Rhododendron taxonomy and diversity of *ex situ* collections for conservation: (subsection) *Maddenia* species as a case study

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MASSEY UNIVERSITY
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UNIVERSITY OF NEW ZEALAND

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Note for Examiners
Explanation of COVID-19 Impacts

Thank you for taking the time to examine this thesis, which has been undertaken during the Covid-19 pandemic. The New Zealand Government's response to Covid-19 includes a system of Alert Levels which have impacted upon researchers. Our University's pandemic plan applied the Government's expectations to our research environment to ensure the health and safety of our researchers, however, research was impacted by restrictions and disruptions, as outlined below.

For a six-week period from March 26 to April 27 2020, New Zealand was placed under very strict lockdown conditions (Level 4 – Lockdown), with students and staff unable to physically access University facilities, unless they were involved in essential research related to Covid-19. All field work ceased and data collection with humans was restricted to online methods, if appropriate. The restrictions were partially lifted on April 27, but students and staff were not generally allowed back into University facilities until May 13.

Ongoing disruptions have also been encountered for some students due to uncertainties over the potential for future Covid-19-related restrictions on activities, and a Covid-19 cluster outbreak based in Auckland in New Zealand on 12 August 2020 led to the imposition of rolling Level 2 (Reduce) and Level 3 (Restrict) conditions until 23 September 2020. Auckland campus based students remained on Level 2 until 7 October 2020.

This Alert Level system continues to be utilised throughout 2021, and in particular from 17 August 2021 when the whole of New Zealand again moved to Level 4 lockdown for an extended period. The Auckland region remained in alert level 3 or 4 for a number of months. Please see the NZ Government website for more information on lockdown dates.

These changing Alert Levels have meant that some research students had experimental, clinical, laboratory, field work, and/or data collection or analysis interrupted, and consequently may have had to adjust their research plans. For some students, the impacts of Covid-19 have been substantial as they may have had to significantly revise their research plans.

Overseas travel is not permitted by the University and restrictions have been placed on the New Zealand borders which are closed to non-New Zealand citizens and permanent residents. This meant that international students who were based offshore at the time of lockdown, were unable to return to New Zealand. A small number of offshore students were provided permission to return to New Zealand in early 2021. Many students have also suffered from anxiety and stress-related issues, and have had financial impacts, meaning their research progress has been significantly delayed.

This form, as completed by the supervisor and student, outlines the extent that the research has been affected by Covid-19 conditions.

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Date: 24-Aug-23

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Ms Ling Hu arrived in New Zealand in February 2020 before the borders closed: however, her study had been underway for only three weeks before New Zealand went into the first lockdown. The key effects of the New Zealand as well as overseas COVID lockdowns on this thesis were as follows:

1. A delay of several months to the start of field work at New Zealand sites. In addition, there was some restraint on further field work as the series of lockdowns were imposed.

2. A delay of about six months for receiving overseas plant samples into New Zealand. Due to lockdown restrictions, plant tissue sampling by staff in the UK or USA was delayed; collection of plant herbaria in the UK or USA was not fulfilled due to labor unavailability. These limited the opportunities of repeating samples that might have failed in DNA extraction, and of herbarium inspection on plant accessions from the UK or USA, particularly in the phylogeny study (Chapter 4).

Notwithstanding the limitations described above, all research objectives were achieved.

Ling did not have a suspension of study during her enrollment.

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Abstract

In the ‘big genus’ *Rhododendron* of over 1,000 species, more than half of the species are threatened[1], at risk[2], or lacking data[3] for biodiversity conservation. *Ex situ* collections, especially those from the wild, are crucial for safeguarding the diversity of species. However, lack of knowledge on existing wild diversity in botanic garden collections, and complex taxonomy, are two main problems in species assessments and conservation decision making. This research studied subsection *Maddenia*, a group of ~65 taxa encountering the two problems but seldom studied, as an exemplar to investigate species taxonomy and *ex situ* diversity.

An *ex situ* conservation gap analysis was undertaken, using ecogeographical representation as a proxy for genetic representation in current botanic garden collections worldwide. Fifty-five of the total 65 taxa were found in cultivation, with over 86% of the living collections conserved in 66% of global botanic gardens. Half of the 18 threatened taxa, and nine of the 12 Data Deficient taxa require further wild collection to achieve a minimum level of ecogeographical representation in *ex situ* collections. Occurrence of *ex situ* collections in countries of origin is limited, and the distribution of *ex situ* collections worldwide is northern hemisphere centric. The results highlight the necessity of having more *ex situ* collections in the 10 native countries, and the importance of inter-institutional data sharing and robust documentation of collections.

Determination of ploidy level of species was the second study, as the presence of polyploid samples may affect phylogenetic analysis. Ploidy levels were estimated for 263 accessions of 47 taxa (including 135 wild accessions) using flow cytometry. Meiotic chromosomes were counted for representative species of both diploids and polyploids to verify the flow cytometry results. This study showed that all taxa except one were diploid. The exception was that polyploids (2–8*x*, 12*x*) occur in the *R. maddenii* complex, where only seven of the 62 accessions tested were diploid while the rest were polyploid. This high level of polyploidy, combined with (i) the wide geographical distribution of the *R. maddenii* complex, and (ii) the previous ‘lumping’ of 12 taxa into the two subspecies, suggests the possibility of either some cryptic

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[1] IUCN categories Extinct in the Wild, Critically Endangered, Endangered, and Vulnerable
[2] IUCN category Near Threatened
[3] IUCN category Data Deficient

species or the need to re-evaluate some of the synonymized species. If new species were revealed, some may require conservation action. However, a greater number of wild-collected accessions and of different geographic origins are needed to explore this possibility.

Following the ploidy study, molecular phylogeny of 40 taxa, including diploids and polyploids, was analysed using target capture sequencing. Phylogenetic trees from maximum likelihood and Bayesian analyses largely supported the morphological groupings of the Maddenii Series, Ciliicalyx Subseries and Megacalyx Subseries, but not the Ciliatum Subseries as classified by Davidian (1982). Of particular interest was the clustering in one clade of all of the *R. maddenii* complex, including all polyploid samples. This occurred irrespective of the method of analysis; however, there was no clear pattern of relationships to ploidy levels within the clade. The molecular phylogeny delimited several species and suggested a revision of the boundary of 'subsection *Maddenia*', although further research, to include a wider range of species, is needed to determine whether the new boundaries should be wider or narrower than before.

The feasibility of using controlled pollination for safeguarding germplasm of prioritised species in *ex situ* collections was studied. Fruit set and seed germination identified the self- and cross-incompatibility of *R. excellens* (Vulnerable), which requires methods other than controlled pollination to conserve the intraspecific diversity in botanic gardens. *R. dalhousiae* var. *dalhousiae* (Least Concern), *R. dalhousiae* var. *rhabdotum* (Vulnerable), *R. lindleyi* (Least Concern), and *R. nuttallii* (Near Threatened) were both self- and cross-compatible, but the compatibility between self and cross pollinations differed from taxon to taxon and from accession to accession. These results suggest the choice of intraspecific pollination should be tested for each species before a programme of propagation is initiated.

These aspects studied for subsection *Maddenia* can be immediately applied to conservation of this group of plants by working with the Global Conservation Consortium for Rhododendron. Meanwhile, the methods used here provide an exemplar for investigating other *Rhododendron* species or plant groups that encounter similar problems, to guide conservation efforts.

Key words: Botanic garden; collection management; *ex situ* conservation; flow cytometry; genetic representation; intraspecific pollination; molecular phylogeny; polyploidy; *Rhododendron*; seed viability; species priority; subsection *Maddenia*; target capture sequencing; taxonomic complexity; wild diversity

Acknowledgements

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My research has received support from various botanic gardens and institutes by sampling inside and outside New Zealand for data analysis across the chapters of different topics. Internationally, I thank Alan Elliott at Royal Botanic Garden Edinburgh in the UK, and Steve Hootman at Rhododendron Species Botanical Garden in the USA, for the provision of plant samples for the genetic analyses and information on rhododendron collections. In New Zealand, I thank Andrew Brooker, Peter Catt & Heather Robson at Pukeiti Gardens, Doug Thomson at Dunedin Botanic Gardens, Lindsay Davies at Heritage Park, Rodney & Faith Wilson at Cross Hills Gardens, and owners of private gardens who provided help during my sample collection as well as gathering of information on rhododendrons. Adrian Grande of the New Zealand Institute of Plant and Food Research Ltd helped me with the DNA extractions, while Cecilia Deng and David Chagné of the same institute provided guidance on the phylogenetic study. At Massey University, Prashant Joshi in the School of Natural Sciences helped me with chromosome counting and for lab instructions, while Gina Aubia and Craig McGill of the New Zealand Indigenous Flora Seed Bank helped with the seed experiments. John Lowry in the School of People, Environment and Planning, and Xiong-zhao He in the School of Agriculture and Environment helped in my consultation on the geo-mapping and statistical analysis, respectively.

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List of Abbreviations

acc.	plant accession
BG	botanic garden (including arboreta)
BGCI	Botanic Gardens Conservation International
ca.	circa, used for ‘about/approximately’
FCM	flow cytometry
Ma	million years ago
ML	maximum likelihood
pg	picogram
PK	Pukeiti Gardens, New Zealand
PMC	pollen mother cell
RBGE	Royal Botanic Garden Edinburgh, UK
RSBG	Rhododendron Species Botanical Garden, USA
SE	standard error
SNP	single nucleotide polymorphism
ss.	subsection
ssp.	subspecies
subgen.	subgenus
syn.	synonym (of a taxon)
var.	variety
wc	wild collection

IUCN Red List Categories:

EX	Extinct
EW	Extinct in the Wild
CR	Critically Endangered
EN	Endangered
VU	Vulnerable
NT	Near Threatened
DD	Data Deficient
LC	Least Concern
NE	Not Evaluated

Chapter 1

General introduction

1.1 Foreword

Rhododendron, named by Linnaeus, is derived from the Greek ‘rhodo’ meaning ‘rose’ and ‘dendron’ meaning ‘tree’ (Hora, 1981). *Rhododendron*s have a place in the mind of many people who are enthusiastic about gardening, especially Asian plants. The magnificent flowers of various colours impress the public when they are blooming. But their influence is far more than just plant beauty. When I tell people that I study conservation of *Rhododendron*s for my PhD, some complained about the harm that *Rhododendron*s bring to the environment where they are exotic. Indeed, *Rhododendron* plants may be invasive, for example in the UK. In New Zealand, I have heard people who love gardening reporting farm animals poisoned by *Rhododendron* plants. While I am not here to help prevent the damages, these stories warn us to understand plants better, if we are to conserve plant biodiversity and continue using the resources they provide. On the positive side, *Rhododendron* provides valuable resources for medicinal functions, cultural symbols, landscaping, and a huge range of horticultural cultivars. Nepal is proud to have *R. arboreum* as the national flower and local people produce the famous ‘mad honey’ from its nectar. At a very young age, I also tried to suck the nectar from the wild *Rhododendron* plants (in Chinese: ‘杜鹃花’) when I used to wander around the mountain forests in my home village in China. Economically, *Rhododendron*s are a source of traditional medicines, as well as wooden products, a food source of edible flowers, and tourism attraction during blooming seasons (Basnett & Ganesan, 2022). More importantly, they are a mega group of plants that are key species in the floras of their local regions, strongly related to the alpine ecosystem, but also found as forest trees and epiphytes.

As we are aware, biodiversity for conservation encompasses species richness, genetic and ecosystem variation (Mace et al., 2012). However for *Rhododendron* biodiversity, the exploitation and people’s ignorance of how to protect these wild resources when destroying natural habitats result in some species under high risk of diversity loss or even extinction (Cameron, 1993; Tiwari & Chauhan, 2006; Nisar et al., 2013; Hart et al., 2017; Rawat et al., 2018; Kumar et al., 2019). Considering the knowledge gaps and challenges faced in *ex situ* conservation of *Rhododendron*, a systematic study is addressed in this thesis. The chapters focus on investigating the taxonomy of *Rhododendron* species and wild diversity in *ex situ* collections towards strategic conservation management. Besides appreciating the beauty of the group of *Rhododendron* subsection *Maddenia* species, I hope this thesis could inspire us a little about why to care, understand and protect the biodiversity of plants that we are surviving with.

1.2 Botanic gardens for plant conservation

1.2.1 *Ex situ* collection management in botanic gardens

The ideal ‘integrated plant conservation’ suggests integrating *in situ* and *ex situ* conservation for plant conservation, with subsequent research, horticulture studies and education ultimately increasing the success of conservation efforts (Guerrant et al., 2004; Heywood, 2019). *In situ* (on site) conservation is often difficult to achieve and may encounter several problems: the material is vulnerable to natural and human-directed disasters, limited genetic diversity can be conserved in any one reserve, and the plants are not easily accessible for research (Hawkes et al., 2000). In contrast, *ex situ* (out of natural habitats) conservation focuses on safeguarding biodiversity by holding plant collections outside their natural habitats such as seed banks or botanic gardens, which ensures back-up materials of the species under threat and providing easy access for utilization and re-introduction (Heywood, 2017) (Fig. 1.1). A general evidence-based approach to managing the *ex situ* collections will effectively preserve a target species' wild diversity. As the IUCN Technical Guidelines state, the primary objectives of maintaining *ex situ* collections encompass selecting priority species, developing *ex situ* protocols, and managing the risk of natural catastrophe, disease or political upheaval on *ex situ* programs (Maunder & Byers, 2005; IUCN SSC, 2014).

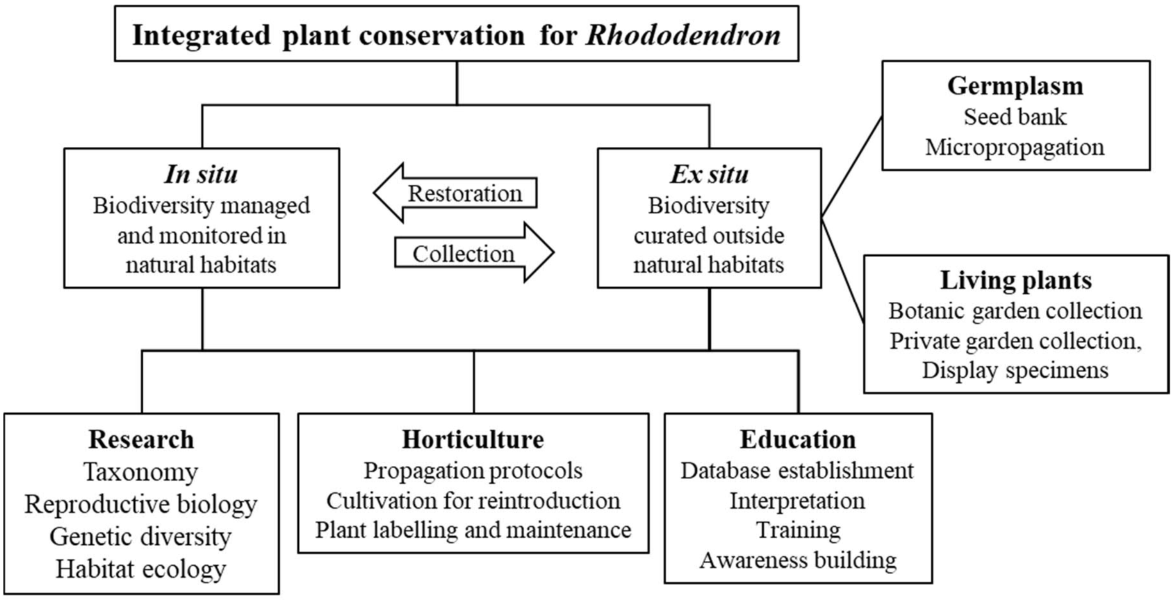


Figure 1.1 Integrated plant conservation for *Rhododendron* (adapted from Guerrant et al., 2004)

Nowadays, botanic gardens (including arboreta) take the main role in plant *ex situ* conservation, with documented collections for scientific research, horticultural development, conservation, plant introduction, display, sustainability, education and outreach (Heywood, 2017; Edwards & Jackson, 2019). Botanic gardens hold a large capacity and potential to conserve wild biodiversity within their collections. As the largest plant conservation network worldwide, Botanic Gardens Conservation International (BGCI, https://www.bgci.org/) monitors global living collections in 1,197 botanic gardens, to measure progress, identify gaps and prioritize species for conservation action.

Current *ex situ* collections need more scientific management to maximise conservation effectiveness (Arnet et al., 2015; Volis, 2017; Heywood, 2019; Griffith et al., 2020; Sharrock, 2020; Westwood et al., 2021). Most of the collections were established as a resource accumulation for horticulture as robust taxa have often been favoured (Maunder et al., 2004), rather than for a conservation purpose (Heywood, 2017). Geographically, botanic gardens and their associated *ex situ* collections are disproportionately in temperate locations with 93% of species held in the Northern Hemisphere (Mounce et al., 2017; Sharrock, 2020); 56% of country-endemic, threatened species are held only in *ex situ* collections outside their country of origin (Mounce et al., 2017); and 11% of globally threatened species are held in only one institution. The majority of botanical gardens hold a small number of accessions and their representation of global *ex situ* collections is poorly known (Maunder, Guerrant, et al., 2004). Also, current identification and documentation of botanic garden collections often lack adequate and up-to-date data management.

1.2.2 Wild diversity in *ex situ* collections

To efficiently utilize the limited space and resources in botanic gardens, conservation strategies should be tailored to conserve maximum wild diversity. Focusing on wild-source collections of species for *ex situ* conservation is a primary method of maintaining genetic diversity (Khoury et al., 2019; Breman et al., 2021). Gap analysis of the wild diversity captured in existing *ex situ* collections can evaluate achievements and direct conservation action by proposing priorities. Usually, the species threatened in the wild should be prioritized for *ex situ* conservation, especially if they are currently unknown to horticulture, so that there will be secured *ex situ* collections available to return the species to the wild, or prevent the taxa from becoming extinct (Heywood, 2017). While early *ex situ* conservation gap analyses usually focused on presence of species in cultivation, recent studies have dug further to understand the geographic and genetic representation of *ex situ* collections. One example showing such progress is *Magnolia* (Cires et al., 2013; Linsky, Crowley, et al., 2022). Accession-level data are necessary to trace the numbers and localities of the wild-source accessions for analysis, but such data require robust documentation of the collections held in the botanic gardens. BGCI PlantSearch database (https://tools.bgci.org/plant_search.php) is a widely acknowledged tool and the only global database to index *ex situ* collections for conservation gap analysis. Taxon-level plant records data are accessible on the public website, whereas accession-level records must be queried to study the wild-source collections.

Ideally, targeted species for *ex situ* management should be identified from the genetic representation in current collections. And for the targeted species, sampling various populations tends to capture greater variation (Havens et al., 2006; Parra-Quijano et al., 2011; Hoban, Bruford, et al., 2020; Rahman et al., 2021). A key part of this strategy is planning regional living collections for biodiversity conservation and deciding species to be preserved in an ‘ideal’ number of living collections by their conservation priority and representation of origins (Heywood, 1992). The problem is that the number of wild accessions in *ex situ* conservation to conserve a species with ‘enough’ genetic diversity remains undetermined (Hoban, 2019). In general, it is suggested to have multiple wild samples collected from diverse populations, and each collection duplicated at multiple sites in case of catastrophic loss (BGCI, 2014; Griffith et al., 2015; Ren et al., 2019). Derived from zoological conservation practice, the concept of ‘metacollection’ (i.e., pooled collection) has been applied in botanic garden management with particular success on palms (Arecaecae) (Griffith et al., 2020). ‘Metacollections’ are suggested for threatened species that are popular in cultivation for efficient *ex situ* management, especially those having a wide distribution and conserved in multiple countries or regions. This practice also enhances the research and conservation capacity of botanic gardens during collaborative data sharing and coordinated sampling (Westwood et al., 2021).

1.3 *Rhododendron* in *ex situ* conservation

1.3.1 *Rhododendron* conservation: from plant hunting to garden collections

Rhododendron L. (Ericaceae) is one of the largest plant genera with more than 1,000 species (Gibbs et al., 2011). In the wild, about 2/3 of the species are found in Asia, North America and Europe, and about 1/3 found in southeast Asia and as far south as northern Australia (Irving & Hebda, 1993; Shrestha et al., 2018) (Fig. 1.2). Species lifeforms range from creeping groundcovers to forest trees and these occupy a range of niches from lowland tropical forests in Papua New Guinea, to alpine tundra in China (Davidian, 1982; M.-Y. Fang et al., 2005; Argent, 2015). The majority of *Rhododendron* species originate from the mountainous regions along the southern Himalayas east into southwestern China, where they form important components of montane ecosystems (Irving & Hebda, 1993; Kumar et al., 2019).

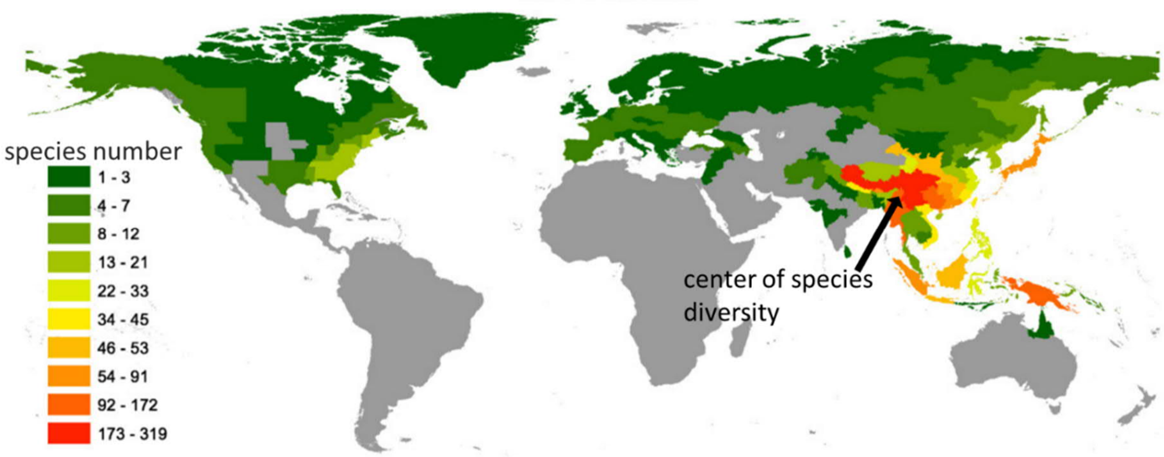


Figure 1.2 Natural distribution of *Rhododendron* worldwide (Adapted from Shrestha et al., 2018)

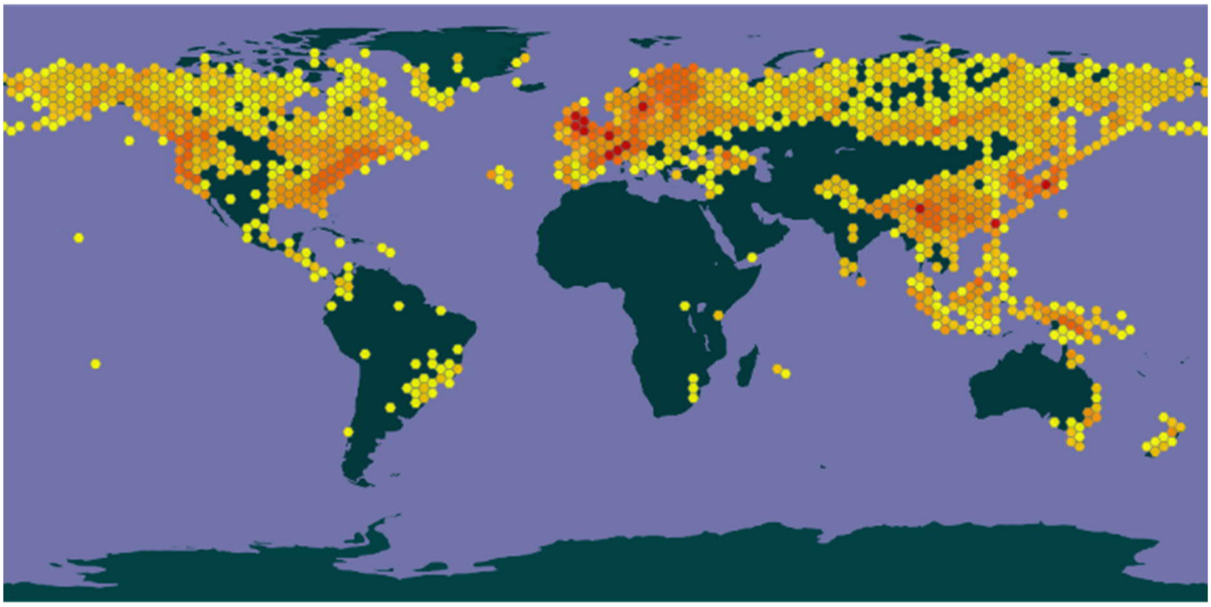


Figure 1.3 *Rhododendron* in cultivation worldwide (Data source: GBIF, 2021. Accessed on 4 April 2023)

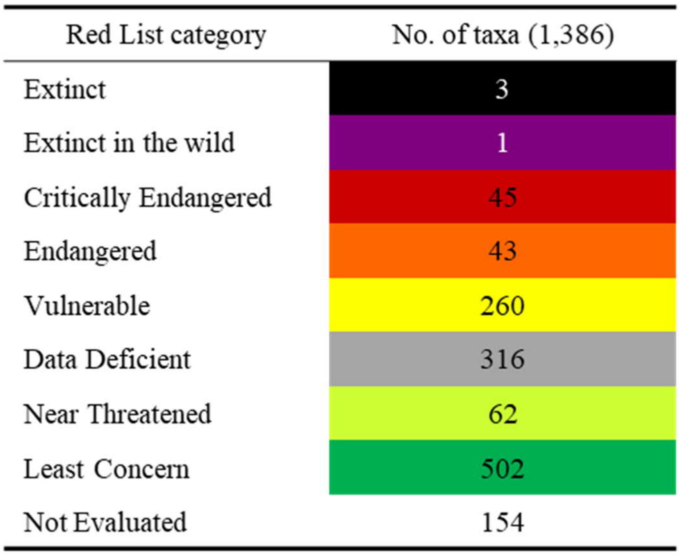
The beauty of *Rhododendron* flowers has been long appreciated by plant hunters and introduced to western gardens (Postan, 1996). Dating back to 1840s when Joseph Hooker discovered 25 new species and collected the very first material from Sikkim, India (Hooker, 1849), the investigation of *Rhododendron* species has been greatly accelerated, and cultivated material has been distributed worldwide (Fig. 1.3). The vast collections of *Rhododendron* provide a large diversity of species that offer their glamor to garden visitors. These cultivated plants sourced originally from the wild form the major components of today's *ex situ* plant conservation, which relates to plants conserved outside their natural habitats.

But this PhD research is based in New Zealand? Indeed, New Zealand does not have native *Rhododendron* species. However, with almost half of the *Rhododendron* species in cultivation (566/1,215 taxa), analysis of *Rhododendron* collections in New Zealand sets a model for examining other introduced plant genera (MacKay et al., 2017; Mackay & Gardiner, 2017a). New Zealand is an outstanding example of *ex situ* conservation of *Rhododendron* in the Southern Hemisphere, and furthermore is one of the leading countries for *ex situ* conservation of *Rhododendron* overall (Mackay & Gardiner, 2017b; MacKay et al., 2018). This study of *ex situ* collections in New Zealand helps us understand the status of *ex situ* conservation of *Rhododendron* as a whole. In favour of the temperate maritime climate, *Maddenia* species grow especially well in New Zealand, and they often flourish even more than in their native countries. Moreover, unlike being 'weedy' in some other countries, rhododendrons in New Zealand seldom disperse naturally and are relatively easy to control.

1.3.2 Conservation assessment and gap analysis

The Global Strategy for Plant Conservation (GSPC) 2011-2020 directs efforts to enhance the global plant diversity (BGCI, 2012a), which are highly relevant to all targets under the Sustainable Development Goals (Sharrock & Wyse Jackson, 2016). The GSPC 2011–2020 emphasizes, an online database for global flora should be established (Target 1), which has been fulfilled with establishment of World Flora Online (Borsch et al., 2020) that includes *Rhododendron* (https://www.worldfloraonline.org/). The GSPC 2011–2020 also emphasizes, with a necessary assessment of the conservation status of all known plant species (Target 2), at least 75% of known threatened species should be conserved *in situ* (Target 7), or over 20% available materials conserved in *ex situ* collections for re-introduction programs (Target 8).

With extensive presence of *Rhododendron* plants in cultivation, people may pose the question: do *Rhododendron* species really require conservation? The answer is yes! According to *The IUCN Red List of Rhododendrons* (Gibbs et al., 2011) together with updates on the global *ex situ* conservation of *Rhododendron* (MacKay et al., 2018), 25% of *Rhododendron* taxa are under threat (Extinct in the Wild, Critically Endangered, Endangered, Vulnerable) and require urgent conservation action. An additional 23% are rated as Data Deficient, for which we lack information on the wild populations for conservation assessment (Fig. 1.4). From 2011 to 2018, there was an increased number of threatened taxa since the IUCN Red List assessment and the Global Survey of *Ex Situ Rhododendron* Collections in 2012 (BGCI, 2012b). Post 2011, Red List assessments for *Rhododendron* species have been conducted to update their conservation status (BGCI & IUCN SSC Global Tree Specialist Group, 2018), which fills a knowledge gap but only for a few species. By 2018, 74% of the 1,386 taxa investigated had at least one wild-source accession, but often from only 1–2 sources at 1–2 sites (MacKay et al., 2018). Also, the extent of wild diversity captured in the *ex situ* collections of *Rhododendron* species has never been studied.



Red List category	No. of taxa (1,386)
Extinct	3
Extinct in the wild	1
Critically Endangered	45
Endangered	43
Vulnerable	260
Data Deficient	316
Near Threatened	62
Least Concern	502
Not Evaluated	154

Figure 1.4 Number of *Rhododendron* taxa in the IUCN Red List categories (modified from Gibbs et al., 2011; BGCI & IUCN SSC Global Tree Specialist Group, 2018; MacKay et al., 2018)

Conservation action for *Rhododendron* is addressed globally and regionally. One highlighted example is the establishment of the Global Conservation Consortium for *Rhododendron* (GCCR, 2023) under the international plant conservation scope of BGCI. Other national organizations also make crucial contributions to global *Rhododendron* conservation and research, such as the American *Rhododendron* Society together with its '*Rhododendron* Research Network' aiming to enhance scientific communication and resource sharing. In countries of origin, apart from the advocated research on wild populations and *in situ* conservation efforts (Basnett, 2022), *ex situ* collections are largely needed to better understand

and safeguard the *Rhododendron* diversity. One example of such efforts of ‘integrative conservation’ is the recent publication *Ex situ flora of China: Ericaceae* (Wang, 2022) revealing the *ex situ* collections held in China’s botanic gardens, apart from research popular on wild populations in China.

There are several challenges in assessing *ex situ* conservation gaps for *Rhododendron*: deficient data on wild populations of species (e.g., distribution, genetic diversity); unresolved taxonomy of species complexes (e.g., ‘lumped’ synonyms, ambiguous species delimitation); incorrect identification of specimens; the degree of participation by collection holders and the dynamic nature of *ex situ* collections that evolve and change over time, etc. While Red List assessments establish a certain priority, and priorities were determined at the subgenus level (Mackay & Gardiner, 2017b), any further guidelines for deciding particular species are lacking for a large and complex genus such as *Rhododendron*. The ‘ideal’ number of wild accessions to be held related to their native range and diversity is also missing. Further to the global updates on the *ex situ* conservation of the genus *Rhododendron* (MacKay et al., 2018), the present research (Chapter 2) investigates the extent and gaps of conserving wild diversity in *ex situ* collections, using subsection *Maddenia* as an exemplar.

1.4 *Rhododendron* taxonomy for conservation

1.4.1 Taxonomic dilemma in *Rhododendron* conservation

The classification of the genus *Rhododendron* has been revised over time, mainly based on morphological data (e.g., features of flowers, leaves, hairs, scales, etc.) (Davidian, 1996; Argent, 2015). The genus is divided into eight subgenera (Chamberlain et al., 1996), with four main subgenera namely *Tsutsusi* (evergreen azaleas, except *Brachycalyx* section), *Pentanthera* (deciduous azaleas), *Rhododendron* (lepidote *Rhododendron*s) and *Hymenanthes* (elepidote *Rhododendron*s). The first two subgenera, together with the *Azaleastrum* subgenus (evergreen), comprise the commonly known ‘azaleas’, while *Rhododendron* and *Hymenanthes* are referred to as ‘rhododendrons’. *Hymenanthes* rhododendrons are evergreen and have large non-scaly leaves; *Rhododendron* (subgenus) rhododendrons have smaller leaves with scales and are usually evergreen but occasionally semi-deciduous (De Keyser et al., 2009) (Figs. 1.5 & 1.6). The leaf scales are unique to subgenus *Rhododendron*. Scale shape, color, size, spacing and stalk length are all useful characters for designating species in this subgenus (Goetsch et al., 2005). However, *Rhododendron* species often show continuous morphological variation, which leaves species delimitation (i.e. determining the boundaries among species) based solely on morphology ambiguous.

'Species' is the basic unit for plant conservation, and it can be defined from various aspects such as morphological, biological, ecological, evolutionary and phylogenetic (Heywood et al., 2006; De Queiroz, 2007). This thesis adopts the concept of species as morphologically recognisable and phylogenetically monophyletic. Well-defined species are required to decide conservation priorities and subsequent actions precisely. *Rhododendron* demonstrates features of a 'big genus' (Frodin, 2004) such as a series of complicated sections and subsections, debates about species delimitation, rapid speciation and frequent occurrence of natural hybrids. One main problem in a 'big genus' is that the unresolved relationships among some species cause difficulties in evaluating their taxonomic status, which results in challenges to assessing species that are threatened and require protection by means of a conservation plan. A further understanding of species relationships may result in changes to conservation investments and priorities, which has happened in cases of critically endangered species such as *R. protistum* (Li et al., 2018) and *R. amesiae* (Ao et al., 2022).

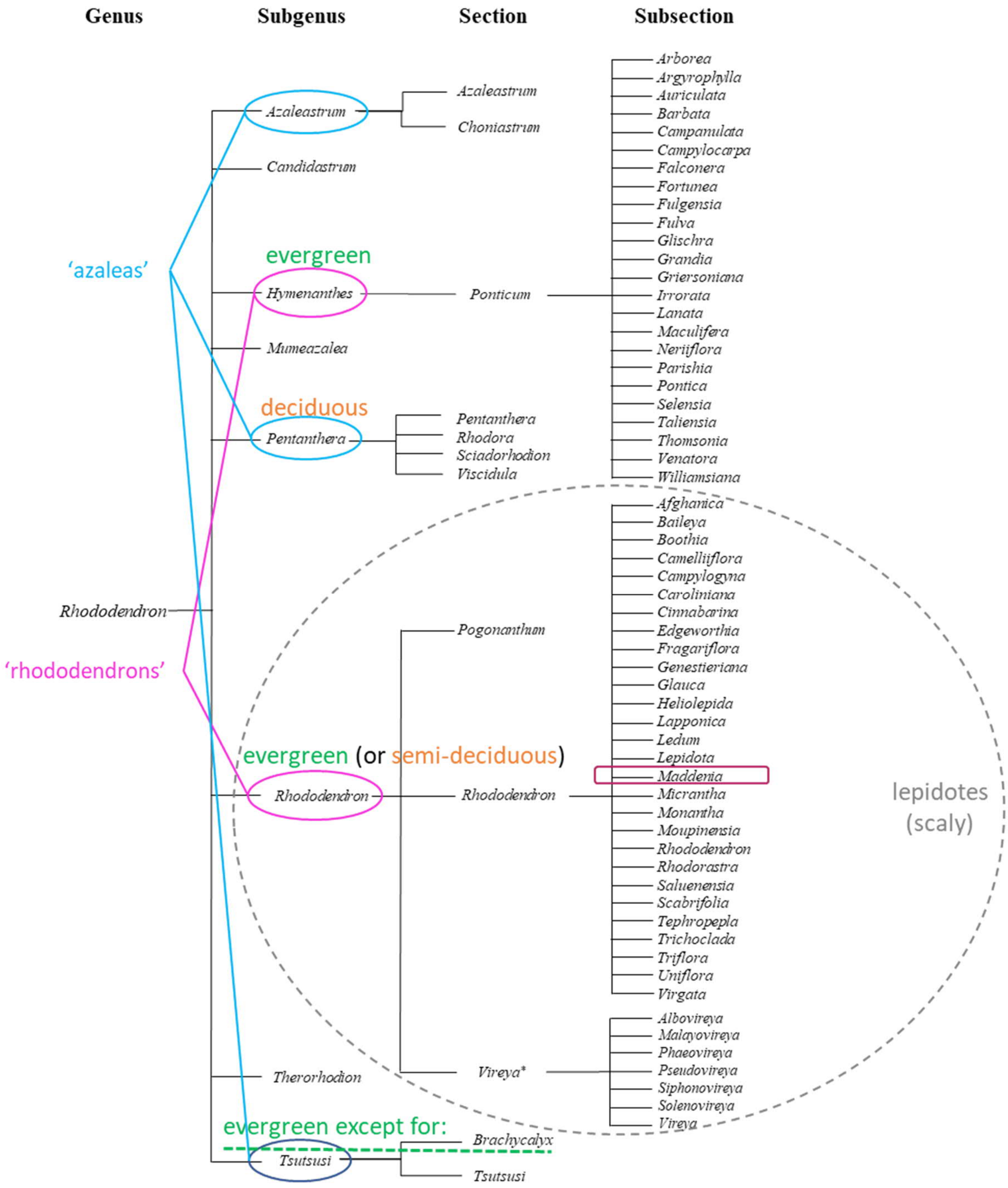


Figure 1.5 Classification of genus *Rhododendron* and features of main groups, based on Chamberlain et al. (1996) and De Keyser et al. (2009). *Section *Vireya* (i.e., section *Schistanthe*, Craven et al., 2011), may appear as 'subgenus *Vireya*' in other literature such as Argent (2015). More details on this taxonomic debate are noted in Chapter 3

Figure 1.6 Representative species from the various subgenera of *Rhododendron*. Subgenus *Azaleastrum*: A) *R. moulmainense*, B) *R. stamineum*; Subgenus *Hymenanthes*: C) *R. arboreum* ssp. *zeylanicum*, D) *R. williamsianum*, E) *R. fortunei*; Subgenus *Pentanthera*: F) *R. atlanticum*, G) *R. canescens*; Subgenus *Rhododendron* – non *Vireya*: H) *R. edgeworthii*, I) *R. triflorum*; Subgenus *Rhododendron* – section *Vireya* (or subgenus *Vireya*, see Fig. 1.4 and Chapter 3): J) *R. notiale*, K) *R. searleanum*, L) *R. laetum*; Subgenus *Therorhodion*: L) *R. camtschaticum*, Subgenus *Tsutsusi*: N) *R. reticulatum*, O) *R. simsii*. Two subgenera with only one species each are not shown: subgenus *Candidastrum* (*R. albiflorum*) and

subgenus *Mumeazaela* (*R. semibarbatum*). Image credit: Marion MacKay, Andrew Brooker, Graham Smith

1.4.2 Molecular phylogeny for understanding taxonomy

Fortunately, modern molecular phylogenetics largely compensates for the limitations of morphological observations for defining species and their taxonomy. Molecular markers have been used to study *Rhododendron* phylogeny and diversity, with many using first-generation sequencing technology (Kron, 1997; Kron, 1998; Milne et al., 1999; Goetsch et al., 2005; Brown et al., 2006; L. Zhou et al., 2008; De Keyser et al., 2009; Caser et al., 2010; Yan et al., 2015; Shrestha et al., 2018; Gardiner et al., December 2019). Most of these phylogenetic studies focused on determining clades of the genus or monophyly of the subgenera, using representative species from different groups (Goetsch et al., 2011; Shrestha et al., 2018; Li et al., 2019; Khan et al., 2021; Xia et al., 2021). Few other genetic studies have been conducted at the species level to inform species priorities in conservation (Li et al., 2018; Ao et al., 2022; Gardiner et al., December 2019). Groups at lower levels (section, subsection) were seldom the focus of molecular phylogenetics to determine species relationships.

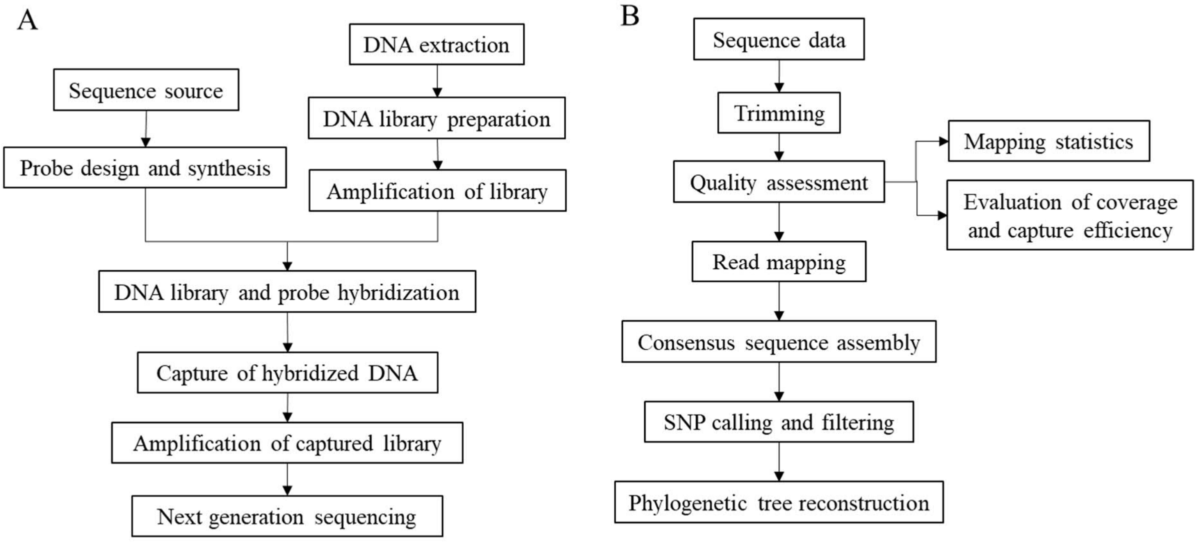


Figure 1.7 Overview of target capture sequencing for molecular phylogeny (modified from Peng et al., 2020). A) General process of target capture sequencing via probe capture; B) Bioinformatic analysis from data evaluation of target capture to phylogenetic tree reconstruction using single nucleotide polymorphisms (SNPs).

When studying *Rhododendron* taxonomy and phylogenetics, the occurrence of polyploids may raise several issues. Polyploids, containing multiple chromosome sets, could form from auto- or allo-polyploidization (Stebbins, 1947). The ploidy level of plants, no matter diploids or polyploids, is usually determined by chromosome counting or alternatively, estimated using flow cytometry (Pellicer et al., 2021). In phylogenetics, polyploid samples may pose problems in the sequencing and data analysis, due to their multiple gene copies causing difficulty in reconstructing each of the distinct homeologues (Rothfels, 2021). However, neither the evolution nor the molecular phylogeny of polyploids has been studied for *Rhododendron*, despite several polyploid species revealed in previous studies by either chromosome counts or flow cytometry (Sax, 1930; Darlington & Janaki Ammal, 1945; Ammal et al., 1950; Mehra & Bawa, 1969; Kehr, 1976; Jones et al., 2007; W.-Y. Zhou et al., 2008; De et al., 2010; Zaytseva et al., 2018; Khan et al., 2021). As subsection *Maddenia* has been reported as having polyploid species (*R. maddenii*) (Cubey, 2003), Chapter 3 investigates two aspects: the ploidy level of species across this subsection, with its impacts on taxonomic classification and the implication of having polyploid collections for biodiversity conservation.

Table 1.1 Published whole genomes of *Rhododendron* species (as of 25 May 2023)

Species	Classification: subgenus – section (– subsection)	Year	Reference	Note
R. delavayi var. *delavayi*	*Hymenanthes – Ponticum* (– *Arborea*)	2017	Zhang et al., 2017	Draft genome
R. williamsianum	*Hymenenthes – Ponticum* (– *Williamsiana*)	2019	Soza et al., 2019	
R. simsii	*Tsutsusi – Tsutsusi*	2020	F.-S. Yang et al., 2020	
R. griersonianum	*Hymenanthes – Ponticum* (– *Griersoniana*)	2021	Ma et al., 2021	
R. ripense	*Tsutsusi - Tsutsusi*	2021	Shirasawa et al., 2021	
R. kiyosumense	*Tsutsusi – Brachycalyx*	2021	Shirasawa et al., 2021	
R. ovatum	*Azaleastrum – Azaleastrum*	2021	Wang et al., 2021	Floral scents
R. molle	*Pentanthera – Pentanthera* (–*Sinensia*)	2022	G.-L. Zhou et al., 2022	Medicinal
R. henanense ssp. *lingbaoense*	*Hymenanthes – Ponticum* (– *Campylocarpa*)	2022	X. J. Zhou et al., 2022	
R. delavayi	*Hymenanthes – Ponticum* (– *Arborea*)	2023	Wu et al., 2023	
R. irroratum	*Hymenanthes – Ponticum* (– *Irrorata*)	2023	Wu et al., 2023	

Based on the examination of ploidy levels in samples for sequencing in Chapter 3, Chapter 4 describes the use of target capture sequencing, to reconstruct a molecular phylogeny for subsection *Maddenia* which has not been studied previously using molecular data. As a high throughput DNA sequencing technology commonly applied for phylogenomic studies, target capture uses designed probes (bait set) to increase sequencing depth (Andermann et al., 2020;

Peng et al., 2020) (Fig. 1.7). It has been reported to be efficient for studying herbarium specimens when there is a limited availability of fresh samples, which suits the scenario of the present case study. Benefiting from several published *Rhododendron* genomes (Table 1.1) to use as reference for reads mapping, phylogenetic trees based on bioinformatic analysis of next-generation (e.g., Illumina) sequence data were reconstructed to enhance our understanding on species relationships. Taxonomic dilemmas in this genus are expected to be more efficiently resolved with the help of a molecular phylogeny to inform conservation policy making.

1.5 Conservation horticulture: maintaining wild diversity in *ex situ* collections

Conservation horticulture in botanic gardens allows genetically diverse *ex situ* collections and representatives of the target populations from the wild to be protected and dispersed (Gratzfeld, 2017; Smith, 2017). Horticultural practice for conservation may be related to research on pollen biology, breeding system, seed banking, etc. In botanic gardens, most taxa are conserved with only a small number of collections, and mostly only from few wild populations without sufficient genetic representation (Heywood, 2017; Volis, 2017). The small sample size of most *ex situ* collections and a need for regeneration inevitably leads to genetic drift and an increase in the level of inbreeding in seed-regenerated collections (Schoen & Brown, 2001). Lack of genetic exchange and stochastic processes in small populations make them susceptible to such detrimental genetic effects (Chen & Sun, 2018).

Cultivating offspring by controlled pollination of *ex situ* collections can be an effective way to capture and conserve the genetic diversity of a species (Hoban et al., 2018). Intraspecific pollination (including self and cross pollinations), especially cross pollination among *ex situ* living collections, is important to maintain the conserved genetic diversity (Maunder, Hughes, et al., 2004). Controlled pollination also avoids the negative effects of random hybridization among collections. Random hybridization may be a limitation to the utility of *ex situ* living collections for conservation purposes. Sympatric gene flow is common when reproductive isolation has not been completely formed between plants, in which case pollen flow from other species can cause genetic pollution to the threatened genotypes (Yan et al., 2018). Natural hybrids (not only inter-specific but also between subspecies and ecotypes) may lack genetic integrity and harbour maladaptive gene combinations (Maunder, Hughes, et al., 2004). Due to weak reproductive barriers among close relatives, hybridization occurs frequently in the wild among sympatrically distributed *Rhododendron* species (Milne & Abbott, 2008; Zha et al., 2008; Ma et al., 2010; Yan et al., 2015; Zhang et al., 2020). To prevent these risks, representative accessions must be maintained separately in botanic gardens, or through controlled breeding and pedigree design (Volis, 2017).

Controlled crosses via hand pollination among wild accessions for prioritised *Rhododendron* species enables genetic diversity to be more efficiently conserved, securing its recovery and availability for reintroduction to the original habitat in the future. Reproductive biology has been studied for a few *Rhododendron* species, which show both self- and cross-incompatibility, but the extent may differ from species to species (Milne et al., 2003; Tiwari & Chauhan, 2007; Bai et al., 2014; Okamoto & Ureshino, 2015; Ma et al., 2016; Yan et al., 2018; Ping, 2019). For species in subsection *Maddenia*, the breeding system for producing viable offspring through selfing or cross pollination is seldom studied (Tiwari & Chauhan, 2007; Tian, 2011). Focusing on this knowledge gap, Chapter 5 investigates intraspecific pollination for the practice of maintaining the germplasm conserved in existing living collections.

Subsection *Maddenia* is in subgenus *Rhododendron* section *Rhododendron* (Fig. 1.5). A total of ~65 taxa (Chapter 2) is summerised in this thesis. Due to complex taxonomy, the number of species or taxa in this subsection varied in different references: 52 species (57 taxa) by Chamberlain et al. (1996), 31 species by Cox and Cox (1997), 56 species by Khan et al. (2021). All taxa in subsection *Maddenia* are lepidotes (scaly). The flowers are showy with white, yellow or pink colours, and they are usually fragrant depending on species (Jamieson, 2021).

Subsection *Maddenia* possesses a series of issues in conservation: a few species are under threat or Data Deficient; wild diversity of species is poorly understood; the taxonomy of several species in this group is not resolved; even the concept of ‘subsection *Maddenia*’ is dubious as it is suspected to be not monophyletic. In *ex situ* conservation, botanic garden collections of this subsection have not been examined to assess the extent of conserved wild diversity, nor their reproductivity for maintaining the germplasm. Due to these hurdles, it is difficult to decide whether species require conservation attention or not, and which species should be prioritized for urgent action. Benefiting from the rich resources in New Zealand together with available material from living collections in leading botanic gardens for sampling, subsection *Maddenia* was chosen as a case study. I believe that this in-depth study of subsection *Maddenia* will make a significant contribution to further research across the genus *Rhododendron*.

1.6 Research framework

1.6.1 Research objectives

This research is conducted to evaluate progress and guide further efforts for conservation of *Rhododendron* species. The thesis focuses on *ex situ* collections of subsection *Maddenia* as a case study, with considerations for studying related issues across the genus. A series of aspects of *ex situ* conservation management is investigated: *ex situ* conservation gaps, species prioritisation and conservation horticulture. As the research framework shows (Fig. 1.8), this thesis includes four main objectives: 1) assess the wild diversity captured in current *ex situ* conservation of subsection *Maddenia*, with *ex situ* data from botanic garden collections analysed for the genetic representation (Chapter 2); 2) estimate ploidy levels in subsection *Maddenia* based on reviewing the reported ploidy of *Rhododendron* species, to discuss the ploidy variation related taxonomy for biodiversity conservation (Chapter 3); 3) reconstruct the molecular phylogeny of subsection *Maddenia* to resolve species delimitation and related taxonomic debates concerning conservation assessment (Chapter 4); and 4) examine the feasibility of controlled pollination for producing viable seeds to maintain the intraspecific diversity in *ex situ* collections (Chapter 5). The detailed research questions are outlined in the corresponding chapters. The results help to identify the knowledge and resource gaps in current *ex situ* conservation and resolve the taxonomic debates to aid conservation decision making, which guides the strategic planning in botanic garden collection management.

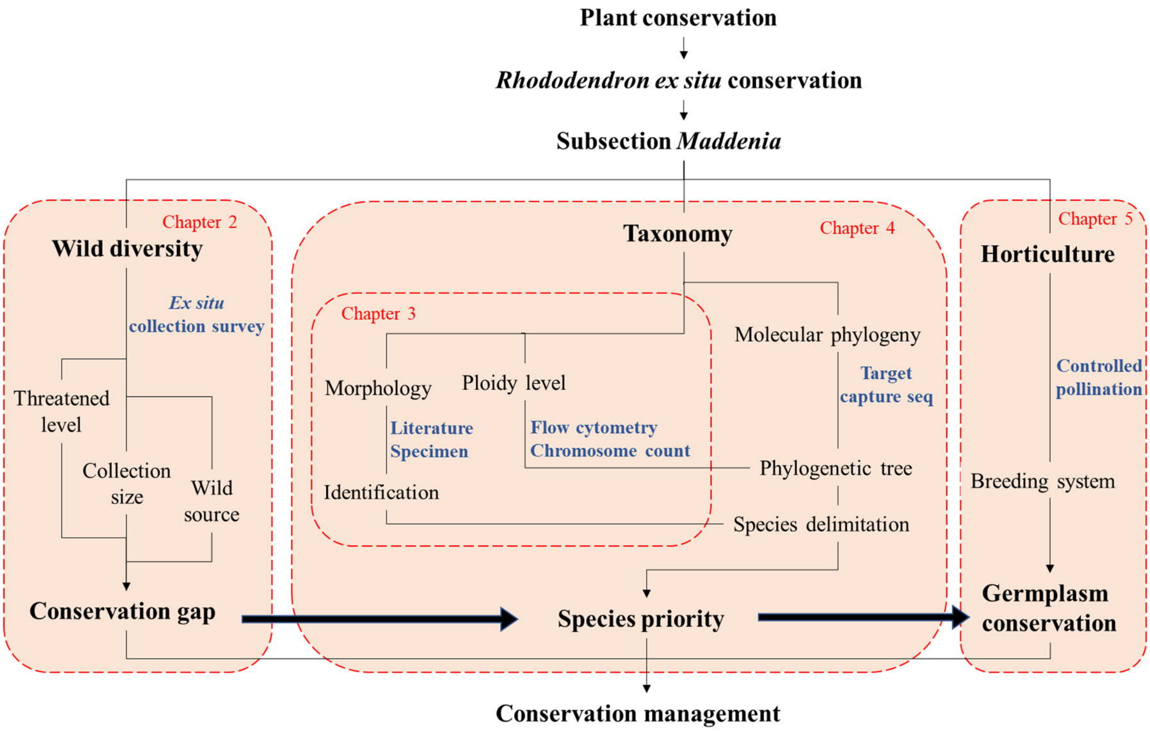


Figure 1.8 Research framework of this thesis

1.6.2 Thesis structure

This thesis is organized into six chapters, including a general introduction (Chapter 1), main body of four research chapters (Chapters 2–5) and a final discussion (Chapter 6). The structure of all chapters is described as below.

Chapter 1 General introduction

This chapter provides basic information of the research background and introduces the research objectives.

Chapter 2 Rhododendron diversity conservation in global botanic gardens: a case study of Maddenia species

This chapter examines the wild-source accessions of subsection *Maddenia* in global botanic gardens, to evaluate the conserved diversity in current *ex situ* collections compared to wild distribution. The findings identify knowledge gaps for conducting such evaluations, as well as suggest species priorities for urgent conservation action.

This chapter is under review for publication in the journal Oryx (https://www.oryxthejournal.org/):

Hu, L., MacKay, M., Gardiner, S. E., & Tate, J. A. (under review). *Rhododendron* diversity conservation in global botanic gardens: a case study of *Maddenia* species. *Oryx*

Chapter 3 Ploidy variation in Rhododendron subsection Maddenia and implications for conservation

This chapter investigates ploidy variation in the genus *Rhododendron* as a whole to illustrate the different levels of biodiversity conservation. Further, because polyploids may confound phylogenetic analyses, this chapter investigates the basic cytogenetics of subsection *Maddenia* by estimating ploidy level, especially for the *R. maddenii* complex with reported polyploidy and the species not yet studied. Two technological issues, the applicability of flow cytometry to *Rhododendron* and data accuracy from herbarium specimens, are also discussed to guide future research.

This chapter has been published:

Hu, L., Tate, J. A., Gardiner, S. E., & MacKay, M. (2023). Ploidy variation in *Rhododendron* subsection *Maddenia* and its implications for conservation. AoB Plants, 15(3), plad016. https://doi.org/10.1093/aobpla/plad016.

Chapter 4 Understanding Rhododendron taxonomy for conservation: molecular phylogeny of subsection Maddenia as a case study

This chapter explains the detailed taxonomic debates on species in subsection *Maddenia* and how this problematic issue impacts conservation decision making. The molecular phylogeny is reconstructed by target capture sequencing the sampled *ex situ* accessions, to assist resolving the species delimitation. The combination of morphological and phylogenetic analyses illustrates the importance of understanding plant taxonomy for biodiversity conservation, which in return, addresses the research function of conserved wild diversity in botanic garden collection management.

This chapter is in preparation for publication.

Chapter 5 Intraspecific pollination of ex situ collections of Rhododendron species for germplasm conservation

This chapter is a case study of applying horticultural practice in *ex situ* collection management. Possibilities of controlled crosses via hand pollination to maintain wild diversity of species when reproducing botanic garden living collections were investigated. Breeding system (outcrossing vs. selfing) and seed viability are evaluated on selected species to identify the fecundity.

This chapter is currently under review for publication in the Australian Journal of Botany (https://www.publish.csiro.au/bt):

Hu, L., Gardiner, S. E., Tate, J. A., & MacKay, M. (under review). Understanding *Rhododendron* intraspecific compatibility in botanic garden collections for species conservation. *Australian Journal of Botany*

Chapter 6 General discussion

This chapter includes general discussion on issues studied in the previous chapters together with future perspectives, and presents overall conclusions and conservation recommendations.

For each of the research chapters (Chapters 2–5) as paper published or in progress, the Statement of Contribution made by all authors is attached at the beginning of the corresponding chapter.

The supplementary files for Chapters 2, 3, 4 are attached in the end of this thesis, as Appendices I, II, III, respectively.

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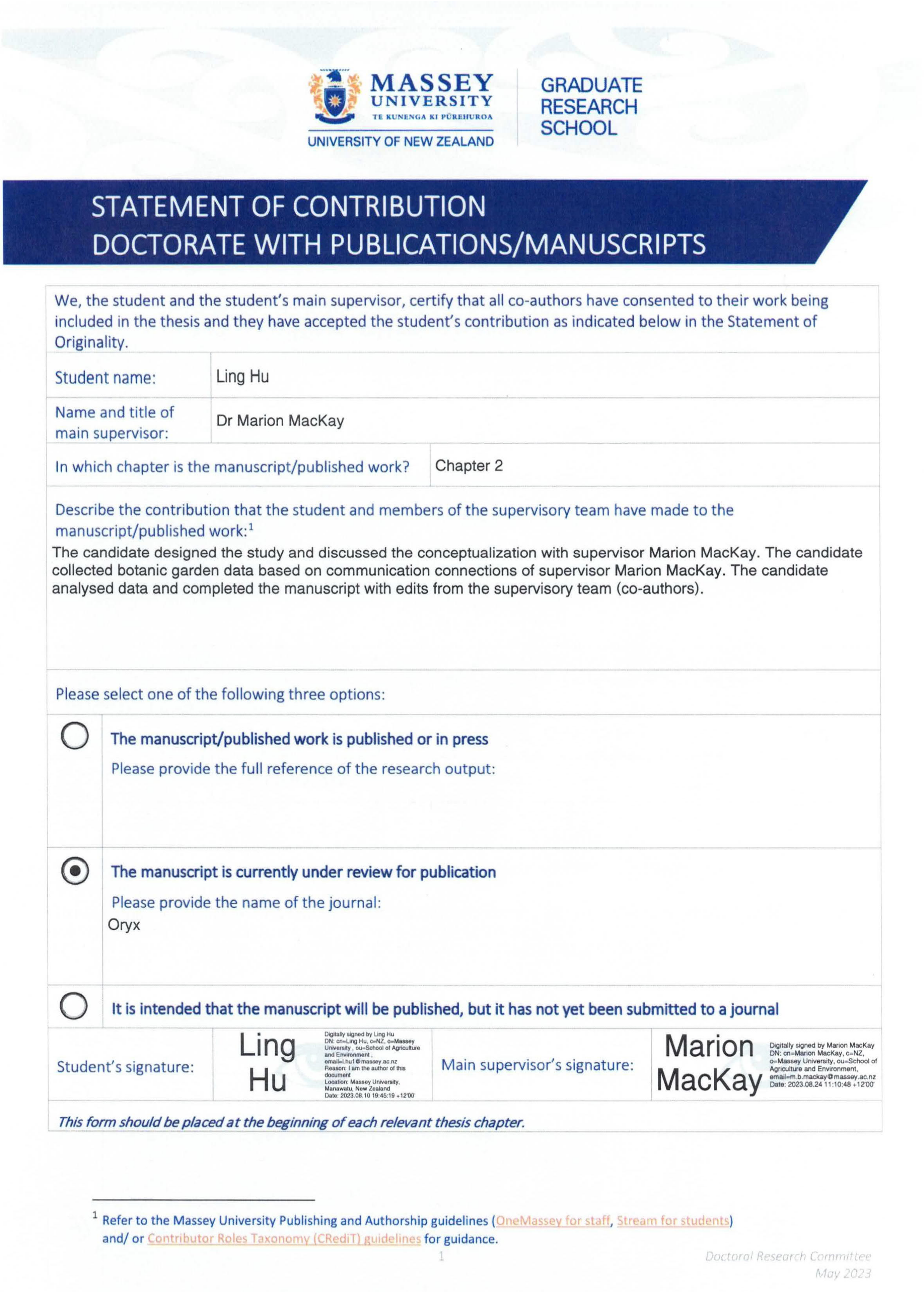
Statement of Contribution – Chapter 2



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STATEMENT OF CONTRIBUTION
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We, the student and the student's main supervisor, certify that all co-authors have consented to their work being included in the thesis and they have accepted the student's contribution as indicated below in the Statement of Originality.

Student name:	Ling Hu
Name and title of main supervisor:	Dr Marion MacKay
In which chapter is the manuscript/published work?	Chapter 2

Describe the contribution that the student and members of the supervisory team have made to the manuscript/published work:[1]

The candidate designed the study and discussed the conceptualization with supervisor Marion MacKay. The candidate collected botanic garden data based on communication connections of supervisor Marion MacKay. The candidate analysed data and completed the manuscript with edits from the supervisory team (co-authors).

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Chapter 2

Rhododendron diversity conservation in global botanic gardens: A case study of *Maddenia* species

Abstract

Effective *ex situ* conservation of plants in botanic gardens requires sufficient wild accessions to represent wild diversity. But data are often lacking in ‘big genera’ such as *Rhododendron* L. (Ericaceae), where almost half of the taxa present conservation issues. Geographical range was used as a proxy for genetic representation in *ex situ* collections of the 65 taxa of *Rhododendron* subsection *Maddenia*, as a case study. The first profile list exhibiting both wild distribution and *ex situ* wild collections of all taxa in subsection *Maddenia* was compiled. The results reveal that 55 of the total 65 *Maddenia* taxa are in cultivation, with over 86% of the living collections conserved in 66% of global botanic gardens. The 18 threatened taxa are all in cultivation, but nine require further wild collection. The 12 Data Deficient taxa await further field investigation, among which nine require wild collection to conserve genetic diversity. The results suggest that wild collections of endemic species of subsection *Maddenia* should be established in all 10 countries of origin, and data shared internationally for metacollections. Apart from proposing priorities, this case study highlights the challenges of data and collection management in achieving effective *ex situ* conservation of *Rhododendron* species.

Keywords: *Ex situ* conservation; genetic representation; geographical range; living collection; prioritisation; taxonomic complexity; wild accession

2.1 Introduction

Plant biodiversity conservation was prioritised for urgent action at the United Nations Biodiversity Conference COP 15, with development of the particular post-2020 global strategy for plant conservation (CBD, 2021). As a component of integrated plant conservation, *ex situ* conservation not only conserves plant diversity but also supports habitat restoration (Havens et al., 2006; Westwood et al., 2021). The genetic variation in *ex situ* collections at the species, population, individual and allelic levels could be drawn from to adapt species to potential environmental changes in habitat, as well as safeguard against introduced diseases and pests (Sharrock, 2020).

Botanic gardens (including arboreta) are key repositories of living collections for plant *ex situ* conservation (Havens et al., 2006; O'Donnell & Sharrock, 2017; Sharrock, 2020; Hudson et al., 2021; Westwood et al., 2021). Target 8 of the Global Strategy for Plant Conservation (CBD, 2010) directs that at least 75% of threatened species be conserved in *ex situ* collections (preferably in countries of origin), with over 20% available for restoration programmes. Examination of *ex situ* conservation status of species against Target 8 and identifying gaps can enable botanic gardens to support *ex situ* conservation more effectively (Godefroid et al., 2011; Linsky, Crowley, et al., 2022). According to analyses on data from the world’s largest plant conservation network Botanic Gardens Conservation International (BGCI), plant collections in global botanic gardens face problems, such as, species are disproportionately held in temperate locations, outside their country of origin and in one institution only (Mounce et al., 2017; Sharrock, 2020). *Ex situ* collections require scientific management to maximise conservation effectiveness.

A fundamental underpinning for effective *ex situ* conservation is a sufficient number of wild-source accessions that represent the wild diversity of species (IUCN SSC, 2014; Mounce et al., 2017; Maxted et al., 2020; Wei & Jiang, 2021; Westwood et al., 2021). The limited space and facilities of botanic gardens have to be allocated to prioritized species (Heywood, 2017; Sharrock, 2020). Factors such as species richness, taxonomic distinctiveness, vulnerabilities of species and threats in the wild as well as on-going *ex situ* conservation activities have been considered to determine priorities for several plant genera (Kozlowski et al., 2012; Toppila, 2012; Hoban et al., 2018; MacKay et al., 2018; Linsky, Crowley, et al., 2022). To estimate the genetic representation of *ex situ* collections, the concept of ‘ecogeographical representativeness’ of wild accessions as a surrogate has been proposed (Rae, 2011; Griffith et al., 2015; Volis, 2017; Chen & Sun, 2018; Griffith et al., 2020; Hudson et al., 2021; Wei & Jiang, 2021). Using the number and provenance of wild accessions to estimate the captured genetic diversity can inform future collection management (Beckman, 2019; Linsky, Crowley, et al., 2022). Current practice includes the concept of 'metacollections' (i.e., pooled collection) to manage pooled collections in botanic gardens obtained from spatially separated populations through data sharing and coordinated sampling at an international or regional level (Griffith et al., 2020; Westwood et al., 2021). The number of wild accessions required to conserve a species with 'enough' genetic diversity differs. However, it is required that multiple wild samples should be collected from diverse populations, with each *ex situ* collection duplicated at multiple sites in case of catastrophic loss (Griffith et al., 2015; Ren et al., 2019).

Rhododendron is a 'big genus' of over 1,000 species from a wide geographical range, with the greatest diversity extending from the southern Himalayas to southwestern China (Frodin, 2004; Gibbs et al., 2011; MacKay et al., 2018; Shrestha et al., 2018). Assessing the number and geographical range of *Rhododendron* populations in the wild is challenging due to their inaccessible habitats in montane or remote regions (Gibbs et al., 2011). Under BGCI's scope, the Global Conservation Consortium for *Rhododendron* was established in 2018 to coordinate conservation action worldwide. Despite the large numbers of conserved *Rhododendron* taxa (78% of threatened taxa in cultivation) in botanic gardens (MacKay & Hootman, 2018; MacKay et al., 2018) and ongoing *ex situ* conservation projects (Ma et al., 2014; McMeekin, 2022), genetic representation of *ex situ* collections of *Rhododendron* species has never been studied.

In this paper, subsection (ss.) *Maddenia* is presented as a case study for examination of the progress of diversity conservation in global *ex situ* collections. Ss. *Maddenia* (subgenus *Rhododendron,* section *Rhododendron*) exhibit various conservation issues that occur across the genus, including under-investigated wild distribution (Gibbs et al., 2011), complex taxonomy (Cubey, 2003; Donald, 2012; McMeekin, 2022; Hu et al., 2023, Chapter 3), taxonomic debates over species' conservation status (Gibbs et al., 2011; Li et al., 2018), and lately published species (Chang et al., 2021; Rushforth et al., 2022). Ecogeographical representation as a proxy for genetic representation in current wild collections of ss. *Maddenia* was analysed, to identify *ex situ* conservation gaps for future action. Data of *ex situ* collections (at taxon- and accession levels) together with taxon distribution are used to (i) update the list of taxa with current knowledge on conservation assessment and wild distribution, (ii) characterize *ex situ* conservation status of taxa, (iii) examine the genetic representation of wild-source accessions, and (iv) identify gaps and derive conservation strategies.

2.2 Materials and Methods

First, a checklist of all ss. *Maddenia* taxa was updated. Second, two sets of data were compiled for ss. *Maddenia*: 1) taxa in the wild: annotated with IUCN Red List category, country/region of distribution, and altitude of habitat; 2) taxa in *ex situ* conservation: annotated with cultivation status (whether a taxon is in cultivation), location of global *ex situ* sites and number of living collections (taxon-level data; Table S2.1), wild collection provenance and number of wild accessions per taxon (accession-level data; Table S2.2). Third, these data were formulated into a profile for each taxon in ss. *Maddenia*, and used to produce a map with known distribution and *ex situ* sites of living collections plotted together with origins of wild accessions (List S2.3). *Ex situ* conservation gap analysis was based on the compiled datasets.

In this study, taxa were defined as ‘in cultivation’ if there was a living collection recorded in any one of the data sources used. A ‘living collection’ was defined as the record of a taxon with living plants cultivated in a botanic garden, and one collection may include multiple accessions.

2.2.1 Checklist of subsection *Maddenia*

In the checklist, all taxa of ss. *Maddenia* (species, subspecies and botanical varieties) with their synonyms were summarized based on Chamberlain et al. (1996), with taxonomic updates referring to post-1996 studies (Argent et al., 2008; Gibbs et al., 2011; Donald, 2012; Mao & Bhaumik, 2015; Mao et al., 2017a; MacKay et al., 2018; Rushforth & Nguyen, 2019; Chang et al., 2021; Rushforth et al., 2022).

Threatened levels of taxa were initially from *The IUCN Red List of Rhododendrons* (Gibbs et al., 2011) and from assessments for recently published species (Mao & Bhaumik, 2015; Chang et al., 2021), or the updated IUCN Red List (BGCI & IUCN SSC Global Tree Specialist Group, 2018) and endemic species referring to national assessments in China (MEP–CAS, 2013; Qin et al., 2017). BGCI’s ThreatSearch database was also indexed for existing conservation assessments (BGCI, 2022b).

Distributions and countries of origin for each taxon were mapped with polygons, based on geographical information from literature and online databases (Cullen, 1980; Davidian, 1982; Feng, 1988, 1992; Feng & Yang, 1999; M.-Y. Fang et al., 2005; Fang et al., 2011; Gibbs et al., 2011; Mao & Bhaumik, 2015; Mao et al., 2017a; RBGE, 2018b, 2018a; Chang et al., 2021; GBIF, 2021; Rushforth et al., 2022). Distribution data were georeferenced and maps generated using QGIS 3.20.3 (QGIS Development Team, 2021). By stacking the polygons for each taxon, a distribution heatmap of all *Maddenia* taxa was generated in QGIS using the ‘count-polygon-overlap’ model. Details of data processing and taxon information can be found in List S2.3.

2.2.2 Presence of subsection *Maddenia* in *ex situ* living collections

Data describing the presence of ss. *Maddenia* taxa in cultivation were collected from three key sources. Firstly, BGCI PlantSearch database (BGCI, 2021b) was used as the primary indicator of presence in cultivation. However, PlantSearch only records *ex situ* collections at taxon level but not accession level. Therefore, an unpublished set of BGCI data (BGCI, 2020) that includes all *Rhododendron* records from GardenSearch and PlantSearch databases, was used as the second source. Taxon-level collections data for ss. *Maddenia* in global botanic gardens were compiled from these two sources (Table S2.1). The unpublished BGCI data (BGCI, 2020) and BGCI’s GardenSearch database (BGCI, 2022a) were used to identify *ex situ* collections held in countries worldwide. The third source was data from seven gardens in New Zealand as a hotspot of *ex situ* conservation of ss. *Maddenia*, together with seven largest collections of ss. *Maddenia* outside New Zealand. Data of the third source include unpublished data from MacKay et al. (2018) and additional data or garden updates in 2020. Accession-level data from the third source were compiled in Table S2.1.

2.2.3 Provenance and number of wild accessions

To evaluate the ecogeographical representation of *Rhododendron* ss. *Maddenia* conserved *ex situ*, provenance and number of wild accessions in the 14 botanic gardens of the third data source were collated. Data were analysed for each taxon, with determinants for the evaluation of conservation: number of wild collections (identified by the unique Collector ID for each wild collection), number of wild accessions per collection (identified by accessions under the same Collector ID), cultivation source material, Collector ID and provenance (habitat location or coordinates and altitude) of wild accessions (Table S2.2).

Wild accessions of each taxon with documented coordinate data were mapped in QGIS. When a wild accession was described from a certain location but without coordinates, a location was assigned around the centre of the geographic area with the taxon's habitat and altitude cross-referenced. When an accession was noted as from the wild but without provenance information, it was considered as a wild accession, but not plotted on the map.

2.3 Results

2.3.1 Checklist of subsection *Maddenia*

In the checklist, a profile was compiled for each of the 65 taxa in *Rhododendron* subsection *Maddenia* (List S2.3). This includes 18 threatened taxa (3 Critically Endangered, 2 Endangered, 13 Vulnerable), 4 Near Threatened, 12 Data Deficient, 20 Least Concern and 11 Not Evaluated. Information for conservation status and wild distribution are included in each profile. The distribution heatmap of subsection *Maddenia* was generated based on maps of all taxa in List S2.3 (Fig. 2.1). Subsection *Maddenia* spans southern Asia across 10 countries including China, India, Myanmar, Vietnam, Bhutan, Thailand, Nepal, Laos, Bangladesh and Indonesia (Fig. 2.1 A & C). China has the greatest number of native taxa (45), followed by Myanmar (20) and India (19). The mountainous areas in the China – NE India and China – Myanmar borders are the geographical hotspot for this subsection.

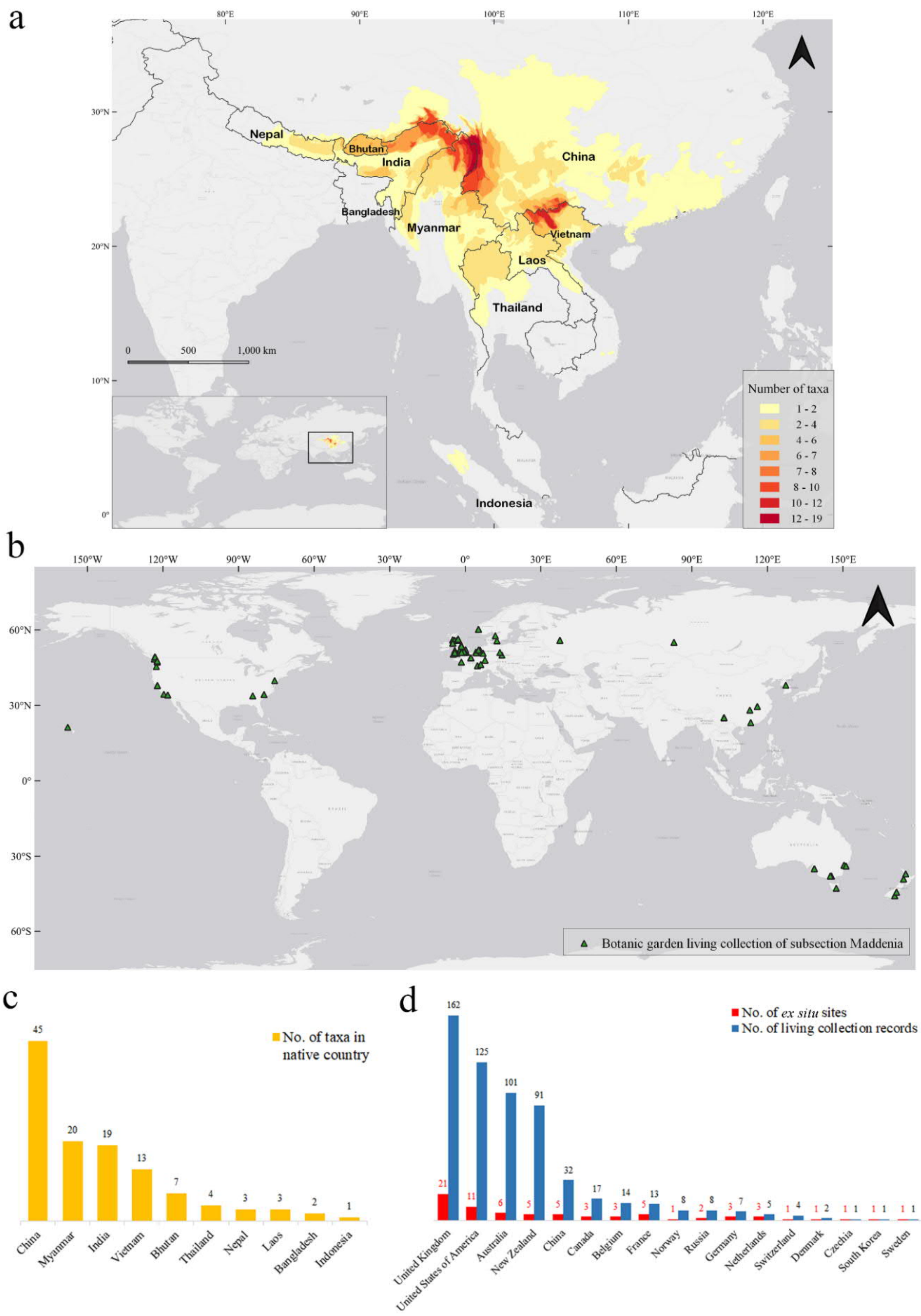


Figure 2.1 *Rhododendron* subsection *Maddenia* in native countries and *ex situ* conservation. A) Taxon distribution and richness in native countries (countries shown on the map). B) The 73 global *ex situ* sites of living collections. C) Number of taxa in each native country and D) Number of *ex situ* sites and living collections by country.

2.3.2 *Ex situ* living collections per taxon by IUCN Red List category

Numbers of *ex situ* sites and countries were summarized per taxon and classified by Red List category (Fig. 2.2A; List S2.3). All threatened taxa (Critically Endangered, Endangered, Vulnerable) are conserved in at least three botanic gardens, so are Near Threatened taxa. However, the 12 Data Deficient taxa have poorer representation. Among them, three (*R. amandum*, *R. yaogangxianense*, *R. yizhangense*) are ‘not in cultivation’ and four (*R. kuomeianum, R. linearilobum, R. rhombifolium*, *R. valentinioides* (ined.)) are cultivated in only one or two botanic gardens. Least Concern taxa are well represented, with only four of the 20 taxa ‘not in cultivation’ or held in fewer than three botanic gardens.

2.3.3 *Ex situ* living collections in native and other countries

A total of 592 collection records of the 55 taxa ‘in cultivation’ were identified at 73 *ex situ* sites in 17 countries. Ten taxa are ‘not in cultivation’ (zero *ex situ* sites, Fig. 2.2A; Table S2.1). *Ex situ* collections of ss. *Maddenia* are widely cultivated in subtropical and temperate areas in Europe, North America, SE Asia and Oceania. There was no record in Africa or South America (Fig. 2.1B). The survey shows that the UK, USA, Australia, New Zealand and China are the top five countries holding *ex situ* collections of ss. *Maddenia* (Fig. 2.1D), where nearly 66% of the *ex situ* sites hold more than 86% of the living collections. While a smaller number of *ex situ* collections are conserved in Canada, Belgium and France, the remaining nine countries hold only ~6% of the *ex situ* collections of this subsection, either in one *ex situ* site or with one collection record.

Among the countries of origin, only China had *ex situ* collections of ss. *Maddenia* reported to BGCI, with 32 collections representing 22 taxa at five sites (Table S2.1). There was no *ex situ* collection of ss. *Maddenia* recorded in the other nine native countries. Using the BGCI GardenSearch database, several botanic gardens were indexed in these native countries, but they did not have data of ss. *Maddenia* reported to BGCI (Table 2.1). Bhutan, Laos and Indonesia each reported one garden holding *Rhododendron* collections, but ss. *Maddenia* was not recorded.

Numbers of ss. *Maddenia* taxa conserved per site were recorded to determine the leading botanic gardens in *ex situ* conservation (Table S2.1). Among all 73 *ex situ* sites, there were 12 holding living collections of more than 10 ss. *Maddenia* taxa, with nearly 66% of the global collections (Table 2.2). Only the three botanic gardens (Royal Botanic Garden Edinburgh, Rhododendron Species Botanical Garden (USA), University of California Botanical Garden at Berkeley) held more than half of the taxa (48, 37, 33, respectively).

Table 2.1 Number of botanic gardens in the countries of origin of *Rhododendron* subsection *Maddenia*. Countries are listed in descending order of taxon number. Numbers of gardens with ss. *Maddenia* or *Rhododendron* collections are from BGCI PlantSearch (BGCI, 2021b), while numbers of BGCI- or non-member botanic gardens are from BGCI GardenSearch (BGCI, 2022a)

Country	No. of gardens with ss. *Maddenia* collections	No. of gardens with *Rhododendron* collections	No. of BGCI member gardens	No. of botanic gardens
China	5	16	40	173
India	0	0	10	138
Myanmar	0	0	1	5
Vietnam	0	0	1	10
Bhutan	0	1	1	1
Thailand	0	0	7	18
Nepal	0	0	0	2
Laos	0	1	1	1
Bangladesh	0	0	0	5
Indonesia	0	1	3	5

Table 2.2 Botanic gardens conserving living collections of more than 10 *Rhododendron* subsection *Maddenia* taxa. Botanic gardens are listed in descending order of number of conserved taxa. Numbers in parentheses represent number of (taxa in cultivation)/(taxa in total) in the corresponding category. [1]including Royal Botanic Garden Edinburgh at Edinburgh, Logan and Benmore; [2]including Royal Botanic Garden Kew at Richmond and Wakehurst. [*]Garden anonymised as permission for naming the garden name was not acquired

Botanic garden (*ex situ* site)	No. of conserved taxa		CR	EN	VU	NT	DD	LC	NE
	Country	(55/65)	(3/3)	(2/2)	(13/13)	(4/4)	(9/12)	(18/20)	(6/11)
Rhododendron Species Botanical Garden	USA	48	3	2	12	4	6	18	3
Royal Botanic Garden Edinburgh[1]	UK	37	2	1	10	3	4	15	2
RhodoBG_72[*]	USA	33	3	1	8	3	2	14	2
National Rhododendron Garden	AU	31	3	1	5	3	4	14	1
Dunedin Botanic Garden	NZ	27	1	1	7	2	2	13	1
RhodoBG_02[*]	AU	25	2	1	5	2	1	13	1
Pukeiti Garden	NZ	23	1	1	4	2	2	12	1
Royal Botanic Gardens Kew[2]	UK	19	1	0	4	1	1	12	0
Blue Mountains Botanic Garden	AU	19	2	0	4	2	0	10	1
Germplasm Bank of Wild Species	CN	14	1	1	0	2	1	8	1
St. Andrews Botanic Garden	UK	14	0	0	4	1	1	8	0
University of British Columbia Botanical Garden	CA	11	0	0	3	3	0	5	0

2.3.4 Number of wild accessions by taxon

The dataset identified 598 wild accessions from 277 documented wild sources of ss. *Maddenia* conserved in the surveyed 14 (botanic) gardens holding wild accessions (Fig. 2.2B; Table S2.2). Overall, the number of wild accessions per taxon showed a similar pattern to the number of *ex situ* sites/countries (Fig. 2.2). However, taxa are generally not well conserved with wild accessions. Among the 18 threatened taxa, *R. coxianum* (1 wild accession), *R. fleuryi* (2), *R. kiangsiense* (1) and *R. taronense* (2) had fewer than three wild accessions, with none for *R. roseatum* and *R. sinonuttallii*. While all four Near Threatened taxa had over 10 wild accessions present, the 12 Data Deficient data had few wild accessions in cultivation. Only four Data Deficient taxa were represented with more than three wild accessions. Notably, *R. linearilobum* and *R. rhombifolium* had no documented wild accessions present, although they were in cultivation (Fig. 2.2). For the 20 Least Concern taxa, although little conservation concern is indicated, *R. crenulatum*, *R. mianningense*, *R. parryae* and *R. pseudomadddenii* had fewer than three wild accessions and two (*R. vanderbiltianum* and *R. yungchangense*) are ‘not in cultivation’. The two subspecies of the *R. maddenii* complex, *R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum* were represented by the greatest number of wild accessions.

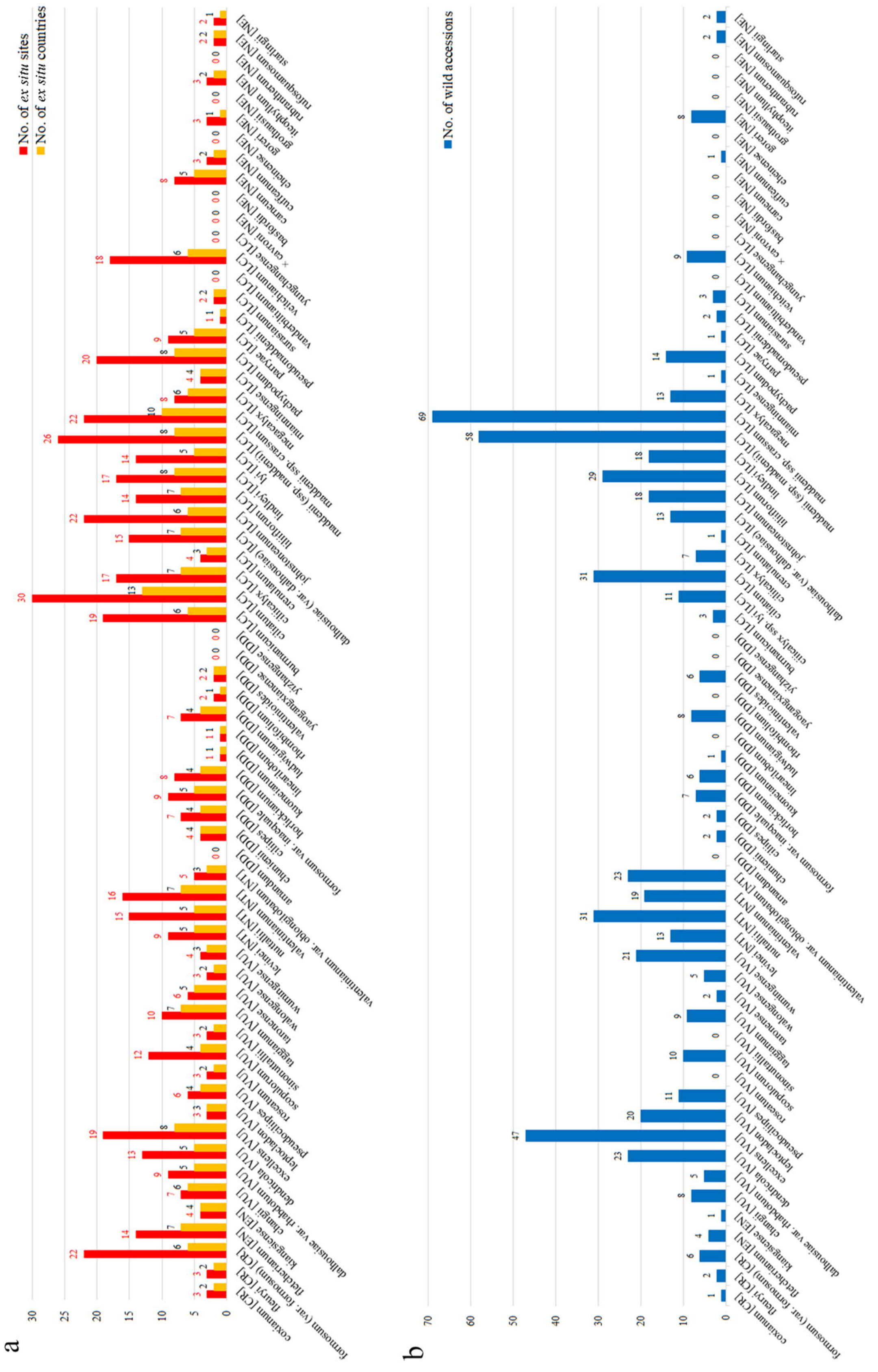


Figure 2.2 *Ex situ* living collections of *Rhododendron* subsection *Maddenia* by taxon. A) Number of sites and countries holding *ex situ* collections; B) Number of accessions in wild collections. Taxa are in alphabetical order under each IUCN Red List category

2.3.5 Ecogeographical representation of *ex situ* collections

Using available provenance data (either coordinates or a described location), 179 of the total 277 wild collections were geo-referenced to show the geographical extent of ss. *Maddenia* in *ex situ* conservation (Figs. 2.3 & 2.4). Most of the wild accessions were collected from southwestern China, north-eastern India, Bhutan, eastern Nepal, northern Myanmar, northern Vietnam and north-western Thailand. Among the taxa threatened or at risk, 10 (2 Critically Endangered, 2 Endangered, 3 Vulnerable, 3 Data Deficient) had documented wild accessions but from fewer than three wild sources (Fig. 2.4A). Due to lack of provenance data, a proportion of wild collections (98/277, 35.4%) were not mapped (Fig. 2.4A; Table S2.2; List S2.3). Although identified as from the wild, these collections were recorded with no geographical information. This resulted in six taxa not mapped (*R. coxianum*, *R. kiangsiense*, *R. taronense*, *R. levinei*, *R. parryae*, *R. pseudomaddenii*), among the 49 taxa having recorded wild accessions in cultivation (Fig. 2.4B).

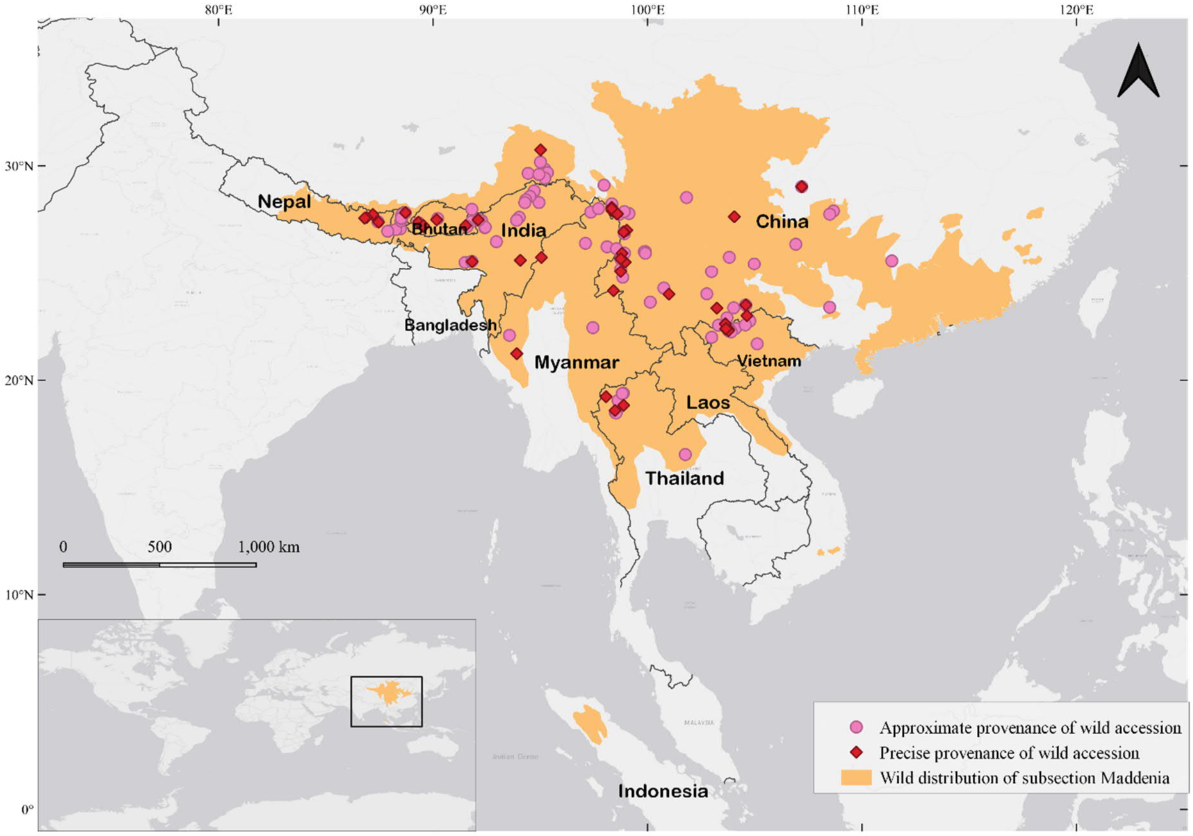
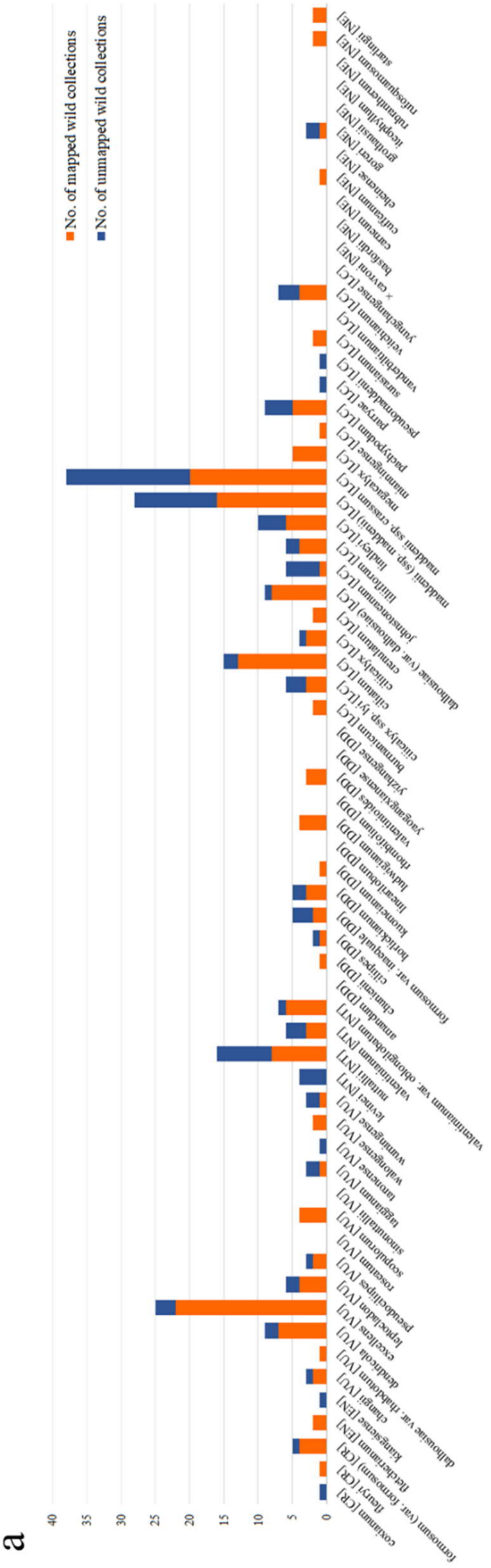


Figure 2.3 Geographical extent of *ex situ* wild collections of *Rhododendron* subsection *Maddenia*. Wild collections are geo-mapped according to provenance data



b

Taxon	Country of origin	Red List category	No. of mapped wild sources	No. of wild sources	No. of living collections
R. coxianum [3]	India	CR	0	1	3
R. kiangsiense [3]	China	EN	0	1	4
R. roseatum [2]	China, Myanmar	VU	0	0	3
R. sinonuttallii [2]	China	VU	0	0	3
R. taronense [3]	China	VU	0	1	6
R. levinei [3]	China	NT	0	4	9
R. amandum [1]	China	DD	0	0	0
R. linearilobum [2]	China	DD	0	0	1
R. rhombifolium [2]	China	DD	0	0	2
R. yaogangxianense [1]	China	DD	0	0	0
R. yizhangense [1]	China	DD	0	0	0
R. parryae [3]	India	LC	0	1	9
R. pseudomaddenii [3]	India	LC	0	1	1
R. vanderbiltianum [1]	Indonesia	LC	0	0	0
R. yungchangense [1]	China	LC	0	0	0
R. × *carvori* [1]	N/A	NE	0	0	0
R. basfordii [1]	Bhutan	NE	0	0	0
R. carneum [2]	Myanmar	NE	0	0	8
R. eheinense [1]	China	NE	0	0	0
R. grothausii [1]	China, Bhutan	NE	0	0	0
R. iteophyllum [2]	India	NE	0	0	3
R. rubrantherum [1]	Myanmar	NE	0	0	0

Figure 2.4 Summary of geo-mapping *ex situ* wild collections of *Rhododendron* subsection *Maddenia*, by taxon. A) Number of mapped and unmapped wild collections per taxon. Of the total 277 wild collections, 179 were mapped with either pink dots or red diamonds as shown in Fig. 2.3. The other 98 were not mapped due to lack of provenance information; B) Summary of [1]taxon 'not in cultivation', [2]Taxon 'in cultivation' but no wild accessions, or [3]Taxon with wild collections of unknown provenances

for geo-mapping (not mapped on Fig. 2.3). Taxa are listed in alphabetical order under each Red List category.

2.4 Discussion

2.4.1 Progress in *ex situ* conservation of *Rhododendron* subsection *Maddenia*

This study is the first of its kind to examine the wild diversity of *Rhododendron* ss. *Maddenia* in current *ex situ* conservation worldwide. Analyses of the living collections inform *ex situ* conservation management of this subsection of 65 taxa towards GSPC Target 8 (CBD, 2010). The 85% of ss. *Maddenia* taxa ‘in cultivation’ show an improved position compared to the 73% for whole genus in 2018 (MacKay et al., 2018), with all threatened taxa now cultivated in at least three sites (Fig. 2.2). This meets the criterion of ‘taxon cultivated in at least three *ex situ* sites and have at least three wild accessions’ optimised from Griffith et al. (2011) and MacKay et al. (2018), to adequately capture genetic diversity in *ex situ* conservation. However, among the 34 taxa threatened or at risk (Critically Endangered, Endangered, Vulnerable, Near Threatened, Data Deficient), only two (*R. excellens*, *R. nuttallii*) are conserved with over 15 wild collections (number of wild sources in Table S2.2 and List S2.3), while half (17/34) do not meet the aforementioned criterion (Figs. 2.2B & 2.4A). Particularly, six threatened taxa (*R. coxianum*, *R. fleuryi*, *R. kiangsiense*, *R. roseatum*, *R. sinonuttallii*, *R. taronense*; Fig. 2.2B) have none or fewer than three wild accessions present on any site, requiring wild collection to safeguard their genetic diversity. Also, Data Deficient taxa account for 27% (18/65 taxa) of the whole subsection. Seven of these Data Deficient taxa are represented by no wild accession or fewer than three, suggesting targeted field work and data collection should be undertaken. In addition, some of the 10 taxa ‘not in cultivation’ (three Data Deficient, two Least Concern and five Not Evaluated; Fig. 2.4B) await further investigation to confirm their conservation status.

In general, the mapping of the wild collections (Fig. 2.1A) showed similar hot spots to the wild distribution of ss. *Maddenia* (Fig. 2.3), indicating a relatively adequate ecogeographical representation of *ex situ* living collections. However, the broad distribution may have not been well sampled for individual taxa. For example, although *R. leptocladon* is native in the China - Vietnam border and assessed Vulnerable globally, its wild populations are still under examination (Data Deficient in China), and current wild accessions have only been collected from northern Vietnam (List S2.3). Also, the geographical extent of *ex situ* collections can be highly related to plant hunting and administrative boundaries. The density of sampling may reflect the collecting patterns rather than natural distribution of a taxon. Under legislations such as the Nagoya Protocol (CBD, 2011), field expeditions, species introduction and plant material exchange may become less frequent, which emphasises the need to understand the wild diversity in existing living collections.

Globally, *ex situ* collections of ss. *Maddenia* are widespread over countries in both the northern and southern hemispheres, but largely in western countries rather than their native countries (Fig. 2.1D; Table 2.1). This trend of threatened species not being held endemically was addressed in the GSPC report 2020 (Sharrock, 2020), and is not unique to *Rhododendron* but also occurs in other plant groups (e.g., *Magnolia* (Magnoliaceae) (Linsky, Crowley, et al., 2022) and *Zelkova* (Ulmaceae) (Kozlowski et al., 2012)). Considering the small number of botanic gardens in countries of origin which report to BGCI (Table 2.1), *ex situ* collections in these countries may not be well covered in the present study. However, while lacking published data on *ex situ* collections, countries of origin may be making more efforts towards *in situ* conservation. In China, where the greatest number of ss. *Maddenia* taxa originates from, more data on *ex situ* collections of *Rhododendron* (Ericaceae) have been published (Wang, 2022), from the project '*Ex Situ Flora of China*' (Huang et al., 2017). In India, plants of the *R. formosum* complex are under on-site observation in Meghalaya (Mao et al., 2017a). Conservation policies in Nepal and Bhutan also indicate *Rhododendron* species are more likely to be protected on site (IUCN Nepal, 2010; DoFSC, 2019; Namgay & Sridith, 2021).

While Gibbs et al. (2011) addressed efforts for *in situ* conservation of *Rhododendron*, challenges also remain for integrating the *ex situ* collections into *in situ* conservation. The countries of origin may hold different conservation priorities which may not be *Rhododendron* species. They may also require further funding and expertise to conduct related research (e.g. evolutionary lineages, ecological components of functioning landscapes and valued economic resources) on the wild species and practice in the botanic gardens. Also, while destruction on *Rhododendron* populations (e.g. for firewood and infrastructure construction) occurs, increasing local awareness of conserving wild species through public education programmes requires more efforts in the botanic gardens.

Nevertheless, results of the present study can be utilized by global databases or organisations such as Global Tree Assessment (BGCI, 2021a), World Flora Online and Global Conservation

Consortium for Rhododendron. Although it is the world’s largest plant conservation network, BGCI’s databases are not exhaustive regarding all *ex situ* collections (Table 2.1). Gardens not in the BGCI GardenSearch database are likely not reporting collection data to BGCI, such as the private gardens in New Zealand that hold *Rhododendron* collections in the present study. The importance of data sharing for research and conservation practice is well illustrated here. To be noted, the sharing of plant material and associated data across national borders should be based on legitimate agreements, so that native biodiversity in both ex- and import countries and data sovereignty can be well protected.

2.4.2 Knowledge gaps in assessing genetic representation of *ex situ* collections of *Rhododendron*

A globally updated taxon list is a necessary basis for studying biodiversity of species. Complex taxonomy is a problematic feature of ‘big genera’ like *Rhododendron*. For example, the unresolved taxonomy of ss. *Maddenia* species remains one big challenge to their conservation assessment; 9 of the 20 taxa threatened or at risk were described with taxonomic debates in Gibbs et al. (2011). Also, new taxa may have been postulated based on morphological observations but not yet been officially published, such as *R. valentinioides* (ined.) (detailed taxonomic debates in List S2.3). In the present study, wild accessions of the infraspecific taxa and affinities were included in the analysis, where their variation was considered as part of the diversity within a species. However, the genetic representation of these variable wild accessions can only be examined realistically based on determined taxonomic status.

Conservation assessments also require further work. Field investigation is needed for Data Deficient taxa (e.g. *R. formosum* var. *inaequale*) in the previous *The Red Lists of Rhododendrons* (Gibbs et al., 2011), or updates are needed for taxa that are re-evaluated. Global and regional (e.g., China and India) conservation status may affect decision-making at different administrative levels. Recent surveys of the wild populations of threatened *Rhododendron* species (Ma et al., 2014), updates of China’s Red Lists (Qin et al., 2017; Qin & Zhao, 2017) together with upcoming assessments coordinated by BGCI would contribute to better understanding of the distribution of *Rhododendron* taxa and their conservation status.

Wild populations of *Rhododendron* ss. *Maddenia* in countries of origin often lack investigation on both size and distribution, due to their localised and fragmented populations in inaccessible habitats of montane regions (Cullen, 1980; Feng, 1988, 1992; Feng & Yang, 1999; Fang et al., 2011; Gibbs et al., 2011; Donald, 2012). Geo-mapping in the present study relied on information derived from published literature and databases, with varying levels of data available for different taxa, hence the extent of capturing distribution may differ among species. Distribution of ss. *Maddenia* is not well localised especially in areas where few taxa have been found (distribution 'edge' area in Fig. 2.1A; List S2.3).

Assessment of ecogeographical representation requires wild collections to be well documented. Adequate geographical data, especially with precise coordinates of the source plants, and regular update on the living status of accessions, are essential to record a wild collection. However, *ex situ* collections of *ss. Maddenia* usually suffer from poor documentation, and the extent of documentating details of wild collections differs among botanic gardens. This causes difficulty in tracing the origin of wild collections and leads to discrepancies in the accuracy of evaluating captured diversity.

For the first time, *ex situ* wild accessions of all ss. *Maddenia* taxa were examined in a global range for their ecogeographical representation, which has greatly enhanced our understanding of genetic representation of taxa in *ex situ* collections. Compared to similar studies of other plants (Godefroid et al., 2011; Kozlowski et al., 2012; Linsky, Crowley, et al., 2022), the present study had more specific data concerning wild accessions. The spatial analysis of *Magnolia* in *ex situ* collections used circular buffers to approximate geographic sizes of habitat, populations and gene flow (Linsky, Crowley, et al., 2022). However, this method of comparing known *in situ* occurrences and *ex situ* collection source localities is not suitable for current *Rhododendron* analysis, considering the greatly limited knowledge of *Rhododendron* wild populations.

2.4.3 Recommendations for urgent conservation action of subsection *Maddenia*

Related botanic gardens are recommended to collaborate to manage further conservation for subsection *Maddenia* by: 1) investigating and/or establishing *ex situ* collections in the countries of origin; 2) botanic gardens sharing *ex situ* data to BGCI and Global Conservation Consortium for Rhododendron. 3) BGCI establishing an accession database with formatted fields for individual gardens, so that genus-wide analyses can be conducted; 4) development of a ‘metacollection’ of subsection *Maddenia* across sites and nations, to pool wild accessions for conservation of genetic diversity.

Field investigation and wild sampling should be established across botanic gardens, particularly in the border regions between countries of origin. Current wild accessions could be summarised in a database with genetic information, to underpin collaborative research within the global conservation network.

Based on the criterion of three wild accessions per taxon for *Rhododendron ex situ* conservation, urgent actions are proposed to: 1) establish *ex situ* collections for the three Data Deficient taxa that are ‘not in cultivation’ (*R. amandum*, *R. yaogangxianense*, *R. yizhangense*), unless they are reassessed as Least Concern; 2) obtain wild collections for the two Vulnerable (*R. roseatum*, *R. sinonuttallii*) and the two Data Deficient taxa (*R. linearilobum*, *R. rhombifolium*) that currently have no wild accessions conserved; 3) extend the geographical range of wild sampling for the 10 taxa that are threatened or at risk but with documented wild accessions from fewer than three wild sources, including two Critically Endangered taxa (*R. coxianum*, *R. fleuryi*), two Endangered (*R. fletcherianum*, *R. kiangsiense*), three Vulnerable (*R. dalhousiae* var. *rhabdotum*, *R. taronense*, *R. walongense*) and three Data Deficient (*R. chunienii*, *R. ciliipes*, *R. kuomeianum*).

2.5 Conclusion

This study has identified that although all 18 threatened taxa of *Rhododendron* subsection *Maddenia* are in cultivation, only half are represented by more than three different wild collections, and they appear to be poorly represented in countries of origin. While GSPC Target 8 is met for the subsection overall, for 17 taxa the ecogeographical representation of wild accessions is insufficient and requires urgent action on wild sampling and *ex situ* cultivation. The dataset was based on long-term holdings of *Rhododendron* ss. *Maddenia* in the main botanic gardens globally, making it the most conclusive study to date, revealing progress and highlighting shortfalls in current *ex situ* conservation of this subsection. Based on the examination of wild accessions in cultivation, recommendations are derived for further conservation action in *ss. Maddenia*. The data process highlights several of the current challenges in *ex situ* plant conservation: the poor representation in cultivation of some threatened species; the problem of poor documentation of wild accessions; the need for comprehensive global datasets to facilitate conservation management; and the need to develop a global metacollection management approach to manage collections across a range of sites. *Ex situ* cultivation of threatened plant species is a valuable component of integrated plant conservation, but analysis on existing collections is necessary to support decision making. Conservation planning of *Rhododendron* ss. *Maddenia* is also affected by taxonomic complexity: views on the 'lumping' or 'splitting' of various taxa differ, and thus far there has not been a comprehensive molecular examination of species relationships in ss. *Maddenia* and the implications for conservation. Chapter 4 of the present thesis contributes to examination of this issue.

Supplementary Files

Supplementary files of Chapter 2 are attached in Appendix I.

Table S2.1 *Ex situ* living collections of *Rhododendron* subsection *Maddenia* in global botanic gardens

Table S2.2 Wild accessions of *Rhododendron* subsection *Maddenia* in the 14 surveyed botanic gardens

List S2.3 Checklist of taxon profiles of *Rhododendron* subsection *Maddenia*

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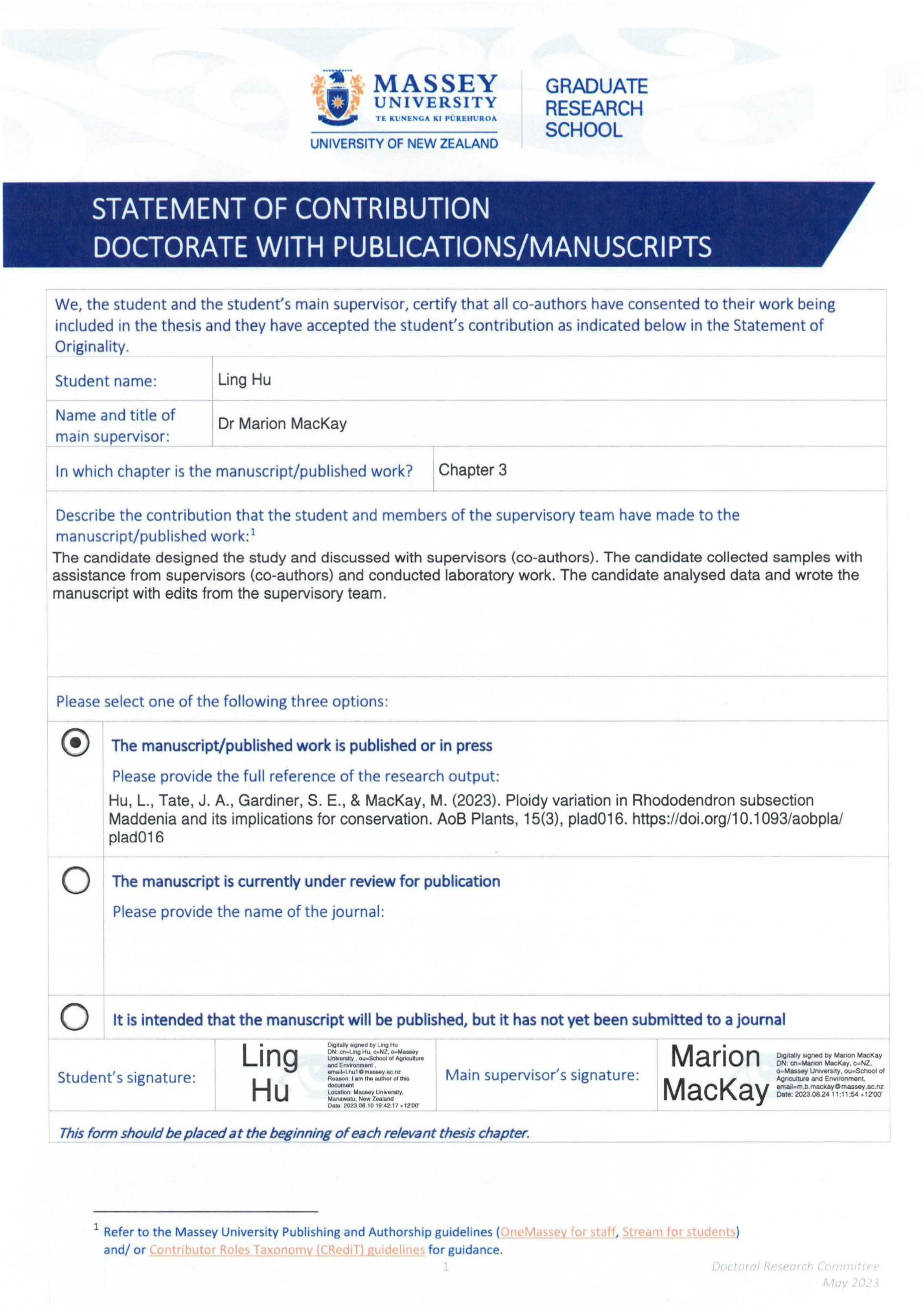

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Chapter 3

Ploidy variation in *Rhododendron* subsection *Maddenia* and its implications for conservation

Abstract

Polyploidy, which is common in plants, can confound taxon recognition and hence conservation assessments. In the taxonomically complex genus *Rhododendron*, 25% of the over 1,300 taxa are considered under threat and 27% Near Threatened or Data Deficient, with their taxonomy needing to be resolved urgently. Although ploidy levels of *Rhododendron* taxa range from diploid (2*x*) to dodecaploid (12*x*) according to previous reports, the extent of polyploidy across the genus has not been examined. This study first summarised the taxonomic distribution of polyploids in the genus based on the literature. Then, ploidy levels of 47 taxa in subsection *Maddenia* (subgenus *Rhododendron*, section *Rhododendron*) were estimated using flow cytometry, together with verification of meiotic chromosome counts for representative taxa. The summary of reported ploidy in *Rhododendron* indicates that polyploidy is most common in subgenera *Pentanthera* and *Rhododendron*. In subsection *Maddenia*, all examined taxa are diploids except for the *R. maddenii* complex that shows a high ploidy variation (2–8*x*, 12*x*). Ploidy level of 12 taxa in subsection *Maddenia* was investigated for the first time, and genome sizes of two *Rhododendron* species were estimated. Knowledge of ploidy levels will inform phylogenetic analysis of unresolved species complexes. Overall, this study of subsection *Maddenia* provides a model for examining multiple issues including taxonomic complexity, ploidy variation and geographic distribution in relation to biodiversity conservation.

Key words: Biodiversity conservation; flow cytometry; polyploidy; *Rhododendron*; subsection *Maddenia*; taxonomic complexity

3.1 Introduction

Polyploidization, or whole genome duplication (WGD), generates organisms containing multiple sets of chromosomes. This major mechanism of plant speciation results from either intraspecific genome duplication (autopolyploidy) or hybridization between different species and chromosome doubling (allopolyploidy) (Stebbins, 1947; Van de Peer et al., 2017). Fertile polyploids can become new species when strong reproductive incompatibilities and distinct phenotypic differences occur, differentiating them from their diploid progenitors. Polyploidization, accompanied by corresponding morphological differences, has been considered as a characteristic for recognition of species which form conservation units (Soltis et al., 2007; Soltis et al., 2010; Laport & Ng, 2017). Due to multiple copies of genes facilitating adaptive processes, polyploids may be more successful at adapting to new environments (Comai, 2005; Van de Peer et al., 2017; Van de Peer et al., 2021). As ploidy variation can be associated with regional biodiversity, it should be included in diversity measurements (e.g., phenotypic, inter- and/or intraspecific diversity) for the consideration of conservation, especially in temperate regions where polyploidization is frequently observed (Comai, 2005; Laport & Ng, 2017; Rice et al., 2019).

Rhododendron L. (Ericaceae) is a megadiverse genus with more than 1,300 taxa (species, subspecies (ssp.) and varieties (var.)) that typically grow in temperate regions (Gibbs et al., 2011). The wild distribution of *Rhododendron* covers a geographic range from the centres of diversity in the south-eastern Himalayas and Malay Archipelago to North America, Europe and northern Australia (Gibbs et al., 2011; Argent, 2015; MacKay et al., 2018; Shrestha et al., 2018). The Himalayan region is characterised by a rich biotic assembly (Fang & Fang, 1979; Yan et al., 2015; Hughes, 2017; Shrestha et al., 2018), where polyploids are likely to diversify under environmental stress (Rice et al., 2019; Van de Peer et al., 2021). Extensive hybridization, due to weak reproductive barriers within *Rhododendron,* is also a possible cause of rapid speciation (Frodin, 2004; Zhang et al., 2007; Zha et al., 2008; Soltis & Soltis, 2009; Ma et al., 2010; Qiu et al., 2020). However, hybridization and polyploidy and their influence on speciation rate in *Rhododendron* are still under investigation (Milne et al., 2010; Schwery et al., 2015; Shrestha et al., 2018; Khan et al., 2021). Taxa produced from introgression of sympatric species often show morphological similarity to their parents, making correct taxon identification challenging (Darlington et al., 1955; Milne et al., 2010; Zhang et al., 2020).

Effective decisions and strategies for species conservation require distinct taxonomy to assess the risk of extinction of species. It has been reported that 25% of *Rhododendron* taxa are under threat (Critically Endangered, Endangered and Vulnerable), and 27% Near Threatened or Data Deficient (MacKay et al., 2018). However, problems of taxon identification due to taxonomic complexity and lack of cytogenetic knowledge of particular accessions still need to be resolved to inform conservation strategies (Mehra, 1976; Jones et al., 2007; Gibbs et al., 2011; Mao et al., 2017a; Khan et al., 2021). Molecular phylogenetic techniques can assist resolution of taxonomic uncertainties (Gibbs et al., 2011; Gardiner et al., December 2019). However, the presence of polyploids can confound analyses due to duplicated genomes that are often derived from multiple species (Yan et al., 2015; Rothfels, 2021). For plant genera that include polyploids, such as *Rhododendron,* any investigation of phylogeny should be preceded by an examination of ploidy levels in the taxa under consideration (Khan et al., 2021).

Cytological studies of *Rhododendron* species began in 1930 (Bowers, 1930; Sax, 1930), with the most extensive and genus-wide chromosome counts reported in the 1950s (Ammal et al., 1950; Darlington et al., 1955). In *Rhododendron* species, mitotic chromosomes in the root tips are notably small and difficult to distinguish under the microscope (Jones et al., 2007; Zaytseva et al., 2018). This difficulty may increase for counting the multiple sets of chromosomes in polyploids (Comai, 2005; Van de Peer et al., 2017). Meiotic chromosome number can be more easily determined by counting haploid chromosomes in pollen mother cells (PMCs) (Windham et al., 2020), but little information is available on optimal bud harvest time for meiotic observation in *Rhododendron*. In contrast, flow cytometry (FCM) saves time by enabling rapid determination of nuclear DNA content (genome size) for a large number of samples (Doležel et al., 1998; De et al., 2010; Zaytseva et al., 2018). Apart from the measurement of genome size (Bou Dagher-Kharrat et al., 2013; Khan et al., 2021; Choi et al., 2022), FCM has been applied to estimate *Rhododendron* ploidy levels in several studies (Doležel et al., 1998; De Schepper et al., 2001; Jones et al., 2007; W.-Y. Zhou et al., 2008; Zaytseva et al., 2018; Khan et al., 2021). Cytological studies and FCM generally require access to living material. However, this can be hindered due to difficulties in accessing remote *Rhododendron* habitats or living accessions on sites of *ex situ* collections internationally. For FCM at least, the use of dehydrated leaf tissues has proven to be reliable for ploidy estimation in other species (Suda & Trávníček, 2006; Tomaszewska et al., 2021), but this approach has not yet been tested on *Rhododendron*.

Rhododendron is taxonomically complex, divided into nine subgenera (if considering *Vireya* as a subgenus) with further sections and subsections of varying sizes (Chamberlain et al., 1996; Frodin, 2004; Argent, 2015). Davidian (1982) systematically described the morphology of *Rhododendron.* Chamberlain et al. (1996) ‘lumped’ a number of previously recognised species as synonyms, which is considered the most comprehensive reference for the taxon checklist to date.

This study initially considers the whole genus, then focuses on subsection (ss.) *Maddenia* (subgenus *Rhododendron,* section *Rhododendron*) as a case study. Due to the complex taxonomy and continuous morphological variation within ss. *Maddenia*, many questions remain about species boundaries, which is identified as a general problem in the genus (Chamberlain et al., 1996; Cullen, 2005; Gibbs et al., 2011; Donald, 2012; MacKay, 2018; Jamieson, 2021). Ss. *Maddenia* is the largest among all the subsections in subgenus *Rhododendron* (if the vireyas are treated as subgenus *Vireya* rather than the broad section *Schistanthe* under subgenus *Rhododendron*), and several new species (Mao & Bhaumik, 2015; Mao et al., 2017a; Chang et al., 2021; Rushforth et al., 2022) have been published since Chamberlain et al. (1996). With ‘lumping’ species as synonyms and/or changes in placement of species over time, the number of accepted species in ss. *Maddenia* varies in treatments by different authors. In *The Rhododendron Species*, Davidian (1982) used the concept of ‘series’ rather than ‘subsection’ and listed a total of 56 species in the two Ciliatum and Maddenii Series. In *The Genus Rhododendron: Its classification & synonymy* that the present study is following as the major reference for taxonomic classification, Chamberlain et al. (1996) listed 52 species (57 taxa) in ss. *Maddenia*. Cox and Cox (1997) included 31 species of ss. *Maddenia* in *The Encyclopedia of Rhododendron Species*, while Khan et al. (2021) defined 56 species in the phylogenetic study. In ss. *Maddenia*, the *R. maddenii* complex is especially problematic, with 12 taxa placed in synonymy under the two subspecies of *R. maddenii* (*R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum*) (Chamberlain et al., 1996). Previous studies also found exceptional occurrence of polyploids (tetraploid, hexaploid, octoploid and dodecaploid) in *R. maddenii*, which raises questions on the uniqueness of this species complex (i.e. with ‘lumped’ synonyms and ambiguous species delimitation) and patterns of species diversification in ss. *Maddenia* (Ammal et al., 1950; Cubey, 2003; Khan et al., 2021).

Previous phylogenetic studies indicate that ss. *Maddenia* may not be monophyletic (Donald, 2012; Shrestha et al., 2018; Khan et al., 2021). However, two of these studies encompassed the whole genus, with few species included from ss. *Maddenia* (Shrestha et al. 2018; Khan et al. 2021), while Donald (2012) only considered the yellow-flowered species that include part of ss. *Maddenia* species. The species coverage as well as number of molecular markers applied in previous studies were limited, which does not provide adequate evidence on the relationships between ss. *Maddenia* and other possibly related species or subsections.

Subsection *Maddenia* includes rhododendrons that are all lepidote (scaly), originating from the Himalayan region through to southern China and northern Vietnam. The taxa not only present great morphological diversity (Fig. 3.1), but also possess unique horticultural value because of their scented flowers and high resistance to thrips (Cullen, 1980; MacKay et al., 2018; Jamieson, 2021). According to conservation assessments for 51 ss. *Maddenia* taxa, 33 were placed in either a threatened category or Data Deficient (Gibbs et al., 2011; MacKay et al., 2018; Chang et al., 2021). Due to the variable taxonomy and species definitions derived from traditional morphology, conservation assessments and subsequent conservation action are subject to debate (Cubey, 2003; Gibbs et al., 2011; Donald, 2012; Jamieson, 2021).

In this study, leaf samples from living accessions were collected to examine the ploidy variation in ss. *Maddenia*. The methodology involved (i) reviewing the literature to establish a comprehensive dataset of ploidy levels across *Rhododendron* taxa, which has not been done previously; (ii) investigating the basic cytogenetics of ss. *Maddenia* by estimating ploidy, especially of the previously reported polyploid taxa in the *R. maddenii* complex and of taxa not previously studied. Flow cytometry was used for ploidy estimation, and when possible, confirmed with meiotic chromosome counts from living material. The resulting data will not only inform future molecular phylogenetic studies (such as Chapter 4 of the present thesis), but also assist in developing an understanding of the speciation and ecological features of ss. *Maddenia* for conservation management.

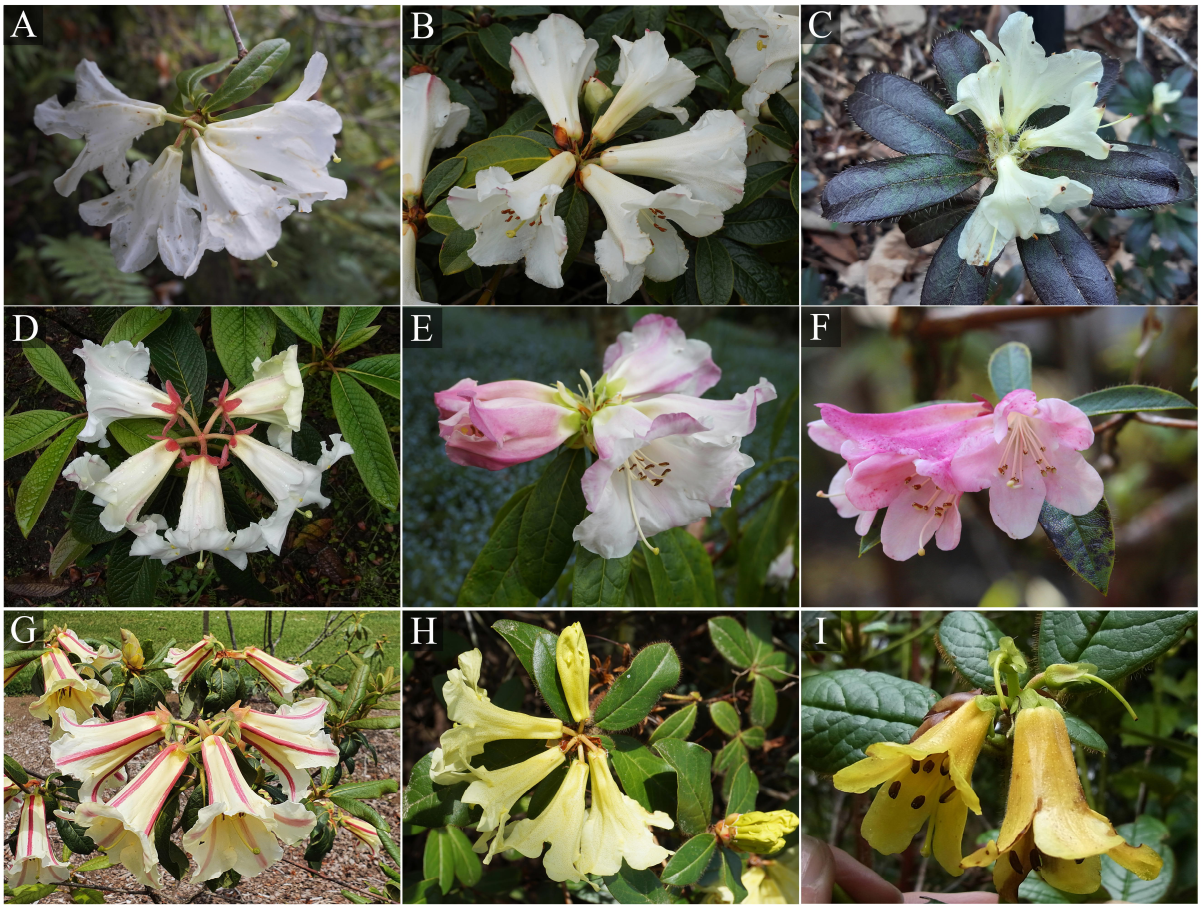

Figure 3.1 Representative taxa of *Rhododendron* subsection *Maddenia* and their conservation status. (A) *R. coxianum*, Critically Endangered. (B) *R. maddenii* ssp. *crassum*, Least Concern. (C) *R. fletcherianum*, Endangered. (D) *R. nuttallii*, Near Threatened. (E) *R. lindleyi*, Least Concern. (F) *R. formosum* var. *formosum*, Critically Endangered. (G) *R. dalhousiae* var. *rhabdotum*, Vulnerable. (H) *R. burmanicum*, Least Concern. (I) *R. valentinianum* var. *oblongilobatum*, Near Threatened. Conservation status of all taxa was published at the global level (Gibbs et al., 2011), except for *R. maddenii* ssp. *crassum* at the national level in China (MEP–CAS, 2013).

3.2 Materials and Methods

3.2.1 Literature review of ploidy in *Rhododendron*

Prior knowledge on ploidy levels of *Rhododendron* taxa was compiled in a spreadsheet, with data from chromosome counting (2*n*) and flow cytometry (*x*) both included but listed separately (Table S3.1). Chromosome data were compiled from the Chromosome Counts Database (CCDB, Rice et al., 2015), Index to Plant Chromosome Numbers (IPCN, Goldblatt & Johnson, 1979) and literature not covered by these two databases (Sax, 1930; Ammal et al., 1950; Li, 1957b; Cubey, 2003; Contreras et al., 2007). FCM ploidy data were collected from previous reports (De Schepper et al., 2001; Jones et al., 2007; De et al., 2010; Khan et al., 2021; Choi et al., 2022). Taxonomic classification (subgenus, section, subsection) followed Chamberlain et al. (1996), except that the vireya species were treated as subgenus *Vireya* following Argent (2015b) (subgenus *Vireya* may be treated as the broad section *Schistanthe* under subgenus *Rhododendron* as in recent studies). Taxa together with their synonyms were indexed according to Chamberlain et al. (1996) except for those in subgenus *Vireya* (Argent, 2015). The classification was integrated for the convenience of indexing taxon names and summarizing ploidy levels, as these two publications are the most comprehensive and latest references for the respective groups. Irrespective of the positioning of the Indomalesian species as subgenus *Vireya* or the broad section *Schistanthe* (Goetsch et al., 2011; Shrestha et al., 2018; Khan et al., 2021), the group of species involved is still largely as described by Argent (2015). Taxa were recorded as polyploids if polyploidy was reported from either chromosome counting or flow cytometry. Reported ploidy, chromosome number and proportion of polyploid taxa were summarized for each taxonomic group.

3.2.2 Plant material collection and taxon identification

For flow cytometry, 263 accessions of ss. *Maddenia* taxa were selected from botanic and/or private gardens and nurseries in New Zealand (164) along with accessions from the Royal Botanic Garden Edinburgh (RBGE, 25), UK, and the Rhododendron Species Botanical Garden (RSBG, 74), USA (Table S3.2). Accessions from RBGE and RSBG are cultivated material of wild origin, while the New Zealand accessions consist of material from wild and horticultural sources. Herbarium specimens for New Zealand accessions are deposited in the Dame Ella Campbell Herbarium (MPN) at Massey University, Palmerston North, New Zealand. Living plants of the accessions in RBGE and RSBG are accessible at the corresponding organizations (Table S3.2).

All taxa of ss. *Maddenia* that have been previously reported for ploidy, except for *R. vanderbiltianum* (Atkinson et al., 2000) and *R. yungchangense* (Cubey, 2003), were included in the present study. Further to the taxa listed by Chamberlain et al. (1996), four taxa were separated from species complexes and analysed as distinct entities: *R. iteophyllum* (Mao et al., 2017b), *R. sinonuttallii* (Gibbs et al., 2011), *R. taronense* (Gibbs et al., 2011) and

R. valentinioides (ined.) (Gibbs et al., 2011; Donald, 2012). Three new species published post-1996 were examined: *R. pseudomaddenii* (Mao & Bhaumik, 2015), *R. leptocladon* (Rushforth & Nguyen, 2019) and *R. kuomeianum* (Chang et al., 2021). *R. vanderbiltianum* was also included because of its suggested placement in this subsection (Argent et al., 2008; Donald, 2012; MacKay et al., 2018). Individual accessions from New Zealand collections were identified following Davidian (1982), based on herbarium specimens and photographs taken in the field.

While fresh leaves were collected locally in New Zealand, overseas samples were silica-gel dried and imported from RBGE and RSBG to New Zealand. In both cases, fully expanded young leaves were routinely sampled for flow cytometry, although sometimes leaves from the previous season’s growth were used when young leaves were unavailable. Fresh samples from the New Zealand sites were chilled and shipped overnight to the laboratory for FCM ploidy estimation. For some local accessions, dehydrated leaf samples from herbarium specimens were used, as fresh or silica gel-dried leaf materials were unavailable at the time of the FCM experiment (Table S3.2). A subset of samples was replicated to verify the consistency of ploidy results for the same accession using fresh leaf *vs.* silica gel-dried leaf *vs.* dried leaf from an herbarium specimen.

Leaf tissue collected from *R. fortunei* was routinely used as the internal diploid standard for flow cytometry. When fresh leaves of *R. fortunei* were unexpectedly unavailable, *R. parryae* was used as the internal standard. Both species were previously reported as diploids (Ammal et al., 1950; Jones et al., 2007) and available as living plants for sampling. Analysis of a subset of samples was repeated to verify the consistency of ploidy results for the same accession using either of the diploid standards. Genome sizes of these two *Rhododendron* species were measured (Table S3.2), using *Pisum sativum* L. (2C = 8.8 pg) and *Zea mays* L. (2C = 5.33 pg) as standards.

3.2.3 Flow cytometry preparation and analysis

Cell nuclei suspensions from leaf tissue were prepared for flow cytometry following Doležel et al. (2007) with minor modifications. Both fresh and dehydrated leaf samples were processed using the same protocol at Manaaki Whenua – Landcare Research (Lincoln, New Zealand).

Approximately 1 cm^2 of leaf tissue of each sample was co-chopped with the diploid standard using a sharp razor blade in approximately 1 mL ice-cold Otto I buffer in a Petri dish, then left to incubate for 1–2 min at room temperature. The homogenate was filtered into a sample tube through a 20-µM nylon mesh to remove large particles. Next, DAPI (4′6-diamidino-2-phenylindole) stain, prepared with Otto II solution, was added to the sample tube at 4 µg/mL. The samples were run on a Partec PAII flow cytometer, using a 375 nm UV laser and FloMax software, until the particle count was at least 5000. Histogram peaks were manually gated for all samples. The relative fluorescence values of the peak positions of DAPI-stained nuclei (Mean-x) and the coefficient of variation (CV-x%) of the RN1/RN2 peak were evaluated. Where there was any uncertainty to gate a peak, the sample was run alone, then co-chopped with the diploid standard to confirm the peak of the standard. Data were transferred to an Excel spreadsheet from which the FCM ploidy (*x*) was calculated (Table S3.2). Genome size measurements of the two diploid standards of *Rhododendron* were performed using the same protocol and reagents, except that 10 µg/mL propidium iodide was used as the stain, and samples were run on a Partec CyFlow Space with a blue laser at 488 nm. Each plant sampled was measured sequentially in triplicate using leaves harvested on the same day, from which the average 2C value (pg) was calculated for the genome size.

3.2.4 Validation of FCM ploidy with meiotic chromosome counts

Chromosome counts were performed on a sub-sample of six accessions to validate the estimated ploidy levels from flow cytometry. Developing flower buds were harvested on sunny mornings in a local garden in New Zealand, mostly between 07:30 and 09: 30 a.m. Prior to the harvest, a series of observations was made to determine the correct stage of the meiotically dividing PMCs. Serial sampling of flower buds was performed during the growth of anthers. The outer layers of bud scales were removed before the buds were immersed in fixative (1 part of glacial acetic acid to 3 parts of absolute ethanol) for at least 24 h. Under a stereo microscope (Leica MZ9.5), young anthers were removed from the buds, mashed and stained with 1% acetocarmine. After removing the debris, slides with a coverslip were heated to ~50 °C for ~30 s and set aside for 1.5–2 h for deeper staining, followed by the final ‘squash’ onto the slide. The meiotic chromosomes of PMCs were observed under a compound microscope (Leica DM500) and images were captured with 100× objective under oil immersion.

3.3 Results

3.3.1 Taxonomic distribution of polyploidy in *Rhododendron*

Summary of ploidy levels from existing databases and the literature demonstrated that polyploidy occurs in five of the nine subgenera of *Rhododendron* (considering *Vireya* as a subgenus) (Tables 3.1 & S3.1). All subgenera have representative taxa investigated for ploidy levels. Of the total 424 taxa reported, 332 are diploids and 92 are polyploids. Subgenus *Rhododendron* contains the largest number of polyploid taxa, followed by subgenera *Vireya*, *Pentanthera*, *Hymenanthes* and *Azaleastrum* (in the descending order of the number of polyploid taxa reported). Sections *Rhododendron* (in subgenus *Rhododendron*) and *Schistanthe* (in subgenus *Vireya*) have the most polyploid taxa at the sectional level. Notably, subsections *Lapponica* and *Triflora* in section *Rhododendron* contain the most polyploid taxa at subsection level. In six subsections, all tested taxa were reported as polyploids, including subsections *Auriculata*, *Baileya*, *Cinnabarina*, *Heliolepida*, *Rhodorastra* and *Williamsiana*. Despite 424 taxa with chromosome counts or ploidy estimates reported to date, there remain some 952 *Rhododendron* taxa for which ploidy has not been studied (Fig. 3.2). Information on total taxa at a taxonomic level can be found in Tables 3.1 and S3.1.

Ploidy level is highly varied in *Rhododendron* taxa, including 2*x* (387 taxa), 3*x* (9), 4*x* (76), 5*x* (1), 6*x* (25), 8*x* (4) and 12*x* (1) (Table S3.1). Only diploids have been reported in four of the nine subgenera and several sections or subsections of the other five subgenera (Table 3.1; Fig. 3.2). Intraspecific ploidy variation has been observed in a total of 55 taxa in subgenera *Hymenanthes* (6), *Pentanthera* (7), *Rhododendron* (35) and *Vireya* (7). The highest number of intraspecific ploidy levels was revealed in the *R. maddenii* complex, with four levels in both *R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum*. Over the genus, polyploidy might be reported only from either chromosome counting or flow cytometry, when both methods have been used to study the same taxon. This discrepancy was observed in 22 taxa among the total 424 reported (Table S3.1). For example, polyploids were identified from only flow cytometry in subgenus *Vireya* and ss. *Rhodorastra* in subgenus *Rhododendron*. In such cases, these taxa were recorded as polyploids for examination of frequency of polyploidy in *Rhododendron* groups.

Table 3.1 Taxonomic distribution of polyploidy in *Rhododendron*. Values in parentheses indicate the number of (polyploid taxa)/(tested taxa)/(all taxa) in the corresponding groups. Ploidy data were combined from flow cytometry and chromosome counts. Taxa were counted as polyploids when there was an occurrence, even if diploids were also found. E.g., of the 38 taxa in subgenus *Azaleastrum*, 11 have been examined for ploidy, in which one taxon was reported with occurrence of polyploids. Taxonomic classification of genus *Rhododendron* is according to Chamberlain et al. (1996) and Argent (2015). Non-vireya taxon names were indexed following Chamberlain et al. (1996) while vireyas (subgenus *Vireya*) following Argent (2015). Other taxonomies may treat the subgenus *Vireya* in this table as the broad section *Schistanthe* under subgenus *Rhododendron* (Goetsch et al., 2011; Shrestha et al., 2018; Khan et al., 2021). *Chromosome counts of taxa in subsection *Saluenensia* by Cubey (2003) are not included due to inaccessibility of data. Reported ploidy data are in Table S3.1

Subgenus	Section	Subsection
Azaleastrum (1/11/38; 2 sections)	*Azaleastrum* (1/3/11) *Choniastrum* (0/8/27)	
Candidastrum (0/1/2)		
Hymenanthes (7/149/427; 1 section)	*Ponticum* (7/149/427; 24 subsections)	*Arborea* (1/4/17), *Argyrophylla* (0/7/31), *Auriculata* (1/1/2), *Barbata* (0/2/5), *Campanulata* (0/2/4), *Campylocarpa* (0/6/10), *Falconera* (1/9/17), *Fortunea* (1/11/51), *Fulgensia* (0/1/3), *Fulva* (0/3/4), *Glischra* (0/5/11), *Grandia* (0/9/17), *Griersoniana* (0/1/1), *Irrorata* (0/7/33), *Lanata* (0/1/9), *Maculifera* (0/5/24), *Neriiflora* (1/19/50), *Parishia* (0/3/8), *Pontica* (1/18/20), *Selensia* (0/5/12), *Taliensia* (0/19/75), *Thomsonia* (0/9/20), *Venatora* (0/1/1), *Williamsiana* (1/1/2)
Mumeazalea (0/1/1)		
Pentanthera (11/29/41; 4 sections)	*Pentanthera* (7/20/20) *Rhodora* (1/2/2) *Sciadorhodion* (3/6/18) *Viscidula* (0/1/1)	
Therorhodion (0/3/3)		
Tsutsusi (0/22/148; 2 sections)	*Brachycalyx* (0/5/34) *Tsutsusi* (0/17/114)	
Rhododendron (57/159/309; 2 sections)	*Pogonanthum* (1/8/26)	
	Rhododendron (56/151/283; 28 subsections)	*Afghanica* (0/0/1), *Baileya* (1/1/1), *Boothia* (0/4/8), *Camelliiflora* (0/1/1), *Campylogyna* (0/1/2), *Caroliniana* (0/1/2), *Cinnabarina* (3/3/8), *Edgeworthia* (0/3/3), *Fragariflora* (0/0/1), *Genestieriana* (0/1/1), *Glauca* (1/8/11), *Heliolepida* (4/4/8), *Lapponica* (17/27/52), *Ledum* (1/3/8), *Lepidota* (0/1/5), *Maddenia* (4/39/65), *Micrantha* (0/1/3), *Monantha* (0/1/4), *Moupinensia* (0/1/3), *Rhododendron* (0/3/3), *Rhodorastra* (4/4/7), *Saluenensia* (4/6/8)*, *Scabrifolia* (0/7/11), *Tephropepla* (0/3/10), *Trichoclada* (0/2/9), *Triflora* (16/22/40), *Uniflora* (1/2/5), *Virgata* (0/2/3)
Vireya (16/49/407; 7 sections)	*Albovireya* (1/2/16) *Discovireya* (0/4/41) *Hadranthe* (*Phaeovireya*) (2/5/54) *Malayovireya* (1/3/21)	
	Pseudovireya (1/5/17)	
	Schistanthe (11/28/244; 5 subsections)	*Euvireya* (7/11/121), *Linnaeopsis* (1/2/16), *Malesia* (2/8/60), *Saxifragoidea* (0/0/1), *Solenovireya* (1/7/46)
	Siphonovireya (0/2/14)	

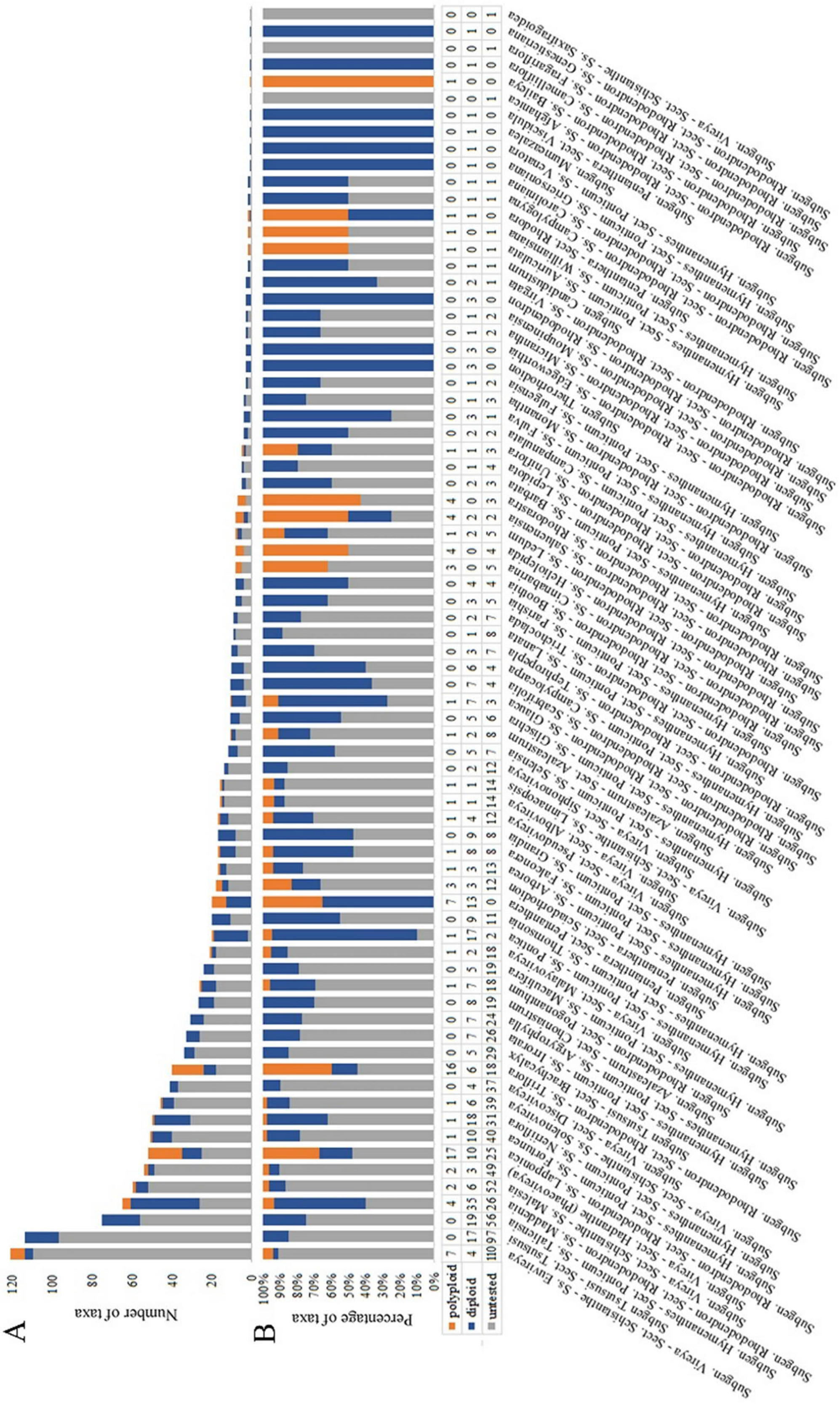

Figure 3.2 Extent of polyploidy in the reported taxa of *Rhododendron*. (A) Number of taxa. (B) Percentage of taxa. Bars are parallel in both graphs, following the descending order of the number of

taxa (A) in each taxonomic group. Each bar represents the reported polyploid taxa (orange), diploid taxa (blue) and untested taxa (grey) in the corresponding taxonomic group (subgenus, section, or subsection), with only the lowest levels listed. Taxa reported include species, subspecies and botanical varieties. A taxon was counted as a polyploid when there was an occurrence from either chromosome counting or flow cytometry. The bottom table shows taxon numbers of the reported ploidy levels in each group. Corresponding to Table 3.1, number of 'diploid' taxa = number of ('tested taxa' – 'polyploid taxa'), while number of 'untested' taxa = number of ('all taxa' – 'tested taxa'). Ploidy data were compiled from literature. Details are shown in Table S3.1

3.3.2 Ploidy levels of taxa in subsection *Maddenia*

3.3.2.1 Ploidy estimation using flow cytometry

Using flow cytometry, ploidy level was assigned to 263 accessions covering 47 of the ca.65 taxa in ss. *Maddenia*. These include 201 accessions of 45 taxa outside the *R. maddenii* complex and 62 accessions within the complex (*R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum* with their synonyms) (Tables 3.2 & S3.2). All taxa outside the *R. maddenii* complex were diploids, with 43 taxa reported using flow cytometry for the first time, among which 12 taxa had no previously reported ploidy data. Polyploids were only identified within the two subspecies of *R. maddenii*, and there were seven diploids as well as 55 polyploid accessions. At least one wild accession was tested for each of 43 taxa (a total of 135 wild accessions examined).

Table 3.2 Ploidy of subsection *Maddenia* in the present study in comparison to published ploidy levels compiled from the literature. Diploids are $2n = 2x = 26$. [1]Identified taxa in alphabetical order. Taxon list follows Chamberlain et al. (1996). [2]‘Yes’ indicates the first report of flow cytometry ploidy estimation from the present study, with chromosome counts reported previously. ‘*’ indicates the first ploidy report from the present study. ‘/’ indicates the accession was not considered as a distinct species, as it is an affinity or synonym and shown in the parentheses. Ploidy data in Table S3.2. [3]Identification of accessions undetermined for subspecific taxonomy in the complex, based on morphology, thus listed as the species. [4]Considered as a distinct species according to literature (M. Fang et al., 2005; Gibbs et al., 2011; Donald, 2012; Cox, 2013b; Mao & Bhaumik, 2015; Mao et al., 2017a; Chang et al., 2021). #Reported as a polyploid from a single accession (Cubey, 2003; Khan et al., 2021)

Ss. *Maddenia* taxon[1]	Present study			Reported 2*n* or *x*
	No. of acc. (wild)	FCM ploidy (no. of acc.)	First report here[2]	
R. burmanicum	8 (1)	2*x*	yes	26
R. carneum	3 (0)	2*x*	no	26; 4*x*#
R. changii	1 (1)	2*x*	yes*	
R. ciliatum	9 (4)	2*x*	yes	26
R. ciliicalyx	4 (2)	2*x*	yes	26
R. ciliipes	3 (2)	2*x*	yes*	
R. coxianum	1 (1)	2*x*	yes	26
R. crenulatum	1 (1)	2*x*	yes	26
R. cuffeanum	1 (1)	2*x*	yes	26
R. dalhousiae var. *dalhousiae*	6 (4)	2*x*	no	26; 2*x*
var. *rhabdotum*	5 (1)	2*x*	yes	26
R. dendricola	8 (4)	2*x*	yes	26
R. excellens	8 (7)	2*x*	yes	26
R. fletcherianum	3 (2)	2*x*	yes	26
R. fleuryi	1 (1)	2*x*	yes	26
R. formosum[3]	5 (3)	2*x*	/	/
var. *formosum* (*R. formosum*)	9 (1)	2*x*	yes	26
(*R. iteophyllum*[4])	3 (0)	2*x*	yes	c.26
var. *inaequale*	2 (1)	2*x*	yes	26
(*R.* aff. *formosum*)	1 (1)	2*x*	/	/
R. goreri	2 (2)	2*x*	yes*	
R. horlickianum	5 (2)	2*x*	yes	26
R. johnstoneanum	8 (3)	2*x*	yes	26
R. kiangsiense	1 (1)	2*x*	yes*	
R. kuomeianum[4]	1 (1)	2*x*	yes*	
R. leptocladon[4]	3 (3)	2*x*	yes	26
R. levinei	2 (2)	2*x*	yes*	
(*R.* aff. *levinei*)	1 (1)	2*x*	/	/
R. liliiflorum	5 (5)	2*x*	yes	26
R. lindleyi	10 (3)	2*x*	no	26; 2*x*
R. ludwigianum	4 (3)	2*x*	yes	26
R. lyi	5 (3)	2*x*	yes	26
(*R.* aff. *lyi*)	1 (1)	2x	/	/
R. maddenii[3]	6 (6)	2*x* (1), 6*x* (4), 8*x* (1)	/	26, 52, 78, 104; 2*x*, 6*x*, 8*x*
R. maddenii ssp. *maddenii*	8 (6)	4-6*x*? (1), 5*x* (1), 6*x* (4), 6-7*x*? (1), 8*x* (1)	no	26 (only in synonym *R. calophyllum*), 52, 78; 6*x*
(*R. maddenii*)	20 (5)	2*x* (1), 6*x* (14), 7*x* (2), 8*x* (3)	/	/
(*R. brachysiphon*)	3 (0)	6*x* (3)	/	/

Ss. *Maddenia* taxon[1]	Present study			Reported 2*n* or *x*
	No. of acc. (wild)	FCM ploidy (no. of acc.)	First report here[2]	
(*R. polyandrum*)	2 (2)	6*x* (2)	/	/
R. maddenii ssp. *crassum*	13 (11)	2*x* (5), 5-6*x*? (1), 8*x* (7)	no	52, 78, 104; 6*x*, 8*x*
(*R. crassum*)	6 (1)	5*x*? (1), 8*x* (3), 7*x* (2)	/	/
(*R. manipurense*)	4 (1)	6*x* (1), 8*x* (3)	/	78, 156
R. megacalyx	5 (2)	2*x*	yes	26
R. nuttallii	9 (6)	2*x*	yes	26
(var. *stellatum*)	2 (0)	2*x*	/	/
R. pachypodum	3 (2)	2*x*	yes	26
(*R. supranubium*)	3 (0)	2*x*	/	26
R. parryae	3 (1)	2*x*	yes	26
R. pseudociliipes	3 (3)	2*x*	yes[*]	
R. pseudomaddenii[4]	1 (1)	2*x*	yes[*]	
R. roseatum	1 (1)	2*x*	yes	26
R. scopulorum	6 (4)	2*x*	yes	26
R. sinonuttallii[4]	2 (0)	2*x*	yes	26
R. surasianum	1 (1)	2*x*	yes[*]	
R. taggianum	5 (1)	2*x*	yes	26
R. taronense[4]	3 (0)	2*x*	yes	c.104[#]
R. valentinianum var. *oblongilobatum*	3 (2)	2*x*	yes[*]	
R. aff. *valentinianum*	1 (0)	2*x*	/	/
R. valentinioides (ined.)[4]	1 (1)	2*x*	yes[*]	
(*R.* aff. *valentinioides* (ined.))	1 (1)	2*x*	/	/
R. veitchianum	6 (5)	2*x*	yes	26
(*R. cubittii*)	5 (1)	2*x*	/	26
R. walongense	2 (2)	2*x*	yes	26
R. wumingense	1 (1)	2*x*	yes[*]	

When 20 accessions that had been first evaluated from fresh leaves were replicated using dehydrated samples (silica gel-dried or herbarium specimen), ploidy of the seven diploid taxa was consistent, regardless of how the sample was dried. For silica gel-dried samples, FCM ploidy was generally the same as from fresh leaves (Tables 3.3 & S3.3). Among the 13 tested polyploids from the *R. maddenii* complex, nine samples showed reproducible ploidy levels, while ploidy for four accessions was not certainly determined. However, when herbarium specimens were used for the same accessions, the ploidy level was the same as using fresh leaves for only three of the polyploid accessions. Polyploidy was not determined for three accessions, or one level lower than ploidy estimated from fresh leaves for five accessions (Table 3.3).

As two species were used as the diploid standard, replicate samples of the *R. maddenii* complex were tested to validate FCM ploidy using both standards. Interestingly, all 10 polyploid accessions showed discrepant ploidy results between the two runs (Tables 3.4 & S3.3). Ploidy estimation using *R. parraye* was one or two levels lower than that using *R. fortunei*, and there was a higher incidence of odd-numbered results with the *R. parryae* standard. Further examination demonstrated that the genome size of *R. parryae* (2C = 1.70–1.75 pg) was larger than *R. fortunei* (2C = 1.52–1.57 pg) (Table S3.4). This explains the lower FCM ploidy level calculated for the same accession, when using the former as the diploid standard.

Table 3.3 Flow cytometry estimates of ploidy level for samples from fresh and dehydrated leaves (silica gel-dried or air-dried herbarium sample). [1]All samples were analysed using *R. fortunei* as the diploid standard. FCM histograms of accessions with inconsistent ploidy in different runs are shown in Table S3.3

Ss. *Maddenia* taxon	Acc. ID	FCM ploidy[1]	Leaf sample
R. burmanicum	OM55	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium
R. ciliicalyx	OM06	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium
R. dalhousiae var. *dalhousiae*	OM32	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium
R. excellens	OM34	2*x*	fresh
		2*x*	silica gel-dried
		Aneuploid < 2*x*?	herbarium
R. formosum var. *formosum*	OM43	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium
R. maddenii ssp. *crassum*	OM17	8*x*	fresh
		8*x*	silica gel-dried
		8*x*	herbarium
	OM47	8*x*	fresh
		8*x*	silica gel-dried
		2*x*	herbarium
R. maddenii ssp. *maddenii*	OM02	6*x*	fresh
		6*x*	silica gel-dried
		5*x*	herbarium
	OM11	6*x*	fresh
		6*x*	silica gel-dried
		6*x*	herbarium
	OM14	8*x*	fresh
		8*x*	silica gel-dried
		2*x*? / 8*x*?	herbarium
	OM18	6*x*	fresh
		6*x*	silica gel-dried
		5*x*	herbarium
	OM20	6*x*	fresh
		6*x*	silica gel-dried

Ss. *Maddenia* taxon	Acc. ID	FCM ploidy[1]	Leaf sample
		5*x*	herbarium
	OM46	6*x*	fresh
		5–6*x*?	silica gel-dried
		5*x*	herbarium
	OM48	7*x*	fresh
		2*x*? / 7*x*?	silica gel-dried
		6–7*x*	herbarium
	OM49	6*x*	fresh
		5–6*x*?	silica gel-dried
		6*x*	herbarium
	OM54	6*x*	fresh
		5–6*x*?	silica gel-dried
		5*x*	herbarium
	OM56	6*x*	fresh
		6*x*	silica gel-dried
		2*x*	herbarium
	OM58	6*x*	fresh
		6*x*	silica gel-dried
		6*x*	herbarium
R. sinonuttallii	OM57	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium
R. taronense	OM40	2*x*	fresh
		2*x*	silica gel-dried
		2*x*	herbarium

Table 3.4 Flow cytometry ploidy estimates of samples repeated with two diploid standards. [1]All results based on fresh leaves. FCM histograms shown in Table S3.3

Ss. *Maddenia* taxon	Acc. ID	FCM ploidy[1]	Diploid standard
R. maddenii ssp. *crassum*	PK22	8*x*	*R. fortunei*
		7*x*	*R. parryae*
	PK45	7*x*	*R. fortunei*
		6*x*	*R. parryae*
	PK59	6*x*	*R. fortunei*
		5*x*	*R. parryae*
	PK61	7*x*	*R. fortunei*
		6*x*	*R. parryae*
R. maddenii ssp. *maddenii*	PK09	7*x*	*R. fortunei*
		5*x*	*R. parryae*
	PK17	8*x*	*R. fortunei*
		7*x*	*R. parryae*
	PK27	6*x*	*R. fortunei*
		5*x*	*R. parryae*
	PK38	6*x*	*R. fortunei*
		5*x*	*R. parryae*
	PK52	6*x*	*R. fortunei*
		5*x*	*R. parryae*
	PK68	6*x*	*R. fortunei*
		5*x*	*R. parryae*

3.3.2.2 Meiotic chromosome counts in representative samples

Representative accessions were selected for meiotic chromosome counting to validate the FCM ploidy estimates (Fig. 3.3). The observed samples included four diploids, one hexaploid (OM20 *R. maddenii* ssp. *maddenii*, Fig. 3.3F) and one octoploid (OM17 *R. maddenii* ssp. *crassum*, Fig. 3.3E). The validated diploid accessions were: OM01 *R. formosum* var. *inaequale* (Fig. 3.3A), OM06 *R. ciliicalyx* (Fig. 3.3B), OM41 *R. carneum* (Fig. 3.3C), and OM55 *R. burmanicum* (Fig. 3.3D). The ploidy results demonstrated consistency with those obtained from flow cytometry, as well as those from previously reported chromosome numbers (Table 3.2).

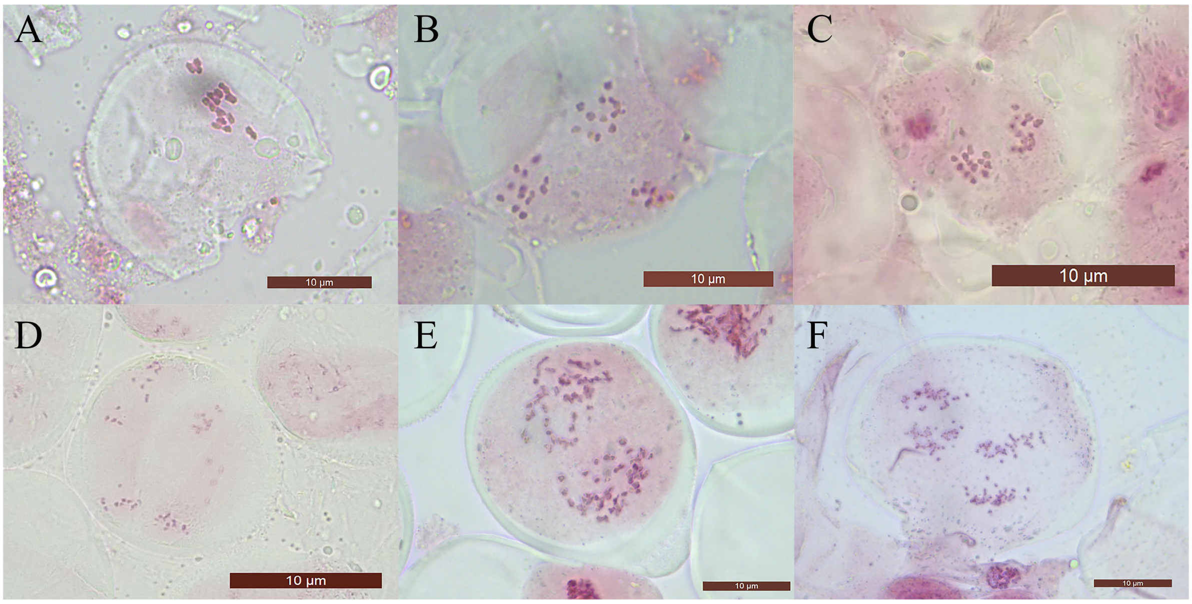

Figure 3.3 Meiotic chromosomes of ss. *Maddenia* taxa sampled from flower buds, with ploidy levels. (A) OM01, *R. formosum* var. *inaequale*, *n* = 13, 2*x*. (B) OM06, *R. ciliicalyx*, *n* = 13, 2*x*. (C) OM41, *R. carneum*, *n* = 13, 2*x*. (D) OM55, *R. burmanicum*, *n* = 13, 2*x*. (E) OM17, *R. maddenii*, *n* = 52, 8*x*. (F) OM20, *R. maddenii*, *n* = 39, 6*x*. All scale bars 10 µm

3.4 Discussion

3.4.1 High ploidy variation in genus *Rhododendron*, with the most frequent polyploidy in subgenera *Pentanthera* and *Rhododendron*

The summary dataset (Fig. 3.2) is the first and most systematic compilation of the ploidy levels of *Rhododendron* species to date. It reveals that 31% of the 1,376 *Rhododendron* taxa have been examined for ploidy while 69% are yet to be investigated. Because databases such as

CCDB do not currently cover all the *Rhododendron* taxa that have been reported, the datasheet (Table S3.1) can be used to update the relevant databases. Of the taxa for which data have been reported, 78% (332) (24% of all *Rhododendron* taxa) are diploids while polyploidy has been found in 22% (92) (7% of all) taxa (Ammal et al., 1950; Väinölä, 2000; Rice et al., 2015; Khan et al., 2021). The larger subgenera (*Azaleastrum, Hymenanthes, Pentanthera, Rhododendron, Vireya*) all exhibit polyploidy to some degree, while in the smaller subgenera (*Candidastrum, Mumeazalea*, *Therorhodion*) and subgenus *Tsutsusi*, all species tested thus far are diploids. The highest frequency of polyploids is in subgenus *Pentanthera* (38% of the reported in this subgenus) then subgenus *Rhododendron* (36%) (Table 3.1), which agrees with the findings in Jones et al. (2007). The highest ploidy variation is found in subgenus *Rhododendron*, ranging from triploid ($3x = 39$) to dodecaploid ($12x = 156$) (Table S3.1). Particularly, taxa reported in subsections *Baileya*, *Cinnabarina*, *Heliolepida*, *Rhodorastra* of subgenus *Rhododendron* are all polyploids (Fig. 3.2; Table 3.1). Chromosome counts for most of the taxa support that the basic chromosome number in genus *Rhododendron* is $x = 13$ ($2n = 26$), although $2n = 24$ has been reported in seven taxa (Table S3.1). This difference may result from accessions that were rare aneuploids (Jones & Brighton, 1972b), or likely miscounts due to technological limitations at the time of early cytological studies of *Rhododendron* (Bowers, 1930).

Natural ploidy series, with both diploids and polyploids, have been reported in several taxa of *Rhododendron*. Ploidy variation has been reported among species in complexes such as *R. maddenii*, *R. telmateium* and *R. yunnanense*, as well as polyploid series within species *R. flavidum* and *R. occidentale* (Table S3.1). Jones et al. (2007) proposed that the polyploid series within *R. occidentale* was from species diversification while that within *R. flavidum* may result from an unresolved species boundary with *R. calendulaceaum*. Ploidy variation could arise from intraspecific variability (i.e., cytotype diversity) (Husband et al., 2013; Farhat et al., 2019) and reflects the high diversification rate of flora in the Himalayan region (Schwery et al., 2015; Yan et al., 2015; Shrestha et al., 2018). However, it could also be related to the unresolved taxonomy. That is, in cases where multiple taxa have been ‘lumped’ into one, it is possible that one or some of the previously recognised taxa had a particular ploidy level, which presents as a series within a set of accessions that encompass the synonymous taxa. A third issue might be incorrect field labelling leading to incorrect grouping of samples, although this could be greatly improved with morphological identification by the researcher. This identification issue was also addressed for taxonomic correction in studies of other plant genera such as *Deutzia* Thunb.

(Hydrangeaceae) (Hembree et al., 2020). Resolving the taxonomy of polyploid complexes will significantly inform decision making on conservation of biodiversity at several levels (e.g., phenotypic, phylogenetic or species diversity) (Ennos et al., 2005; Laport & Ng, 2017).

Notably, a discrepancy among ploidy levels was found between chromosome counts and flow cytometry reported in previous studies of *Rhododendron*. Polyploids were identified only from either flow cytometry (e.g., subgenus *Vireya*, subsection *Rhodorastra*) or chromosome counting (e.g., *R. baileyi*) when both methods have been applied (Table S3.1). This occasional discrepancy is observed more likely from the two largest ploidy studies of *Rhododendron*: Ammal et al. (1950) using chromosome counting and Khan et al. (2021) using flow cytometry. Limited coverage of samples might be the primary reason for this discrepancy, such that intraspecific ploidy variation was not captured. Another factor that may influence the ploidy discovered is more recent sampling from garden cultivation rather than from the wild, as in cultivation there may be more polyploids due to their favourable horticultural features (Jones et al., 2008; Rodionov et al., 2019). Given that flow cytometry is less time-consuming than chromosome counting, additional sampling for flow cytometry from wild populations should be considered to further understand the ploidy variation in *Rhododendron* taxa.

3.4.2 Subsection *Maddenia* consisting of diploids except for the *R. maddenii* complex

Ploidy estimations using flow cytometry present the most comprehensive ploidy analysis of ss. *Maddenia* reported to date. Ploidy of 12 taxa is reported for the first time, increasing the known number of diploid taxa in this subsection to 47 of the total 51 taxa studied (Tables 3.2 & S3.2). In agreement with previous studies, polyploids are present in ss. *Maddenia*, but only in the two subspecies of *R. maddenii*. The only two polyploid exceptions reported outside the *R. maddenii* complex were one octoploid ($2n$ = ca.104) *R. taronense* (Cubey, 2003) and one tetraploid ($4x$) *R. carneum* (Khan et al., 2021), but both were from one accession only. FCM results from multiple accessions together with other previous chromosome counts identified only diploids in both species, supporting the conclusion that these two species are diploids (Tables 3.2 & S3.1).

The *R. maddenii* complex reveals a ploidy series consisting of diploids and polyploids varying from pentaploid to octoploid (5–$8x$) (Table 3.2). This is consistent with the previous reports from flow cytometry (Jones et al., 2007; De et al., 2010; Khan et al., 2021), where hexaploids (6*x*) and octoploids (8*x*) were reported. Tetraploids ($2n = 52$) were identified in previous chromosome counts but not in the present study (Ammal et al., 1950; Darlington et al., 1955). However, it is not known whether the polyploid complex within *R. maddenii* results from intraspecific variability or a combination of ploidy levels due to the ‘lumped’ taxa. Also, data are lacking as to whether the *R. maddenii* polyploids are allopolyploids or autopolyploids. Cubey (2003) proposed an autopolyploid origin of the polyploids in *R. maddenii*, when there were no distinguishable morphological characters among plants of different ploidy levels, and diploids were rarely found in this species. Although *R. maddenii* was assessed as a species of Least Concern in the Red List (Gibbs et al., 2011), the two putative subspecies should be studied to determine whether the synonymous taxa require species recognition, which might result in a revision of their conservation status.

In the whole genus, natural anisoploidy is not common, although triploids (3*x* or $2n = 39$) have been reported in nine species and a pentaploid (5*x*) in one species (Table S3.1). This study of ss. *Maddenia* revealed some anisoploids (5*x*, 7*x*) in the *R. maddenii* complex (Table 3.2). More *Rhododendron* anisoploids, usually triploids, are bred for horticulture, but little is known about their reproductive biology (Li, 1957b; Jones & Ranney, 2009). The pentaploid (5*x*) and heptaploid (7*x*) plants in the present study do produce flowers, but their fertility and the mechanism as to how these anisoploids arose await further investigation.

In general, *R. maddenii* ssp. *crassum* tends to present a higher ploidy level with more octoploids (8*x*) than *R. maddenii* ssp. *maddenii* which includes more hexaploids (6*x*) (Tables 3.2 & S3.1). This may be an infraspecific distinction and related to the geographic distribution of the two subspecies. Cullen (1980) compared the geographic distribution of the two subspecies of *R. maddenii*. While he suggested that the morphological variation in *R. maddenii* was unrelated to geography, results in the present study show a possible trend in the ploidy levels between the two subspecies. However, the relationship between ploidy and geographic pattern in this species complex is still under investigation and requires further carefully structured field surveys.

The *R. maddenii* complex shows a similar pattern of ploidy variation and geographic distribution as the genus *Buddleja* L. (Scrophulariaceae) which is also from the Sino-Himalayan region (Cullen, 1980; Chen et al., 2007). One hypothesis for the ploidy differences between the two subspecies of *R. maddenii* may be the ongoing *in situ* speciation in this area (Hughes, 2017).

As one of the world's youngest mountain ranges, with a high frequency of polyploidy in plants, the Sino-Himalayan region has been identified as a centre of species diversification that may be attributed to polyploidization (Irving & Hebda, 1993; Schwery et al., 2015; Xing & Ree, 2017; Shrestha et al., 2018; Rice et al., 2019; Xia et al., 2021). However, the Sino-Himalayan origin does not explain why polyploids should have continued to occur in *R. maddenii*, while other species in ss. *Maddenia* which are predominantly from the same region do not exhibit polyploids. Further research on a wider range of wild samples, from across the geographic range, and particularly from the *R. maddenii* complex, would inform this question.

3.4.3 Flow cytometry as a useful tool for estimating ploidy level of *Rhododendron,* even with dehydrated leaves

Despite few reports in previous studies (De Schepper et al., 2001; Jones et al., 2007; Khan et al., 2021), the consistency of ploidy identified by flow cytometry and meiotic chromosome counts in the present study supports the reliability of flow cytometry for ploidy estimation of *Rhododendron* (Fig. 3.3). The trial with replicated samples verified higher reliability of silica gel-dried over herbarium leaves of *Rhododendron* for FCM ploidy assessment (Table 3.3). Although not preferred, dehydrated, particularly silica gel-dried leaf tissue, has been successful in other plant groups for ploidy estimation with the standard DAPI protocol using flow cytometry, thereby eliminating the inconvenience of collecting and preserving fresh samples (Šmarda, 2006; Šmarda & Stančík, 2006; Suda & Trávníček, 2006; Farhat et al., 2019; Tomaszewska et al., 2021). The efficiency of flow cytometry with dehydrated leaves from herbarium specimens might be limited by several factors, including insufficient amount of tissue, sampling of mature leaves rather than newly expanding ones, incorrect drying, storage and preservation of samples, and the limited efficacy of nuclei isolation due to degradation (Tomaszewska et al., 2021).

Although flow cytometry can be convenient for ploidy determination of a large number of samples, especially for identifying the frequency of polyploids (Jones et al., 2007; Kron et al., 2007; Hembree et al., 2020; Tomaszewska et al., 2021), this technique may not always yield definitive results (Suda et al., 2006). In the results for all samples that were interpreted as polyploids, histogram peaks of the higher-ploidy samples tended to be significantly lower than that of the diploid standard. Such small peaks may be missed, or the decision between diploid or polyploid may be difficult to interpret in data analysis (Table S3.3). In addition, in some cases the ratio of two peaks on the histogram was near the midpoint between euploids, and the interpreted ploidy was therefore approximate (e.g., PK17 *R. maddenii* ssp. *maddenii*: 7–8*x*; Tables 3.4 & S3.3). In such cases, samples were repeated without co-chopped standard tissue, to verify the results. In addition, the use of two diploid standards (*R. fortunei* and *R. parryae*) due to constraints on availability of fresh material in some gardens, brought further challenge to interpreting the ploidy of some accessions. Differing values of DNA contents from different standards slightly change the calculated ploidy ratio, particularly for polyploids. The results for *R. fortunei* and *R. parryae* fall within the range of genome sizes of reported *Rhododendron* diploids (Bou Dagher-Kharrat et al., 2013; Khan et al., 2021; Choi et al., 2022). However, the larger genome size of *R. parryae* likely caused the interpreted ploidy for the same accessions being one level lower than using *R. fortunei* as the standard (Tables 3.4 & S3.4). Consistent use of a single standard in a study is therefore recommended, and further use of these two *Rhododendron* species as diploid standards is anticipated in future research for the genus. Nevertheless, due to the degree of unavoidable uncertainty of ploidy determination by flow cytometry, chromosome counting is still the ‘gold standard’ approach to determining ploidy level.

In previous studies, most *Rhododendron* chromosome counts were made from root tips grown from seed (Jones et al., 2007; De et al., 2010; Zaytseva et al., 2018). However, this may introduce errors in the ploidy determination, as seedlings from species in cultivation are likely to be from open-pollinated seeds and hence may be hybrids. For this reason, developing stamens in flower buds were used as the source of tissue for chromosome counts, which requires careful observation of the timing of flower bud development. *Rhododendron* flower buds move into dormancy shortly after flower differentiation. The onset and duration of rest depend upon the presence of the flower bud scales (Schneider, 1968). Mirgorodskaya et al. (2015) reported that the microspores of the evergreen species *R. catawbiense* in Russia underwent meiosis at the end of the summer (i.e., in August) and overwintered at the vacuolization stage. Mitosis with the formation of bicellular pollen grains occurred shortly before flowering at the beginning of summer in the following year (i.e., in June). In light of these observations, flower buds with dividing microspore mother cells should be harvested after blooming and close to winter dormancy, at the late stage of flower differentiation. However, it may take the entire season to observe development and identify the correct stage for sampling. Meiotic chromosomes can only be observed once the buds are dissected under the microscope after fixation and staining, which increases the difficulty of harvesting inflorescence buds at the desired development stage and requires constant sampling in the field. *Rhododendron* chromosomes are small and difficult to view under the microscope (Jones et al., 2007), which makes it more difficult to assess polyploids with multiple sets of chromosomes (Windham et al., 2020). In some cases, even a physical chromosome count cannot confirm the number of chromosomes, due to overlapping chromosomes, or abnormal chromosome behaviours (e.g., lagging chromosomes) in polyploids (Li, 1957b; Contreras et al., 2007). Other possible approaches to ploidy estimation such as targeted capture sequencing may allow discovery of polyploid characteristics (Viruel et al., 2019; Tahir et al., 2020).

3.5 Conclusion

Phylogenetic analysis, commonly used to provide knowledge on species relationships and in turn for conservation planning, can be confounded by the presence of polyploids in a set of samples. In the ‘big genus’ (Frodin, 2004) *Rhododendron* that presents both complex taxonomy and considerable conservation problems, prior studies reported polyploids in several species. The taxonomic distribution of polyploidy in the whole genus was investigated, and particularly ploidy levels of taxa in ss. *Maddenia*. Polyploidy occurs across the genus with 22% polyploids among the reported 424 species, with the highest frequency in subgenera *Pentanthera* and *Rhododendron*. However, the genus remains largely underexamined for ploidy, with no report for 69% of *Rhododendron* taxa.

Flow cytometry is a suitable tool for ploidy estimation in *Rhododendron*. When fresh tissue is unavailable, silica gel-dried leaves are more reliable than leaves from herbarium samples. Ploidy for 47 taxa in ss. *Maddenia* was estimated using flow cytometry, including 12 taxa that had never been investigated in previous studies. In this subsection, polyploids have been definitively identified in only the *R. maddenii* complex, where its two subspecies exhibit ploidy series consisting of diploids and various polyploidy levels. The ploidy variation in the *R. maddenii* complex may be a factor of the unresolved taxonomy or of the diversification of the species across a broad geographic range. Broader sampling from wild population should be considered in future research to resolve the relationship between taxon geography and ploidy levels.

Current botanic garden accessions of ss. *Maddenia*, especially those from the wild, can be analysed with next-generation sequences mapped against published *Rhododendron* genomes (Zhang et al., 2017; Soza et al., 2019; F.-S. Yang et al., 2020; Ma et al., 2021; X. J. Zhou et al., 2022) to understand character evolution, especially for those characters used to resolve species taxonomy. More immediately, the present samples tested for ploidy estimations prompt the phylogenetic study of ss. *Maddenia* in Chapter 4. Eventually, knowledge of resolved taxonomic debates will underpin the priorities in ss. *Maddenia* for conservation actions.

Supplementary Files

Supplementary files of Chapter 3 are attached in Appendix II.

Table S3.1 Reported ploidy of taxa in *Rhododendron* L. (Ericaceae), $2n = 2x = 26$

Table S3.2 Ploidy estimation of taxa in subsection *Maddenia* in the present study, using flow cytometry

Table S3.3 Flow cytometry histograms of subsection *Maddenia* accessions with inconsistent ploidy in different runs

Table S3.4 Genome size measurements of *R. fortunei* Lindl. and *R. parryae* Hutch.

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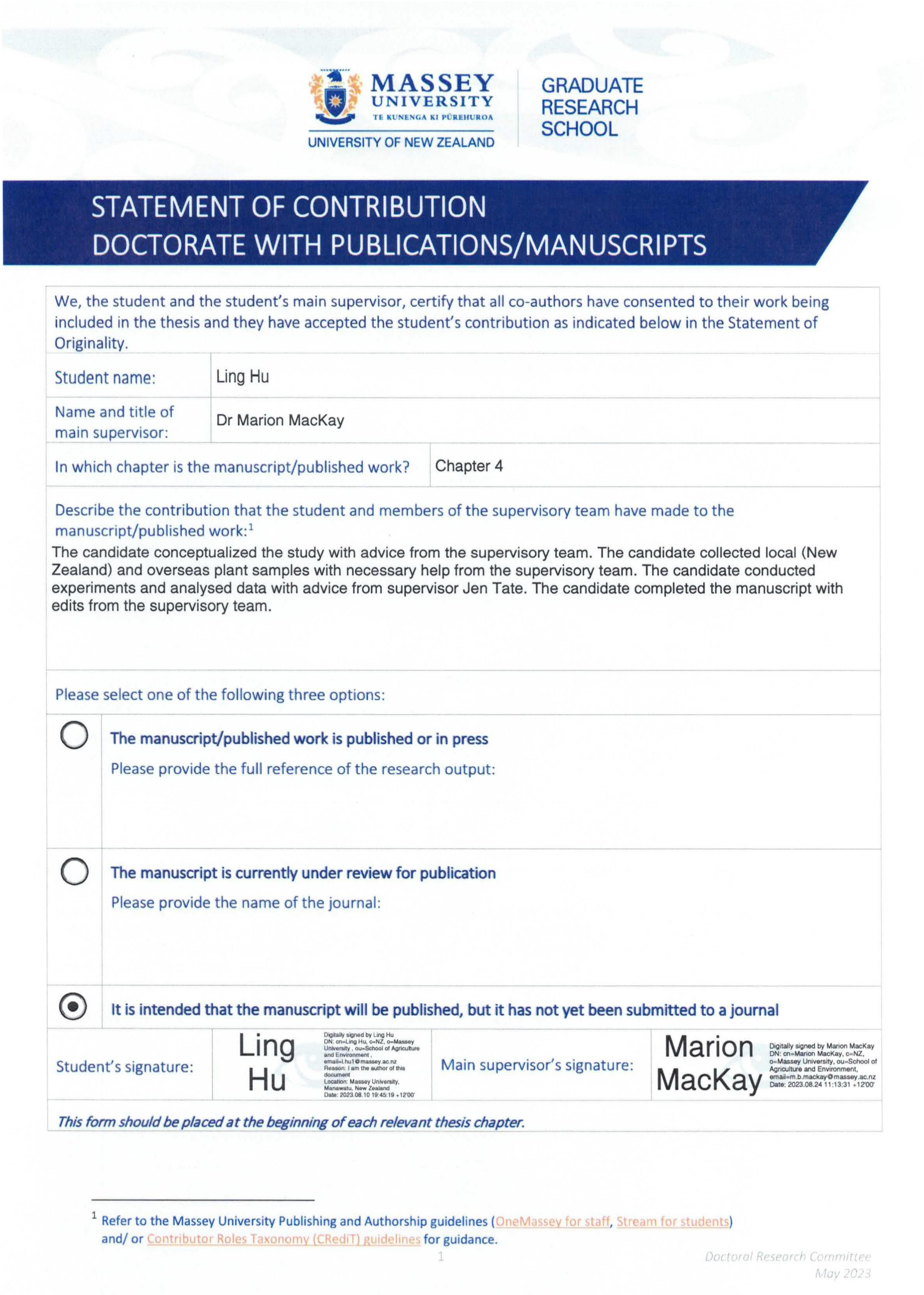
Statement of Contribution – Chapter 4



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The candidate conceptualized the study with advice from the supervisory team. The candidate collected local (New Zealand) and overseas plant samples with necessary help from the supervisory team. The candidate conducted experiments and analysed data with advice from supervisor Jen Tate. The candidate completed the manuscript with edits from the supervisory team.

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Chapter 4

Understanding molecular phylogeny of *Rhododendron* species and its conservation implications: Subsection *Maddenia* as a case study

Abstract

Taxonomic complexity is problematic in species prioritisation when deciding conservation action. The 'big genus' *Rhododendron* illustrates this problem as it has many species that are not well defined, thus hindering conservation assessments and decision making. The species of *Rhododendron* subsection *Maddenia* are notable for their extent of taxonomic uncertainty. Valued in horticulture because of their showy flowers, about half of the species in the subsection are of conservation concern. Yet, this group has not been the focus of a molecular phylogenetic study. Here, phylogenetic analysis was conducted with target capture DNA sequencing data from 40 of the total 65 taxa in subsection *Maddenia*. Replicate samples of taxa were used to assess taxon delimitation. The overall phylogeny was found to reflect species relationships inferred from morphology, although some species were not monophyletic. Polyploidisation exclusively in the *R. maddenii* complex was confirmed but did not affect the overall phylogenetic interpretation of the results. As previous studies have suggested, subsection *Maddenia* is likely paraphyletic, with species of subsections *Edgeworthia*, *Boothia* and *Triflora* phylogenetically nested within it. Conservation actions for several species are proposed based on their delimitation as clades.

Key words: Conservation; herbarium identification; polyploid; species delimitation; target capture sequencing; taxonomic complexity

4.1 Introduction

Clear species boundaries are important in species prioritisation for biodiversity conservation (Ennos et al., 2005). ‘Taxonomic complexity’ usually indicates that species delimitation (i.e. determining the boundaries among species) is ambiguous and occurs where morphological features are highly variable, particularly in ‘big genera’ of more than 500 species, which have high variation at the specific and intraspecific levels (Frodin, 2004). When morphological features are not able to provide sufficient evidence to resolve species taxonomy, a molecular phylogeny is required to resolve species boundaries and species complexes, which then informs conservation assessment (Heywood et al., 2006). As conservation action is based on defined species, debates on species’ taxonomic status as well as lack of taxonomic expertise will hinder the determination of species’ conservation status (Hollingsworth, 2003).

Rhododendron L. (Ericaceae) is one example of a ‘big genus’ that frequently encounters such taxonomic problems in conservation assessments (Gibbs et al., 2011). In this genus, some 52% of the more than 1,000 species are under risk of extinction (25% threatened, 27% Near Threatened or Data Deficient) (Gibbs et al., 2011; MacKay et al., 2018). *Rhododendron* species often encounter taxonomic debates, which can confuse decisions on their conservation status (Gibbs et al., 2011). Taxonomic complexity (i.e., species not well defined), plus lack of a recent and comprehensive taxonomic revision, makes species prioritization for conservation difficult to decide. Thorough understanding on species delimitation may lead to strategic changes on conservation priority, which has been seen in case studies for the examples of *R. protistum* var. *giganteum* in relation to *R. protistum* var. *protistum* (Li et al., 2018), and *R. amesiae* (Ao et al., 2022).

Taxonomic complexity of *Rhododendron* is reflected in the repeated re-organisation of species groupings over time. Taxonomists have used two classification hierarchies for *Rhododendron* and its species: one is genus – series – subseries (Stevenson, 1930; Davidian, 1982), while the other is genus – subgenus – section – subsection (Sleumer, 1949; Cullen, 1980; Chamberlain et al., 1996). Davidian (1982), following the first form of hierarchy, provided a comprehensive taxonomic key to *Rhododendron* species, as well as descriptions for each species. In contrast, using the second form of hierarchy, Chamberlain et al. (1996) provided the most recent comprehensive taxon checklist for the genus, but without species descriptions. Chamberlain et al. (1996) largely follow the taxonomic organisation used by Cullen (1980), where several species described by Davidian (1982) were 'lumped' as synonyms.

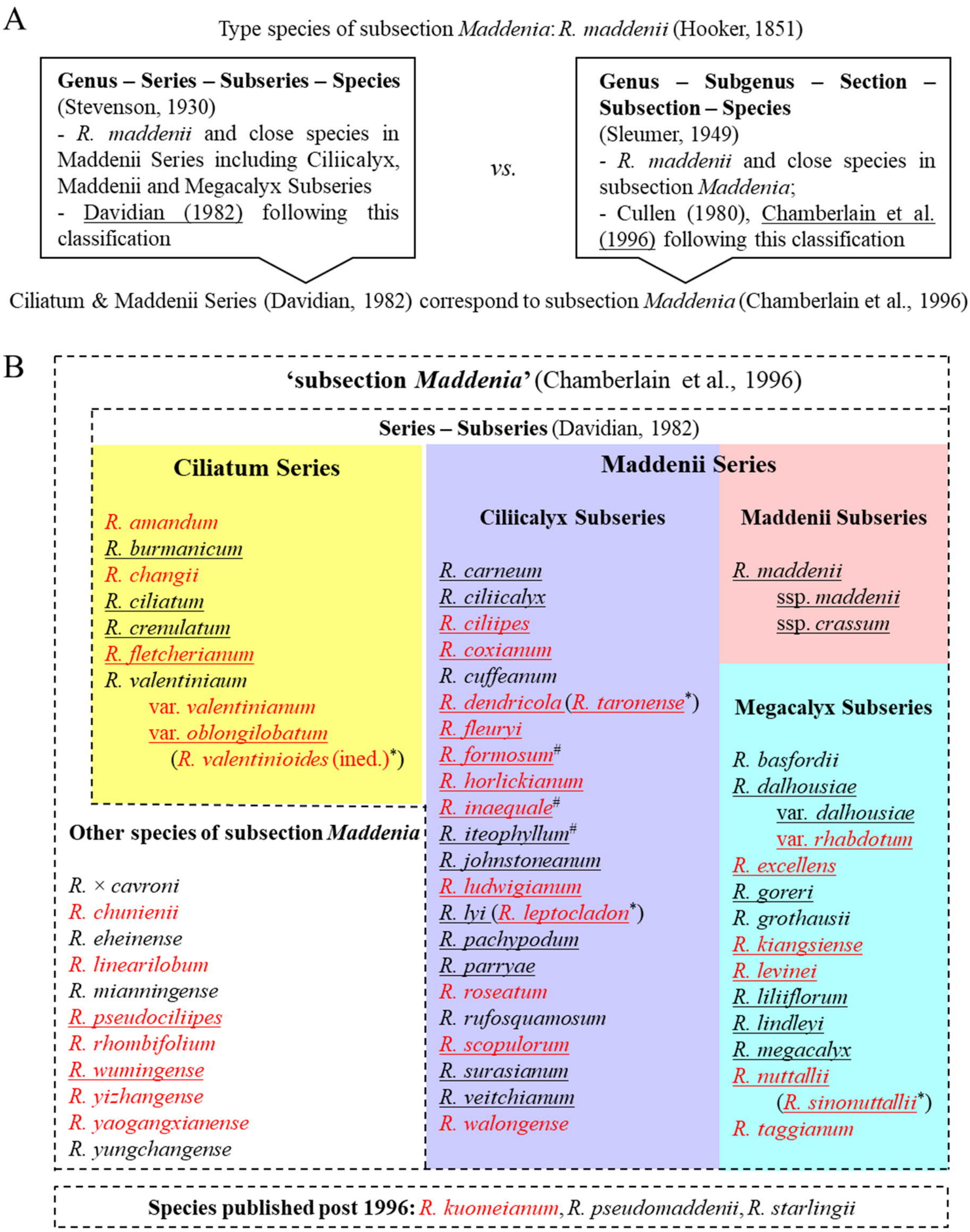

Figure 4.1 Species of subsection *Maddenia*. A) classification debate on species in subsection *Maddenia*. B) *Maddenia* species showing different groupings in the two classifications debated between Chamberlain et al. (1996) and Davidian (1982). Species are listed in alphabetical order within each box.

Synonyms of each species (Chamberlain et al., 1996) are not shown, except for those noted with an asterisk (*) that were assessed as distinct species in the IUCN Red List (Gibbs et al., 2011). Hash symbol (#) indicates the three morphologically distinct species suggested by Mao et al. (2017), which were listed as belonging to the *R. formosum* complex in Chamberlain et al. (1996). Taxa in red are the threatened (Critically Endangered, Endangered, Vulnerable), Near Threatened or Data Deficient. Underlined taxa were sampled in the present study. For all species, taxonomic notes and Red List updates can be found in the taxon checklist of subsection *Maddenia* in Chapter 2, except that the dubious species *R. vanderbiltianum* (List S2.3) included there is not listed here.

Subsection *Maddenia* is clearly one of the groups in which the unresolved species relationships hinders conservation decision making. The definition of 'subsection *Maddenia*' used here follows the classification in Chamberlain's checklist (1996), which corresponds to the Ciliatum and Maddenii Series of Davidian's classification (1982) (Fig. 4.1 A). There is a total of 65 taxa (61 species, 2 subspecies and 4 botanical varieties) in this subsection (List S2.3, Chapter 2). These taxa originate from the Himalayan region through to southern China and northern Vietnam (Fig. 2.1A, Chapter 2). This group of species exhibits great morphological variation (Cullen, 1980; Davidian, 1982; Cubey, 2003). The species are all lepidotes, with scales on leaves, seed capsules, and sometimes also other parts such as petioles, pedicels, corolla outside (outer surface, corolla always sympetalous), and styles (Fig. 4.2). The corolla can be white, pink or (creamy) yellow (Fig. 4.2-I; Fig. 3.1, Chapter 3, Hu et al., 2023). Some species are ciliate, bristly, or hairy on the branches, leaves, calyx, and filaments (Fig. 4.2-II & III). The under surface of the leaves (abaxial surface of lamina) shows various appearances (e.g., brown, glaucous, green) (Fig. 4.2-IV).

As landscaping plants, *Maddenia* plants possess outstanding horticultural value because of the showy and scented flowers of many species, as well as their high resistance to pests such as thrips (Cullen, 1980; Donald, 2012; MacKay et al., 2018; Jamieson, 2021; McMeekin, 2022). Even though well outside their original habitats, they grow vigorously in the temperate maritime climate of New Zealand (MacKay et al., 2017; Jamieson, 2021). Globally, 55 of the total 65 taxa are known to be in cultivation (Chapter 2). The ~33 taxa grown in New Zealand form an essential contribution to the *ex situ* conservation of *Rhododendron* species. Indeed, locations of *ex situ* collections are northern hemisphere dominant, so the relatively few collections in the southern hemisphere are a key resource (Mounce et al., 2017; Chapter 2).

Figure 4.2 Representative species of subsection *Maddenia*, showing flower and leaf features. Each row: A) PK40 *R. ciliatum*; B) OM06 *R. ciliicalyx*; C) OM11 *R. maddenii* ssp. *maddenii*; D) PK31 *R. megacalyx*. Each column: I) inflorescence – flower number and appearance vary; II) pistil and stamens – base of filaments sometimes hairy (A-II, B-II, D-II), and number usually 10 except for *R. excellens* (12–15) and *R. maddenii* (15–25, C-II); III) calyx and pedicel – sometimes scaly and/or bristly (A-III, B-III), and base of corolla outside – sometimes scaly (C-III); IV) leaf under surface – colouration varies; scales are always present and the density varies

In subsection *Maddenia*, 18 taxa are threatened (3 Critically Endangered, 2 Endangered, 13 Vulnerable) and 16 are at risk (4 Near Threatened, 12 Data Deficient) (Gibbs et al., 2011; Chapter 2). Determination of conservation status and prioritisation of action in this subsection is hindered by four main issues.

The first issue is the presence of species of uncertain definition where authorities differ about ‘lumping’ or ‘splitting’ of taxa. Davidian (1982) defined 47 species in subsection *Maddenia*, while Chamberlain et al. (1996) reclassified them together with later-published species into 52 species (56 taxa) (Fig. 4.1B). Some species are ‘lumped’; for example, Chamberlain et al. (1996) included *R. supranubium* with *R. pachypodum* as a synonym. The question arises as to whether some of the ‘lumped’ species are in fact distinct and require separate conservation consideration.

The second issue is the presence of species complexes where the rank and definition of several closely related species is subject to debate. For example, the species/subspecies status of members in the *R. formosum* complex has changed over time (Mao et al., 2017) (Fig. 4.1B), but their molecular phylogeny has not been reconstructed for assessment of the complex. This issue of species complex is particularly problematic in the type species of subsection *Maddenia*: *R. maddenii* (Hooker, 1851). Five species in the Maddenii Subseries described by Davidian (1982) were ‘lumped’ into the two subspecies (ssp. *maddenii* and ssp. *crassum*) of *R. maddenii* in Chamberlain et al. (1996), including *R. brachysiphon*, *R. calophyllum*, *R. manipurense*, *R. odoriferum*, and *R. polyandrum*. As there is high and continuous morphological variation within this species complex (Cullen, 1980), as well as a lack of genetic studies, definition of the taxonomic distinction in the two subspecies as well as the synonyms is challenging.

The third issue is the presence of polyploids in the *R. maddenii* complex. Within the whole subsection examined to date, polyploids were found only in the *R. maddenii* complex, exhibiting the greatest ploidy variation in the genus (2–12x) (Chapter 3, Hu et al. 2023). In phylogenetics, polyploids could cause issues in data generation and analysis when reconstructing distinct homeologues, due to the multiple gene copies in each sample (Rothfels, 2021). In a few studies, *R. maddenii* was included in a *Rhododendron* phylogeny, but it was sampled as a species representative (Donald, 2012; Shrestha et al., 2018; Chang et al., 2021; Fu et al., 2021; Khan et al., 2021), rather than at the intraspecific level.

The fourth issue is the concept of ‘subsection *Maddenia*’. Morphologically, species in subsections *Edgeworthia*, *Triflora* and *Boothia* show a strong resemblance to those in subsection *Maddenia* (Cox, 1985; Cox, 1990; Cullen, 1980). Although usually only few subsection *Maddenia* species were studied in phylogenetic studies, the results suggest that species from close subsections *Edgeworthia*, *Boothia*, *Tephropepla,* also possibly *Monantha* and *Moupinensia,* are either in subsection *Maddenia* or a sister clade (Donald, 2012; Shrestha et al., 2018; Fu et al., 2021; Khan et al., 2021; Xia et al., 2021). So far, no phylogenetic study has included sufficient species from subsection *Maddenia* nor other species from closely related subsections, to define the true boundary of subsection *Maddenia*.

The issues outlined above are not easily resolved by morphological research. The high and continuous variation from species to species, such as stamen number, filament indumentum, density of scales, corolla size and shape, leaf width and fruit shape (Cullen, 1980; Davidian, 1982; Cox & Cox, 1997) makes species delimitation difficult. Similarly, the presence of continuous clines in geographically widespread species, such as *R. maddenii* (Cullen, 1980; Chapter 2), makes the species boundaries difficult to define. Phylogenetic studies could be used to address these issues raised in relation to morphology. Yet, subsection *Maddenia* has not been studied for these issues as an entire group.

For *Rhododendron* in general, a few phylogenetic studies have used different sequencing methods, such as nuclear/chloroplast markers (Milne et al., 2010; Donald, 2012; Zhou et al., 2013; Hart et al., 2017; Shrestha et al., 2018), Restriction-site Associated DNA sequencing (Li et al., 2019; Chang et al., 2021), and genome skimming (Fu et al., 2021). These studies help us to understand the taxonomic classification of *Rhododendron*, but mostly at higher taxonomic levels (genus, subgenus) that do not comprehensively cover a wide range of close species. Considering the great number of *Rhododendron* species and the many problematic species complexes, phylogenetic studies have yet to address all of the species relationships at the section or subsection level. Donald (2012) and Chang et al. (2021) partially analysed the molecular phylogeny in subsection *Maddenia*, but only for a very limited number of species. For subsection *Maddenia* as a whole, a comprehensive species-level phylogeny with intraspecific sampling has not been reconstructed.

Therefore, this study reconstructs the molecular phylogeny using as many species as were accessible, in replicate, to develop an understanding of species relationships in subsection

Maddenia. Target capture sequencing (Fig. 1.7, Chapter 1) is tested for the analysis of *Rhododendron* phylogeny. This sequencing technology has grown in popularity for handling polyploids (Kamneva et al., 2017; Brandrud et al., 2020; Debray et al., 2021) and/or herbarium samples with degraded DNA (Andermann et al., 2020), which both occur in the present case.

The unit for plant conservation, 'species', has been defined in various ways from different research aspects (Heywood et al., 2006; De Queiroz, 2007). This study adopts the concept of species as morphologically recognisable and phylogenetically monophyletic. Species relationships in subsection *Maddenia* together with several close subsections are studied to address the following questions: 1) Can the molecular phylogeny delimit close species and the species complexes of *R. maddenii* and *R. formosum*? 2) How well does the clustering of taxa in the phylogenetic results agree with the previous morphological classification? 3) Does the occurrence of polyploids in the present study affect phylogenetic inference? 4) Is 'subsection *Maddenia*' monophyletic? 5) Is target capture sequencing efficient for studying the molecular phylogeny of *Rhododendron* species? The findings are discussed with respect to resolution of the taxonomic debates for conservation of the *Maddenia* species, and to propose wider conservation action in the genus *Rhododendron*.

4.2 Materials and Methods

4.2.1 Sample collection

As many taxa as possible of subsection *Maddenia* were included for a high coverage of this subsection. Leaf samples were acquired from botanic and/or private gardens and nurseries in New Zealand (160 samples), along with accessions from the Royal Botanic Garden Edinburgh (RBGE, 25 samples), UK, and the Rhododendron Species Botanical Garden (RSBG, 74 samples), USA for sampling plant accessions. Accessions from RBGE and RSBG are cultivated materials of wild origin with known provenance, while the New Zealand accessions consist of materials from either wild or horticultural sources. Herbarium specimens for New Zealand accessions were deposited in the Dame Ella Campbell Herbarium (MPN) at Massey University, Palmerston North, New Zealand. Living plants of the accessions in RBGE and RSBG are accessible at the corresponding organizations. Taxon names within 'subsection *Maddenia*' followed the updated taxon list in Chapter 2 (List S2.3) based on Chamberlain's taxon checklist

(Chamberlain et al., 1996), which consists of taxa in Davidian's Maddenia Series and Ciliatum Series. The voucher specimens, together with field photos, were used to identify and verify the sampled accessions, following Davidian's taxonomic key (Davidian, 1982), as it is still the most comprehensive morphological set of descriptions to date.

Samples for several species from other subsections of section *Rhododendron* were collected to test the monophyly of subsection *Maddenia*: *R. boothii* and *R. leucaspis* (subsection *Boothia*), *R. edgeworthii* (subsection *Edgeworthia*), *R. yunnanense* (subsection *Triflora*). Species from subgenus *Hymenanthes* section *Ponticum* were collected as outgroup: *R. arboreum* ssp. *delavayi* (subsection *Arborea*), *R. fortunei* and *R. decorum* (subsection *Fortunea*), and *R. williamsianum* (subsection *Williamsiana*) (Fig. 1.5) (Donald, 2012; Shrestha et al., 2018; Fu et al., 2021; Khan et al., 2021; Xia et al., 2021). All samples were collected from November 2020 to October 2021. A list of all samples and voucher specimens is provided in Supplementary Table S4.1.

4.2.2 DNA extraction, library preparation and Illumina sequencing

Fully expanded young leaves were sampled and dried in silica gel prior to DNA extraction. DNA was extracted following a modified protocol from the DNeasy Plant Kit (Qiagen) used for *Rhododendron* in Gardiner et al. (December 2019). An aliquot of 2 µL DNA was electrophoresed in a 1% agarose gel to evaluate the DNA quality for each sample. DNA concentration was tested using the Qubit dsDNA HS Assay Kit (ThermoFisher Scientific). DNA samples were stored at –20 °C for later use.

After the quantity was standardised for 500–1000 ng per sample, the DNA samples were sent to DArT (Diversity Arrays Technology, Canberra, Australia) for Illumina sequencing. Prior to sequencing, DNA samples were run through a quality control by DArT. DArTag, a high-throughput genotyping method using DArTseq^{TM} technology (https://www.diversityarrays.com/services/targeted-genotying/) was employed to genotype all samples. Samples were genotyped using an available set of blueberry baits developed in collaboration between DArT and Breeding Insight (https://breedinginsight.org/) at Cornell University. The marker panel was initially selected from blueberry cultivars in North America, and is suitable for genotyping the tetraploid blueberry *Vaccinium corymbosum* 'Draper'

(Ericaceae) (Colle et al., 2019) for breeding decisions and selection. However, in the present study, this panel of markers was used to test its applicability to reconstructing *Rhododendron* phylogeny. One advantage of using the DArTag method is that any SNP (or a small indel) can be targeted if there is some genomic sequence available around the variant base/indel. Because the two genera *Vaccinium* and *Rhododendron* are from the same family (Ericaceae), but their extent of homology is unknown, the 200 bp flanking sequences of the blueberry 3K SNP markers for the DArTag panel was subjected to a BLAST search against two published *Rhododendron* genomes: *R. williamsianum* (subgenus *Hymenanthes*, section *Ponticum*, subsection *Williamsiana*) (Soza et al., 2019) and *R. simsii* (subgenus *Tsutsusi*, section *Tsutsusi*) (F.-S. Yang et al., 2020). From the blast results using either genome, the baits set showed high homology for ~200 loci (> 90% identity), indicating that these baits should successfully capture *Rhododendron* loci. Of the two genomes, the *R. simsii* genome showed a relatively higher homology: there were 218 blast hits, and each chromosome (chr 1–13) had 6–26 hits; compared to the 188 hits, with 5–20 hits on each chromosome for *R. williamsianum* (at base identity > 90% for both species; Fig. S4.1).

In the first DArTag step, molecular probes select the small target regions containing sequence variants. In the second step the targeted regions are amplified and, in parallel, the sample-specific barcode (a short stretch of sequence) is attached. The libraries generated were next sequenced on the Illumina HiSeq. Of the 259 samples sent for sequence analysis, 205 were successfully genotyped and yielded sequence data. To analyse all SNPs detected in the *Rhododendron* sequences for the phylogenetic analysis, raw FASTQ data were processed using the pipeline below.

4.2.3 Bioinformatic analysis

4.2.3.1 Read quality control and trimming

Raw FASTQ files received from DArT (demultiplexed single-end reads) were processed for bioinformatic analyses. Data were analysed on the HPC platform ‘JupyterHub’ (JupyterLab/.2023.1.0-gimkl-2022a-3.4.3) of New Zealand eSource Infrastructure (NeSI, 2023). To inspect the sequence quality, FASTQ files were run through FastQC/0.11.9 (Babraham Institute, 2010) to check the Phred score, sequence duplication, adapter content, etc.

Reads were then trimmed (5′ end 29 bp, 3′ end 39 bp) and cleaned using Fastp/0.23.2-GCC-11.3.0 (Chen et al., 2018), where sample barcodes and possible adapters were removed to obtain clean reads.

4.2.3.2 Reads mapping to reference genome, assembly and variant calling

Using ipyrad/0.9.85-gimkl-2022a-Python-3.10.5 (Eaton & Overcast, 2020), clean reads were mapped to the published genome of *R. simsii* for reference based assembly. The basic assembly included seven steps following the defaults in ipyrad: sorting, filtering, clustering, consensus, clustering, and formatting (https://ipyrad.readthedocs.io/en/latest/7-outline.html). The output files include different formats, including the called variants (SNPs and Indels), PHYLIP*.phy for RAxML and NEXUS*.nex for Bayesian analysis. To separately analyse subsets of the *R. maddenii* complex, diploids only and polyploids only, samples were partitioned as subsets from the whole dataset, using the branching function in ipyrad.

Excluding the two samples that were filtered out in read mapping due to a disqualifying number of determined sites per locus (ipyrad step 4 & 5), a final total of 203 samples were analysed in the phylogenetic inference. They include eight species (16 samples) outside of subsection *Maddenia*, and 40 taxa in subsection *Maddenia* with 39 samples of the *R. maddenii* complex plus 146 samples of other taxa (Table S4.1).

4.2.3.3 Phylogenetic tree inference

To reconstruct the phylogenetic trees, ipyrad output files were used as input data for different software on the NeSI HPC platform, to compare trees built with different algorithms. Due to the high proportion of missing data and for efficient running of the algorithms, only SNP data, rather than all recovered loci were used to generate the phylogenetic trees. RAxML/8.2.12-gimkl-2022a (Stamatakis, 2014) and MrBayes/3.2.7-gimpi-2022a (Ronquist et al., 2012) were used for maximum likelihood (ML) and Bayesian analyses, respectively. For Bayesian analysis, GPU/A100-1g.5gb together with beagle-lib/4.0.0-GCC-11.3.0 on the NeSI HPC platform were used to speed up the Bayesian analysis. Two chains of MrBayes were run for up to 50 million generations with a burn-in value of 0.25. Average standard deviation of the split frequencies was set as the default value as ≤ 0.1 to indicate the convergence of the two chains, and the convergence from the results was verified using Tracer v1.7.2 (Rambaut et al., 2018). Phylogenetic trees were annotated using FigTree v.1.4.4 (Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK). Further, splits networks were generated to examine incompatibilities in the phylogenetic dataset (Huson & Bryant, 2006; Marin et al., 2020). For this, the Nexus file of SNP data was used as input in SplitsTree v4 (Huson & Bryant, 2006).

To examine the possible impact of polyploidization on phylogenetic inference, analyses were also performed to reconstruct trees for two subsets of samples separately: diploids only (including the two diploids of *R. maddenii*), and the *R. maddenii* complex (all polyploids plus the two diploids). The subsets were partitioned from the full dataset to generate separate consensus sequences, using the 'branching and merging' function of ipyrad (https://ipyrad.readthedocs.io/en/master/8-branching.html). ML and Bayesian trees were inferred for each subset, respectively.

For data availability, the FASTQ sequences of all samples are uploaded to NCBI SRA database (PRJNA1069350). Information for bioinformatic analysis in this study are deposited in Github repository (https://github.com/linghu114/RhododendronMaddenia.git), including flanking sequence of the blueberry 3K DArTag baits panel and the blast script, scripts used in reads mapping and assembly using ipyrad, and phylogenetic tree building using RAxML and MrBayes.

4.3 Results

4.3.1 Reads mapping and genome-reference assembly of all samples

Target capture sequencing of the 205 accessions that passed DNA quality control yielded ~4 GB data. The mean length of the single-end reads was 69 bp, and the size of Q30 bases was 39.96 M (93.3%). After mapping to the reference genome of *R. simsii* using ipyrad, a total of 1,176 loci were recovered. The full sequence matrix included 203 samples and 73,616 bp, with 72.28% missing sites. The aligned SNP matrix included 203 samples and 5,299 sites, with 60.64% missing sites. A map of recovered loci is shown in Fig. S4.2. No pronounced difference of recovered loci was found between ingroup and outgroup samples.

4.3.2 Phylogenetic tree

4.3.2.1 Phylogenetic inference of subsection Maddenia using maximum likelihood and Bayesian analyses

Maximum likelihood (ML) and Bayesian analyses were performed on the full dataset with loci filtered to minimize the impact of missing data. In most instances, replicates of the same species were clustered together, reflecting the confidence of grouping of the species. A few samples were not grouped with others within the same species according to the collection label, and the identity of these were further investigated using herbarium specimens from the present collection (Table S4.1). Despite low bootstrap support for some subclades, ML analysis of all samples (Figs. 4.3 & S4.3A) generated a tree reflecting meaningful biological relationships of *Maddenia* species as discussed in section 4.4.1.

MrBayes analyses yielded a similar phylogeny as the ML tree (Fig. S4.3B). However, there are two issues that indicate a lower accuracy for the Bayesian trees. Firstly, when the whole dataset was analysed, the two chains in the Bayesian analysis were not converged as observed in Tracer v1.7.2 (average deviation 0.410648 – greater than the standard value 0.1) after 50 million generations. However, each of the two chains for separate subsets (e.g., diploids only vs. the *R. maddenii* complex only) converged well. Secondly, although the Bayesian tree generated a similar topology to the morphological taxonomic classification of subsection *Maddenia*, clustering for a few samples in the Ciliicalyx Subseries formed a polytomy.

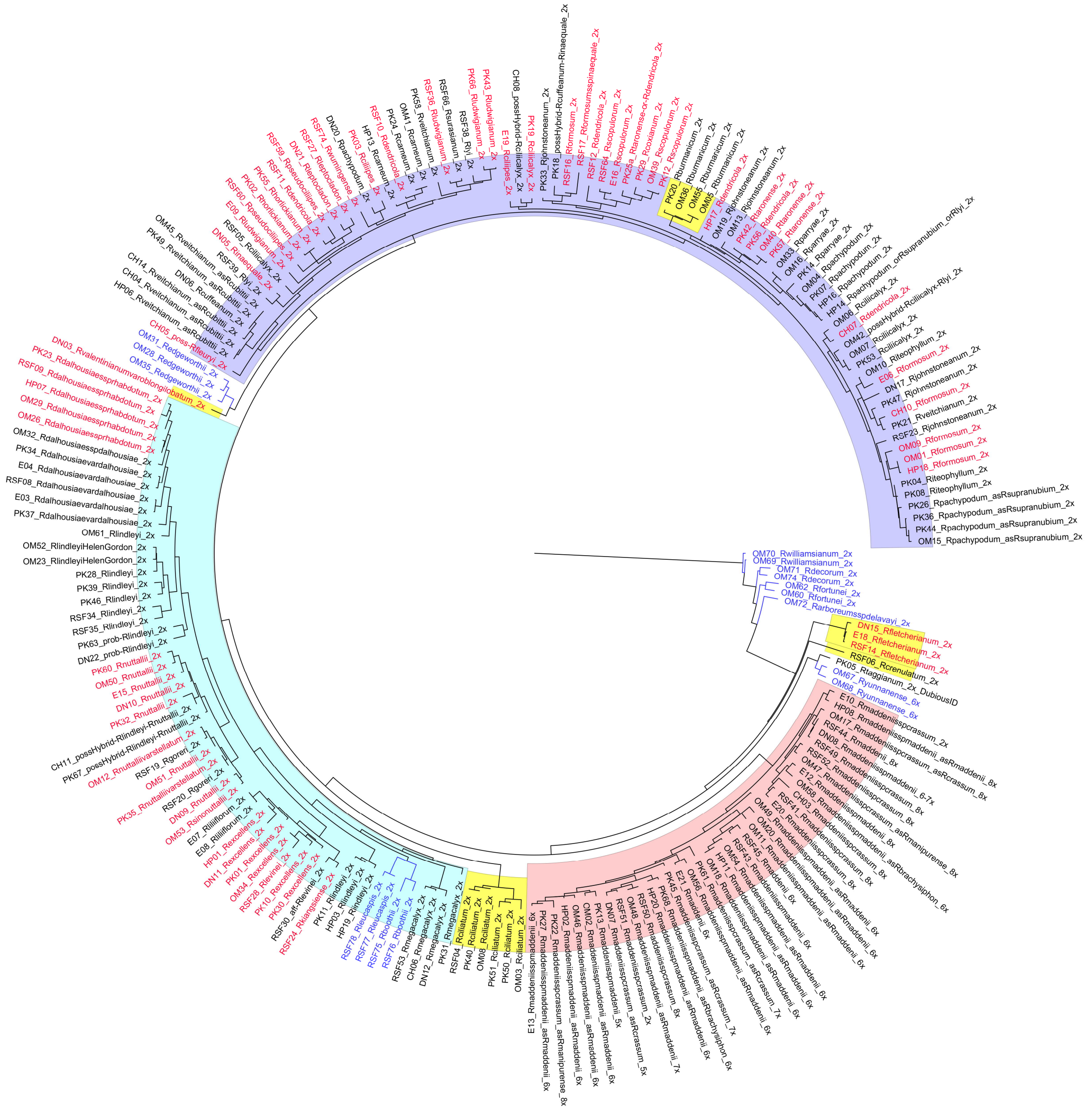

Figure 4.3 RAxML tree from analysis of blueberry baits for all 203 samples of *Rhododendron* subsection *Maddenia* and outgroup. Samples include diploids and polyploids. The tree is rooted with OM70 (*R. williamsianum*, 2*x*). Background highlight colours indicate the Davidian (1982) classification: yellow – Ciliatum Series; purple – Maddenii Series Ciliicalyx Subseries; ocean blue – Maddenii Series Megacalyx Subseries; pink – Maddenii Series Maddenii Subseries. Annotated names in navy blue are outgroup. Names in red are samples of species that are threatened or at risk following IUCN Red List assessments (Chapter 2). See supplementary file Fig. S4.3A for the rectangular ML tree with bootstrap values annotated.

4.3.2.2 Phylogeny of subsection Maddenia and species from close subsections

In general, the subsection *Maddenia* samples were resolved into three main clades aligning with Davidian's (1982) classification of the subseries of Maddenii Series (Maddenii, Ciliicalyx and Megacalyx Subseries) (Figs. 4.3 & S4.3). The Maddenii Subseries (bootstrap in percentage, posterior probability in decimal value = BS: 46, PP: 0.53) formed a well-supported clade that included both diploid and polypoid species. Also, species of Ciliicalyx Subseries formed one clade (BS: 21, PP: 0.97), the same as for the Megacalyx Subseries (BS: 21, PP: 0.97)

In contrast, samples of species from Davidian's Ciliatum Series (*R. fletcherianum*, *R. crenulatum*, *R. ciliatum*, *R. burmanicum*, *R. valentinianum* var. *oblongilobatum*) were not grouped in one clade but were scattered over the phylogenetic tree (Fig. S4.3). *R. fletcherianum* and *R. crenulatum*, clustered closer to the root with the outgroup, *R. ciliatum* was placed sister to clades of *Maddenii* Series and Megacalyx Subseries (BS: 74, PP: 1), and *R. burmanicum* was included in Ciliicalyx Subseries (BS: 98, PP: 1). *R. valentianum* var. *oblongilobatum* clustered together with the outgroup *R. edgeworthii* (BS: 55, PP: 0.50). The clade of *R. edgeworthii* and *R. valentinianum* var. *oblongilobatum* forms a clade sister to the clade of Ciliicalyx Subseries.

However, clustering of the reportedly close species from related subsections showed that subsection *Maddenia* was not monophyletic (Figs. 4.3 & S4.3). In the tree rooted with the outgroup sample *R. williamsianum* OM70 (diploid), species outside of subgenus *Rhododendron*: *R. williamsianum*, *R. decorum*, *R. fortunei*, *R. arboreum* ssp. *delavayi*, were clearly distant from samples in the subgenus. However, representative species from other subsections within subgenus *Rhododendron* were interspersed amongst the *Maddenia* samples. *R. yunnanense* (subsection *Triflora*) was relatively distinct from other samples but nested between clades of the scattered Ciliatum Series and Maddenii Series (BS: 65, PP: 0.50). The subclade of *R. boothii* and *R. leucaspis* (subsection *Boothia*) was clustered among species of Megacalyx Subseries (BS: 14, PP: 1). *R. edgeworthii* (subsection *Edgeworthia*) was clustered with *R. valentinianum* var. *oblongilobatum* (BS: 55, PP: 0.50) in a subclade, sister to clade of Megacalyx Subseries and clade of Ciliicalyx Subseries (Fig. S4.3).

4.3.2.3 Phylogeny of the R. maddenii complex

R. maddenii samples of varying ploidy levels, with *R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum* as well as their synonyms forming the Maddenii Subseries, were all located in one clade (Fig. 4.3). When samples within the *R. maddenii* complex were analysed separately using either RAxML or MrBayes, the subspecies *R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum* were not clearly clustered in separate clades (Fig. S4.4). These findings suggest that while the *R. maddenii* complex itself is monophyletic, there is no clear phylogenetic division intra-specifically between the two subspecies. However, the hexaploid (6*x*) samples (mostly identified as *R. maddenii* ssp. *maddenii*) tended to be clustered in a separate subclade from the octoploids (8*x*) (mostly identified as *R. maddenii* ssp. *crassum*) (Fig. S4.3).

The ML and Bayesian trees of the two subsets (the *R. maddenii* complex, Fig. S4.4; all diploids, Fig. S4.5) identified a similar topology of species relationships to that for the full dataset (Fig. S4.3). This indicates the consistency of phylogeny between the full dataset and subsets. However, some parts in subclades of the Bayesian tree were not as resolved as the ML tree (Figs. S4.3B & S4.5). Also, the two MCMC runs of Bayesian analysis for the full dataset did not converge despite the high number of 50 million generations (checked with Tracer).

4.3.3 Splits network

When SplitsTree was employed to analyse the SNPs of the full dataset, the networks showed conflicts among some samples (Fig. 4.4). In general, samples were split into groups: the *R. maddenii* complex, the Megacalyx Subseries, a mix of part outgroup and part Ciliatum Series, and two divisions of the Ciliicalyx Subseries. Some of the outgroup species, already mentioned in section 4.3.2.2 above, are included within the main set of *Maddenia* samples, while the others are well separated. The split of these groups largely matches the clustering of samples in the phylogenetic tree (Fig. 4.3 & S4.3).

The extent of the conflicts shown in the SplitsTree analysis indicates the presence of factors that generate ambiguous signals. For example, several samples that were suspected to be hybrids or were difficult to determine the morphological identification (e.g., DN05, OM42, HP03 as indicated with the arrows), were associated with edges (i.e., connections) to other samples (Fig. 4.4).

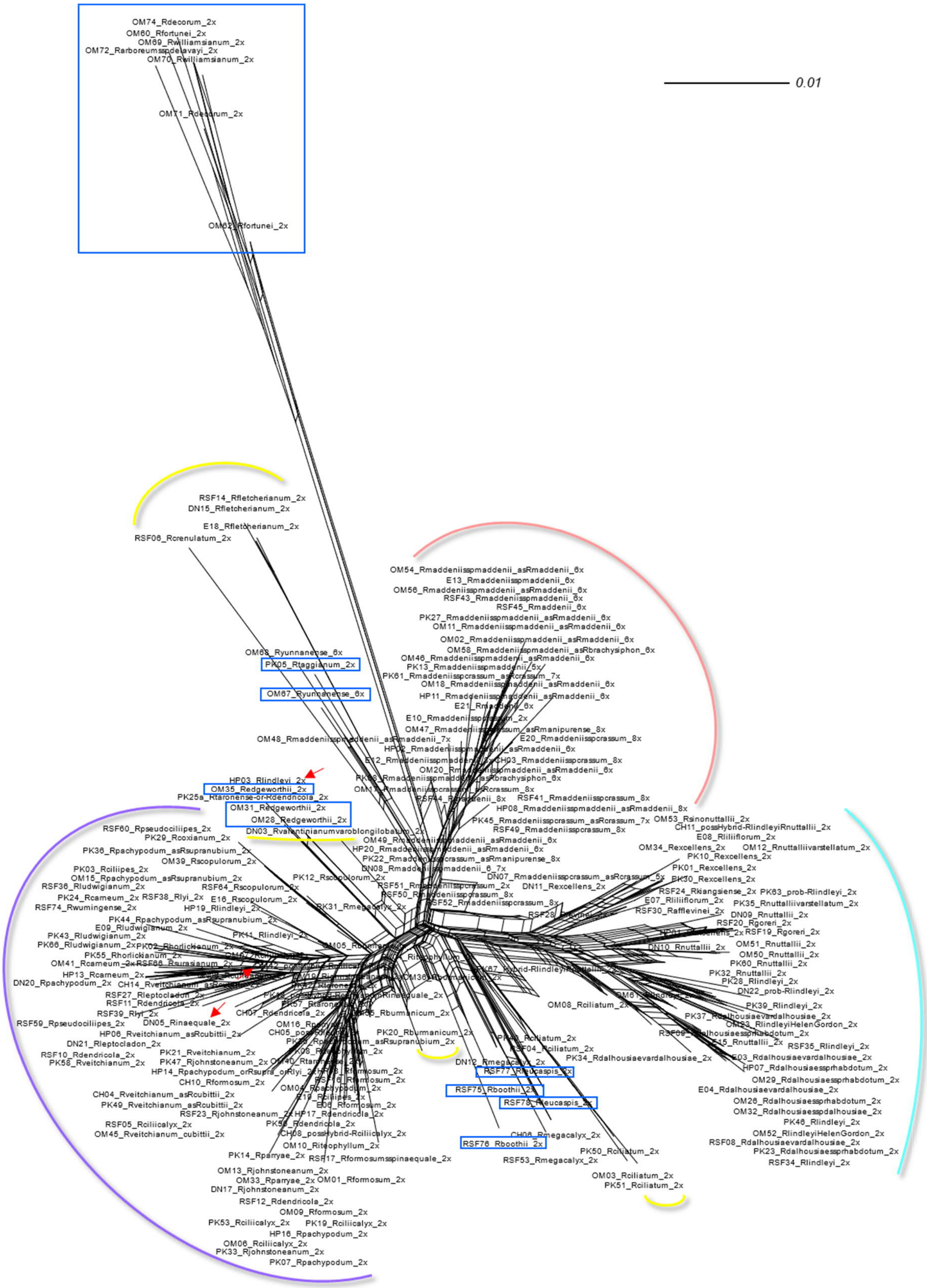

Figure 4.4 Split networks representing incompatibilities within the full dataset, with EqualAngle view showing Neighbornet network using SplitsTree v4. Networks are annotated with coloured curves

indicating the Davidian (1982) series (corresponding to Figs. 4.1 & 4.2): yellow – Ciliatum Series; purple – Maddenii Series Ciliicalyx Subseries; ocean blue – Maddenii Series Megacalyx Subseries; pink – Maddenii Series Maddenii Subseries. Taxon names in navy blue rectangles are outgroup. Red arrows indicate example samples (DN05, OM42, HP03), that were suspected to be hybrids and/or encountered difficult morphological identification, showing data conflicts here. The scale bar represents 0.01 substitutions per site.

4.4 Discussion

4.4.1 Understanding the phylogeny of subsection *Maddenia*

Comparison of the molecular phylogeny of subsection *Maddenia* with the previous morphological taxonomy enables a review of the species classification in this subsection. Prior research in *Rhododendron* has not made many breakthroughs in developing an understanding of species relationships in this subsection, which is needed to answer questions that impact conservation decisions, related to the geographic distribution, taxonomy and intraspecific variation of taxa. This case study provides an example of the merit of focusing on a particular group (subsection) to examine these big questions.

According to the present phylogenetic results, Davidian's (1982) separation of the three subseries within Maddenii Series (Maddenii, Ciliicalyx and Megacalyx) is supported (Figs. 4.1B & 4.3). But the separation between the two series (Ciliatum and Maddenii) is not well supported, as samples of the two series do not form single clades. Also, subsection *Maddenia* is not monophyletic. Details are discussed as below and in section 4.4.3.

Both ML and Bayesian trees support the separation of the three subseries of Maddenii Series (Fig. S4.3). One exception is that *R. excellens* should belong to the Megacalyx Subseries (in agreement with Cullen (1980)), rather than in the Maddenii Subseries as Davidian (1982) placed. In addition, two species (i.e., *R. pseudociliipes*, *R. wumingense*) that were published post Chamberlain et al. (1996), belong phylogenetically to the Ciliicalyx Subseries of Davidian's classification (1982).

However, the Ciliatum Series does not form a coherent phylogenetic group as the species are scattered. *R. crenulatum* and *R. fletcherianum* are clustered in a subclade sister to the outgroup. Either *R. ciliatum* or *R. valentinianum* var. *oblongilobatum* forms a subclade outside of the three subseries of Maddenii Series but intercalated within the Maddenii Series (Fig. 4.3). This clustering of species within Ciliatum Series largely agrees with previous molecular phylogeny of the yellow-flowered *Maddenia* species (Donald, 2012). However, in this study, *R. valentinianum* var. *oblongilobatum* is sister to *R. edgeworthii* (subsection *Edgeworthia*), and both species are nested between the clades of Megacalyx and Ciliicalyx Subseries, while *R. burmanicum* is included in the clade of Ciliicalyx Subseries. However, in Donald (2012), *R. burmanicum* was close to *R. valentinianum*, both distant from *R. edgeworthii*. Nevertheless, Ciliicalyx Subseries is phylogenetically nested with some species from the Ciliatum Series in both studies, which is consistent with their strong morphological resemblance addressed by Davidian (1982).

An understanding of species delimitation and species complexes in subsection *Maddenia* is achieved from the present study. When available, multiple samples were used to test the monophyly of examined species. For most species, their replicates grouped together, indicating these species are themselves distinct. Conversely, replicates of some species were not clustered in one clade, including *R. lindleyi*, *R. dendricola*/*R. taronense*, *R. johnstoneanum*, and *R. ciliicalyx* (Fig. 4.3), indicating these species may not be monophyletic (details discussed in the following section 'Species delimitation'). With respect to the 'lumping' of species by Chamberlain et al. (1996), some of these were supported while others are not. For the two species complexes (*R. maddenii* and *R. formosum*), results of their internal resolution were different (details discussed in following section 4.4.1.2 'Species complexes'). Detailed resolution of species, and remaining questions concerning species and the species complexes in subsection *Maddenia* can be found below.

4.4.1.1 Delimitation of 'lumped' species

- *R. veitchianum*/*R. cubittii* – Ciliicalyx Subseries

The phylogenetic tree identified all *R. cubittii* samples in one clade that is separate from *R. veitchianum* (however there was only one sample PK58, Figs. 4.3 & S4.3), suggesting *R. cubittii* should be recognized as a distinct species. Davidian (1982) recognized *R. veitchianum* and *R. cubittii* as distinct species, while Cullen (1980) and Chamberlain et al. (1996) treated *R. cubittii* as a synonym of *R. veitchianum*. Although sharing some morphological features, the two species appear morphologically and phylogenetically different, suggesting that *R. cubittii* should be treated as a distinctive species. *R. cubittii* has smooth brown flaky bark, bristly petioles and branchlets, oblong-lanceolate leaves, leaf underside greenish, while in *R. veitchianum* the leaf underside is glaucous and usually less scaly, the corolla usually smaller, and calyx margin is usually not bristly (Davidian, 1982, p.237).

- *R. pachypodum*/*R. supranubium* – Ciliicalyx Subseries

In the phylogenetic tree (Fig. 4.3), samples of these two putative species were clustered in two different clades: *R. pachypodum* next to *R. parryae*, but *R. supranubium* was included within the *R. formosum*/*R. iteophyllum* clade. This separation suggests that *R. pachypodum* and *R. supranubium* are distinct species. *R. supranubium* has been considered as a synonym of *R. pachypodum* by Chamberlain et al. (1996). But Davidian (1982, p.248) described the two species separately while addressing their resemblance. In Davidian's key (1982, p.231), the four species (*R. formosum, R. lyi, R. inaequale, R. supranubium*) were not easily distinguishable, as they only exhibit minor differences on leaf width, scale density on under surface of leaves and outside of corolla. This could explain a close relationship between *R. supranubium* and *R. formosum*, for which identifying the specimens is more difficult. For example, the identification of sample HP14 was not certain to be *R. pachypodum* or *R. supranubium* or *R. lyi*, as its morphological features partially matched descriptions of the three species according to Davidian's key.

- *R. dendricola* (*syn: R. taronense*) – Ciliicalyx Subseries

The phylogenetic tree (Fig. 4.3) suggests *R. taronense* to be a synonym of *R. dendricola*, as multiple accessions of the two species were jointly clustered together. *R. taronense* has been considered synonymous with *R. dendricola* by Chamberlain et al. (1996). But Davidian (1982) described the two species separately, and the IUCN Red list (Gibbs et al., 2011) assessed *R. taronense* as a separate entity. While both species were rated Vulnerable and may represent different genetic variation, a re-assessment of their conservation status using one combined entity of *R. dendricola* is recommended.

- *R. nuttallii*– Ciliicalyx Subseries

According to the phylogenetic trees, *R. sinonuttallii* is likely a variation of *R. nuttallii* and therefore suggested to be a synonym, considering that the *R. sinonuttallii* sample (OM53, Figs.

4.3 & S4.3) was nested in *R. nuttallii*. This agrees with their morphological classification: *R. sinonuttallii* has been considered synonymous with *R. nuttallii* (Chamberlain et al., 1996), and also suggested by Davidian (1982) to be a synonym based on morphological features. Therefore, the species status of *R. sinonuttallii* that was assessed as a single entity in the IUCN Red List (Gibbs et al., 2011) is not supported. However, this conclusion needs to be further confirmed, as only one sample of *R. sinonuttallii* was tested. Botanic gardens usually label related accessions as *R. nuttallii* rather than differentiating these two species (Chapter 2), which is reasonable considering the high degree of resemblance between the two species and the overlapping geographic distribution of *R. sinonuttallii* and *R. nuttallii* (List S2.3).

The phylogenetic tree (Fig. 4.3) also identified the close relatives to be in the *R. nuttallii* clade: *R. nuttallii* var. *stellatum* and *R. goreri*. Davidian (1982) described both as distinct entities while addressing their resemblance to *R. nuttallii*, which is supported by the molecular phylogeny here. The reason why the two samples of each *R. nuttallii* var. *stellatum* and *R. goreri* were not grouped together could be specimen misidentification or baits efficacy but is yet to be confirmed.

- *R. ciliicalyx* – Ciliicalyx Subseries

In the phylogenetic tree (Fig. 4.3), *R. ciliicalyx* is not monophyletic. The samples are scattered, sister to samples of *R. ciliipes*, *R. dendricola* and possibly *R. lyi* (identification uncertain). The highly overlapped distributions, especially at the border between China (SE Xizang, NW Yunnan) and N Myanmar, may be the primary reason for the taxonomic complexity among these four species (Cullen, 1980; Chapter 2).

As *R. ciliicalyx* and *R. johnstoneanum* often occur together in the wild, Cullen addressed the main distinguishing feature was that *R. johnstoneanum* has an impressed style while *R. ciliicalyx* does not (i.e., ovary tapering into the style) (Cullen, 1980, p.50). However, this feature was not recognised by Davidian (1982). Instead, Davidian described *R. ciliicalyx* as having a truncate ovary (i.e., contrary to Cullen's description), and the bristly and long calyx ('*ciliicalyx*') was the main feature. The *R. ciliicalyx* samples in the present study were identified based on herbarium observations and following Davidian's key, based on etymology of the species name.

- *R. johnstoneanum* – Ciliicalyx Subseries

Davidian (1982) pointed out that *R. johnstoneanum* was originally classified as *R. formosum* var. *johnstoneanum*. In the phylogenetic tree (Fig. 4.3), samples of *R. johnstoneanum* are scattered (not monophyletic), some with *R. formosum* as suggested by Davidian, but others with *R. dendricola*. There are two possibilities for this pattern: (i) *R. johnstoneanum* as morphologically defined is not a separate species but is part of a continuum with *R. formosum* (or maybe *R. dendricola)*, or (ii) some of the overseas samples are incorrectly identified, which would change the interpretation of the results.

- *R. lindleyi* – Megacalyx Subseries

There are two clades of *R. lindleyi* in the reconstructed phylogenetic tree (Fig. 4.3), suggesting this species is not monophyletic. One clade contains 10 samples and is next to clades containing *R. nuttallii* and *R. dalhousiae*, which is in keeping with the proposed morphological relationship to *R. dalhousiae* (Davidian, 1982; Cox & Cox, 1997). Two of the samples in this clade (PK46, PK63) were field labelled as *R. lindleyi* ‘Ludlow & Sherriff’, and other two (OM23, OM52) as the cultivar *R. lindleyi* ‘Helen Gordon’ for which the parentage partially includes *R. lindleyi* ‘Geordie Sherriff’ and ‘Ludlow & Sherriff’ (New Zealand Rhododendron Association Bulletin, 2000, p.35). Davidian (1982, pp.275, 278) states that two wild forms under *R. lindleyi*, ‘Geordie Sherriff’ and ‘Ludlow & Sherriff’, are likely *R. grothausii*, but Cox & Cox (1997) argued the differences simply represent variation and *R. grothausii* should be synonymous to *R. lindleyi*. These four samples are nested with other *R. lindleyi* samples in the phylogenetic tree (Fig. 4.3 & S4.3), suggesting *R. grothausii* is likely to be a variation of *R. lindleyi* rather than a distinct species.

The second clade of *R. lindleyi* contains three samples and is not a neighbour to the first clade (Fig. 4.3 & S4.3). Of the three samples, two (HP03, HP19) were field labelled as *R. taggianum* but keyed as *R. lindleyi*, and one (PK11) was the wild collected KW16029 (labelled by Kingdon-Ward as *R. inaequale*), but also keyed to *R. lindleyi*.

The separation of these two clades could be related to its wide distribution in N Bangladesh, Bhutan, China (S Xizang), NE India, N Myanmar, and E Nepal (List S2.3, Chapter 2) and its high degree of variation within the species (Davidian, 1982; Cox & Cox, 1997). However, the reason why the two clades are distant remains to be investigated.

4.4.1.2 Species complexes

- *R. maddenii* complex (*R. maddenii* ssp. *maddenii* and *R. maddenii* ssp. *crassum*, together with synonymous species) – Maddenii Subseries

The *R. maddenii* samples are all located in one clade, well defining the boundary of this species (Fig. S4.3). Within the species complex, the two subspecies appear to be divided into two subclades to a certain extent. The subclade of more *R. maddenii* ssp. *maddenii* samples, with mainly hexaploids (6*x*), is naturally distributed farther west to Bhutan, and Sikkim in northeastern India. The other subclade of more *R. maddenii* ssp. *crassum* samples, with mainly octoploids (8*x*), is naturally distributed farther east to southwestern China (Yunnan) and northern Vietnam. This division is possibly in a relation to the intraspecific ploidy variation and geographic distribution of *R. maddenii* as discussed in Chapter 3 (Hu et al., 2023). However, distributions of both subspecies do overlap in northeastern India (Arunachal Pradesh), southwestern China (S Xizang, NW Yunnan) and perhaps northern Vietnam (List S2.3, Chapter 2). Also, there were some morphological differences observed in their samples with respect to stamen hair, bark smoothness, corolla size, stamen number, leaf width, calyx and anther lengths, as Davidian (1982) mentioned. However, the intraspecific phylogeny related to species distribution and ploidy evolution should be further investigated in future studies, with more samples of wild source included to capture the geographic distribution of the two subspecies.

- *R. formosum* complex (*R. formosum*, *R. inaequale*, *R. iteophyllum*) – Ciliicalyx Subseries

The phylogenetic tree (Fig. 4.3) supports distinctness of the three species (considered as subspecies previously) in the *R. formosum* complex, which agrees with the morphological reassessment by Mao et al. (2017). The *R. formosum* samples are all in the clade of Ciliicalyx Subseries but separated into different subclades. Meanwhile, considering the *R. iteophyllum* clade is sister to the *R. formosum* clade, these two species are closer than to *R. inaequale*. Although the two species appear to be distinct, the treatment of *R. iteophyllum* as a synonym of *R. formosum* var. *formosum* by Chamberlain et al. (1996) is reasonable to some extent. However, *R. inaequale* (DN05, Figs. 4.3 & S4.3) is in a different clade distant from the *R. formosum*/*R. iteophyllum* clade, suggesting that *R. inaequale* is a distinct species. Among the three species, Davidian (1982) mentioned that *R. formosum* and *R. iteophyllum* were similar in morphology, but *R. inaequale* rather has a stronger resemblance to an ‘outsider’ species

R. veitchianum on general features. The molecular phylogeny agrees with the previously stated morphological similarity between *R. formosum* and *R. iteophyllum* as well as the distinction of *R. inaequale* but may not support the resemblance between *R. inaequale* and *R. veitchianum* (PK58, Figs. 4.3 & S4.3) as the two species are not close in the phylogenetic tree. More samples of *R. inaequale* and *R. veitchianum* are required to further describe their relationship.

4.4.1.3 Phylogenetic networks in subsection Maddenia

SplitsTree networks showed a high degree of genetic conflicts among the tested samples. The possibility of evolutionary processes creating this conflict (e.g., hybridization) may be a principal reason for the complex taxonomy in the group of *Maddenia* species. For example, as distributions of *Maddenia* species usually overlap (List S2.3, Chapter 2), wild-source accessions could be natural hybrids resulting from hybridization among species (Jamieson, 2021). The network reticulation supplements the phylogenetic trees to explain the undetermined taxa. But reasons for the reticulation require investigation.

In summary, a few factors may be responsible for the unresolved molecular phylogeny of *Rhododendron* species examined (i.e., not monophyletic): 1) multiple samples represent intraspecific variation, including continuous morphological variation in most examined species, as well as the ploidy variation in the *R. maddenii* complex (Chapter 3, Hu et al., 2023); 2) taxon misidentification in the field sampling. Particularly, for the samples from RBGE and RSBG outside of New Zealand, it was not possible for the researcher to verify the identification of the specimens; 3) low efficiency of the blueberry baits when used for *Rhododendron*; and/or 4) rapid radiation (recent speciation/diversification) of *Maddenia* species (within the recent ca. 10 Ma (Shrestha et al., 2018)), which is common in species from the Himalayan mountainous regions (Schwery et al., 2015; Xing & Ree, 2017), causing inefficient locus recovery as well as SNP capture by the baits (Fig. S4.2). Among them, factors 3) and 4) are suspected to be also the main reasons for the large amount of missing data resulting in low confidence (support values) in some areas of the phylogeny.

4.4.2 Polyploidisation did not change phylogenetic structure of subsection *Maddenia*

Polyploidisation in samples of the *R. maddenii* complex did not impact the phylogenetic structure in subsection *Maddenia*. In the present study, polyploids only occur in the *R. maddenii* complex, and this species complex forms a coherent clade (Figs. 4.3 & S4.3). As the results show, ML and Bayesian trees identified a similar topology of species relationships, for either subsection *Maddenia* or subsets of diploids/polyploids (Figs. S4.3 & S4.4). In the ML analysis, polyploids in the *R. maddenii* complex had little impact on the phylogenetic inference. Although there were polyploids in the full dataset, almost all samples were resolved, identifying the genetic polymorphism captured by the blueberry baits.

However, the combination of diploid and polyploid samples increased the issue of data convergence in the Bayesian analysis (Fig. S4.3B). The separation of diploids and polyploids, as suggested in other studies (Andermann et al., 2020; Brandrud et al., 2020; Wang et al., 2020), yielded higher convergence for either dataset (Figs. S4.4B & S4.5B). Low data convergence for several samples in the clade of Ciliicalyx Subseries is a persistent problem in the Bayesian trees, no matter whether in the full dataset or the diploid subset (Figs. S4.3B & S4.5). Hence, the phylogenetic interpretation primarily referred to the better-resolved maximum likelihood tree (Fig. 4.3) rather than the Bayesian tree (Fig. S4.3).

4.4.3 Concept of ‘subsection *Maddenia*’

The molecular phylogeny suggests that the morphological taxonomy of ‘subsection *Maddenia*’ (Chamberlain et al., 1996), or Maddenii Series plus Ciliatum Series following Davidian (1982), does not define the boundary of this group well. This agrees with results in other studies covering the genus or *Rhododendron* groups of species, which reveal several species from other subsections are nested in subsection *Maddenia* (Donald, 2012; Shrestha et al., 2018; Fu et al., 2021; Khan et al., 2021; Xia et al., 2021). In the present phylogenetic study, *R. yunnanense* (subsection *Triflora*), *R. edgeworthii* (subsection *Edgeworthia*), as well as *R. boothii* and *R. leucaspis* (subsection *Boothia*) are included within subsection *Maddenia*. In particular, *R. yunnanense* and *R. edgeworthii* are close to species in the scattered Ciliatum Series, while *R. boothii* and *R. leucaspis* are close to species in Ciliicalyx Subseries (Fig. 4.3).

The concept of subsection *Maddenia* requires refinement even in morphological terms, as the key character to this group is not well defined. Using Davidian's key (1982), once a species is identified to subgenus *Rhododendron* (plants scaly) (Fig. 1.5), *Maddenia* species are characterized by the presence or absence of several features. First, the absence of a woolly leaf underside (otherwise Edgeworthia Series, or subsection *Edgeworthia* in Chamberlain et al., 1996). Second, that the scales are not lacerate, the corolla is not salverform, and the inflorescence is not capitate (otherwise Anthopogon Series; or section *Pogonanthum* in Chamberlain et al. (1996)). Third, that the seeds do not have an elongated tail at each end (longer than the seed body (Cullen, 1980, p22)), and the capsule is not spindle-shaped (otherwise Vaccinoides Series, or subsection *Pseudovireya* in Chamberlain et al. (1996)). Next, the style is long and slender and straight, and the corolla is of various shapes (short and bent style leads to several other series). After that, the large-corolla species are keyed to Maddenii Series, while a small corolla along with some other features leads to Ciliatum Series, but also several other series.

Therefore, once section *Pogonanthum* and section *Vireya* (*Schistanthe*) are separated out of subgenus *Rhododendron* (Fig. 1.5), species identification is narrowed down to subsection *Maddenia* and several other subsections in section *Rhododendron*. Integrating Davidian's classification, the Maddenii Series is primarily characterized by a long straight style and large flowers. Defining the Ciliatum Series is rather complicated, as apart from the smaller-corolla feature, certain other features need to be checked so that several related series can be ruled out. This morphological complexity of Ciliatum Series is reflected in the scattered species located in the phylogenetic tree (Fig. 4.3), which suggests this series is not monophyletic and adds difficulty to defining the boundary of subsection *Maddenia*.

Given that the previous morphological definition of subsection *Maddenia* appears incomplete, for now it may be better to call the group of species in the current subsection *Maddenia* as '*Maddenia* species', until the classification can be refined to define a monophyletic subsection *Maddenia*. This could be fulfilled by (i) integrating an expanded subsection *Maddenia* that includes nested species from close subsections (i.e., subsections *Edgworthia*, *Boothia* and possibly *Triflora*, perhaps together with others not included here such as subsections *Monantha*, *Moupinensia* and *Tephropepla* (Shrestha et al., 2018; Fu et al., 2021; Khan et al., 2021; Xia et al., 2021)); Or (ii) excluding some of the species in Ciliatum Series (e.g., *R. fletcherianum* and *R. crenulatum*) and only including the other species that are nested in the clades of Maddenii

Series (e.g., *R. burmanicum*, *R. ciliatum*, *R. valentianianum*). As to the question whether 'expanding' or 'shrinking' subsection *Maddenia* is more appropriate to verify the composition of subsection *Maddenia* and determine an appropriate solution for the clear boundary of subsection *Maddenia*, more studies are needed utilizing additional (wild) samples from subsection *Maddenia* and all close subsections.

4.4.4 Analysing molecular phylogeny of *Rhododendron* species using target capture sequencing

The present case study has demonstrated the applicability of target capture sequencing for studying the molecular phylogeny of *Rhododendron.* The relatively low number of recovered loci (Fig. 4.2) had no negative effect on phylogenetic reconstruction for subsection *Maddenia*. Several phylogenomic studies such as Ufimov et al. (2021) have suggested that a probe set can be phylogenetically informative despite a high level of missing data. In our application of the blueberry baits for reconstructing the *Maddenia* phylogeny, the phylogenetic trees, especially the ML tree, provided information on relationships among the taxa. The clustering of close species and species complexes matched relationships derived from the morphological features suggesting that the DArT 3K blueberry baits set is relatively efficient for phylogenetic resolution of *Maddenia* species. This efficiency is also reflected in the clustering of sample replicates for tested taxa, and consistent topology at higher taxonomic levels (i.e. series, subseries) between the ML and Bayesian trees.

However, although the phylogenetic tree is informative, it is not optimal, as conclusions on relationships among several species could not be made until further confirmation is available with data from more wild samples and/or sequence datasets. The ML tree (Fig. S4.3A), although greatly helping species delimitation, could be improved with higher support values. Also, low data convergence and poor sample divergence were shown for the clade of subseries Ciliicalyx Subseries in the Bayesian analysis (Fig. S4.3). Therefore, the blueberry baits set is not recommended for future *Rhododendron* phylogenetic research. Instead, *Rhododendron*-specific baits could be developed in the future to enable the use of target capture sequencing for fully understanding *Rhododendron* phylogeny. Considering the efficiency of target capture sequencing demonstrated in our case study and the rapidly increasing availability of *Rhododendron* genome data (Table 1.1, Chapter 1), a probe set from *Rhododendron* species could be developed readily. Alternatively, the universal baits set for flowering plant phylogeny reconstruction, Angiosperms353 baits (Johnson et al., 2018; Ufimov et al., 2021), could be tested on *Rhododendron*. While existing phylogenetic studies of *Rhododendron* have focused on genus-wide analyses, detailed taxonomic assessment of many species complexes may benefit from the efficiency of target capture sequencing. Other techniques, including genome skimming (Fu et al., 2021), could be used for higher-quality sequences or for capturing chloroplast regions. This could add more data sets to compare with the present study to refine the phylogenetic tree, as well as to achieve a better understanding concerning evolutionary issues (e.g., hybridization, incomplete linage sorting) that cause phylogenetic networks in *Rhododendron* species (Huson & Bryant, 2006; Marin et al., 2020).

4.4.5 Implications for biodiversity conservation

The goal of biodiversity conservation is to conserve not only species diversity, but also the variation within species (Volis, 2017; Khoury et al., 2019). The findings from the present molecular phylogeny of subsection *Maddenia* will help to guide the next phase of conservation efforts, as we begin to understand whether a species in the species complexes is monophyletic or not, and how a species is taxonomically delineated. In particular, successful species delimitation supports conservation of the 21 threatened or Data Deficient taxa examined in this study (Fig. 4.1).

Conservation assessments, for species that are ‘lumped’ or ‘synonymised’ in species complexes but later recognised as phylogenetically distinct species, should be re-evaluated. For example, *R. supranubium* should be separated from *R. pachypodum* (Least Concern), and *R. cubittii* separated from *R. veitchianum* (Least Concern) as distinct species for conservation assessments. *R. formosum* (Critically Endangered), *R. iteophyllum* (Not Evaluated), *R. inaequale* (Data Deficient) should be treated as separate species in conservation rather than a joint species complex of *R. formosum*. Existing accessions of *R. formosum* are likely to include those of *R. iteophyllum* due to their high morphological resemblance, and the accessions should be re-identified, if available. In contrast, although assessed as a Vulnerable species (Gibbs et al., 2011), *R. sinonuttallii* is likely to be a variation of *R. nuttallii* as discussed above. Existing conservation efforts for *R. sinonuttallii* are suggested to be combined with *R. nuttallii* (Near Threatened) as one entity.

When species of complex taxonomy result from evolutionary processes (such as uniparental lineages and reticulate evolution) and represent taxonomic biodiversity, they should be given attention for biodiversity conservation (Ennos et al., 2005). For example, although *R. dendricola* (Vulnerable) may be not monophyletic, the diversity from different populations may be sampled separately under the 'metacollection' principle (Westwood et al., 2021). While *R. taronense* (Vulnerable) is clustered with *R. dendricola* and considered as a synonym, the conservation for the variant *R. taronense* is less urgent. For *R. excellens* (Vulnerable), all tested samples were wild accessions cultivated in New Zealand, which indicates a rich wild resource in *ex situ* conservation. As there are two divisions in the phylogenetic tree representing genetic variation, plant accessions in both divisions should be considered for diversity conservation. Although the multiple wild accessions were sampled from China or Vietnam (Table S4.1), there was no geographic division of these samples in the phylogenetic tree. The inclusion of further wild samples from a wider geographic range (Chapter 2) would better illustrate the species relationships and possible geographic distribution of different populations. Also, as the *R. excellens* clade is embedded with *R. liliiflorum* (Least Concern) and *R. levinei* (Near Threatened), indicating their close relationship, the identification of cultivated accessions must be robust to confirm the correct species required to be under protection.

Especially for species with unclear boundaries and complex taxonomy, detailed morphological study is essential when justifying accession identification (Besnard et al., 2018). Existing identification of cultivated plant accessions should be used with caution in conservation management. During observations of the specimens to verify their placement in the phylogenetic tree in this study, several specimens were found to be wrongly labelled in the source collections and therefore a name change at their respective curation site has been suggested (Table S4.1). For example, in this study, accessions from garden collections may have been misidentified as *R. formosum* (Critically Endangered) instead of *R. veitchianum* (Least Concern), or vice versa. Considering all botanic garden *ex situ* collections, we may have more (or fewer) *R. formosum* accessions in cultivation than expected, based on plant labels. As *R. formosum* appears to be paraphyletic, the delimitation of *R. formosum* from close species (e.g., *R. veitchianum*, *R. johnstoneanum*, *R. inaequale*) should be performed carefully (Figs. 4.3 & S4.3). Similarly, *R. supranubium* (Least Concern) may have been misidentified as *R. taggianum* (Vulnerable) in the present study, suggesting there is in fact less diversity of *R. taggianum* conserved than is recorded. Another example, from this study, advises that caution should be taken with delimitation of *R. coxianum* from *R. formosum* in the plant collections, due to their close morphological resemblance (Davidian, 1982). *R. coxianum* (Critically Endangered) has only one accession known to be conserved in global *ex situ* collections (Pukeiti Garden, New Zealand) (Table S2.2, Chapter 2), suggesting more material should be brought into cultivation and distributed to other botanic gardens in case of death of living plants. In such situations, botanic gardens should verify that their wild collections are distinct from closely related species, to ensure the diversity of the targeted species is safeguarded.

4.5 Conclusion

In this case study, target capture sequencing was used to develop an understanding of molecular phylogeny of *Rhododendron* species. By successfully delimiting a number of species in subsection *Maddenia* and identifying the unclear boundary of subsection *Maddenia* in relation to adjacent subsections, this case study provides an exemplar for further resolution of taxonomy of *Rhododendron* and suggests actions for conservation management. The maximum likelihood and Bayesian analyses generated consistent phylogenetic structures, although confidence levels were low for some inferences due to difficulty in data convergence. Target capture sequencing proved to be phylogenetically informative, despite the presence of polyploids which revealed no clear phylogenetic pattern within the *R. maddenii* complex. Evolutionary processes in the species (e.g., hybridization, incomplete linage sorting) are likely to cause uncertainty regarding monophyly of some species, for which the species delimitation remains unresolved.

Following the phylogenetic results and detailed discussions, actions are proposed with respect to conservation as below:

- A review of the conservation status of delimited species that are found to be either distinct from a previous ‘lumping’ (e.g., *R. cubittii*, *R. supranubium*, *R. iteophyllum*), or not distinct from the closely related species (e.g., *R. sinonuttallii, R. taronense*);
- Robust morphological identification of the samples collected outside of New Zealand, to confirm the monophyly/paraphyly of concerned species that are scattered in the phylogenetic tree (e.g., *R. ciliipes, R. ludwigianum, R. pseudociliipes*);

- Robust identification of plant accessions in *ex situ* conservation, for species that could be easily misidentified as morphologically close species, as happened in this study, such as *R. taggianum* for *R. supranubium*, or between *R. formosum* and *R. veitchianum*. In another example, the sample RSF30 from RSBG (USA) that is labelled as an affinis to *R. levinei*, is likely *R. kiangsiense* according to the molecular phylogeny;
- The further acquisition or reproduction of wild samples for certain distinct but rarely collected species, such as *R. coxianum* and *R. excellens*.

Despite the progress achieved in this study, resolving the complex taxonomy of *Rhododendron* species requires more thorough sampling especially of wild sources. Benefiting from the sequencing technologies and published *Rhododendron* genomes, future studies are anticipated to further reconstruct a comprehensive molecular phylogeny of species in the sections and subsections of genus *Rhododendron*.

Supplementary Files

Supplementary files of Chapter 4 are attached in Appendix III.

Figure S4.1 BLAST results of the blueberry 3K DArTag baits against *Rhododendron* genomes

Figure S4.2 Recovered loci for each of the 203 samples in the full dataset

Figure S4.3 A) Maximum likelihood vs. B) Bayesian trees of the full dataset

Figure S4.4 A) Maximum likelihood vs. B) Bayesian trees of samples in the *R. maddenii* complex

Figure S4.5 A) Maximum likelihood vs. B) Bayesian trees of all diploids including the two diploid samples of *R. maddenii*

Table S4.1 Specimen information for the accessions sampled for phylogenetic study

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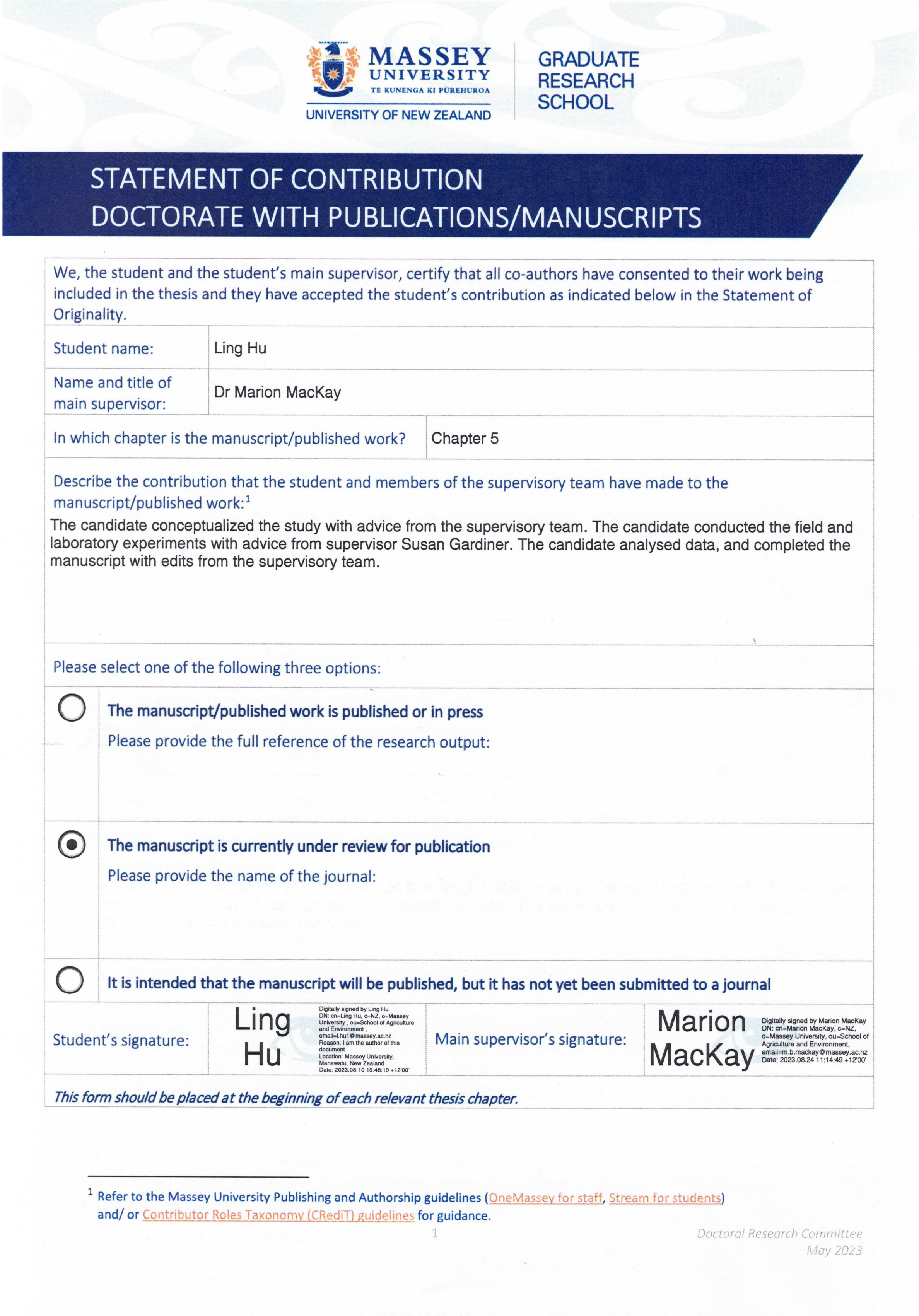
Statement of Contribution – Chapter 5



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May 2023

Chapter 5

Intraspecific pollination of *ex situ* collections of *Rhododendron* species for germplasm conservation

Abstract

Controlled pollination is an important technique for maintaining germplasm to support species diversity in integrated plant conservation, particularly in genera where open pollination usually generates hybrids with unknown male parents. This study investigated the fruit set and seed viability of self and intraspecific crosses for five *Rhododendron* taxa with different IUCN Red list categories, to guide conservation management of threatened species in botanic garden collections. Controlled pollinations were performed on selected garden accessions, and germination of seeds was tested under the incubation condition of 15/25℃, 16h/8h, ~6 µmol m^{-2} s^{-1}. The species studied, all from subsection *Maddenia*, showed different levels of intraspecific compatibilities. *R. dalhousiae* var. *dalhousiae* (Least Concern) was both self- and cross-compatible, with seeds from cross-pollination having a higher germination rate. *R. dalhousiae* var. *rhabdotum* (Vulnerable) was also self- and cross-compatible, but seeds from self-pollination had a higher germination rate. *R. lindleyi* (Least Concern) had similar, relatively low, seed germination from both self- and cross-pollinations. For *R. nuttallii* (Near Threatened), self-pollination produced more seeds than the outcross, but the self-compatibility was significantly different between the two pollinated accessions. *R. excellens* (Vulnerable) was incompatible for all combinations of accessions tested here, with no seed set in either cross or self-pollination. For quickly testing seed viability, X-ray images for *Rhododendron* seeds had low resolution and showed limited correlation with the seed germination. The treatments of X-ray scan and fungicide (Ridomil) had little impact on seed germination, which is beneficial for seed banking of *Rhododendron* species with respect to assessing seed quality and preventing fungal infection. This study indicates that controlled intraspecific pollination can be used to maintain diversity of *ex situ* accessions for some *Rhododendron* species; however, the zero or low compatibility demonstrated in some, such as *R. excellens*, may require a different approach.

Key words: Controlled pollination; diversity; *ex situ* conservation; intraspecific compatibility; outcross; seed viability; self; subsection *Maddenia*

5.1 Introduction

As part of ‘integrated conservation’ for safeguarding plant biodiversity, *ex situ* conservation focuses on holding plant collections outside their natural habitats in facilities such as seed banks or botanic gardens, which hold materials of the species under threat and provide easy access for utilization and re-introduction (Oldfield & Newton, 2012; Gratzfeld, 2017; Heywood, 2017; Smith & Pence, 2017) (Fig. 1.3, Chapter 1). Maintaining genetic diversity in collections is essential for *ex situ* conservation, which requires strategic breeding to generate new plants through sexual (seed) reproduction (Gratzfield, 2017; Smith and Pence, 2017). *Ex situ* management of seed reproduction is particularly necessary for species such as *Rhododendron* which hybridise easily (Zha et al., 2008; Ma et al., 2010; Jamieson, 2021), and where open-pollinated seeds are likely to be hybrids. Indeed, collections of taxa and populations that are geographically isolated in nature and brought together in a botanic garden can generate an extreme form of artificial sympatry (Maunder, Hughes, et al., 2004), which is undesirable in species conservation. Careful management is needed to facilitate the safe or ‘pure’ propagation of threatened taxa for conservation (Volis, 2017; Forgiarini et al., 2023). Therefore, controlled pollination increases genetic exchange between representative (ideally wild) accessions, which helps to maintain the germplasm of prioritized species (Maunder, Guerrant, et al., 2004; Volis, 2017).

Rhododendron is a large genus which contains some 349 (25%) threatened species (Gibbs et al., 2011; MacKay et al., 2018). Some species, such as *R. coxianum* and *R. fleuryi* (both Critically Endangered), have small wild populations and are also scarce in cultivation (Chapter 2), while *R. kanehirae* (Extinct in the Wild) presently relies on botanic garden cultivation for its continued existence. For many *Rhododendron* species there is a limited number of accessions held in *ex situ* collections (Chapter 2) and use of controlled pollination to increase the number of individuals in cultivation is desirable for these species.

Understanding the reproductive biology and breeding system (i.e. selfing vs. outcrossing) is important to produce viable seeds and offspring in conservation horticulture of threatened species (Schoen & Brown, 1991; Hollingsworth et al., 2006; van der Walt et al., 2022). Williams et al. (1990) summarized the detailed reproductive biology of *Rhododendron*, describing the morphological characteristics of reproductive structures, fertilization process, seed development, etc. *Rhododendron* species are mostly pollinated by bees, butterflies and birds, with pollen tetrads connected by viscin threads that can be easily attached to the pollinator (Bowers, 1930; Williams et al., 1990; Basnett & Ganesan, 2022). Reproductive biology of *Rhododendron* species has been generally studied to develop an understanding of the process of fertilization (Palser, 1986; Barbara F Palser et al., 1989; Williams et al., 1990). Breeding systems have been studied for several taxonomic groups (Williams et al., 1990; Rouse et al., 1993) or species (Mejias et al., 2002; Okamoto & Suto, 2004; Okamoto & Ureshino, 2015; Ma et al., 2016; Yan et al., 2018); but these usually focused on interspecific crosses and for the generation of horticultural hybrids. Only a few have investigated the reproductive biology of *Rhododendron* species with respect towards species conservation (Li et al., 2018; T. Li et al., 2018; Cai et al., 2022).

Intraspecific pollination, including selfing and outcrossing, is important for conservation of genetic diversity of a species in *ex situ* collections (van der Walt et al., 2022; Forgiarini et al., 2023). However, not all species are able to produce seeds through selfing or intraspecific crossing. Williams et al. (1990) concluded that most *Rhododendron* species were fully self-compatible. But some *Rhododendron* species (e.g., *R. catawbiense*) have been reported as self-incompatible (Bowers, 1930; Ping, 2019). Indeed, Williams et al. (1984) noted that post-zygotic abortion may inhibit production of seeds; or even if seeds are formed, they may have problems such as emptiness, failure to germinate, or non-viable seedlings (Rouse et al., 1993). Following the self pollinations of several species by Rouse et al. (1993), the seed yield varied from species to species. Also, Takahashi and Itino (2021) reported inbreeding depression (i.e. decrease or loss of fitness due to inbreeding) of *R. kaempferi*, with the fruit set from self-pollination significantly lower than outcrossing. Whether a species is self- and/or cross-compatible and the extent of compatibility needs to be investigated for each individual species, prior to making a conservation decision for *ex situ* collections (e.g., seedbanking, living collections).

Investigation of compatibility should primarily focus on the production of fruit and seed from controlled pollinations. Then the quality of seeds including seed purity, seed fill and seed viability should be evaluated to ensure healthy offspring that can be established in a collection (Martyn Yenson, 2021). Germination rate is a key criterion for evaluation of seed quality for generating viable seedlings (ISTA, 2023). Radiography of seeds (X-ray scan) is a quick non-destructive approach to determine seed fill, which predicts the germination rate before sowing the seeds (Medeiros et al., 2018; Musaev et al., 2022). However, there is no available information on using X-ray scans to test *Rhododendron* seed quality. There is also limited information for species in subsection *Maddenia* (subgenus *Rhododendron*, section *Rhododendron*) on intraspecific pollination and seed germination (Barbara F. Palser et al., 1989; Rouse et al., 1993; Tiwari & Chauhan, 2007; Tian, 2011).

This case study investigates the feasibility of controlled pollination to generate viable seeds to conserve intraspecific germplasm of *ex situ* collections of *Rhododendron* species in subsection *Maddenia*. This follows prior work on *ex situ* conservation, including examining *ex situ* conservation status (Chapter 2), cytogenetics (Chapter 3, Hu et al., 2023) and molecular phylogeny of species (Chapter 4), studied as a means of prioritising urgent and distinct species for conservation action. Knowledge about the breeding system of subsection *Maddenia* species informs *ex situ* conservation management. When the species is compatible for selfing or intraspecific cross, it is suggested to increase gene exchange among accessions through planned pollination especially between distant gardens. Otherwise, efforts should be put more on wild collection.

This study examines the following issues: 1) Can the selected species produce viable seeds through controlled pollination? If yes: 2) Is there difference in seed germination rate between self- and out-cross pollinations? 3) Can X-ray images of *Rhododendron* seeds indicate seed quality and hence predict seed germination? 4) Learning from this case study, what issues should botanic gardens be concerned with about conservation of *Rhododendron* through controlled pollination for *ex situ* collections?

5.2 Materials and Methods

5.2.1 Species selection and sample accession

A total of 13 accessions of four species (five taxa) from subsection *Maddenia* were used for controlled pollination. All samples were from plants growing in New Zealand: *R. dalhousiae* var. *dalhousiae* (Least Concern; OM32, CH15 – both cultivated source; both flowering in mid-November 2021), *R. dalhousiae* var. *rhabdotum* (Vulnerable; OM26, OM29 – both cultivated source; both flowering in early January 2022), *R. excellens* (Vulnerable; HP01, PK01, PK10 – all wild origin but source unknown; all flowering in early January 2022), *R. lindleyi* (Least Concern; OM52, PK39 – all cultivated source; both flowering in early November 2021), *R. nuttallii* (Near Threatened; CH16 – cultivated source, flowering in late November 2021;

OM50 – wild source from northern Viet Nam, flowering in late November 2021; OM51 – wild source from China, flowering in early November 2021) (Fig. 5.1). Accessions were selected based on their different threatened levels, availability and accessibility of plants in nearby gardens, appropriate blooming season for pollination, as well as lack of information on pollination compatibility of the species. OM61, labelled as species *R. lindleyi*, was originally also included in the pollination experiments. However, it was only maternally fertile and failed to produce pollen; and the morphology and molecular phylogeny suggested it was a hybrid (Fig. 4.3, Chapter 4). The living accessions are currently located in New Zealand at: CH15, CH16 - Cross Hills Gardens, Kimbolton; HP01 - Heritage Park, Kimbolton; OM26, OM29, OM32, OM50, OM51, OM52, Omahuri Garden (private), Palmerston North; PK01, PK10, PK39 - Pukeiti garden, New Plymouth.

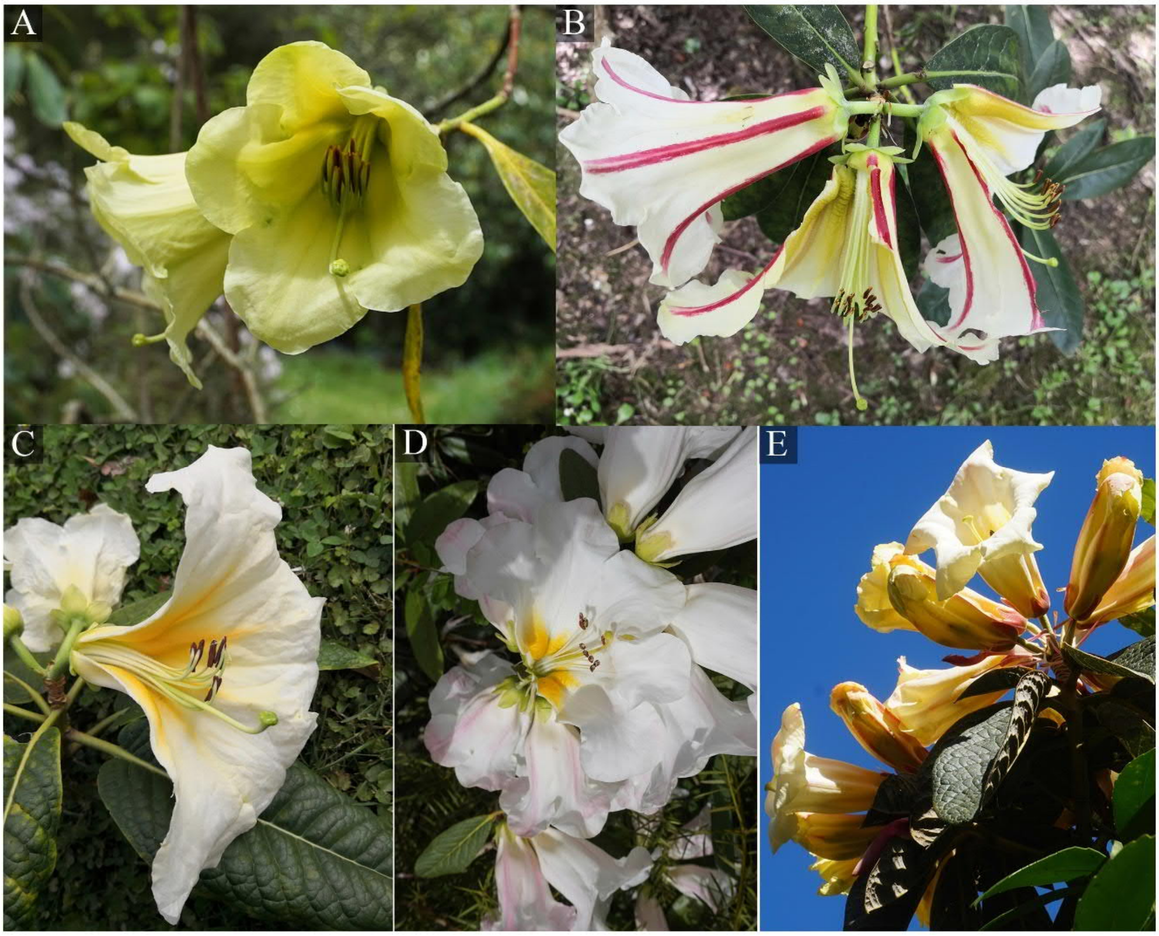

Figure 5.1 Taxa of subsection *Maddenia* used for controlled pollination in this study. A) *R. dalhousiae* var. *dalhousiae* (OM32); B) *R. dalhousiae* var. *rhabdotum* (OM26); C) *R. excellens* (HP01); D) *R. lindleyi* (OM52); E) *R. nuttallii* (OM50)

5.2.2 Controlled pollination

Flowers were first emasculated by removing anthers immediately before, or when the flowers started to open (anthesis). Stigmas were carefully sealed with surgical tape (micropore tape) to prevent contamination from self pollen or insect-borne foreign pollen. Fresh pollen was used for self-pollination, and for cross-pollination when the accessions of the same taxon were in flower at the same time. Otherwise, mature and fresh anthers were collected before dehiscing, dried and preserved over silica gel at 4°C until pollination (Fig. 5.2A). When the stigmas turned receptive (sticky and visibly wet), controlled pollinations, either selfing or outcrossing, were made on at least three flowers for each plant (Table 5.1). Both selfing and intraspecific crosses were made 5–7 days after anthesis when the stigma presented a visible exudate indicating receptivity, on plants between 10:00am–12:00pm on sunny days in November 2021 or January 2022, in New Zealand, depending on blooming time. After the micropore tape was carefully removed from the stigma, pollen was applied to the moist surface by dipping the stigma in the stored anthers (Fig. 5.2A). For selfing, pollen grains were applied by touching dehiscing anthers from the same plant to the stigma. Pollen grains were visibly attached to the stigma. Pollinated stigmas were covered with surgical tape to stop pollen contamination from other sources while the stigmas were still fertile. Each pollinated flower was tagged with the parental combination (or selfing) and pollination date.

Pollinations were replicated on at least three flowers per plant and on two plants for each selfing or intraspecific cross (Fig. 5.2; Table 5.1). Due to different flowering times of plants causing limited availability of pollen and geographical distance between different accessions, crosses were only made one-way rather than reciprocally, or only intraspecific crosses, but no selfing for some accessions. Details of plant accessions, pollination sets and the number of pollinated flowers per plant are shown in Table 5.1.

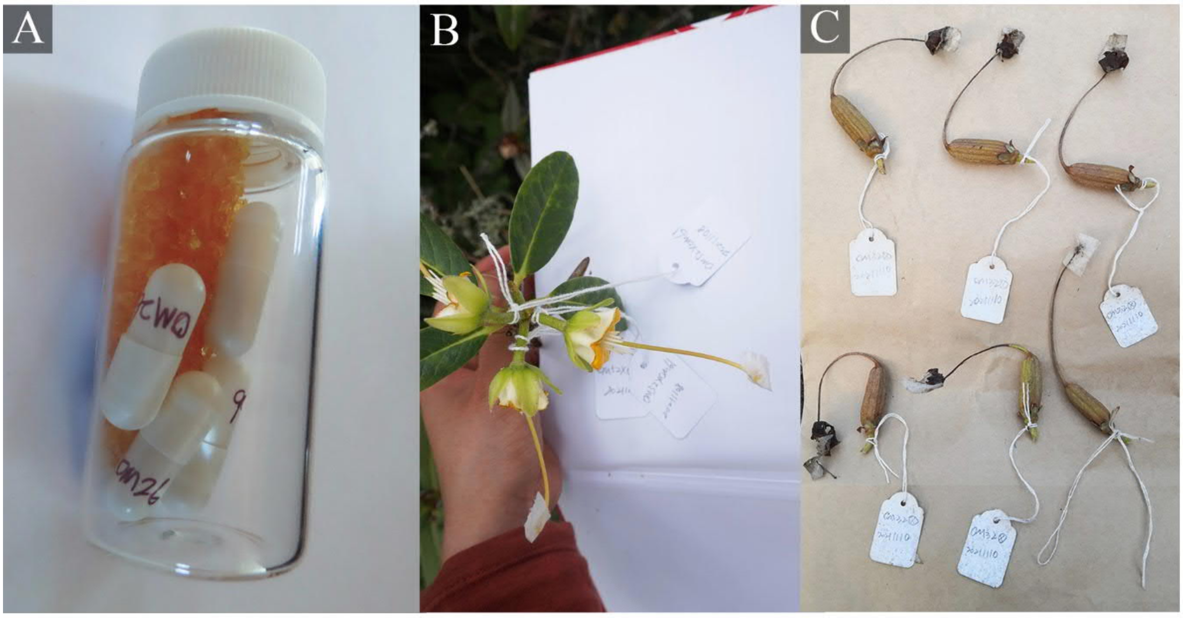

Figure 5.2 Controlled pollination. A) pollen grains preserved over silica gel; B) stigma taped and labelled after hand pollination; C) harvested seed capsules

5.2.3 Harvest and storage of seed capsules

Seed capsules were harvested before dehiscing when they were turning brown (ripe), approximately four months post-pollination. The fruit set was recorded (Table 5.1). The seed capsules, harvested separately in paper bags, were stored at room temperature (~20°C) for ~6 months. After they became ripe (i.e., most had dehisced), the capsules were stored in a cold room (~4°C) until seed germination experiments were conducted (within one year).

5.2.4 Seed viability

5.2.4.1 Seed cleaning and weight measurement

Seed capsules were cracked by hand and all seeds shaken off, then filtered with a sieve (355 mic) to remove debris. Seed weight was measured for each of three random capsules per pollination. For each capsule, five lots and 50 seeds for each lot were measured to calculate thousand-seed weight (Fig. 5.3). Weight of all seeds in each capsule was also measured to calculate the approximate seed number.

Figure 5.3 Cleaning seed capsules and measuring seed weight. A) cracking seed capsules, removing debris, and filtering seeds with a sieve (355 mic); B) counting 50 seeds for each of five lots; C) weighing each lot of 50 seeds

5.2.4.2 Seed germination

Seeds from each pollination were germinated to examine their viability. For each pollination set, 50 randomly selected seeds with three replicates (capsules) were sown on blotting paper in a sealed transparent box. All seeds were incubated in a plant growth chamber (Conviron Adaptis CMP6010, Canada) for germination. The thermoperiod was set to 15/25°C and photoperiod at 16h dark/8h light at ~6 µmol m^{-2} s^{-1}, following the optimal germination conditions for other *Rhododendron* species (Tiwari & Chauhan, 2007; Lin & Wang, 2017). Seeds were watered and seed germination was recorded weekly for 7 weeks, after which no more seeds germinated. Seeds showing radicle emergence were recorded as germinated. Germination rate was calculated as the percentage of germinated seeds among the total number of seeds sown.

Two more seed sets from the same capsules of the ‘Control’ group as described above, were sown and used to identify the possible impact of X-ray scanning or fungicide treatment on the germination of *Rhododendron* seeds. For one of these additional sets, seeds were scanned under X-ray to confirm seed fill before they were sowed, with a dosage of 31 kilovoltage, ~7s (UltraFocus 60, Faxitron®, USA). Following mould development being observed during germination in the ‘Control’ and ‘X-ray’ groups, another three replicates each with 50 seeds from the corresponding accession, were treated with Ridomil fungicide (Gold® MZ WG, 1 g/L) during sowing (‘Ridomil’ group). Seeds were then sprayed with water weekly as for the ‘Control’ group.

Data were analysed using SAS 9.13 (SAS Institute Inc, USA) with a rejection level set at P = 0.05. A generalized linear model (GLIMMIX procedure) was used to compare seed germination of each taxon between treatments (i.e., 'Control', 'X-ray', 'Ridomil') for each pollination or between pollinations (i.e., self, outcross) of each treatment with a Binomial distribution followed by a *Logit* function after the model. A Tukey-Kramer test was applied for multiple comparisons. The number of seeds and number of germinated seeds were '*x*+1' transferred before analysis, as some data on germination were zero.

5.2.4.3 seed X-ray – germination positional test

To examine whether seed fill shown by X-ray can indicate seed germination, a positional test was performed to investigate the correlation between seed radioscopy and germination rate. Six lots of 25 seeds each from different pollinations were scanned under X-ray (setting the same as in 5.2.4.2) then moved directly onto blotting paper. Seeds were sprayed with Ridomil prior to sowing to limit fungal infection. Seeds of each pollination (self/outcross) were also observed under a stereo microscope (Olympus) to assess maturity and fullness.

5.3 Results

5.3.1 Fruit set and seed weight

Fruit set was recorded for different pollinations in each of the five experimental taxa (Table 5.1). Most pollinations, both self and outcross, produced fruit(s) and seeds in the different taxa. The one exception was *R. excellens*, that yielded no seed; although the self and outcross had one fruit set each, there was no seed in the capsule. In other taxa, most pollinations produced seeds successfully, with all pollinated flowers setting fruit (e.g., *R. lindleyi*).

Thousand-seed weight was recorded for each pollination (Table 5.1). Thousand-seed weight of the four taxa (except for *R. excellens* that did not produce seeds) ranged from 0.0704 to 0.1139 g. Thousand-seed weight of *R. dalhousiae* (including the two subspecies) was higher than *R. lindleyi* and *R. nuttallii*. For *R. dalhousiae* var. *dalhousiae*, *R. lindleyi* and *R. nuttallii*, the thousand-seed weight of self-pollination was lower than that of the outcross. In contrast, for *R. dalhousiae* var. *rhabdotum*, the thousand-seed weight of the outcross was lower.

Table 5.1 Intraspecific pollination (self and outcross) of subsection Maddenia species. *Following Gibbs et al. (2011) and the updated Red List category in Chapter 2 (List S2.3). In the ‘Pollination’ column, self is represented by ‘⊗’ while outcross is ‘(maternal parent) × (paternal parent)’

Species	Red List*	Pollination	Number		Thousand-weight (g)	Approx. seed number/capsule
			Stigmas	Capsules		
R. dalhousiae var. *dalhousiae*	LC	OM32 ⊗	5	5	0.0940±0.0022	4580
		OM32 × CH15	4	1	0.1007±0.0013	3512
R. dalhousiae var. *rhabdotum*	VU	OM29 ⊗	9	6	0.1139±0.0015	4150
		OM29 × OM26	5	4	0.1065±0.0039	3553
		OM26 × OM29	3	3	0.0895±0.0008	4081
R. excellens	VU	HP01 ⊗	6	1 (empty)	-	-
		HP01 × PK01	7	1 (empty)	-	-
		HP01 × PK10	11	0	-	-
R. lindleyi	LC	OM52⊗	7	7	0.0803±0.0080	2423
		OM52 × PK39	10	10	0.0821±0.0205	2377
R. nuttallii	NT	OM50 ⊗	11	9	0.0704±0.0069	6825
		OM51 ⊗	11	11	0.0727±0.0029	5428
		OM50 × OM51	13	13	0.0780±0.0044	6512
		OM50 × CH16	11	11	0.0804±0.0041	7522

The approximate number of seeds in each capsule was calculated based on weights of thousand seeds and total seeds in the capsule (Table 5.1). The approximate seed number in each capsule showed different ranges in the four taxa measured. While seed numbers in the capsule of the two *R. dalhousiae* subspecies are similar (3512–4580), seed capsules of *R. lindleyi* had fewer (2377–2400) seeds, and *R. nuttallii* had as many as 5428–7522 seeds.

5.3.2 Seed germination

Seeds reached peak germination mostly within 6 weeks after the time of sowing. Few seeds germinated in the seventh week, while some seeds that germinated earlier had started to die. Treatment with fungicide (‘Ridomil’ group), prevented the fungal contamination that occurred in the ‘Control’ and ‘X-ray’ groups. Figure 5.4 shows the seed fill observed under stereo microscope and X-ray, the germination test and a developing seedling.

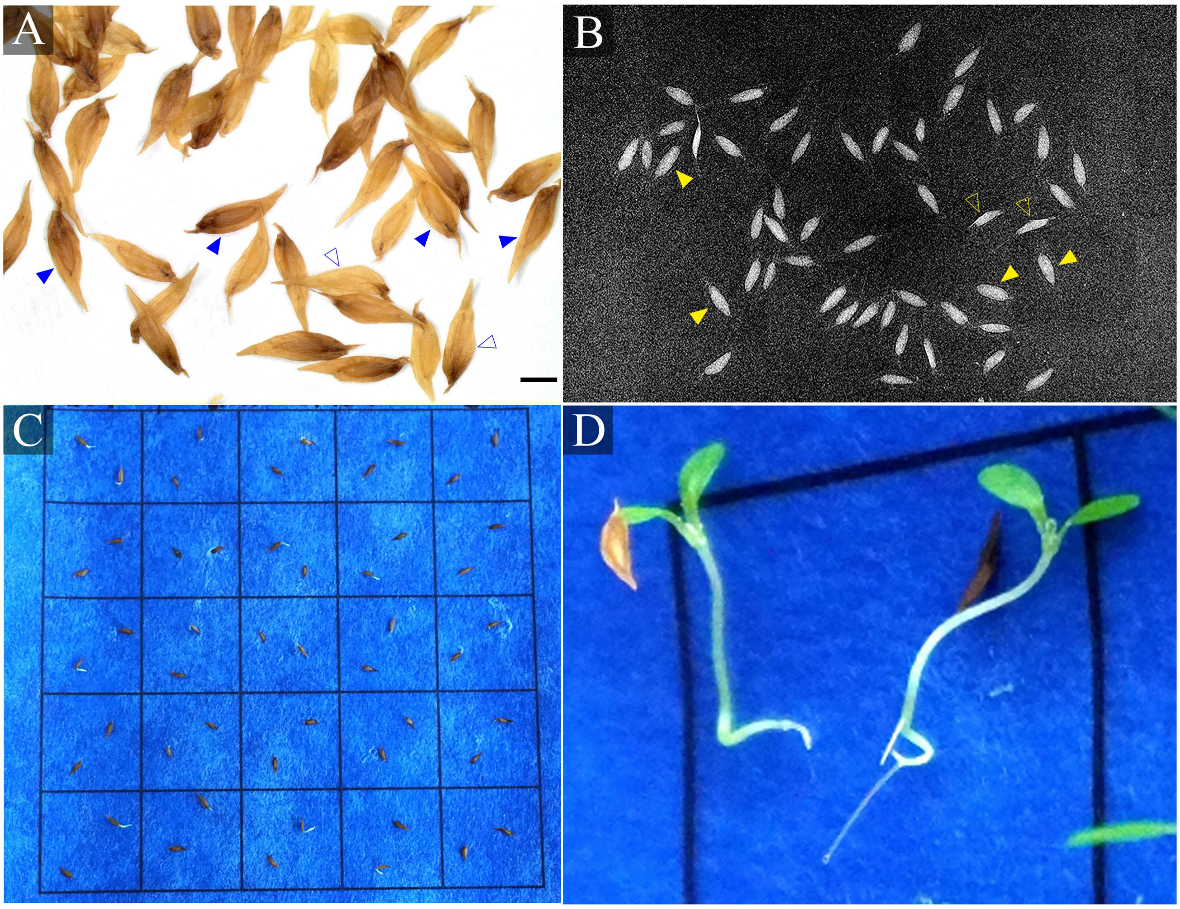

Figure 5.4 Example of the result from experiments on seed fill and germination (*R. dalhousiae* var. *dalhousiae* OM32×CH15). A) seed morphology under stereo microscope (scale bar 1 mm); B) X-ray scan showing the bright seed and faint seed appendage including the 'wing' structure and 'tails' (micropylar and chalazal ends); C) germination test (control set) D) seedlings with emerged cotyledons. Full triangles in A) and B) point to examples of full seeds, while empty triangles point to partially-full seeds.

Table 5.2 Effects of different pollinations and treatments on seed germination rate (%) for different taxa. In the ‘Pollination’ column, self is represented by ‘⊗’ while outcross is ‘(maternal parent) × (paternal parent)’. Within each taxon, means (± SE) followed by the same letter in each column (English) comparing pollinations or row (Greek) comparing treatments are not significantly different ($P > 0.05$), using a Tukey-Kramer test. The F value represents statistical significance of the test. The (d,f) values represent numbers of degrees of freedom, in the model and associated with the model errors, respectively

Taxon	Pollination		Treatment			$F_{(d,f)}$	P
			Control	Ridomil	X-ray		
R. dalhousiae var. *dalhousiae*	OM32 ⊗		47.660±6.385 b α	38.667±13.283 b α	52.667±21.674 b α	$3.01_{(2,6)}$	0.125
	OM32 × CH15		92.544±2.472 a α	86.667±1.764 a αβ	81.755±1.185 a β	$3.64_{(2,6)}$	0.092
		$F_{(d,f)}$	$54.20_{(1,4)}$	$62.70_{(1,4)}$	$26.69_{(1,4)}$		
		P	0.0018	0.0014	0.0067		
R. dalhousiae var. *rhabdotum*	OM29 ⊗		71.333±9.684 a α	59.714±5.353 a α	65.583±1.960 a α	$2.19_{(2,6)}$	0.1933
	OM29 × OM26		72.667±5.696 a α	38.667±8.511 b β	48.000±14.189 b αβ	$17.43_{(2,6)}$	0.0032
	OM26 × OM29		50.722±2.443 b α	47.518±3.390 ab α	43.333±8.743 b α	$0.80_{(2,6)}$	0.4928
		$F_{(d,f)}$	$9.58_{(2,6)}$	$6.50_{(2,6)}$	$7.88_{(2,6)}$		
		P	0.0136	0.0315	0.0210		
R. lindleyi	OM52 ⊗		36.667±20.276 a α	34.000±18.148 a α	32.000±16.371 a α	$0.32_{(2,6)}$	0.7381
	OM52 × PK39		24.000±15.875 a α	17.801±9.102 b α	25.061±17.675 a α	$1.20_{(2,6)}$	0.3632
		$F_{(d,f)}$	$5.40_{(1,4)}$	$9.48_{(1,4)}$	$1.89_{(1,4)}$		
		P	0.0809	0.0370	0.2411		
R. nuttallii	OM50 ⊗		5.333±5.333 b α	1.333±1.333 b α	6.6667±6.667 b α	$1.80_{(2,6)}$	0.2447
	OM51 ⊗		64.667±3.528 a α	65.333±6.766 a α	52.259±7.860 a α	$3.28_{(2,6)}$	0.1091
	OM50 × OM51		2.083±2.083 b α	0 b α	0.667±0.667 bc α	$0.56_{(2,6)}$	0.5976
	OM50 × CH16		0 b α	0 b α	0 c α	$0_{(2,6)}$	1.0000
		$F_{(d,f)}$	$54.22_{(3,8)}$	$51.51_{(3,8)}$	$40.53_{(3,8)}$		
		P	<0.0001	<0.0001	<0.0001		

The germination rates were compared between self and outcross within each taxon, which varied among different taxa (Table 5.2). In *R. dalhousiae* var. *dalhousiae,* seeds from the outcrosses had a significantly higher germination rate than those from the self (P = 0.0018, 0.0014, 0.0067 for the 'Control', 'Ridomil', 'X-ray' group, respectively). While in *R. dalhousiae* var. *rhabdotum*, the selfing seeds had a relatively higher germination rate (P = 0.0136, 0.0315, 0.0210). In *R. lindleyi*, seeds from self and outcross showed similar germination rates (P = 0.0809, 0.0370, 0.2411). In *R. nuttallii,* seeds from the OM51 selfed showed a significantly higher germination rate than OM50 selfed plant or crossed plants (P < 0.0001 for all three treatments).

The results of the germination rate were also compared among different treatments ('Control', 'Ridomil', 'X-ray') for each pollination. In general, germination of seeds scanned under X-ray or treated with Ridomil were not significantly different from the 'Control' group. However, for two intraspecific outcrosses, *R. dalhousiae* var. *dalhousiae* OM32×CH15 (P = 0.092) and *R. dalhousiae* var. *rhabdotum* OM29×OM26 (P = 0.0032, significant), seed germination of the 'Ridomil' and 'X-ray' groups was lower than for the 'Control' group (Table 5.2).

5.3.3 X-ray seed quality for seed germination

The positional test of X-ray seed fullness and seed germination was performed to investigate the correlation of radiography results in relation to germination. Seeds that were identified as empty in the X-ray image (invisible) did not germinate (Fig. 5.5A-A3). When the X-ray image indicated a seed to be partially full (embryo faintly visible or deformed), the seed in some cases did not germinate, for example, this was observed especially for *R. nuttallii* OM50×OM51 (Fig. 5.5F). Others of the partially full seeds exhibited poor growth (unable to develop cotyledons and/or showing brownness) (Fig. 5.5 E-C3). Some of these apparently partially full seeds might or might not establish normal seedlings (Fig. 5.5C-B4).

The stereo microscopy image was also used as a reference of seed maturity and fullness. The structure of seeds, including the embryo and the appendage (wing structure) could be easily observed. Seeds of *R. nuttallii* (Fig. 5.5E&F) showed a smaller embryo and greater area of appendage than *R. dalhousiae* and *R. lindleyi*. The seeds of *R. nuttallii* OM50×OM51 (Fig. 5.5F) showed a lower maturity (as indicated by the pale colour) and less full embryo, compared to OM51 selfed (Fig. 5.5E).

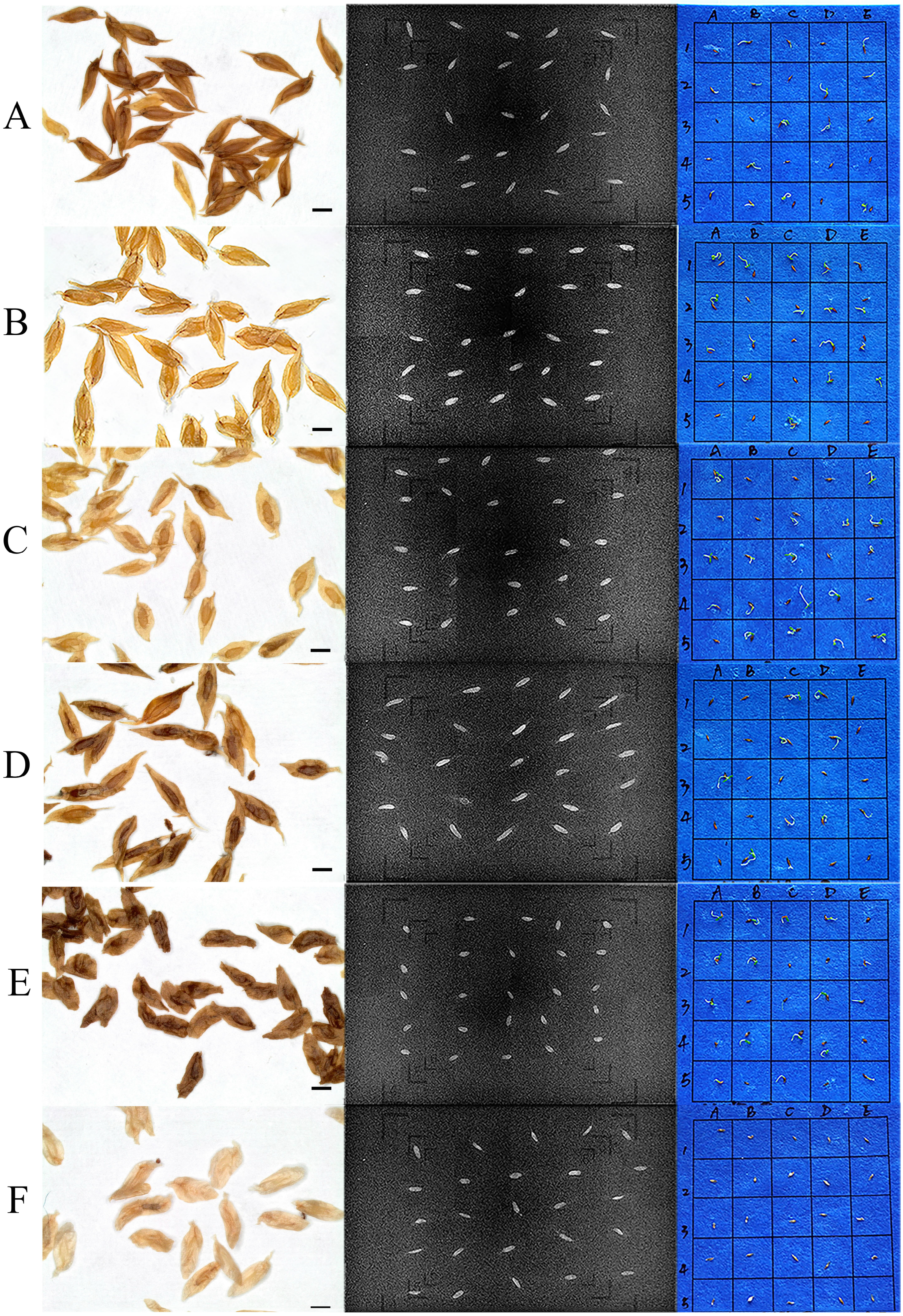

Figure 5.5 Positional test of *Rhododendron* seeds comparing fullness under stereo microscope (left) and by X-ray imaging (middle) with seed germination (right). Seed position in the X-ray image corresponds to that in the germination in the same row. Every row represents seeds from the same pollination: A)

R. dalhousiae var. *dalhousiae* OM32⊗; B) *R. dalhousiae* var. *rhabdotum* OM29⊗; C) *R. lindleyi* OM52⊗; D) *R. lindleyi* OM52×PK39; E) *R. nuttallii* OM51⊗; F) *R. nuttallii* OM50×OM51. Self is represented by '⊗' while outcross is '(maternal parent) × (paternal parent)'. Scale bar 1 mm

5.4 Discussion

5.4.1 Intraspecific compatibility of the examined species

This case study examined the intraspecific compatibility of five taxa in subsection *Maddenia*. Both fruit set and seed germination were investigated as measures of compatibility. The taxa showed different levels of intraspecific compatibility, and the compatibility between self and cross pollinations varied.

The Vulnerable taxon *R. dahousiae* var. *rhabdotum* showed relatively high intraspecific compatibility together with *R. dalhousiae* var. *dalhousiae* (Least Concern). This is consistent with the only result of intraspecific pollinations previously performed for *R. dalhousiae* by Williams et al. (1990). The conservation efforts for this taxon should be focused on collecting more wild samples, as fewer than three wild plant accessions were recorded in the *ex situ* collection survey (Chapter 2). As *R. dalhousiae* var. *rhabdotum* is morphologically recognizable and phylogenetically distinct from *R. dalhousiae* var. *dalhousiae* (Fig 4.3, Chapter 4), collections of these two subspecies should be always differentiated, which is often neglected by botanic gardens as some accessions were recorded as the species *R. dalhousiae*.

Rhododendron excellens (Vulnerable) in the present study was unable to produce seeds from selfing or outcrossing even through fruits formed. This agrees with the low self compatibility concluded from previous studies where the numbers of seeds produced were significantly lower than outcrosses; and varied seed set was observed in cross pollinations, where a fruit might have no seeds (Tian, 2011; Cai et al., 2022). The low compatibility may be the main reason why it is Vulnerable in the wild (Gibbs et al., 2011), as the wild populations remain small and face difficulties in producing offspring. The high inbreeding depression of *R. excellens* requires particular attention for conservation of this species both *in situ* and *ex situ*. Sampling more accessions from the wild is suggested to capture the diversity of this species in *ex situ* conservation, especially from distribution areas which current *ex situ* collections have not covered (details of ecogeographical representation referring to Chapter 2). Investigation on causes of the inbreeding depression of this species could also be conducted for possible solutions to increase seed production, such as *in vitro* cultivation (van der Walt et al., 2022). Furthermore, as *R. excellens* has a close relationship with *R. liliiflorum* (Least Concern) and *R. levinei* (Near Threatened) (Fig 4.3, Chapter 4), morphological identification should be rigorous in field sampling.

Rhododendron lindleyi (Least Concern) showed partial self- and intraspecific cross-compatibilities, but smaller seed number per capsule than other species in the present study. However, this species did not produce seeds following self pollination of multiple plants by Rouse et al. (1993). Further investigation is needed to understand the breeding system of *R. lindleyi*, as well as to verify its possible paraphyly observed in Chapter 4.

For *R. nuttallii* (Near Threatened), self-compatibility was observed to be higher than for the intraspecific cross, although the low seed germination observed from crosses may also have resulted from seed immaturity. This partial compatibility agrees with its certain degree of self compatibility in prior work (Rouse et al., 1993). Also, the difference in seed production through self-pollination between the two wild accessions of *R. nuttallii* may indicate different levels of compatibility in wild populations from different geographic ranges. In turn, this may suggest that more wild sampling should be the priority of diversity conservation for wild populations in China due to their low compatibility, while the diversity of populations in Vietnam could be maintained employing the other option of controlled pollination in *ex situ* collections. As the molecular phylogeny in Chapter 4 supports the synonymy of *R. sinonuttallii* (Vulnerable) with *R. nuttallii*, botanic gardens may consider the diversity conservation of *R. sinonuttallii* as variation of *R. nuttallii*. However, the confirmation of relationship between these two species requires further investigation with more samples.

In summary, to conserve threatened species, the present study shows that selfing and outcrossing could be beneficial for maintaining germplasm of *R. dalhousiae* var. *rhabdotum* (Vulnerable) and *R. nuttallii* (Near Threatened) by performing intraspecific pollination. In contrast, *R. excellens* (Vulnerable) was found to be self-incompatible with no seed set, which is in keeping with its extremely low self-compatibility and varied outcross compatibility (possibly zero seed set) reported in previous studies (Tian, 2011; Cai et al., 2022). More wild sampling rather than strategic breeding, should be scheduled to increase the genetic diversity of this species conserved in *ex situ* collections.

5.4.2 Testing seed viability for *Rhododendron* species

For *Rhododendron* species, limited information is available for seed weight and germination on the Seed Information Database (https://ser-sid.org/). In particular, there are no data for thousand-seed weight and germination rate for seeds of *R. dalhousiae* var. *dalhousiae*, *R. dalhousiae* var. *rhabdotum*, *R. lindleyi* and *R. nuttallii*. Data from the present study fill this knowledge gap for the four examined taxa and provide information for future research.

Different studies have reported that *Rhododendron* seeds can germinate when mature, without any pre-treatment (Williams et al., 1990; Glenn et al., 1999; Tiwari & Chauhan, 2007; Lin & Wang, 2017). *Rhododendron* seeds retain viability for one year or often longer without special storage conditions (apart from chilling and dryness), and appropriate temperature, water, humidity and light conditions are necessary for germination (Williams et al., 1990). In the present study, as the incubation conditions were set at optimal thermoperiod (15/25°C) and photoperiod (16/8h) according to prior studies (Glenn et al., 1999; Tiwari & Chauhan, 2007; Tian, 2011; Lin & Wang, 2017), the apparently viable seeds that did not germinate were likely to be affected by other factors, such as seed maturity. This was observed for seeds from *R. nuttallii* OM50×OM51, for which the seeds showed little brown colour (immature) in the microscopy images, and none of them germinated, although they were observed to be viable in the X-ray image (Fig. 5.5). A Tetrozolium test, used as a backup method in seed banking (ISTA, 2023) could be performed to confirm the viability of these seeds that did not germinate, but which appeared to be viable in the X-ray image. However, the applicability of the Tetrazolium test for *Rhododendron* seeds also awaits investigation, as there is very little information available except for a single study (Kumar & Sharma, 2020).

Seed fullness was demonstrated with X-ray images, with seed viability verified with the germination test. The results in this study suggest that although the X-ray image can show fullness of *Rhododendron* seeds, the image resolution was too low to identify the internal structure (i.e., embryo and endosperm), thus was unable to predict the seed germinability. The accuracy of X-ray imaging has been reported to depend on seed size and structure (Martyn Yenson et al., 2021, pp.140-145). For *Rhododendron* seed, the present study showed that the X-ray image can assist in identifying ‘dead’ seeds (invisible under X-ray) that will not germinate, but it has a low accuracy for predicting viability through differential seed fullness (Fig. 5.7). The small size (~1.5 mm long by ~0.5 mm wide, Fig. 5.5) of the *Rhododendron* seeds is likely a main cause of the low image resolution, as multiple (25) seeds were captured at a time for the convenience of positional test. The resolution could possibly be improved by adjusting the X-ray settings and focusing on fewer seeds. The low image resolution also makes it difficult to manually or automatically measure seed characteristics for seed quality analysis through the X-ray images, as performed for other species in such as Brassicaceae, *Leucaena* (Fabaceae) or *Pinus* (Pinaceae) (Tay & Hu, 2005; Medeiros et al., 2018; Karamysheva et al., 2020; Musaev et al., 2022). Other factors such as water content may as well affect the image quality (Gagliardi & Marcos-Filho, 2011), and this requires investigation. For the effect of X-ray on seed quality, there is limited information in existing studies. The lack of reliability of X-ray technology for testing the quality of *Rhododendron* seeds agrees with another study on lettuce seeds (Tay & Hu, 2005).

Williams (1990) mentioned the high risk of fungal diseases of *Rhododendron* seedlings during the emergence of the cotyledons. In this study, the application of fungicide when sowing seeds effectively prevented infection but had little impact on the germination rate, although it is unlikely that the seedlings would have survived beyond a few weeks without treatment. Seed germination rate did not change significantly after the treatment with Ridomil fungicide for all species. A single exception was that the fungicide might have inhibited the germination of seeds from outcrosses of *R. dalhousiae* var. *dalhousiae* and *R. dalhousiae* var. *rhabdotum* (Table 5.2). Fungicide seed treatment might inhibit the growth of seedlings of plant species due to decrease of endophytes associated with root systems (Zhang et al., 2009; Ayesha et al., 2021). For some orchid seeds, fungicides were reported to inhibit the growth in vitro of shoot tip explants but no negative effect on the germination (Brown et al., 1981). Further work is needed on the possible effect of fungicide on *Rhododendron* seed germination and seedling growth. Nevertheless, as this study has identified, fungicide is effective for protecting *Rhododendron* seeds/seedlings from infection. Therefore, the application of fungicide should be a necessary precaution in the raising of healthy offspring from intraspecific pollinations in botanic garden practice.

5.4.3 Maintaining germplasm in botanic garden collections of *Rhododendron*

In germplasm conservation, controlled pollination is an important tool used to maintain diversity of *ex situ* accessions, particularly in genera where open pollination cannot be used because of the potential for cross hybridization. For *Rhododendron* species in particular, existing botanic garden collections can be valuable for maintaining conserved germplasm, as the wild populations of many species are either very limited, or under considerable threat (Gibbs et al., 2011). For these species, *ex situ* collections provide backup material for the threatened species, and collection management should include maintenance of diversity through sexual reproduction via strategic breeding.

There are three main issues to consider in intraspecific controlled pollination in *ex situ* collections. Firstly, it is desirable to increase genetic diversity by making crosses among unique accessions, possibly at different botanic gardens. This requires knowledge on origin and genetic diversity of the accessions present in different collections. Secondly, pollen collection and storage are required if the pollination is performed among accessions at different locations. For example, there was only one accession of *R. lindleyi* nearby in this study, but three at a distant garden, requiring pollen to be collected and stored. Thirdly, flowering time of different accessions of the same species is an important factor when selecting the parental plants. Pollen storage (Rouse, 1984) is required if the blooming times do not overlap. In outcrosses, when there is no preserved pollen available, the plant flowering later can only be used for pollen collection in that season, as a paternal parent. Its use as a maternal parent has to be in the next blooming season, receiving pollen collected in the prior season.

The varied compatibility of taxa or their different accessions, together with variation in other aspects studied in previous chapters, represent intraspecific diversity and should be taken in account for species conservation. These intraspecific variations can be seen in different varieties of the same species. For example, *R. dalhousiae* var. *dalhousiae* in this study shows lower self compatibility than intraspecific cross, while *R. dalhousiae* var. *rhabdotum* is the opposite. *R. dalhousiae* var. *dalhousiae* flowers earlier (December in New Zealand) than *R. dalhousiae* var. *rhabdotum* (January). While the two varieties show distinct division in the molecular phylogeny (Figs. 4.3 & S4.3), their natural distributions show a certain degree of difference, although greatly overlapping in Bhutan and China (S Xizang). *R. dalhousiae* var. *rhabdotum* has narrower distribution and spreads farther east to Arunachal Pradesh in India, while *R. dalhousiae* var. *dalhousiae* spreads wider and farther west to NE India (Sikkim and West Bengal) and E Nepal (List S2.3).

Another example of intraspecific variation is exhibited in the two wild accessions of *R. nuttallii*. The two accessions were from two different origins (OM50 from northern Vietnam and OM51 from China, Table 5.1) and showed significantly different levels of self-compatibility (Table 5.2). While they are located adjacent to each other in the local *ex situ* garden, they flower at different times (OM51 flowered about two weeks earlier as observed in November 2021 in New Zealand). The two samples (OM50, OM51) are also clustered in different subclades in the molecular phylogeny, reflecting their genetic difference (Figs. 4.3 & S4.3). These variations on flowering time, geographic origin, and molecular phylogeny and pollination compatibility, among different varieties or different accessions of same species/taxon, all represent their intraspecific diversity.

5.5 Conclusion

This study investigated the intraspecific compatibility of five taxa in *Rhododendron* subsection *Maddenia* that have been classified in different IUCN Red List categories: *R. dalhousiae* var. *dalhousiae* (Least Concern), *R. dalhousiae* var. *rhabdotum* (Vulnerable), *R. excellens* (Vulnerable), *R. lindleyi* (Least Concern) and *R. nuttallii* (Near Threatened). Fruit set and germination rate of these taxa varied. Self and intraspecific outcross compatibilities differ among different species/taxa. Different conservation actions were therefore proposed depending on the taxon. The compatibility also varied among different varieties and/or different accessions of the same species, suggesting intraspecific diversity, which should be taken into consideration in biodiversity conservation. However, datasets of the selected species in this study are limited. Future research should evaluate more accessions (preferably of wild origin) to confirm the intraspecific compatibility of related taxa.

With respect to data and techniques, the seed data from this study (i.e., thousand-seed weight and germination rate) contribute to knowledge required for seed banking of the studied species. When the popularly used technology of X-ray radiography was tested on *Rhododendron* species, it proved to have limited applicability for predicting viability of *Rhododendron* seeds. The technology needs to be optimised by undertaking further investigation.

Overall, this study provides information on intraspecific compatibility and seed characterization for the species examined. It also presents an exemplar of how to incorporate various aspects of knowledge about a species (conservation status, diversity captured in *ex situ* collections, taxonomic distinction and pollination compatibility) that are used to choose the optimised strategy for species conservation in botanic garden practice.

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Chapter 6

General discussion

Both taxonomy and diversity of *Rhododendron* species in subsection *Maddenia* have been investigated in this thesis and discussed in relation to *ex situ* conservation. In previous chapters, several aspects of *Rhododendron ex situ* conservation (Fig. 1.1) were examined and the main challenges highlighted: genetic representation of wild accessions in *ex situ* living collections (Chapter 2); ploidy variation in *Rhododendron* and its implications for conservation (Chapter 3); application of a molecular phylogeny to resolve taxonomic issues among *Maddenia* species (Chapter 4); horticultural practice for maintaining conserved diversity in living collections (Chapter 5). This final chapter summarises the main findings of the thesis and highlights their implications for *Rhododendron* conservation. Directions for future research are proposed, including those related to the limitations of the present research.

6.1 Diversity of *Maddenia* species conserved in *ex situ* collections

Living collections in botanic gardens are invaluable resources for the integrated conservation of threatened species. Wild-source collections in particular represent genetic diversity of wild populations (Heywood, 2017), and assessment of the diversity of existing *ex situ* living collections in global botanic gardens should inform further conservation action. Based on the data compiled for each of the 65 taxa updated, examinations of the living collections at both taxon and accession levels suggest that the *Maddenia* species are relatively well represented in cultivation (Chapter 2). At the taxon level, 55 of the 65 *Maddenia* taxa are cultivated, with over 86% of the living collections conserved in 66% of global botanic gardens. At the accession level, half of the 18 threatened taxa (Critically Endangered, Endangered, Vulnerable) and the 12 Data Deficient taxa require more wild collections to capture sufficient diversity of accessions. Such an assessment is important for the monitoring of current *Rhododendron* collections of species under threat, as well as recommending species for urgent action. This kind of diversity analysis enables further efforts to reduce potential diversity loss, which is under the scope of the GSPC 2011–2020 targets (especially Target 8, BGCI, 2012a) and the CBD post-2020 Global Biodiversity Framework (Hoban, Bruford, et al., 2020; CBD, 2021).

Most existing gap studies evaluating *ex situ* collections have focussed primarily at the taxon (or species) level for identification of species presence in living collections (Kozlowski et al., 2012; MacKay et al., 2018). Some have performed analyses more deeply, at the accession level, in order to develop an understanding of the wild diversity represented (Christe et al., 2014). One of the main reasons for this is that increased knowledge has been gained about the populations comprising the species. An example is the *ex situ* gap analysis for *Magnolia* species, which first studied taxon-level collections, then in-depth accession-level data (Linsky, Crowley, et al., 2022). Due to the remote mountainous habitats, sizes of *Rhododendron* wild populations are still largely lacking investigation, hence their genetic diversity is poorly understood (Gibbs et al., 2011), with the exception of some species that do not include *Maddenia* species (Wu et al., 2014; Yadav et al., 2019). This lack of knowledge regarding the extent of wild populations makes the method of using geographic circles to scale the size of represented wild populations used in studies of other species (Beckman, 2019; Khoury et al., 2019; Bruns et al., 2022) not feasible for *Rhododendron*. The present diversity analysis using wild-source accessions in botanic gardens establishes a method of using ecogeographical representation as a proxy for genetic representation (Khoury et al., 2019; Linsky, Coffey, et al., 2022) of *Rhododendron* species diversity. Despite the approximation, this method can temporarily deal with the lack of quantification of genetic diversity for most *Rhododendron* species through population genetics, which greatly helps us to understand the represented wild diversity in *ex situ* collections.

In the present study, the method of compiling taxon profiles that take into account both wild distribution and *ex situ* wild collections has proved to be informative for presenting data (List S2.3). This enables us to understand the approximate extent of diversity present in *ex situ* collections and how much is not captured or is unknown in the wild. More importantly, this method addresses several widely identified issues (Westwood et al., 2021) that challenge diversity analysis and conservation planning, particularly in current *Rhododendron* botanic garden living collections.

The first knowledge gap relates to the outdated conservation status assigned to species. The size and distribution of wild populations as well as species taxonomy are encountered as the main difficulties in making conservation assessments for *Rhododendron*. So far, GBIF and IUCN Red List maps are not specific enough to describe species distribution, as they use administrative units (state, province or country, etc.) as natural areas. This is understandable, as current GIS mapping software can only recognize locations based on manually defined places. The case study of *Rhododendron* species in this thesis suggests that more field investigations are needed to understand the size and geography of wild populations. If based on thorough geographic data, deeper understanding on the geographic source of wild collections will contribute to developing an understanding of the possible geographic patterns that are contributing to *Rhododendron* speciation and diversity.

Secondly, collection data are poorly shared among botanic gardens, hindering international collaboration towards the mutual goal of biodiversity conservation. The results in Chapter 2 highlight the importance of a global network in curating living collections collaboratively under the concept of ‘metacollection’ (Griffith et al., 2020; Breman et al., 2021; Westwood et al., 2021). However, the number of individual plants needed to capture the genetic diversity of *Rhododendron* species is yet to be determined. This difficulty in deciding the required number of plants is a common challenge in plant biodiversity assessment and it differs from species to species (Breman et al., 2021). This is also why recent genetic diversity studies on wild plants have used the geographic size of wild collections as a proxy for genetic representation (Khoury et al., 2019; Linsky, Coffey, et al., 2022). In the ‘metacollection’ approach, recording taxon-level information, i.e., solely identifying whether a species is in cultivation, is not adequate to determine the genetic representation in living collections. For species in ‘big genera’ such as *Rhododendron* that has over 1,000 species, accession-level data are urgently needed to quantify and map the wild collections and make comparisons among species for decision making. Currently, online databases (e.g., BGCI PlantSearch database) do not record accession-level data for living collections (Hudson et al., 2021). Hopefully, coordination by organizations such as Global Conservation Consortium *Rhododendron* and BGCI, will enable the establishment of a database for botanic garden accessions based on data from individual botanic gardens. Such a database might be expected to record the geographic source of wild collections more systematically, monitoring the progress of capturing wild diversity and guiding future collection to guard against the further reduction of diversity. Future research would benefit from the meta data in established databases and use programming tools to rapidly analyse information for decision making, as in the ‘meta-analysis’ outlined by Wei and Jiang (2021). This is very possible once sufficient data are captured for each species, such as the information shown in the taxon profiles of subsection *Maddenia* (List S2.3, Chapter 2).

A third common problem in *ex situ* collection management, as well as ‘metacollection’ decision making, is that many wild collections are missing documentation and/or the survival status of the accessions is out of date (Breman et al., 2021). This problem explicitly occurs within genus *Rhododendron*, and the present study was challenged by low consistency among botanic gardens when compiling the provenance data of wild accessions **(**Table S2.2**)**. It should be noted that the mapping of the species distribution and geographic source of wild accessions were processed manually, which is time demanding but more precise than following the administrative geography.

Also, the study of existing *ex situ* collections may inspire different countries to initiate their own strategies for collecting and conserving wild collections (Chapter 2). Current *ex situ* conservation of *Rhododendron* is mostly conducted in countries with many introduced *Rhododendron* species (e.g., the United Kingdom, the USA, Australia, New Zealand) rather than their countries of origin. The case study reveals that the number of wild collections of *Rhododendron* species in the 10 countries of origin is extremely small (e.g., China, Myanmar, India, Vietnam). Conservation of endemic *Rhododendron* species should be actioned urgently in case of rapid diversity loss, especially for the threatened species with small populations, such as the two Critically Endangered species *R. coxianum* and *R. fleuryi*. Programmes such as the ‘Plant Species with Extremely Small Populations’ programme developed in China (Liu et al., 2020; J. Yang et al., 2020) could be developed for the other threatened species.

6.2 Molecular phylogeny of *Maddenia* species

Effective conservation efforts should target distinct species (Heywood et al., 2006). Species delimitation may lead to changes in conservation priority and thus the conservation action that is implemented (Li et al., 2018; Ao et al., 2022; Gardiner et al., December 2019). Complex taxonomy is one of the confounding factors affecting conservation assessments in *Rhododendron* (Gibbs et al., 2011) and this is a feature of ‘big genera’ (Frodin, 2004) where species often show varied and continuous morphological features (Cullen, 1980; Davidian, 1982). Thus, in the present work, a major focus was construction of the molecular phylogeny of subsection *Maddenia*, to assist species delimitation and so enhance the development of conservation strategies.

In Chapter 4, the molecular phylogeny of *Maddenia* species was examined using a range of wild derived accessions. The main clades revealed in the phylogenetic clustering largely support the 'series – subseries' classification suggested by early taxonomists such as Stevenson (1930) and Davidian (1980) (or the 'informal groups' in Cullen, 1980). Except for the Ciliatum Series whose members were scattered (but outside of the other main clades), the three subseries of Maddenii Series were clustered in different clades. This separation supports the phylogeny of yellow-flowered species together with close species by Donald (2012). Despite the polyploidy in the *R. maddenii* samples, all were in a single clade, indicating the distinct diversification of this species complex from the other complexes in the Maddenii Subseries. This phylogenetic study addresses the importance of careful identification of the accessions sampled, highlighting the value of herbarium specimens in providing morphological evidence for rigorous identification. In addition, as suggested in Chapter 4, the first use of target capture sequencing with the blueberry baits set for construction of a *Rhododendron* phylogeny proved to be relatively informative. Future phylogenetic studies on *Rhododendron* species may continue to test more bait sets (e.g., Angiosperm353) or other sequencing technologies (e.g., genome skimming) (Chapter 4) to obtain further datasets, so that a species tree with higher confidence might be achieved.

The present study suggests that 'subsection *Maddenia*', as previously defined, is paraphyletic (Chapter 4). Species from closely related subsections (ss. *Edgeworthia*, *Boothia*) were embedded with *Maddenia* species in the phylogenetic tree, suggesting subsection *Maddenia* is not monophyletic. This confirms earlier studies where paraphyly was indicated but where only a limited number of *Maddenia* species were considered (Donald, 2012; Shrestha et al., 2018; Khan et al., 2021). In consequence, the definition of subsection *Maddenia* might be refined, by excluding some of the species (e.g., *R. fletcherianum, R. crenulatum*) to fit 'subsection *Maddenia*' as a monophyletic group, and/or broadening this subsection to include species in closely related subsections. The present work indicates that subsections *Edgeworthia*, *Boothia*, *Triflora*, could be included, while other evidence indicates subsections *Tephropepla*, *Monantha* and *Moupinensia* should be considered (Donald, 2012; Shrestha et al., 2018; Fu et al., 2021; Khan et al., 2021; Xia et al., 2021). Considering the limited sampling of wild *Maddenia* species and related species from close subsections in the present study, future phylogenetic studies are suggested to include species from all close subsections in subgenus *Rhododendron*. This will complement the present research, enabling construction of a thorough phylogeny among related subsections, as well as the species within. With respect to the concept of 'subsection *Maddenia*'

(Fig 5.1), given the strong indication that this grouping is not monophyletic, it is proposed that the species in current subsection *Maddenia* be denoted as '*Maddenia* species', in line with the use of '*Maddenia* species' in the title of this thesis.

Polyploidy represents part of the biodiversity of species and the presence of polyploids can impact phylogenetic analysis. Polyploids have been reported in some *Rhododendron* species, but the impact of polyploidy on phylogenetic analysis has not been discussed for *Rhododendron*. Therefore, after summarising the reported occurrence of polyploidy in *Rhododendron* species in general, this thesis specifically examined the ploidy variation in subsection *Maddenia* (Chapter 3; Hu, 2023). The present study identified that polyploidy in *Maddenia* species occurs only in the *R. maddenii* complex, with a high degree of ploidy variation, ranging from 4–12*x*, according to the present and previous studies. There are some prior reports of polyploids in *R. maddenii*, among which only Cubey (2003) included the whole group of *Maddenia* species but did not investigate the genetics. The present study is therefore the first using cytogenetic data to reveal the unique polyploidy of *R. maddenii* within subsection *Maddenia*.

Polyploid samples can be troublesome in genotyping, especially with short-read sequences, as the sequencing reads need to be sorted in reference to the origin of sub-genomes during sequence assembly (Mason, 2015; Andermann et al., 2020; Rothfels, 2021). Ploidy levels of all samples in the present study were therefore examined prior to their use in the phylogenetic reconstruction (Chapter 3). The maximum likelihood and Bayesian phylogenetic trees, as well as splits networks, identified the monophyly of the *R. maddenii* complex, regardless of the different ploidy levels of samples. However, the unique polyploidy of the *R. maddenii* complex in subsection *Maddenia* is yet to be explained. On one hand, it could be related to the wide distribution of wild populations and their rapid diversification in the mountainous regions. On the other side, it could result from the complex taxonomy of the species, as *R. maddenii* is 'lumped' with a few synonymous species showing a high degree of morphological variation (Chapter 3, Hu et al., 2023). The evolutionary mechanism of mixed-ploidy species is complicated (Kolář et al., 2017), and has not been studied in *Rhododendron*. For a species with a high ploidy variation as *R. maddenii*, extensive wild sampling is needed for future research to develop a robust understanding of the evolution of polyploids, as well as any possible geographic pattern associated with ploidy variation.

Despite the findings achieved in this phylogenetic study, some limitations should be noted with regard to the confidence in the results. All the discussion is based on limited prior knowledge, as nobody has undertaken a comprehensive molecular phylogeny of subsection *Maddenia*; Donald (2012) only included the yellow-flowered species (most species of the Ciliatum Series in Davidian (1982)). More samples of *Maddenia* species should be added in future studies to verify the species relationships inferred in the present study and to further resolve the molecular phylogeny of related species. This includes species for which this study was unable to define the boundary (e.g., *R. ciliicalyx*, *R. johnstoneanum*, *R. lindleyi*) (Chapter 4), or the ones not included due to lack of access to samples (e.g., *R. kiangsiense*, *R. walongense*, *R. roseatum*) (Chapter 2). In addition, *Rhododendron* hybrids could easily be present in the living collections, which challenges specimen identification and our ability to make accurate phylogenetic conclusions. An increased number of wild collected samples may more robustly illustrate the molecular phylogeny, as well as other factors impacting speciation, including geographic variation and polyploidization of species in the Himalayan region (Schwery et al., 2015; Shrestha et al., 2018; Basnett & Ganesan, 2022).

6.3 Maintaining intraspecific diversity of *Rhododendron* species in living collections

Safeguarding genetic diversity conserved in *ex situ* collections is important for maintaining species capacity to adapt to environmental changes *in situ* and *ex situ* and for provision of material to recovery programmes (Guerrant et al., 2004; IUCN SSC, 2014). In Chapters 2–4, diversity of *ex situ* collections, ploidy variation in species and molecular phylogeny of subsection *Maddenia* were examined to guide species prioritisation and highlight criteria for conservation management.

Chapter 5 followed up with respect to conservation action in botanic gardens, to conserve the genetic diversity in *ex situ* collections through horticultural practice. In species for which open pollinated seeds are frequently not ‘true’ due to hybridisation, controlled pollination is needed to maintain the germplasm conserved in botanic gardens by producing good-quality seeds for seedbanking, to back up plant material in case of diversity loss or species extinction (Schoen & Brown, 2001). Controlled intraspecific pollinations (including self and outcross) increase genetic exchange among plant accessions, which is especially beneficial for genetic conservation of a species across collections in multiple locations, under the collaborative ‘metacollection’ scheme (Hoban, Callicrate, et al., 2020; Westwood et al., 2021).

In Chapter 5, intraspecific compatibility was examined for five taxa in subsection *Maddenia* that are classified in different IUCN Red List categories: *R. dalhousiae* var. *dalhousiae* (Least Concern), *R. dalhousiae* var. *rhabdotum* (Vulnerable), *R. excellens* (Vulnerable), *R. lindleyi* (Least Concern) and *R. nuttallii* (Near Threatened). Among each of the studied taxa, fruit set and seed germination rate varied following self and cross pollination. The results were then discussed together with conservation priority of these taxa based on conservation status, diversity captured in *ex situ* collections and taxonomic distinction reported in previous chapters (Chapters 2–4). Conservation strategies were finally proposed for each taxon studied. The findings in Chapter 5 address the principle that as species self and/or outcross compatibilities differ, the breeding system of species must be studied individually to develop a tailored breeding plan for species conservation. In extreme cases, if existing accessions cannot successfully generate offspring (e.g., *R. excellens* HP01), further collections from the wild should be prioritized for species conservation.

The variations in intraspecific compatibility and flowering time among different varieties (e.g., *R. dalhousiae* var. *dalhousiae* and *R. dalhousiae* var. *rhabdotum*) or different accessions of the same species (e.g., OM50 and OM51 for *R. nuttallii*) was outlined in Chapter 5. Together with intraspecific variation in other aspects (e.g., morphological variation, geographic distribution, ploidy variation, phylogenetic relatedness) that have been discussed in the previous chapters (Chapters 2–4), they reflect the intraspecific diversity. A focus on intraspecific diversity must be incorporated into botanic garden management for biodiversity conservation of the species.

6.4 Conclusion and recommendations

Integrated plant conservation, where *in situ* and *ex situ* programmes are managed together, requires an exacting execution of both practices. This thesis investigated key elements of *ex situ* conservation by examining the existing *ex situ* collections internationally, with respect to: *ex situ* conservation gaps, species taxonomy, and conservation horticulture. The research focused on the *Rhododendron* species in subsection *Maddenia* (subgenus *Rhododendron*, section *Rhododendron*) that includes a total of 65 taxa (List S2.3, Chapter 2). Despite the high horticultural value of these species and the need for research related to undertaking conservation, subsection *Maddenia* has seldom been studied. This case study of *Maddenia* species is an exemplar of how examination of species taxonomy and diversity represented in existing *ex situ* collections can be used to guide conservation management. This thesis can also be used as a reference for similar studies in the overall genus *Rhododendron*.

In this research, *ex situ* conservation gap analysis for *Rhododendron* was developed by examining botanic garden living collections at both taxon- and accession- levels of subsection *Maddenia* (Chapter 2). The method of using the ecogeographical representation of wild-source accessions helped to examine the *ex situ* conservation gaps for *Maddenia* species, and suggested that half (9/18) of the threatened taxa and nine of the 12 Data Deficient taxa require further collection to capture adequate wild diversity. The importance of sampling the wild *Rhododendron* populations for *ex situ* conservation in their countries of origin was emphasized.

This research has progressed our understanding of the taxonomy of *Rhododendron* species particularly in subsection *Maddenia*. By reviewing the ploidy variation in genus *Rhododendron* and then estimating the ploidy levels of species in subsection *Maddenia*, Chapter 3 identified the high cytogenetic variation in *Rhododendron* species, which is part of the biodiversity to be conserved. Chapter 3 also addressed the high research value of *Rhododendron* species for studying the evolution of polyploidisation. By investigating ploidy variation (Chapter 3) and molecular phylogeny with testing of target capture sequencing in *Rhododendron* (Chapter 4), further understanding was gained concerning existing taxonomic debates for species delimitation in subsection *Maddenia*. Also, the possible paraphyly of subsection *Maddenia*, embedded with species from close subsections such as *Edgeworthia*, *Boothia* and *Triflora*, has been identified.

This research also investigated the feasibility of employing controlled pollination, as a method to be used in conservation horticulture, to maintain the intraspecific diversity in *ex situ Rhododendron* collections (Chapter 5). The different levels of intraspecific compatibility of the five taxa examined inform the necessity of developing different conservation strategies for individual species.

Therefore, this thesis provides a comprehensive study to inform decision making in botanic garden practice towards *Rhododendron* conservation. The methods, results and recommendations could be adopted by institutions as a reference for planning conservation action, both in botanic garden management (*ex situ*) and wild population assessment (*in situ*). As a general principle, this thesis addresses the importance of documenting the wild collections in botanic gardens. Maintaining the records of plant accessions is the primary step to safeguard the germplasm of the correct species. With plant biodiversity conservation as a global goal, effective action can only be achieved through frequent communication and collaboration among institutions. With the aim of maximising the function of integrated plant conservation as demonstrated in Figure 1.1, this research has discussed further efforts related to living collections, germplasm and horticulture in the previous chapters. Other aspects, such as education programmes, should also be addressed to increase public awareness of plant biodiversity conservation.

From this study it is recommended for *Rhododendron* conservation:

- That an analysis of the number and diversity of wild-sourced accessions of all threatened species of *Rhododendron* (Critically Endangered, Endangered, and Vulnerable) be undertaken and that these analyses be used to direct collection management and further field collecting;
    - That further research on the source of accessions be undertaken, to overcome the issue of poor documentation
    - That the true geographic distribution of all threatened species be investigated, to overcome the problem of poor definition of distribution
    - That collaboration with Chinese scientists be strengthened, to accomplish the above work for the Chinese species
- That further research into the polyploidy of *R. maddenii* be undertaken, with a view to examining any geographic pattern or possible cryptic speciation
- That further application of target capture sequencing on *Rhododendron* phylogenetics with testing more existing probe sets and/or baits yet to be developed from *Rhododendron* genomes, to develop a thorough understanding of species relationships especially in lower-level groups (i.e., section or subsection)
- That further phylogenetic studies of subsections in subgenus *Rhododendron* be undertaken, starting with a broader examination of the monophyly of subsection *Maddenia* and then progressing to other subsections
- That breeding systems of all threatened species be investigated to determine whether self or intraspecific cross pollination can be used to generate offspring when wild populations are small
- That subgenus by subgenus, international datasets are formed to facilitate management of metacollections of each group. Data should include details of wild accessions on

provenance (geographic coordinates) and number of living plants based on robust morphological identification. Collecting these information for each taxon should also consider data from the sites that are not yet included in the BGCI GardenSearch database. The metacollections should be managed nationally and/or internationally, based on cooperation and shared data across institutions.

This research has studied *Rhododendron* to investigate various aspects of *ex situ* conservation, in a genus where some 59% of species have a conservation issue and where conservation action is confounded by the features of a 'big genus'. It has been demonstrated how the technologies developed and used across the four research-based chapters can inform conservation efforts in (subsection) *Maddenia* species. Extrapolation of the findings to *Rhododendron* in general will assist in the long-term conservation of this genus. That said, despite the vast number of species in *Rhododendron* or other genera, efforts on understanding and protecting the biodiversity of many species are needed, so that we take care of them as of ourselves towards a sustainable environment where we live together.

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Appendix I: Supplementary Files – Chapter 2

Table S2.1 *Ex situ* living collections of *Rhododendron* subsection *Maddenia* in global botanic gardens

Table S2.2 Wild accessions of *Rhododendron* subsection *Maddenia* in the 14 surveyed botanic gardens

List S2.3 Checklist of taxon profiles of *Rhododendron* subsection *Maddenia*

Table S2.1 *Ex situ* living collections of *Rhododendron* subsection *Maddenia* in global botanic gardens

Data describing the presence of ss. *Maddenia* taxa in cultivation were collected from three key sources. Firstly, BGCI PlantSearch database (BGCI, 2021) was used as the primary indicator of presence in cultivation. However, PlantSearch only records *ex situ* collections at taxon level but not accession level. An unpublished set of BGCI data (BGCI, 2020), which contained details of the accessions held at individual botanic gardens, was therefore used as the second source. BGCI data were used, compiled and published under the BGCI Data Sharing Agreement (signed between Marion MacKay and the BGCI representative Abby Meyer on 10 July 2020).

The third source was data from seven gardens in New Zealand as a hotspot of *ex situ* conservation of ss. *Maddenia*, together with seven largest collections of ss. *Maddenia* outside New Zealand (Table 2.2). Sites in New Zealand are Pukeiti garden (Taranaki region) (BGCI member), Dunedin Botanic Garden (BGCI member), Tannock Glen and one private garden (Dunedin), Heritage Park, Cross Hills Gardens and one private garden (Manawatū region). Sites outside New Zealand are: Rhododendron Species Botanical Garden (RSBG, USA), Royal Botanical Garden Edinburgh (RBGE, UK; including RBGE at Edinburgh, Logan and Benmore), Royal Botanic Garden Kew (UK; including RBGK at Kew and Wakehurst), the Dandenong Ranges Botanic Garden (previously Olinda Garden of Parks Victoria, Australia), Arboretum Wespelaar (Belgium), University of British Columbia Botanic Garden (UBCBG, Canada) and the Arnold Arboretum of Harvard University (USA). Data include an unpublished dataset from an earlier survey by MacKay et al. (2018), together with additional data or individual garden updates in 2020. The use of collections data and permission of publishing compiled dataset were approved by the source botanic gardens.

Based on current presence of ss. *Maddenia* taxa, numbers of living collections at each *ex situ* site and per taxon were counted. Taxa were defined as ‘in cultivation’ if there was a record in any one of the data sources used, while taxa with no record in any of the data sources used were considered ‘not in cultivation’. The exception was the newly published species *R. kuomeianum* (Chang et al., 2021) that is in cultivation at RSBG, with one accession collected from the wild (Hootman, 2021 & personal communication). For the new species *R. starlingii*, wild accessions were reported earlier under its ally *R. crenulatum* (Rushforth et al., 2022), thus listed separately in the present dataset (Table S2.2; List S2.3). For other taxa, wild accessions of the synonyms were listed under the corresponding allied species. For example, accessions identified as *R. cubittii* were listed under *R. veitchianum*.

This table lists the 592 records of subsection *Maddenia* in the 73 *ex situ* sites (botanic gardens) globally. The number of records identifies the number of taxa per site; however, one taxon may have more than one record with different plant codes in the source databases, which usually arises from collections of synonyms, varieties or botanical cultivars.

Botanic garden codes in the table column ‘BG code’ are assigned by the author. Each code anonymously corresponds to a botanic garden in BGCI’s internal database.

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_01	Australia	*R. burmanicum*			LC
RhodoBG_01	Australia	*R. carneum*			NE
RhodoBG_01	Australia	*R. ciliatum*			LC
RhodoBG_01	Australia	*R. ciliicalyx*			LC
RhodoBG_01	Australia	*R. ciliicalyx*		Charisma	LC
RhodoBG_01	Australia	*R. crassum*			LC
RhodoBG_01	Australia	*R. dalhousiae*			LC
RhodoBG_01	Australia	*R. dendricola*			VU
RhodoBG_01	Australia	*R. excellens*			VU
RhodoBG_01	Australia	*R. fleuryi*			CR
RhodoBG_01	Australia	*R. formosum*			CR
RhodoBG_01	Australia	*R. johnstoneanum*			LC
RhodoBG_01	Australia	*R. johnstoneanum*		DoubleDiamond	LC
RhodoBG_01	Australia	*R. lindleyi*			LC
RhodoBG_01	Australia	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_01	Australia	*R. nuttallii*			NT
RhodoBG_01	Australia	*R. pachypodum*			LC
RhodoBG_01	Australia	*R. scopulorum*			VU
RhodoBG_01	Australia	*R. taggianum*			VU
RhodoBG_01	Australia	*R. valentinianum*			NT
RhodoBG_01	Australia	*R. veitchianum*			LC
RhodoBG_01	Australia	*R. veitchianum*		Ã—Cilipense	LC
RhodoBG_02	Australia	*R. burmanicum*			LC
RhodoBG_02	Australia	*R. carneum*			NE
RhodoBG_02	Australia	*R. ciliatum*			LC
RhodoBG_02	Australia	*R. ciliicalyx*			LC
RhodoBG_02	Australia	*R. ciliicalyx*		Hybrid	LC
RhodoBG_02	Australia	*R. ciliicalyx*		Pink	LC
RhodoBG_02	Australia	*R. coxianum*			CR
RhodoBG_02	Australia	*R. dalhousiae*			LC
RhodoBG_02	Australia	*R. dendricola*			VU
RhodoBG_02	Australia	*R. dendricola-taronense*		TaronenseGroup	VU
RhodoBG_02	Australia	*R. excellens*			VU
RhodoBG_02	Australia	*R. fletcherianum*			EN
RhodoBG_02	Australia	*R. formosum*	var. *formosum*		CR
RhodoBG_02	Australia	*R. horlickianum*			DD
RhodoBG_02	Australia	*R. johnstoneanum*			LC
RhodoBG_02	Australia	*R. johnstoneanum-parryae*		Parryaegroup	LC
RhodoBG_02	Australia	*R. liliiflorum*			LC
RhodoBG_02	Australia	*R. lindleyi*			LC
RhodoBG_02	Australia	*R. lindleyi*		Ludlow&Sherriffform	LC
RhodoBG_02	Australia	*R. lyi*			LC
RhodoBG_02	Australia	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_02	Australia	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_02	Australia	*R. maddenii*			LC
RhodoBG_02	Australia	*R. nuttallii*			NT
RhodoBG_02	Australia	*R. pachypodum*			LC
RhodoBG_02	Australia	*R. scopulorum*			VU
RhodoBG_02	Australia	*R. taggianum*			VU
RhodoBG_02	Australia	*R. valentinianum*			NT
RhodoBG_02	Australia	*R. veitchianum*			LC
RhodoBG_02	Australia	*R. veitchianum*		Ashcombe	LC
RhodoBG_03	Australia	*R. burmanicum*			LC
RhodoBG_03	Australia	*R. carneum*			NE
RhodoBG_03	Australia	*R. chunienii*			DD
RhodoBG_03	Australia	*R. ciliatum*			LC
RhodoBG_03	Australia	*R. ciliicalyx*			LC
RhodoBG_03	Australia	*R. ciliipes*			DD
RhodoBG_03	Australia	*R. coxianum*			CR
RhodoBG_03	Australia	*R. dalhousiae*			LC
RhodoBG_03	Australia	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_03	Australia	*R. dendricola*			VU
RhodoBG_03	Australia	*R. excellens*			VU
RhodoBG_03	Australia	*R. fletcherianum*			EN
RhodoBG_03	Australia	*R. fletcherianum*		YellowBunting	EN
RhodoBG_03	Australia	*R. formosum*			CR
RhodoBG_03	Australia	*R. formosum*	var. *formosum*		CR

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_03	Australia	*R. formosum*	var. *inaequale*		DD
RhodoBG_03	Australia	*R. horlickianum*			DD
RhodoBG_03	Australia	*R. johnstoneanum*			LC
RhodoBG_03	Australia	*R. johnstoneanum*		Buff	LC
RhodoBG_03	Australia	*R. levinei*			NT
RhodoBG_03	Australia	*R. liliiflorum*			LC
RhodoBG_03	Australia	*R. lindleyi*			LC
RhodoBG_03	Australia	*R. lindleyi*		Ludlow&Sherriffform	LC
RhodoBG_03	Australia	*R. ludwigianum*			CR
RhodoBG_03	Australia	*R. lyi*			LC
RhodoBG_03	Australia	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_03	Australia	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_03	Australia	*R. maddenii*			LC
RhodoBG_03	Australia	*R. megacalyx*			LC
RhodoBG_03	Australia	*R. nuttallii*			NT
RhodoBG_03	Australia	*R. pachypodum*			LC
RhodoBG_03	Australia	*R. parryae*			LC
RhodoBG_03	Australia	*R. polyandrum*			LC as *maddenii* ssp. *maddenii*
RhodoBG_03	Australia	*R. scopulorum*			VU
RhodoBG_03	Australia	*R. taggianum*			VU
RhodoBG_03	Australia	*R. valentinianum*			NT
RhodoBG_03	Australia	*R. veitchianum*			LC
RhodoBG_03	Australia	*R. veitchianum*		Ashcombe	LC
RhodoBG_04	Australia	*R. ciliicalyx*			LC
RhodoBG_04	Australia	*R. veitchianum*			LC
RhodoBG_05	Australia	*R. ciliatum*			LC
RhodoBG_05	Australia	*R. ciliicalyx*			LC
RhodoBG_05	Australia	*R. formosum*			CR
RhodoBG_05	Australia	*R. johnstoneanum*			LC
RhodoBG_05	Australia	*R. lindleyi*			LC
RhodoBG_05	Australia	*R. nuttallii*			NT
RhodoBG_05	Australia	*R. pachypodum*			LC
RhodoBG_06	Australia	*R. burmanicum*			LC
RhodoBG_06	Australia	*R. nuttallii*		Highborn	NT
RhodoBG_07	Belgium	*R. changii*			VU
RhodoBG_07	Belgium	*R. ciliatum*			LC
RhodoBG_07	Belgium	*R. horlickianum*			DD
RhodoBG_07	Belgium	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_07	Belgium	*R. maddenii*			LC
RhodoBG_07	Belgium	*R. mianningense*			LC
RhodoBG_07	Belgium	*R. pachypodum*			LC
RhodoBG_07	Belgium	*R. pseudociliipes*			VU
RhodoBG_07	Belgium	*R. taggianum*			VU
RhodoBG_08	Belgium	*R. carneum*			NE
RhodoBG_08	Belgium	*R. excellens*			VU
RhodoBG_08	Belgium	*R. kiangsiense*			EN
RhodoBG_08	Belgium	*R. liliiflorum*			LC
RhodoBG_09	Belgium	*R. cuffeanum*			NE
RhodoBG_10	Canada	*R. valentinianum*			NT
RhodoBG_11	Canada	*R. changii*			VU
RhodoBG_11	Canada	*R. ciliatum*			LC
RhodoBG_11	Canada	*R. crenulatum*			LC
RhodoBG_11	Canada	*R. excellens*			VU
RhodoBG_11	Canada	*R. levinei*			NT
RhodoBG_11	Canada	*R. liliiflorum*			LC
RhodoBG_11	Canada	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_11	Canada	*R. nuttallii*			NT
RhodoBG_11	Canada	*R. pachypodum*			LC
RhodoBG_11	Canada	*R. valentinianum*			NT
RhodoBG_11	Canada	*R. wumingense*			VU
RhodoBG_12	Canada	*R. ciliatum*			LC
RhodoBG_12	Canada	*R. fletcherianum*			EN
RhodoBG_12	Canada	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_12	Canada	*R. pachypodum*			LC
RhodoBG_12	Canada	*R. valentinianum*			NT
RhodoBG_13	China	*R. changii*			VU
RhodoBG_13	China	*R. ciliicalyx*			LC
RhodoBG_13	China	*R. dalhousiae*			LC
RhodoBG_13	China	*R. excellens*			VU

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_13	China	*R. liliiflorum*			LC
RhodoBG_13	China	*R. lindleyi*			LC
RhodoBG_13	China	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_13	China	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_13	China	*R. maddenii*			LC
RhodoBG_13	China	*R. megacalyx*			LC
RhodoBG_13	China	*R. pachypodum*			LC
RhodoBG_13	China	*R. rhombifolium*			DD
RhodoBG_13	China	*R. roseatum*			VU
RhodoBG_13	China	*R. taggianum*			VU
RhodoBG_13	China	*R. valentinianum*			NT
RhodoBG_14	China	*R. excellens*			VU
RhodoBG_14	China	*R. levinei*			NT
RhodoBG_15	China	*R. ciliatum*			LC
RhodoBG_15	China	*R. liliiflorum*			LC
RhodoBG_15	China	*R. linearilobum*			DD
RhodoBG_15	China	*R. maddenii*			LC
RhodoBG_15	China	*R. pachypodum*			LC
RhodoBG_15	China	*R. rhombifolium*			DD
RhodoBG_15	China	*R. roseatum*			VU
RhodoBG_15	China	*R. taronense*			VU
RhodoBG_16	China	*R. chunienii*			DD
RhodoBG_16	China	*R. kiangsiense*			EN
RhodoBG_16	China	*R. levinei*			NT
RhodoBG_16	China	*R. liliiflorum*			LC
RhodoBG_16	China	*R. pachypodum*			LC
RhodoBG_17	China	*R. levinei*			NT
RhodoBG_17	China	*R. liliiflorum*			LC
RhodoBG_18	Czechia	*R. ciliatum*			LC
RhodoBG_19	Denmark	*R. ciliatum*			LC
RhodoBG_19	Denmark	*R. johnstoneanum*			LC
RhodoBG_20	France	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_20	France	*R. dendricola*			VU
RhodoBG_20	France	*R. excellens*			VU
RhodoBG_20	France	*R. kiangsiense*			EN
RhodoBG_21	France	*R. ciliatum*			LC
RhodoBG_22	France	*R. burmanicum*			LC
RhodoBG_22	France	*R. odoriferum*			LC as *maddenii* ssp. *crassum*
RhodoBG_23	France	*R. lindleyi*			LC
RhodoBG_24	France	*R. ciliatum*			LC
RhodoBG_24	France	*R. excellens*			VU
RhodoBG_24	France	*R. fletcherianum*			EN
RhodoBG_24	France	*R. sinonuttallii*			VU
RhodoBG_24	France	*R. valentinianum*			NT
RhodoBG_25	Germany	*R. lindleyi*			LC
RhodoBG_25	Germany	*R. maddenii*			LC
RhodoBG_25	Germany	*R. megacalyx*			LC
RhodoBG_25	Germany	*R. taggianum*			VU
RhodoBG_26	Germany	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_26	Germany	*R. maddenii*			LC
RhodoBG_27	Germany	*R. ciliatum*			LC
RhodoBG_28	Netherlands	*R. ciliatum*			LC
RhodoBG_29	Netherlands	*R. johnstoneanum*			LC
RhodoBG_30	Netherlands	*R. mianningense*			LC
RhodoBG_30	Netherlands	*R. pachypodum*			LC
RhodoBG_30	Netherlands	*R. pseudociliipes*			VU
RhodoBG_31	New Zealand	*R. burmanicum*			LC
RhodoBG_31	New Zealand	*R. dendricola*			VU
RhodoBG_31	New Zealand	*R. johnstoneanum*		KenBurns	LC
RhodoBG_31	New Zealand	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_31	New Zealand	*R. maddenii*			LC
RhodoBG_31	New Zealand	*R. nuttallii*			NT
RhodoBG_32	New Zealand	*R. brachysiphon*			LC as *maddenii* ssp. *maddenii*
RhodoBG_32	New Zealand	*R. burmanicum*			LC
RhodoBG_32	New Zealand	*R. carneum*			NE
RhodoBG_32	New Zealand	*R. ciliatum*			LC
RhodoBG_32	New Zealand	*R. ciliicalyx*			LC
RhodoBG_32	New Zealand	*R. ciliipes*			DD
RhodoBG_32	New Zealand	*R. crassum*			LC

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_32	New Zealand	*R. cubittii*			LC as *veitchianum*
RhodoBG_32	New Zealand	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_32	New Zealand	*R. dalhousiae*			LC
RhodoBG_32	New Zealand	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_32	New Zealand	*R. dendricola*			VU
RhodoBG_32	New Zealand	*R. excellens*			VU
RhodoBG_32	New Zealand	*R. fletcherianum*			EN
RhodoBG_32	New Zealand	*R. formosum*	var. *inaequale*		DD
RhodoBG_32	New Zealand	*R. inaequale*			DD
RhodoBG_32	New Zealand	*R. johnstoneanum*			LC
RhodoBG_32	New Zealand	*R. johnstoneanum*		Double Diamond	LC
RhodoBG_32	New Zealand	*R. leptocladon*			VU
RhodoBG_32	New Zealand	*R. lindleyi*			LC
RhodoBG_32	New Zealand	*R. lindleyi*	F Ludlow & Sheriff 6562		LC
RhodoBG_32	New Zealand	*R. ludwigianum*			CR
RhodoBG_32	New Zealand	*R. lyi*			LC
RhodoBG_32	New Zealand	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_32	New Zealand	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_32	New Zealand	*R. maddenii*			LC
RhodoBG_32	New Zealand	*R. manipurense*			LC as *maddenii* ssp. *crassum*
RhodoBG_32	New Zealand	*R. megacalyx*			LC
RhodoBG_32	New Zealand	*R. nuttallii*			NT
RhodoBG_32	New Zealand	*R. nuttallii*		Stellata	NT
RhodoBG_32	New Zealand	*R. pachypodum*			LC
RhodoBG_32	New Zealand	*R. polyandrum*			LC as *maddenii* ssp. *maddenii*
RhodoBG_32	New Zealand	*R. rhabdotum*			VU
RhodoBG_32	New Zealand	*R. scopulorum*			VU
RhodoBG_32	New Zealand	*R. surasianum*			LC
RhodoBG_32	New Zealand	*R. taggianum*			VU
RhodoBG_32	New Zealand	*R. taronense*			VU
RhodoBG_32	New Zealand	*R. valentinianum*			NT
RhodoBG_32	New Zealand	*R. veitchianum*			LC
RhodoBG_32	New Zealand	*R. veitchianum*		IceWhite	LC
RhodoBG_33	New Zealand	*R. burmanicum*			LC
RhodoBG_33	New Zealand	*R. burmanicum*		xMyLadyxRoseScott	LC
RhodoBG_33	New Zealand	*R. carneum*			NE
RhodoBG_33	New Zealand	*R. ciliatum*			LC
RhodoBG_33	New Zealand	*R. ciliipes*			DD
RhodoBG_33	New Zealand	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_33	New Zealand	*R. dendricola*			VU
RhodoBG_33	New Zealand	*R. excellens*			VU
RhodoBG_33	New Zealand	*R. fletcherianum*			EN
RhodoBG_33	New Zealand	*R. formosum*	var. *formosum*		CR
RhodoBG_33	New Zealand	*R. formosum*	var. *inaequale*		DD
RhodoBG_33	New Zealand	*R. johnstoneanum*			LC
RhodoBG_33	New Zealand	*R. johnstoneanum*		Double Diamond	LC
RhodoBG_33	New Zealand	*R. johnstoneanum*		KenBurns	LC
RhodoBG_33	New Zealand	*R. lindleyi*			LC
RhodoBG_33	New Zealand	*R. lyi*			LC
RhodoBG_33	New Zealand	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_33	New Zealand	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_33	New Zealand	*R. maddenii*			LC
RhodoBG_33	New Zealand	*R. megacalyx*			LC
RhodoBG_33	New Zealand	*R. nuttallii*			NT
RhodoBG_33	New Zealand	*R. nuttallii*		LilacTime	NT
RhodoBG_33	New Zealand	*R. pachypodum*			LC
RhodoBG_33	New Zealand	*R. parryae*			LC
RhodoBG_33	New Zealand	*R. scopulorum*			VU
RhodoBG_33	New Zealand	*R. taggianum*			VU
RhodoBG_33	New Zealand	*R. valentinianum*	var. *oblongilobatum*		NT
RhodoBG_33	New Zealand	*R. veitchianum*			LC
RhodoBG_33	New Zealand	*R. veitchianum*		Ashcombe	LC
RhodoBG_33	New Zealand	*R. veitchianum*		IceWhite	LC
RhodoBG_34	New Zealand	*R. burmanicum*			LC
RhodoBG_34	New Zealand	*R. crassum*			LC
RhodoBG_34	New Zealand	*R. johnstoneanum*			LC
RhodoBG_34	New Zealand	*R. maddenii*			LC

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_34	New Zealand	*R. nuttallii*			NT
RhodoBG_34	New Zealand	*R. parryae*			LC
RhodoBG_34	New Zealand	*R. polyandrum*			LC as *maddenii* ssp. *maddenii*
RhodoBG_34	New Zealand	*R. scopulorum*			VU
RhodoBG_34	New Zealand	*R. veitchianum*			LC
RhodoBG_35	New Zealand	*R. burmanicum*			LC
RhodoBG_35	New Zealand	*R. formosum*			CR
RhodoBG_35	New Zealand	*R. johnstoneanum*			LC
RhodoBG_35	New Zealand	*R. johnstoneanum*		KenBurnsForm	LC
RhodoBG_35	New Zealand	*R. maddenii*		WaddersbillK.B.	LC
RhodoBG_35	New Zealand	*R. veitchianum*			LC
RhodoBG_36	Norway	*R. changii*			VU
RhodoBG_36	Norway	*R. ciliatum*			LC
RhodoBG_36	Norway	*R. ciliicalyx*			LC
RhodoBG_36	Norway	*R. fletcherianum*			EN
RhodoBG_36	Norway	*R. formosum*		Shillong	CR
RhodoBG_36	Norway	*R. liliiflorum*			LC
RhodoBG_36	Norway	*R. lindleyi*			LC
RhodoBG_36	Norway	*R. mianningense*			LC
RhodoBG_37	Russia	*R. burmanicum*			LC
RhodoBG_37	Russia	*R. ciliicalyx*			LC
RhodoBG_37	Russia	*R. cubittii*			LC as *veitchianum*
RhodoBG_37	Russia	*R. formosum*	var. *inaequale*		DD
RhodoBG_37	Russia	*R. lyi*			LC
RhodoBG_37	Russia	*R. parryae*			LC
RhodoBG_38	Russia	*R. ciliicalyx*			LC
RhodoBG_38	Russia	*R. lyi*			LC
RhodoBG_39	South Korea	*R. dalhousiae*			LC
RhodoBG_40	Sweden	*R. maddenii*			LC
RhodoBG_41	Switzerland	*R. cubittii*			LC as *veitchianum*
RhodoBG_41	Switzerland	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_41	Switzerland	*R. formosum*			CR
RhodoBG_41	Switzerland	*R. odoriferum*			LC as *maddenii* ssp. *crassum*
RhodoBG_42	UK	*R. excellens*			VU
RhodoBG_43	UK	*R. ciliatum*			LC
RhodoBG_43	UK	*R. fletcherianum*			EN
RhodoBG_43	UK	*R. johnstoneanum*			LC
RhodoBG_43	UK	*R. liliiflorum*			LC
RhodoBG_43	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_43	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_43	UK	*R. pachypodum*			LC
RhodoBG_43	UK	*R. wumingense*			VU
RhodoBG_44	UK	*R. excellens*			VU
RhodoBG_45	UK	*R. ciliatum*			LC
RhodoBG_45	UK	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_46	UK	*R. ciliatum*			LC
RhodoBG_46	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_46	UK	*R. valentinianum*			NT
RhodoBG_47	UK	*R. dalhousiae*			LC
RhodoBG_48	UK	*R. formosum*			CR
RhodoBG_48	UK	*R. iteophyllum*			NE
RhodoBG_48	UK	*R. ludwigianum*			CR
RhodoBG_48	UK	*R. lyi*			LC
RhodoBG_48	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_48	UK	*R. maddenii*			LC
RhodoBG_48	UK	*R. pachypodum*			LC
RhodoBG_48	UK	*R. taronense*			VU
RhodoBG_49	UK	*R. burmanicum*			LC
RhodoBG_49	UK	*R. burmanicum*		ElizabethDavid	LC
RhodoBG_49	UK	*R. carneum*			NE
RhodoBG_49	UK	*R. changii*			VU
RhodoBG_49	UK	*R. chunienii*			DD
RhodoBG_49	UK	*R. ciliatum*			LC
RhodoBG_49	UK	*R. ciliicalyx*		WalterMaynard	LC
RhodoBG_49	UK	*R. ciliipes*			DD
RhodoBG_49	UK	*R. crenulatum*			LC
RhodoBG_49	UK	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_49	UK	*R. dalhousiae*			LC
RhodoBG_49	UK	*R. dalhousiae*	var. *dalhousiae*		LC

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_49	UK	*R. dendricola*			VU
RhodoBG_49	UK	*R. excellens*			VU
RhodoBG_49	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_49	UK	*R. formosum*	var. *inaequale*		DD
RhodoBG_49	UK	*R. horlickianum*			DD
RhodoBG_49	UK	*R. johnstoneanum*			LC
RhodoBG_49	UK	*R. leptocladon*			VU
RhodoBG_49	UK	*R. liliiflorum*			LC
RhodoBG_49	UK	*R. lindleyi*			LC
RhodoBG_49	UK	*R. ludwigianum*			CR
RhodoBG_49	UK	*R. lyi*			LC
RhodoBG_49	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_49	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_49	UK	*R. maddenii*			LC
RhodoBG_49	UK	*R. megacalyx*			LC
RhodoBG_49	UK	*R. nuttallii*			NT
RhodoBG_49	UK	*R. pachypodum*			LC
RhodoBG_49	UK	*R. parryae*			LC
RhodoBG_49	UK	*R. pseudociliipes*			VU
RhodoBG_49	UK	*R. rufosquamosum*			NE
RhodoBG_49	UK	*R. scopulorum*			VU
RhodoBG_49	UK	*R. valentinianum*	var. *oblongilobatum*		NT
RhodoBG_49	UK	*R. valentinianum*	var. *valentinianum*		NT
RhodoBG_49	UK	*R. veitchianum*			LC
RhodoBG_49	UK	*R. walongense*			VU
RhodoBG_50	UK	*R. johnstoneanum*			LC
RhodoBG_51	UK	*R. maddenii*			LC
RhodoBG_52	UK	*R. ciliatum*			LC
RhodoBG_53	UK	*R. ciliatum*			LC
RhodoBG_53	UK	*R. ciliipes*			DD
RhodoBG_53	UK	*R. crenulatum*			LC
RhodoBG_53	UK	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_53	UK	*R. dalhousiae*			LC
RhodoBG_53	UK	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_53	UK	*R. dendricola*			VU
RhodoBG_53	UK	*R. excellens*			VU
RhodoBG_53	UK	*R. fletcherianum*			EN
RhodoBG_53	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_53	UK	*R. formosum*	var. *inaequale*		DD
RhodoBG_53	UK	*R. horlickianum*			DD
RhodoBG_53	UK	*R. liliiflorum*			LC
RhodoBG_53	UK	*R. ludwigianum*			CR
RhodoBG_53	UK	*R. lyi*			LC
RhodoBG_53	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_53	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_53	UK	*R. maddenii*			LC
RhodoBG_53	UK	*R. nuttallii*			NT
RhodoBG_53	UK	*R. scopulorum*			VU
RhodoBG_53	UK	*R. valentinianum*	var. *oblongilobatum*		NT
RhodoBG_53	UK	*R. veitchianum*			LC
RhodoBG_54	UK	*R. burmanicum*			LC
RhodoBG_54	UK	*R. ciliatum*			LC
RhodoBG_54	UK	*R. dendricola*			VU
RhodoBG_54	UK	*R. formosum*			CR
RhodoBG_54	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_54	UK	*R. manipurense*			LC as *maddenii* ssp. *crassum*
RhodoBG_54	UK	*R. valentinianum*			NT
RhodoBG_55	UK	*R. burmanicum*			LC
RhodoBG_55	UK	*R. ciliatum*			LC
RhodoBG_55	UK	*R. ciliicalyx*			LC
RhodoBG_55	UK	*R. dalhousiae*			LC
RhodoBG_55	UK	*R. dalhousiae*		FrankLudlow	LC
RhodoBG_55	UK	*R. dendricola*			VU
RhodoBG_55	UK	*R. formosum*			CR
RhodoBG_55	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_55	UK	*R. formosum*	var. *inaequale*		DD

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_55	UK	*R. johnstoneanum*			LC
RhodoBG_55	UK	*R. lindleyi*			LC
RhodoBG_55	UK	*R. lindleyi*		DameEdithSitwell	LC
RhodoBG_55	UK	*R. lyi*			LC
RhodoBG_55	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_55	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_55	UK	*R. maddenii*			LC
RhodoBG_55	UK	*R. manipurense*			LC as *maddenii* ssp. *crassum*
RhodoBG_55	UK	*R. pachypodum*			LC
RhodoBG_55	UK	*R. parryae*			LC
RhodoBG_55	UK	*R. scopulorum*			VU
RhodoBG_55	UK	*R. taggianum*			VU
RhodoBG_55	UK	*R. taronense*			VU
RhodoBG_55	UK	*R. valentinianum*			NT
RhodoBG_55	UK	*R. veitchianum*			LC
RhodoBG_56	UK	*R. johnstoneanum*			LC
RhodoBG_57	UK	*R. changii*			VU
RhodoBG_57	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_58	UK	*R. burmanicum*			LC
RhodoBG_58	UK	*R. fletcherianum*			EN
RhodoBG_58	UK	*R. johnstoneanum*			LC
RhodoBG_58	UK	*R. lyi*			LC
RhodoBG_58	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_58	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_58	UK	*R. maddenii*			LC
RhodoBG_58	UK	*R. scopulorum*			VU
RhodoBG_58	UK	*R. veitchianum*			LC
RhodoBG_59	UK	*R. dalhousiae*			LC
RhodoBG_59	UK	*R. formosum*			CR
RhodoBG_59	UK	*R. johnstoneanum*			LC
RhodoBG_59	UK	*R. lindleyi*			LC
RhodoBG_59	UK	*R. maddenii*			LC
RhodoBG_59	UK	*R. nuttallii*			NT
RhodoBG_60	UK	*R. brachysiphon*			LC as *maddenii* ssp. *maddenii*
RhodoBG_60	UK	*R. burmanicum*			LC
RhodoBG_60	UK	*R. burmanicum*		(GlenarnForm)	LC
RhodoBG_60	UK	*R. ciliatum*			LC
RhodoBG_60	UK	*R. ciliicalyx*			LC
RhodoBG_60	UK	*R. crassum*			LC
RhodoBG_60	UK	*R. cubittii*			LC as *veitchianum*
RhodoBG_60	UK	*R. fletcherianum*			EN
RhodoBG_60	UK	*R. formosum*			CR
RhodoBG_60	UK	*R. formosum*	var. *formosum*		CR
RhodoBG_60	UK	*R. formosum*	var. *inaequale*		DD
RhodoBG_60	UK	*R. iteophyllum*			NE
RhodoBG_60	UK	*R. johnstoneanum*			LC
RhodoBG_60	UK	*R. levinei*			NT
RhodoBG_60	UK	*R. lindleyi*			LC
RhodoBG_60	UK	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_60	UK	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_60	UK	*R. manipurense*			LC as *maddenii* ssp. *crassum*
RhodoBG_60	UK	*R. nuttallii*			NT
RhodoBG_60	UK	*R. polyandrum*		(PinkForm)	LC as *maddenii* ssp. *maddenii*
RhodoBG_61	UK	*R. valentinianum*			NT
RhodoBG_62	UK	*R. burmanicum*			LC
RhodoBG_62	UK	*R. ciliatum*			LC
RhodoBG_62	UK	*R. ciliicalyx*			LC
RhodoBG_62	UK	*R. horlickianum*			DD
RhodoBG_62	UK	*R. lindleyi*			LC
RhodoBG_62	UK	*R. valentinianum*			NT
RhodoBG_63	USA	*R. ciliicalyx*	ssp. *lyi*		LC
RhodoBG_63	USA	*R. pseudociliipes*			VU
RhodoBG_64	USA	*R. excellens*			VU
RhodoBG_64	USA	*R. levinei*			NT
RhodoBG_64	USA	*R. liliiflorum*			LC
RhodoBG_65	USA	*R. ciliicalyx*			LC
RhodoBG_65	USA	*R. ciliicalyx*		WaltMaynard	LC
RhodoBG_65	USA	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_65	USA	*R. fletcherianum*			EN

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_65	USA	*R. fletcherianum*		YellowBunting(R#22302)	EN
RhodoBG_65	USA	*R. goreri*			NE
RhodoBG_65	USA	*R. johnstoneanum*			LC
RhodoBG_65	USA	*R. johnstoneanum*		DoubleDiamond	LC
RhodoBG_65	USA	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_65	USA	*R. maddenii*			LC
RhodoBG_65	USA	*R. pachypodum*			LC
RhodoBG_66	USA	*R. formosum*			CR
RhodoBG_67	USA	*R. formosum*			CR
RhodoBG_68	USA	*R. cubittii*		Ashcombe	LC as *veitchianum*
RhodoBG_68	USA	*R. cuffeanum*			NE
RhodoBG_68	USA	*R. formosum*		Edinburgh	CR
RhodoBG_68	USA	*R. taronense*			VU
RhodoBG_69	USA	*R. excellens*			VU
RhodoBG_70	USA	*R. johnstoneanum*			LC
RhodoBG_71	USA	*R. burmanicum*			LC
RhodoBG_71	USA	*R. carneum*			NE
RhodoBG_71	USA	*R. changii*			VU
RhodoBG_71	USA	*R. chunienii*			DD
RhodoBG_71	USA	*R. ciliatum*			LC
RhodoBG_71	USA	*R. ciliicalyx*			LC
RhodoBG_71	USA	*R. ciliicalyx*		WaltMaynard	LC
RhodoBG_71	USA	*R. ciliipes*			DD
RhodoBG_71	USA	*R. coxianum*			CR
RhodoBG_71	USA	*R. crenulatum*			LC
RhodoBG_71	USA	*R. cuffeanum*			NE
RhodoBG_71	USA	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_71	USA	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_71	USA	*R. dendricola*			VU
RhodoBG_71	USA	*R. dendricola*		Cons.best	VU
RhodoBG_71	USA	*R. excellens*			VU
RhodoBG_71	USA	*R. excellens*		Clark	VU
RhodoBG_71	USA	*R. fletcherianum*			EN
RhodoBG_71	USA	*R. fletcherianum*			EN
RhodoBG_71	USA	*R. fletcherianum*		YellowBunting	EN
RhodoBG_71	USA	*R. fleuryi*			CR
RhodoBG_71	USA	*R. formosum*			CR
RhodoBG_71	USA	*R. formosum*	var. *formosum*		CR
RhodoBG_71	USA	*R. formosum*	var. *inaequale*		DD
RhodoBG_71	USA	*R. formosum*		Khasia	CR
RhodoBG_71	USA	*R. goreri*			NE
RhodoBG_71	USA	*R. horlickianum*			DD
RhodoBG_71	USA	*R. johnstoneanum*			LC
RhodoBG_71	USA	*R. johnstoneanum*		Double Diamond	LC
RhodoBG_71	USA	*R. johnstoneanum*		rubrolineatum	LC
RhodoBG_71	USA	*R. kiangsiense*			EN
RhodoBG_71	USA	*R. kuomeianum*			DD
RhodoBG_71	USA	*R. leptocladon*			VU
RhodoBG_71	USA	*R. levinei*			NT
RhodoBG_71	USA	*R. liliiflorum*			LC
RhodoBG_71	USA	*R. lindleyi*			LC
RhodoBG_71	USA	*R. lindleyi*		GeordieSherriff	LC
RhodoBG_71	USA	*R. ludwigianum*			DD
RhodoBG_71	USA	*R. lyi*			LC
RhodoBG_71	USA	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_71	USA	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_71	USA	*R. maddenii*			LC
RhodoBG_71	USA	*R. maddenii*		PinkTrumpet	LC
RhodoBG_71	USA	*R. megacalyx*			LC
RhodoBG_71	USA	*R. mianningense*			LC
RhodoBG_71	USA	*R. nuttallii*			NT
RhodoBG_71	USA	*R. nuttallii*		JohnPaulEvans	NT
RhodoBG_71	USA	*R. pachypodum*			LC
RhodoBG_71	USA	*R. parryae*			LC
RhodoBG_71	USA	*R. pseudociliipes*			VU
RhodoBG_71	USA	*R. pseudomaddenii*			LC
RhodoBG_71	USA	*R. roseatum*			VU
RhodoBG_71	USA	*R. scopulorum*			VU
RhodoBG_71	USA	*R. sinonuttallii*			VU

BG code	Country	Species	ssp./var.	cultivar	Red List
RhodoBG_71	USA	*R. surasianum*			LC
RhodoBG_71	USA	*R. taggianum*			VU
RhodoBG_71	USA	*R. taggianum*		DelJames	VU
RhodoBG_71	USA	*R. valentinianum*			NT
RhodoBG_71	USA	*R. valentinianum*	var. *oblongilobatum*		NT
RhodoBG_71	USA	*R. veitchianum*			LC
RhodoBG_71	USA	*R. veitchianum*		Ashcombe	LC
RhodoBG_71	USA	*R. walongense*			VU
RhodoBG_71	USA	*R. wumingense*			VU
RhodoBG_72	USA	*R. burmanicum*			LC
RhodoBG_72	USA	*R. ciliatum*			LC
RhodoBG_72	USA	*R. ciliicalyx*			LC
RhodoBG_72	USA	*R. ciliipes*			DD
RhodoBG_72	USA	*R. crassum*			LC
RhodoBG_72	USA	*R. dalhousiae*	var. *dalhousiae*		LC
RhodoBG_72	USA	*R. dalhousiae*	var. *rhabdotum*		VU
RhodoBG_72	USA	*R. dendricola*			VU
RhodoBG_72	USA	*R. excellens*			VU
RhodoBG_72	USA	*R. fletcherianum*			EN
RhodoBG_72	USA	*R. fleuryi*			CR
RhodoBG_72	USA	*R. formosum*			CR
RhodoBG_72	USA	*R. formosum*	var. *formosum*		CR
RhodoBG_72	USA	*R. formosum*	var. *iteophyllum*		NE
RhodoBG_72	USA	*R. goreri*			NE
RhodoBG_72	USA	*R. horlickianum*			DD
RhodoBG_72	USA	*R. johnstoneanum*			LC
RhodoBG_72	USA	*R. levinei*			NT
RhodoBG_72	USA	*R. liliiflorum*			LC
RhodoBG_72	USA	*R. lindleyi*			LC
RhodoBG_72	USA	*R. ludwigianum*			CR
RhodoBG_72	USA	*R. lyi*			LC
RhodoBG_72	USA	*R. maddenii*	ssp. *maddenii*		LC
RhodoBG_72	USA	*R. maddenii*	ssp. *crassum*		LC
RhodoBG_72	USA	*R. maddenii*			LC
RhodoBG_72	USA	*R. megacalyx*			LC
RhodoBG_72	USA	*R. pachypodum*			LC
RhodoBG_72	USA	*R. parryae*			LC
RhodoBG_72	USA	*R. pseudociliipes*			VU
RhodoBG_72	USA	*R. scopulorum*			VU
RhodoBG_72	USA	*R. sinonuttallii*			VU
RhodoBG_72	USA	*R. valentinianum*			NT
RhodoBG_72	USA	*R. valentinianum*	var. *oblongilobatum*		NT
RhodoBG_72	USA	*R. veitchianum*			LC
RhodoBG_72	USA	*R. veitchianum*		Ashcombe	LC
RhodoBG_72	USA	*R. walongense*			VU
RhodoBG_72	USA	*R. wumingense*			VU
RhodoBG_73	USA	*R. ciliatum*			LC

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Table S2.2 Wild accessions of *Rhododendron* subsection *Maddenia* in the 14 surveyed botanic gardens

A ‘wild collection’ was defined as a series of accessions collected from a plant in the wild that carries a unique Collector ID and represents a single wild source. In this table, a wild collection is identified by the ‘Collector ID’. A wild accession is identified by the Accession ID (‘Acc. ID’) under each wild collection.

The nature of original plant material, seeds or cuttings, was not distinguished. Plants under that collector’s number could be held at different *ex situ* sites and included multiple accessions (‘Acc. ID’ column). Subspecies, varieties, species synonyms, species cultivars of wild sources, and affinities (aff.) of taxa were included in the wild collection, as they may represent variable forms of a taxon. Accessions that were recorded as dead (‘Dead acc.’ column) and when there was no progeny recorded in other botanic gardens surveyed, were coded as invalid, even though they had previously occurred in cultivation and might represent unique origins. However, their provenance data were used in geo-mapping.

Data sources are seven gardens in New Zealand as a hotspot of *ex situ* conservation of ss. *Maddenia*, together with seven largest collections of ss. *Maddenia* outside New Zealand. Sites in New Zealand are Pukeiti garden (Taranaki region) (BGCI member), Dunedin Botanic Garden (BGCI member), Tannock Glen and one private garden (Dunedin), Heritage Park, Cross Hills Gardens and one private garden (Manawatū region). Sites outside New Zealand are: Rhododendron Species Botanical Garden (RSBG, USA), Royal Botanical Garden Edinburgh (RBGE, UK; including RBGE at Edinburgh, Logan and Benmore), Royal Botanic Garden Kew (UK; including RBGK at Kew and Wakehurst), the Dandenong Ranges Botanic Garden (previously Olinda Garden of Parks Victoria, Australia), Arboretum Wespelaar (Belgium), University of British Columbia Botanic Garden (UBCBG, Canada) and the Arnold Arboretum of Harvard University (USA).

Data include an unpublished dataset from an earlier survey by MacKay et al. (2018), together with additional data or individual garden updates in 2020. The use of collections data and permission of publishing compiled dataset were approved by the source botanic gardens.

Numbers in the table column ‘Wc no.’ are assigned by the author for identifying the number of wild collections per taxon.

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc burmanicum #1		*R. burmanicum*		1981/118	KW#21921		wc, 1956, Burma Expedition (Mt Victoria, Burma by Kingdon-Ward [Davidian,1982 pp99])	
wc burmanicum #1		*R. burmanicum*		1999/095	KW#21921		wc, 1956, Burma Expedition (Mt Victoria, Burma by Kingdon-Ward [Davidian,1982 pp99])	
wc burmanicum #2		*R. burmanicum*		12333		1	Collected by Prue Crome, 2700 m, Mt Victoria, Myanmar, 21/5/13	
wc changii #1		*R. changii*		2015/043	JN#11029		wc, Nov. 2011, S Chongqing, 2200 m	
wc changii #1		*R. changii*		2015/014	JN#11029		wc, Nov. 2011, S Chongqing, 2200 m	
wc changii #1		*R. changii*		2015/028	JN#11029		wc, Nov. 2011, S Chongqing, 2200 m	
wc changii #2		*R. changii*		20091273	COH	3	China: Sichuan Province: Jinfo Shan. Epiphytic on rocks. 2,100 m	
wc changii #3		*R. changii*		09254	1811: no fruits	1	(CH 9001)	
wc changii #3		*R. changii*		09253	CH 9001	1		
wc changii #3		*R. changii*		09252	1811: no fruits	1	(CH 9001)	
wc changii #1	dead	*R. changii*		2012-0163	JN11029	0	China: Sichuan Province, s Chongqing, 2200 m	
wc changii #1		*R. changii*		2014-0440	JN.11029	1	China: Sichuan Province, s Chongqing, 2200 m	
wc chunienii #1		*R. chunienii*		2013/262	AC#			
wc chunienii #1?		*R. chunienii*		12240		1	Royal Horticultural Society seed exchange 2003 #02196, A Clark (AC 5092). Sown 26/4/03	
wc ciliatum #1		*R. ciliatum*		2008/315	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #1		*R. ciliatum*		2008/201	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #1		*R. ciliatum*		2008/157	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #1		*R. ciliatum*		2008/245	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #1		*R. ciliatum*		2008/286	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #1		*R. ciliatum*		2008/360	SEH#587		wc, Spring 1997, Sikkim, India, 8500'	
wc ciliatum #2		*R. ciliatum*		2000/094	SEH#545		wc, 1997, Yumthang Valley, Sikkim Himalaya, India, 3340 m	
wc ciliatum #2		*R. ciliatum*		2000/082	SEH#545		wc, 1997, Yumthang Valley, Sikkim Himalaya, India, 3340 m	
wc ciliatum #2		*R. ciliatum*		2000/111	SEH#545		wc, 1997, Yumthang Valley, Sikkim Himalaya, India, 3340 m	
wc ciliatum #2		*R. ciliatum*		2000/069	SEH#545		wc, 1997, Yumthang Valley, Sikkim Himalaya, India, 3340 m	
wc ciliatum #2		*R. ciliatum*		2000/064	SEH#545		wc, 1997, Yumthang Valley, Sikkim Himalaya, India, 3340 m	
wc ciliatum #3		*R. ciliatum*		1995/072	BLM#324		wc, 1971, E Nepal	
wc ciliatum #3?		*R. ciliatum*		19720860	BLM	1	Nepal: Barun Khola. 3,200 m	
wc ciliatum #3?		*R. ciliatum*		1974-1936	BLRM 324		Nepal	
wc ciliatum #4		*R. ciliatum*		1980/077	LS&H#16019		wc, 1949, Bhutan Expedition	
wc ciliatum #5		*R. ciliatum*		1982/172	HED#378		wc, Milke Danda, Nepal, 3500 m	
wc ciliatum #6		*R. ciliatum*		19860321	LSH	1	Bhutan: Ha Dist.: Ha. Boggy ground. 9,500 ft. Shrub about 3 ft; K pale green; C pinkish-white; A filaments white, anthers brown; G style white, stigma green	27°22' N, 89°19' E

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc ciliatum #7		*R. ciliatum*		19932596	SIN	2	Bhutan: Wangdi Phodrang Dist.: 1 km north of Gangtey Gompa. South facing wet flush in blue pine forest. 2,880 m. Shrub to 1.2 m; flowers very good white	
wc ciliatum #8		*R. ciliatum*		20031365	BSL	4	Possibly Bhutan	
wc ciliatum #9		*R. ciliatum*		19850526	NEE	1	Nepal: By the bridge south of Poyan. Open forest. 9,000 ft. Single plant	
wc ciliatum #10		*R. ciliatum*		19820583	PRA	9	India: Sikkim, N: Yumthang. 11,600 ft	
wc ciliatum #11		*R. ciliatum*		19850525	NEE	13	Nepal: Surkie La. Open summit of pass. 10,122 ft	
wc ciliatum #12?		*R. ciliatum*		19840909	DIN	3	Nepal: Milke Danda, E. 8,000-9,000 ft	
wc ciliatum #12?		*R. ciliatum*		19840910	DIN	1	Nepal: Milke Danda. 9,000 ft	
wc ciliatum #13		*R. ciliatum*	var. nov.	19941445	WIC	2	Indonesia: Irian Jaya: Near Mt. Trikora. Plant small; flowers red	
wc ciliatum #14		*R. ciliatum*		1989-2085	FOXD 86134	3	Nepal	
wc ciliatum #14		*R. ciliatum*		08552		1	C.W D. Fox, DF 86134	
wc ciliatum #14		*R. ciliatum*		08553		1	C.W D. Fox, DF 86134	
wc ciliatum #15		*R. ciliatum*		07500		1	RS 1642	
wc ciliatum #15		*R. ciliatum*		07514		1	RS1642	
wc ciliatum #15		*R. ciliatum*		07517		1	RS1642	
wc ciliatum #16?	dead	*R. ciliatum*		1965-0029	RSF.352	0	India: Sikkim	
wc ciliatum #17?	dead	*R. ciliatum*			Ron Gordon?	0	Wild collected material imported from the Ron Gordon expedition to Sikkim (NZRA Bulletin 67, 1977 p23)	
wc ciliatum #18?	dead	*R. ciliatum*			Sikkim	0	In 1990 Pukeiti Plants for Members sold material from Sikkim	
wc ciliicalyx #1		*R. ciliicalyx*		2013/203	BASE#9726			
wc ciliicalyx #2		*R. ciliicalyx*		03445		1	Maddenii Walk above road., Ex. Burma, NS 34	
wc ciliicalyx #2		*R. ciliicalyx*		03446		1	Maddenii Walk above road., Ex. Burma, NS 34	
wc ciliicalyx #2		*R. ciliicalyx*		03447		1	Maddenii Walk above road., Ex. Burma, NS 34	
wc ciliicalyx #2		*R. ciliicalyx*		03448		1	Ex. Burma, NS 34, Maddenii Walk above road	
wc ciliicalyx #3		*R. ciliicalyx*		08556		1	A.R.S. 87/250, C.W. Yunnan	
wc ciliicalyx #4		*R. ciliicalyx*	'Charisma'		KW20280		At PK. collected 1950 Lokit valley Assam, above Rima (Pukeiti 2016 list as Charisma)	
wc ciliipes #1		*R. ciliipes*		19991313	BSL	9	China: [Yunnan]: [Nujiang Lisu Aut. Pref.]: [Gongshan Drung-Nu Aut. Co.]: On the Mekong - Salween divide at Kawa Gepo and between the Salween and the Irrawady watershed. ca 3,000-4,000 m	28° N, 91° E
wc ciliipes #2		*R. ciliipes*			K56		Kew seed China	
wc coxianum #1		*R. coxianum*			1984-443		Pukeiti had accession 1984-443 (PK29) (RSF 78-068, Glendoick, cutting) which was alive in 2005 (PRT 2005)	
wc crenulatum #1		*R. crenulatum*		20141542	HNE#184	1	Vietnam: Lao Cai: Fanipan Peak. 3,110 m	103°46' 31.02" E, 22°18' 11.82" N
wc crenulatum #2	dead	*R. crenulatum*		2008-0062	PW.177	0	Vietnam: Sa Pa, Phan Xi Păng (Fansipan) summit	
wc starlingii #1		*R. crenulatum*		20020810	RUS#7369	4	Vietnam: Lao Cai: Sapa, Fansipan, from the campsite by the first river (station282 at 22°19'11.6N, 103°46'58.9E 2074m)	

Wc no.	Dead acc.	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
							via the knoll at station 283 (22°18'50.1N, 103°46'52.7E, 2450m) to station 284 at upper knoll (22°18'31.8N, 103°46'36.2E 2875m). 2,900 m	
wc cuffeanum #1		*R. cuffeanum*		2001/148	KW#21909		wc, 1956, Burma Expedition	
wc dalhousiae var. dalhousiae #10?	dead	*R. dalhousiae*			Ron Gordon	0	Wild collected material imported from the Ron Gordon expedition to Nepal (NZRA Bulletin 67, 1977 p23)	
wc dalhousiae var. dalhousiae #5		*R. dalhousiae*		19880631	FOX	3	India: Sikkim	
wc dalhousiae var. dalhousiae #8?		*R. dalhousiae*		01668		1	Ex. Sikkim	
wc dalhousiae var. dalhousiae #9?		*R. dalhousiae*			Jellyman		Jellyman ws (PK34) photographed at Pukeiti Dec 2019	
wc dalhousiae var. dalhousiae #1		*R. dalhousiae*	var. *dalhousiae*	2001/131	SEH#502		wc, Spring, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. dalhousiae #1		*R. dalhousiae*	var. *dalhousiae*	2001/029	SEH#502		wc, Spring, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. dalhousiae #2		*R. dalhousiae*	var. *dalhousiae*	1997/133			wc, near Kalimpong, West Bengal, India	
wc dalhousiae var. dalhousiae #2		*R. dalhousiae*	var. *dalhousiae*	1997/134			wc, near Kalimpong, West Bengal, India	
wc dalhousiae var. dalhousiae #3		*R. dalhousiae*	var. *dalhousiae*	1999/132	SEH#522		wc, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. dalhousiae #3		*R. dalhousiae*	var. *dalhousiae*	1999/153	SEH#522		wc, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. dalhousiae #3		*R. dalhousiae*	var. *dalhousiae*	1999/170	SEH#522		wc, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. dalhousiae #4		*R. dalhousiae*	var. *dalhousiae*	1999/643	SEH#521		wc, 1997, Sikkim Himalaya, India, 2100 m	
wc dalhousiae var. rhabdotum #1		*R. dalhousiae*	var. *rhabdotum*	2006/046	KCSH#0310		wc, 10-10-2003, to the Se La, east side, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8600'	
wc dalhousiae var. rhabdotum #1		*R. dalhousiae*	var. *rhabdotum*	2006/081	KCSH#0310		wc, 10-10-2003, to the Se La, east side, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8600'	
wc dalhousiae var. rhabdotum #1		*R. dalhousiae*	var. *rhabdotum*	2011/117	KCSH#0310		wc, 10-10-2003, to the Se La, east side, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8600'	
wc dalhousiae var. rhabdotum #1		*R. dalhousiae*	var. *rhabdotum*	2009/005	KCSH#0310		wc, 10-10-2003, to the Se La, east side, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8600'	
wc dalhousiae var. rhabdotum #1		*R. dalhousiae*	var. *rhabdotum*	2009/014	KCSH#0310		wc, 10-10-2003, to the Se La, east side, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8600'	
wc dalhousiae var. dalhousiae #6		*R. dalhousiae*	var. *dalhousiae*	19722633	SAI	1	India: W Bengal: Nr Darjeeling. 2,280 m	
wc dalhousiae var. dalhousiae #7		*R. dalhousiae*	var. *dalhousiae*	19722217	BLM	1	Nepal: 1,829 m	
wc dendricola #1		*R. dendricola*		2007/293	SEH#25037		wc, 5-29-05, out of Baoshan, S Gaoligong Shan, Yunnan, China, 2360 m	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc dendricola #1		*R. dendricola*		2007/325	SEH#25037		wc, 5-29-05, out of Baoshan, S Gaoligong Shan, Yunnan, China, 2360 m	
wc dendricola #1		*R. dendricola*		2007/246	SEH#25037		wc, 5-29-05, out of Baoshan, S Gaoligong Shan, Yunnan, China, 2360 m	
wc dendricola #1		*R. dendricola*		2007/231	SEH#25037		wc, 5-29-05, out of Baoshan, S Gaoligong Shan, Yunnan, China, 2360 m	
wc dendricola #1		*R. dendricola*		2007/263	SEH#25037		wc, 5-29-05, out of Baoshan, S Gaoligong Shan, Yunnan, China, 2360 m	
wc dendricola #10	dead	*R. dendricola*			KW20601	0	NZRA received seed of KW20601 R. dendricola in 1954 (NZRA Bulletin 2003 p48)	
wc dendricola #2		*R. dendricola*		2015/044	JN#11048		wc, Nov 2011, Salween Region, W Yunnan, 1600 m	
wc dendricola #2		*R. dendricola*		2015/059	JN#11048		wc, Nov 2011, Salween Region, W Yunnan, 1600 m	
wc dendricola #2		*R. dendricola*		2015/029	JN#11048		wc, Nov 2011, Salween Region, W Yunnan, 1600 m	
wc dendricola #2		*R. dendricola*		2015/016	JN#11048		wc, Nov 2011, Salween Region, W Yunnan, 1600 m	
wc dendricola #2		*R. dendricola*		2015/003	JN#11048		wc, Nov 2011, Salween Region, W Yunnan, 1600 m	
wc dendricola #3		*R. dendricola*		2011/163	BASE#9507		wc, southern Gaoligong Shan N of Datang, Salween, China, 2235 m	
wc dendricola #3		*R. dendricola*		2011/155	BASE#9507		wc, southern Gaoligong Shan N of Datang, Salween, China, 2235 m	
wc dendricola #3		*R. dendricola*		2011/092	BASE#9507		wc, southern Gaoligong Shan N of Datang, Salween, China, 2235 m	
wc dendricola #3		*R. dendricola*		2011/118	BASE#9507		wc, southern Gaoligong Shan N of Datang, Salween, China, 2235 m	
wc dendricola #3		*R. dendricola*		2011/142	BASE#9507		wc, southern Gaoligong Shan N of Datang, Salween, China, 2235 m	
wc dendricola #3		*R. dendricola*			BASE 9507		DBR had BDM1348, BASE 9507, ended up at DBG	
wc dendricola #4		*R. dendricola*		1998/019	KW#20981		wc, 1953, The Triangle Expedition, N Burma	
wc dendricola #5		*R. dendricola*		1998/021	F#17227		wc, 1917-19, NE Burma, Yunnan, Sichuan & Tibet Frontiers Expedition	
wc dendricola #6		*R. dendricola*		2013/490	DGEY#046		wc, 9-29-01, track along Dulong Jiang north of Kongdan, NW Yunnan, China, N27º 54.461', E098º 20.577, 1600m	
wc dendricola #7		*R. dendricola*		19191023	FOR	6	China: Yunnan, W: Shweli-Salween divide	
wc dendricola #8		*R. dendricola*		19754089	KWA	5	Myanmar: Kachin State: Ngawchang Valley, N of Htawgaw to Keng fang, Pyepat ridge, N of Htawgaw, & Black Rock. Chung-tien plateau. 3,505 m	
wc dendricola #9		*R. dendricola*		1988-2299		4	China	
wc taronense #1		*R. dendricola*	(*R. taronense*)	02974		1	T.L. 1977	
wc taronense #1		*R. dendricola*	(*R. taronense*)	03744		1	1977 T.L.	
wc dendricola #5		*R. dendricola*	aff.	1980/087	F#17227		wc, 1917-19, NE Burma, Yunnan, Sichuan & Tibet Frontiers Expedition	
wc excellens #1		*R. excellens*		2015/123	FMWJ#13398		wc. N Vietnam	
wc excellens #10		*R. excellens*		20020815	RUS	4	Vietnam: Lao Cai: Sapa, excellens ex raod, on roadside bank	
wc excellens #11		*R. excellens*		20001560	TRN	1	Vietnam: Lào Cai: Sapa, Fansipan	
wc excellens #12		*R. excellens*		2015-1587	VIET 375	4	Vietnam	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc excellens #12		*R. excellens*		2017-1410	VIET 375	1	Vietnam	
wc excellens #12		*R. excellens*		2017-767	VIET 375	7	Vietnam	
wc excellens #12		*R. excellens*		2017-1057	VIET 375	6	Vietnam	
wc excellens #12		*R. excellens*		2017-634	VIET 375	3	Vietnam	
wc excellens #12		*R. excellens*		2017-1401	VIET 375	1	Vietnam	
wc excellens #12		*R. excellens*		2017-528	VIET 375	5	Vietnam	
wc excellens #12		*R. excellens*		2017-523	VIET 375	5	Vietnam	
wc excellens #13		*R. excellens*		2017-893	VIET 329	9	Vietnam	
wc excellens #13		*R. excellens*		2017-894	VIET 329	7	Vietnam	
wc excellens #13		*R. excellens*		2017-895	VIET 329	6	Vietnam	
wc excellens #13		*R. excellens*		2017-536	VIET 329	5	Vietnam	
wc excellens #14		*R. excellens*		2015-1577	VIET 364	3	Vietnam	
wc excellens #14		*R. excellens*		2017-632	VIET 364	3	Vietnam	
wc excellens #14		*R. excellens*		2017-495	VIET 364	3	Vietnam	
wc excellens #15		*R. excellens*		09526		1	K.R.2998, S.E. Maddenia Walk	
wc excellens #15		*R. excellens*		09658		1	Messmate forest, Mathias Rd. track, K.R. 2998	
wc excellens #15		*R. excellens*		09797		1	K.R. 2998, Vietnam 1994	
wc excellens #16		*R. excellens*		12235		1	American Rhododendron Society seed exchange 1993 AC370. Sown 3/4/93 at Parks Victoria	
wc excellens #2		*R. excellens*		1994/380			seed w.c. at 6,500' in the Sapa region of N Vietnam	
wc excellens #27?		*R. excellens*				2	Wild collected by Alan Clark 1996 Yunnan, no collection number	
wc excellens #3		*R. excellens*		2017/047	SEH#227			
wc excellens #3		*R. excellens*		1999/039	SEH#227		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2000m	
wc excellens #3		*R. excellens*		1999/025	SEH#227		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2000m	
wc excellens #3		*R. excellens*		1999/050	SEH#227		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2000m	
wc excellens #3		*R. excellens*		1999/081	SEH#227		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2000m	
wc excellens #4		*R. excellens*		2006/243	KR#7916		wc, 2003, Lao Cai, Vietnam, 1750m	
wc excellens #4		*R. excellens*		2006/338	KR#7916		wc, 2003, Lao Cai, Vietnam, 1750m	
wc excellens #4		*R. excellens*		2006/289	KR#7916		wc, 2003, Lao Cai, Vietnam, 1750m	
wc excellens #5		*R. excellens*		2011/094			wc, N. Vietnam, 2400m	
wc excellens #6		*R. excellens*		1996/053	KR#3092		wc, 1994, Vietnam Expedition	
wc excellens #9		*R. excellens*		20170743	LGCKH	2	Vietnam: Lao Cai: Treck up Y Ty Mnt from Nhiu Co San Village past camps 1 & 2 to summit returning via camps to Nhiu Co San Village. 1,861 m	103°37' 27.72" E, 22°37' 28.8" N
wc excellens #28?		*R. excellens*	aff.	19951644	RUS	1	Vietnam: Lào Cai: Sapa, Fansipan, NE ridge above the village of Sin Chay. 2,300 m	
wc excellens #29?		*R. excellens*	aff.	19941651	TRN	1	Vietnam: Lào Cai: Sapa, Fansipan. 2,377 m. Leaves small, narrow, to 23-33 mm wide, 9 cm. long. Capsule ca. 4 cm., 5 cells	
wc excellens #15		*R. excellens*			KR2998		Wild collected seed of *R. excellens* KR2998 (PK01) came to Pukeiti via Os Blumhardt in 1994 (NZRA Bulletin 2003 p21)	
wc excellens #17	dead	*R. excellens*		2015-0258	HN-E003	0	San Sa Ho	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc excellens #18	dead	*R. excellens*		2015-0325	HN-E329	0	Tay Con Linh Mountain, Xan Xa Ho Village Lao Commune	
wc excellens #19	dead	*R. excellens*		2015-0330	HN-E375	0	Tay Con Linh Mountain, Xan Xa Ho Village Lao Commune	
wc excellens #20	dead	*R. excellens*		2015-0620	HN-E364	0	Tay Con Linh Mountain, Xan Xa Ho Village Lao Commune	
wc excellens #21	dead	*R. excellens*		2016-0094	HN-UBC.31A	0	Sa Pa, Phan Xi Păng (Fansipan)	
wc excellens #22		*R. excellens*			AC5630		*R. excellens* AC5630 (PK30), collected North Vietnam, offered for sale in 2012 (PPM2012)	
wc excellens #23		*R. excellens*			TVO-064		Sapa, Fansipan? (RBGE Herbarium: *R. excellens* TVO27)	
wc excellens #24		*R. excellens*			AC435			
wc excellens #25		*R. excellens*			DT307-98		Seed purchased from the RHS in 1993 by L Davies (NZRA Bulletin 88, 2000, p58). DT307-98 (HP01) at Heritage Park	
wc excellens #26?		*R. excellens*			NthVietnam		Nth Vietnam (OM34) via Hudson (in colln 198)	
wc excellens #5		*R. excellens*			SEH227		Hootman collection (DBR spreadsheet)	
wc excellens #30		*R. excellens*	aff.	2009-0218	NVD.0718	1	Lao Cai, Sa Pa; 2323 m	
wc excellens #31?	dead	*R. excellens*	aff.	2007-0376	NA	0	Yunnan Province, Kumming; 1950 m	
wc excellens #31?	dead	*R. excellens*	aff.	2007-0377	NA	0	Yunnan Province, Kumming; 1950 m	
wc excellens #32?	dead	*R. excellens*	aff.	2013-0131	NA	0	NA	
wc excellens #32?	dead	*R. excellens*	aff.	2013-0133	NA	0	NA	
wc excellens #7		*R. excellens*	aff.	1998/008	KR#2948		wc, 1994, Vietnam Expedition	
wc excellens #8		*R. excellens*	aff.	1998/007	KR#3093		wc, 1994, Vietnam Expedition	
wc fletcherianum #1	dead	*R. fletcherianum*			Rock 22302	0	Imported by Pukeiti from the Species Foundation (SF65/355) in 1975 (NZRA Bulletin 67, 1979, p 24). Seedlings of Rock 22302 offered for sale in 2011 (PPM2011) and 2012 (PPM2012)	
wc fletcherianum #1		*R. fletcherianum*		1968/858	R#22302		wc, 1932, NW Yunnan, China Expedition	
wc fletcherianum #2		*R. fletcherianum*		19754070	ROC	11	China: Xizang (Tibet) Aut. Reg.: Solo La. 4,250 m	
wc fletcherianum #2		*R. fletcherianum*		20171082	ROC	3	China: Xizang (Tibet) Aut. Reg.: Solo La. 4,250 m	
wc fletcherianum #2	dead	*R. fletcherianum*		20191134	ROC	0	China: Xizang (Tibet) Aut. Reg.: Solo La. 4,250 m	
wc fletcherianum #1		*R. fletcherianum*	'Yellow Bunting'	1974/071	R#22302		wc, 1932, NW Yunnan, China Expedition	
wc fleuryi #1		*R. fleuryi*		1998/009	KR#3286		wc, 1994, Vietnam Expedition	
wc fleuryi #1		*R. fleuryi*		1996/040	KR#3286		wc, 1994, Vietnam Expedition	
wc formosum var. formosum #2		*R. formosum*	var. *formosum* 'Khasia'	1998/012	C&H#320		wc, 1965, Khasia, Arunachal Pradesh, & Bengal N India Expedition	
wc formosum var. inaequale #1		*R. formosum*	var. *inaequale*	1998/002	C&H#301		wc, 1965, Khasia, Arunachal Pradesh, & Bengal N India Expedition	
wc formosum var. inaequale #1		*R. formosum*	var. *inaequale*	2002-2122	COHU 301	3	India	
wc formosum var. formosum #1		*R. formosum*	aff.	2007/267	APA#008		wc, 10-11-05, floodplain of Yang Sang, Arunachal Pradesh, India, (Arunachal Pradesh Abroka Expedition), 5000'	
wc formosum var. formosum #3		*R. formosum*	var. *formosum*	19751328	CHA	20	India: Meghalaya: Shillong, below Elephant Falls. 1,750 m	
wc formosum var. formosum #3	dead	*R. formosum*	var. *formosum*	20191121	CHA	0	India: Meghalaya: Shillong, below Elephant Falls. 1,750 m	
wc formosum var. formosum #4		*R. formosum*	var. *formosum*	20141092		2	India: Sikkim	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc formosum var. formosum #4		*R. formosum*	var. *formosum*	19731586		1	India: Sikkim	
wc formosum var. formosum #6		*R. formosum*	var. *formosum* 'Ten Tashi'		Ten Tashi		*R. formosum* 'Ten Tashi' (PK18) imported by Pukeiti from Greer Gardens, USA, in 1985 (NZRA Bulletin 1986 p64)	
wc formosum var. inaequale #2		*R. formosum*	var. *inaequale*	19730900	COH	3	India: Meghalaya: Khasia Hills: Nr Morphlong to Shillong Rd.	
wc formosum var. inaequale #2		*R. formosum*	var. *inaequale*	20141083	COH	3	India: Meghalaya: Khasia Hills: Nr Morphlong to Shillong Rd.	
wc formosum var. inaequale #2		*R. formosum*	var. *inaequale*	20141085	COH	4	India: Meghalaya: Khasia Hills: Nr Morphlong to Shillong Rd.	
wc formosum var. inaequale #3		*R. formosum*	var. *inaequale*	19803103	COH	1	India: Arunchal Pradesh: W Peak of Ridge SE of Apa Tani Valley. 3,000 m	
wc formosum var. inaequale #4		*R. formosum*	var. *inaequale*		KW16029		PK has KW16029 (Windsor 1975, cuttings)	
wc formosum var. inaequale #5	dead	*R. formosum*	var. *inaequale*		KW20301	0	*R. formosum* var. *inaequale* KW20301 offered for sale in 2008 (PPM2008) but not listed at Pukeiti now. KW20301 came from NZRA in 1955	
wc goreri #1		*R. goreri*		2005/235	RR#112		wc, fall 2002, Tibet	
wc goreri #2		*R. goreri*		2005/249	RR#122		wc, fall 2002, Tibet	
wc goreri #2		*R. goreri*		2005/213	RR#122		wc, fall 2002, Tibet	
wc goreri #3		*R. goreri*		2003/168	KR#6027		wc, 10-2-99, Rong chu valley below Trulong at station 30, Tibet, 2020 m	
wc goreri #3		*R. goreri*		2003/188	KR#6027		wc, 10-2-99, Rong chu valley below Trulong at station 30, Tibet, 2020m	
wc goreri #3		*R. goreri*		2003/195	KR#6027		wc, 10-2-99, Rong chu valley below Trulong at station 30, Tibet, 2020 m	
wc goreri #3		*R. goreri*		2003/112	KR#6027		wc, 10-2-99, Rong chu valley below Trulong at station 30, Tibet, 2020 m	
wc goreri #3		*R. goreri*		2003/139	KR#6027		wc, 10-2-99, Rong chu valley below Trulong at station 30, Tibet, 2020 m	
wc goreri #3	dead	*R. goreri*			KR6027	0	DBR had BDM1203 (KR6027) but it was never offered for sale	
wc horlickianum #1		*R. horlickianum*		2002/004	CCHH#8074		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000 m	
wc horlickianum #1		*R. horlickianum*		2002/011	CCHH#8074		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000 m	
wc horlickianum #2		*R. horlickianum*		1987/053	KW#9403		wc, 1931, Upper Burma & Tibetan Frontier Expedition	
wc horlickianum #3		*R. horlickianum*		19321007	KWA	13	Myanmar: Chin Special Division: Adung Valley. In thickets along river bank or on cliffs. 2,134 m	
wc horlickianum #4?		*R. horlickianum*		17417	BE 1219	3	MaDoi Mountains, MM,2700 m	
wc horlickianum #5?		*R. horlickianum*			GDK		Colln 200 (wc?) has a plant from GDK, could that be ws?	
wc johnstoneanum #1		*R. johnstoneanum*		2013/407	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	

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wc johnstoneanum #1		*R. johnstoneanum*		2013/436	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/460	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/471	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/427	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/402	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/489	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/451	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/294	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/324	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/375	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #1		*R. johnstoneanum*		2013/358	NAPE#024		wc, Nagaland-Araunchal Pradesh (& adjacent Bhutan), 8500-9000'	
wc johnstoneanum #2		*R. johnstoneanum*		1990/070	KW#12585		wc, 1935, Tibet, Assam-Himalaya Frontier Tract Expedition	
wc johnstoneanum #3		*R. johnstoneanum*		2015/215	KW#7732			
wc johnstoneanum #4		*R. johnstoneanum*		19832095	KWA	5	India: Assam: Naga Hills: Japvo. On steep ridge leading to the summit and on the final cliff in deep shade. 2,743-3,048 m. Small bushy shrub	
wc johnstoneanum #4		*R. johnstoneanum*		19870984	KWA	1	India: Assam: Naga Hills.: Japvo. On steep ridge leading to the summit and on the final cliff in deep shade. 2,743-3,048 m. Small bushy shrub	
wc johnstoneanum #5		*R. johnstoneanum*			KW20305		KW20305 (PK33) at Pukeiti ex NZRA 1955	
wc johnstoneanum #6		*R. johnstoneanum*			AC5532		Pukeiti also has AC5532 (PK47)	
wc kiangsiense #1		*R. kiangsiense*		2013/269	EN#			
wc kuomeianum #1		*R. kuomeianum*			SEH		wc, collected from type location	
wc leptocladon #1		*R. leptocladon*		1996/070	KR#2932		wc, 1994, Vietnam Expedition. Vietnam: Lào Cai Prov: Dèo Hoàng Liên Sòn, on the Phong Tho Road	
wc leptocladon #1		*R. leptocladon*		1996/073	KR#2932		wc, 1994, Vietnam Expedition	
wc leptocladon #1		*R. leptocladon*		1996/072	KR#2932		wc, 1994, Vietnam Expedition	
wc leptocladon #1		*R. leptocladon*		1996/066	KR#2932		wc, 1994, Vietnam Expedition	
wc leptocladon #1		*R. leptocladon*		1996/068	KR#2932		wc, 1994, Vietnam Expedition	
wc leptocladon #2		*R. leptocladon*		2005/035	HWJ#99688			
wc leptocladon #2		*R. leptocladon*		2005/076	HWJ#99688			
wc leptocladon #2		*R. leptocladon*		2005/068	HWJ#99688			
wc leptocladon #2		*R. leptocladon*		2005/054	HWJ#99688			

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc leptocladon #2		*R. leptocladon*		2005/011	HWJ#99688			
wc leptocladon #3		*R. leptocladon*		2016/150	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/233	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/103	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/114	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/208	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/168	PZVN#13-075		wc, Vietnam	
wc leptocladon #3		*R. leptocladon*		2016/096	PZVN#13-075		wc, Vietnam	
wc leptocladon #4?		*R. leptocladon*		2015-1398	VIET 188		Vietnam	
wc leptocladon #5?		*R. leptocladon*		2015-657	VIET 31		Vietnam	
wc leptocladon #6		*R. leptocladon*			BDM1345		Pictured at DBG (The Rhododendron 2013, p41). DBG has BDM1345, HP P. Cox	
wc levinei #1		*R. levinei*		2013/006	CGG#14162			
wc levinei #1		*R. levinei*		2013/014	CGG#14162			
wc levinei #1		*R. levinei*		2013/018	CGG#14162			
wc levinei #1		*R. levinei*		2013/024	CGG#14162			
wc levinei #1		*R. levinei*		2013/036	CGG#14162			
wc levinei #1		*R. levinei*		2013/040	CGG#14162			
wc levinei #1		*R. levinei*		2013/001	CGG#14162			
wc levinei #2		*R. levinei*		2002/006			wc	
wc levinei #4		*R. levinei*		12239		1	Royal Horticultural Society seed exchange 2003 #02214, A Clark (AC5128). Sown 26/4/03. Needs verification	
wc levinei #1		*R. levinei*		2014-0441	CGG.14162	1	CHN: 3200 m	
wc levinei #3		*R. levinei*	aff.	2013/229	TH#2805			
wc levinei #3		*R. levinei*	aff.	2013/244	TH#2805			
wc levinei #3		*R. levinei*	aff.	2013/267	TH#2805			
wc liliiflorum #1		*R. liliiflorum*		2005/166	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/233	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/223	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/175	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/269	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/262	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/208	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/211	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/268	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/214	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/170	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/186	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2015/251	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/250	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #1		*R. liliiflorum*		2005/236	PW#116		wc, spring 2003, Guizhou, China	
wc liliiflorum #2		*R. liliiflorum*		2012/052	CGG#14066			
wc liliiflorum #2		*R. liliiflorum*		2012/072	CGG#14066			
wc liliiflorum #2		*R. liliiflorum*		2012/063	CGG#14066			

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wc liliiflorum #2		*R. liliiflorum*		2012/104	CGG#14066			
wc liliiflorum #2		*R. liliiflorum*		2012/036	CGG#14066			
wc liliiflorum #3		*R. liliiflorum*		1998/001	ex. Guiz#163			
wc liliiflorum #3		*R. liliiflorum*		19911969	GUI#163	1	China: Guizhou: 1,500 m.	
wc liliiflorum #3		*R. liliiflorum*		19861179	GUI#163	1	China: Guizhou: On boulders on steep rocky slopes in forest. 1,500 m. Shrub of up to 1.5 m. Scarce	
wc liliiflorum #3		*R. liliiflorum*			Guiz163		Offered for sale by BLM before 1999 (Gaddum 1999). Guiz163 held in collection 200, ex GDK	
wc liliiflorum #4	dead	*R. liliiflorum*		19861177	GUI#75	0	China: Guizhou: 1,000-1,200 m	
wc liliiflorum #5		*R. liliiflorum*		20140724	COX	3	China: Fan Jing Shan Summit ridge	
wc liliiflorum #6		*R. liliiflorum*		04323		1	Ex. T.L.	
wc liliiflorum #6		*R. liliiflorum*		04324		1	Ex. T.L.	
wc liliiflorum #1		*R. liliiflorum*		2006-0211	PW 116	1	Guizhou Province, not listed	
wc liliiflorum #7		*R. liliiflorum*		2021-0619	NN0958	1	Guizhou Province, SW Guizhou, 1850 m	
wc lindleyi #1		*R. lindleyi*		2007/252	AC#5308		wc, 2004, Chander to Thungri, W Kameng, Arunachal Pradesh, India, mean alt. 3100m	
wc lindleyi #1		*R. lindleyi*		2007/305	AC#5308		wc, 2004, Chander to Thungri, W Kameng, Arunachal Pradesh, India, mean alt. 3100m	
wc lindleyi #1		*R. lindleyi*		2007/235	AC#5308		wc, 2004, Chander to Thungri, W Kameng, Arunachal Pradesh, India, mean alt. 3100m	
wc lindleyi #10		*R. lindleyi*			KW8546		KW8546 ex Gwavas (PK28)	
wc lindleyi #11	dead	*R. lindleyi*			KR8635	0	*R. lindleyi* KR8635 offered for sale in 2012 (PPM2012)	
wc lindleyi #12	dead	*R. lindleyi*			RCM90107?	0	PK used to have RCM90107, accessioned 1990, M9	
wc lindleyi #2		*R. lindleyi*		2013/230	HECC#10023			
wc lindleyi #2		*R. lindleyi*		2013/216	HECC#10023			
wc lindleyi #3		*R. lindleyi*		2000/253	BB#8840			
wc lindleyi #4		*R. lindleyi*		2001/191	SEH#534		wc, 1997, Sikkim Himalaya, India, 2700m	
wc lindleyi #4		*R. lindleyi*		2001/174	SEH#534		wc, 1997, Sikkim Himalaya, India, 2700m	
wc lindleyi #4		*R. lindleyi*		2001/239	SEH#534		wc, 1997, Sikkim Himalaya, India, 2700m	
wc lindleyi #4		*R. lindleyi*		2001/221	SEH#534		wc, 1997, Sikkim Himalaya, India, 2700m	
wc lindleyi #5		*R. lindleyi*		2008/022	KR#8074		wc, 2005, W. Kameng district, Arunachal Pradesh, India, 3020 m	
wc lindleyi #5		*R. lindleyi*		2008/100	KR#8074		wc, 2005, W. Kameng district, Arunachal Pradesh, India, 3020 m	
wc lindleyi #5		*R. lindleyi*		2008/067	KR#8074		wc, 2005, W. Kameng district, Arunachal Pradesh, India, 3020m	
wc lindleyi #6		*R. lindleyi*		1978/067	LS&T#6562		wc, 1938, SE Tibet Expedition	
wc lindleyi #7		*R. lindleyi*		2011/096	GR#0822		wc, Chandar/Tongri, Arunachal Predesh, India	
wc lindleyi #9?		*R. lindleyi*		19803104	COH	1	India: Arunachal Pradesh: Subansiri Div.: Ridge SE of Api Tani Valley. 2,500-2,650 m	
wc lindleyi #8?		*R. lindleyi*	aff.	19771142		1	India	
wc ludwigianum #1		*R. ludwigianum*		2004/065			wc, Doi Ang Kang, (Limestone mountain) Chiengmai, Thailand, 1800m	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc ludwigianum #1		*R. ludwigianum*		2004/048			wc, Doi Ang Kang, (Limestone mountain) Chiengmai, Thailand, 1800m	
wc ludwigianum #1		*R. ludwigianum*		2004/030			wc, Doi Ang Kang, (Limestone mountain) Chiengmai, Thailand, 1800m	
wc ludwigianum #1		*R. ludwigianum*					Imported by Pukeiti in 1985 from Greer Gardens USA (NZRA Bulletin, 1986 p64). Pukeiti has ws Doi Ang Kang, Thailand (PK43)	
wc ludwigianum #2		*R. ludwigianum*		19631492	SMN	3	Thailand: Chiang Mai: Doi Chiengdo (Doi Chiang Dao). 2,000 m	
wc ludwigianum #2		*R. ludwigianum*		19850478	SMN	3	Thailand: Chiang Mai: Doi Chiang Dao. On limestone, barren rocks. 2,000 m	
wc ludwigianum #3		*R. ludwigianum*		01352		1	Ex. Thailand 1318172	
wc ludwigianum #4		*R. ludwigianum*		12236		1	John Rouse collection, collected by Peter Valder, Thailand 1975? Cutting 19/2/06	
wc lyi #1		*R. lyi*		1996/060	KR#2962		wc, 1994, Vietnam Expedition	
wc lyi #1?		*R. lyi*		1998/010	KR#269(?)			
wc lyi #2		*R. lyi*		2015/034	FMWJ#13042		wc, N Vietnam	
wc lyi #2		*R. lyi*		2015/018	FMWJ#13042		wc, N Vietnam	
wc lyi #2		*R. lyi*		2015/049	FMWJ#13042		wc, N Vietnam	
wc lyi #3		*R. lyi*		2001/152	Valder#19			
wc lyi #3		*R. lyi*		2001/146	Valder#		wc, Vietnam (? probably Thailand - SEH)	
wc lyi #4		*R. lyi*		2017/073	SEH#27010			
wc lyi #4		*R. lyi*		2017/064	SEH#27010			
wc lyi #5		*R. lyi*		1981/125	PGV#19			
wc lyi #6?		*R. lyi*		1963-23402		7	Thailand	
wc maddenii ssp. maddenii #1		*R. maddenii*		2011/156	NVD#19		wc, N Vietnam, 2323m	
wc maddenii ssp. maddenii #1		*R. maddenii*		2011/120	NVD#19		wc, N Vietnam, 2323m	
wc maddenii ssp. maddenii #1		*R. maddenii*		2011/144	NVD#19		wc, N Vietnam, 2323m	
wc maddenii ssp. maddenii #10		*R. maddenii*		19872083	BSL	1	Bhutan: Tashigang Dist.: Gamri Chu. 2,591 m	
wc maddenii ssp. maddenii #11		*R. maddenii*		19942904	BSL	2	Bhutan: West side of Pele La	
wc maddenii ssp. maddenii #12		*R. maddenii*		19831844	HED	1	Bhutan: Thimphu Dist.: Near Chapcha. 2,500 m	27°10' N, 89°33' E
wc maddenii ssp. maddenii #13		*R. maddenii*		19872103	BSL	4	Bhutan: Bhutan, E: S of Kaling. 2,286 m	
wc maddenii ssp. maddenii #19		*R. maddenii*		2017-1415	VIET 458	1	Vietnam	
wc maddenii ssp. maddenii #19		*R. maddenii*		2017-1432	VIET 458	1	Vietnam	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc maddenii ssp. maddenii #19		*R. maddenii*		2017-496	VIET 458	5	Vietnam	
wc maddenii ssp. maddenii #19		*R. maddenii*		2017-497	VIET 458	5	Vietnam	
wc maddenii ssp. maddenii #19		*R. maddenii*		2017-518	VIET 458	5	Vietnam	
wc maddenii ssp. maddenii #2		*R. maddenii*		2005/237	NAPE#109		wc, 10-2-2003, Tom Hill, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8400'	
wc maddenii ssp. maddenii #2		*R. maddenii*			NAPE109			
wc maddenii ssp. maddenii #20		*R. maddenii*		2015-1732	VIET 192		Vietnam	
wc maddenii ssp. maddenii #21		*R. maddenii*		00504		1	Wada, Bhutan	
wc maddenii ssp. maddenii #22	dead	*R. maddenii*		01337		0	T.L. Sikkim 72/30	
wc maddenii ssp. maddenii #22		*R. maddenii*		01338		1	T.L. Sikkim 72/30	
wc maddenii ssp. maddenii #23?		*R. maddenii*		01657		1	Ex. Wada Bhutan 1977	
wc maddenii ssp. maddenii #23?		*R. maddenii*		01658		1	Ex. Wada Bhutan 1977	
wc maddenii ssp. maddenii #23?		*R. maddenii*		01659		1	Ex. Wada Bhutan 1977	
wc maddenii ssp. maddenii #25		*R. maddenii*		06376		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06377		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06378		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06379		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06380		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06381		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06382		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06383		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06384		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06385		1	RS 1659 Wada's Pink	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc maddenii ssp. maddenii #25		*R. maddenii*		06386		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06387		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06388		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06389		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #25		*R. maddenii*		06390		1	RS 1659 Wada's Pink	
wc maddenii ssp. maddenii #26		*R. maddenii*			TH237			
wc maddenii ssp. maddenii #27		*R. maddenii*			SD1104			
wc maddenii ssp. maddenii #28?		*R. maddenii*			Burma Road		at Heritage Park	
wc maddenii ssp. maddenii #29	dead	*R. maddenii*			KW21005	0	1954: NZRA received seed of *R. polyandrum* KW21005	
wc maddenii ssp. maddenii #3		*R. maddenii*		2005/220	KC#0108A&B		wc, October 2001, Arunachal Pradesh, India	
wc maddenii ssp. maddenii #3		*R. maddenii*		2005/263	KC#0108A&B		wc, October 2001, Arunachal Pradesh, India	
wc maddenii ssp. maddenii #3	dead	*R. maddenii*		2006-0214	KC 108	0	Arunachal Pradesh, not listed	
wc maddenii ssp. maddenii #3		*R. maddenii*			KC0108			
wc maddenii ssp. maddenii #4		*R. maddenii*		2006/393	KCSH#0345		wc, 10-11-2003, back to the Se La, Arunachal Pradesh, 9000'	
wc maddenii ssp. maddenii #6	dead	*R. maddenii*		2006-0215	KCSH 388	0	Arunachal Pradesh, not listed	
wc maddenii ssp. maddenii #8		*R. maddenii*		20161203	LGCKH	6	Vietnam: Lao Cai: Treck up Y Ty Mnt from Nhiu Co San Village past camps 1 & 2 to summit returning via camps to Nhiu Co San Village. 1,983m	22°36' 42.48" N, 103°37' 26.94" E
wc maddenii ssp. maddenii #9		*R. maddenii*		20141093	PRL	3	India: Sikkim	
wc maddenii ssp. maddenii #9		*R. maddenii*		19870430	PRL	2	India: Sikkim	
wc maddenii ssp. crassum #1		*R. maddenii*	ssp. *crassum*	2011/054	DJHV#8163		wc, Vietnam & Sichuan, China	
wc maddenii ssp. crassum #1		*R. maddenii*	ssp. *crassum*	2011/041	DJHV#8163		wc, Vietnam & Sichuan, China	
wc maddenii ssp. crassum #1		*R. maddenii*	ssp. *crassum*	2013/049	DJHV#8163		wc, Vietnam & Sichuan, China	
wc maddenii ssp. crassum #1		*R. maddenii*	ssp. *crassum*	2011/067	DJHV#8163		wc, Vietnam & Sichuan, China	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	1996/048	KR#2978		wc, 1994, Vietnam Expedition	
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	09788		1	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	09789		1	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #11		*R. maddenii*	ssp. *crassum*	1996/027	KR#3116		wc, 1994, Vietnam Expedition	
wc maddenii ssp. crassum #11		*R. maddenii*	ssp. *crassum*	2000-0472	KR.3116	1	Yunnan Province, ne Yunnan, 2800 m	
wc maddenii ssp. crassum #12		*R. maddenii*	ssp. *crassum*	20092025		1		
wc maddenii ssp. crassum #2		*R. maddenii*	ssp. *crassum*	1999/544	CCHH#8217		wc, 10-12-97, Cangshan, Yunnan, China, 2650m	
wc maddenii ssp. crassum #2		*R. maddenii*	ssp. *crassum*	1999/631	CCHH#8217		wc, 10-12-97, Cangshan, Yunnan, China, 2650m	
wc maddenii ssp. crassum #2	dead	*R. maddenii*	ssp. *crassum*	2000-0627	CCHH.8217	0	Yunnan Province, Cangshan	
wc maddenii ssp. crassum #26		*R. maddenii*	ssp. *crassum*	1958-32204	KWRD 21005	1		
wc maddenii ssp. crassum #27		*R. maddenii*	ssp. *crassum*	2015-1375	VIET 168	2	Vietnam	
wc maddenii ssp. crassum #27		*R. maddenii*	ssp. *crassum*	2017-1417	VIET 168	5	Vietnam	
wc maddenii ssp. crassum #27		*R. maddenii*	ssp. *crassum*	2017-498	VIET 168	9	Vietnam	
wc maddenii ssp. crassum #27		*R. maddenii*	ssp. *crassum*	2017-514	VIET 168	3	Vietnam	
wc maddenii ssp. crassum #27		*R. maddenii*	ssp. *crassum*	2017-1588	VIET 168	5	Vietnam	
wc maddenii ssp. crassum #29		*R. maddenii*	ssp. *crassum*	17425	Rhododendron-Park Bremen 2009/09	1	Japfu Peak, Nagaland, IN,2850 m	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*	2007/253	NAPE#025		wc, 9-19-2003, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8500'	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*	2007/236	NAPE#025		wc, 9-19-2003, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8500'	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*	2007/306	NAPE#025		wc, 9-19-2003, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8500'	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*	2007/337	NAPE#025		wc, 9-19-2003, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8500'	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*	2007/273	NAPE#025		wc, 9-19-2003, Nagaland-Araunchal Pradesh (& adjacent Bhutan) Expedition, 8500'	
wc maddenii ssp. crassum #31		*R. maddenii*	ssp. *crassum*	2000-0574	HWJ.99559	3	Lao Cai, Sa Pa, Phan Xi Păng (Fansipan), 2050 m	

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc maddenii ssp. crassum #32		*R. maddenii*	ssp. *crassum*	2005-0275	PW.153	2	Lao Cai, Sa Pa, Phan Xi Păng (Fansipan), 2890 m	
wc maddenii ssp. crassum #32	dead	*R. maddenii*	ssp. *crassum*	2013-0136	PW.153	0	Lao Cai, Sa Pa, Phan Xi Păng (Fansipan)	
wc maddenii ssp. crassum #33	dead	*R. maddenii*	ssp. *crassum*	2009-0216	NVD.0719	0	Lao Cai, Sa Pa, 2323 m	
wc maddenii ssp. crassum #34?		*R. maddenii*	ssp. *crassum*	2013-0286	NA	2	NA	
wc maddenii ssp. crassum #4		*R. maddenii*	ssp. *crassum*	2014/032	DJHV#8146		wc, Vietnam & Sichuan, China	
wc maddenii ssp. crassum #5		*R. maddenii*	ssp. *crassum*	2007/080	GR#0407			
wc maddenii ssp. crassum #6		*R. maddenii*	ssp. *crassum*	1994/378			wc, Yunnan, China, 2800m	
wc maddenii ssp. crassum #7		*R. maddenii*	ssp. *crassum*	2009/017	BASE#9539		wc, 5-21-00, up from Gongshan on new road to Dulong Valley, Salween, China, 2690m	27º 45' 47, 98º 35' 39
wc maddenii ssp. crassum #7		*R. maddenii*	ssp. *crassum*	2009/008	BASE#9539		wc, 5-21-00, up from Gongshan on new road to Dulong Valley, Salween, China, 2690m	27º 45' 47, 98º 35' 39
wc maddenii ssp. crassum #8		*R. maddenii*	ssp. *crassum*	2009/054	DJHMV #104		wc, 10-06, N Vietnam	
wc maddenii ssp. crassum #8		*R. maddenii*	ssp. *crassum*	2010/005	DJHMV #104		wc, 10-06, N Vietnam	
wc maddenii ssp. crassum #8		*R. maddenii*	ssp. *crassum*	2010/013	DJHMV #104		wc, 10-06, N Vietnam	
wc maddenii ssp. crassum #8		*R. maddenii*	ssp. *crassum*	2010/021	DJHMV #104		wc, 10-06, N Vietnam	
wc maddenii ssp. crassum #8		*R. maddenii*	ssp. *crassum*	2009/090	DJHMV #104		wc, 10-06, N Vietnam	
wc maddenii ssp. crassum #9		*R. maddenii*	ssp. *crassum*	2002/163			wc, Cang Shan, 9000'	
wc maddenii ssp. crassum #9		*R. maddenii*	ssp. *crassum*	2002/165			wc, Cang Shan, 9000'	
wc maddenii ssp. crassum #28		*R. maddenii*	ssp. *crassum* (*R. manipurense*)	1978-6210	KWRD 7136	5		
wc maddenii ssp. maddenii #5		*R. maddenii*	ssp. *maddenii*	2001/222	SEH#599		wc, 1997, Sikkim Himalaya, India, 1690m	
wc maddenii ssp. maddenii #5		*R. maddenii*	ssp. *maddenii*	2001/175	SEH#599		wc, 1997, Sikkim Himalaya, India, 1690m	
wc maddenii ssp. maddenii #5		*R. maddenii*	ssp. *maddenii*	2001/232	SEH#599		wc, 1997, Sikkim Himalaya, India, 1690m	
wc maddenii ssp. maddenii #6		*R. maddenii*	ssp. *maddenii*	2006/153	KCSH#0388		wc, 10-15-2003, around Tawang and back to Dirang, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8750'	

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc maddenii ssp. maddenii #6		*R. maddenii*	ssp. *maddenii*	2006/059	KCSH#0388		wc, 10-15-2003, around Tawang and back to Dirang, Arunachal Pradesh, Nagaland-Araunchal Pradesh Expedition, 8750'	
wc maddenii ssp. maddenii #7		*R. maddenii*	ssp. *maddenii*	1979/014			wc, Sikkim	
wc maddenii ssp. maddenii #24		*R. maddenii*	(*R. callophyllum*)	02970		1	C.W. India T.L. 1977	
wc maddenii ssp. crassum #10	dead	*R. maddenii*	ssp. *crassum*	09787		0	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	09790		1	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	09791		1	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #10		*R. maddenii*	ssp. *crassum*	09792		1	K.R.2978, Madd. Wlk, sth bank	
wc maddenii ssp. crassum #13		*R. maddenii*	ssp. *crassum*	20141091	YTT	1	China: Yunnan: Kiuchiang valley. 1,600 m	
wc maddenii ssp. crassum #13		*R. maddenii*	ssp. *crassum*	20141084	YTT	2	China: Yunnan: Kiuchiang valley. 1,600 m	
wc maddenii ssp. crassum #13		*R. maddenii*	ssp. *crassum*	19391048	YTT	1	China: Yunnan	
wc maddenii ssp. crassum #13		*R. maddenii*	ssp. *crassum*	19391033	YTT	16	China: Yunnan: Kiuchiang valley. 1,600 m	
wc maddenii ssp. crassum #14		*R. maddenii*	ssp. *crassum*	19662449		1	Myanmar: Sagaing Division: Mann Gale, Mt. Saramati. 600 m	25°44' N, 95°3' E
wc maddenii ssp. crassum #15		*R. maddenii*	ssp. *crassum*	19754044	LST	2	China: Xizang (Tibet) Aut. Reg.: Le. 2,350 m	
wc maddenii ssp. crassum #15		*R. maddenii*	ssp. *crassum*	20141081	LST	3	China: Xizang (Tibet) Aut. Reg.: Le. 2,350 m	
wc maddenii ssp. crassum #16		*R. maddenii*	ssp. *crassum*	19772713	FOR	10	China: Yunnan, W: Mekong Salween divide. 3,050-3,350 m	27° N, 99°2' E
wc maddenii ssp. crassum #17		*R. maddenii*	ssp. *crassum*	20141088	FOR	1	China: Yunnan. An unusual varient with white, petaloid calyx. [Locality not able to be traced]	
wc maddenii ssp. crassum #17		*R. maddenii*	ssp. *crassum*	19321024	FOR	4	China: Yunnan. An unusual varient with white, petaloid calyx. [Locality not able to be traced]	
wc maddenii ssp. crassum #18		*R. maddenii*	ssp. *crassum*	19951908	RUS	6	Vietnam: Lào Cai: Sapa, Fansipan, NE ridge above the village of Sin Chay. 2,280 m	
wc maddenii ssp. crassum #19		*R. maddenii*	ssp. *crassum*	19300234	FOR	1	China: Yunnan. [Herbarium source traced, no field notes with specimen].	
wc maddenii ssp. crassum #20		*R. maddenii*	ssp. *crassum*	19772716	FOR	2	China: Yunnan, W: Baoshan Pref.: Shweli-Salween divide. 2,600 m	25°40' N, 98°45' E
wc maddenii ssp. crassum #21		*R. maddenii*	ssp. *crassum*	19832535	KWA	13	India: Arunachal Pradesh: Di Chu Valley. Grows socially in thickets or on boulders in the river bed, preferring shade. 2,438-2,743 m	

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc maddenii ssp. crassum #22		*R. maddenii*	ssp. *crassum*	19941656	TRN	1	Vietnam: Lào Cai: Sapa, Fansipan. 2,987 m	
wc maddenii ssp. crassum #23		*R. maddenii*	ssp. *crassum*	19772715	FOR	1	China: Xizang (Tibet) Aut. Reg.: Salween-Kiuchiang divide. 2,750 m	
wc maddenii ssp. crassum #23		*R. maddenii*	ssp. *crassum*	19832494	FOR	1	China: Xizang (Tibet) Aut. Reg.: Salween-Kiuchiang divide. 2,750 m	
wc maddenii ssp. crassum #24		*R. maddenii*	ssp. *crassum*	19491022	ROC	4	China: Xizang (Tibet) Aut. Reg. - Yunnan border	
wc maddenii ssp. crassum #25		*R. maddenii*	ssp. *crassum*	19763208	FOR	8	China: Yunnan, W: Shweli-Salween divide. 3,050 m	
wc maddenii ssp. crassum #3		*R. maddenii*	ssp. *crassum*		NAPE025		NAPE025 (PK59) at Pukeiti	
wc maddenii ssp. crassum #30		*R. maddenii*	ssp. *crassum*	17413	JN 11082	1	W C Yunnan, CN,2800m	
wc maddenii ssp. crassum #35		*R. maddenii*	ssp. *crassum*		TH268?		TH268 (OM14) (crassum?) is sold as Spiced Ice. Vietnam	
wc maddenii ssp. crassum #36?		*R. maddenii*	ssp. *crassum*		DT 98		A Dayal Thomson collection from 1998 (S. Gardiner, pers comm). It may have been obtained through Brent Murdoch of Dalebroojk Nursery	
wc maddenii ssp. crassum #37?		*R. maddenii*	ssp. *crassum*				*R. maddenii* ssp. *crassum* as *R. manipurense* (wc?) is ‘poss Nth Vietnam’	
wc maddenii ssp. crassum #38		*R. maddenii*	ssp. *crassum*		JN1058?		DBG spreadsheet	
wc maddenii ssp. crassum #39	dead	*R. maddenii*	ssp. *crassum*		KW20839	0	*R. crassum* KW20839 (big form) imported by Pukeiti from Achamore House, Isle of Gigha, UK, in 1971 (Pukeiti archive, Imports 1971) but is now dead	
wc maddenii ssp. crassum #40		*R. maddenii*	ssp. *crassum*		DT 43	2	Wild collected by Doug Thomson 1996 Yunnan	
wc maddenii ssp. maddenii #14		*R. maddenii*	ssp. *maddenii*	19715035	LSE	3	China: Xizang (Tibet) Aut. Reg.: Tsakohugong, Tsangpo Gorge. 2,000 m	
wc maddenii ssp. maddenii #15		*R. maddenii*	ssp. *maddenii*	19150028	COO	4	Bhutan: Thimphu Dist.: Chapcha. 6,000 ft. Sparse, straggly bush; underleaf copper	27°13' N, 89°33' E
wc maddenii ssp. maddenii #16		*R. maddenii*	ssp. *maddenii*	20141090	LST	1	Bhutan: Tashigang Dist.: Jiri Chu. Rhododendron arboreum/Quercus forest. 6,500 ft. Shrub 4-10 ft	27°13' N, 91°31' E
wc maddenii ssp. maddenii #16		*R. maddenii*	ssp. *maddenii*	19754068	LST	8	Bhutan: Tashigang Dist.: Jiri Chu. Rhododendron arboreum/Quercus forest. 6,500 ft. Shrub 4-10 ft	27°13' N, 91°31' E
wc maddenii ssp. maddenii #17		*R. maddenii*	ssp. *maddenii*	19141003	BAI	2	China: Xizang (Tibet) Aut. Reg.: Upper Nyamsang Valley. 2,450 m	
wc maddenii ssp. maddenii #18		*R. maddenii*	ssp. *maddenii*	19730904	COH	3	India: Arunachal Pradesh: Subansiri Div., SE of Ziro	
wc megacalyx #1		*R. megacalyx*		2005/212	BASE#9544		wc, 5-21-2000, up from Gongshan on new road to Dulong Valley, Salween, China 2280 m	27º 45' 47, 98º 35' 39
wc megacalyx #1		*R. megacalyx*		2005/152	BASE#9544		wc, 5-21-2000, up from Gongshan on new road to Dulong Valley, Salween, China 2280 m	27º 45' 47, 98º 35' 39

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ ‘cultivar’	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc megacalyx #1		*R. megacalyx*		2005/243	BASE#9544		wc, 5-21-2000, up from Gongshan on new road to Dulong Valley, Salween, China 2280 m	27º 45' 47, 98º 35' 39
wc megacalyx #2		*R. megacalyx*		2002/009	CCHH#8076		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000 m	
wc megacalyx #2		*R. megacalyx*		2002/016	CCHH#8076		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000 m	
wc megacalyx #2		*R. megacalyx*		2000/020	CCHH#8076		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000 m	
wc megacalyx #2		*R. megacalyx*		2000/019	CCHH#8076		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000m	
wc megacalyx #3		*R. megacalyx*		2006/304	DGEY#026		wc, 9-27-01, along new Dulong road from Gongshan to Kongdan (Nu Jiang side), NW Yunnan, China, 2600 m	N27 45.540', E098 34.565'
wc megacalyx #3		*R. megacalyx*		2006/254	DGEY#026		wc, 9-27-01, along new Dulong road from Gongshan to Kongdan (Nu Jiang side), NW Yunnan, China, 2600 m	N27 45.540', E098 34.565'
wc megacalyx #3		*R. megacalyx*		2006/352	DGEY#026		wc, 9-27-01, along new Dulong road from Gongshan to Kongdan (Nu Jiang side), NW Yunnan, China, N27 45.540', E098 34.565', 2600 m	N27 45.540', E098 34.565'
wc megacalyx #4		*R. megacalyx*		2005/238	BASE#9532		wc, 5-21-2000, up from Gongshan on new road to Dulong Valley, Salween, China 2500 m	27º 45' 47, 98º 35' 39
wc megacalyx #4		*R. megacalyx*		2005/219	BASE#9532		wc, 5-21-2000, up from Gongshan on new road to Dulong Valley, Salween, China 2500 m	27º 45' 47, 98º 35' 39
wc megacalyx #5		*R. megacalyx*		1980/134	KW#20836		wc, 1953, The Triangle Expedition, N Burma	
wc mianningense #1		*R. mianningense*		17408	JN 12300	1	Mianning, Sichuan, CN, 4050 m	
wc nuttallii #1		*R. nuttallii*		2004/349	DGEY#079		wc, 9-30 to 10-2-01, track along Dulong Jiang north of Kongdan, NW Yunnan, China, 1850 m	N28 04.017', E098 20.002'
wc nuttallii #1		*R. nuttallii*		2004/374	DGEY#079		wc, 9-30 to 10-2-01, track along Dulong Jiang north of Kongdan, NW Yunnan, China, 1850 m	N28 04.017', E098 20.002'
wc nuttallii #10		*R. nuttallii*		20042030	GLGS2	5	China: Yunnan: Gongshan: Zizhixian: E side of the Dulong Jiang near and on cliff to the S of Bailai village ca. 7.4 direct km S of Dizhengdang (Lengdang) and ca. 15 direct km N of Kongdang. 1,620 m. Undisturbed	28°0' 35.5" N, 98°19' 24.2" E
wc nuttallii #11		*R. nuttallii*		20092021		2		
wc nuttallii #12		*R. nuttallii*		19941669	TRN	3	Vietnam: Lào Cai: Sapa, Fansipan. 2,498 m	
wc nuttallii #13		*R. nuttallii*		2015-630	VIET 3	2	Vietnam	
wc nuttallii #13		*R. nuttallii*		2017-1054	VIET 3	3	Vietnam	
wc nuttallii #13		*R. nuttallii*		2017-630	VIET 3	7	Vietnam	
wc nuttallii #13		*R. nuttallii*		2017-631	VIET 3	13	Vietnam	
wc nuttallii #13		*R. nuttallii*		2017-525	VIET 3	8	Vietnam	
wc nuttallii #14		*R. nuttallii*		2009-0217	NVD.0715	1	Sa Pa	
wc nuttallii #15	dead	*R. nuttallii*		2019-0155	KR11277	0	Upper Dibang District, Anini District, drive from Anini (28 47' 38.8" N, 95 54' 15.0" E, 1657m) via station 35 (just inside the Mipi Mithun fencing - 28 53' 25.3" N, 95 50' 00.2" E, 1478m), to Mipi (28 57' 01.5" N, 95 48' 51.5" E, 1534m) to Mipi 2	

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc nuttallii #16?		*R. nuttallii*					China ex ARS at Pukeiti (PK60)	
wc nuttallii #17?		*R. nuttallii*					OM-50 – Hudson ex Vietnam	
wc nuttallii #18	dead	*R. nuttallii*			AC435	0	*R. nuttallii* AC435 offered for sale in 1999 (PPM1999)	
wc nuttallii #19	dead	*R. nuttallii*			TH1419	0	*R. nuttallii* TH1419 offered for sale in 2001 (PPM2001)	
wc nuttallii #2		*R. nuttallii*		2001/315	CCHH#8077		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000m	
wc nuttallii #2		*R. nuttallii*		2001/289	CCHH#8077		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000m	
wc nuttallii #2		*R. nuttallii*		2001/267	CCHH#8077		wc, 9-27-97, Biluoxueshan, up from Fugong, Yunnan, China, 2000m	
wc nuttallii #2		*R. nuttallii*		20040721	CCHH	1	China: Biluo xue shan above Fugong. Cliff side. 2,000 m	
wc nuttallii #3		*R. nuttallii*		2017/075	HECC#10005			
wc nuttallii #3		*R. nuttallii*		2017/080	HECC#10005			
wc nuttallii #3		*R. nuttallii*		2017/091	HECC#10005			
wc nuttallii #3	dead	*R. nuttallii*			Cox10005	0	*R. nuttallii* Cox 10005 (ws, but does not say where) offered for sale in 2010 (PPM2010) – this plant dead now	
wc nuttallii #4		*R. nuttallii*		2008/175	APA#009		wc, 10-11-05, ridge running S from Singa to Abroka, Arunachal Pradesh, India, (Arunachal Pradesh Abroka Expedition), 5000'	
wc nuttallii #4		*R. nuttallii*		2008/263	APA#009		wc, 10-11-05, ridge running S from Singa to Abroka, Arunachal Pradesh, India, (Arunachal Pradesh Abroka Expedition), 5000'	
wc nuttallii #4		*R. nuttallii*		2008/219	APA#009		wc, 10-11-05, ridge running S from Singa to Abroka, Arunachal Pradesh, India, (Arunachal Pradesh Abroka Expedition), 5000'	
wc nuttallii #5		*R. nuttallii*		2001/150	KW#?			
wc nuttallii #6		*R. nuttallii*		2007/338	CCHH#8104		wc, 10-2-97, Gongshan, Yunnan, China, 1900m	
wc nuttallii #6		*R. nuttallii*		2007/308	CCHH#8104		wc, 10-2-97, Gongshan, Yunnan, China, 1900m	
wc nuttallii #6		*R. nuttallii*		2007/275	CCHH#8104		wc, 10-2-97, Gongshan, Yunnan, China, 1900m	
wc nuttallii #6	dead	*R. nuttallii*			CCHH8104	0	DBR2001 offered for sale (BDM669 -ws P. Cox CCHH8104)	
wc nuttallii #7		*R. nuttallii*		1996/028	KR#3056		wc, 1994, Vietnam Expedition	
wc nuttallii #8		*R. nuttallii*	aff.	19951632	RUS	3	Vietnam: Lào Cai: Sapa, Ban Khoang Road. Bank near waterfall 2-3 km from Ban Khoang. 1,500 m. Shrub to 1m.	
wc nuttallii #9		*R. nuttallii*	aff.	20092023		2		
wc nuttallii #9		*R. nuttallii*	aff.	20092024		1		
wc pachypodum #1		*R. pachypodum*		2014/226	JN#11046		wc, Nov 2011, Cangshan, Yunnan, 2600m	
wc pachypodum #1		*R. pachypodum*		2014/172	JN#11046		wc, Nov 2011, Cangshan, Yunnan, 2600m	
wc pachypodum #1		*R. pachypodum*		2014/217	JN#11046		wc, Nov 2011, Cangshan, Yunnan, 2600m	
wc pachypodum #10	dead	*R. pachypodum*			K60 seed.	0	1990-1450e (seed ex China, Kew, K60) which was in the Pukeiti nursery in 1992	
wc pachypodum #10	dead	*R. pachypodum*			RGY 003	0	1990-1450d (RGY003, Bublitz, Yunnan, seed) which was G28	
wc pachypodum #2		*R. pachypodum*		1999/197	AC#1993		wc, 1995, China	

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wc pachypodum #2		*R. pachypodum*		1999/149	AC#1993		wc, 1995, China	
wc pachypodum #2		*R. pachypodum*		1999/175	AC#1933		wc, 1995, China	
wc pachypodum #2		*R. pachypodum*			AC1993	1	DBG has AC1993 ex DBR (DBG spreadsheet)	
wc pachypodum #3		*R. pachypodum*		1999/089			grown from 88ARS# 399 which is seed imported by RSF from Yunnan, China, wc, 3100m	
wc pachypodum #4		*R. pachypodum*		2002/168			wc, Cang Shan, 9000'	
wc pachypodum #5		*R. pachypodum*		1979-74	FORR 7516	9		
wc pachypodum #6	dead	*R. pachypodum*		03707		0	SBEC 0115 Ex. NS 299 UK	
wc pachypodum #6		*R. pachypodum*		03714		1	SBEC 0115 Ex. NS 358 UK	
wc pachypodum #6		*R. pachypodum*		03723		1	SBEC 0115	
wc pachypodum #6	dead	*R. pachypodum*		03724		0	SBEC 0115	
wc pachypodum #6	dead	*R. pachypodum*			SBEC0115	0	1980-1450 (Cox, SBEC0115, 8600ft China, seed) which was A10	
wc pachypodum #7		*R. pachypodum*		17415	JN 11076	1	SW Yunnan, CN, 2800 m	
wc pachypodum #1	dead	*R. pachypodum*		2012-0164	JN11046	0	midwest Yunnan	
wc pachypodum #7	dead	*R. pachypodum*		2012-0165	JN11076	0	SW Yunnan	
wc pachypodum #8	dead	*R. pachypodum*		2004-0382	KR.7721	0	Dali, Cangshan	
wc pachypodum #9		*R. pachypodum*		2011-0559	MD.97	1	Kunming	
wc parryae #1		*R. parryae*			Fischer 146		Pukeiti got Fischer 146 from RBGE in 1972	
wc pseudociliipes #1		*R. pseudociliipes*		2017/090	SEH#1534			
wc pseudociliipes #1		*R. pseudociliipes*		2017/082	SEH#1534			
wc pseudociliipes #2		*R. pseudociliipes*		2014/184	JN#11070		wc, Nov. 2011, Salween Region, W. Yunnan, China, 2800m	
wc pseudociliipes #2		*R. pseudociliipes*		2014/210	JN#11070		wc, Nov. 2011, Salween Region, W. Yunnan, China, 2800m	
wc pseudociliipes #2		*R. pseudociliipes*		2014/249	JN#11070		wc, Nov. 2011, Salween Region, W. Yunnan, China, 2800 m	
wc pseudociliipes #2		*R. pseudociliipes*		17414	JN 11070	1	W Yunnan, CN, 2800 m	
wc pseudociliipes #3		*R. pseudociliipes*		2005/084	BASE#9697		wc, 6-11-2000, Ziben Shan, Biluoxue Shan, Salween, China, 2500m	
wc pseudociliipes #3		*R. pseudociliipes*		2005/098	BASE#9697		wc, 6-11-2000, Ziben Shan, Biluoxue Shan, Salween, China, 2500m	
wc pseudociliipes #3		*R. pseudociliipes*		2005/132	BASE#9697		wc, 6-11-2000, Ziben Shan, Biluoxue Shan, Salween, China, 2500m	
wc pseudociliipes #3		*R. pseudociliipes*		2005/147	BASE#9697		wc, 6-11-2000, Ziben Shan, Biluoxue Shan, Salween, China, 2500m	
wc pseudociliipes #3		*R. pseudociliipes*		2005/120	BASE#9697		wc, 6-11-2000, Ziben Shan, Biluoxue Shan, Salween, China, 2500m	
wc pseudomaddenii #1		*R. pseudomaddenii*		2017/072	HECC#10083			
wc pseudomaddenii #1		*R. pseudomaddenii*		2017/066	HECC#10083			
wc roseatum #1	dead	*R. roseatum*				0	Wild collected material imported in 1992 by L. Davies (NZRA Bulletin 2001 p55). At Heritage Park (NZRA Bulletin 2003 p40)	
wc rufosquamosum #1		*R. rufosquamosum*	aff.	19962587	RUS	1	China: Yunnan: Mengzi, Li Hua Shan; by tin mines. Growing on cliff edge and in pockets in the kharst limestone. ca 2,400 m.Shrub to 0.7 m; petioles bristly as in _*R. barbatum*	103°14' E, 23°21' N

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ ‘cultivar’**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc scopulorum #1		*R. scopulorum*		2005/110	AC#3669		wc, 1997, Bayi	
wc scopulorum #1		*R. scopulorum*		2005/129	AC#3669		wc, 1997, Bayi	
wc scopulorum #1		*R. scopulorum*		2005/088	AC#3669		wc, 1997, Bayi	
wc scopulorum #1		*R. scopulorum*			AC3669		DBG has BDM 919(AC3669) and BDM1365 (DBG spreadsheet)	
wc scopulorum #2		*R. scopulorum*		1998/014	KW#6354		wc, 1924-25, Tibet & Bhutan Expedition	
wc scopulorum #2		*R. scopulorum*		19730921	KWA	27	China: Xizang (Tibet) Aut. Reg.: Gompa La, Tsangpo Gorge. On steep, sun-scorched boulder screes and on steep rocky slopes in thickets. 1,829 m. Stout bush 6-8 ft	
wc scopulorum #2		*R. scopulorum*		1996-4618	KWRD 6354	9	Bhutan	
wc scopulorum #3		*R. scopulorum*		2002/007	CC#7571		wc, Spring 1996, SE Tibet Expedition	
wc scopulorum #3		*R. scopulorum*		2002/003	CC#7571		wc, Spring 1996, SE Tibet Expedition	
wc scopulorum #4		*R. scopulorum*		19980429	RUS	1	China: Xizang (Tibet) Aut. Reg.: Near the confluence of the Yigrong Tsangpo and the Tongkyuk chu; near station 62. Amongst cliffs. ca 2,100 m. Shrub 1-1.5 m	30.01°44' 4" N, 95°0' 39.3" E
wc surasianum #1		*R. surasianum*		2003/148			wc, Chiengmai Province, Thailand, 5000-5700'	
wc surasianum #1		*R. surasianum*		2003/177			wc, Chiengmai Province, Thailand, 5000-5700'	
wc surasianum #2		*R. surasianum*			BDM1067		Doi Langka Noi, Chiangmai Thailand 1700m, should be at DBG	
wc taggianum #1		*R. taggianum*		2001/108	CCHH#8108		wc, 10-3-97, Gongshan, up trail from Quzi, Yunnan, China, 2130m	
wc taggianum #1		*R. taggianum*		2001/123	CCHH#8108		wc, 10-3-97, Gongshan, up trail from Quzi, Yunnan, China, 2130m	
wc taggianum #1		*R. taggianum*		2001/070	CCHH#8108		wc, 10-3-97, Gongshan, up trail from Quzi, Yunnan, China, 2130m	
wc taggianum #1		*R. taggianum*		2001/132	CCHH#8108		wc, 10-3-97, Gongshan, up trail from Quzi, Yunnan, China, 2130m	
wc taggianum #1		*R. taggianum*			CCHH8108	1	DBG has BDM748 (CCHH8108)	
wc taggianum #2		*R. taggianum*		1992-1272	GUIZ 163	3	China	
wc taggianum #3		*R. taggianum*		00311		1	J. Basford says plant is *R. lindleyi* Ghia form of RS 499, said to be American form of *R. lindleyi*	
wc taggianum #3		*R. taggianum*		00312		1	J. Basford says plant is *R. lindleyi* Ghia form of RS 499, said to be American form of *R. lindleyi*	
wc taggianum #3		*R. taggianum*		00313		1	J. Basford says plant is *R. lindleyi* Ghia form of RS 499, said to be American form of *R. lindleyi*	
wc valentinianum #3		*R. valentinianum*		2015-1730	VIET 166			
wc valentinianum #4		*R. valentinianum*		2018-0539	DJHV 13180	3	Lao Cai, Sa Pa, Phan Xi Păng (Fansipan) Fansipan?	
wc valentinianum #5		*R. valentinianum*			BDM895		DBG has BDM895 (Cox form selfed, hp) (DBG spreadsheet).	
wc valentinianum #6	dead	*R. valentinianum*			F27715	0	PK once had valentinianum F27715	
wc valentinioides #1		*R. valentinianum*	(SEH#235 noted as *R. valentinioides*)	2000-0483	SEH.235	3	Yunnan Province, ne Yunnan, 2800 m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/155	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	

Wc no.	**Dead acc.**	***Rhododendron* species**	**ssp./var./(syn.)/ 'cultivar'**	**Acc. ID**	**Collector ID**	**No. of plants**	**Collection provenance**	**Provenance coordinates**
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/128	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/137	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/222	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/144	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/211	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/161	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/174	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/257	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/235	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/180	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum var. oblongilobatum #1		*R. valentinianum*	var. *oblongilobatum*	2014/193	JN#11080		wc, Wuliang Shan, Yunnan, 2800m	
wc valentinianum #1		*R. valentinianum*	aff.	2014/185	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/166	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/173	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/197	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/150	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/219	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/234	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/256	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/203	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/126	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/135	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #1		*R. valentinianum*	aff.	2014/142	DJHMV#106		wc, 10-06, N Vietnam	
wc valentinianum #2		*R. valentinianum*	aff.	2016/040	FMWJ#13298		wc, N Vietnam	
wc valentinianum #2		*R. valentinianum*	aff.	2016/062	FMWJ#13298		wc, N Vietnam	
wc valentinianum #2		*R. valentinianum*	aff.	2016/082	FMWJ#13298		wc, N Vietnam	
wc valentinianum #7	dead	*R. valentinianum*	aff.		DT31598	0	An aff. DT31598 in colln 97	
wc valentinianum #8		*R. valentinianum*	aff.		DT319		DT319 valentinianum aff.	
wc valentinianum var. oblongilobatum #2		*R. valentinianum*	var. *oblongilobatum*	19960619	KYE	1	China: Yunnan: Wenshan Zhuang-Miao Aut. Pref.: Laujunshan, Wenshan. Amongst bamboo. ca 2,600 m. Shrub to 2 m (like AC 1221 but terrestrial)	104°35' E, 23°30' N

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc valentinianum var. oblongilobatum #3		*R. valentinianum*	var. *oblongilobatum*	19960621	KYE	8	China: Yunnan: Wenshan Zhuang-Miao Aut. Pref.: Xichou, Wenshan. ca 1,800 m. Shrub to 2 m; epiphytic on Lithocarpus sp.	104°38' E, 23° N
wc valentinianum var. oblongilobatum #3		*R. valentinianum*	var. *oblongilobatum*		AC1258		PK has AC1258 (PK16) (ex S. Dahal?)	
wc valentinianum var. oblongilobatum #4		*R. valentinianum*	var. *oblongilobatum*		C&H7186		*R. valentinianum* var. *oblongilobatum* C&H7186 at Orton Bradley (NZRA Bulletin 2003 p21)	
wc valentinioides #1		*R. valentinioides*		1997/137	SEH#235		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2800m	
wc valentinioides #1		*R. valentinioides*		1997/136	SEH#235		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2800m	
wc valentinioides #1		*R. valentinioides*		1997/139	SEH#235		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2800m	
wc valentinioides #2		*R. valentinioides*		1997/128	SEH#237		wc, Sept. & Oct. 1995, NE Yunnan Province, China, 2800m	
wc valentinioides #3		*R. valentinioides*		2017-628	VIET 183	5	Vietnam	
wc valentinioides #3		*R. valentinioides*		2015-1731	VIET 183	16	Vietnam	
wc veitchianum #1		*R. veitchianum*		2002/012	C#9001		wc, Doi Inthanon, Thailand	
wc veitchianum #1		*R. veitchianum*		2002/001	C#9001		wc, Doi Inthanon, Thailand	
wc veitchianum #1		*R. veitchianum*		1998/017	C#9001		wc, Doi Inthanon, Thailand (mountain)	
wc veitchianum #2		*R. veitchianum*		19750211	VLD	12	Thailand: Chiang Mai: Doi Pui. 160 m	
wc veitchianum #3		*R. veitchianum*		19991627	TH99	1	Thailand: Thailand, NW: Above Huay Hee village, near Mae Hong	
wc veitchianum #4		*R. veitchianum*			KR2247		*R. veitchianum* aff. KR2247 (OM44)	
wc veitchianum #5?		*R. veitchianum*			Thailand		Collected in Thailand (PK58) by Os Blumardt (The Rhododendron 2015, p39) – this form is in the Bublitz garden	
wc veitchianum #6		*R. veitchianum*			BDM1066		DBG has BDM1066 (Thailand) (DBG spreadsheet)	
wc veitchianum #7	dead	*R. veitchianum*			AC5645	0	*R. veitchianum* AC5645 (North Vietnam) offered for sale in 2012 (PPM2012)	
wc veitchianum #8		*R. veitchianum*	'Ice White'		Thailand		*R. veitchianum* Ice White (PK21, wild collected, Thailand) offered for sale in 1994 (PPM1994)	
wc walongense #1		*R. walongense*		2007/355	HECC#10004		wc, 10-17-2002, Arunachal Pradesh, 5400'	
wc walongense #1		*R. walongense*		2007/312	HECC#10004		wc, 10-17-2002, Arunachal Pradesh, 5400'	
wc walongense #2		*R. walongense*		2005/253	HECC#10006		wc, 10-22-2002, Arunachal Pradesh, 6600'	
wc walongense #2		*R. walongense*		2005/239	HECC#10006		wc, 10-22-2002, Arunachal Pradesh, 6600'	
wc walongense #2		*R. walongense*		2005/167	HECC#10006		wc, 10-22-2002, Arunachal Pradesh, 6600'	
wc wumingense #1		*R. wumingense*		2014/014	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/044	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/025	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/080	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/111	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/036	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/020	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/076	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/053	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/061	CGG#14150			
wc wumingense #1		*R. wumingense*		2014/098	CGG#14150			

Wc no.	Dead acc.	*Rhododendron* species	ssp./var./(syn.)/ 'cultivar'	Acc. ID	Collector ID	No. of plants	Collection provenance	Provenance coordinates
wc wumingense #1		*R. wumingense*		2014/010	CGG#14150			
wc wumingense #2		*R. wumingense*		2016/027	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/071	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/077	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/060	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/046	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/091	CDHM#14724			
wc wumingense #2		*R. wumingense*		2016/038	CDHM#14724			
wc wumingense #3		*R. wumingense*		20140719	COX	3	China: Daming Shan	
wc wumingense #1		*R. wumingense*		2014-0449	CGG.14150	1	no specific location	

Reference

MacKay, M. B., Hootman, S. E., Smith, G. F., Thomson, D., Gardiner, S. E., & Smith, P. (2018). *Updated global analysis for ex situ conservation of Rhododendron L. (Ericaceae)*. Massey University, Palmerston North, New Zealand & Botanic Gardens Conservation International, Richmond, UK. Retrieved from https://www.globalconservationconsortia.org/resources/updated-global-analysis-for-ex-situ-conservation-of-rhododendron-l-ericaceae/

List S2.3 Checklist of taxon profiles of *Rhododendron* subsection *Maddenia*

The 65 taxa of *Rhododendron* subsection *Maddenia* are listed in alphabetical order. Each taxon profile includes information on taxon name with commonly seen synonyms in cultivation, IUCN Red List category, wild distribution locality and altitude range, and status of *ex situ* cultivation. The list of taxa includes all species currently defined (as described below) and does not consider issues of unresolved taxonomy.

This list summarises all taxa of ss. *Maddenia* (species, subspecies and botanical varieties) with their synonyms, based on the 56 taxa classified by Chamberlain et al. (1996). In addition, four taxa are listed separately from species complexes and analysed as distinct entities due to unresolved taxonomy: *R. iteophyllum* (Mao et al., 2017b), *R. sinonuttallii* (Gibbs et al., 2011), *R. taronense* (Gibbs et al., 2011), *R. valentinioides* (ined.) (Gibbs et al., 2011; Donald, 2012). *R. vanderbiltianum* is also included despite its doubtful placement (Argent et al., 2008; Donald, 2012; MacKay et al., 2018). Another four recently published species are updated: *R. pseudomaddenii* (Mao & Bhaumik, 2015), *R. leptocladon* (Rushforth & Nguyen, 2019), *R. kuomeianum* (Chang et al., 2021) and *R. starlingii* (Rushforth et al., 2022).

IUCN Red List categories for subsection *Maddenia* are listed as CR (Critically Endangered), EN (Endangered), VU (Vulnerable), NT (Near Threatened), LC (Least Concern), DD (Data Deficient) and NE (Not Evaluated) (BGCI & IUCN SSC Global Tree Specialist Group, 2018). Taxa of ss. *Maddenia* were categorized according to their conservation status: CR, EN, VU, NT, DD, LC or NE (no taxon known as EX or EW). Threatened levels of taxa were initially from *The IUCN Red List of Rhododendrons* (Gibbs et al., 2011) or from assessments for the recently published species: *R. pseudomaddenii* (Mao & Bhaumik, 2015) and *R. kuomeianum* (Chang et al., 2021), or the updated IUCN Red List (BGCI & IUCN SSC Global Tree Specialist Group, 2018) and endemic species referring to national assessments in China: the China Red List of higher plants (MEP–CAS, 2013) and threatened species list of China's higher plants (Qin et al., 2017). BGCI's ThreatSearch database was also indexed for reference of existing conservation assessments globally or regionally (BGCI, 2022b).We prioritize global assessments to decide the IUCN Red List category, but some national assessments in China are considered at a global level for endemic taxa. Finally, the **Red List status in bold** for each taxon was adopted for our analysis.

Each taxon profile is initially described with two maps including information of wild distribution (upper map) and *ex situ* collections (lower map). The distribution area was geo-mapped for each taxon, referring to literature and online databases that describe taxon distribution in administrative or natural regions within an altitudinal range (Cullen, 1980; Davidian, 1982; Feng, 1988, 1992; Feng & Yang, 1999; M.-Y. Fang et al., 2005; Fang et al., 2011; Gibbs et al., 2011; Mao & Bhaumik, 2015; Mao et al., 2017a; Chang et al., 2021;

Rushforth et al., 2022). For particular taxa with limited geographical information, especially those ‘not in cultivation’ (e.g., *R. amandum*), provenance of type specimens (Davidian, 1982) or documented wild collections (RBGE, 2018b, 2018a; Table S2.2 from the present study) were also referenced. Region or site names were initially searched using the QGIS ‘GeoCoding’ plugin and/or by manual confirmation on Google maps. When there was no direct result for the geo-reference search, the distribution was manually located referring to the taxon’s habitat, altitude and administrative address as described. Herbarium occurrence in the Global Biodiversity Information Facility database (GBIF, 2021) was referenced only when the distribution in the literature was geographically broad and not defined with specific geographical information, and where there was no related information in the Red List (Gibbs et al., 2011) or *Flora of China* (M.-Y. Fang et al., 2005).

Data describing the presence of ss. *Maddenia* taxa in cultivation were collected from three key sources: 1) BGCI PlantSearch public website (BGCI, 2021); 2) an unpublished set of BGCI data for *Rhododendron* records (BGCI, 2020) (see taxon-level data in the compiled Supplementary Table S2.1); 3) accession-level data from seven gardens in New Zealand and seven largest collections of ss. *Maddenia* outside New Zealand (see Supplementary Table S2.2), which includes unpublished data from MacKay et al. (2018) and additional data or individual garden updates in 2020.

Number (no.) of *ex situ* sites represents count of occurrences holding collections of the corresponding taxon in the BGCI database. *Ex situ* collection sites are geo–located with green triangles on the bottom map in each taxon profile.

Number (no.) of wild sources was counted as for number of wild collections according to collectors’ number. When a collector’s number was unavailable, other information about the collection was referenced to establish a reliable identification. No. of mapped wild sources represents the count of wild accessions mapped with available provenance information according to the compiled dataset; others were counted for number of wild sources but not mapped. No. of wild accessions represents the total count of plants from different wild sources in the surveyed botanic gardens. For example, different plants are cultivated from seeds collected from the same accession in the wild, which does not take the plant clones into account.

Maps for each taxon were georeferenced and generated using QGIS 3.20.3 (QGIS Development Team, 2021). GIS layers were used as the base for the two maps, with ESRI grey layer in the top (regional) map for wild distribution and provenance of wild accessions, and KG layer in the bottom (global) map for locating *ex situ* sites. For geo-mapping, several layers were used to cross check various factors as mapping references. Most distribution records were at different administrative units (e.g., country, province/state, city, county, town). Natural Earth layers (cultural) at a resolution of 10 m (Natural Earth, 2021) and ‘ESRI National Geographic’ layer and ‘Google.cn Normal’ layer (QGIS plugin: ‘QuickMapServices’ for the latter two layers) were used as base maps to recognize the national geographical area in administrative units. Data for range of altitude (Davidian, 1982; M.-Y. Fang et al., 2005) were also referenced when drawing distribution polygons. The altitude was inferred from the 'ESRI Topo' base map (QGIS plugin: 'QuickMapServices'), which presents contour lines at a resolution of 20 m. The shape layer at a 1 km resolution of the latest Köppen–Geiger climate classification system was used as a reference for regional climate, which presents the spatial climate classes based on air temperature and precipitation integrated with topographic effects (Beck et al., 2018). Only the natural range was considered, and the extent of distribution mapping of different taxa may differ due to the availability of information on their distribution.

On the lower map of each profile, there may be two types of plots representing provenance of the wild accessions. Red diamonds represent accurate origins of wild collections with available coordinates or precise collection locations described; pink dots represent approximate origins of wild collections with an approximate description of the source, usually mapped near the center of the described region with a reference of habitat altitude if available. Therefore, it is possible that accessions are identified as from the wild but not mapped due to lack of provenance data. Because the mapping of taxa distribution and wild accessions are manually generated based on literature and garden records, maps presented here should be viewed as estimates to compare among taxa for conservation prioritization rather than the actual diversity captured in *ex situ* collections.

The designations employed and plant data analysed in this study do not imply any opinion of the author's concerning country territory and legal status of plant material.

Legend for the taxon profiles:

🟧 light orange polygon - wild distribution
■ dark orange square - location of type specimen
◆ red diamond - precise provenance of wild accession
● pink dot - approximate provenance of wild accession
▲ green triangle - botanic garden living collection of taxon

Rhododendron × cavroni André

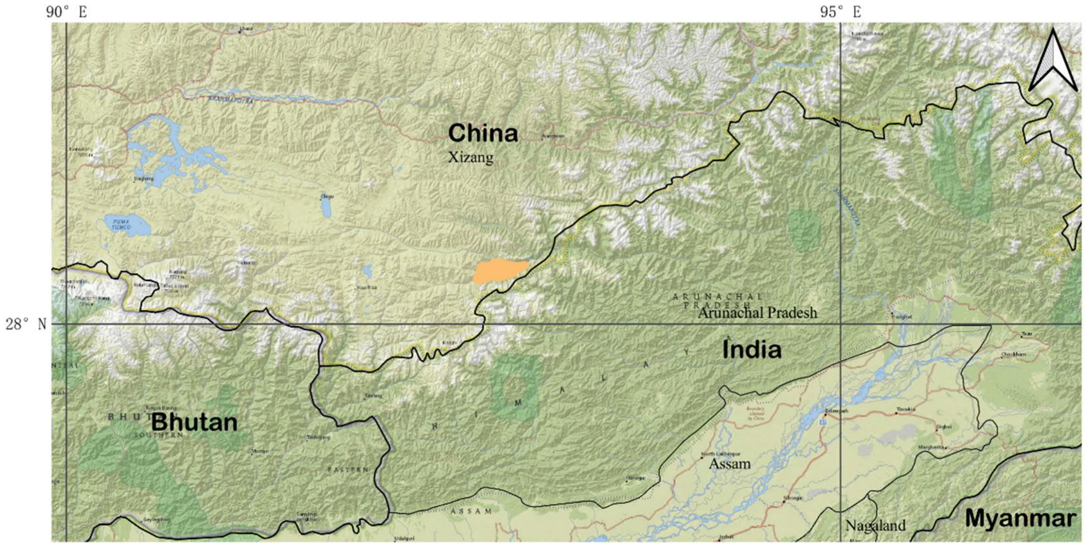
Taxonomic references: Chamberlain et al. (1996); International Plant Names Index (2022)

IUCN Red List status: NE
No distribution data.
Not in cultivation.

Due to lack of data and no published materials, we suggest removing this species from subsection *Maddenia*. It is not included by World Flora Online (WFO, 2022).

Rhododendron amandum Cowan

IUCN Red List status: **DD** (Gibbs et al., 2011; Qin et al., 2017)
Distribution: China (Xizang)*
Altitude: ca. 3,500 m
Not in cultivation.



*Lacking distribution data. This map shows the location where the type specimen was collected (Davidian, 1982).

Rhododendron basfordii Davidian

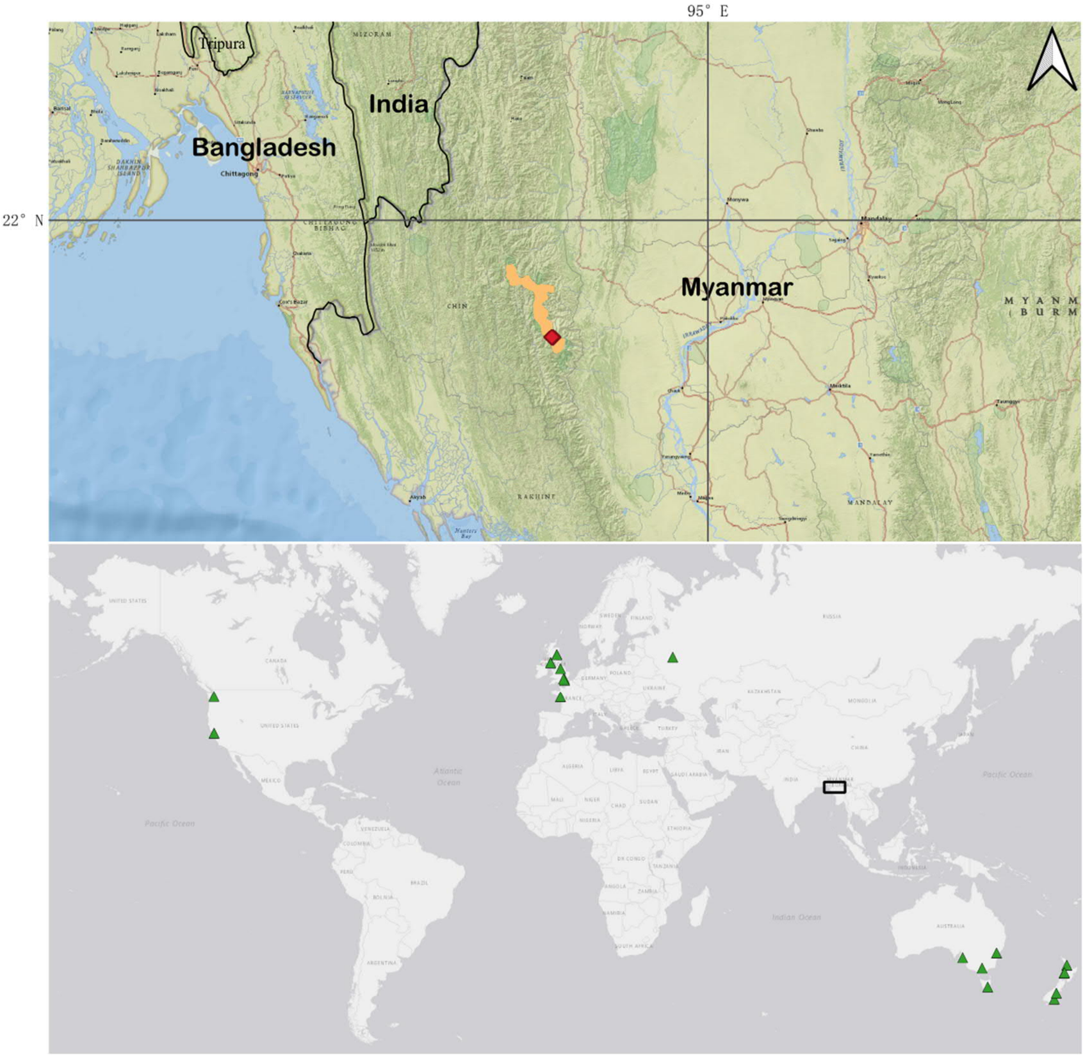
IUCN Red List status: NE
Distribution: Bhutan*
Altitude: ca. 2,593 m
Not in cultivation.

*Lacking distribution data. This map shows the location where the type specimen was collected (Davidian, 1982).

Rhododendron burmanicum Hutch.

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: Myanmar
Altitude: 2,745–3,020 m

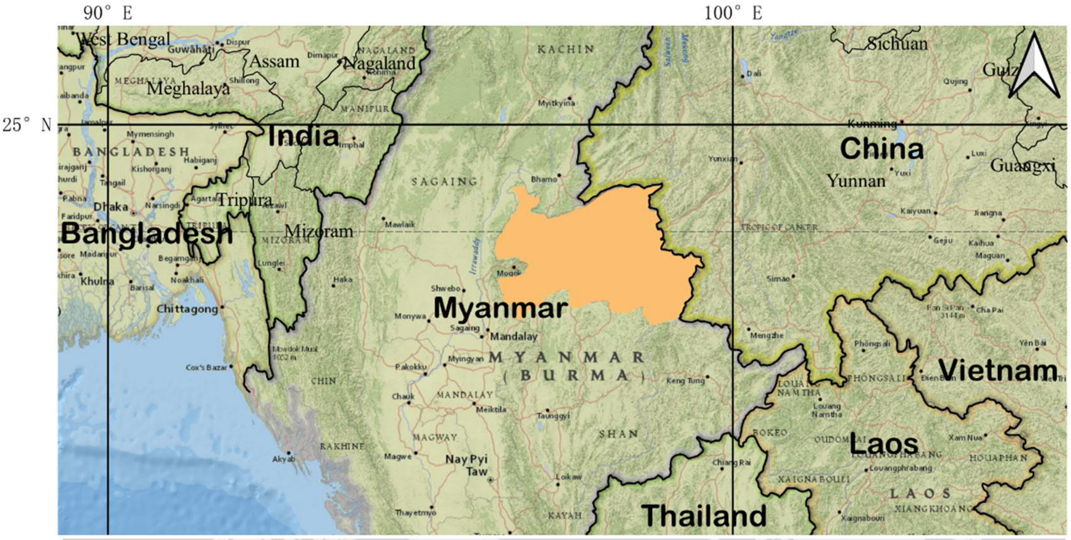
No. of *ex situ* sites/countries: 19/6
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 3



Rhododendron carneum Hutch.

IUCN Red List status: NE
Distribution: Myanmar
Altitude: ca. 2,288 m

No. of *ex situ* sites/countries: 8/5
No. of (mapped) wild sources: 0
No. of wild accessions: 0

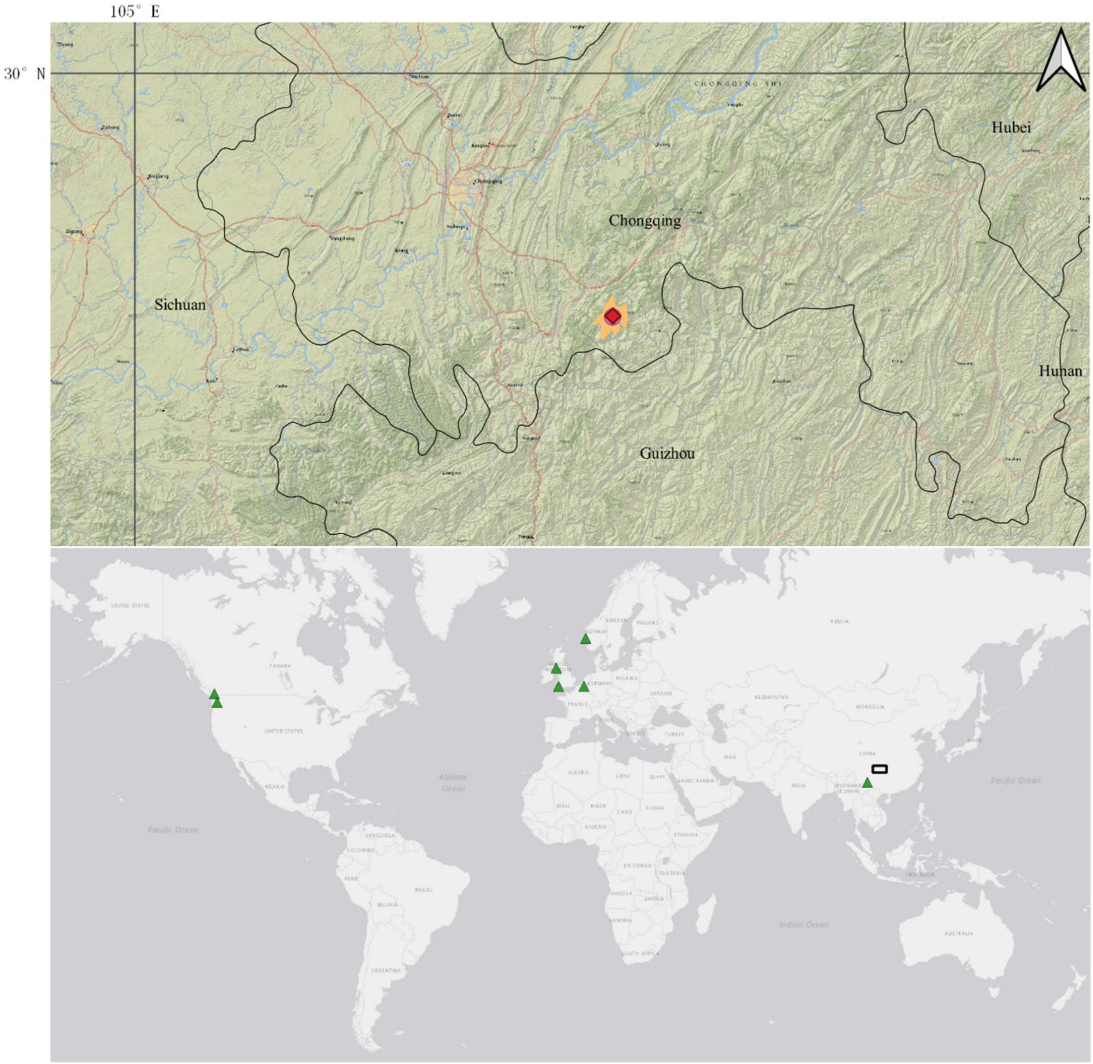


Rhododendron changii (W.P.Fang) W.P.Fang

IUCN Red List status: globally CR (Gibbs et al., 2011), **VU** in China (Qin et al., 2017)

Distribution: China (S Chongqing)
Altitude: 1,600–2,000 m

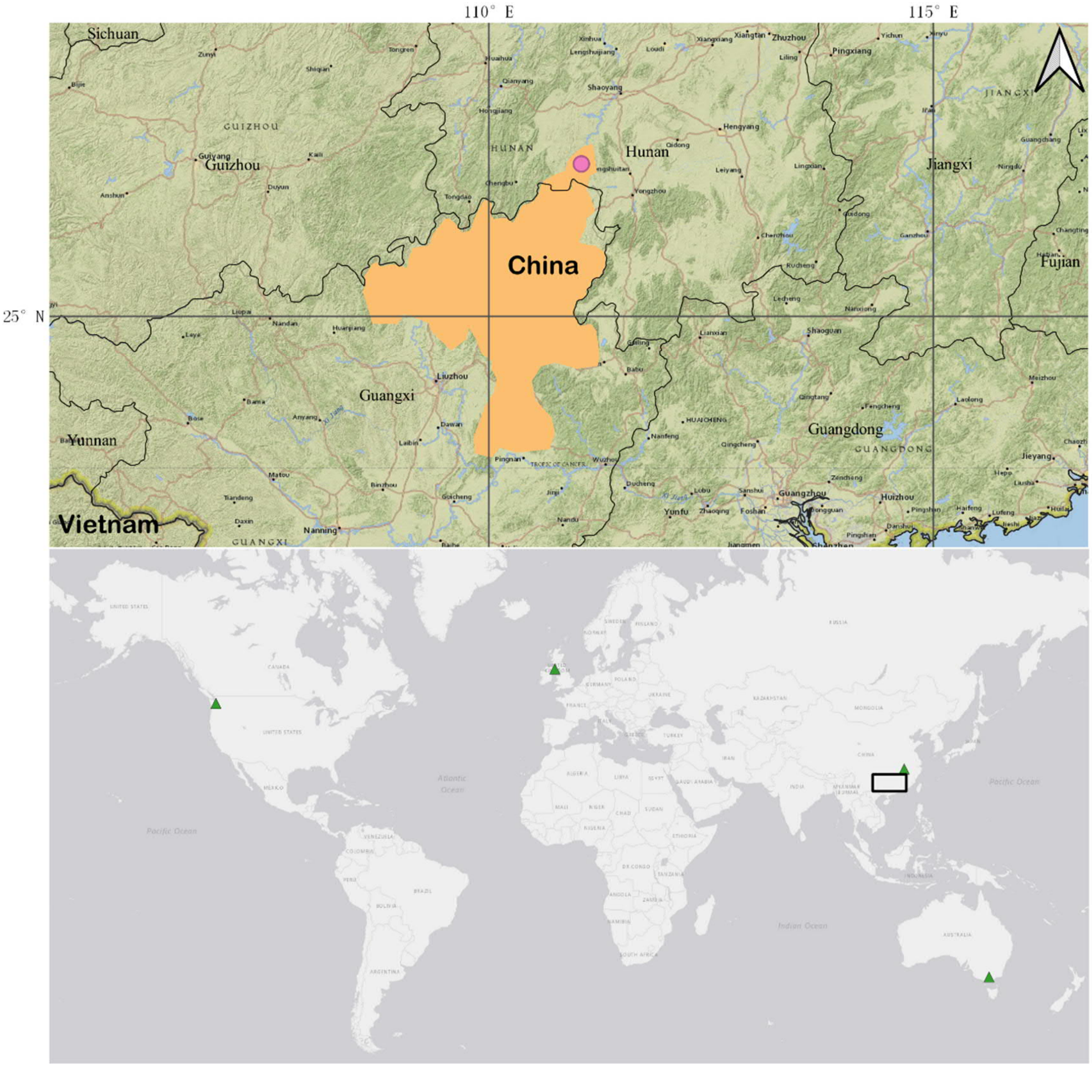
No. of *ex situ* sites/countries: 7/6
No. of (mapped) wild sources: (2) 3
No. of wild accessions: 8



Rhododendron chunienii Chun & W.P.Fang

IUCN Red List status: **DD** (Gibbs et al., 2011)
Distribution: China (NE Guangxi, SW Hunan)
Altitude: 1,300–1,400 m (M.-Y. Fang et al., 2005); ca. 1,700 m (Feng & Yang, 1999)

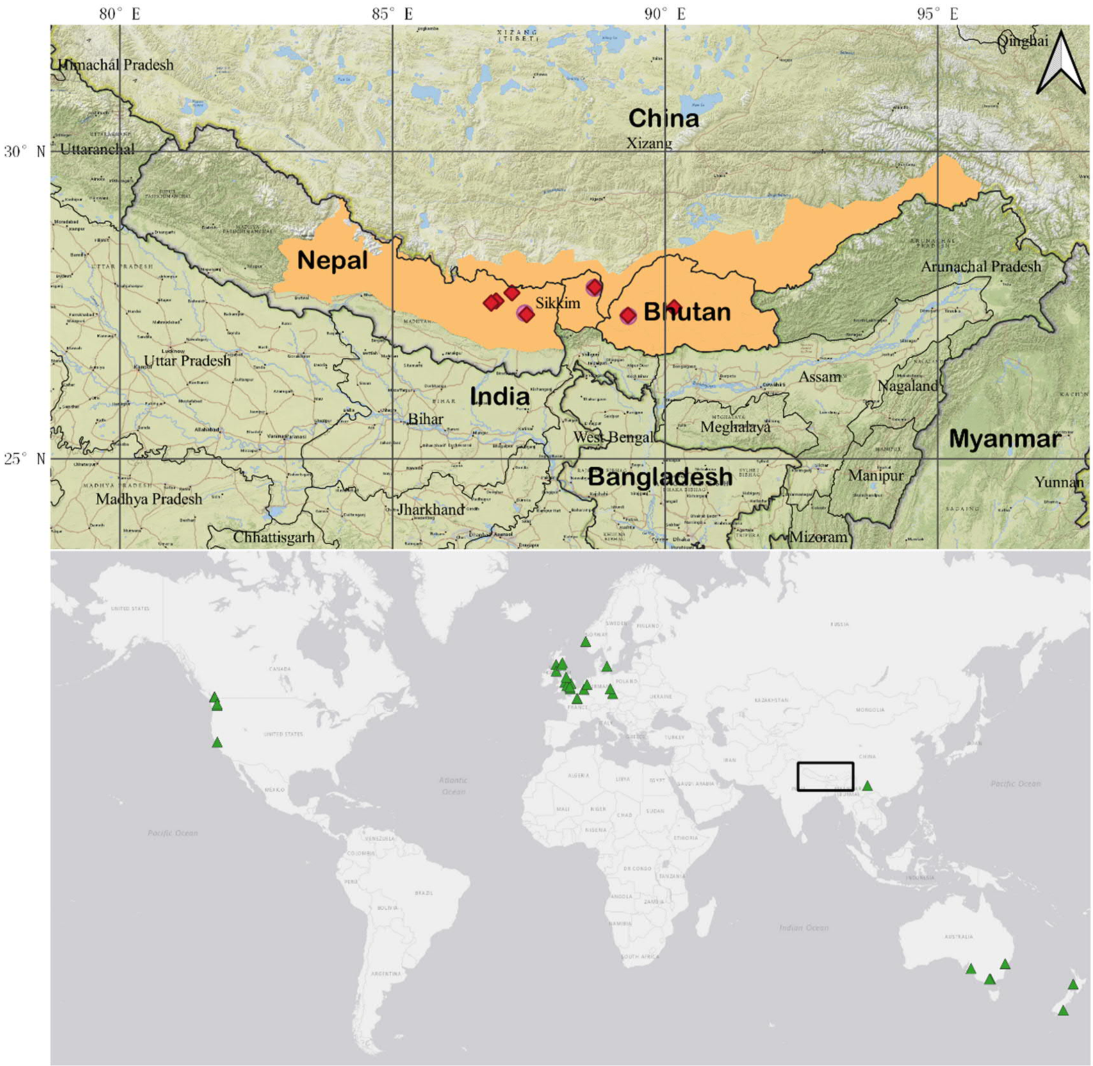
No. of *ex situ* sites/countries: 4/4
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 2



Rhododendron ciliatum Hook.f.

IUCN Red List status: **LC** (Gibbs et al., 2011; MEP–CAS, 2013)
Distribution: China (S Xizang), Bhutan, E Nepal, India (Sikkim)
Altitude: 2,700–3,500 m

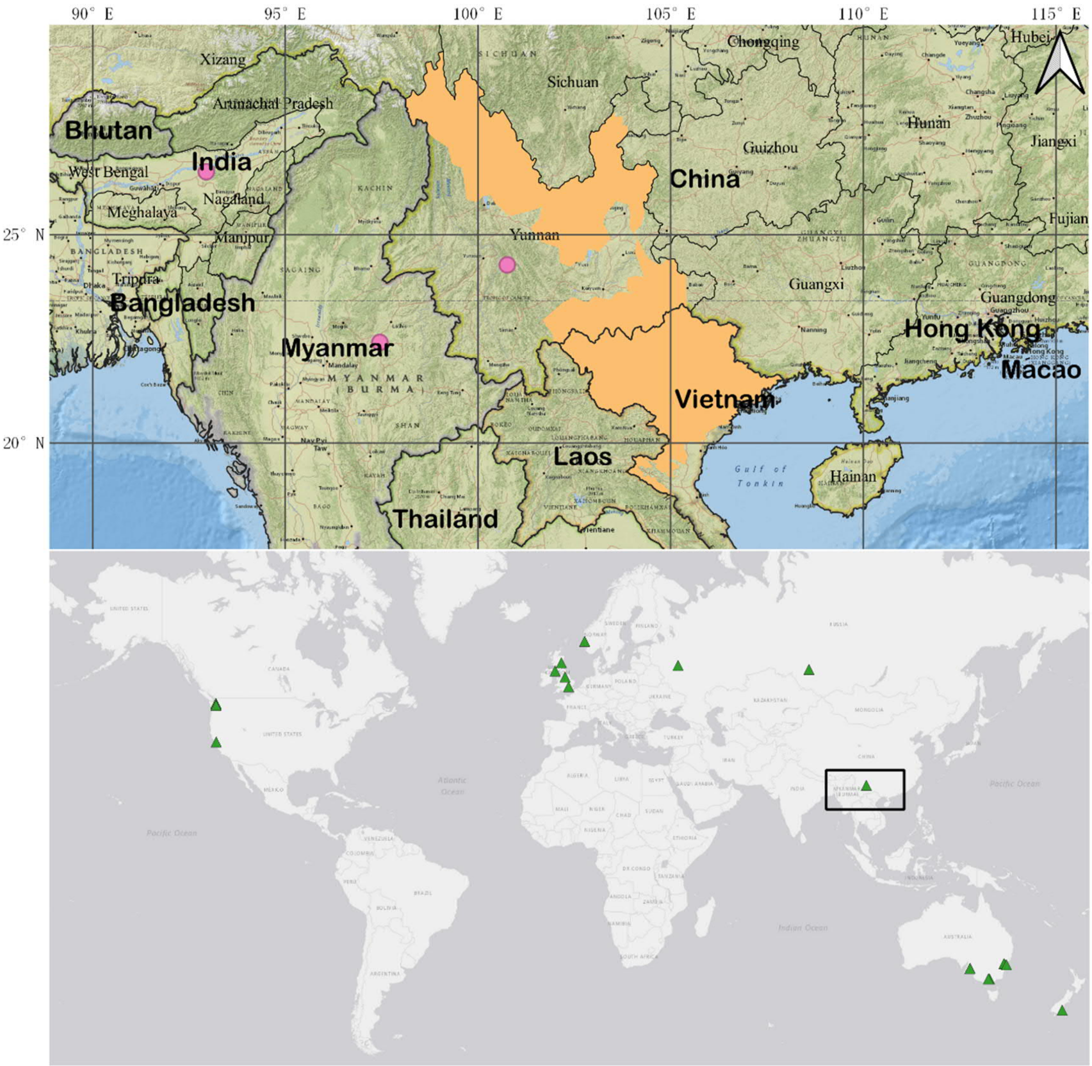
No. of *ex situ* sites/countries: 13/30
No. of (mapped) wild sources: (13) 15
No. of wild accessions: 31



Rhododendron ciliicalyx Franch.

IUCN Red List status: **LC** (BGCI & IUCN SSC Global Tree Specialist Group, 2018)
Distribution: China (Yunnan)*, N Vietnam. Lacking data
Altitude: 1,000–3,100 m (M.-Y. Fang et al., 2005); 2,700–3,500 m (Feng, 1992)

No. of *ex situ* sites/countries: 17/7
No. of (mapped) wild sources: (3) 4#
No. of wild accessions: 7



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*Fang et al. (2011) mapped the distribution which is different from other references (Davidian, 1982; Feng & Yang, 1999; M.-Y. Fang et al., 2005). The map here follows the latter.

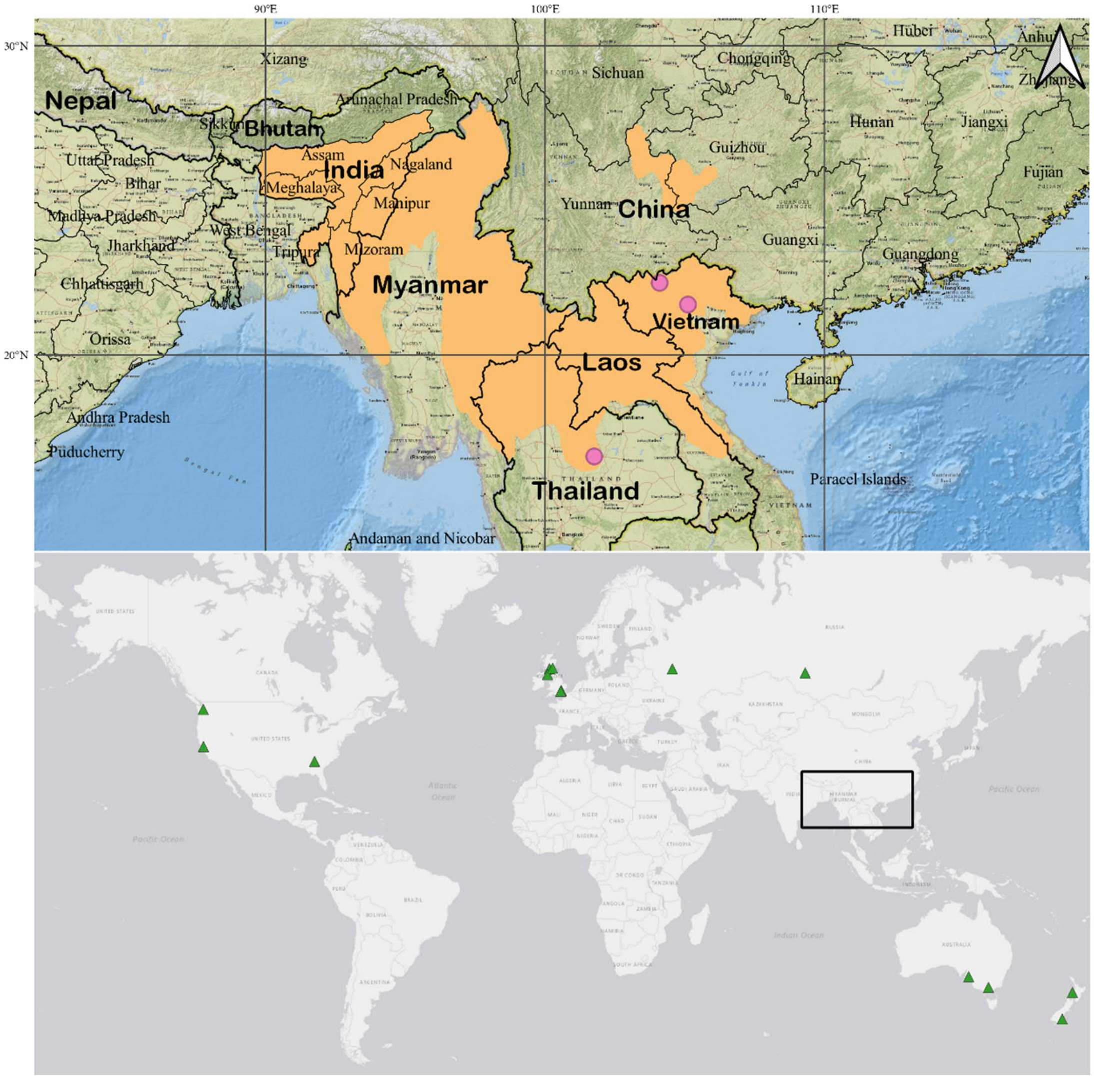
Wild accessions labelled as *R. ciliicalyx* may be in fact *R. ciliicalyx* ssp. *lyi*, or wild distribution of the former is wider than presently described (in the regions where the pink dots are located).

Rhododendron ciliicalyx Franch. ssp. *lyi* (H.Lév.) R.C.Fang

Note: treated as a subspecies of *R. ciliicalyx* in descriptions of Chinese species (Feng & Yang, 1999; M.-Y. Fang et al., 2005; Fang et al., 2011) and the Red List (Gibbs et al., 2011), but as a distinct species as *R. lyi* by Davidian (1982) and Chamberlain et al. (1996).

IUCN Red List status: **LC** (Gibbs et al., 2011, MEP–CAS, 2013)
Distribution: China (Guizhou, Yunnan)*, NE India, Laos, Myanmar, Thailand, Vietnam.
Lacking data
Altitude: 1,300–2,200 m

No. of *ex situ* sites/countries: 14/5
No. of (mapped) wild sources: (3) 6
No. of wild accessions: 11



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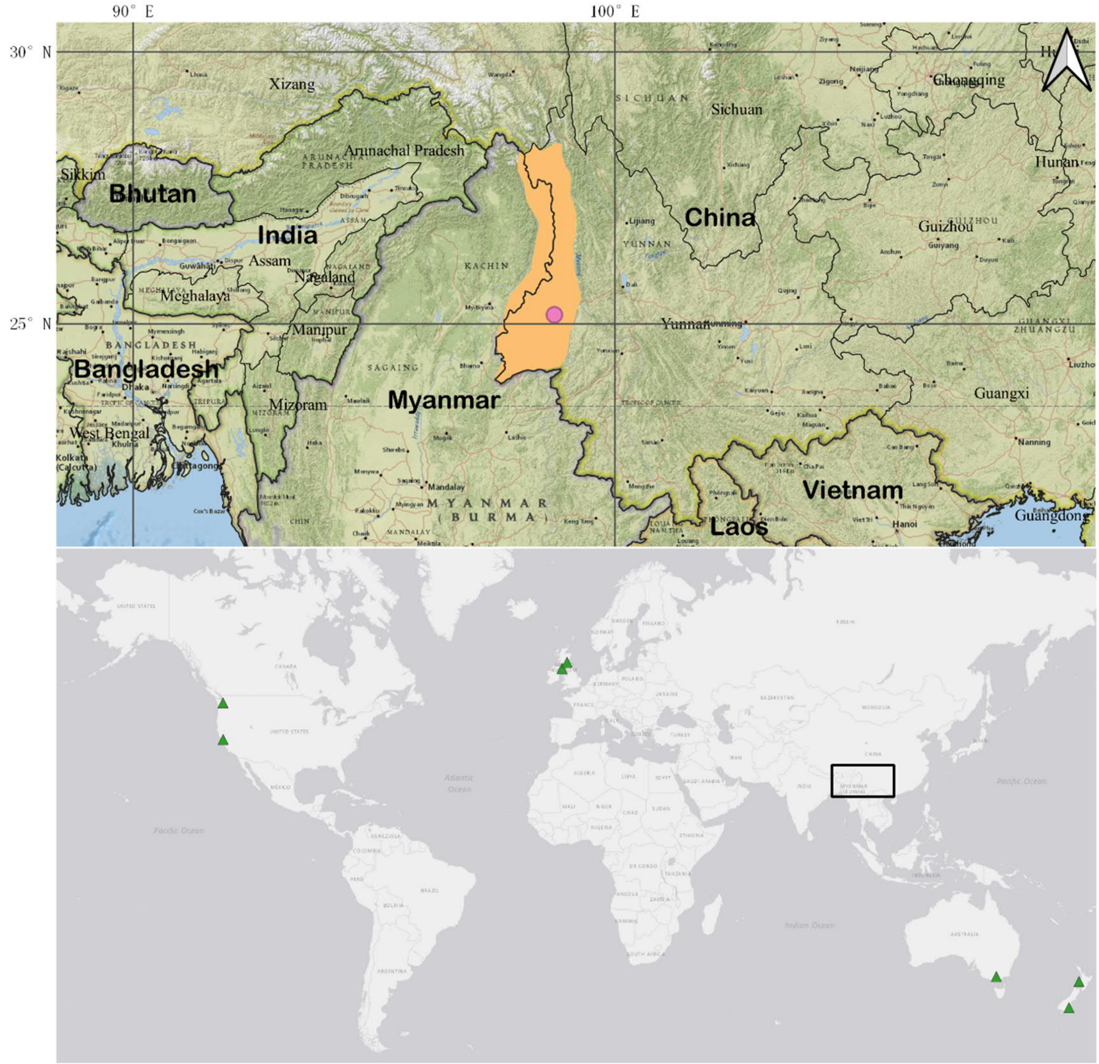
[*] Fang et al. (2011) mapped the distribution which is different from other references (Davidian, 1982; Feng & Yang, 1999; M.-Y. Fang et al., 2005). The map here follows the latter.

Rhododendron ciliipes **Hutch.**

IUCN Red List status: **DD** (Gibbs et al., 2011, MEP–CAS, 2013)
Distribution: China (W Yunnan), NE Myanmar
Altitude: 2,300–3,000 m

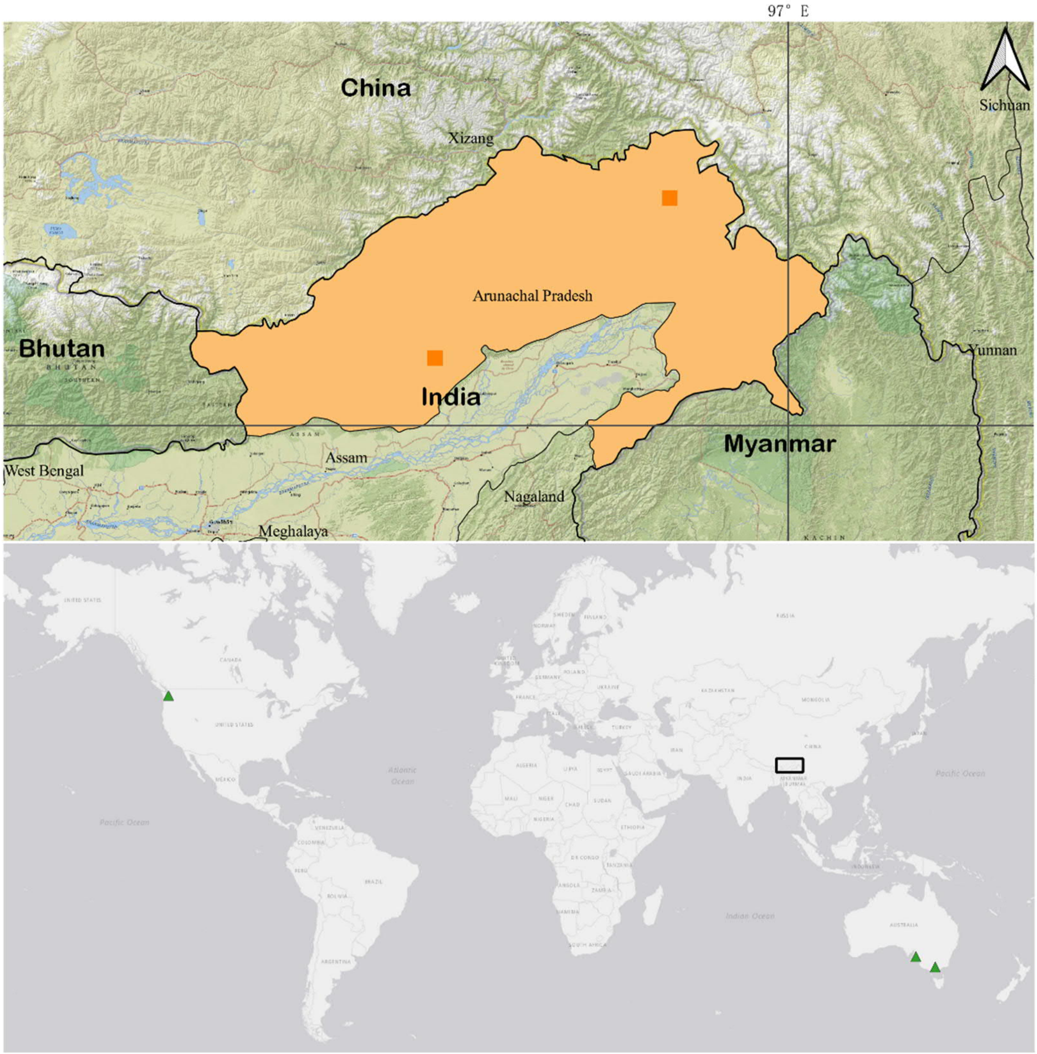
No. of *ex situ* sites/countries: 7/4
No. of (mapped) wild sources: (1) 2
No. of wild accessions: 2



Rhododendron coxianum Davidian

IUCN Red List status: **CR** (Gibbs et al., 2011)
Distribution: India (Arunachal Pradesh[1])*
Altitude: ca. 1,647 m

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: (0) 1
No. of wild accessions: 1



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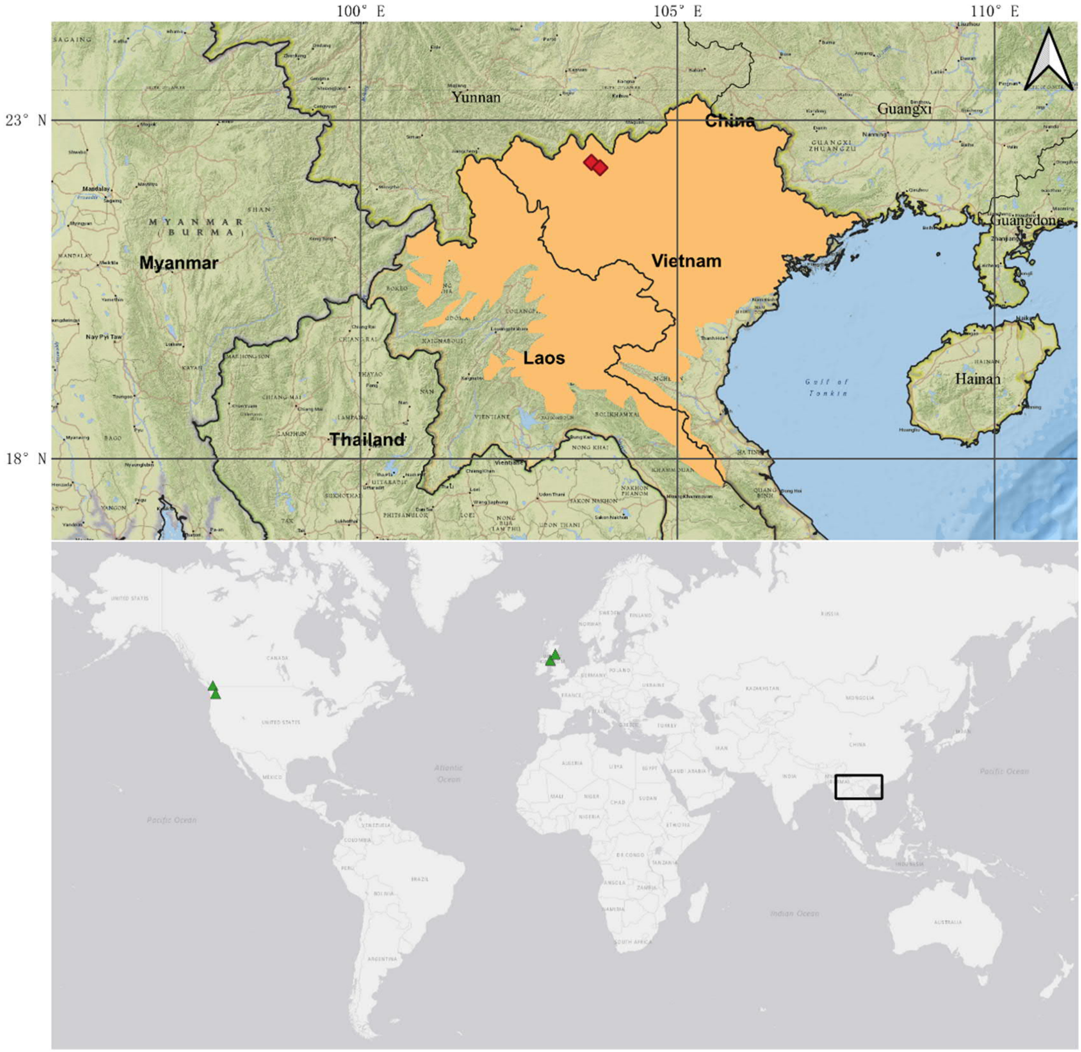
[1] Disputed area between China and India. In this study, Arunachal Pradesh is included in India following the geography of QGIS base layers.

[*] Lacking distribution data. This map shows the location where the type specimens were collected in Apa Tani Valley (now Ziro Valley, type specimen) and Debang Valley in Arunachal Pradesh (Davidian, 1982; Gibbs et al., 2011).

Rhododendron crenulatum Hutch. ex Sleumer

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: N Vietnam, N Laos
Altitude: ca. 2,800 m

No. of *ex situ* sites/countries: 4/3
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 1 (only one living)

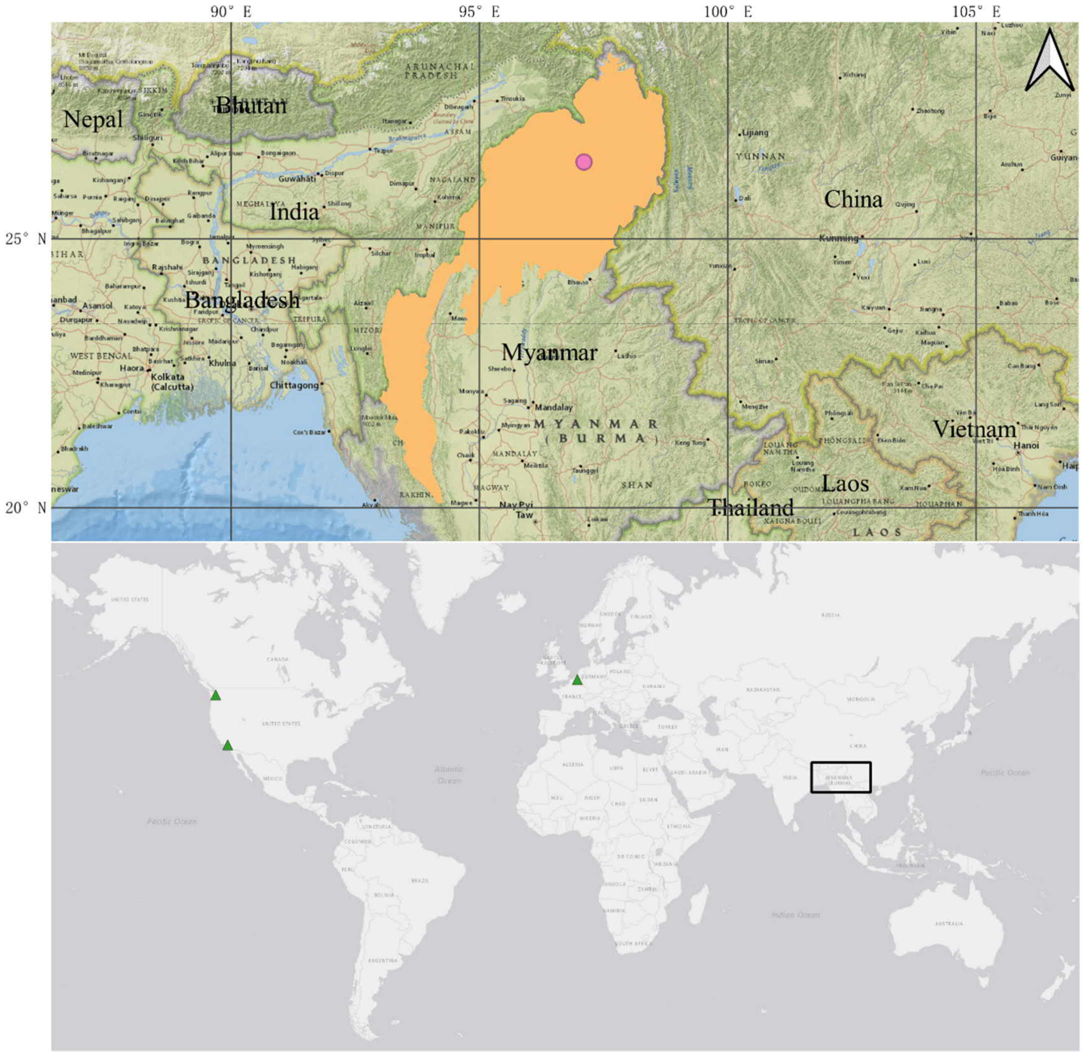


R. starlingii is separated from *R. crenulatum* (Rushforth et al., 2022). The two wild collections of *R. starlingii* were previously under *R. crenulatum*: AC#5685 and KR#7369.

Rhododendron cuffeanum Hutch.

IUCN Red List status: NE
Distribution: N and W Myanmar[*]
Altitude: N/A

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 1

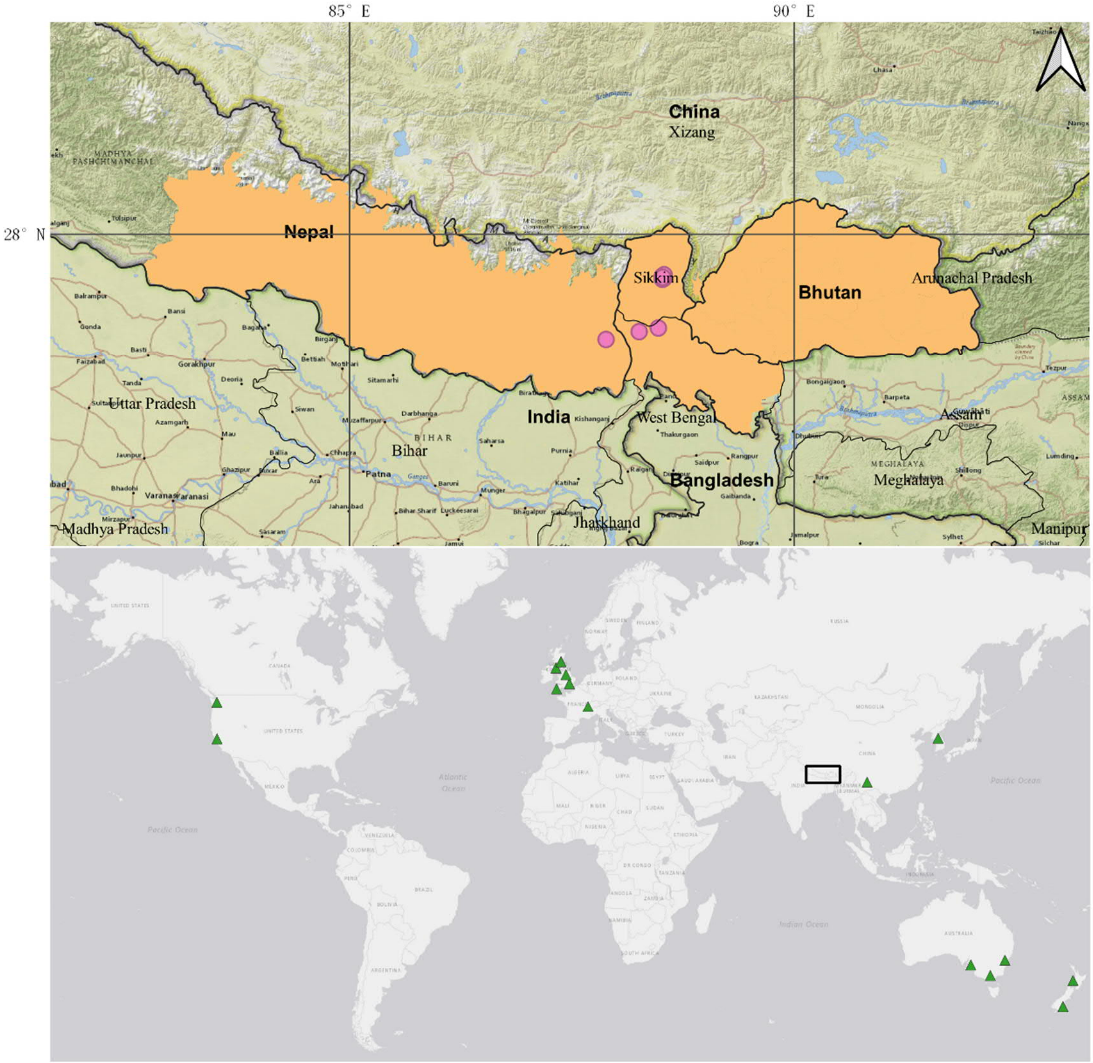


[*] Based on locations of the two wild collections due to unavailable data of wild distribution.

Rhododendron dalhousiae Hook.f. var. *dalhousiae*

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: China (S Xizang), India (West Bengal, Sikkim), Bangladesh, Bhutan, E Nepal
Altitude: 2,000–2,500 m

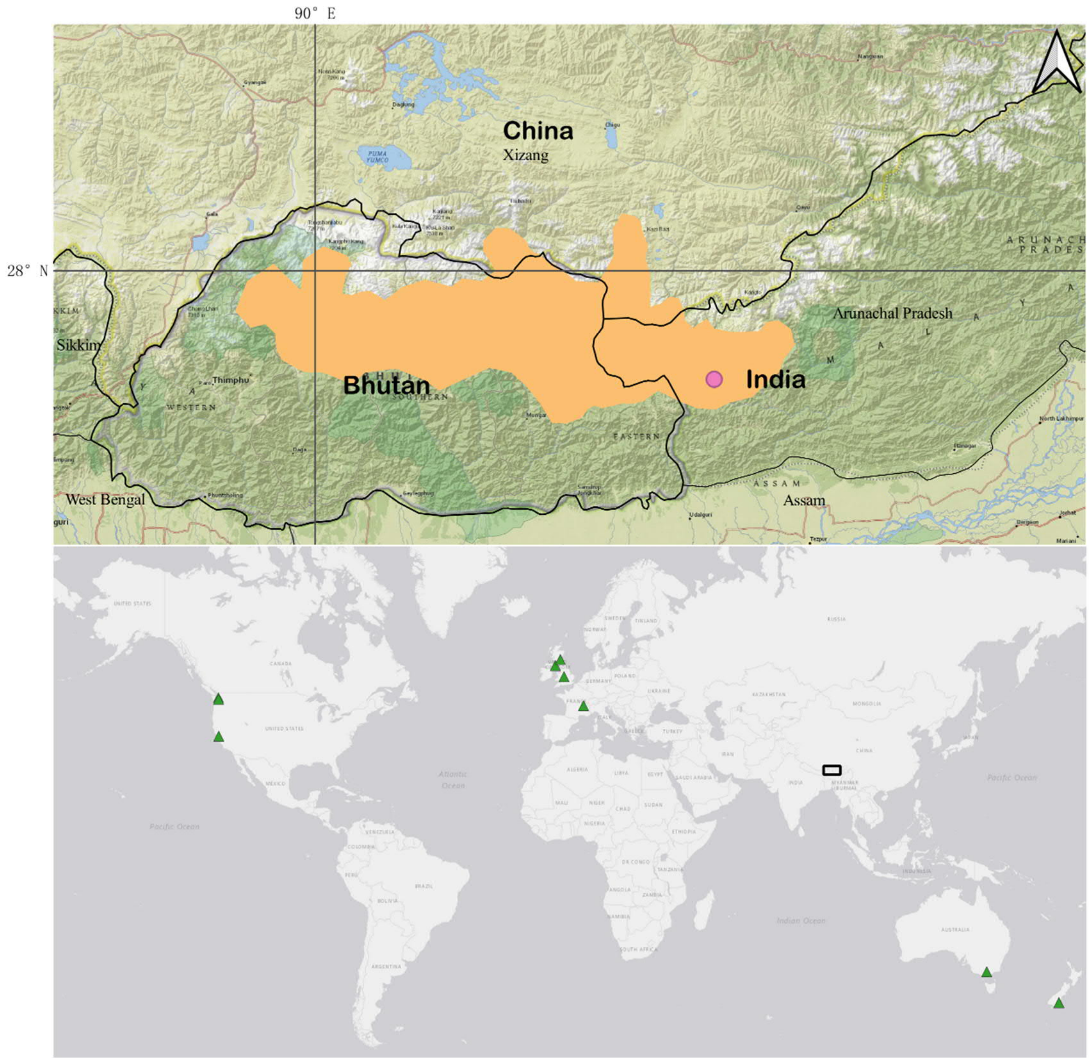
No. of *ex situ* sites/countries: 15/7
No. of (mapped) wild sources: (8) 9
No. of wild accessions: 13



Rhododendron dalhousiae Hook.f. var. *rhabdotum* (Balf.f. & R.E.Cooper) Cullen

IUCN Red List status: **VU** (Gibbs et al., 2011)
Distribution: Bhutan, NE India (Arunachal Pradesh), China (S Xizang)
Altitude: 1,500–2,600 m

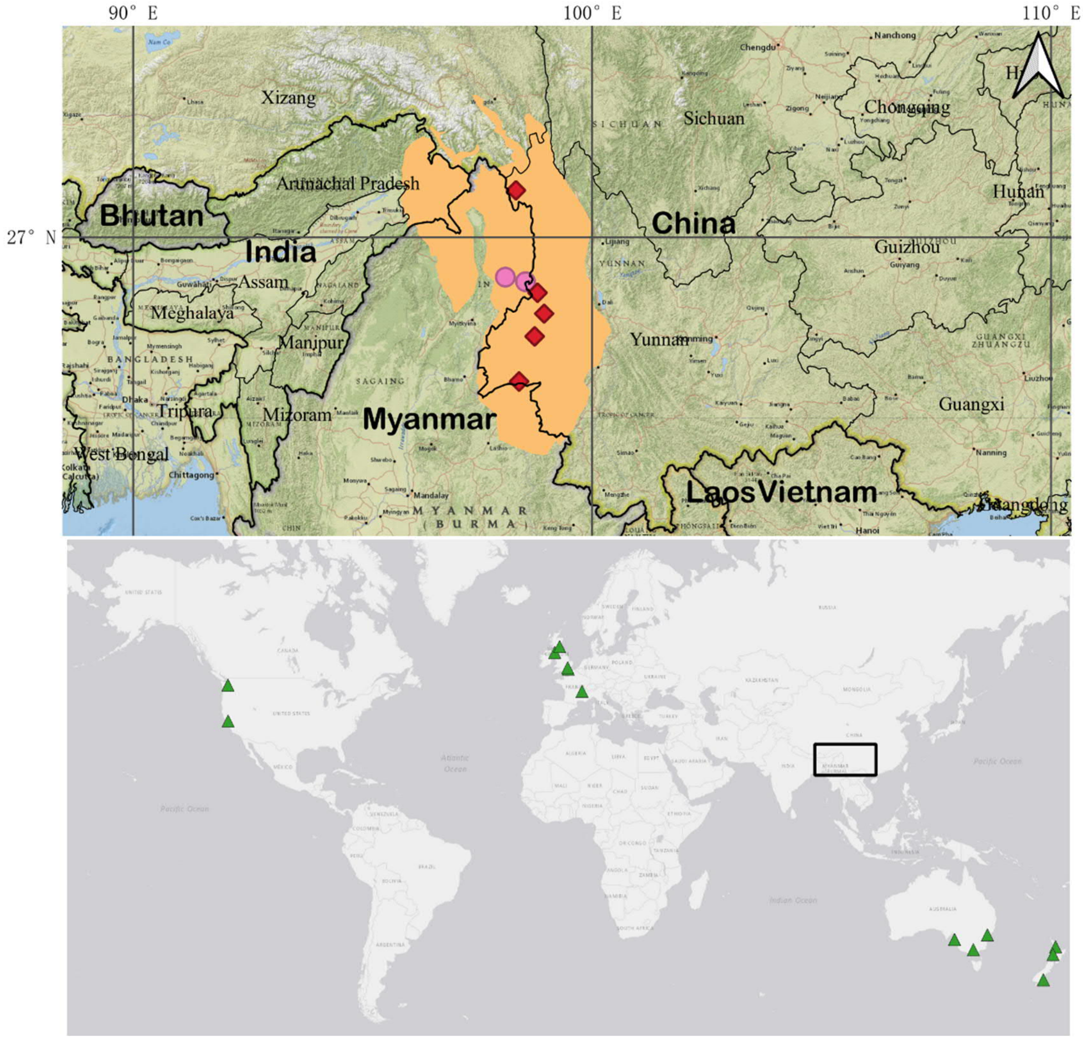
No. of *ex situ* sites/countries: 9/5
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 5



Rhododendron dendricola Hutch.

IUCN Red List status: **VU** (Gibbs et al., 2011; Qin et al., 2017)
Distribution: China (SE Xizang, NW Yunnan), India (Arunachal Pradesh), N Myanmar
Altitude: 2,135–3,050 m (Davidian, 1982). In Yunnan, China: 1,350–2,700 m (Feng, 1988); 1,200–2,800 m (Li & Zhou, 2005); 1,300–1,900 m (M.-Y. Fang et al., 2005)

No. of *ex situ* sites/countries: 13/5
No. of (mapped) wild sources: (7) 9
No. of wild accessions: 23



Rhododendron eheinense M.Y.He & Z.J.Zhao

IUCN Red List status: NE
Distribution: China (Sichuan). Lacking distribution data. No information of type specimen
Altitude: N/A
Not in cultivation.

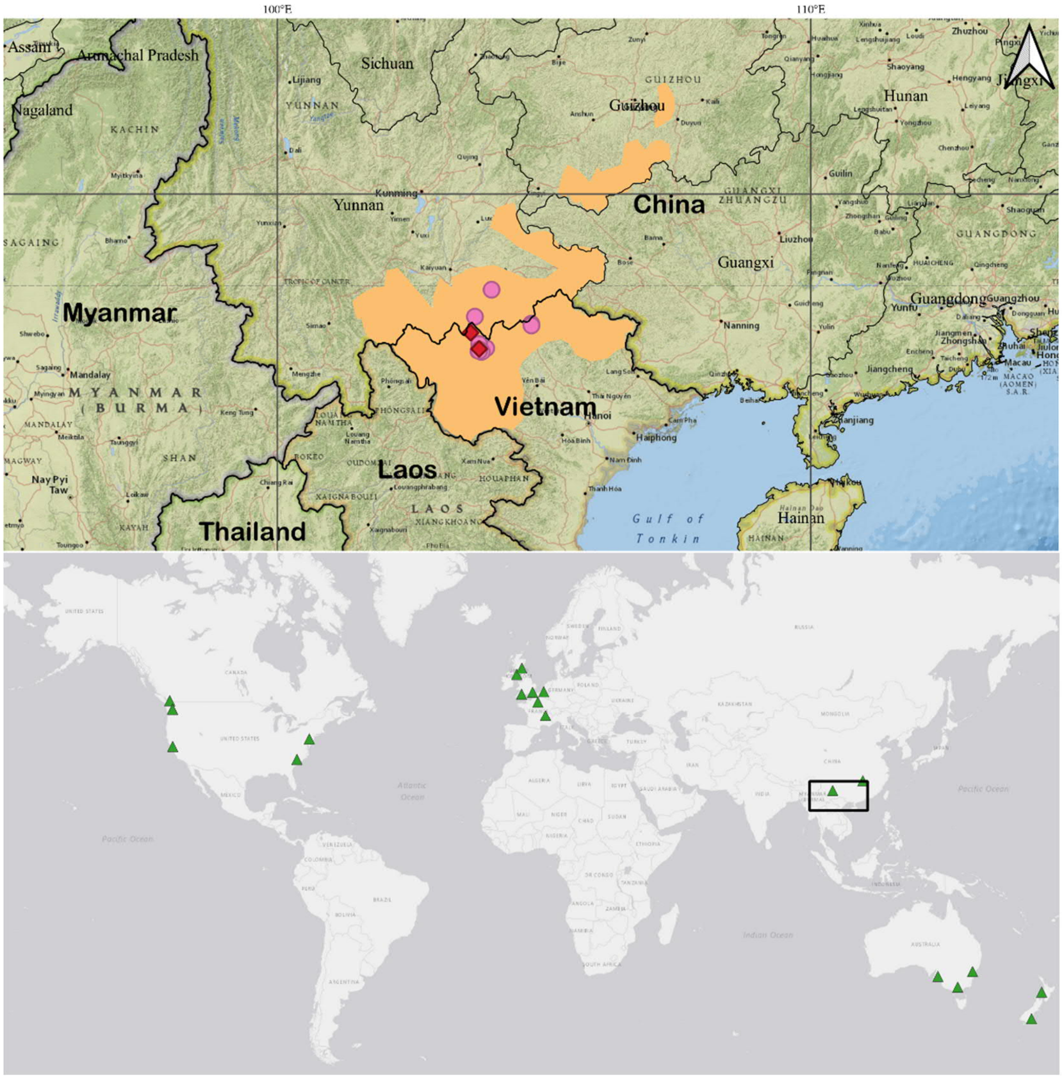
R. eheinense is an accepted species endemic to Sichuan, China (https://www.ipni.org/n/985026–1). It was not listed in contents of *Flora of China* (M.-Y. Fang et al., 2005) but mentioned in the appendix as a valid species.

Rhododendron excellens Hemsl. & E.H.Wilson

IUCN Red List status: globally **VU** (Gibbs et al., 2011), NT in China (MEP–CAS, 2013)

Distribution: China (SE Yunnan, S Guizhou), N Vietnam
Altitude: 1,100–2,400 m

No. of *ex situ* sites/countries: 19/8
No. of (mapped) wild sources: (22) 25
No. of wild accessions: 47#

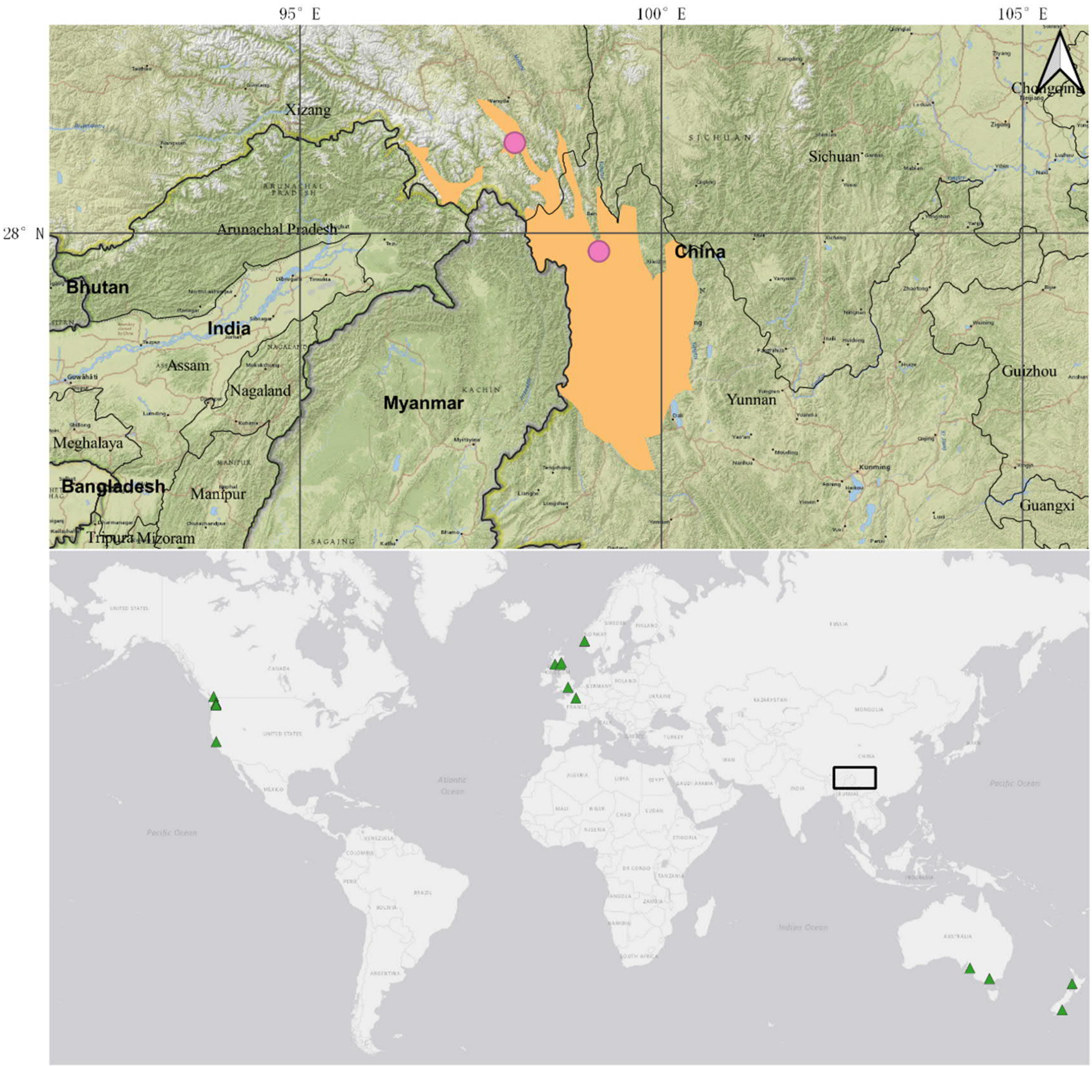


R. excellens (SEH#227) (Table S2.2) is suspected to be mistakenly recorded as from NE Yunnan rather than actually SE Yunnan (according to Steve Hootman's description of the 1995 expedition https://rhodygarden.org/new–r–valentinioides–646/).

Rhododendron fletcherianum Davidian

IUCN Red List status: **EN** (Gibbs et al., 2011)
Distribution: China (SE Xizang, NW Yunnan)
Altitude: ca. 3,400 m

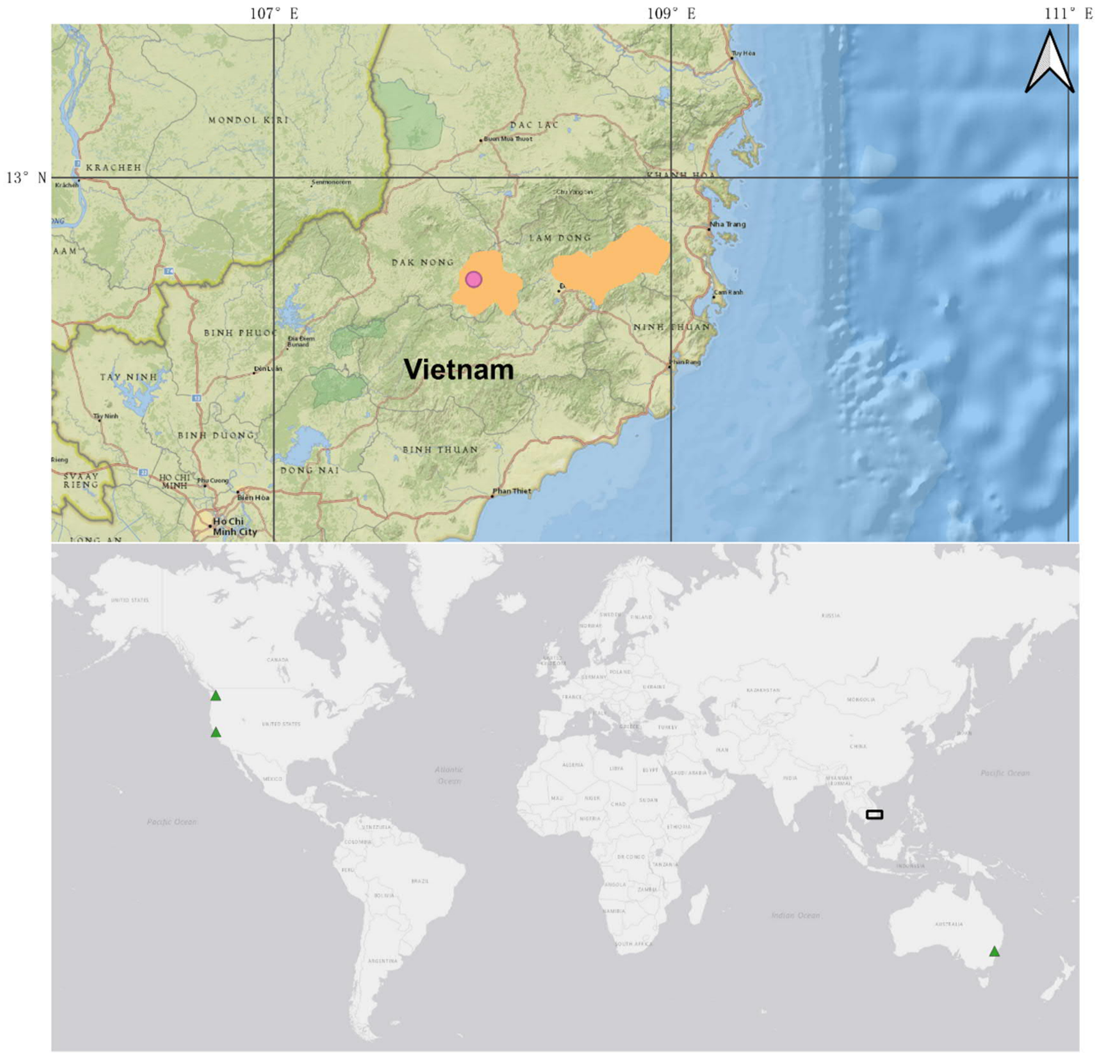
No. of *ex situ* sites/countries: 14/7
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 4



Rhododendron fleuryi Dop

IUCN Red List status: **CR** (Gibbs et al., 2011)
Distribution: S Vietnam[*]
Altitude: 2,000–2,500 m

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 1



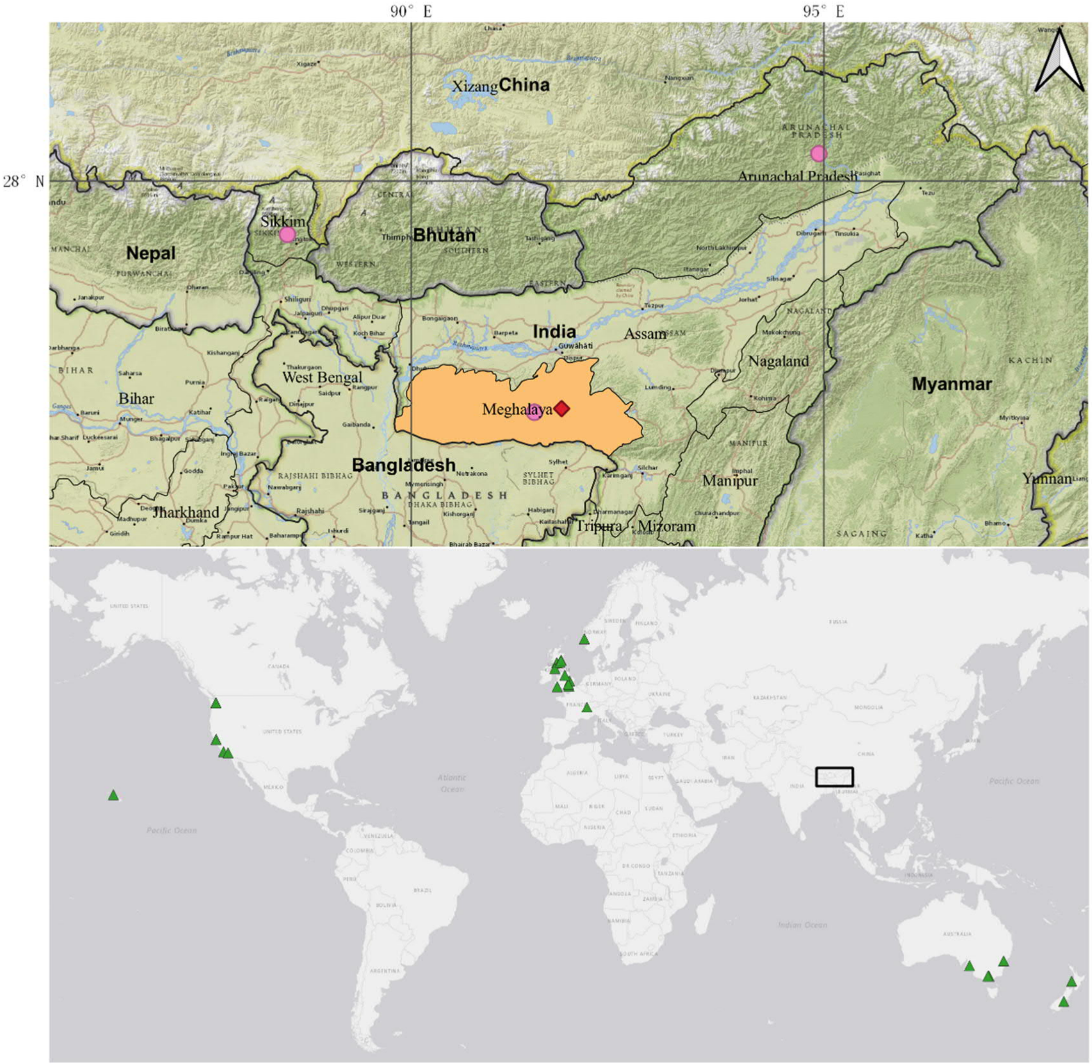
[*] The distribution of *R. fleuryi* in northern Vietnam in the Red List (Gibbs et al., 2011) is suspected to be an error. Langbiang, where the specimen plant was discovered, is in S Vietnam.

Rhododendron formosum Wall. var. *formosum*

Chamberlain et al. (1996) listed *R. iteophyllum* as a synonym. Mao et al. (2017) suggested to separate *R. iteophyllum* out from *R. formosum* as a distinct species.

IUCN Red List status: globally **CR** as *R. formosum* var. *formosum* (Gibbs et al., 2011), EN as *R. formosum* in India (Meghalaya) (https://www.nationalredlist.org/), VU as *R. formosum* in India (Arunachal Pradesh) (https://www.nationalredlist.org/).
Distribution: India (Meghalaya)[*]
Altitude: 1,400–2,300 m[*]

No. of *ex situ* sites/countries: 22/6
No. of (mapped) wild sources: (4) 5
No. of wild accessions: 6



[*] According to Mao et al. (2017). Davidian (1982) described the distribution as in India (Assam) and north–west Upper Burma, at altitude 736–2,196 m. However, he located the specimen in Khasia Hills, Assam, which is suspected to be today's Khasi Hills, Meghalaya.

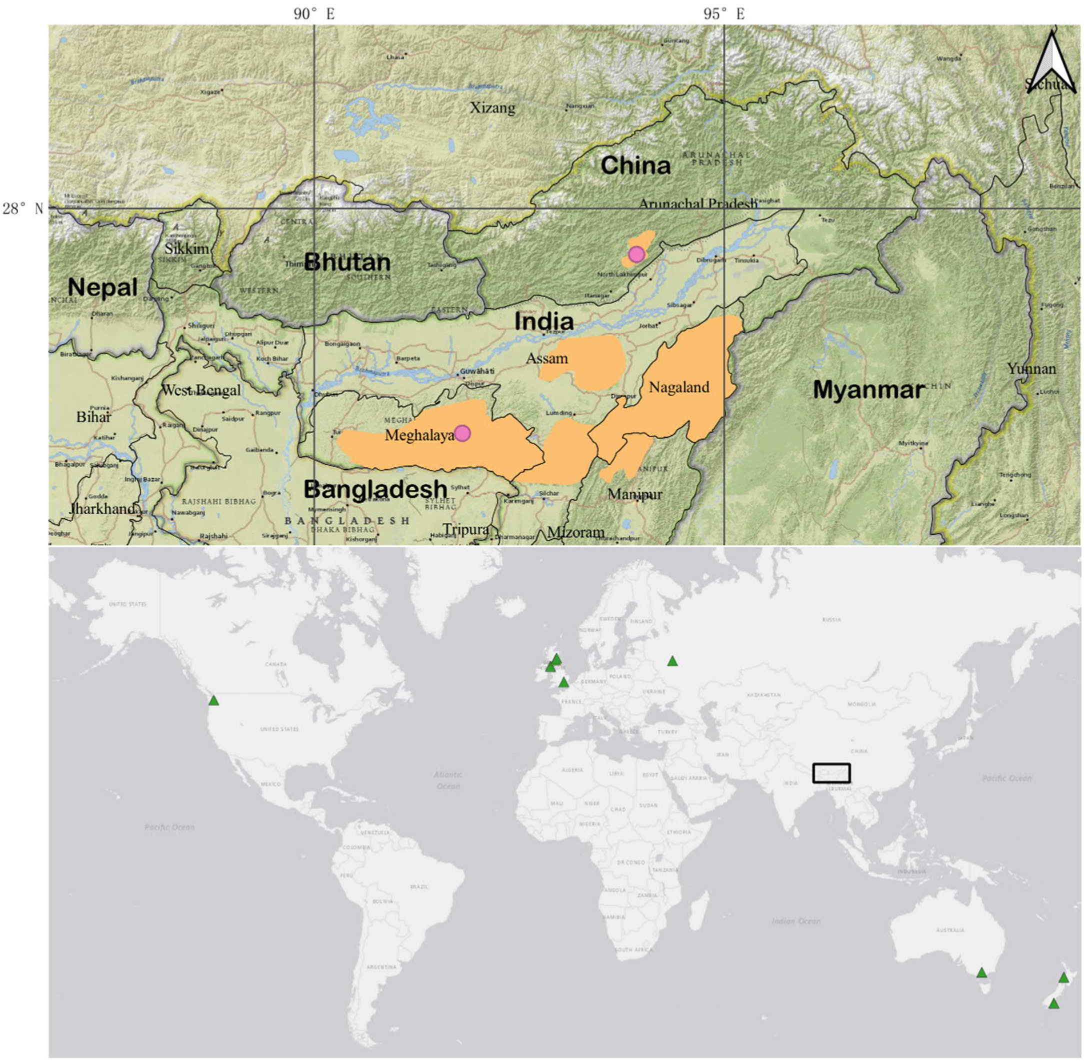
Although *R. formosum* var. *formosum* is listed CR and has few wild accessions, it has many living collections worldwide.

Rhododendron formosum Wall. var. *inaequale* (Hutch.) Cullen

Note: considered as a distinct species as *R. inaequale* by Mao et al. (2017).

IUCN Red List status: **DD** (Gibbs et al., 2011)
Distribution: India (Arunachal Pradesh, Assam, Manipur, Meghalaya, Nagaland)[*]
Altitude: 1,400–2,230 m

No. of *ex situ* sites/countries: 9/5
No. of (mapped) wild sources: (2) 4
No. of wild accessions: 7

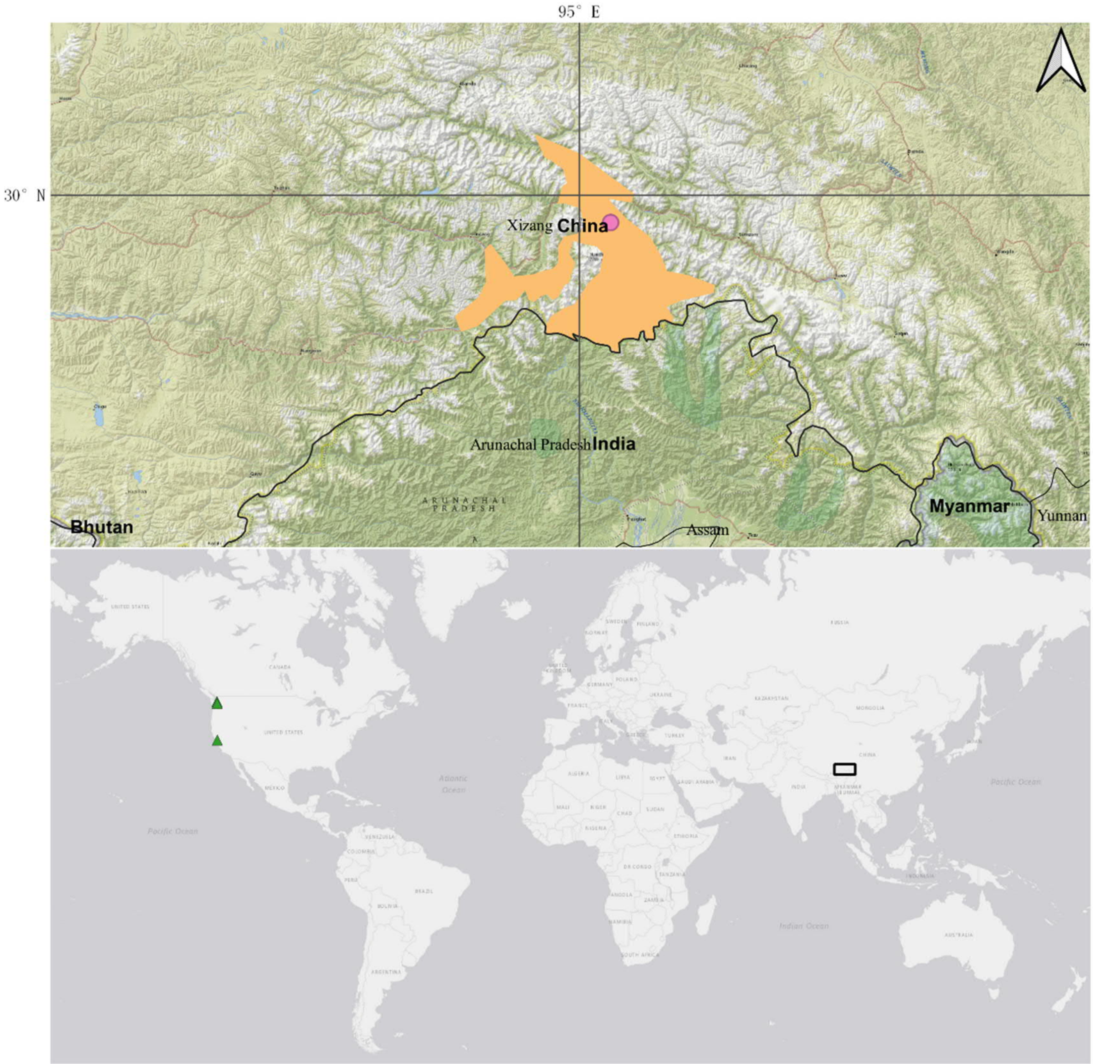


[*] According to Mao et al. (2017) and the location of specimens in Assam, Meghalaya and Nagaland at 1,220–2,135m (Davidian, 1982). The Red List (Gibbs et al., 2011) notes as Arunachal Pradesh, Meghalaya, Nagaland.

Rhododendron goreri Davidian

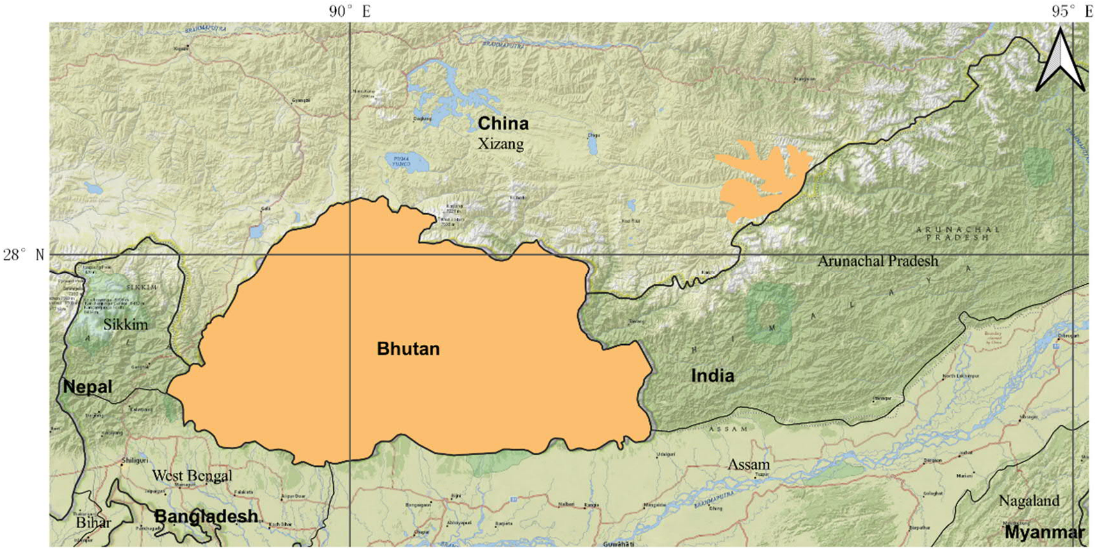
IUCN Red List status: NE
Distribution: China (SE Xizang)
Altitude: 2,020–2,188 m

No. of *ex situ* sites/countries: 3/1
No. of (mapped) wild sources: (1) 3
No. of wild accessions: 8



Rhododendron grothausii Davidian

IUCN Red List status: NE
Distribution: China (S Xizang), Bhutan
Altitude: 2,593–2,745 m
Not in cultivation*.



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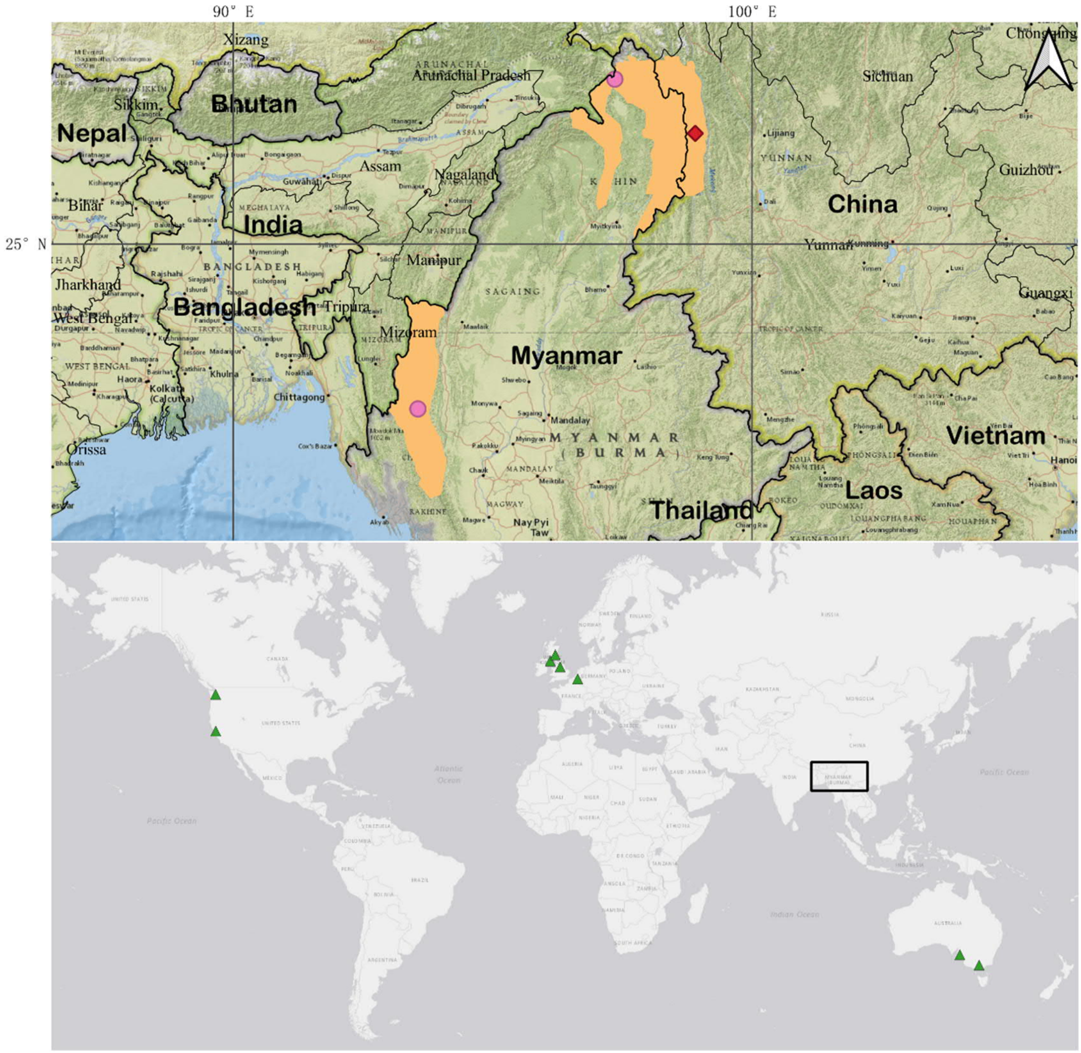
*Davidian (1982, pp.275, 278) stated that the wild form ‘Ludlow & Sherriff’ of *R. lindleyi* was likely *R. grothausii*, in which situation, *R. grothausii* is in cultivation.

Rhododendron horlickianum Davidian

IUCN Red List status: **DD** (Gibbs et al., 2011)
Distribution: N and W Myanmar, China (NW Yunnan)*
Altitude: 1,220–2,135 m

No. of *ex situ* sites/countries: 8/4
No. of (mapped) wild sources: (3) 5
No. of wild accessions: 6



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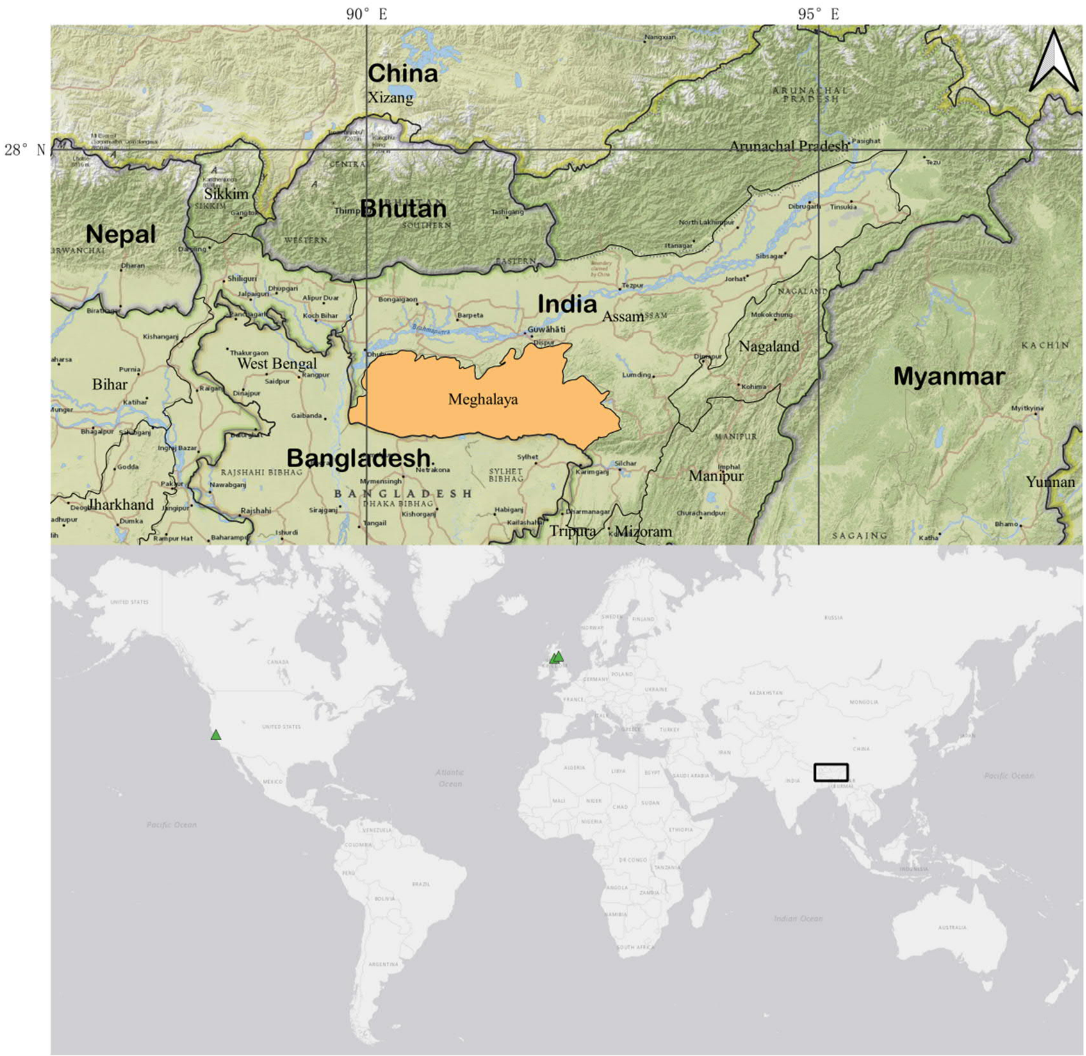
*N Myanmar and China (NW Yunnan) are newly added according to mapped distribution in the Red List (Gibbs et al., 2011) and location of wild accessions. This species is however not included in *Flora of China* (M.-Y. Fang et al., 2005).

Rhododendron iteophyllum Hutch.

Chamberlain et al. (1996) listed *R. iteophyllum* as a synonym of *R. formosum* var. *formosum*. Mao et al. (2017) suggested to separate *R. iteophyllum* out as a distinct species.

IUCN Red List status: NE
Distribution: India (Meghalaya)
Altitude: 890–1,500 m[*]

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: 0
No. of wild accessions: 0



[*] According to Mao et al. (2017).

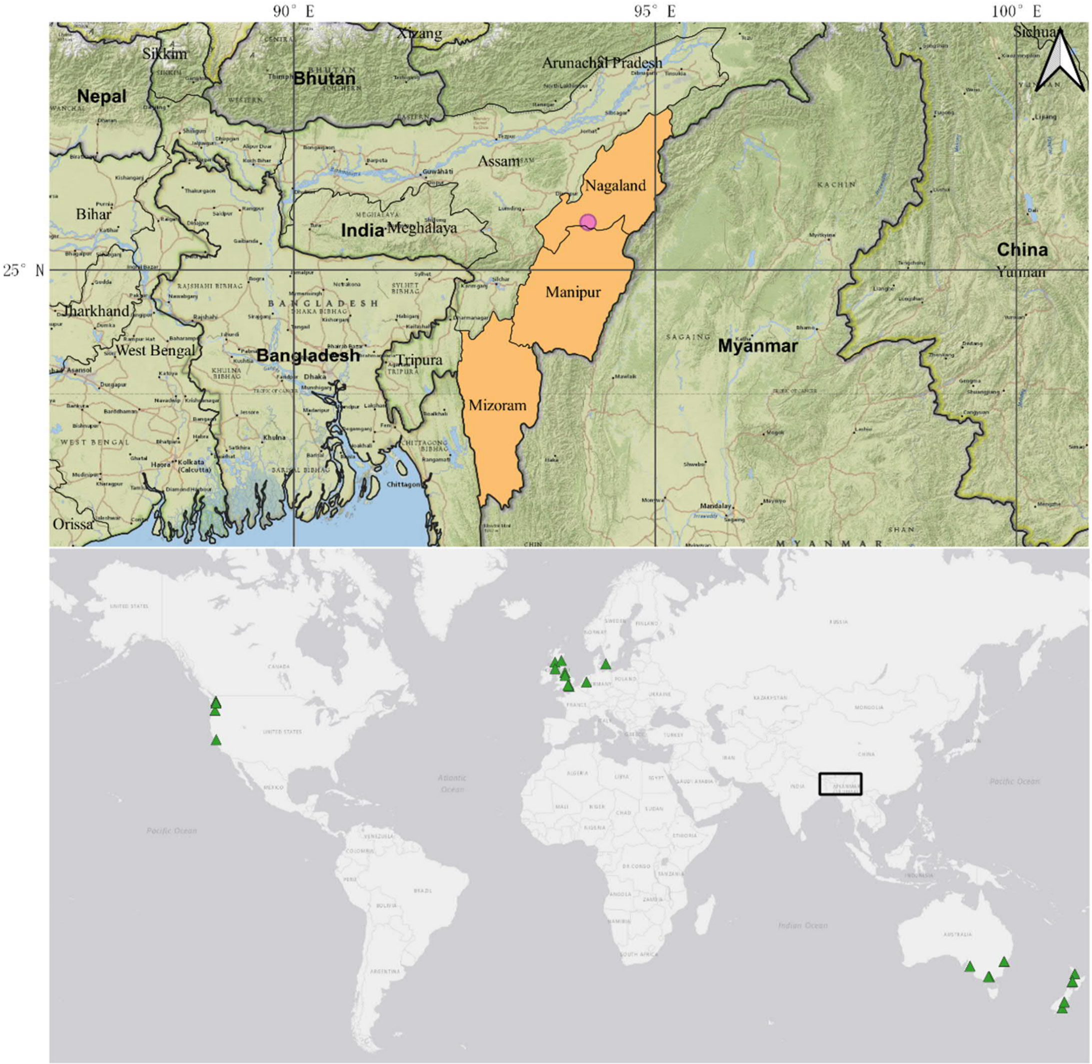
There are living collections of *R. iteophyllum* at three botanic gardens that conserve *R. formosum* (Table S2.1). Davidian (1982) noted there were wild collections at altitude 610–

1,830 m. However, no wild collection is noted as *R. iteophyllum* in our datasheet. It may have been conserved under *R. formosum* due to unresolved taxonomy (Cullen, 1980).

Rhododendron johnstoneanum G.Watt. ex Hutch.

IUCN Red List status: globally **LC** (Gibbs et al., 2011), EN in India (Mizoram) (https://www.nationalredlist.org/)
Distribution: India (Manipur, Mizoram, Nagaland)*
Altitude: 1,830–3,355 m

No. of *ex situ* sites/countries: 22/6
No. of (mapped) wild sources: (1) 6
No. of wild accessions: 18



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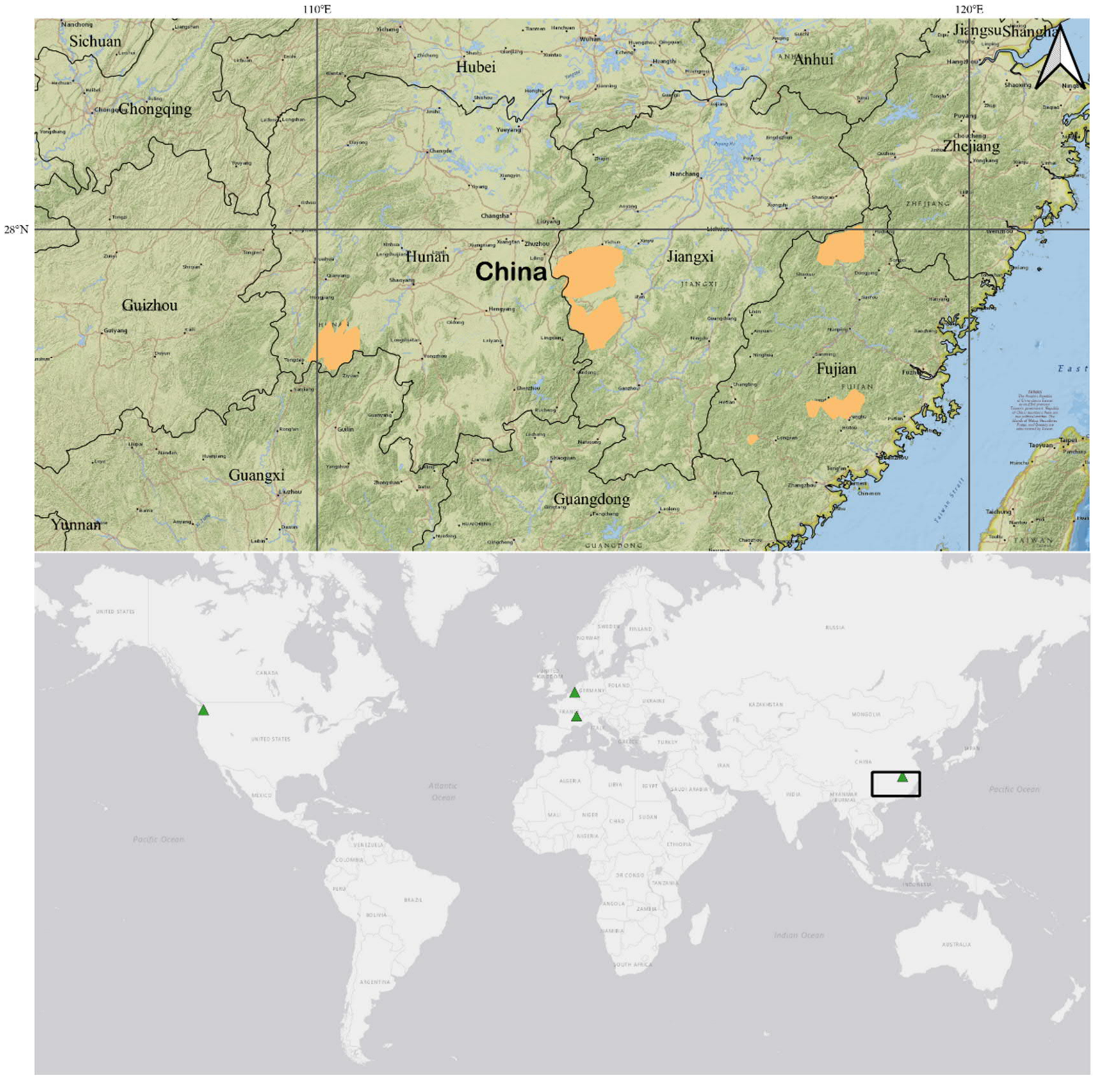
*Cullen (1980, pp. 44–47) noted a specimen from western central Myanmar (Mindat ridge, KW #22200) that may be a variant of *R. johnstoneanum*. However, no other wild record of this species is found in this study.

Rhododendron kiangsiense W.P.Fang

IUCN Red List status: globally NT (Gibbs et al., 2011), **EN** in China (Qin et al., 2017)
Distribution: China (W Jiangxi, Fujian, SW Hunan)
Altitude: 1,100–1,500 m

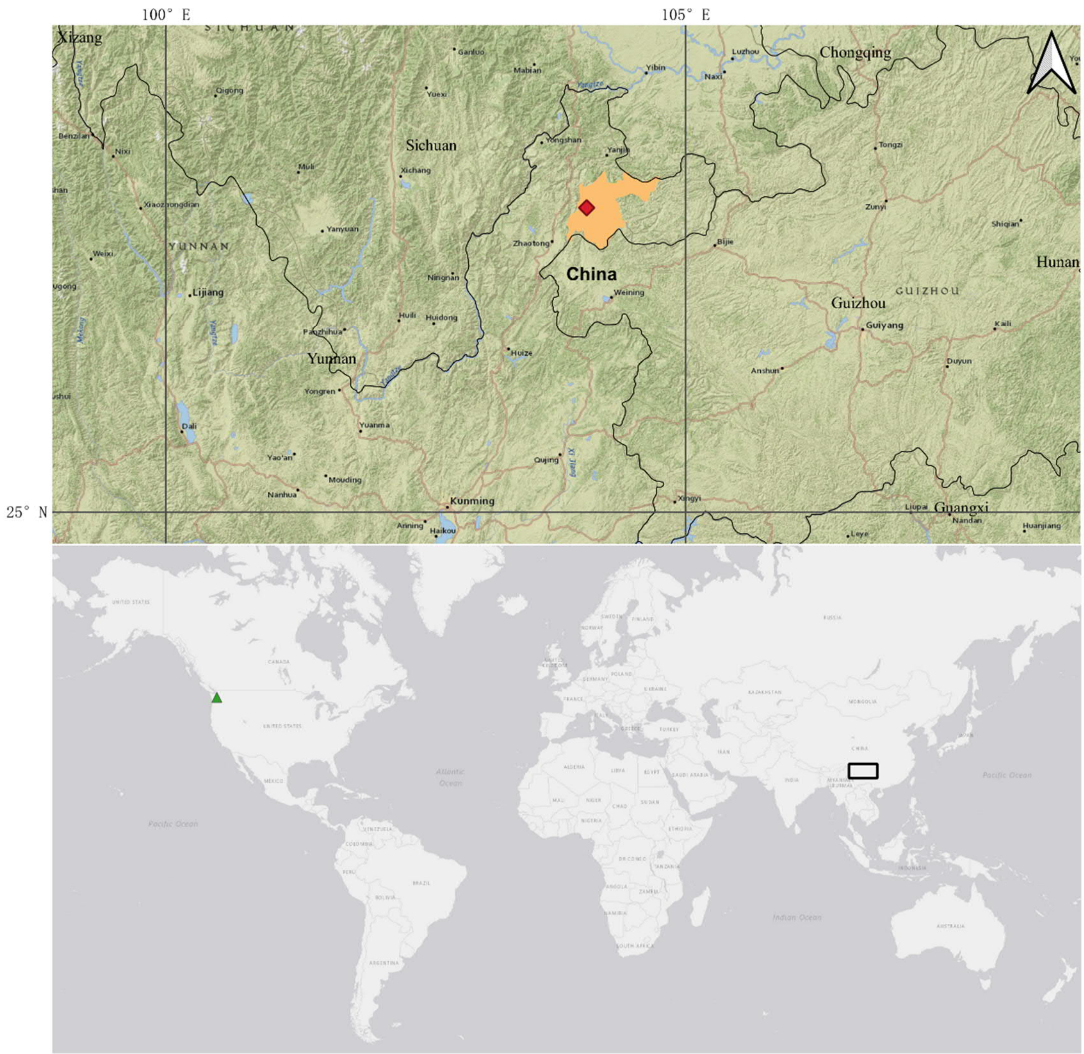
No. of *ex situ* sites/countries: 4/4
No. of (mapped) wild sources: (0) 1
No. of wild accessions: 1



Rhododendron kuomeianum Y.H. Chang, J.Nielsen &Y.P. Ma

IUCN Red List status: **DD** (Chang et al., 2021)
Distribution: China (NE Yunnan)
Altitude: 1,800–2,000 m

No. of *ex situ* sites/countries: 1/1
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 1*



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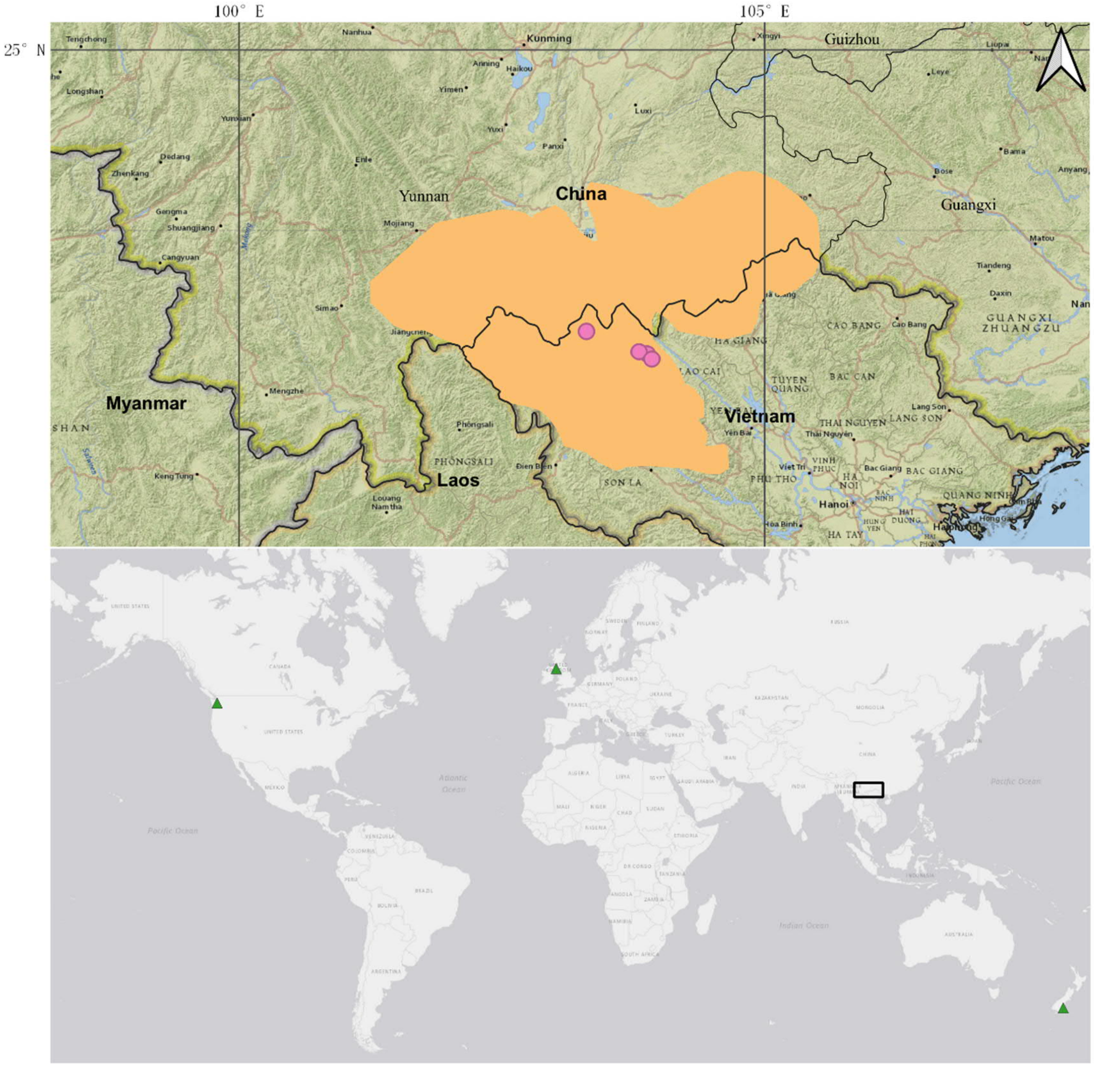
*One wild accession is in cultivation at Rhododendron Species Botanical Garden, USA, collected from the area where the type specimen was found (Table S2.2).

Rhododendron leptocladon Dop

Syn: *R. nemorosum* R.C.Fang (No accessions in cultivation under this name)

IUCN Red List status: globally **VU** (Gibbs et al., 2011), DD in China (MEP–CAS, 2013)
Distribution: China – Vietnam border region
Altitude: 2,000–2,300 m

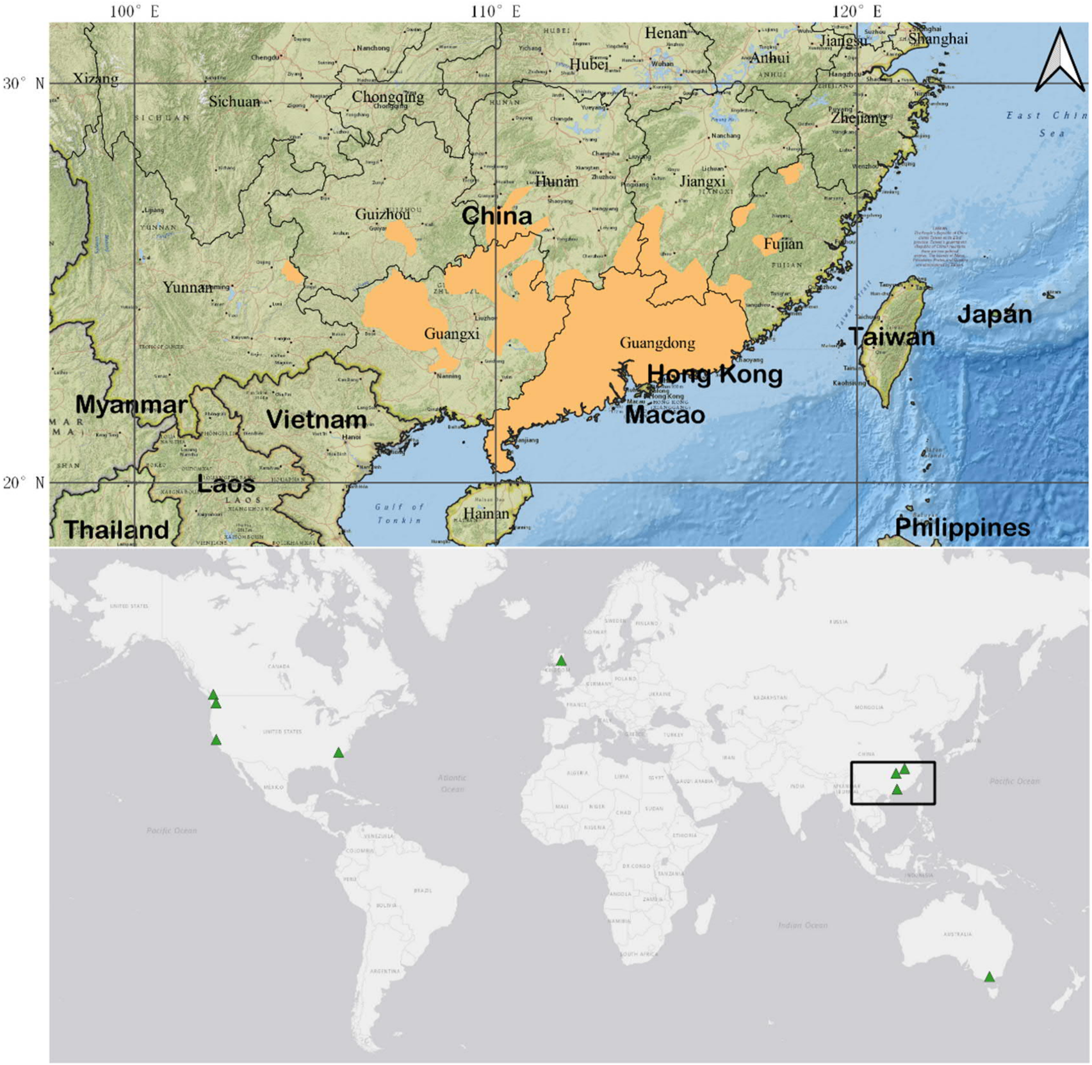
No. of *ex situ* sites/countries: 3/3
No. of (mapped) wild sources: (4) 6
No. of wild accessions: 20



Rhododendron levinei Merr.

IUCN Red List status: globally DD (Gibbs et al., 2011), **NT** in China (MEP–CAS, 2013)
Distribution: China (Fujian, Guangdong, Guangxi, Guizhou, Hunan; S Jiangxi and E Yunnan? (Fang et al., 2011). Lacking geographic data on specific distribution
Altitude: 800–1,000 m (Feng, 1992); 1,300–1,500 m (M.-Y. Fang et al., 2005)

No. of *ex situ* sites/countries: 9/5
No. of (mapped) wild sources: (0) 4*
No. of wild accessions: 13



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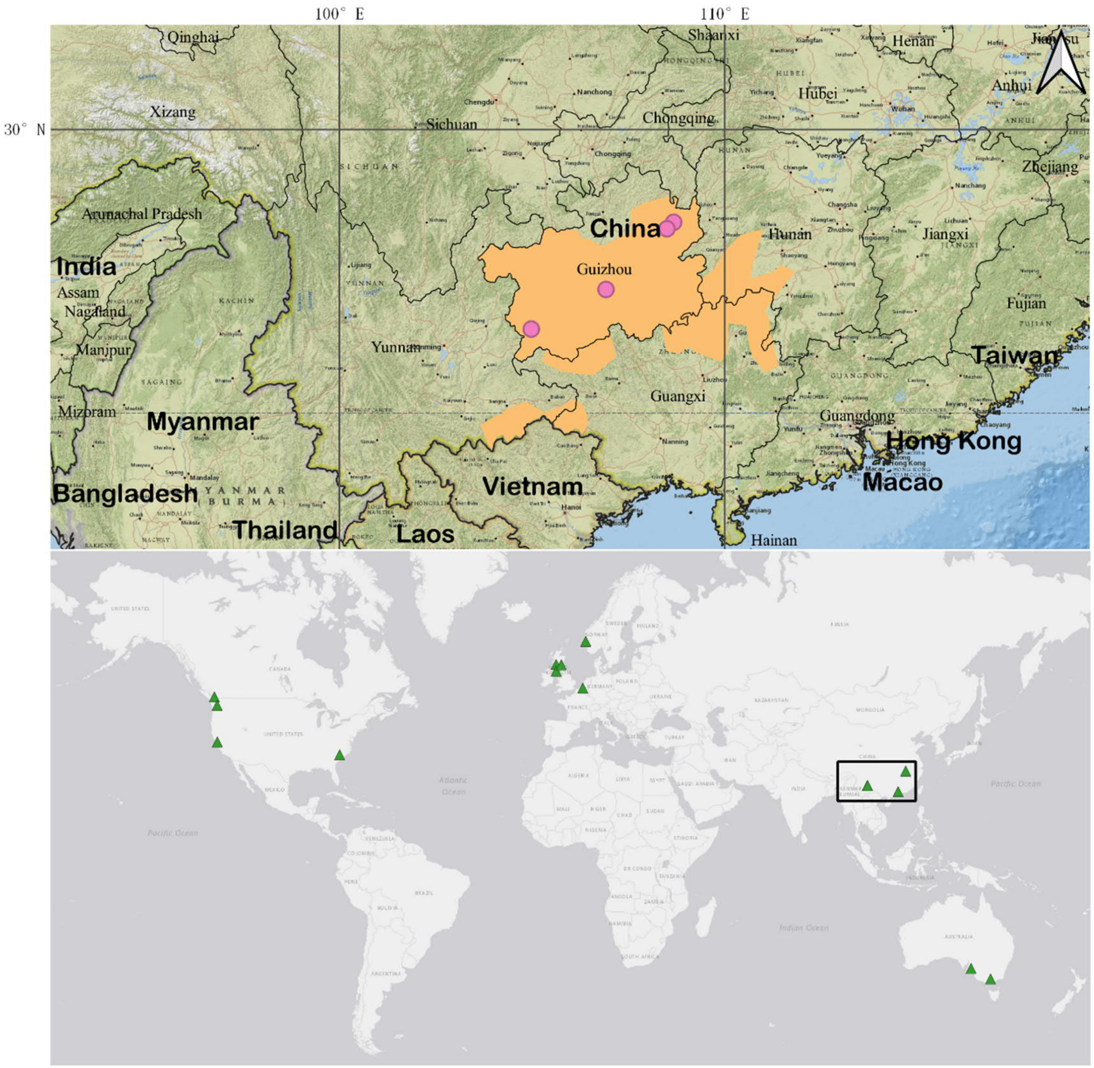
*No wild accession was recorded with provenance data due to poor documentation.

Rhododendron liliiflorum H.Lév.

IUCN Red List status: globally NT (Gibbs et al., 2011), **LC** in China (MEP–CAS, 2013)
Distribution: China (NE & W Guangxi, Guizhou, SW Hunan, SE Yunnan)
Altitude: 750–1,900 m (Feng, 1992); 600–1,400 m (M.-Y. Fang et al., 2005)

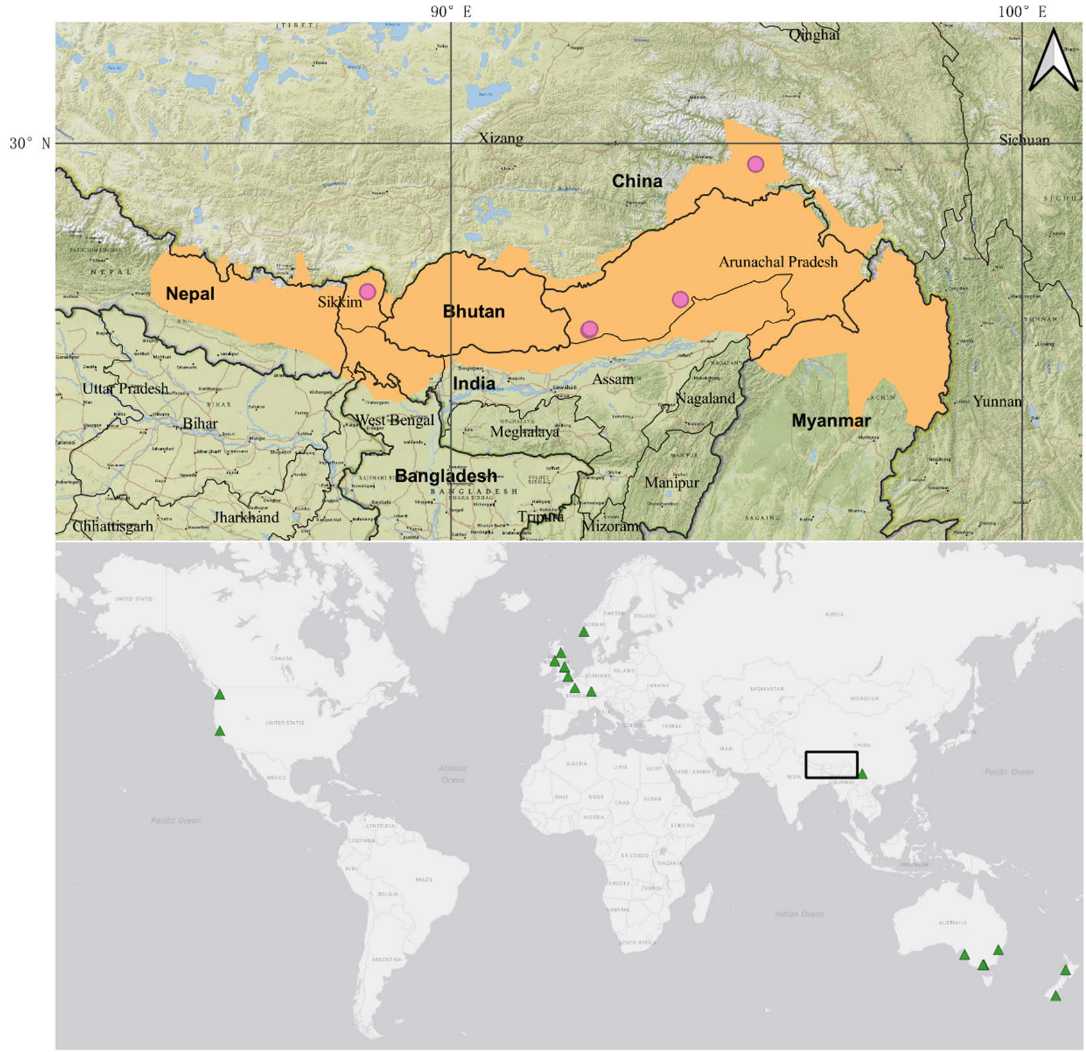
No. of *ex situ* sites/countries: 14/7
No. of (mapped) wild sources: (4) 6
No. of wild accessions: 29



Rhododendron lindleyi T.Moore

IUCN Red List status: globally **LC** (Gibbs et al., 2011), VU in China (Qin et al., 2017)
Distribution: N Bangladesh, Bhutan, China (S Xizang), NE India, N Myanmar, E Nepal
Altitude: 1,600–3,355 m

No. of *ex situ* sites/countries: 17/8
No. of (mapped) wild sources: (6) 10
No. of wild accessions: 18



Rhododendron linearilobum R.C. Fang & A.L.Zhang

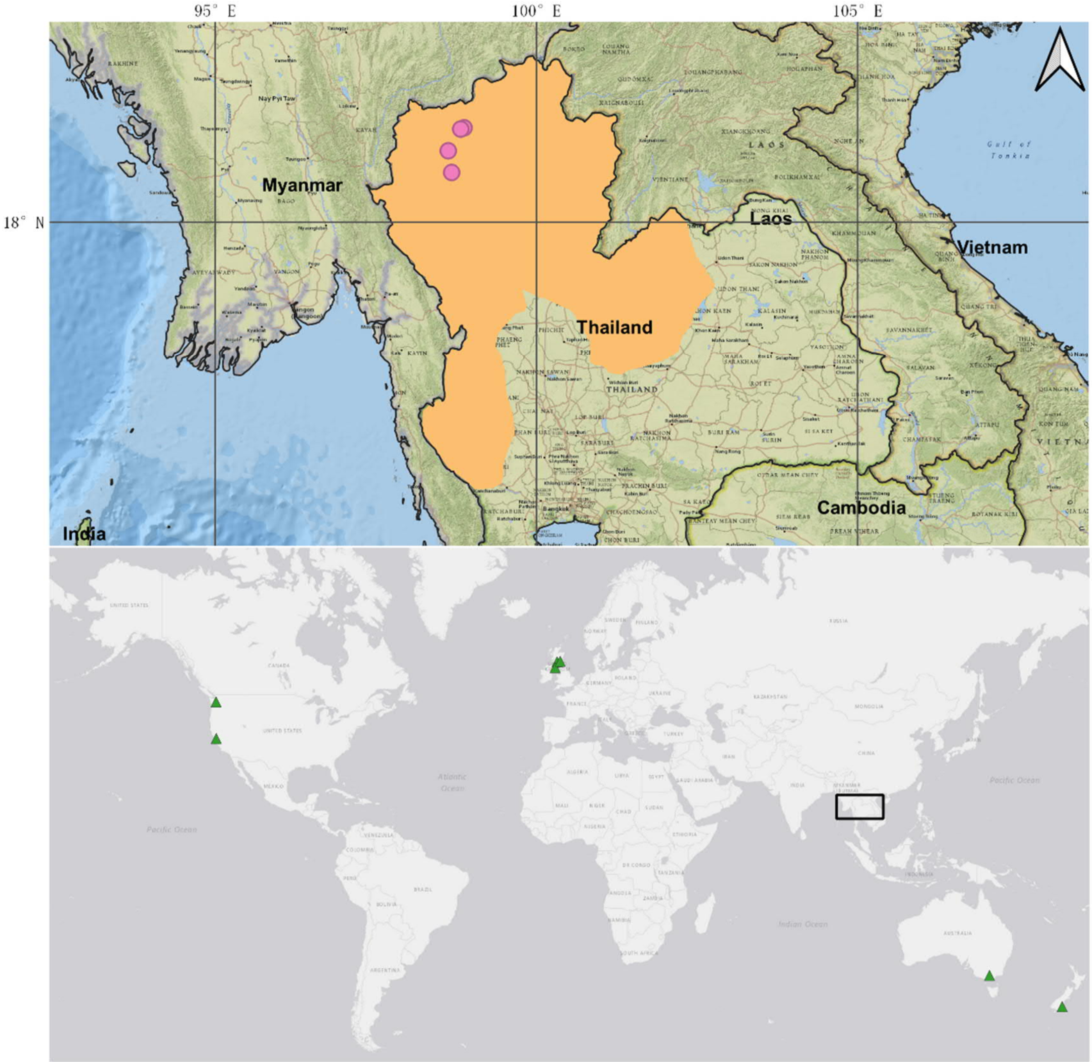
IUCN Red List status: globally CR (Gibbs et al., 2011), **DD** in China (MEP–CAS, 2013)
Distribution: China (SE Yunnan)
Altitude: 1,400–2,200 m

No. of *ex situ* sites/countries: 1/1
No. of (mapped) wild sources: 0
No. of wild accessions: 0

Rhododendron ludwigianum Hosseus

IUCN Red List status: **DD** (Gibbs et al., 2011)
Distribution: N Thailand
Altitude: 1,600–2,180 m

No. of *ex situ* sites/countries: 7/4
No. of (mapped) wild sources: (4) 4
No. of wild accessions: 8

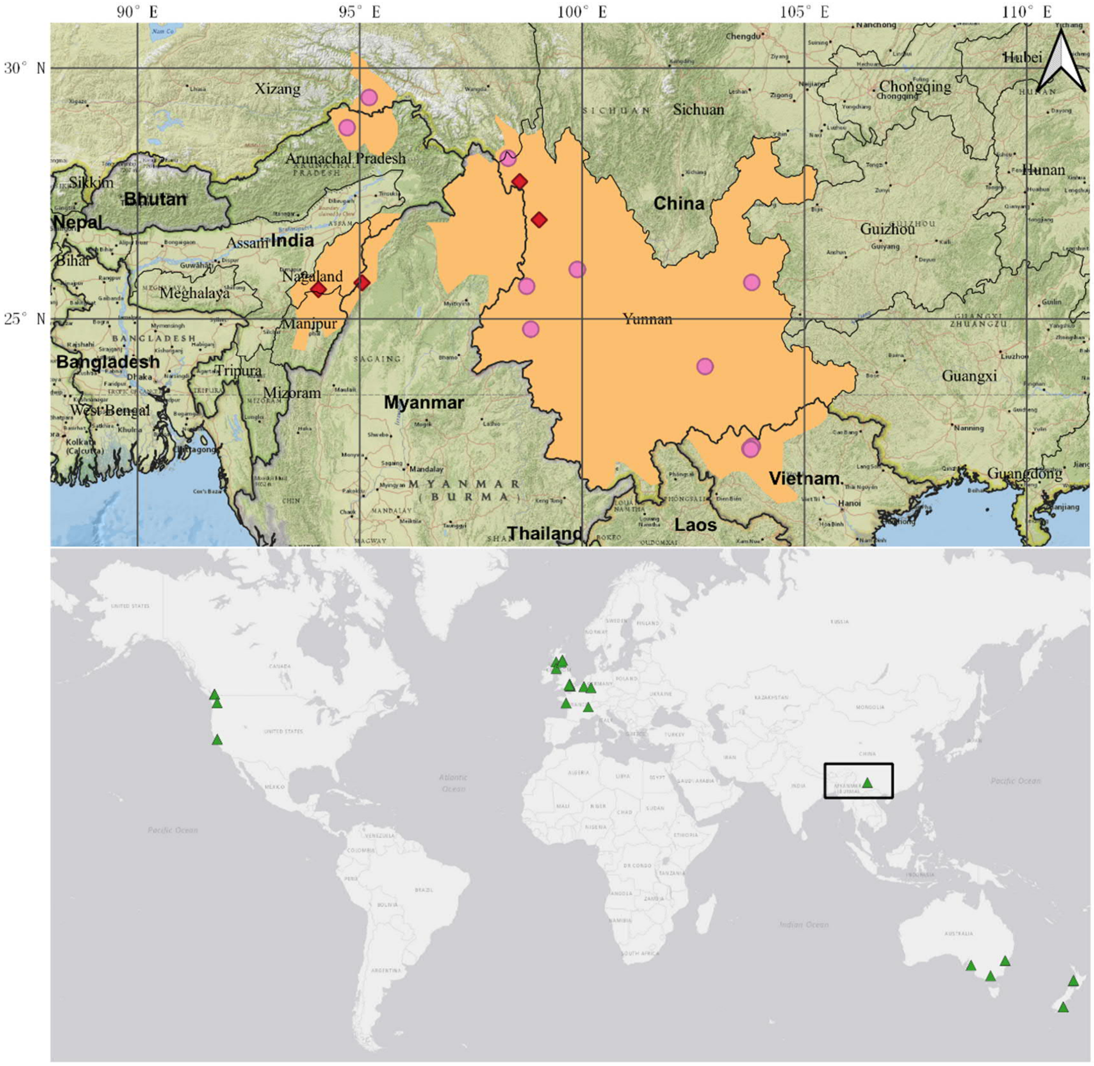


Rhododendron maddenii Hook.f. ssp. *crassum* (Franch.) Cullen

Note: data below including synonyms *R. manipurense* Balf.f. & Watt and *R. odoriferum* Hutch.

IUCN Red List status: **LC** (MEP–CAS, 2013)
Distribution: China (S Xizang, Yunnan), India (Arunachal Pradesh, Nagaland, Manipur), N Myanmar, N Vietnam
Altitude: 1,500–3,200 m

No. of *ex situ* sites/countries: 22/10
No. of (mapped) wild sources: (20) 38
No. of wild accessions: 69

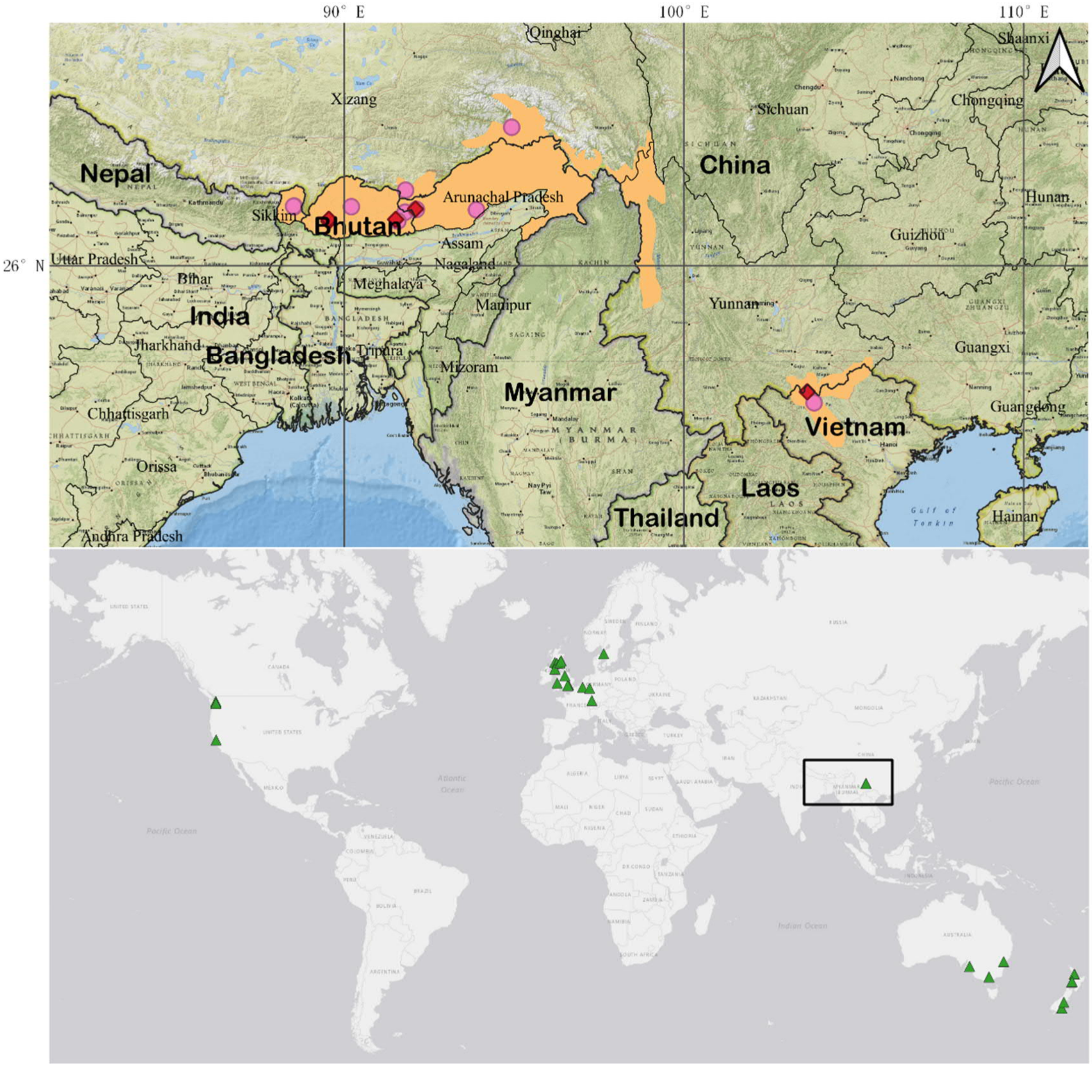


Rhododendron maddenii Hook.f. (ssp. *maddenii*)

Note: data below including synonyms *R. brachysiphon* Hutch., *R. calophyllum* Nutt. and *R. polyandrum* Hutch.

IUCN Red List status: **LC** (MEP–CAS, 2013; BGCI & IUCN SSC Global Tree Specialist Group, 2018)
Distribution: China (S Xizang, Yunnan), India (Arunachal Pradesh, Sikkim), Bhutan, N Vietnam
Altitude: ca. 2,600 m

No. of *ex situ* sites/countries: 26/8
No. of (mapped) wild sources: (16) 28
No. of wild accessions: 58

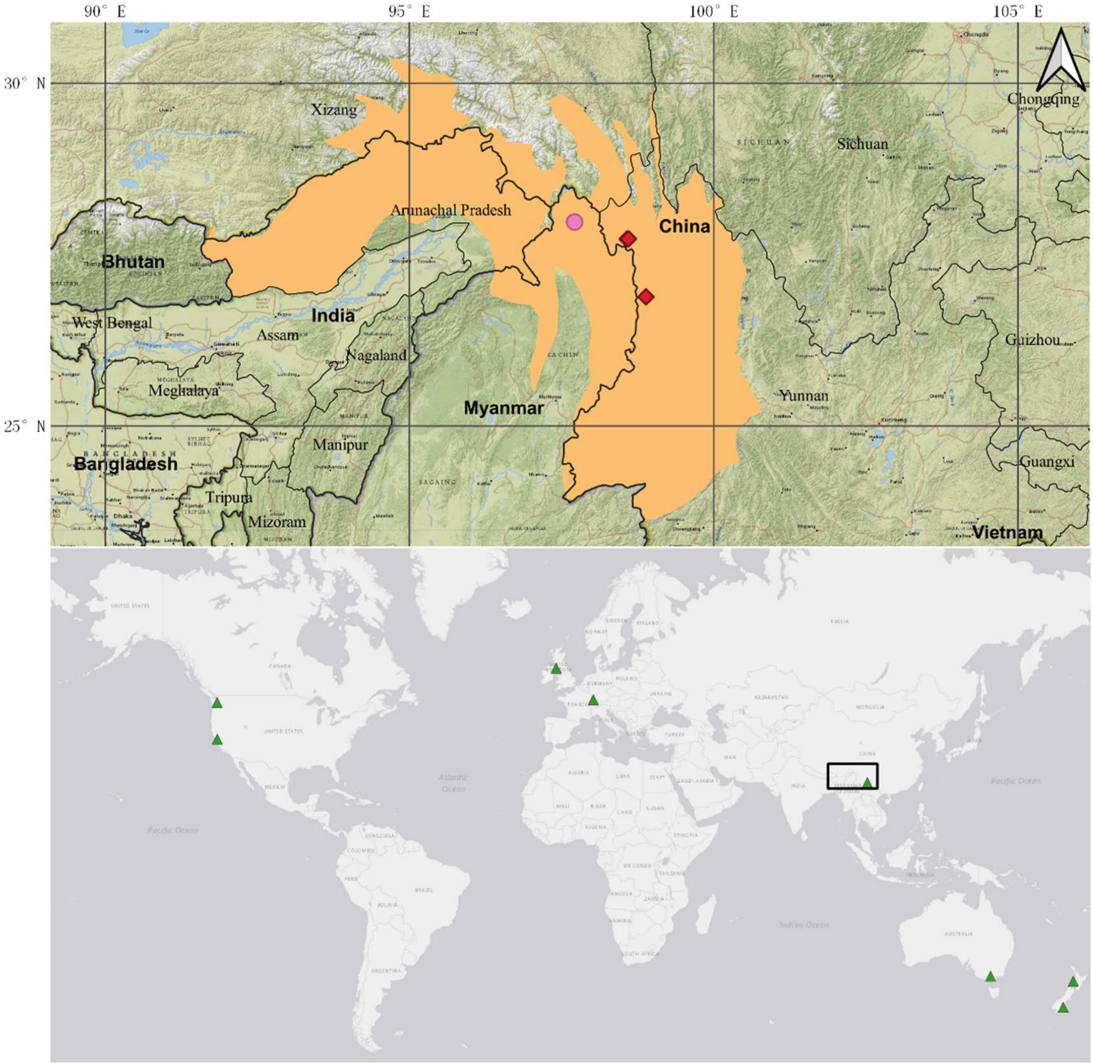


Rhododendron megacalyx Balf.f.

IUCN Red List status: globally **LC** (Gibbs et al., 2011), VU in China (Qin et al., 2017)

Distribution: China (SE Xizang, NW Yunnan), NE India (Arunachal Pradesh), NE Myanmar
Altitude: 2,200–3,000 m

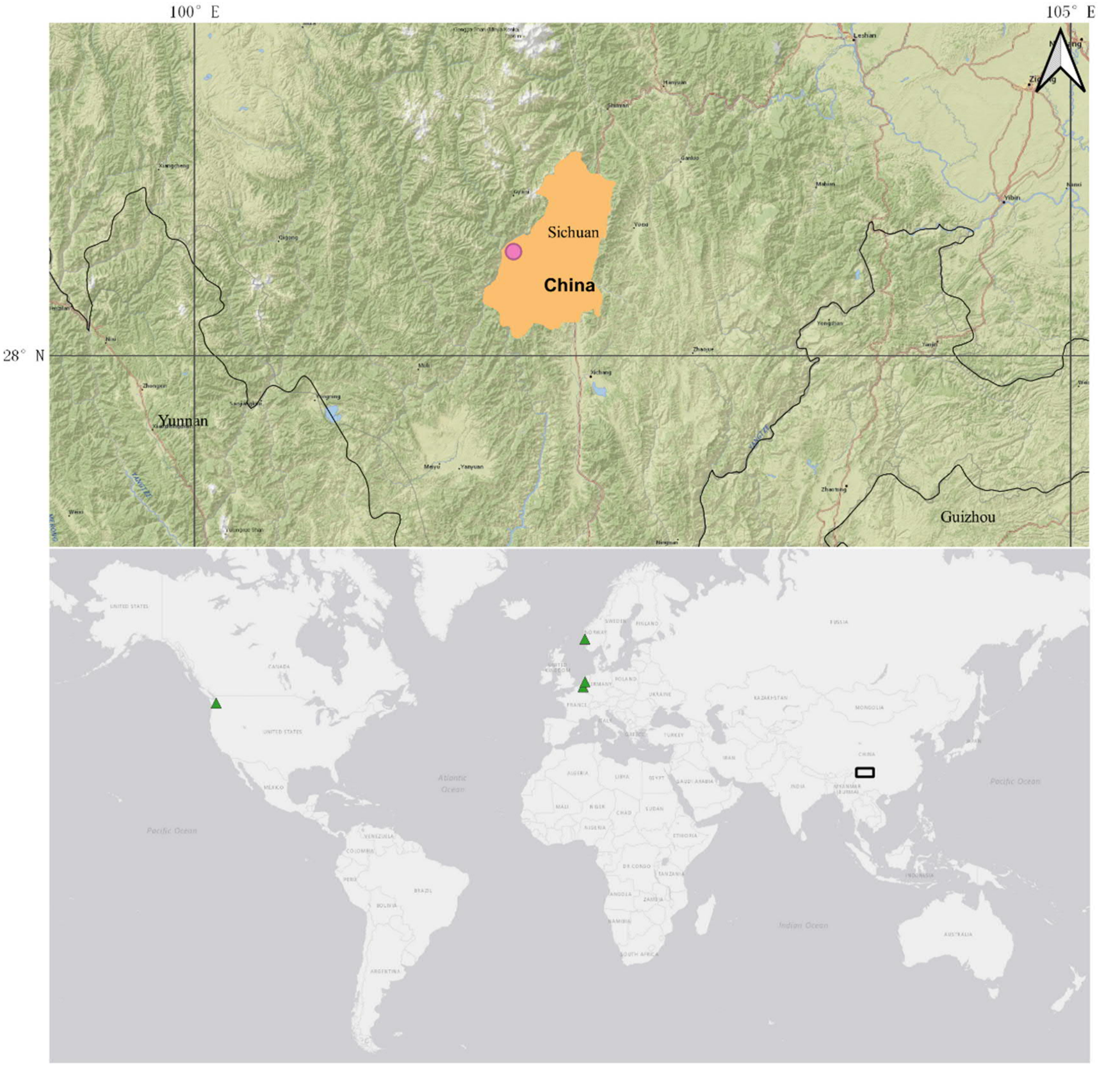
No. of *ex situ* sites/countries: 8/6
No. of (mapped) wild sources: (5) 5
No. of wild accessions: 13



Rhododendron mianningense Z.J.Zhao

IUCN Red List status: globally CR (Gibbs et al., 2011), **LC** in China (MEP–CAS, 2013)
Distribution: China (Mianning in S Sichuan)
Altitude: ca. 3,500 m

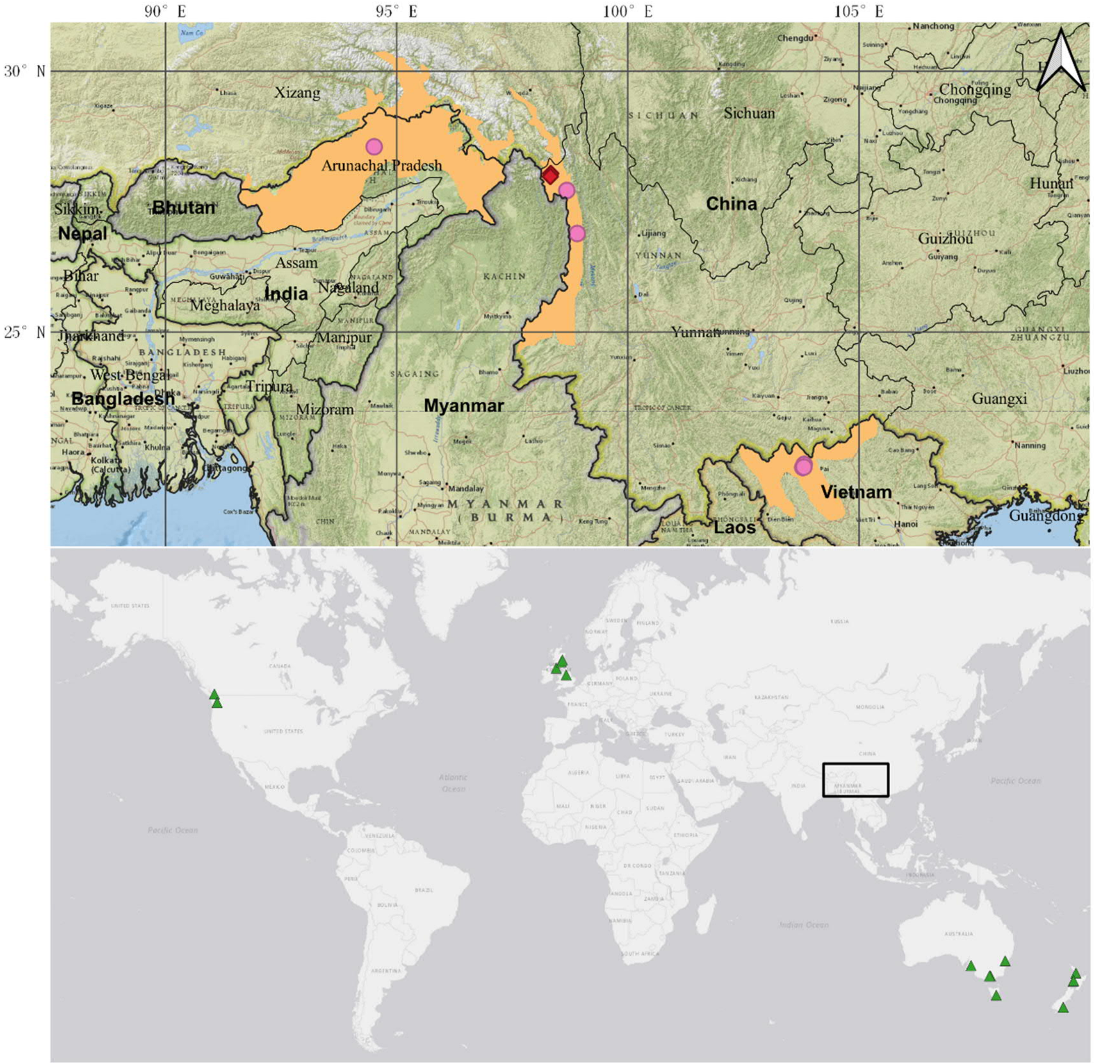
No. of *ex situ* sites/countries: 4/4
No. of (mapped) wild sources: (1) 1
No. of wild accessions: 1



Rhododendron nuttallii Booth

IUCN Red List status: globally **NT** (Gibbs et al., 2011), VU in China (Qin et al., 2017)
Distribution: China (SE Xizang, NW Yunnan*), N India (Arunachal Pradesh), N Vietnam, N Myanmar?
Altitude: 1,800–2,400 m

No. of *ex situ* sites/countries: 15/5
No. of (mapped) wild sources: (8) 16
No. of wild accessions: 31



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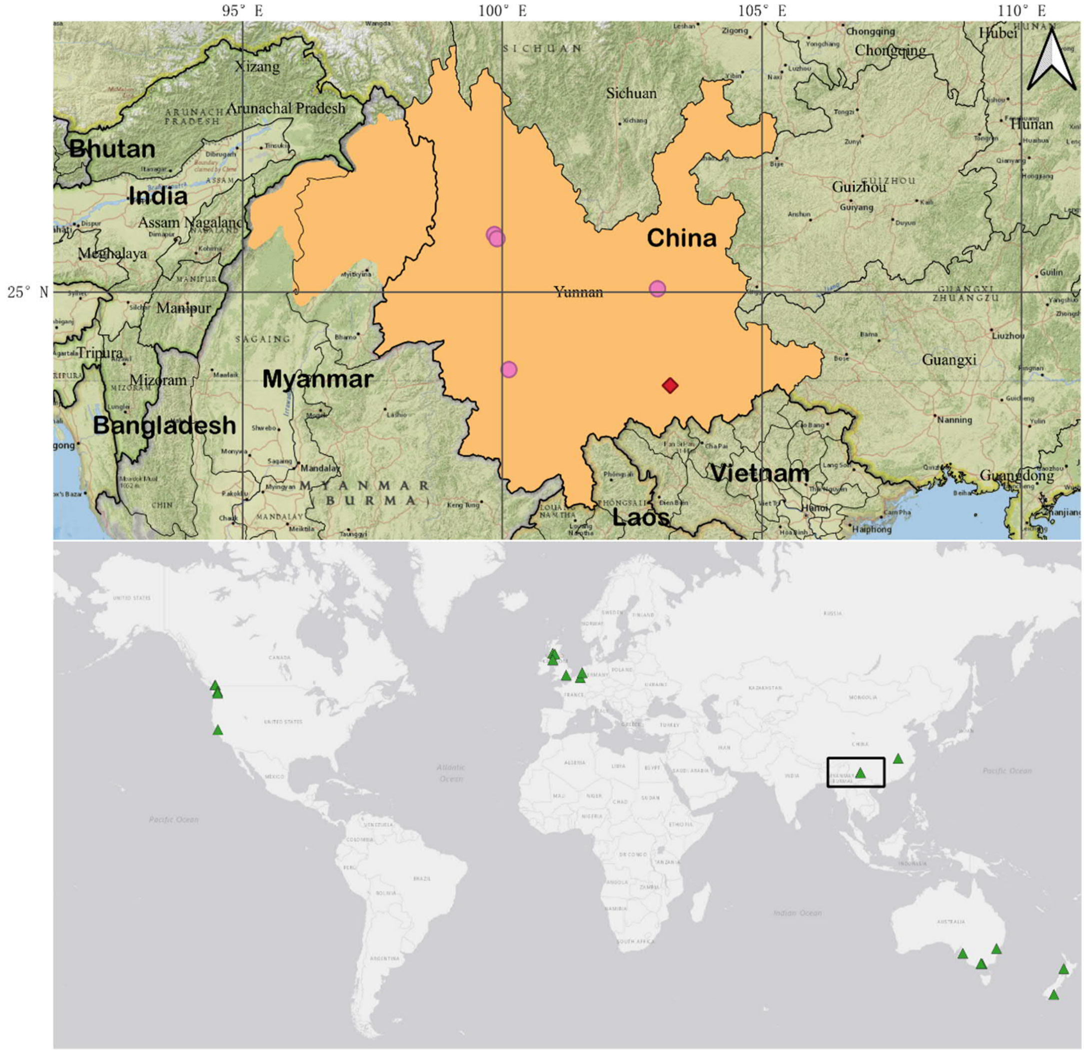
*Distribution in NW Yunnan was not recorded by Feng (1992) and Fang et al. (2011), but by Gibbs et al. (2011). Specimens from this area may possibly be of *R. sinonuttallii*.

***Rhododendron pachypodum* Balf. f. & W.W.Sm.**

Syn: *R. supranubium* Hutch.

IUCN Red List status: **LC** (MEP–CAS, 2013; BGCI & IUCN SSC Global Tree Specialist Group, 2018)
Distribution: China (Yunnan), N Myanmar[*]
Altitude: 1,200–2,800(–3,100) m[*] (*R. supranubium* 1,220–3,660 m)

No. of *ex situ* sites/countries: 20/8
No. of (mapped) wild sources: (5) 9
No. of wild accessions: 14

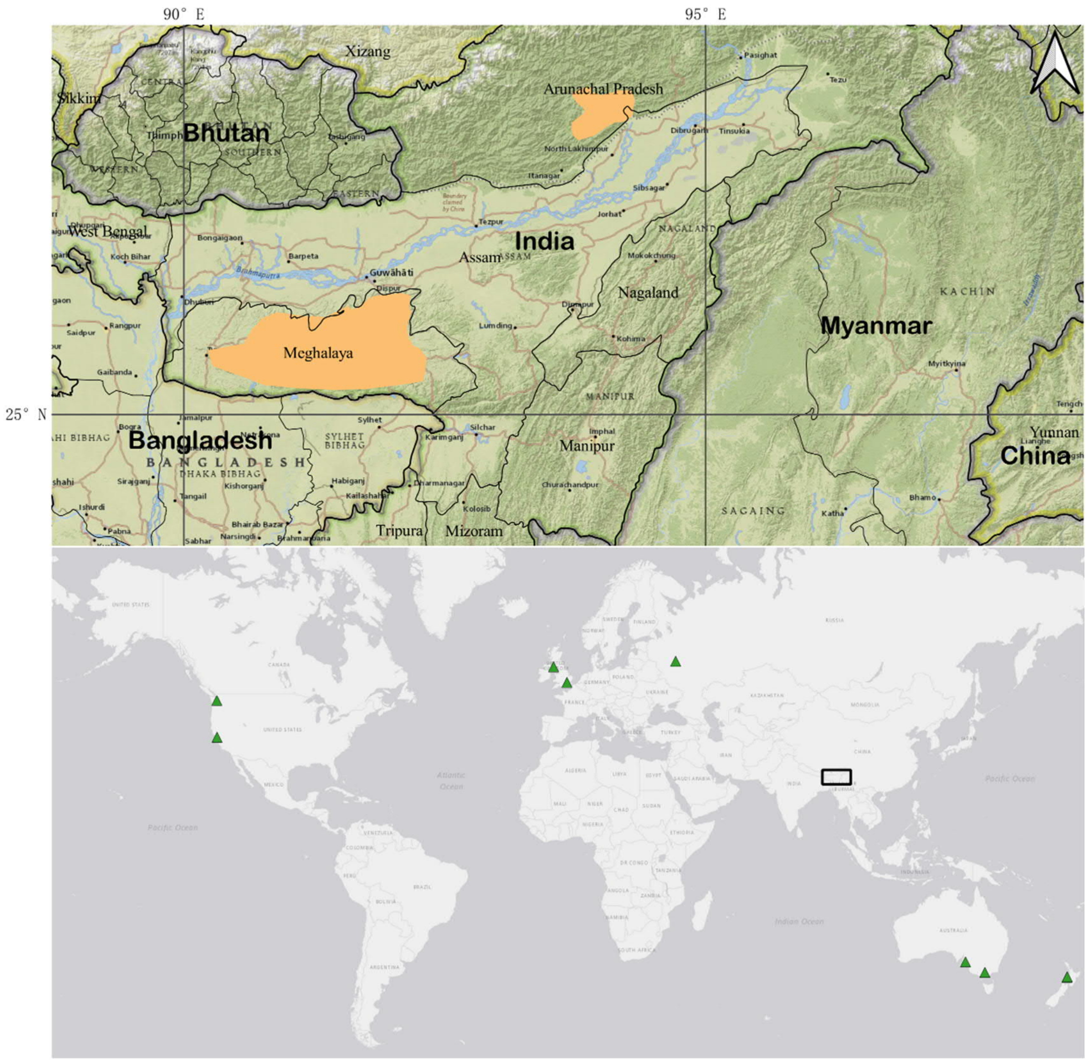


[*] Altitude according to *Flora of China* (M.-Y. Fang et al., 2005) but the distribution is changed here from ‘NE Myanmar’ to ‘N Myanmar’ referring to the geographic description of ‘North Triangle’.

Rhododendron parryae Hutch.

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: India (Arunachal Pradesh, Meghalaya)*
Altitude: 1,769–2,135 m

No. of *ex situ* sites/countries: 9/5
No. of (mapped) wild sources: (0) 1
No. of wild accessions: 1



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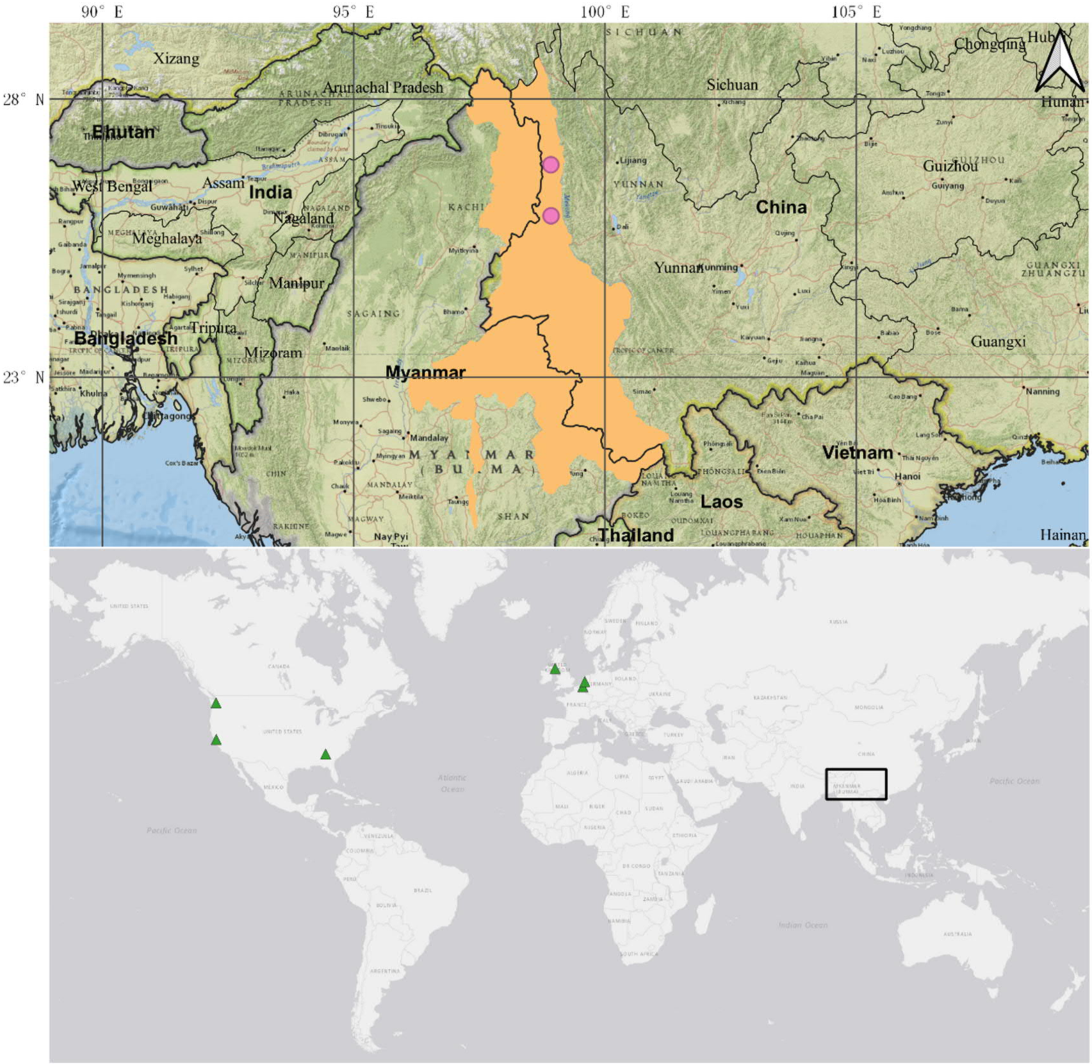
*According to locations of type specimens (Davidian, 1982), which were described as in ‘Assam’ in 1927 and 1965. By then ‘Assam’ included today’s Arunachal Pradesh, Assam, Meghalaya, Nagaland and Mizoram, which alerts modern readers/scholars to be careful about the administrative change when checking the documented plant collections before 1970s in this area.

Rhododendron pseudociliipes Cullen

IUCN Red List status: globally **VU** (Gibbs et al., 2011), NT in China (MEP–CAS, 2013)
Distribution: China (NW Yunnan), NE Myanmar
Altitude: 2,400–3,100 m

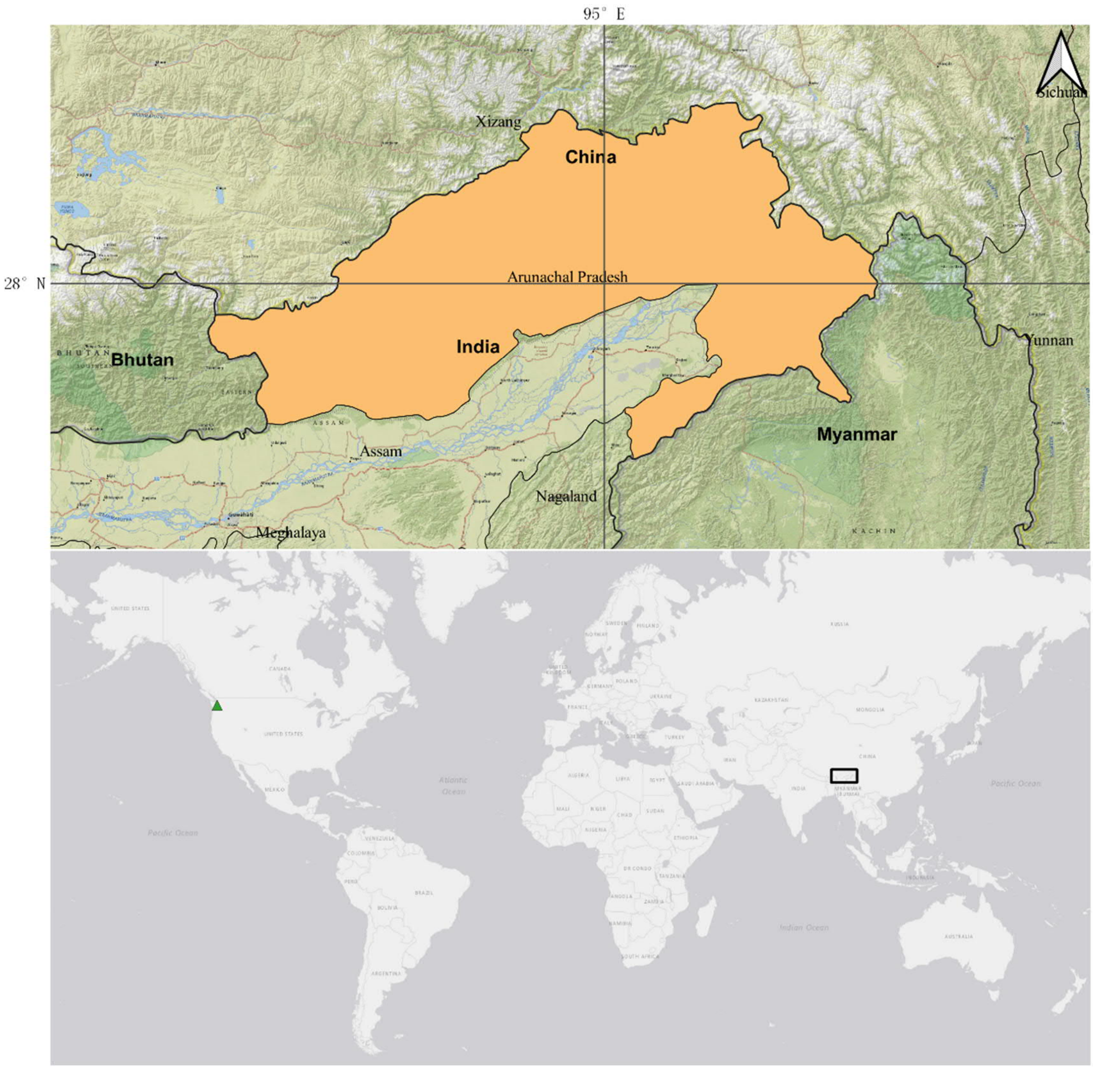
No. of *ex situ* sites/countries: 6/4
No. of (mapped) wild sources: (2) 3
No. of wild accessions: 11



Rhododendron pseudomaddenii A.A.Mao & M.Bhaumik

IUCN Red List status: **LC** (Mao & Bhaumik, 2015)
Distribution: India (Arunachal Pradesh)
Altitude: 1,900–3,000 m

No. of *ex situ* sites/countries: 1/1
No. of (mapped) wild sources: (0) 1
No. of wild accessions: 2



Rhododendron rhombifolium R.C.Fang

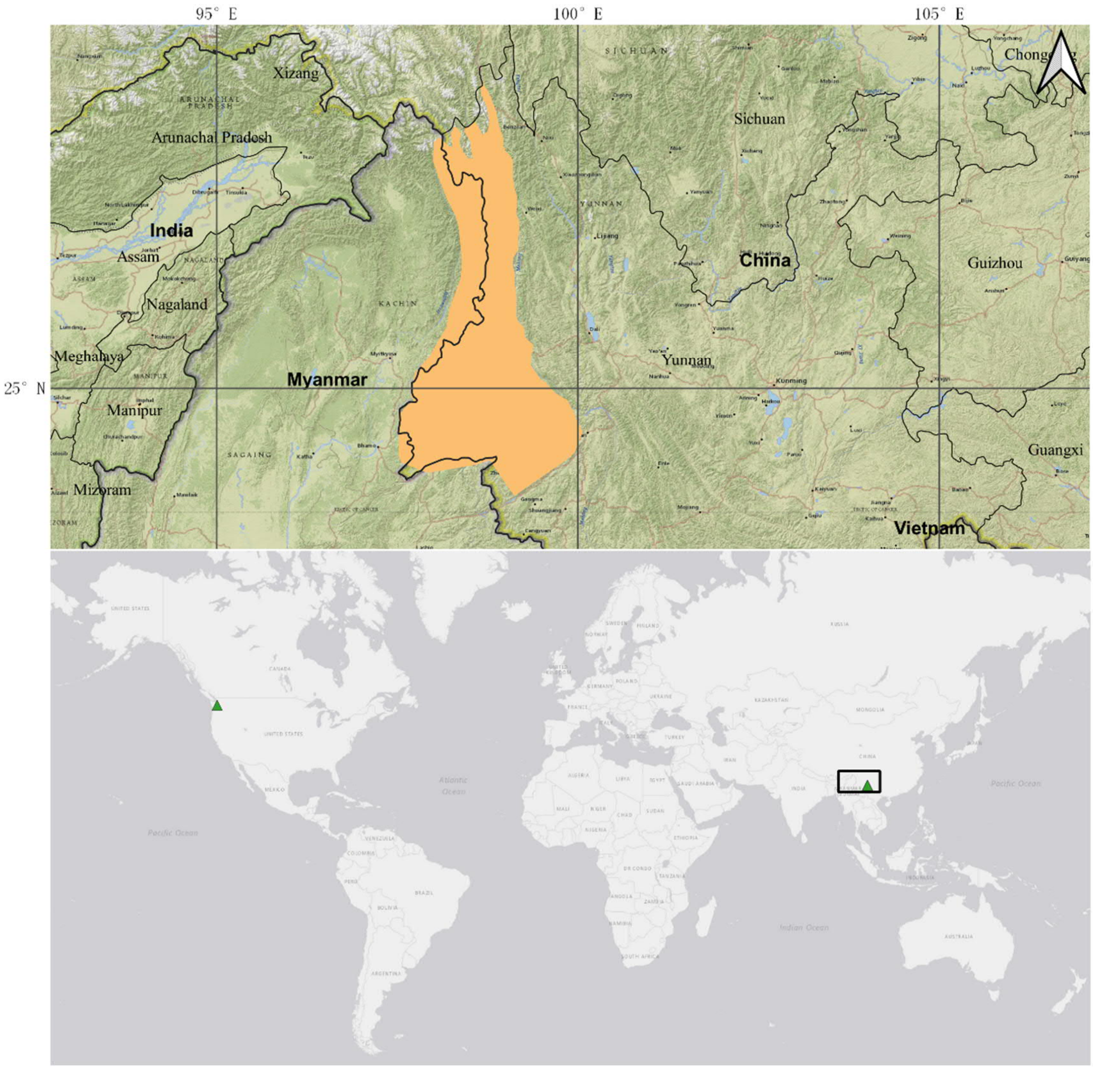
IUCN Red List status: globally CR (Gibbs et al., 2011), **DD** in China (MEP–CAS, 2013)
Distribution: China (Yunnan)
Altitude: 1,800–1,900 m (Feng & Yang, 1999; M.-Y. Fang et al., 2005); 3,000–4,450 m (Li & Zhou, 2005);

No. of *ex situ* sites/countries: 2/1
No. of (mapped) wild sources: 0
No. of wild accessions: 0

Rhododendron roseatum Hutch.

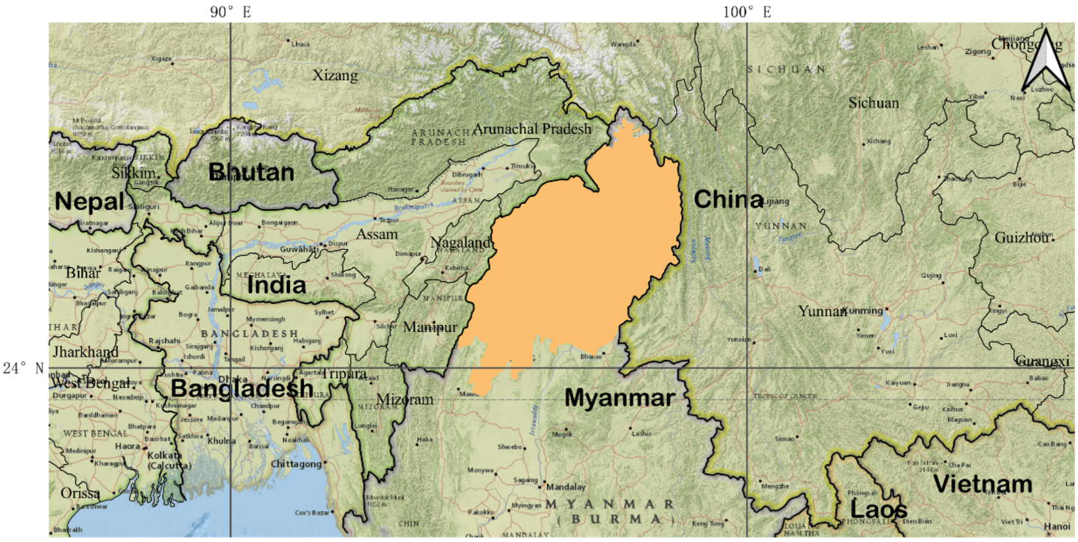
IUCN Red List status: globally **VU** (Gibbs et al., 2011), NT in China (MEP–CAS, 2013)
Distribution: China (Yunnan), NE Myanmar
Altitude: 2,000–3,000 m

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: 0
No. of wild accessions: 0



Rhododendron rubrantherum Kingdon–Ward

IUCN Red List status: NE
Distribution: upper Burma (https://www.ipni.org/n/333258–1). Lacking data.
Not in cultivation.



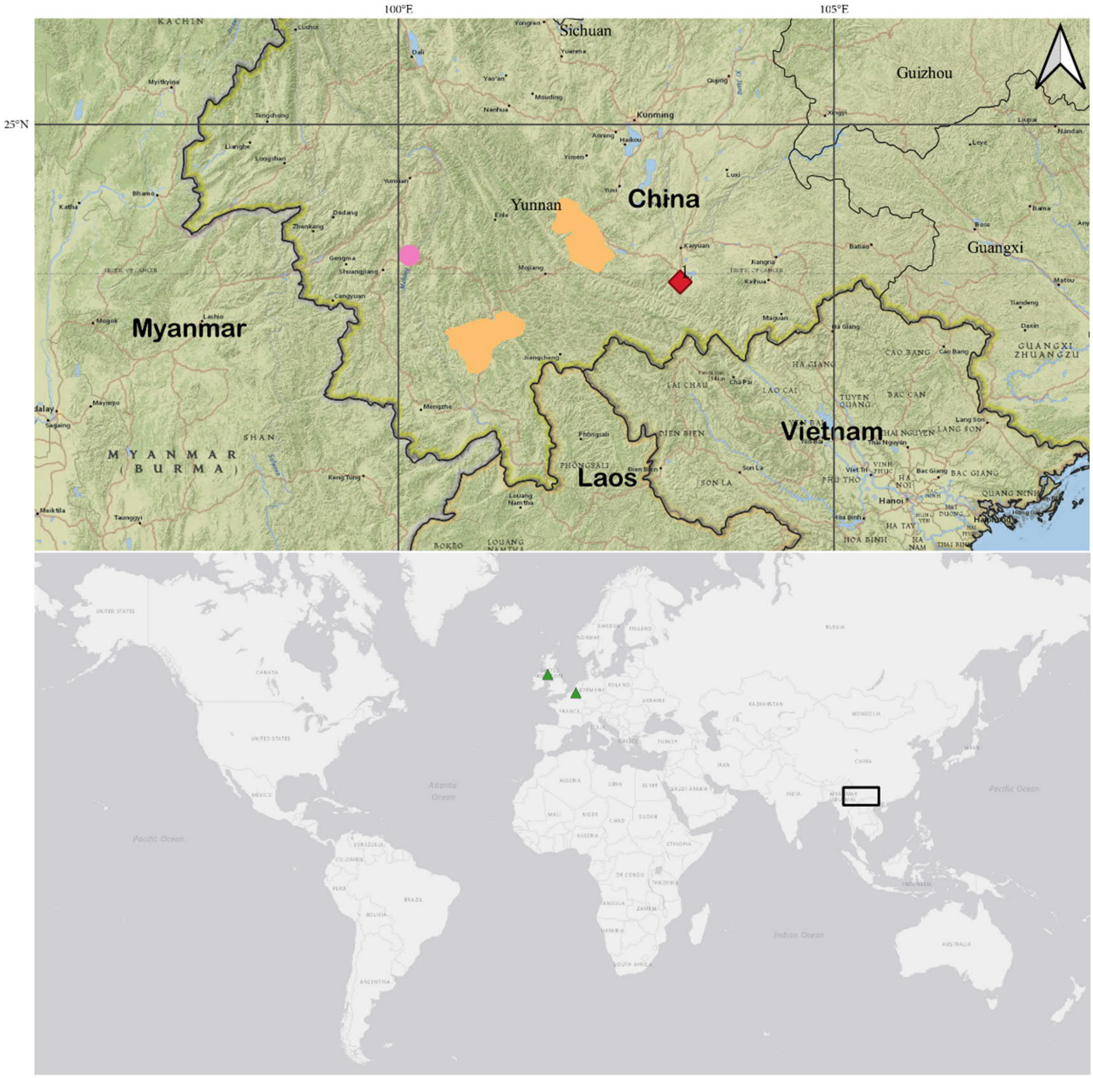
R. rubrantherum was listed by Chamberlain et al. (1996), but there is no further information on taxonomy or distribution of this species (http://www.worldfloraonline.org/taxon/wfo–0000405521). There is no current concern about conservation as the species has not been assessed.

Rhododendron rufosquamosum Hutch.

Note: *Flora of China* (M.-Y. Fang et al., 2005) listed *R. rufosquamosum* as a synonym of *R. pachypodum*, but other references (Cullen, 1980; Feng, 1988, 1992; Chamberlain et al., 1996) listed the two species separately.

IUCN Red List status: NE
Distribution: China (S Yunnan)
Altitude: ca. 1,464 m (Davidian, 1982); ca. 2,000 m (Feng, 1992)

No. of *ex situ* sites/countries: 2/2
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 2*



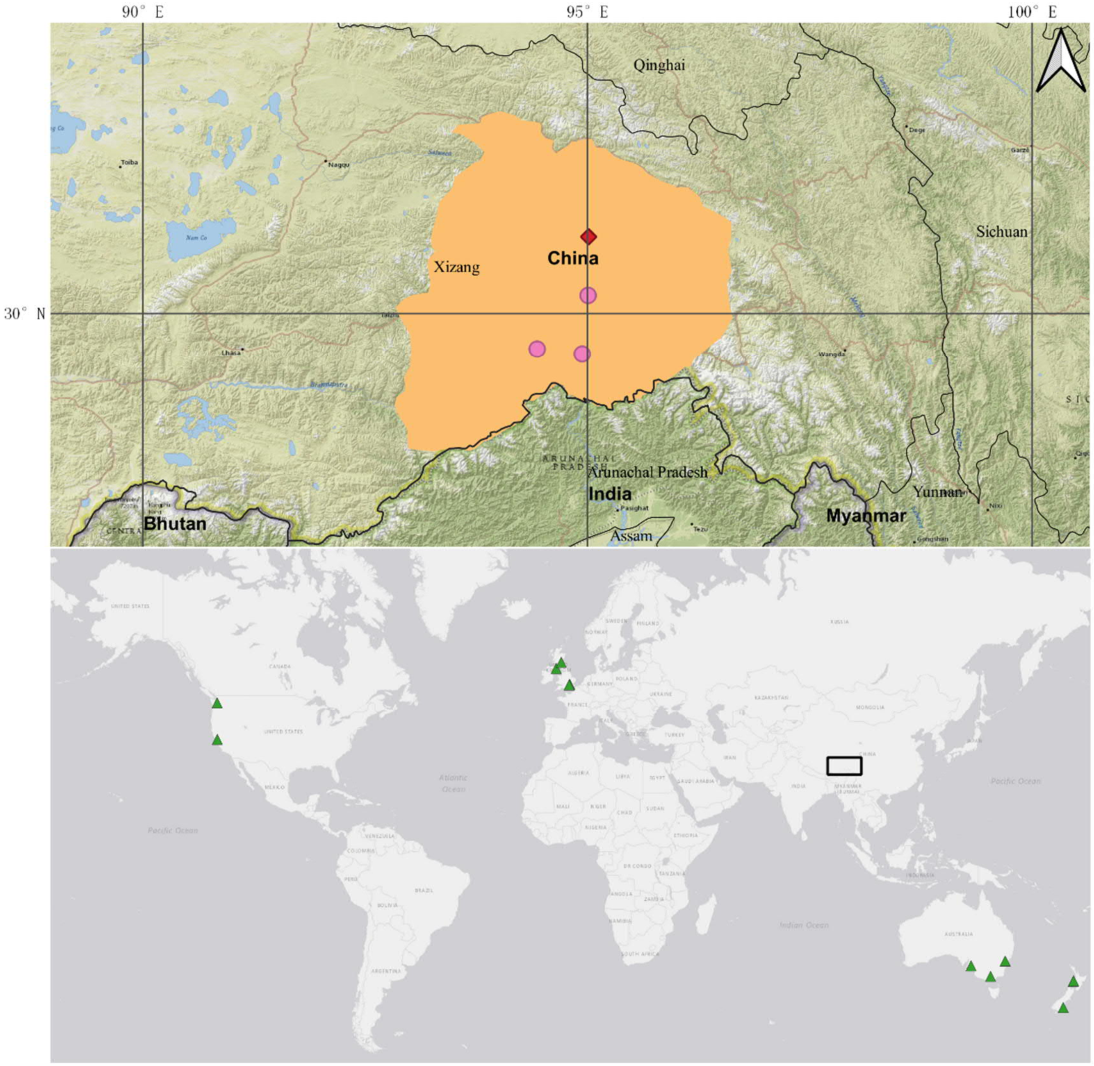
*Two possible wild collections (Table S2.2):
1) *R.* aff. *rufosquamosum* KR#4303 as #19962587 cultivated in Royal Botanic Garden Edinburgh (Logan garden);

2) *R. pachypodum*/*rufosquamosum*? JN#11076 as #17415 cultivated in Arboretum Wespelaar, Germany; Another accession was cultivated as #2012–0165 at University of British Columbia Botanic Garden but it died.

Rhododendron scopulorum **Hutch.**

IUCN Red List status: globally VU (Gibbs et al., 2011), **LC** in China (MEP–CAS, 2013)
Distribution: China (SE Xizang)
Altitude: 1,830–2,440 m

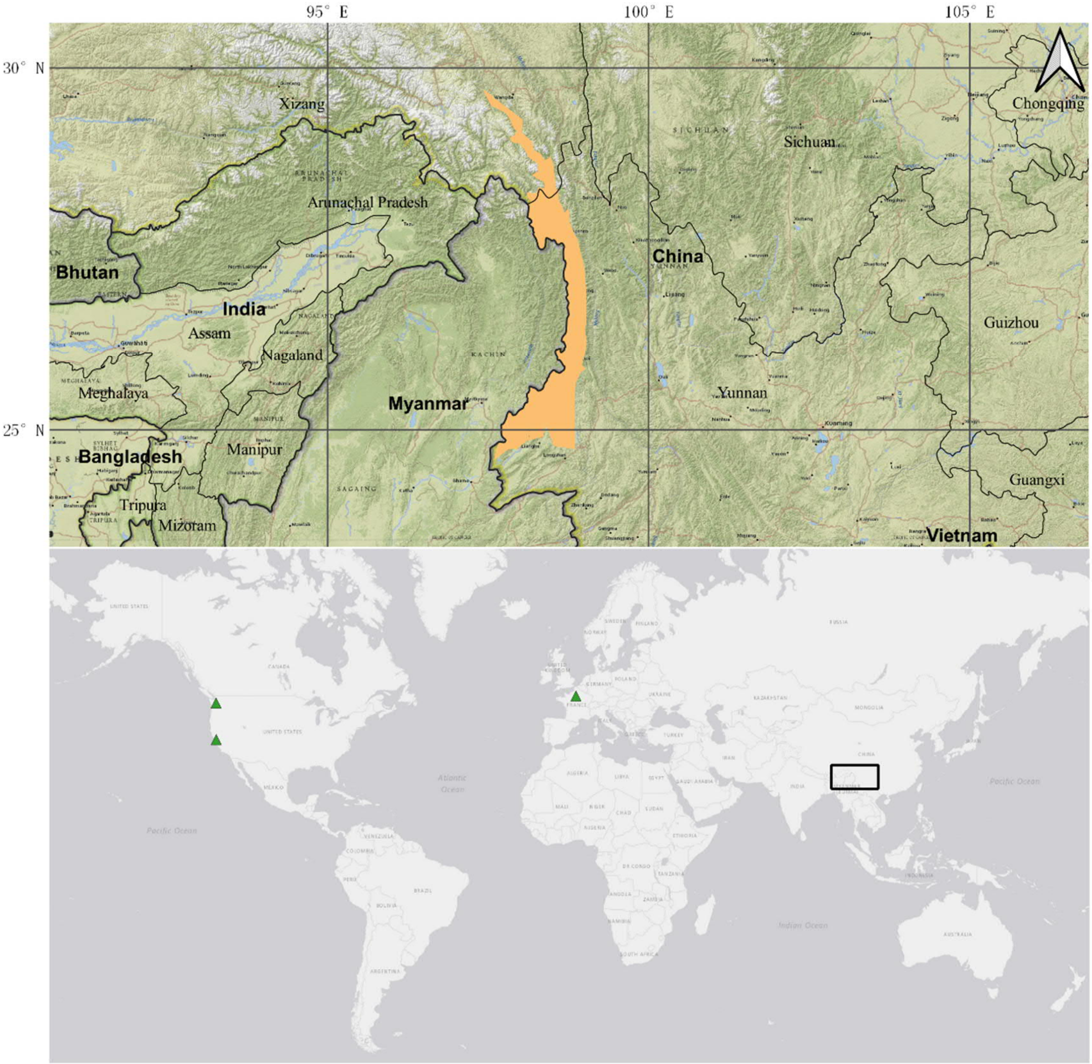
No. of *ex situ* sites/countries: 12/4
No. of (mapped) wild sources: (4) 4
No. of wild accessions: 10



Rhododendron sinonuttallii Balf.f. & Forrest

IUCN Red List status: **VU** (Gibbs et al., 2011)
Distribution: China (SE Xizang, NW Yunnan), N Myanmar?[*]
Altitude: 1,200–2,800 m

No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: 0
No. of wild accessions: 0



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[*] Myanmar was mentioned in the Red List (Gibbs et al., 2011) but not in *Flora of China* (M.-Y. Fang et al., 2005).

Rhododendron starlingii **Rushforth & Nguyen Thi Thanh Huong**

IUCN Red List status: NE (Rushforth et al., 2022)
Distribution: Vietnam (Upper parts of Fansipan)
Altitude: ca. 2,800–3,000 m

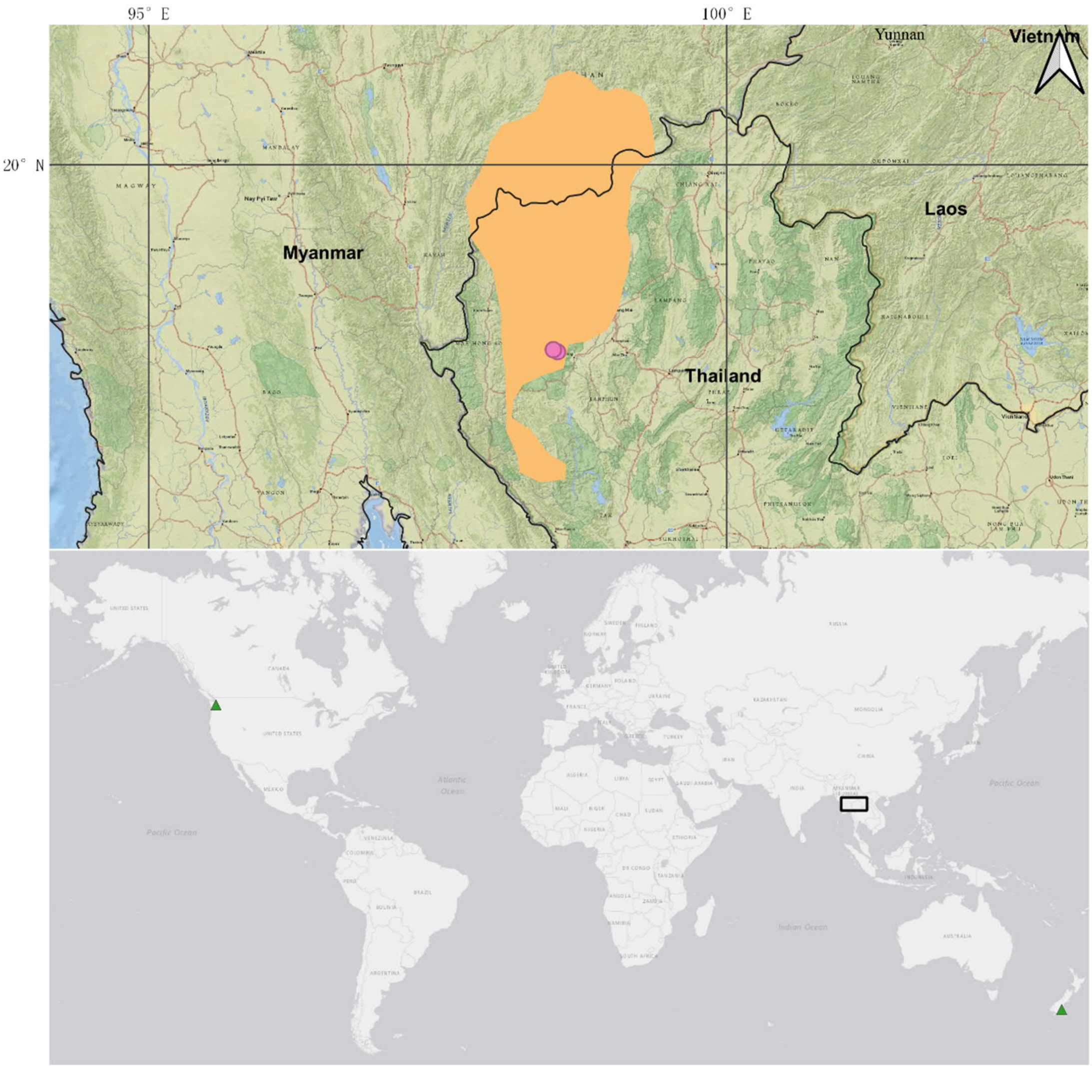
No. of *ex situ* sites/countries: 2/1*
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 2

*In Keith Rushforth's and Barry Starling's private gardens which are in UK and not members of BGCI. The two wild collections were previously under *R. crenulatum*: AC#5685 and KR#7369 (Rushforth et al., 2022).

Rhododendron surasianum Balf.f. & Craib

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: N Thailand, SE Myanmar
Altitude: 1,400–1,737 m

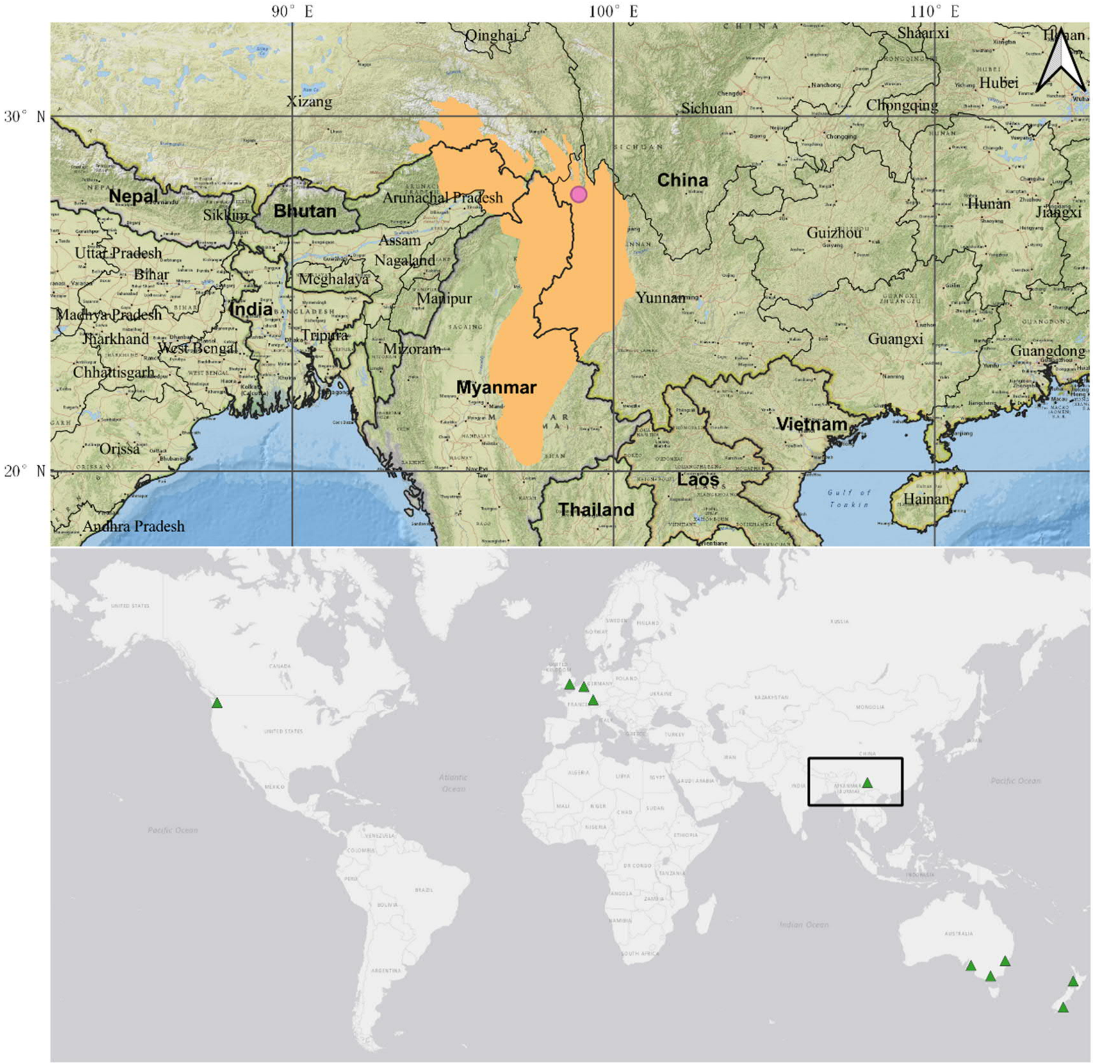
No. of *ex situ* sites/countries: 2/2
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 3



Rhododendron taggianum Hutch.

IUCN Red List status: globally **VU** (Gibbs et al., 2011), NT in China (MEP–CAS, 2013)
Distribution: China (SE Xizang, Yunnan), NE India (Arunachal Pradesh), NE Myanmar
Altitude: 1,800–2,300 m

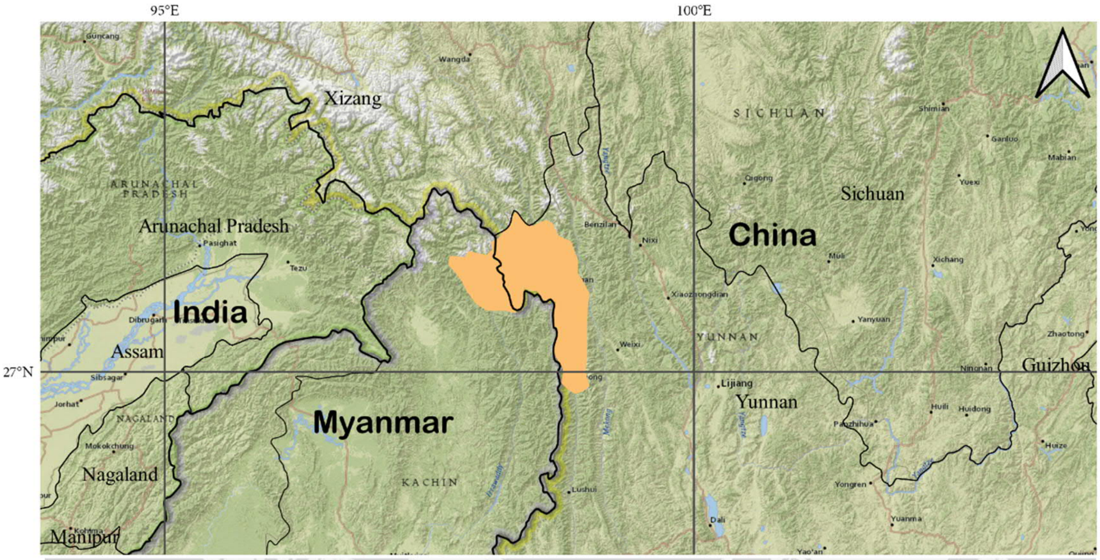
No. of *ex situ* sites/countries: 10/7
No. of (mapped) wild sources: (1) 3
No. of wild accessions: 9



Rhododendron taronense Hutch.

IUCN Red List status: **VU** (Gibbs et al., 2011, Qin et al., 2017)
Distribution: China (NW Yunnan), N Myanmar
Altitude: 1,250–2,300 m (Feng, 1988); 1,200–1,600 m (M.-Y. Fang et al., 2005)

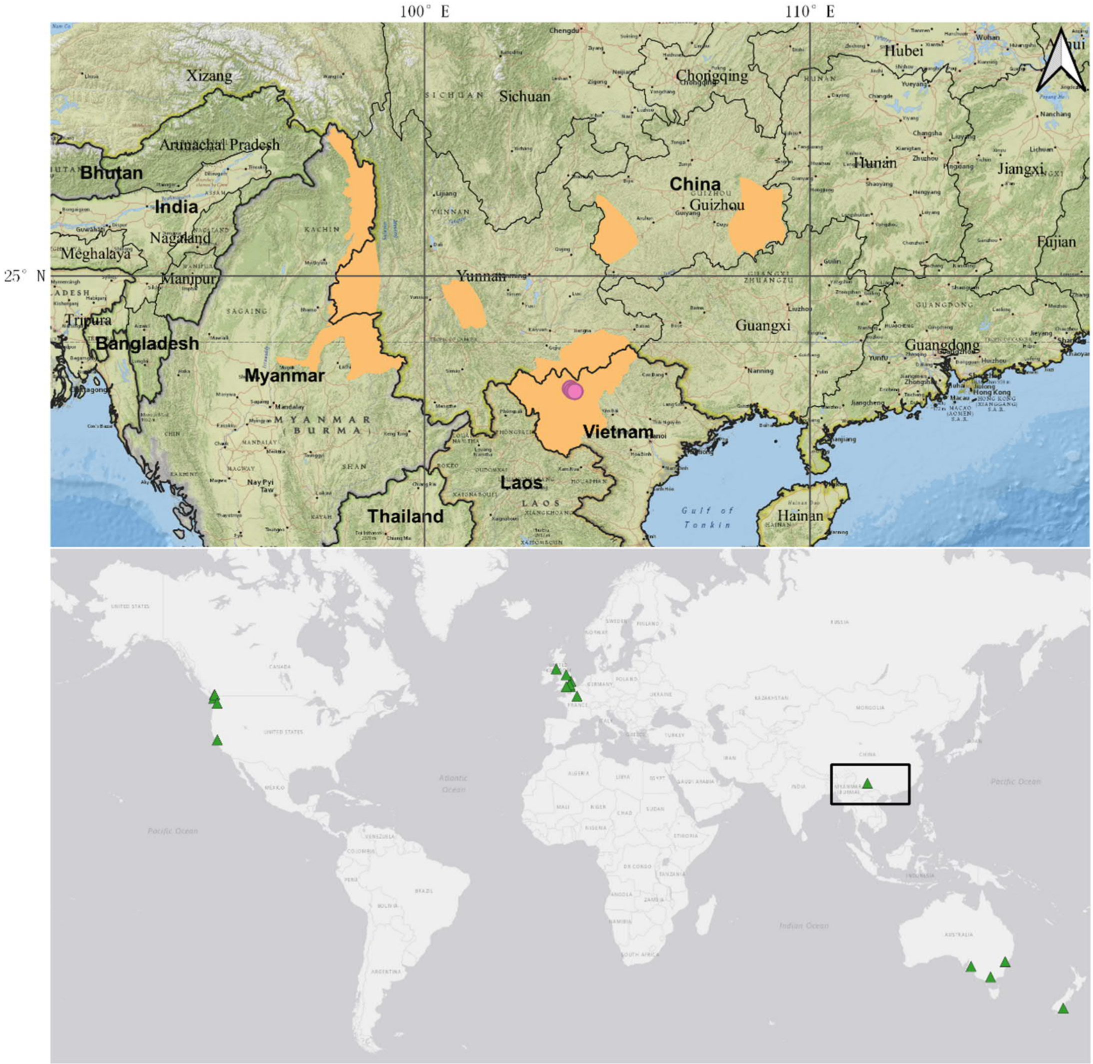
No. of *ex situ* sites/countries: 6/5
No. of (mapped) wild sources: (0) 1
No. of wild accessions: 2



Rhododendron valentinianum (var. *valentinianum*) Forrest ex Hutch.

IUCN Red List status: **NT** (Gibbs et al., 2011, MEP–CAS, 2013)
Distribution: China (Guizhou, Yunnan), NE Myanmar, N Vietnam*
Altitude: ca. 2,400 m

No. of *ex situ* sites/countries: 16/7
No. of (mapped) wild sources: (3) 6
No. of wild accessions: 19



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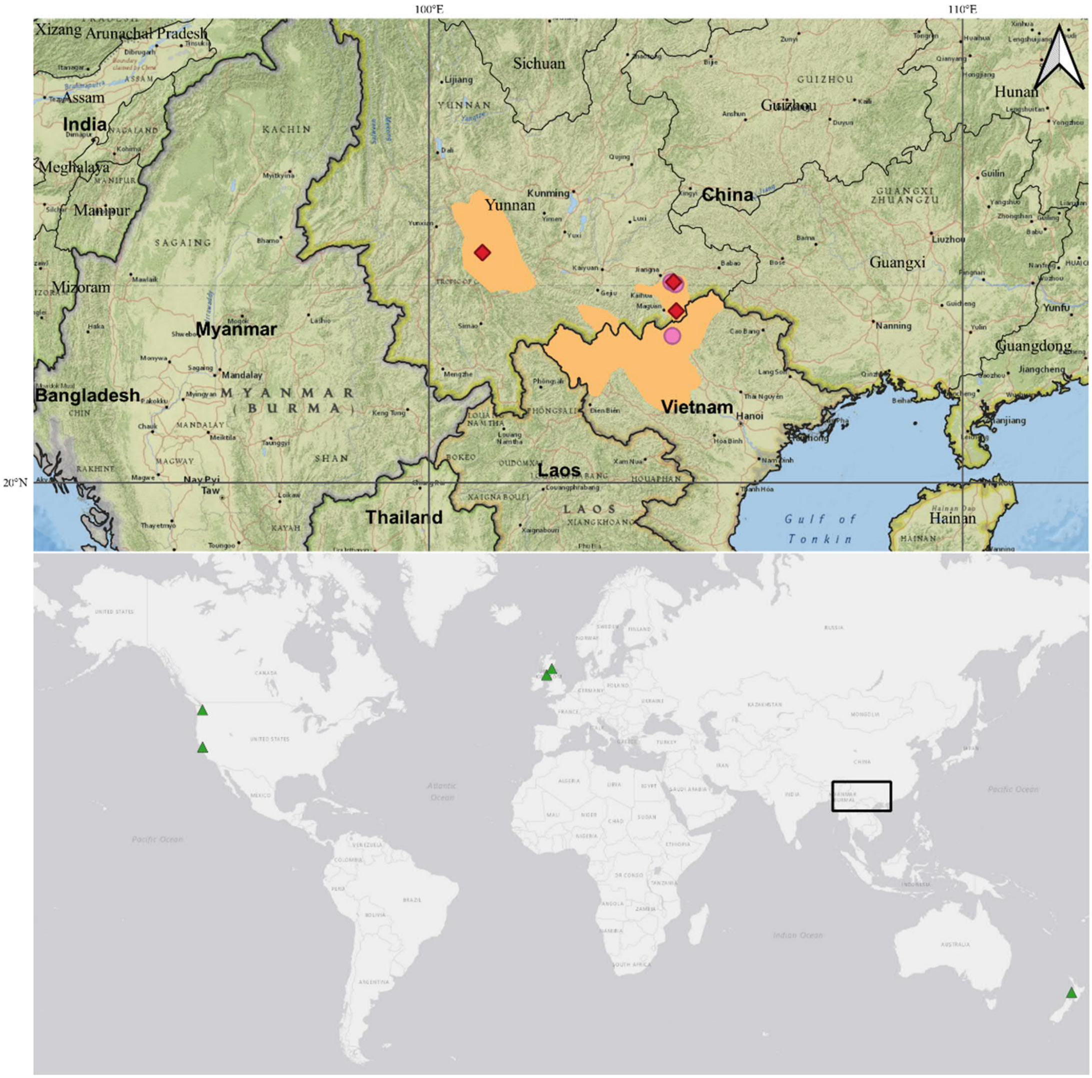
*Scattered distribution in Guizhou (Guiding, Anlong), Yunnan (Tengchong, Jingdong, Jinping) and wide in NE Myanmar and N Vietnam (*Flora of China*, http://www.iplant.cn/info/%E6%AF%9B%E6%9F%84%E6%9D%9C%E9%B9%83?t=z)

Rhododendron valentinianum var. *oblongilobatum* R.C.Fang

IUCN Red List status: **NT** (MEP–CAS, 2013)
Distribution: China (Yunnan), N Vietnam
Altitude: 1,800–3,100 m

No. of *ex situ* sites/countries: 5/3
No. of (mapped) wild sources: (6) 7
No. of wild accessions: 23



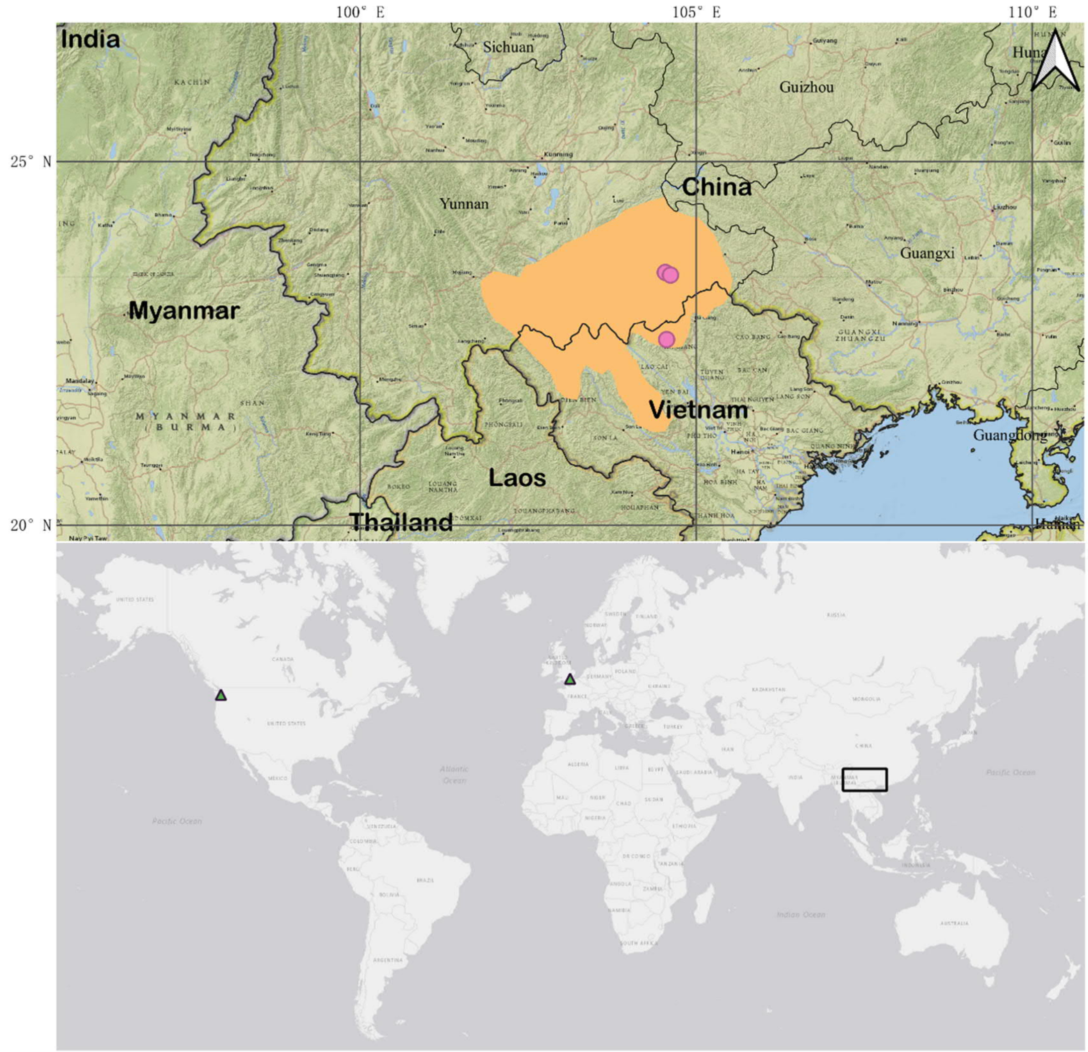
Distribution and wild collections of *R. valentinioides* may be lumped with *R. valentinianum* var. *oblongilobatum* due to unresolved taxonomy (Hootman, 2021).

Rhododendron valentinioides (ined.) Chamb., Cox and Hutchison

IUCN Red List status: **DD** (Gibbs et al., 2011, MEP–CAS, 2013)

Distribution: China (Yunnan), N Vietnam
Altitude: ca. 2,800 m (referring to wild accessions)

No. of *ex situ* sites/countries: 2/2
No. of (mapped) wild sources: (3) 3
No. of wild accessions: 6



R. valentinioides was listed separately in the Red List (Gibbs et al., 2011), with narrower distribution in the border area between China (Yunnan) and Vietnam. It was identified phylogenetically close to *R. valetinianum* var. *oblongilobatum* and both distinct from *R. valentinianum* (Donald, 2012). Cox (2013a) and Steve Hootman (https://rhodygarden.org/new–r–valentinioides–646/) mentioned *R. valentinioides* was a new species yet to be accepted. However, the Cox Glendoick website lumps *R. valentinioides* C.&H.7186 with *R. valentinianum* var. *oblongilobatum* (https://www.glendoick.com/Maddenia–Rhododendrons).

Rhododendron vanderbiltianum Merr.

IUCN Red List status: **LC** (Gibbs et al., 2011)
Distribution: Indonesia, a small group of mountains in the Losir area of Aceh Province: Mt. Losir; Mt. Goh Lembuh; Mt. Kemiri and Pang–mog (Argent et al., 2008)
Not in cultivation.

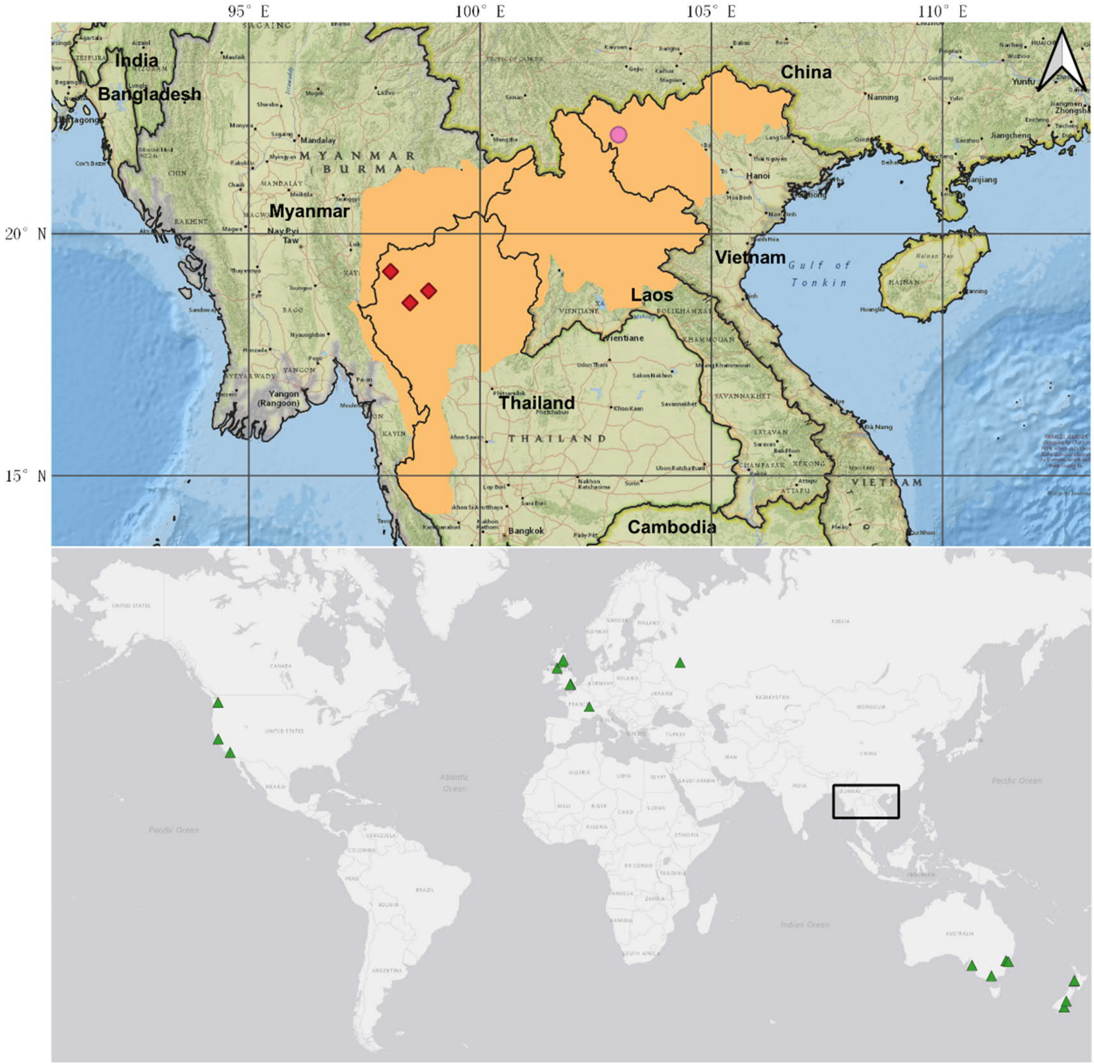
R. vanderbiltianum is an accepted species (http://www.plantsoftheworldonline.org/taxon/urn:lsid:ipni.org:names:333537–1) but its taxonomic position remains unknown (http://www.worldfloraonline.org/taxon/wfo–0000405704). Argent et al. (2008) confirmed *R. vanderbiltianum* was not a vireya species. He also noted it was morphologically similar to *R. crenulatum* (subsection *Maddenia*) and difficult to cultivate as the latter. Donald (2012) included *R. vanderbiltianum* as a yellow–flower species and verified it phylogenetically close to species in ss. *Maddenia*. However, as yet there is no other evidence to confirm its placement. Previously the global *ex situ* conservation update of *Rhododendron* (MacKay et al., 2018) included *R. vanderbiltianum* in ss. *Maddenia* based on existing evidence. Hereby, it is included as a species of ss. *Maddenia* in this study.

Rhododendron veitchianum Hook. f.

Note: data below includes the synonym *R. cubittii* Hutch.

IUCN Red List status: **LC** (Gibbs et al., 2011), Rare in India (Mizaram)
Distribution[*]: Myanmar, Laos, Thailand, Vietnam
Altitude: 1,220–2,288 m

No. of *ex situ* sites/countries: 18/6
No. of (mapped) wild sources: (4) 7
No. of wild accessions: 9

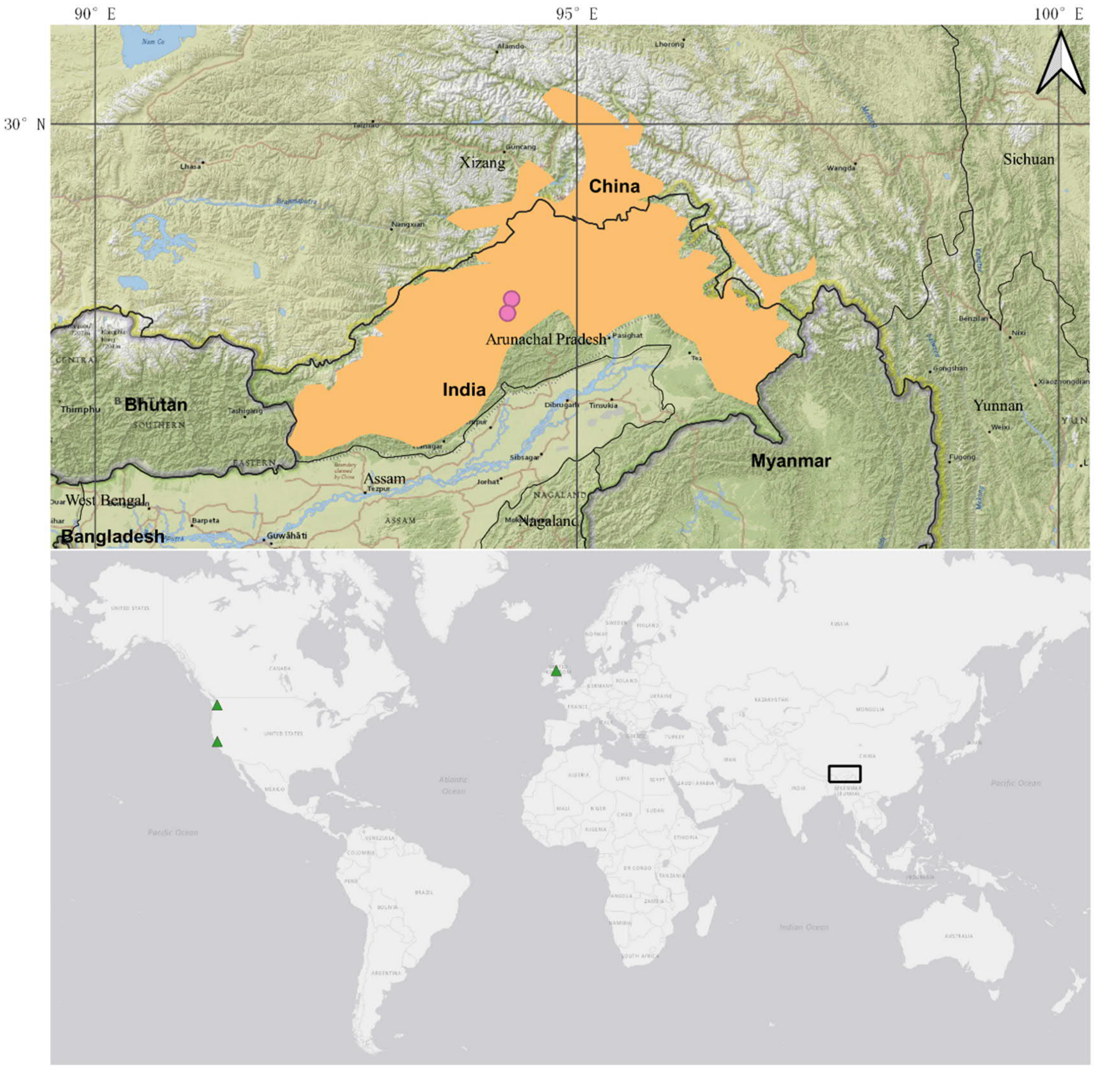


[*] Distribution in N Myanmar (Cullen, 1980, pp. 55–56) and India (Mirazam) (https://archive.nationalredlist.org/species-information/?speciesID=229666) is possible.

Rhododendron walongense Kingdon–Ward

IUCN Red List status: globally **VU** (Gibbs et al., 2011), LC in China (MEP–CAS, 2013)
Distribution: China (S Xizang), India (Arunachal Pradesh)
Altitude: 1,500–2,200 m

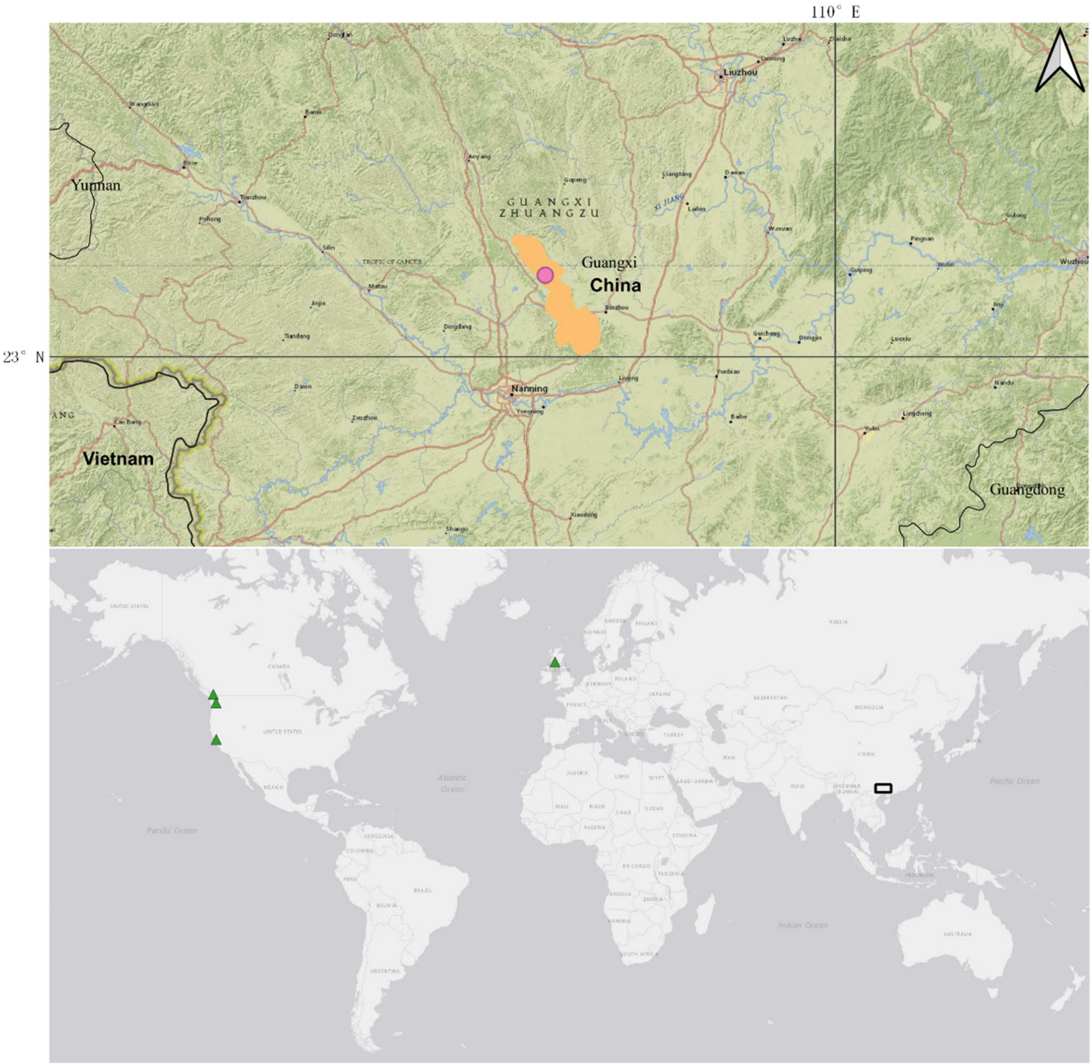
No. of *ex situ* sites/countries: 3/2
No. of (mapped) wild sources: (2) 2
No. of wild accessions: 5



Rhododendron wumingense W.P.Fang

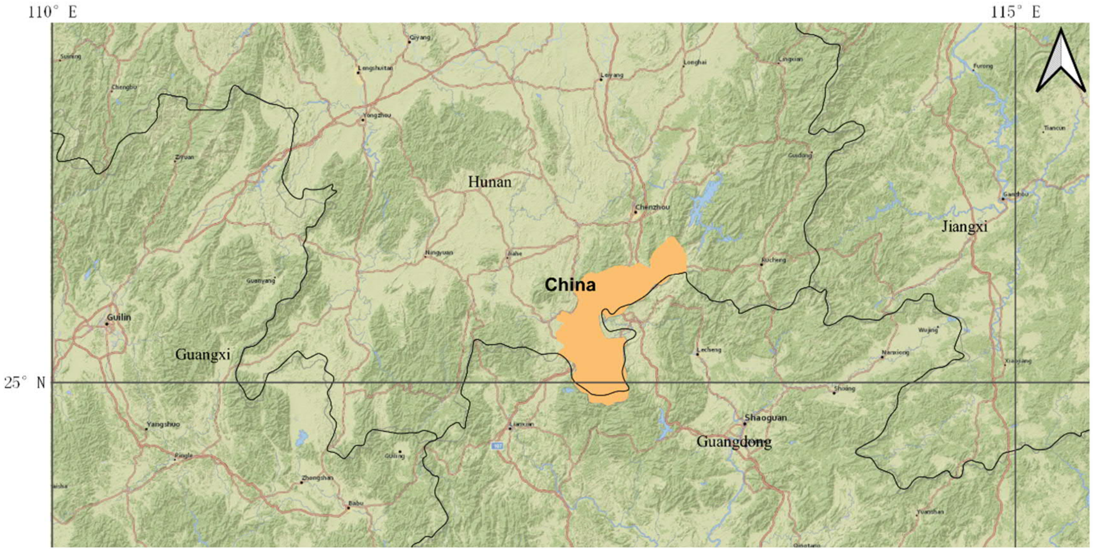
IUCN Red List status: **VU** (Gibbs et al., 2011, Qin et al., 2017)
Distribution: China (Wuming in central Guangxi)
Altitude: ca. 1,000 m

No. of *ex situ* sites/countries: 4/3
No. of (mapped) wild sources: (1) 3
No. of wild accessions: 21



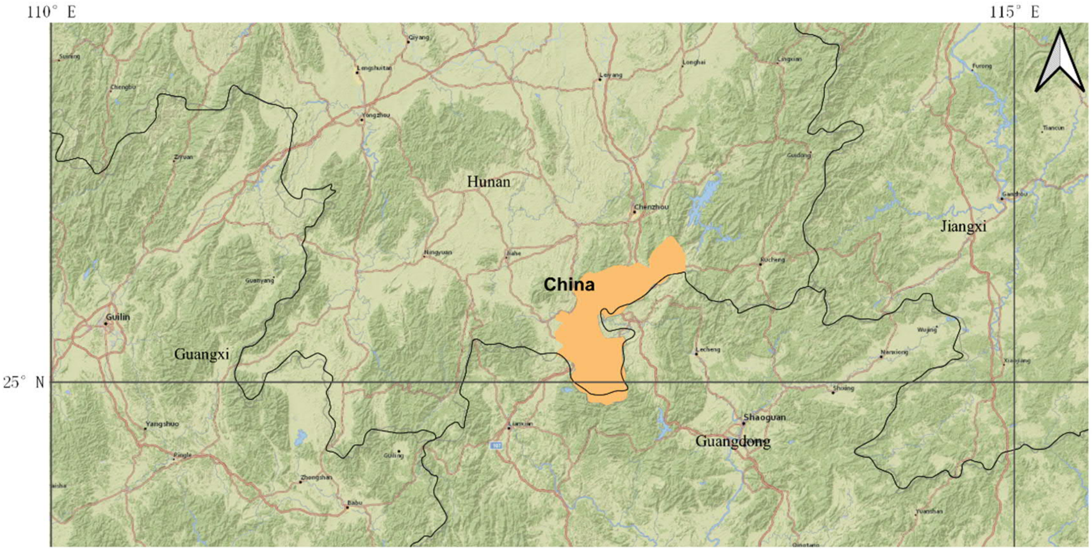
Rhododendron yaogangxianense Q.X.Liu

IUCN Red List status: **DD** (Gibbs et al., 2011, MEP–CAS, 2013)
Distribution: China (Yizhang in Hunan)
Altitude: ca. 1,100 m
Not in cultivation.



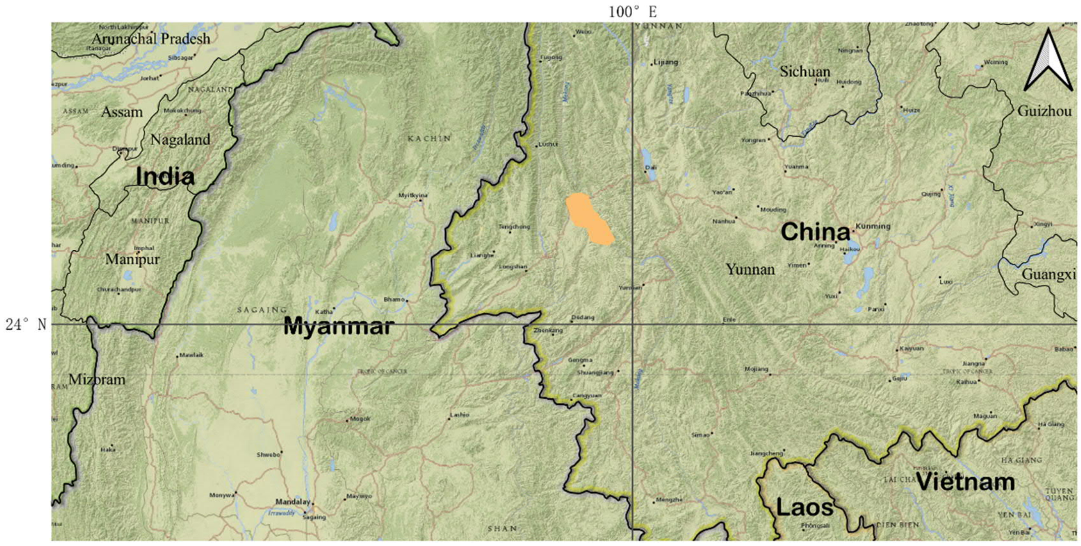
Rhododendron yizhangense Q.X.Liu

IUCN Red List status: **DD** (Gibbs et al., 2011, MEP–CAS, 2013)
Distribution: China (Yizhang in Hunan)
Altitude: ca. 1,600 m
Not in cultivation.



Rhododendron yungchangense Cullen

IUCN Red List status: globally DD (Gibbs et al., 2011), **LC** in China (MEP–CAS, 2013)
Distribution: China (W Yunnan)*
Altitude: 2,100–2,500 m
Not in cultivation.



*Lacking distribution data. This map shows the location where type specimen was collected (Davidian, 1982).

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Appendix II: Supplementary Files – Chapter 3

Table S3.1 Reported ploidy of taxa in *Rhododendron* L. (Ericaceae), $2n = 2x = 26$

Table S3.2 Ploidy estimation of taxa in subsection *Maddenia* in the present study, using flow cytometry

Table S3.3 Flow cytometry histograms of subsection *Maddenia* accessions with inconsistent ploidy in different runs

Table S3.4 Genome size measurements of *R. fortunei* Lindl. and *R. parryae* Hutch.

Table S3.1 Reported ploidy of taxa in *Rhododendron* L. (Ericaceae), $2n = 2x = 26$

1) Taxonomic classification (subgenus – section – subsection) followed Chamberlain et al. (1996) and Argent (2015) [1, 2]. For resolved names, non-vireya taxa were indexed according to Chamberlain et al. [1] while vireyas (subgenus Vireya, also known as section *Schistanthe*) followed Argent (2015) [2]. **2)** Data of horticultural cultivars that were studied previously are presented here (noted as ‘cultivation source’ in column ‘Resolved name’), but not included in our calculation of taxon numbers (Table 3.1 and Fig. 3.2), as our study focuses on ‘taxa’ which include species, subspecies and botanical varieties. **3)** Despite unresolved taxonomy, *R. vanderbiltianum* is included because of its suggested placement in subsection *Maddenia* [3-5]. **4)** Data in Cubey (2003) [6] are partially presented due to inaccessibility of the PhD thesis, with chromosome counts of subsection *Maddenia* included, but not subsection *Saluenensia*.

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (x)**	**Chromosome count ($2n$)**	**Reference**
unknown	unknown	unknown	*R. cunninghamii* T. Moore	*R.* 'Cunninghamii'? (cultivation source)		26	[7]
unknown	unknown	unknown	*R. cunninghamii* T. Moore (*R. cinnamomeum* C. Paxt.)	*R.* 'Cunninghamii'? (cultivation source)		26	[8]
unknown	unknown	unknown	*R. omurasaki*	*R.* o-murasaki ‘Makino’ (cultivation source)		26	[9]
unknown	unknown	unknown	*R. lateritium*	*R.* 'Lateritium' (cultivation source)		26	[10]
unknown	unknown	unknown	*R. praecox*	(cultivation source)		26	[10]
unknown	unknown	unknown	*R. viscosepalum*	(cultivation source)		26	[10]
Azaleastrum (1/11/38; 2 sections)	*Azaleastrum* (1/3/11)	\	*R. leptothrium* Balf. f. & Forrest	*R. leptothrium* Balf. & Forrest		26	[11, 12]
			R. ovatum (Lindley) Maximowicz	*R. ovatum* (Lindley) Maximowicz	4*x*		[13]
			R. vialii Delavay & Franch.	*R. vialii* Delavay & Franch.		26	[11]
	Choniastrum (0/8/27)	\	*R. championae* Hooker	*R. championae* Hooker	2*x*		[13]
			R. hancockii Hemsl.	*R. hancockii* Hemsl.		26	[11]
			R. amamiense Ohwi	*R. latoucheae* Franch.		26	[11]
			R. mackenzianum Forrest	*R. moulmainense* Hook.f.		26	[11]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (x)**	**Chromosome count ($2n$)**	**Reference**
			R. stamineum Franch.	*R. stamineum* Franch.		26	[11]
			R. truncatovarium L.M. Gao & D.Z. Li	*R. truncatovarium* L. M. Gao & D. Z. Li		26	[11]
			R. tutcherae Hemsl. & E.H. Wilson	*R. tutcherae* Hemsl. & E. H. Wilson		26	[11]
			R. tutcherae var. *glabrifolium* L.M. Gao & D.Z. Li	*R. tutcherae* var. *glabrifolium* L.M. Gao & D.Z. Li		26	[11]
Candidastrum (0/1/2)	\	\	*R. albiflorum*	*R. albiflorum* Hook.		26	[12]
Hymenanthes (7/149/(436 - 9 unplaced) = 7/149/427; 1 section - 24 subsections)	*Ponticum* [7/(148 + 1 diploid taxon unplaced for subsection)/427 = 7/149/427]	(unplaced)	*R. batemanii* Hook.	*R.* × *batemannii* Hook.f. (1863) (cultivation source)		26	[12]
		(unplaced)	*R. beimaense*	*R.* × *erythrocalyx* Balf.f. & Forrest (cultivation source)		26	[12]
		(unplaced)	*R. planetum*	*R. planetum* Balf.f.		26	[12]
		Arborea (1/4/17)	*R. arboreum* (ssp. *arboreum*) Smith	*R. arboreum* (ssp. *arboreum*) Smith	$2x$	26	[7, 8, 12, 13]
			R. zeylanicum	*R. arboreum* Sm. ssp. *zeylanicum* (Booth) Tagg		26	[12]
			R. silvaticum	*R. lanigerum* Tagg		26	[12]
			R. niveum Hook. f.	*R. niveum* Hook. f.	$6x$	26	[12, 14]
		Argyrophylla (0/7/31)	*R. adenopodum*	*R. adenopodum* Franch.		26	[12]
			R. argyrophyllum	*R. argyrophyllum* Franch.		26	[12]
			R. argyrophyllum ssp. *nankingense* (Cowan) Chamberlain	*R. argyrophyllum* ssp. *nankingense* (Cowan) Chamberlain	$2x$		[13]
			R. hunnewellianum	*R. hunnewellianum* Rehder & E.H.Wilson		26	[12]
			R. insigne	*R. insigne* Hemsl. & E.H.Wilson		26	[12]
			R. ririei Hemsley & Wilson	*R. ririei* Hemsley & Wilson	$2x$	26	[12, 13]
			R. thayerianum Rehder & Wilson	*R. thayerianum* Rehder & Wilson	$2x$	26	[12, 13]
		Auriculata (1/1/2)	*R. auriculatum* Hemsley	*R. auriculatum* Hemsley	$2x$, $4x$	26	[12, 13]
		Barbata (0/2/5)	*R. smithii* Nutt.	*R. argipeplum* Balf.f. & R.E.Cooper		26	[12]
			R. barbatum Wall. ex G. Don	*R. barbatum* Wall. ex G. Don		26	[8, 12]
		Campanulata (0/2/4)	*R. campanulatum* Don	*R. campanulatum* D. Don		26	[8, 12]
			R. wallichii /*R. campanulatum* var. *wallichii* Hook.	*R. wallichii* Hook.f.		26	[8, 12]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (*x*)**	**Chromosome count (2*n*)**	**Reference**
		Campylocarpa (0/6/10)	*R. callimorphum*/*R. cyclium*	*R. callimorphum* Balf.f. & W.W.Sm. (var. *callimorphum*)		26	[12]
			R. campylocarpum Hook. f.	*R. campylocarpum* Hook.		26	[12]
			R. campylocarpum ssp. *caloxanthum* /*R. caloxanthum*/*R. telopeum*	*R. campylocarpum* ssp. *caloxanthum* (Balfour & Farrer) Chamberlain	2*x*	26	[12, 13]
			R. souliei	*R. souliei* Franch.		26	[12]
			R. wardii/*R. croceum*/*R. litiense*	*R. wardii* W.W.Sm. (var. *wardii*)		26	[12]
			R. wardii var. *puralbum* (Balfour & Smith) Chamberlain	*R. wardii* var. *puralbum* (Balfour & Smith) Chamberlain	2*x*		[13]
		Falconera (1/9/17)	*R. decipiens* Lacaita	*R.* × *decipiens* Lacaita (cultivation source)	2*x*		[14]
			R. arizelum	*R. arizelum* Balf. & Forrest		26	[12]
			R. basilicum	*R. basilicum* Balf.f. & W.W.Sm.		26	[12]
			R. coriaceum	*R. coriaceum* Franch.		26	[12]
			R. falconeri Hook. f	*R. falconeri* Hook. f	2*x*	26	[12, 14]
			R. eximium Nutt.	*R. falconeri* Hook.f. ssp. *eximium* (Nutt.) D.F.Chamb.		26	[12]
			R. galactinum Tagg	*R. galactinum* Tagg	2*x*	26	[12, 13]
			R. hodgsonii Hook. f.	*R. hodgsonii* Hook.		26	[7, 8, 12]
			R. rex	*R. rex* H. Lév.		52	[15]
			R. fictolacteum	*R. rex* H. Lév. ssp. *fictolacteum* (Balf.f.) D.F.Chamb.		26	[12]
		Fortunea (1/11/51)	*R. calophytum*	*R. calophytum* Franch.		26	[12]
			R. decorum	*R. decorum* Franch.		26	[12]
			R. diaprepes/*R. decorum* ssp. *diaprepes* (Balfour & Smith) Ming	*R. decorum* ssp. *diaprepes* (Balfour & Smith) Ming	2*x*	26, 39	[13, 16]
			R. discolor	*R. fortunei* Lindl. ssp. *discolor* (Franch.) D.F.Chamb.		26	[12]
			R. fortunei	*R. fortunei* Lindl.	2*x*		[17]
			R. griffithianum Cooper	*R. griffithianum* Wight		26	[12]
			R. orbiculare	*R. orbiculare* Decne.		26	[12]
			R. oreodoxa	*R. oreodoxa* Franch.		26	[12]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (*x*)**	**Chromosome count (2*n*)**	**Reference**
			R. fargesii/*R. erubescens*	*R. oreodoxa* Franch. var. *fargesii* (Franch.) D.F.Chamb.		26	[12]
			R. praevernum Hutchinson	*R. praevernum* Hutchinson	2*x*	26	[12, 13]
			R. sutchuenense	*R. sutchuenense* Franch.		26	[12]
		Fulgensia (0/1/3)	*R. fulgens* Hook. f.	*R. fulgens* Hook. f.	2*x*	26	[12, 14]
		Fulva (0/3/4)	*R. fulvoides*	*R. fulvoides* Balf.f. & Forrest		26	[12]
			R. fulvum	*R. fulvum* Balf.f. & W.W.Sm.		26	[12]
			R. niphargum	*R. uvarifolium* Diels var. *uvarifolium*		26	[12]
		Glischra (0/5/11)	*R. crinigerum*	*R. crinigerum* Franch.		26	[12]
			R. diphrocalyx	*R. diphrocalyx* Balf.f.		26	[12]
			R. glischrum	*R. glischrum* Balf.f. & W.W.Sm.		26	[12]
			R. habrotrichum	*R. habrotrichum* Balf.f. & W.W.Sm.		26	[12]
			R. recurvoides Tagg & Kingdon-Ward	*R. recurvoides* Tagg & Kingdon-Ward	2*x*		[13]
		Grandia (0/9/17)	*R. grande Wight*	*R. grande* Wight	2*x*	26	[7, 8, 14, 18]
			R. macabeanum Watt.	*R. macabeanum* Watt ex Balf.f.	2*x*	26	[12, 13]
			R. montroseanum Davidian	*R. montroseanum* Davidian	2*x*		[13]
			R. coryphaeum	*R. praestans* Balf.f. & W.W.Sm.		26	[12]
			R. protistum Balfour & Forrest	*R. protistum* Balfour & Forrest	2*x*	26	[12, 13]
			R. giganteum	*R. protistum* Balfour & Forrest var. *gigantum* (Forrest ex Tagg) D.F.Chamb.		26	[12]
			R. sidereum	*R. sidereum* Balf.f.		[12]	[12]
			R. sinogrande	*R. sinogrande* Balf.f. & W.W.Sm.	2*x*	26	[12, 17]
			R. watsonii	*R. watsonii* Hemsl. & E.H.Wilson		26	[12]
		Griersonian a (0/1/1)	*R. griersonianum* Balfour & Forrest	*R. griersonianum* Balfour & Forrest	2*x*		[12, 13]
		Irrorata (0/7/33)	*R. aberconwayi*	*R. aberconwayi* Cowan		26	[12]
			R. annae Franchet/*R. hardingii*	*R. annae* Franchet	2*x*	26	[12, 13]
			R. araiophyllum	*R. araiophyllum* Balf. & W. W. Sm.		26	[12]
			R. hylothreptum	*R. anthosphaerum* Diels		26	[12]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (*x*)**	**Chromosome count (2*n*)**	**Reference**
			R. irroratum/*R. ningyuenense* (correction: *ninguenense*)	*R. irroratum* Franch. (ssp. *irroratum*)		26	[12]
			R. lukiangense/*R. cerasinum*	*R. lukiangense* Franch.		26	[12]
			R. shepherdii Nutt.	*R. kendrickii* Nutt.		26	[12]
		Lanata (0/1/9)	*R. lanatum* Hook. f	*R. lanatum* Hook.		26	[12]
		Maculifera (0/5/24)	*R. longesquamatum*	*R. longesquamatum* C.K.Schneid		26	[12]
			R. maculiferum	*R. maculiferum* Franch.		26	[12]
			R. morii	*R. morii* Hayata		26	[12]
			R. pachytrichum	*R. pachytrichum* Franch.		26	[12]
			R. strigillosum Franchet	*R. strigillosum* Franchet	2*x*	26	[12, 13]
		Neriiflora (1/19/50)	*R. aperantum*	*R. aperantum* Balf. & Kingdon-Ward		26	[12]
			R. beanianum	*R. beanianum* Cowan		26	[12]
			R. citriniflorum (var. *citriniflorum*)	*R. citriniflorum* Balf.f. & Forrest (var. *citriniflorum*)	4*x*	26	[12, 13]
			R. dichroanthum	*R. dichroanthum* Diels		26	[12]
			R. apodectum	*R. dichroanthum* Diels ssp. *apodectum* (Balf. & W. W. Sm.) Cowan		26	[12]
			R. scyphocalyx	*R. dichroanthum* Diels ssp. *scyphocalyx* (Balf.f. & Forrest) Cowan		26	[12]
			R. floccigerum	*R. floccigerum* Franch.		26	[12]
			R. repens	*R. forrestii* Balf.f. ex Diels ssp. *forrestii*		26	[12]
			R. haematodes	*R. haematodes* Franch.		26	[12]
			R. chaetomallum Balf. f & Forrest	*R. haematodes* subsp. *chaetomallum* (Balf. & Forrest) D. F. Chamb.		26	[12]
			R. mallotum	*R. mallotum* Balf.f. & Kingdon-Ward		26	[12]
			R. neriiflorum Franchet	*R. neriiflorum* Franchet	2*x*	26	[12, 13]
			R. euchaites	*R. neriiflorum* Franch. ssp. *neriiflorum*		26	[12]
			R. phaedropum	*R. neriiflorum* Franch. ssp. *phaedropum* (Balf.f. & Barrer) Tagg		26	[12]
			R. pocophorum	*R. pocophorum* Balf.f. ex Tagg		26	[12]
			R. sanguineum	*R. sanguineum* Franch.		26	[12]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. didymum	*R. sanguineum* Franch. ssp. *didymum* (Balf.f. & Forrest) Cowan		26	[12]
			R. haemaleum	*R. sanguineum* Franch. ssp. *sanguineum* var. *haemaleum* (Balf.f. & Forrest) D.F.Chamb.		26	[12]
			R. sperabile	*R. sperabile* Balf.f. & Farrer		26	[12]
		Parishia (0/3/8)	*R. elliottii Watt*	*R. elliottii* Watt ex Brandis	2*x*	26	[12, 13]
			R. facetum/*R. eriogynum*	*R. facetum* Balf.f. & Kingdon-ward		26	[12]
			R. kyawi (*R. prophantum*)	*R. kyawi* Lace & W.W.Sm.		26	[12]
		Pontica (1/18/20)	*R.* × *sochadzeae* Kharadze & Davlian.	*R. caucasicum* × *ponticum* (cultivation source)		26	[19]
			R. ungernii	*R. ungernii* Trautv.		26	[12]
			R. hyperythrum	*R. hyperythrum* Hayata		26	[12]
			R. makinoi	*R. makinoi* Tagg		26	[12]
			R. metternichii	*R. degronianum* Carrière ssp. *heptamerum* (Maxim.) H.Hara (Maxim.) Sealy		26	[12]
			R. yakushimanum	*R. degronianum* Carrière ssp. *yakushimanum* (Nakai) Kitam. var. *yakushimanum* (Nakai) Kitam.		26	[12]
			R. aureum Georgi	*R. aureum* Georgi		26, 52	[12, 20-27]
			R. brachycarpum	*R. brachycarpum* D.Don ex G.Don	2*x*	26	[12, 13, 28]
			R. fauriei	*R. brachycarpum* D.Don ex G.Don ssp. *fauriei* (Franch.) D.F.Chamb.		26	[12]
			R. catawbiense	*R. catawbiense* Michx.		24, 26	[10, 12, 29, 30]
			R. caucasicum Pall.	*R. caucasicum* Pall.		26	[12, 31]
			R. degronianum	*R. degronianum* Carrière		26	[12]
			R. degronianum ssp. *yakushimanum* (Nakai) Hara	*R. degronianum* ssp. *yakushimanum* (Nakai) Hara	2*x*		[13]
			R. obtusum 'Kaempferi'/*R. kaempferi*	*R. kaempferi* Planch.		26	[10, 12, 30]
			R. obtusum japonicum	*R. kiusianum* Makino var. *kiusianum*		26	[10, 30]
			R. macrophyllum/R. californicum	*R. macrophyllum* D. Don ex G. Don	2*x*	26	[12, 13, 32]
			R. maximum/R. purpureum	*R. maximum* L.	2*x*	24, 26	[10, 12, 17, 29, 30]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. ponticum/R. obtusum/R. speciosum	*R. ponticum* L.	2*x*	26	[9, 10, 12, 13, 17, 33]
			R. smirnowii Trautvetter	*R. smirnowii* Trautvetter	2*x*	26	[10, 13]
		Selensia (0/5/12)	*R. bainbridgeanum*	*R. bainbridgeanum* Tagg & Forrest		26	[12]
			R. martinianum	*R. martinianum* Balf.f. & Forrest		26	[12]
			R. selense (ssp. *probum*)	*R. selense* Franch. (ssp. *selense*)		26	[12]
			R. rhaibocarpum	*R. selense* Franch. ssp. *dasycladum* (Balf.f. & W.W.Sm.) D.F.Chamb.		26	[12]
			R. selense ssp. *jucundum* (Balfour & Smith) Chamberlain	*R. selense* Franch. ssp. *jucundum* (Balfour & Smith) Chamberlain	2*x*		[13]
		Taliensia (0/19/75)	*R. adenophorum*	*R. adenogynum* Diels		26	[12]
			R. aganniphum	*R. aganniphum* Balf.f. & Kingdon-Ward		26	[12]
			R. flavorufum	*R. aganniphum* Balf.f. & Kingdon-Ward var. *flavorufum* (Balf.f. & Forrest) D.F.Chamb.		26	[12]
			R. alutaceum var. *iodes* (Balfour & Forrest) Chamberlain	*R. alutaceum* var. *iodes* (Balfour & Forrest) Chamberlain	2*x*		[13]
			R. tritifolium	*R. alutaceum* var. *russotinctum* (Balfour & Forrest) Chamberlain		26	[12]
			R. balfourianum	*R. balfourianum* Diels		26	[12]
			R. bathyphyllum	*R. bathyphyllum* Balf.f & Forrest		26	[12]
			R. beesianum	*R. beesianum* Diels		26	[12]
			R. bureavii	*R. bureavii* Franch.		26	[12]
			R. dumicola	*R. dumicola* Tagg & Forrest		26	[12]
			R. lacteum	*R. lacteum* Franch.		26	[12]
			R. mimetes var. *simulans*	*R. mimetes* Tagg & Forrest var. *simulans* Tagg & Forrest		26	[12]
			R. prattii	*R. prattii* Franch.		26	[12]
			R. roxieanum	*R. roxieanum* Forrest		26	[12]
			R. traillianum	*R. traillianum* Forrest & W.W.Sm.		26	[12]
			R. vellereum	*R. principis* Bureau & Franch.		26	[12]
			R. wasonii Hemsley & Wilson	*R. wasonii* Hemsley & Wilson	2*x*	26	[12, 13]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (*x*)**	**Chromosome count (2*n*)**	**Reference**
			R. wightii Hook. f.	*R. wightii* Hook.		26	[12]
			R. wiltonii	*R. wiltonii* Hemsl. & E.H.Wilson		26	[12]
		Thomsonia (0/9/20)	*R. cyanocarpum*	*R. cyanocarpum* (Franch.) W.W.Sm.		26	[12]
			R. eclecteum	*R. eclecteum* Balf.f. & Forrest		26	[12]
			R. sikkimense Pradhan & Lachungpa	*R.* × *sikkimense* Pradhan & Lachungpa (1990) (cultivation source)	2*x*		[14]
			R. hookeri Nutt. aff.	*R. hookeri* Nutt. aff.		26	[12]
			R. hylaeum Balfour & Farrer	*R. hylaeum* Balfour & Farrer	2*x*		[13]
			R. meddianum	*R. meddianum* Forrest		26	[12]
			R. sherriffii Cowan	*R. sherriffii* Cowan	2*x*	26	[12, 13]
			R. stewartianum	*R. stewartianum* Diels		26	[12]
			R. thomsonii	*R. thomsonii* Hook.f.		26	[12]
			R. thomsonii ssp. *lopsangianum* Hooker	*R. thomsonii* ssp. *lopsangianum* Hooker	2*x*		[13]
		Venatora (0/1/1)	*R. venator* Tagg	*R. venator* Tagg	2*x*	26	[12, 13]
		Williamsiana (1/1/2)	*R. williamsianum* Rehder & Wilson	*R. williamsianum* Rehder & Wilson	4*x*	26	[12, 13]
Mumeazalea (0/1/1)	\	\	*R. semibarbatum* Maximowicz	*R. semibarbatum* Maximowicz	2*x*	26	[12, 13]
Pentanthera (11/29/41; 4 sections)	*Pentanthera* (7/20/20)	\	*R. bakeri*	*R.* × *bakeri* (Lemmon & McKay) Hume (1948) (cultivation source)		26	[33]
			R. alabamense	*R. alabamense* Rehder	2*x*	26	[12, 17, 33-35]
			R. arborescens	*R. arborescens* (Pursh) Torr.	2*x*	24, 26	[10, 12, 13, 17, 29, 30, 33-35]
			R. atlanticum (Ashe) Rehd.	*R. atlanticum* (Ashe) Rehder	3*x*, 4*x*	26	[12, 13, 17, 30, 34, 35]
			R. austrinum	*R. austrinum* (Small) Rehder	2*x*, 3*x*, 4*x*	26	[13, 17, 33-35]
			R. calendulaceum	*R. calendulaceum* (Michx.) Torr.	3*x*, 4*x*	24, 52	[10, 12, 16, 17, 29, 30, 33, 35]
			R. canescens/R. roseum	*R. canescens* (Michx.) Sweet	2*x*	26	[10, 12, 13, 30, 33, 35]
			R. colemanii R. Miller	*R. colemanii* R. Miller	4*x*		[35]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. cumberlandense	*R. cumberlandense* E. L. Braun	2*x*	26	[13, 17, 33, 35]
			R. eastmanii	*R. eastmanii* Kron & Creel	2*x*		[17, 35]
			R. flammeum	*R. flammeum* (Michx.) Sarg.	2*x*, 4*x*	26	[17, 32, 35]
			R. japonicum/R. metternichii	*R. japonicum*		26	[10, 12, 30]
			R. luteum Sweet/*R. flavum* G. Don	*R. luteum* Sweet	4*x*	26	[10, 12, 13, 35, 36]
			R. molle	*R. molle* (Blume) G.Don	2*x*	26	[10, 12, 35]
			R. mortieri	*R.* × *mortieri* (Sweet) ? (*R. calendulaceum* × *periclymenoides*) (cultivation source)		26	[10]
			R. japonicum Sur.	*R. molle* (Blume) G.Don ssp. *japonicum* (A.Gray) Kron		26	[37]
			R. occidentale	*R. occidentale* (Torr. & A. Gray) A. Gray	2*x*	26, 52, 78	[10, 12, 13, 17, 32, 35, 38]
			R. periclymenoides/R. nudiflorum	*R. periclymenoides* (Michx.) Shinners	2*x*	26	[12, 13, 17, 33, 35]
			R. prinophyllum	*R. prinophyllum* (Small) Millais	2*x*	26	[13, 17, 35]
			R. prunifolium	*R. prunifolium* (Small) Millais	2*x*	26	[12, 13, 17, 33, 35]
			R. serrulatum	*R. serrulatum* (Small) Millais	2*x*	26	[12, 17]
			R. viscosum/R. oblongifolium/R. serrulatum	*R. viscosum* (L.) Torr.	2*x*	26	[10, 12, 13, 17, 30, 33, 35]
	Rhodora (1/2/2)	\	*R. canadense*	*R. canadense* (L.) Torr.	2*x*	52	[10, 12, 13, 16, 30, 35, 39]
			R. vaseyi	*R. vaseyi* A. Gray	2*x*	26	[10, 12, 13, 17, 30]
	Sciadorhodion (3/6/18)	\	*R. albrechtii*	*R. albrechtii* Maxim.	2*x*	26	[12, 13, 34]
			R. benhallii Craven var. *purpurea* (*Menziesia ciliicalyx* var. *purpurea*)	*R. benhallii* Craven var. *purpurea* (*Menziesia ciliicalyx* var. *purpurea*)	4*x*		[13]
			R. pentaphyllum	*R. pentaphyllum* Maxim.		26	[12]
			R. pilosum Craven (*Menziesia pilosa* (Michaux) Juspieu)	*R. pilosum* (Michx.) Craven	4*x*		[13]
			R. quinquefolium	*R. quinquefolium* Bisset & S.Moore		26	[12]
			R. schlippenbachii	*R. schlippenbachii* Maxim.	2*x*, 3*x*	26	[9, 10, 12, 13, 25, 28, 30]
	Viscidula (0/1/1)	\	*R. nipponicum*	*R. nipponicum* Matsum.		26	[12]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
Rhododendron (57/159/309; 2 sections)	*Pogonanthum* (1/8/26)	\	*R. anthopogon* D. Don	*R. anthopogon* D. Don	2*x*	26	[12, 13]
		\	*R. adamsii* Rehder	*R. fragrans* (Adams) Maxim.	3*x*	26, 55-58	[28, 40-43]
		\	*R. cephalanthum/R. crebreflorum*	*R. cephalanthum* Franch. (ssp. *cephalanthum*)		26	[12]
		\	*R. kongboense*	*R. kongboense* Hutch.		26	[12]
		\	*R. sargentianum*	*R. sargentianum* Rehder & E.H.Wilson		26	[12]
		\	*R. temoense*	*R. laudandum* Cowan var. *temoense* Kingdon-Ward ex Cowan & Davidian		26	[12]
		\	*R. trichostomum/R. ledoides/R. radinum/R. sphaeranthum*	*R. trichostomum* Franch.		26	[12]
		\	*R. tsarongense*	*R. primuliflorum* Bureau & Franch.		26	[12]
	Rhododendron [56/151/(287 - 4 unplaced) = 56/151/283; 28 subsections]	*Baileya* (1/1/1)	*R. baileyi*	*R. baileyi* Balf.f.	2*x*	52	[12, 13]
		Boothia (0/4/8)	*R. boothii* Nutt.	*R. boothii* Nutt.		26	[12]
			R. chrysodoron	*R. chrysodoron* Tagg ex Hutch.		26	[12]
			R. leucaspis Tagg	*R. leucaspis* Tagg	2*x*	26	[12, 13]
			R. megeratum	*R. megeratum* Balf.f.		26	[12]
		Camelliiflora (0/1/1)	*R. lucidum* Nutt./*R. camelliiflorum* Hook. f	*R. camelliiflorum* Hook.		26	[12]
		Campylogyna (0/1/2)	*R. campylogynum/R. myrtilloides*	*R. campylogynum* Franch.		26	[12]
		Caroliniana (0/1/2)	*R. minus/R. carolinianum*	*R. minus Michx.*	2*x*	24, 26	[10, 12, 13, 29, 30, 32]
		Cinnabarina (3/3/8)	*R. cinnabarinum* Hook. f. (var. *roylei;* var. *blandfordiaeflorum)*	*R. cinnabarinum* Hook. (ssp. *cinnabarinum*)	6*x*	78	[12, 13, 16]
			R. xanthocodon/R. concatenans	*R. cinnabarinum* Hook.f. ssp. *xanthocodon* (Hutch.) (Ref: Cullen, 1980)		78	[12, 16]
			R. keysii Nutt.	*R. keysii* Nutt.		78	[12]
		Edgeworthia (0/3/3)	*R. edgeworthii* Hook. f./*R. bullatum*	*R. edgeworthii* Hook.		26	[12]
			R. pendulam Hook. f.	*R. pendulum* Hook. f.	2*x*	26	[12-14]
			R. seinghkuense	*R. seinghkuense* Kingdon-Ward		26	[12]
		Genestieriana (0/1/1)	*R. genestierianum* Forrest	*R. genestierianum* Forrest	2*x*		[13]
			R. brachyanthum	*R. brachyanthum* Franch.		26	[12]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
		Glauca (1/8/11)	*R. charitostreptum*/*R. hypolepidotum*	*R. brachyanthum* Franch. ssp. *hypolepidotum* (Franch.) Cullen		26	[12]
			R. charitopes	*R. charitopes* Balf.f. & Farrer		26	[12]
			R. charitopes ssp. *tsangpoense*/*R. tsangpoense*	*R. charitopes* Balf.f. & Farrer ssp. *tsangpoense* (Kingdon-Ward) Cullen	2*x*	52	[12, 13, 16]
			R. curvistylum	*R. charitopes* ssp. *tsangpoense* (Kindon-Ward) Cullen × *campylogynum* Franch.		26	[12]
			R. glaucophyllum	*R. glaucophyllum* Rehder		26	[12]
			R. glaucum Hook. f.	*R. glaucophyllum* Rehder ssp. *glaucophyllum* var. *glaucophyllum*		26	[12]
			R. pruniflorum	*R. pruniflorum* Hutch.		26	[12]
		Heliolepida (4/4/8)	*R. bracteatum* Rehder & Wilson	*R. bracteatum* Rehder & Wilson	6*x*		[13]
			R. heliolepis/*R. aporinum*(correction: *R. oporinum*)/*R. heliolepis* var. *fumidum* (Balfour & Smith) Fang	*R. heliolepis* Franch. (var. *heliolepis*)	6*x*	52, 78	[12, 13, 16]
			R. brevistylum/*R. pholidotum*	*R. heliolepis* Franch. var. *brevistylum* (Franch.) Cullen		52, 104	[12, 16]
			R. rubiginosum/*R. desquamatum*	*R. rubiginosum* Franch.	6*x*	52, 78	[12, 13, 16]
		Lapponica (17/27/52)	*R. capitatum*	*R. capitatum* Maxim.		52	[12, 16]
			R. complexum	*R. complexum* Balf. & W. W. Sm.		78	[12, 16]
			R. cuneatum/*R. ravum*	*R. cuneatum* W. W. Sm.	6*x*	52, 78	[12, 13, 16]
			R. dasypetalum	*R. dasypetalum* Balf. & Forrest		52	[12, 16]
			R. edgarianum	*R. edgarianum* Rehder & E. H. Wilson		52	[12, 16]
			R. fastigiatum	*R. fastigiatum* Franch.		26, 52	[12, 16]
			R. flavidum	*R. flavidum* Franch.		26, 52, 78	[12, 16]
			R. fimbriatum	*R. hippophaeoides* Balf.f. & W.W.Sm. var. *hippophaeoides*		26	[12]
			R. hippophaeoides	*R. hippophaeoides* Balf.f. & W.W.Sm.		26	[12]
			R. impeditum/*R. litangense*	*R. impeditum* Balf.f. & W.W.Sm.		26	[12]
			R. intricatum	*R. intricatum* Franch.		26, 52	[12, 16]
			R. lapponicum (L.) Wahlenb./*R. parvifolium* Adams/*R. parvifolium* Adams subsp. *alpinum* (Glehn) Dostalek	*R. lapponicum* (L.) Wahlenb.	2*x*	26, 52	[12, 16, 28, 43-49]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. lysolepsis	*R.* × *lysolepsis* Hutch. (1930) = *R. flavidum* × ? (cultivation source)		26, 52	[12, 16]
			R. ramosissimum/R. violaceum/R. stictophyllum	*R. nivale* subsp. *boreale* Philipson & M. N. Philipson		26, 52	[12, 16]
			R. paludosum	*R. nivale* Hook.f. ssp. *nivale*		26	[12]
			R. orthocladum	*R. orthocladum* Balf.f. & Forrest		26	[12]
			R. microleucum	*R. orthocladum* Balf.f. & Forrest var. *microleucum* (Hutch.) M.N.Philipson & Philipson		26	[12]
			R. polycladum Franchet/*R. scintillans/R. compactum*	*R. polycladum* Franchet	2*x*	26, 52	[12, 13]
			R. rupicola/R. achroanthum	*R. rupicola* W. W. Sm.		26, 52	[12, 16]
			R. chryseum	*R. rupicola* W.W.Sm. var. *chryseum* (Balf.f. & Kingdon-Ward) M.N.Philipson & Philipson		26	[12]
			R. russatum	*R. russatum* Balf. & Forrest		39, 52	[12, 16]
			R. setosum D. Don	*R. setosum* D. Don	2*x*	26	[12-14]
			R. tapetiforme	*R. tapetiforme* Balf. & Kingdon-Ward	4*x*	78	[12, 13, 16]
			R. drumonium/R. idoneum	*R. telmateium* Balf. & W. W. Sm.		26, 52, 78	[12, 16]
			R. polifolium/R. spilanthum	*R. thymifolium* Maxim.		26	[12]
			R. websterianum	*R. websteranum* Rehder & E.H.Wilson		26	[12]
			R. yungningense/R. glomerulatum	*R. yungningense* Balf. ex Hutch.		26, 52	[12, 16]
		Ledum (1/3/8)	*R. columbianum*	*R. columbianum* (Piper) Harmaja		26	[32]
			R. groenlandicum	*R. groenlandicum* (Oeder) Kron & Judd		26	[32]
			R. tomentosum	*R. tomentosum* (Stokes) Harmaja	4*x*	26,52	[13, 32, 50]
		Lepidota (0/1/5)	*R. lepidotum* Wall. ex G. Don/*R. obovatum* Hook. f	*R. lepidotum* Wall. ex G. Don		26	[12]
		Maddenia (4/39/65)	*R. burmanicum*	*R. burmanicum* Hutch.		26	[6]
			R. carneum Hutchinson	*R. carneum* Hutchinson	4*x*	26	[6, 12, 13]
			R. ciliatum Hook. f.	*R. ciliatum* Hook.		26	[6, 10, 12]
			R. ciliicalyx	*R. ciliicalyx* Franch.		26	[6, 12]
			R. coxianum	*R. coxianum* Davidian		26	[6]

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			R. crenulatum	*R. crenulatum* Hutch. ex Sleumer		26	[6]
			R. cuffeanum	*R. cuffeanum* Hutch.		26	[12]
			R. dalhousiae Hooker (var. *dalhousiae*)	*R. dalhousiae* Hooker (var. *dalhousiae*)	2*x*	26	[6, 12, 13]
			R. dalhousiae var. *rhabdotum*	*R. dalhousiae* Hook.f. var. *rhabdotum* (Baff.f. & R.E.Cooper) Cullen		26	[6]
			R. dendricola	*R. dendricola* Hutch.		26	[6, 12]
			R. excellens	*R. excellens* Hemsl. & E.H.Wilson		26	[6]
			R. fletcheranum	*R. fletcherianum* Davidian		26	[6]
			R. fleuryi	*R. fleuryi* Dop		26	[6]
			R. formosum Wall.	*R. formosum* Wall.		26	[6, 12]
			R. inaequale	*R. formosum* Wall. var. *inaequale* (Hutch.) Cullen		26	[6, 12]
			R. formosum var. *iteophyllum*	*R. iteophyllum* Hutch.		c.26	[6]
			R. horlickianum	*R. horlickianum* Davidian		26	[6]
			R. johnstoneanum Watt.	*R. johnstoneanum* Watt ex Hutch.		26	[6, 12]
			R. leptocladon	*R. leptocladon* Dop		26	[6]
			R. liliiflorum	*R. liliiflorum* H.Lév.		26	[6]
			R. lindleyi Moore	*R. lindleyi* Moore	2*x*	26	[6, 12, 13]
			R. ludwigianum	*R. ludwigianum* Hosseus		26	[6]
			R. lyi	*R. lyi* H.Lév.		26	[6, 12, 51]
			R. maddenii (ssp. *maddenii*)/*R. polyandrum* Hutch./*R. calophyllum* Nutt.	*R. maddenii* Hook. f. (ssp. *maddenii*)	2*x*, 6*x*, 8*x*	26, 52, 78	[6, 12-14, 16, 17]
			R. maddenii ssp. *crassum*/R. *crassum*/R. *manipurense*	*R. maddenii* Hook.f. ssp. *crassum* (Franch.) Cullen	6*x*, 8*x*	52, 78, 104, 156	[6, 12, 16, 17]
			R. megacalyx	*R. megacalyx* Balf.f.		26	[6, 12]
			R. nuttallii	*R. nuttallii* Booth		26	[6, 12]
			R. parryae Hutch.	*R. parryae* Hutch.		26	[6, 12]
			R. pachypodum/R. *scottianum*/R. *supranubium*	*R. pachypodum* Balf.f. & W.W.Sm.		26	[6, 12]
			R. roseatum	*R. roseatum* Hutch.		26	[6]

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			R. scopulorum	*R. scopulorum* Hutch.		26	[6, 12]
			R. sinonuttallii	*R. sinonuttallii* Balf.f. & Forrest		26	[6]
			R. taggianum	*R. taggianum* Hutch.		26	[12]
			R. taronense	*R. taronense* Hutch.		c.104	[6]
			R. valentinianum	*R. valentinianum* Forrest ex. Hutch.		26	[6, 12]
			R. vanderbiltianum Merr.	*R. vanderbiltianum* Merr.		26	[52]
			R. veitchianum/*R. cubittii*	*R. veitchianum* Hook.f.		26	[6, 12]
			R. walongense	*R. walongense* Kingdon-Ward		26	[6]
			R. yungchangense	*R. yungchangense* Cullen		26	[6]
		Micrantha (0/1/3)	*R. micranthum* Turczaninow	*R. micranthum* Turcz.	2*x*	26	[12, 13]
		Monantha (0/1/4)	*R. flavantherum*	*R. flavantherum* Hutch. & Kingdon-Ward		26	[12]
		Moupinensia (0/1/3)	*R. moupinense* Franchet	*R. moupinense* Franchet	2*x*	26	[12, 13]
		Rhododendron (0/3/3)	*R. ferrugineum* L.	*R. ferrugineum* L.	2*x*	26	[10, 12, 13]
			R. hirsutum L.	*R. hirsutum* L.	2*x*	26	[12, 13, 53]
			R. kotschyi Simonk.	*R. myrtifolium* Schott & Kotschy		26	[54]
		Rhodorastra (4/4/7)	*R. da(h)uricum* L.	*R. dauricum* L.	3*x*	26	[10, 12, 20, 27, 30, 55]
			R. ledebourii	*R. ledebourii* Pojark.	3*x*		[55]
			R. mucronulatum Turcz.	*R. mucronulatum* Turcz.	4*x*, 5*x*	26	[10, 12, 13, 20, 55]
			R. sichotense Pojark.	*R. sichotense* Pojark.	2*x*, 6*x*	26	[13, 20, 25, 27, 55]
		Saluenensia (4/6/8)	*R. calostrotum*	*R. calostrotum* Balf.f. & Kingdon-Ward		26	[12]
			R. keleticum/*R. radicans*	*R. calostrotum* Balf.f. & Kingdon-Ward ssp. *keleticum* (Balf.f. & Forrest) Cullen		26	[12]
			R. calciphilum/*R. riparium* Ward/*R. nitens*	*R. calostrotum* Balf.f. & Kingdon-Ward ssp. *riparium* (Kingdon-Ward) Cullen		26, 52	[12, 16]
			R. saluenense	*R. saluenense* Franch.		26, 52	[12, 16]
			R. cosmetum/*R. chameunum*/*R. charidotes*	*R. saluenense* Franch. ssp. *chameunum* (Balf.f. & Forrest) Cullen		26, 52	[12, 16]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. prostratum	*R. saluenense* var. *prostratum* (W. W. Sm.) R. C. Fang		52	[12, 16]
		Scabrifolia (0/7/11)	*R. hemitrichotum*	*R. hemitrichotum* Balf.f. & Forrest		26	[12]
			R. mollicomum	*R. mollicomum* Balf.f.& W.W.Sm.		26	[12]
			R. pubescens	*R. pubescens* Balf.f. & Forrest		26	[12]
			R. racemosum Franchet	*R. racemosum* Franchet	2*x*	26	[12, 13]
			R. scabrifolium	*R. scabrifolium* Franch.		26	[12]
			R. spiciferum Franchet	*R. spiciferum* Franchet	2*x*	26	[12, 13]
			R. spinuliferum Franchet	*R. spinuliferum* Franchet	2*x*	26	[12, 13]
		Tephropepla (0/3/10)	*R. auritum* Tagg	*R. auritum* Tagg	2*x*	26	[12, 13]
			R. tephropeplum	*R. tephropeplum* Balf.f. & Farrer		26	[12]
			R. xanthostephanum Merrill	*R. xanthostephanum* Merrill	2*x*	26	[12, 13]
		Triflora (16/22/40)	*R. ambiguum* Hemsl.	*R. ambiguum* Hemsl.	6*x*	52	[12, 13, 16]
			R. amesiae	*R. amesiae* Rehder & E. H. Wilson	4*x*	52	[12, 13]
			R. augustinii	*R. augustinii* Hemsl.	4*x*	52	[12, 16, 17]
			R. augustinii ssp. chasmanthum Cullen/*R. chasmanthum*	*R. augustinii* ssp. *chasmanthum* Cullen/*R. chasmanthum*	4*x*	52	[12, 13, 16]
			R. concinnum/R. pseudoyanthinum	*R. concinnum* Hemsl.	2*x*, 6*x*	52	[12, 13, 16]
			R. davidsonianum/R. charianthum	*R. davidsonianum* Rehder & E. H. Wilson	4*x*	52, 78	[12, 13, 16]
			R. keiskei Miquel	*R. keiskei* Miquel	2*x*	26	[10, 12, 13]
			R. keiskei var. *hypoglaucum*	*R. keiskei* Miq. var. *hypoglaucum* Sutô & Suzuki		26	[56]
			R. lutescens Franchet	*R. lutescens* Franchet	2*x*	26	[12, 13]
			R. oreotrephis/R. artosquamatum/R. exquisitum/R. timeteum	*R. oreotrephes* W. W. Sm.		52,78	[12, 16]
			R. pleistanthum Balfour ex Wilding	*R. pleistanthum* Balfour ex Wilding	4*x*		[13]
			R. polylepis Franchet	*R. polylepis* Franchet	2*x*	26	[12, 13]
			R. searsiae	*R. searsiae* Rehder & E. H. Wilson		52	[12, 16]
			R. siderophyllum Franch.	*R. siderophyllum* Franch.	6*x*	78	[12, 13, 16]
			R. trichanthum Rehder	*R. trichanthum* Rehder	6*x*		[13]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. triflorum Hook. f.	*R. triflorum* Hook. f.	2*x*, 6*x*	26	[12-14]
			R. bauhiniiflorum Watt. ex Hutch	*R. triflorum* var. *bauhiniiflorum* (Watt) C. I. Cullen & D. F. Chamb.		26	[12]
			R. yunnanense/R. aechmophyllum/R. chartophyllum/R. suberosum	*R. yunnanense* Franch.	4*x*	26, 52, 78	[12, 13, 16]
			R. zaleucum	*R. zaleucum* Balf. & W. W. Sm.		52	[12, 16]
			R. zaleucum var. *flaviflorum* Balfour & Smith	*R. zaleucum* var. *flaviflorum* Balfour & Smith	2*x*		[13]
			R. rigidum Franchet	*R. rigidum* Franchet	4*x*	26	[12, 13]
			R. tatsienense Franchet	*R. tatsienense* Franchet	6*x*		[13]
		Trichoclada (0/2/9)	*R. chloranthum*	*R. mekongense* var. *melinanthum* (Balf.f. & Kingdon-Ward) Cullen		26	[12]
			R. trichocladum	*R. trichocladum* Franch.		26	[12]
		Uniflora (1/2/5)	*R. imperator*	*R. uniflorum* Hutch. & Kingdon-Ward var. *imperator* (Kingdon-ward) Cullen		26	[12]
			R. pemakoense/R. patulum	*R. pemakoense* Kingdon-Ward		26, 52	[12, 16]
		Virgata (0/2/3)	*R. oleifolium*	*R. virgatum* Hook.f. ssp. *oleifolium* (Franch.) Cullen		26	[12]
			R. virgatum Hook. f.	*R. virgatum* Hook.		26	[12]
Therorhodion (0/3/3)	\	\	*R. camtschaticum* Pall. (ssp. *camtschaticum*)	*R. camtschaticum* Pall. (ssp. *camtschaticum*)	2*x*	24, 26	[12, 13, 39, 57-59]
			Therorhodion glandulosum	*R. camtschaticum* var. *glandulosum* (Standl.) B. Boivin		24,26	[32]
			R. redowskianum Maxim.	*R. redowskianum Maxim.*		26	[40]
Tsutsusi (0/22/148; 2 sections)	*Brachycalyx* (0/5/34)	\	*R. amagianum*	*R. amagianum* (Makino) Makino ex H. Hara		26	[12]
			R. dilatatum Miquel	*R. dilatatum* Miquel	2*x*		[13]
			R. mariesii	*R. mariesii* Hemsl. & E.H.Wilson		26	[12]
			R. reticulatum	*R. reticulatum* D.Don (1834)		26	[10, 12, 30]
			R. weyrichii	*R. weyrichii* Maxim.		26	[12]
	Tsutsusi (0/17/114)	\	*R. eriocarpum* (Hayata) Nakai/*R. phoeniceum* var. *eriocarpum*	*R. eriocarpum* (Hayata) Nakai	2*x*	26	[12, 13]
			R. indicum/R. macranthum G. Don/*R. eriocarpum*	*R. indicum* (L.) Sweet	2*x*	26	[9, 10, 12, 60, 61]
			R. pulchrum	*R. indicum* × 'Ledifolia' (cultivation source)		26	[12]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
			R. kaempferi	*R. kaempferi* Planch.	2*x*	26	[9, 13]
			R. kiusianum	*R. kiusianum* Makino	2*x*	26	[9, 60]
			R. mucronatum/R. ledifolium	*R. mucronatum* (Blume) G.Don	2*x*	26	[10, 12, 60]
			R. mucronatum (Blume) G. Don var. *ripense* (Makino) Wilson	*R. mucronatum* (Blume) G. Don var. *ripense* (Makino) Wilson	2*x*		[13]
			R. nakaharai Hay	*R. nakaharai* Hayata		26	[62]
			R. noriakianum	*R. noriakianum* Suzuki	2*x*		[60]
			R. oldhamii Maximowicz	*R. oldhamii* Maximowicz	2*x*	26	[12, 13]
			R. scabrum	*R. scabrum* G.Don	2*x*		[60]
			R. simsii Planch.	*R. simsii* Planch.	2*x*	26	[60, 63]
			R. linearifolium (var. *macrosepalum*)/*R. hortense*	*R. stenopetalum* (Hogg) Mabb.		26	[10, 12]
			R. stenopetalum 'Linearifolium'	*R. stenopetalum* (Hogg) Mabb. 'Linearifolium' (cultivation source)	2*x*	26	[12, 17]
			R. tashiroi Maximowicz	*R. tashiroi* Maximowicz	2*x*		[13]
			R. tosaense	*R. tosaense* Makino		26	[12]
			R. tschonoskii	*R. tschonoskii* Maxim.		26	[12]
			R. yedoense	*R. yedoense* Maxim.		26	[10, 12]
			R. yedoense poukhanense	*R. yedoense* var. *poukhanense* (H.Lév.) Nakai		26	[30]
Vireya (16/49/407; 7 sections)	*Albovireya* (1/2/16)	\	*R. aequabile* J.J. Sm.	*R. aequabile* J. J. Sm.		26	[51, 52]
			R. album Blume	*R. album* Blume	4*x*	26	[13, 52]
	Discovireya (0/4/41)	\	*R. cuneifolium* Stapf	*R. cuneifolium* Stapf		c.26	[52]
			R. gaultheriifolium J.J.S.	*R. gaultheriifolium* J. J. Sm.		26	[51]
			R. quadrasianum Vidal	*R. quadrasianum* S. Vidal		26	[52]
			R. retusum	*R. retusum* (Blume) Benn.	2*x*	26	[12, 13]
	Hadranthe (Phaeovireya) (2/5/54)	\	*R. beyerinckianum* Koord.	*R. beyerinckianum* Koord.		26	[51, 52]
			R. dianthosmum Sleumer	*R. dianthosmum* Sleumer		26	[52]
			R. konori	*R. konori* Becc.	4*x*	26	[13, 51]

Subgenus	**Section**	**Subsection**	**Taxon in original literature**	**Resolved taxon name**	**FCM ploidy (*x*)**	**Chromosome count (2*n*)**	**Reference**
			R. phaeopeplum Sleum.	*R. konori* Becc. var. *phaeopeplum* (Sleumer) Argent		26	[51]
			R. phaeochitum F. Muell.	*R. phaeochitum* F. Muell.	4*x*	26	[13, 52]
			R. caliginis Kores × *R. vitis-idaea* Sleumer	*R. caliginis* Kores × *R. vitis-idaea* Sleumer (cultivation source)		26	[52]
	Malayovireya (1/3/21)	\	*R. acuminatum* Hook. f.	*R. acuminatum* Hook.		26	[51]
			R. apoanum Stein	*R. apoanum* Stein	4*x*	26	[13, 52]
			R. himantodes Sleumer	*R. himantodes* Sleumer		26	[52]
	Pseudovireya (1/5/17)	\	*R. emarginatum*	*R. emarginatum* Hemsl. & E.H.Wils.	4*x*		[13]
			R. kawakamii Hayata	*R. kawakamii* Hayata (1911)	2*x*		[13]
			R. rushforthii Argent & D.F. Chamb.	*R. rushforthii* Argent & D. F. Chamb.	2*x*	26	[13, 52]
			R. santapaui Sastry & et al.	*R. santapaui* Sastry & al.		26	[52]
			R. vaccinioides Hook. f.	*R. vaccinioides* Hook.		26	[12]
	Schistanthe (11/28/244; 5 subsections)	*Euvireya* (7/11/121)	*R. aurigeranum*	*R. aurigernum* Sleumer	4*x*		[13]
			R. christianae Sleum.	*R. christianae* Sleumer		26	[51]
			R. crassifolium Stapf	*R. crassifolium* Stapf		26	[52]
			R. javanicum (ssp. *javanicum*)	*R. javanicum* (Blume) Benn.	4*x*	26	[12, 13]
			R. laetum J.J.S.	*R. laetum J.* J. Sm.	4*x*	26	[13, 51]
			R. lochiae F. Muell.	*R. lochiae* F.Muell.		26	[12, 51, 52]
			R. lochiae/viriosum (unidentified sample)	*R. lochiae/viriosum* (unidentified sample)	4*x*		[13]
			R. macgregoriae	*R. macgregoriae* F. Muell.	4*x*	26	[13, 51]
			R. orbiculatum	*R. orbiculatum* Ridl.	4*x*	26	[13, 51, 52]
			R. polyanthemum	*R. polyanthemum* Sleumer	4*x*		[13]
			R. praetervisum Sleumer	*R. praetervisum* Sleumer		26	[52]
			R. verticillatum	*R. verticillatum* Low ex Lindl.	4*x*		[13]
		Linnaeopsis (1/2/16)	*R. anagalliflorum* Wernham	*R. anagalliflorum* Wernham		26	[52]
			R. gracilentum	*R. gracilentum* F. Meull.	4*x*		[13]
			R. bagobonum H.F. Copel.	*R. bagobonum* H. F. Copel.		26	[52]

Subgenus	Section	Subsection	Taxon in original literature	Resolved taxon name	FCM ploidy (*x*)	Chromosome count (2*n*)	Reference
		Malesia (2/8/60)	*R. burttii*	*R. burttii* R.Woods	4*x*		[13]
			R. buxifolium Low ex Hook. f.	*R. buxifolium* H. Low ex Hook.		26	[51]
			R. commonae Foerst.	*R. commonae* Foerst.		26	[51, 52]
			R. inconspicuum J.J.S./*R. invasorium* Sleum.	*R. inconspicuum* J.J.Sm.		26	[51]
			R. multicolor Miq.	*R. multicolor* Miq.		26	[51]
			R. taxifolium	*R. taxifolium* Merr.	4*x*		[13]
			R. wrightianum var. *cyclopense* J.J. Sm.	*R. wrightianum* var. *cyclopense* J.J. Sm.		26	[52]
		Solenovireya (1/7/46)	*R. cruttwellii*	*R. cruttwellii* Sleumer	4*x*		[13]
			R. pneumonanthum Sleumer	*R. edanoi* var. *pneumonanthum*		26	[52]
			R. jasminiflorum	*R. jasminiflorum* Hook.		26	[12]
			R. loranthiflorum Sleumer	*R. loranthiflorum* Sleumer		26	[52]
			R. ruttenii J.J. Sm.	*R. ruttenii* J. J. Sm.		26	[52]
			R. stapfianum Hemsl. ex Prain	*R. stapfianum* Hemsl. ex Prain		c.26	[52]
			R. tuba Sleumer	*R. tuba* Sleumer		26	[52]
	Siphonovireya (0/2/14)	\	*R. herzogii* Warb.	*R. herzogii* Warb.		26	[52]
			R. inundatum Sleumer	*R. psammogenes* var. *inundatum*		26	[52]

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Table S3.2 Ploidy estimation of taxa in subsection *Maddenia* in the present study, using flow cytometry

For diploids (RN1 only), FCM ploidy = diploid standard (2*x*); for polyploids (RN1 and RN2), $\text{FCM ploidy} = \frac{\text{Mean}-\text{x (RN2: polyploid peak)}}{\text{Mean}-\text{x (RN1: standard or diploid peak)}} \times 2$, round number. **1)** Sample IDs marked with an asterisk (*) were also evaluated using silica gel-dried and herbarium leaves (Tables 3.3 and S3.3). Sample IDs marked with a hashtag (#) were evaluated using both *R. fortunei* Lindl. and *R. parryae* Hutch. as diploid standards (Tables 3.4 and S3.3). Ploidy shown here was from the most reliable result. **2)** Voucher specimen ID of diploid standards: *R. fortunei*, MPN52690; *R. parryae*, MPN52773. **3)** Herbarium specimens for New Zealand accessions are deposited in the Dame Ella Campbell Herbarium (MPN) at Massey University, Palmerston North, New Zealand (listed with voucher specimen ID). Living plants of the accessions in the Royal Botanic Garden Edinburgh (RBGE), UK and Rhododendron Species Botanical Garden (RSBG), Washington, USA are accessible at the corresponding organizations (listed with living accession ID). When there is no specimen ID provided, the living accession can be traced on site, with the original collection number as a note to 'Taxon labelled as'. **4)** When a sample accession is recorded as from the wild, it is noted as a 'Wild accession' with original locality, when the information is available. Samples are otherwise from a cultivated source. **5)** Underlined name in the 'Taxon' column was later re-identified to a different taxon in the phylogeny study (Chapter 4), see Table S4.1 for the final taxon name.

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
CH02	*R. maddenii* ssp. *maddenii* (as *R. brachysiphon*)	*R. maddenii* (as *R. brachysiphon*)	6*x*	51.08	5.07	149.21	2.88	*R. fortunei*	fresh		MPN52752; MPN52753
CH03	*R. maddenii* ssp. *crassum*	*R. maddenii*	8*x*	51.16	6.03	204.03	2.93	*R. fortunei*	fresh		MPN52754; MPN52755; MPN52756; MPN52757

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
CH04	*R. veitchianum* (as *R. cubittii*)	*R. cubittii*	2*x*	54.96	8.17	n/a	n/a	*R. fortunei*	fresh		MPN52758
CH05	*R. carneum*	*R. carneum*	2*x*	55.31	8	n/a	n/a	*R. fortunei*	fresh		MPN52759; MPN52760
CH06	*R. megacalyx*	*R. megacalyx*	2*x*	50.19	8.87	n/a	n/a	*R. fortunei*	fresh		MPN52761; MPN52762
CH07	*R. dendricola*	*R. dendricola*	2*x*	56.68	8.44	n/a	n/a	*R. fortunei*	fresh		MPN52763; MPN53021
CH08	*R. formosum*	*R. assamicum*	2*x*	53.18	6.48	n/a	n/a	*R. fortunei*	fresh		MPN52764
CH09	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	*R. crassum*	8*x*	48.23	6.85	190.77	3.2	*R. fortunei*	fresh		MPN52765
CH10	*R. formosum* var. *formosum* (as *R. formosum*)	*R. formosum*	2*x*	50.28	5.94	n/a	n/a	*R. fortunei*	fresh		MPN52766; MPN53014
CH11	*R. lindleyi*	*R. lindleyi*	2*x*	51.98	7.82	n/a	n/a	*R. fortunei*	fresh		MPN52767
CH14	*R. veitchianum* (as *R. cubittii*)	*R. ciliicalyx*	2*x*	52.94	9.69	n/a	n/a	*R. fortunei*	fresh		MPN52770; MPN52771
DN01	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	5-6*x*?	51.37	5.31	129.1	9.11	*R. fortunei*	herbarium		MPN52952
DN02	*R. formosum* var. *formosum* (as *R. formosum*)	*R. formosum*	2*x*	55.54	6.7	n/a	n/a	*R. fortunei*	herbarium		MPN52953
DN03	*R. valentinianum* var. *oblongilobatum*	*R. valentinianum* var. *oblongilobatum*	2*x*	47.33	11.47	n/a	n/a	*R. fortunei*	herbarium		MPN52954
DN05	*R. formosum* var. *inaequale* (as *R. inaequale*)	*R. formosum* var. *formosum*	2*x*	46.78	9.79	n/a	n/a	*R. fortunei*	fresh		MPN52956
DN06	*R. formosum*	*R. formosum* var. *inaequale*	2*x*	52.01	8.06	n/a	n/a	*R. fortunei*	herbarium		MPN52957; MPN53007
DN07	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* (*R. polyandrum*)	5*x*?	45.87	10.53	106.08	7.26	*R. fortunei*	herbarium		MPN52958; MPN52959; MPN52999
DN08	*R. maddenii* ssp. *maddenii*	*R. maddenii* (*R. polyandrum*)	6-7*x*?	50.58	7.16	167.81	7.14	*R. fortunei*	herbarium		MPN52960
DN09	*R. nuttallii*	*R. nuttallii*	2*x*	39.62	8.32	n/a	n/a	*R. fortunei*	herbarium		MPN52961
DN10	*R. nuttallii*	*R. nuttallii*	2*x*	45.79	12.51	n/a	n/a	*R. fortunei*	herbarium		MPN52962

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
DN11	*R. excellens*	*R. excellens*	2*x*	42.9	11.12	n/a	n/a	*R. fortunei*	herbarium		MPN52963
DN12	*R. megacalyx*	*R. megacalyx*	2*x*	42.08	9.48	n/a	n/a	*R. fortunei*	herbarium		MPN52964
DN14	*R. horlickianum*	*R. horlickianum*	2*x*	44.52	10.46	n/a	n/a	*R. fortunei*	herbarium		MPN52966
DN15	*R. fletcherianum*	*R. fletcherianum*	2*x*	45.69	11.78	n/a	n/a	*R. fortunei*	herbarium		MPN52967
DN16	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* 'Kotuku'	2*x*	44.6	10.07	n/a	n/a	*R. fortunei*	herbarium		MPN52968
DN17	*R. johnstoneanum*	*R. johnstoneanum*	2*x*	47.3	8.79	n/a	n/a	*R. fortunei*	fresh		MPN52969
DN18	*R. horlickianum*	*R. horlickianum*	2*x*	47.02	11.88	n/a	n/a	*R. fortunei*	fresh		accession died
DN20	*R. pachypodum*	*R. pachypodum* AC 1993	2*x*	44.33	11.42	n/a	n/a	*R. fortunei*	fresh	wild	MPN52970
DN21	*R. leptocladon*	*R. leptocladon* (H.P. Cox) ex Murdoch	2*x*	46.51	10.58	n/a	n/a	*R. fortunei*	herbarium	wild	MPN52971
DN22	*R. taggianum*	*R. taggianum* CCHH 108 ex Murdoch	2*x*	44.77	9.65	n/a	n/a	*R. fortunei*	fresh	wild	MPN52972
E01	*R. ciliatum*	*R. ciliatum*	2*x*	43.48	10.67	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India: Sikkim, N	RBGE#19820583*F
E02	*R. ciliatum*	*R. ciliatum*	2*x*	44.97	10.86	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Nepal	RBGE#19850525*K
E03	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae*	2*x*	45.24	11.83	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India: W Bengal	RBGE#19722633*F
E04	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae*	2*x*	45.42	12.23	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India: Sikkim	RBGE#19880631*F
E05	*R. dendricola*	*R. dendricola*	2*x*	48.36	11.63	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Myanmar: Kachin State	RBGE#19754089*F
E06	*R. formosum*	*R. formosum*	2*x*	49.2	12.41	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India: Meghalaya	RBGE#19751328*G
E07	*R. liliiflorum*	*R. liliiflorum*	2*x*	48	10.09	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Guizhou	RBGE#19911969*B
E08	*R. liliiflorum*	*R. liliiflorum*	2*x*	48.61	13.55	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Guizhou	RBGE#19861177*A
E09	*R. ludwigianum*	*R. ludwigianum*	2*x*	45.74	12.91	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Thailand: Chiang Mai	RBGE#19850478*D
E10	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	2*x*	51.41	8.83	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Yunnan	RBGE#19391033*N

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
E11	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	8*x*	48.61	7.37	186.9	5.09	*R. fortunei*	silica gel-dried	wild: India: Arunachal Pradesh	RBGE#19832535*I
E12	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii*	8*x*	51.28	10.35	200.65	5.02	*R. fortunei*	silica gel-dried	wild: Bhutan: Thimphu Dist.	RBGE#19150028*L
E13	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii*	6*x*	45.87	10.2	131.31	5.14	*R. fortunei*	silica gel-dried	wild: Bhutan: Tashigang Dist.	RBGE#19754068*I
E14	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii*	4-6*x*?	47.6	9.69	122.64	7.48	*R. fortunei*	silica gel-dried	wild: China: Xizang (Tibet) Aut. Reg.	RBGE#19141003*C
E15	*R. nuttallii*	*R. nuttallii*	2*x*	49.04	10.01	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Yunnan - Gaoligong Shan	RBGE#20042030*E
E16	*R. scopulorum*	*R. scopulorum*	2*x*	53.15	10.61	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Xizang (Tibet) Aut. Reg.	RBGE#19730921*P
E17	*R. veitchianum*	*R. veitchianum*	2*x*	55.37	11.33	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Thailand: Chiang Mai	RBGE#19750211*H
E18	*R. fletcherianum*	*R. fletcherianum*	2*x*	51.96	8.21	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Xizang (Tibet) Aut. Reg.	RBGE#19754070*J
E19	*R. ciliipes*	*R. ciliipes*	2*x*	54.99	7.22	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Yunnan	RBGE#19991313*B
E20	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	8*x*	54.88	9.12	208.28	4.37	*R. fortunei*	silica gel-dried	wild: China: Xizang (Tibet) Aut. Reg. - Yunnan border	RBGE#19491022*B
E21	*R. maddenii*	*R. maddenii*	6*x*	52.42	8.36	141.88	5.46	*R. fortunei*	silica gel-dried	wild: Bhutan: Thimphu Dist.	RBGE#19831844*B
E22	*R. maddenii*	*R. maddenii*	6*x*	54.1	6.46	142.24	5.48	*R. fortunei*	silica gel-dried	wild: India: Sikkim	RBGE#19890430*B
E23	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	2*x*	53.07	8.79	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China: Yunnan	RBGE#19321024*D
E24	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii*	6*x*	53.14	7.56	154.4	5.5	*R. fortunei*	silica gel-dried	wild: China: Xizang (Tibet) Aut. Reg.	RBGE#19715035*G
E25	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii*	6*x*	48.63	10.04	128.7	3.46	*R. fortunei*	silica gel-dried	wild: India: Arunachal Pradesh	RBGE#19730904*E

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
HP01	*R. excellens*	*R. excellens* DT307/98	2*x*	50.59	6.84	n/a	n/a	*R. fortunei*	fresh	wild	MPN52703; MPN52704
HP02	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* (as *R. polyandrum*)	6*x*	54.09	5.33	156.12	3.05	*R. fortunei*	fresh		MPN52705; MPN52706; MPN52707
HP03	*R. taggianum*	*R. taggianum*	2*x*	58.91	6.89	n/a	n/a	*R. fortunei*	fresh		MPN52708; MPN52709
HP05	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii*	6*x*	53.15	6	151.36	2.76	*R. fortunei*	fresh	wild: Burma road, Yunnan, China	MPN52712; MPN52713; MPN52714
HP06	*R. veitchianum* (as *R. cubittii*)	*R. veitchianum*? (*as* *R. cubittii*)	2*x*	47.26	9.15	n/a	n/a	*R. fortunei*	fresh		MPN52715
OM45	*R. veitchianum* (as *R. cubittii*)	*R. veitchianum*? (*as* *R. cubittii*)	2*x*	70.09	5.75	n/a	n/a	*R. fortunei*	fresh		MPN52661; MPN52662
HP07	*R. dalhousiae* var. *rhabdotum*	*R. dalhousiae* var. *rhabdotum*	2*x*	45.24	6.42	n/a	n/a	*R. fortunei*	fresh		MPN52716; MPN52717; MPN52718
HP08	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* No. 1, ex Cullinane	8*x*	42.97	6.24	169.24	2.81	*R. fortunei*	fresh		MPN52719; MPN52720
HP09	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* ssp. *crassum* DT 98	8*x*	42.73	5.43	170.83	3.48	*R. fortunei*	fresh	wild	MPN52721; MPN52722
HP10	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ssp. *crassum* Jury selection	6*x*	50.97	5.15	148.24	2.93	*R. fortunei*	fresh		MPN52723; MPN52724; MPN52725
HP11	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ssp. *crassum* Jury selection (as *R. polyandrum*)?	6*x*	51.07	4.64	143.23	3.42	*R. fortunei*	fresh		MPN52726; MPN52727
HP13	*R. ciliipes*	*R. ciliipes*	2*x*	54.61	9.42	n/a	n/a	*R. fortunei*	fresh		MPN52730; MPN52731; MPN52732; MPN52733
HP14	*R. lyi*	*R. ciliicalyx* ssp. *lyi* Gigha form (as *R. lyi*)	2*x*	56.11	6.54	n/a	n/a	*R. fortunei*	fresh		MPN52734; MPN52735
HP15	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* ssp. *maddenii*	8*x*	51.25	6.69	197.97	3.62	*R. fortunei*	fresh		MPN52736; MPN52737
HP16	*R. pachypodum* (as *R. supranubium*)	*R. pachypodum* (as *R. supranubium*)	2*x*	52.89	8.84	n/a	n/a	*R. fortunei*	fresh		MPN52738; MPN52739

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
HP17	*R. taggianum*	*R. taggianum*	2*x*	56.5	7.5	n/a	n/a	*R. fortunei*	fresh		MPN52740; MPN52741
HP19	*R. taggianum*	*R. taggianum*	2*x*	53.68	11.68	n/a	n/a	*R. fortunei*	silica gel-dried		MPN52743; MPN52744; MPN53025
HP20	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. polyandrum*	6*x*	50.25	7.02	143.21	3.72	*R. fortunei*	fresh		MPN52745; MPN52998
HP21	*R.* aff. *valentinianum*	*R. valentinianum* aff.	2*x*	57.2	8.31	n/a	n/a	*R. fortunei*	fresh		MPN52746; MPN53022
OM01	*R. formosum* var. *formosum* (as *R. formosum*)	*R. inaequale*	2*x*	67.55	5.04	n/a	n/a	*R. fortunei*	fresh		MPN52583; MPN52584
HP18	*R. formosum* var. *formosum* (as *R. formosum*)	*R. inaequale*	2*x*	54.39	7.2	n/a	n/a	*R. fortunei*	fresh		MPN52742
OM02*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* (as *R. manipurense*)	6*x*	63.14	6.78	178.28	2.77	*R. fortunei*	fresh		MPN52585; MPN52586
OM03	*R. ciliatum*	*R. ciliatum*	2*x*	65.45	6.69	n/a	n/a	*R. fortunei*	fresh		MPN52587; MPN52588
OM04	*R. pachypodum*	*R. pachypodum* (as *R. supranubium*)	2*x*	67.71	10.75	n/a	n/a	*R. fortunei*	fresh		MPN52589; MPN52590; MPN52591
HP04	*R. pachypodum*	*R. pachypodum* (as *R. supranubium*)	2*x*	57.68	6.35	n/a	n/a	*R. fortunei*	fresh		MPN52710; MPN52711; MPN53015
OM05	*R. burmanicum*	*R. burmanicum*	2*x*	61.06	6.95	n/a	n/a	*R. fortunei*	fresh		MPN52592; MPN52592
OM06*	*R. ciliicalyx*	*R. ciliicalyx*	2*x*	66.52	6.88	n/a	n/a	*R. fortunei*	fresh		MPN52594; MPN52595
OM07	*R. ciliicalyx*	*R. ciliicalyx* ‘Charisma’	2*x*	61.99	6.78	n/a	n/a	*R. fortunei*	fresh		MPN52596; MPN52597
OM08	*R. ciliatum*	*R. ciliatum*	2*x*	60.91	5.02	n/a	n/a	*R. fortunei*	fresh		MPN52598; MPN52599
OM09	*R. formosum* var. *formosum* (as *R. formosum*)	*R. formosum* (as *R. assamicum*)	2*x*	64.14	5.39	n/a	n/a	*R. fortunei*	fresh		MPN52600; MPN52601

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
OM10	*R. formosum* var. *formosum* (as *R. iteophyllum*)	*R. formosum* (as *R. iteophyllum*)	2*x*	62.94	5.96	n/a	n/a	*R. fortunei*	fresh		MPN52602; MPN52603
OM11*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* SD1104	6*x*	63.34	6.33	180.47	2.66	*R. fortunei*	fresh	wild: Sikkim	MPN52604; MPN52605
OM12	*R. nuttallii* var. *stellatum*	*R. nuttallii* 'Stellata'	2*x*	58.75	5.71	n/a	n/a	*R. fortunei*	fresh		MPN52606; MPN52607
OM13	*R. johnstoneanum*	*R. johnstoneanum* KB form	2*x*	62.09	6.81	n/a	n/a	*R. fortunei*	fresh		MPN52608; MPN52609
OM14*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* TH268?	8*x*	62.33	6.37	250.59	2.84	*R. fortunei*	fresh	wild: Vietnam	MPN52610; MPN52611
OM15	*R. formosum* var. *formosum* (as *R. formosum*)	*R. veitchianum* (as *R. cubittii*)	2*x*	59.87	7.99	n/a	n/a	*R. fortunei*	fresh		MPN52612; MPN52613
OM16	*R. parryae*	*R. parryae*	2*x*	59.26	7.05	n/a	n/a	*R. fortunei*	fresh		MPN52614; MPN52615
OM17*	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* ssp. *crassum*	8*x*	59.75	7.05	239.78	2.45	*R. fortunei*	fresh		MPN52616; MPN52617; MPN53000
OM18*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ‘Late Pink’	6*x*	61.73	6.62	174.45	3.19	*R. fortunei*	fresh		MPN52618; MPN52619
OM19	*R. johnstoneanum*	*R. johnstoneanum*	2*x*	56.03	7.16	n/a	n/a	*R. fortunei*	fresh		MPN52620; MPN52621
OM20*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii*	6*x*	58.28	6.42	166.06	2.64	*R. fortunei*	fresh		MPN52622; MPN52623
OM22	*R. lindleyi*	*R. lindleyi*	2*x*	61.42	5.64	n/a	n/a	*R. fortunei*	fresh		accession died
OM23	*R. lindleyi*	*R. lindleyi* ‘Helen Gordon’	2*x*	60.31	5.58	n/a	n/a	*R. fortunei*	fresh		MPN52679; MPN52680 (accession is a clone of OM52)
OM52	*R. lindleyi*	*R. lindleyi* ‘Helen Gordon’	2*x*	79.22	4.58	n/a	n/a	*R. fortunei*	fresh		MPN52679; MPN52680
OM24	*R. lindleyi*	*R. lindleyi*	2*x*	59.88	5.52	n/a	n/a	*R. fortunei*	fresh		accession died

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
OM25	*R. veitchianum*	*R. veitchianum*	2*x*	59.44	6.15	n/a	n/a	*R. fortunei*	fresh		MPN52624; MPN52625
OM26	*R. dalhousiae* var. *rhabdotum*	*R. dalhousiae* var. *rhabdotum*	2*x*	59.3	6.39	n/a	n/a	*R. fortunei*	fresh		MPN52626
OM29	*R. dalhousiae* var. *rhabdotum*	*R. dalhousiae* var. *rhabdotum*	2*x*	56.6	6.3	n/a	n/a	*R. fortunei*	fresh		MPN52630
OM30	*R. johnstoneanum*	*R. johnstoneanum*	2*x*	55.29	6.53	n/a	n/a	*R. fortunei*	fresh		MPN52631; MPN52632
OM32*	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae* var. *dalhousiae*	2*x*	63.83	6.58	n/a	n/a	*R. fortunei*	fresh		MPN52634; MPN52635
OM33	*R. parryae*	*R. parryae*	2*x*	59.15	5.09	n/a	n/a	*R. fortunei*	fresh		MPN52636; MPN52637
OM34*	*R. excellens*	*R. excellens*	2*x*	62.49	6	n/a	n/a	*R. fortunei*	fresh	wild: Nth Vietnam	MPN52638; MPN52639
OM36	*R. burmanicum*	*R. burmanicum*	2*x*	56.1	4.93	n/a	n/a	*R. fortunei*	fresh		MPN52643; MPN52644
OM37	*R. johnstoneanum*	*R. johnstoneanum* KB form	2*x*	59.89	5.4	n/a	n/a	*R. fortunei*	fresh		MPN52645; MPN52646
OM38	*R. burmanicum*	*R. burmanicum* Marchant form	2*x*	57.78	5.9	n/a	n/a	*R. fortunei*	fresh		MPN52647; MPN52648
OM39	*R. scopulorum*	*R. scopulorum*	2*x*	64.34	4.91	n/a	n/a	*R. fortunei*	fresh		MPN52649; MPN52650
OM40*	*R. taronense*	*R. taronense*	2*x*	63.58	6.14	n/a	n/a	*R. fortunei*	fresh		MPN52651; MPN52652
OM41	*R. carneum*	*R. carneum*	2*x*	65.51	8.44	n/a	n/a	*R. fortunei*	fresh		MPN52653; MPN52654
OM42	*R. formosum* var. *formosum* (as *R. formosum*)	*R. veitchianum* (as *R. cubittii*)	2*x*	70.64	7.02	n/a	n/a	*R. fortunei*	fresh		MPN52655; MPN52656
OM43*	*R. formosum* var. *formosum* (as *R. formosum*)	*R. formosum*	2*x*	62.36	6.61	n/a	n/a	*R. fortunei*	fresh		MPN52657; MPN52658
OM44	*R. formosum*	*R. aff. veitchianum* KR2247	2*x*	64.47	5.27	n/a	n/a	*R. fortunei*	fresh	wild	MPN52659; MPN52660
OM46*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* 'Jury Selection' (*R. polyandrum*)	6*x*	59.02	4.98	165.86	2.9	*R. fortunei*	fresh		MPN52663; MPN52664

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
OM47*	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	8*x*	57.87	6.34	228.08	2.63	*R. fortunei*	fresh		MPN52665; MPN52666
OM48*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	7*x*	57.4	6.48	197.92	3.84	*R. fortunei*	fresh	wild: possibly Nth Vietnam	MPN52667; MPN52668; MPN52669
OM49*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii*	6*x*	58.46	5.54	179.98	2.86	*R. fortunei*	fresh		MPN52670; MPN52671
OM50	*R. nuttallii*	*R. nuttallii*	2*x*	71.09	7.08	n/a	n/a	*R. fortunei*	fresh	wild: Nth Vietnam	MPN52672; MPN52673; MPN52674; MPN52675
OM51	*R. nuttallii*	*R. nuttallii*	2*x*	71.66	10.14	n/a	n/a	*R. fortunei*	fresh	wild: China	MPN52676; MPN52677; MPN52678; MPN53018
OM53	*R. sinonuttallii*	*R. sinonuttallii* (possibly a hybrid, L. Davies pers comm)	2*x*	71.29	4.98	n/a	n/a	*R. fortunei*	fresh		MPN52681; MPN52682; MPN52683
OM54*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* 'Virginalis'	6*x*	58.98	5.97	170.11	2.87	*R. fortunei*	fresh		MPN52684; MPN52685
OM55*	*R. burmanicum*	*R. burmanicum*	2*x*	57.16	4.7	n/a	n/a	*R. fortunei*	fresh		MPN52686
OM56*	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. crassum*	6*x*	58.53	6.9	167.38	3.5	*R. fortunei*	fresh		MPN52687
OM57*	*R. sinonuttallii*	*R. sinonuttallii*	2*x*	57.44	6.64	n/a	n/a	*R. fortunei*	fresh		MPN52688
OM58*	*R. maddenii* ssp. *maddenii* (as *R. brachysiphon*)	*R. brachysiphon*	6*x*	54.99	5.97	163.53	3.42	*R. fortunei*	fresh		MPN52689
PK01	*R. excellens*	*R. excellens* KR2998	2*x*	50.58	5.7	n/a	n/a	*R. parryae*	fresh	wild	MPN52774; MPN52775
PK02	*R. horlickianum*	*R. horlickianum* Gwavas	2*x*	52.72	4.49	n/a	n/a	*R. parryae*	fresh		MPN52776
PK03	*R. ciliipes*	*R. ciliipes* K56	2*x*	52.18	4.51	n/a	n/a	*R. parryae*	fresh	wild	MPN52777; MPN52778; MPN52779; MPN52780

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
PK04	*R. formosum* var. *formosum* (as *R. iteophyllum*)	*R. iteophyllum* Gigha form	2*x*	52.12	4.62	n/a	n/a	*R. parryae*	fresh		MPN52781; MPN52782; MPN52783; MPN52784
PK05#	*R. taggianum*	*R. taggianum*	2*x*	54.11	7.93	n/a	n/a	*R. parryae*	fresh		accession died
PK06	*R. excellens*	*R. excellens* AC435	2*x*	49.56	6.48	n/a	n/a	*R. parryae*	fresh	wild	MPN52785; MPN52786
PK07	*R. pachypodum* (as *R. supranubium*)	*R. pachypodum* (as *R. supranubium*)	2*x*	50.77	5.69	n/a	n/a	*R. parryae*	fresh		MPN52787; MPN52788; MPN52789; MPN52790
PK08	*R. formosum* var. *formosum* (as *R. iteophyllum*)	*R. iteophyllum* Brodick (*R. formosum* var. *formosum* on the tag)	2*x*	50.91	5.25	n/a	n/a	*R. parryae*	fresh		MPN52791; MPN52792; MPN52793
PK09#	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ssp. *maddenii* (as *R. brachysiphon*)	7*x*	61.12	5.09	163.18	2.74	*R. fortunei*	fresh		MPN52794; MPN52795; MPN52796; MPN52797
PK10	*R. excellens*	*R. excellens* TVO 064	2*x*	58.56	5.27	n/a	n/a	*R. parryae*	fresh	wild	MPN52798; MPN52799; MPN52800
PK11	*R. lindleyi*	*R. formosum* var. *inaequale* KW16029	2*x*	75.65	4.21	n/a	n/a	*R. parryae*	fresh	wild	MPN52801; MPN52802; MPN52803
PK12	*R. scopulorum*	*R. scopulorum*	2*x*	72.55	5.05	n/a	n/a	*R. parryae*	fresh		MPN52804; MPN52805; MPN52806; MPN52807; MPN52808
PK13	*R. maddenii* ssp. *maddenii*	*R. maddenia* ssp. *maddenii* (as *R. polyandrum*)	5*x*	72.22	4.05	232.19	2.33	*R. fortunei*	fresh		MPN52809; MPN52810
PK14	*R. parryae*	*R. parryae* RBGE146 Fischer form	2*x*	74.35	4.39	n/a	n/a	*R. parryae*	fresh	wild	MPN52811; MPN52812
PK15	*R. burmanicum*	*R. burmanicum* Brodick form	2*x*	74.48	4.61	n/a	n/a	*R. parryae*	fresh		MPN52813; MPN52814

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
PK16	*R. valentinianum* var. *oblongilobatum*	*R. valentinianum* var. *oblongilobatum* AC1258?	2*x*	58.74	5.67	n/a	n/a	*R. parryae*	fresh	wild	MPN52815; MPN52816; MPN52817
PK17#	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* TH. 237	8*x*	59.74	5.13	216.78	2.24	*R. fortunei*	fresh	wild	MPN52818; MPN52819; MPN52820
PK18	*R. formosum* var. *formosum* (as *R. formosum*)	*R. formosum* 'Ten Tashi'	2*x*	58.52	4.93	n/a	n/a	*R. parryae*	fresh	wild	MPN52821; MPN52822; MPN52823
PK19	*R. dendricola*	*R. dendricola*	2*x*	55.41	5.46	n/a	n/a	*R. parryae*	fresh		MPN52824; MPN52825; MPN52826; MPN52827; MPN52828
PK20	*R. burmanicum*	*R. burmanicum* 'Deep Yellow'	2*x*	54.3	6.13	n/a	n/a	*R. parryae*	fresh		MPN52829; MPN52830; MPN52831
PK21	*R. veitchianum*	*R. veitchianum* 'Ice White'	2*x*	58.45	5.1	n/a	n/a	*R. parryae*	fresh	wild: Thailand	MPN52832; MPN52833; MPN52834
PK22#	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	*R. maddenii* ssp. *maddenii* (as *R. polyandrum*)	8*x*	56.84	5.26	204.51	2.81	*R. fortunei*	fresh		MPN52836; MPN52837; MPN52838
PK23	*R. dalhousiae* var. *rhabdotum*	*R. dalhousiae* var. *rhabdotum*	2*x*	54.64	5.8	n/a	n/a	*R. parryae*	fresh		MPN52839; MPN52840
PK24	*R. carneum*	*R. carneum*	2*x*	58.22	5.73	n/a	n/a	*R. parryae*	fresh		MPN52841; MPN52842; MPN52843
PK25a	*R. dendricola*	*R. dendricola*	2*x*	56.41	6.39	n/a	n/a	*R. parryae*	fresh		MPN52844; MPN52845; MPN52846
PK26	*R. pachypodum* (as *R. supranubium*)	*R. pachypodum*	2*x*	56.29	4.85	n/a	n/a	*R. parryae*	fresh		MPN52847; MPN52848; MPN52849; MPN52850
PK27#	*R. maddenii* ssp. *maddenii* (as *R. maddenii*)	*R. maddenii* ssp. *crassum*	6*x*	56.24	6.01	146.7	2.75	*R. fortunei*	fresh		MPN52851; MPN52852; MPN52853

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
PK28	*R. lindleyi*	*R. lindleyi* KW8546 ex Gwavas	2*x*	55.16	6.57	n/a	n/a	*R. parryae*	fresh	wild	MPN52854; MPN52855
PK29	*R. coxianum*	*R. coxianum* 1984-443, Glendoick?	2*x*	69.92	5.2	n/a	n/a	*R. parryae*	fresh	wild	MPN52856; MPN52857
PK30	*R. excellens*	*R. excellens* AC5630	2*x*	72.97	4.49	n/a	n/a	*R. parryae*	fresh	wild: Ban Khoang, Vietnam	MPN52860; MPN52861; MPN52862
PK31	*R. megacalyx*	*R. megacalyx*	2*x*	54.33	6.9	n/a	n/a	*R. parryae*	fresh		MPN52863; MPN52864; MPN52865; MPN52866
PK32	*R. nuttallii*	*R. nuttallii*	2*x*	55.08	5.6	n/a	n/a	*R. parryae*	fresh		MPN52867; MPN52868; MPN52869; MPN52870
PK33	*R. johnstoneanum*	*R. johnstoneanum* KW20305	2*x*	64.84	6.53	n/a	n/a	*R. parryae*	fresh	wild	MPN52871; MPN52872
PK34	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae*	2*x*	72.38	4.76	n/a	n/a	*R. parryae*	fresh	wild: Solu Khumbu, Nepal	MPN52873; MPN52874
PK35	*R. nuttallii* var. *stellatum*	*R. nuttallii* 'Stellata'	2*x*	70.17	5.3	n/a	n/a	*R. parryae*	fresh		MPN52875; MPN52876; MPN52877; MPN53024
PK36	*R. formosum* var. *formosum* (as *R. formosum*)	*R. veitchianum* 'Ashcombe'	2*x*	70.74	5.04	n/a	n/a	*R. parryae*	fresh		MPN52878; MPN52879
PK37	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae*	2*x*	72.98	4.38	n/a	n/a	*R. parryae*	fresh		MPN52880; MPN52881
PK38#	*R. maddenii* ssp. *maddenii* (as *R. polyandrum*)	*R. maddenii* NAPE 109	6*x*	69.55	5.22	178.2	3.52	*R. fortunei*	fresh	wild: Nagaland-Araunchal Pradesh	MPN52882; MPN52883
PK39	*R. lindleyi*	*R. lindleyi* Hollard form	2*x*	70.39	5.22	n/a	n/a	*R. parryae*	fresh		MPN52884; MPN52885
PK40	*R. ciliatum*	*R. ciliatum*	2*x*	67.11	4.75	n/a	n/a	*R. parryae*	fresh		MPN52886; MPN52887; MPN52888; MPN52889

Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
PK41	*R. burmanicum*	*R. burmanicum*	2*x*	68.67	4.86	n/a	n/a	*R. parryae*	fresh		MPN52890; MPN52891
PK42	*R. taronense*	*R. taronense*	2*x*	69.37	4.58	n/a	n/a	*R. parryae*	fresh		MPN52892; MPN52893; MPN52894
PK43	*R. ludwigianum*	*R. ludwigianum* Doi Ang Kang, Thailand	2*x*	69.28	4.36	n/a	n/a	*R. parryae*	fresh	wild	MPN52895; MPN52896; MPN52897
PK44	*R. lyi*	*R. lyi*	2*x*	69.81	5.16	n/a	n/a	*R. parryae*	fresh		MPN52898; MPN52899
PK45#	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* ssp. *crassum*	7*x*	67.11	4.97	212.12	2.47	*R. fortunei*	fresh		MPN52900; MPN52901; MPN52902; MPN53001
PK47	*R. johnstoneanum*	*R. johnstoneanum* AC5532	2*x*	71.3	4.87	n/a	n/a	*R. parryae*	fresh	wild	MPN52906; MPN52907
PK49	*R. veitchianum* (as *R. cubittii*)	*R. veitchianum*	2*x*	63.18	5.54	n/a	n/a	*R. parryae*	fresh		MPN52911
PK50	*R. ciliatum*	*R. ciliatum*	2*x*	64.04	4.86	n/a	n/a	*R. parryae*	fresh		MPN52912; MPN52913; MPN52914
PK51	*R. ciliatum*	*R. ciliatum*	2*x*	66.76	4.78	n/a	n/a	*R. parryae*	fresh		MPN52915; MPN52916
PK52#	*R. maddenii* ssp. *maddenii* (as *R. polyandrum*)	*R. maddenii* KC0108	6*x*	68.34	4.53	181.49	2.13	*R. fortunei*	fresh	wild: Araunchal Pradesh	MPN52917; MPN52918; MPN52919; MPN52920; MPN52921
PK53	*R. ciliicalyx*	*R. ciliicalyx* 'Charisma' KW20280	2*x*	67.43	4.4	n/a	n/a	*R. parryae*	fresh	wild	MPN52922; MPN52923
PK56	*R. dendricola*	*R. dendricola*	2*x*	64.77	5.28	n/a	n/a	*R. parryae*	fresh		MPN52928; MPN52929
PK57	*R. taronense*	*R. taronense*	2*x*	65.14	5.02	n/a	n/a	*R. parryae*	fresh		MPN52930; MPN52931
PK58	*R. veitchianum*	*R. veitchianum* Os Blumhardt collection	2*x*	62.66	5.45	n/a	n/a	*R. parryae*	fresh	wild: Thailand	MPN52932; MPN52933
PK59#	*R. maddenii* ssp. *crassum* (as *R. manipurense*)	*R. maddenii* ssp. *crassum* Nape 025	6*x*	66.14	4.43	171.57	2.52	*R. fortunei*	fresh	wild: Aranachal Pradesh	MPN52934; MPN52935

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
PK60	*R. nuttallii*	*R. nuttallii*	2*x*	63.97	4.72	n/a	n/a	*R. parryae*	fresh	wild: China	MPN52936; MPN52937; MPN52938
PK61#	*R. maddenii* ssp. *crassum* (as *R. crassum*)	*R. maddenii* ssp. *crassum* (*R. odoriferum*)	7*x*	63.57	5.48	197.26	2.68	*R. fortunei*	fresh		MPN52939; MPN52940
PK63	*R. lindleyi*	*R. lindleyi*	2*x*	63.42	5.47	n/a	n/a	*R. parryae*	fresh		MPN52942
PK66	*R. ludwigianum*	*R. ludwigianum*	2*x*	65.03	5.28	n/a	n/a	*R. parryae*	fresh		MPN52948; MPN52949
PK67	*R. lindleyi*	*R. lindleyi*	2*x*	63.03	5.68	n/a	n/a	*R. parryae*	fresh		MPN52950
PK68#	*R. maddenii* ssp. *maddenii* (as *R. brachysiphon*)	*R. maddenii ssp. maddenii* (as *R. brachysiphon*)	6*x*	60.92	5.05	158.64	3.14	*R. fortunei*	fresh		MPN52951
RSF01	*R. burmanicum*	*R. burmanicum*	2*x*	61.84	10.23	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#99/095
RSF02	*R. changii*	*R. changii* JN 11029, wc Nov 2011	2*x*	51.74	10.45	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2015/043
RSF03	*R. ciliatum*	*R. ciliatum* LS&H 16019	2*x*	59.49	9.8	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Bhutan	RSBG#1980/077
RSF04	*R. ciliatum*	*R. ciliatum* SEH 545	2*x*	63.07	9.51	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Sikkim	RSBG#2000/094
RSF05	*R. ciliicalyx*	*R. ciliicalyx* TH#1276 2013/113	2*x*	61.25	10.19	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG
RSF06	*R. crenulatum*	*R. crenulatum* NV#072	2*x*	64.31	9.84	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG
RSF07	*R. cuffeanum*	*R. cuffeanum* KW 21909	2*x*	58.33	9.39	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2001/148
RSF08	*R. dalhousiae* var. *dalhousiae*	*R. dalhousiae* var. *dalhousiae* SEH 522	2*x*	60.91	11.02	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#99/153
RSF09	*R. dalhousiae* var. *rhabdotum*	*R. dalhousiae* var. *rhabdotum* KCSH 0310	2*x*	56.4	9.21	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India	RSBG#2006/046
RSF10	*R. dendricola*	*R. dendricola* F 17227	2*x*	66.51	10.15	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Himalaya	RSBG#1998/021
RSF11	*R. dendricola*	*R. dendricola* SEH 25037	2*x*	60.33	11.17	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2007/246
RSF12	*R. dendricola*	*R. dendricola* DGEY#046 2013/490	2*x*	63.31	9.07	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG
RSF13	*R. excellens*	*R. excellens* TH#3773	2*x*	61.12	11.07	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2019/054
RSF14	*R. fletcherianum*	*R. fletcherianum*	2*x*	56.78	12.88	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#65/355
RSF15	*R. fleuryi*	*R. fleuryi* KR 3286	2*x*	62.99	9.21	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam	RSBG#1998/009

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
RSF16	*R. formosum*	*R. formosum* C&H 320	2*x*	60.62	10.92	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Khasia, India	RSBG#1998/012
RSF17	*R. formosum* var. *inaequale*	*R. formosum* var. *inaequale* C&H 301	2*x*	59.38	11.37	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India	RSBG#1998/002
RSF18	*R.* aff. *formosum*	*R. formosum* aff. APA#008	2*x*	59.2	10.72	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#07/249
RSF19	*R. goreri*	*R. goreri* KR 6027	2*x*	63.48	10.24	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2003/188
RSF20	*R. goreri*	*R. goreri* RR 112	2*x*	63.42	9.26	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2005/249
RSF21	*R. horlickianum*	*R. horlickianum* CCHH 8074	2*x*	61.13	10.29	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2002/011
RSF22	*R. horlickianum*	*R. horlickianum* KW 9403	2*x*	59.4	12.3	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Burma&China	RSBG#1987/053
RSF23	*R. johnstoneanum*	*R. johnstoneanum* NAPE 024	2*x*	64.52	10.35	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India&Bhutan	RSBG
RSF24	*R. kiangsiense*	*R. kiangsiense* EN	2*x*	69.48	9.59	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2013/269
RSF25	*R. kuomeianum*	*R. kuomeianum* SEH#171	2*x*	55.19	12.14	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG
RSF26	*R. leptocladon*	*R. leptocladon* KR 2932	2*x*	65.64	9.45	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam	RSBG#1996/066
RSF27	*R. leptocladon*	*R. leptocladon* HWJ#99688	2*x*	69.75	8.54	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2005/035
RSF28	*R. levinei*	*R. levinei* CGG#14162	2*x*	62.15	11.67	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2020/142
RSF29	*R. levinei*	*R. levinei*	2*x*	67.55	9.42	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2002/006
RSF30	*R.* aff. *levinei*	*R. levinei* aff.TH#2805	2*x*	67.52	10.33	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2013/244
RSF31	*R. liliiflorum*	*R. liliiflorum* CGG 14066	2*x*	68.14	10.16	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2012/036
RSF32	*R. liliiflorum*	*R. liliiflorum* PW 116	2*x*	70.59	9.57	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2005/166
RSF33	*R. liliiflorum*	*R. liliiflorum* NN#0958	2*x*	64.7	8.71	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2017/143
RSF34	*R. lindleyi*	*R. lindleyi* KR 8074	2*x*	75.17	6.53	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India	RSBG#2008/100
RSF35	*R. lindleyi*	*R. lindleyi* SEH#534	2*x*	74.16	8.21	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2001/239
RSF36	*R. ludwigianum*	*R. ludwigianum*	2*x*	75.29	8.09	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2004/030
RSF37	*R. lyi*	*R. lyi* KR 2962	2*x*	75.38	6.9	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam	RSBG#1996/060

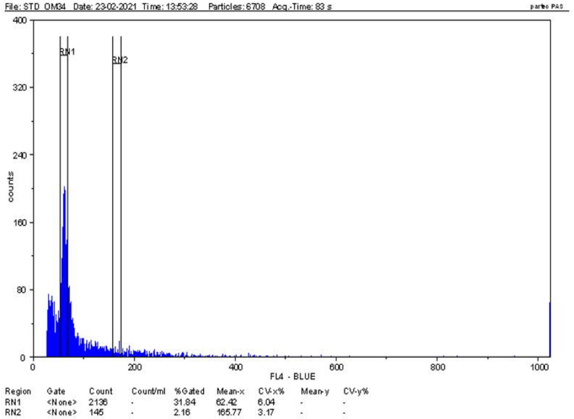
Sample	Taxon	Taxon labelled as	FCM ploidy	RN1		RN2		Diploid SD	Leaf sample	Wild accession	Specimen location and ID
				Mean-x	CV-x%	Mean-x	CV-x%				
RSF38	*R. lyi*	*R. lyi* KR Valder#	2*x*	79.34	6.79	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam (? probably Thailand)	RSBG#2001/146
RSF39	*R. lyi*	*R. lyi* FMWJ#13042	2*x*	78.11	8.34	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2015/018
RSF40	*R.* aff. *lyi*	*R. lyi* affinity NV#03	2*x*	81.1	8.16	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2019/083
RSF41	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	8*x*	43.25	9.08	181.55	3.48	*R. fortunei*	silica gel-dried	wild	RSBG#2011/120
RSF42	*R. maddenii*	*R. maddenii* KCSH#0345	6*x*	38.11	6.52	109.27	7.31	*R. fortunei*	silica gel-dried	wild: Arunachal Pradesh, India	RSBG#2006/393
RSF43	*R. maddenii* ssp. *maddenii*	*R. maddenii* ssp. *maddenii* SEH#599	6*x*	45.45	8.93	125.85	6.98	*R. fortunei*	silica gel-dried	wild: Sikkim, India	RSBG#2001/192
RSF44	*R. maddenii*	*R. maddenii*	8*x*	44.61	8.92	179.51	9.76	*R. fortunei*	silica gel-dried	wild	RSBG#2005/237
RSF45	*R. maddenii*	*R. maddenii*	6*x*	44	9.83	127.67	4	*R. fortunei*	silica gel-dried	wild	RSBG#2006/153
RSF46	*R. maddenii*	*R. maddenii*	2*x*	44.18	8.72	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2008/046
RSF47	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	2*x*	46.2	7.95	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2010/005
RSF48	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	2*x*	49.47	8.72	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#1999/631
RSF49	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum*	8*x*	50.18	7.93	199.1	5.47	*R. fortunei*	silica gel-dried	wild	RSBG#2007/273
RSF50	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum* BASE#9539	8*x*	51.17	6.21	206.78	4.12	*R. fortunei*	silica gel-dried	wild: China	RSBG#2009/017
RSF51	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum* KR#3116	2*x*	51.7	6.94	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam	RSBG#1996/027
RSF52	*R. maddenii* ssp. *crassum*	*R. maddenii* ssp. *crassum* DJHM#13057	8*x*	50.45	6.76	199.02	5.03	*R. fortunei*	silica gel-dried	wild: Burma	RSBG
RSF53	*R. megacalyx*	*R. megacalyx* BASE 9544	2*x*	51.38	7.05	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2005/243
RSF54	*R. megacalyx*	*R. megacalyx* DGEY#026	2*x*	51.62	5.86	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2006/304
RSF55	*R. nuttallii*	*R. nuttallii* DGEY 079	2*x*	52.5	7.68	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2004/374
RSF56	*R. nuttallii*	*R. nuttallii* HECC#10005	2*x*	49.76	8.13	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Arunachal Pradesh	RSBG
RSF57	*R. pachypodum*	*R. pachypodum* JN 11046	2*x*	52.3	7.27	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2014/217
RSF58	*R. pseudociliipes*	*R. pseudociliipes* JN 11070	2*x*	47.59	7.4	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2014/184
RSF59	*R. pseudociliipes*	*R. pseudociliipes* BASE 9697	2*x*	55.55	8.21	n/a	n/a	*R. fortunei*	silica gel-dried	wild: China	RSBG#2005/132

Sample	**Taxon**	**Taxon labelled as**	**FCM ploidy**	**RN1**		**RN2**		**Diploid SD**	**Leaf sample**	**Wild accession**	**Specimen location and ID**
				Mean-x	**CV-x%**	**Mean-x**	**CV-x%**				
RSF60	*R. pseudociliipes*	*R. pseudociliipes*	2*x*	56.16	8.79	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Vietnam	RSBG#2018/162
RSF61	*R. pseudomaddenii*	*R. pseudomaddenii* HECC#10083	2*x*	42.84	12.72	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2017/066
RSF62	*R. roseatum*	*R. roseatum* GLEN - RBGE	2*x*	39.72	11.53	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#1998/016
RSF63	*R. scopulorum*	*R. scopulorum* AC 3669	2*x*	41.93	11.89	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Bayi in Tibet, China	RSBG#2005/110
RSF64	*R. scopulorum*	*R. scopulorum* KW 6354	2*x*	46.7	12.34	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Tibet & Bhutan	RSBG#1998/014
RSF65	*R. scopulorum*	*R. scopulorum* CC 7571	2*x*	45.02	12.08	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Tibet	RSBG#2002/007
RSF66	*R. surasianum*	*R. surasianum* (no detail)	2*x*	44.13	13.34	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2003/177
RSF67	*R.* aff. *valentinioides* (ined.)	*R. valentinioides* affinity	2*x*	42.42	13.73	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2014/166
RSF68	*R. valentinianum* var. *oblongilobatum*	*R. oblongilobatum*	2*x*	37.54	12.57	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2014/211
RSF69	*R. valentinioides* (ined.)	*R. valentinioides*	2*x*	35.06	10.17	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#1997/139
RSF70	*R. veitchianum*	*R. veitchianum* C 9001	2*x*	41.85	13.63	n/a	n/a	*R. fortunei*	silica gel-dried	wild: Thailand	RSBG#2002/012
RSF71	*R. veitchianum*	*R. veitchianum*	2*x*	43.33	11.5	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#1998/017
RSF72	*R. walongense*	*R. walongense* HECC 10004	2*x*	44.18	10.86	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India	RSBG#1998/003
RSF73	*R. walongense*	*R. walongense* HECC 10006	2*x*	44.1	11.69	n/a	n/a	*R. fortunei*	silica gel-dried	wild: India	RSBG#2005/253
RSF74	*R. wumingense*	*R. wumingense* CGG 14150	2*x*	43.51	13.51	n/a	n/a	*R. fortunei*	silica gel-dried	wild	RSBG#2014/111

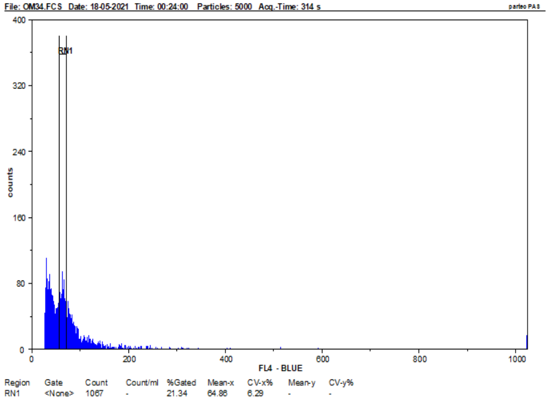
Table S3.3 Flow cytometry histograms of subsection *Maddenia* accessions with inconsistent ploidy in different runs

Samples are listed in alphabetical order of species names. Histogram graphs for each of the accessions are presented below the table correspondingly.

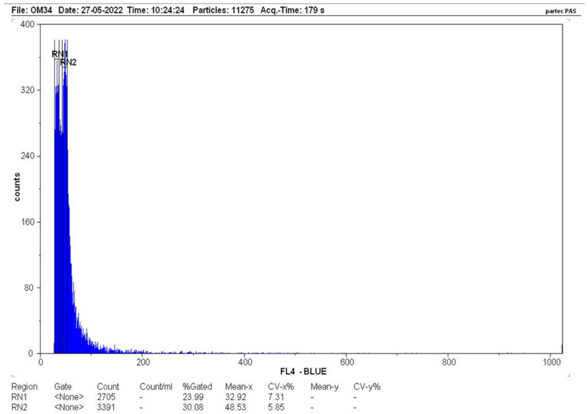
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. excellens	OM34	2*x*	*R. fortunei* (OM60)	fresh	62.49	6	n/a	n/a	23-02-2021 (left)
		2*x*	*R. fortunei* (OM60)	silica gel-dried	64.86	6.15	n/a	n/a	18-05-2021 (middle)
		Aneuploid lower than diploid standard?	*R. fortunei* (OM60)	Herbarium	48.46	5.85	33	7.35	27-05-2022 (right)



```
Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   2136    -          31.84    62.42    6.04    -        -
RN2      <None>   145     -          2.16     165.77   3.17    -        -
```

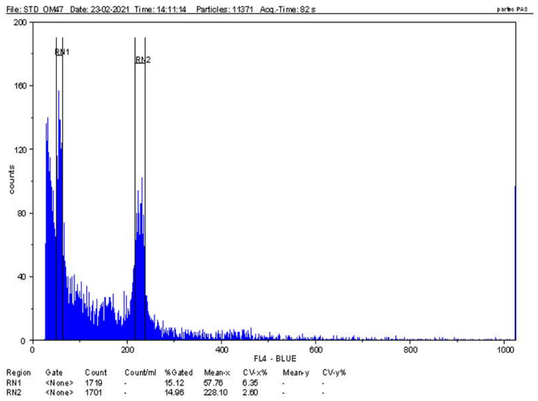


```
Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1067    -          21.34    64.86    6.29    -        -
```

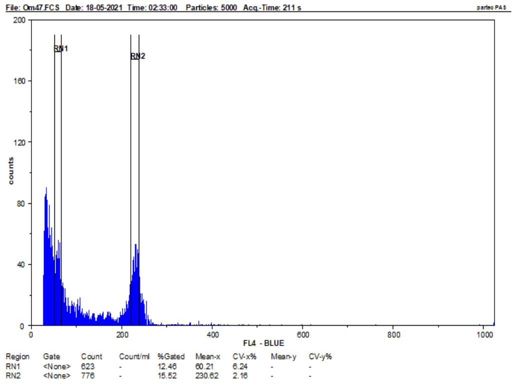


```
Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   2705    -          23.99    32.92    7.31    -        -
RN2      <None>   3391    -          30.08    48.53    5.85    -        -
```

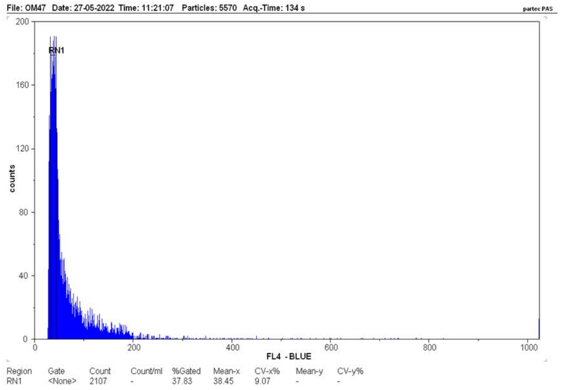
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *crassum*	OM47	8*x*	*R. fortunei* (OM60)	fresh	57.87	6.34	228.08	2.63	23-02-2021 (left)
		8*x*	*R. fortunei* (OM60)	silica gel-dried	60.13	6.2	230.52	2.14	18-05-2021 (middle)
		2*x*	*R. fortunei* (OM60)	Herbarium	38.46	9.12	n/a	n/a	27-05-2022 (right)


File: STD_OM47 Date: 23-02-2021 Time: 14:11:14 Particles: 11371 Acq.-Time: 82 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1719	-	15.12	57.76	6.35	-	-
RN2	<None>	1701	-	14.96	228.10	2.60	-	-

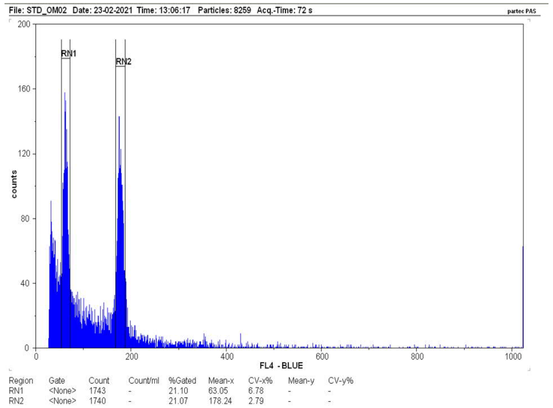

File: Om47.FCS Date: 18-05-2021 Time: 02:33:00 Particles: 5000 Acq.-Time: 211 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	623	-	12.46	60.21	6.24	-	-
RN2	<None>	776	-	15.52	230.62	2.16	-	-

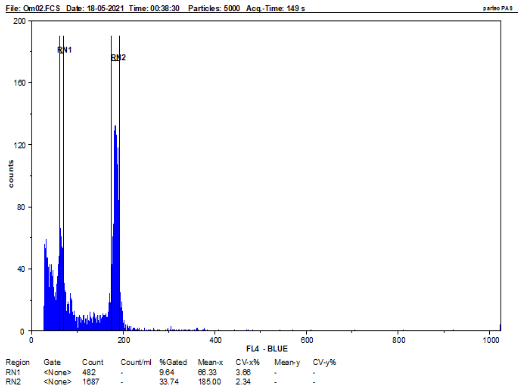

File: OM47 Date: 27-05-2022 Time: 11:21:07 Particles: 5570 Acq.-Time: 134 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2107	-	37.83	38.45	9.07	-	-

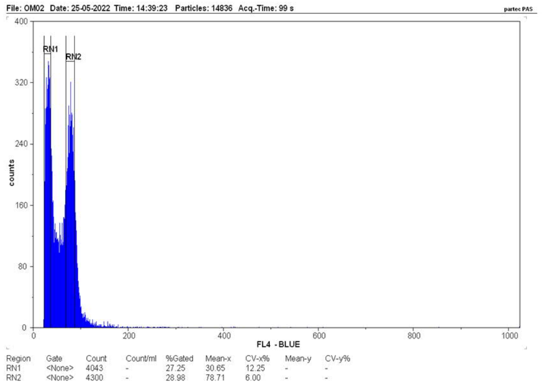
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM02	6*x*	*R. fortunei* (OM60)	fresh	63.14	6.78	178.28	2.77	23-02-2021 (left)
		6*x*	*R. fortunei* (OM60)	silica gel-dried	66.4	3.66	184.92	2.36	18-05-2021 (middle)
		5*x*	*R. fortunei* (OM60)	Herbarium	30.76	12.21	78.66	6.02	25-05-2022 (right)


File: STD_OM02 Date: 23-02-2021 Time: 13:06:17 Particles: 8259 Acq.-Time: 72 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1743	-	21.10	63.05	6.78	-	-
RN2	<None>	1740	-	21.07	178.24	2.79	-	-

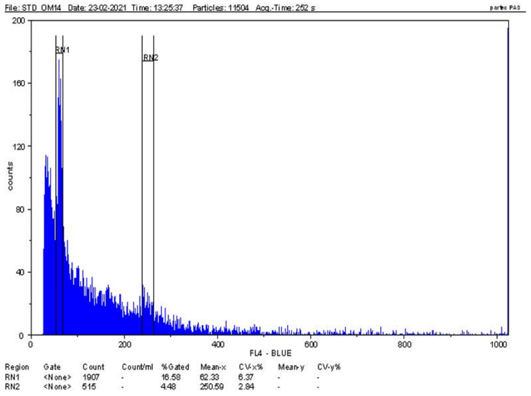

File: Om02.FCS Date: 18-05-2021 Time: 00:38:30 Particles: 5000 Acq.-Time: 149 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	482	-	9.64	66.33	3.66	-	-
RN2	<None>	1687	-	33.74	185.00	2.34	-	-

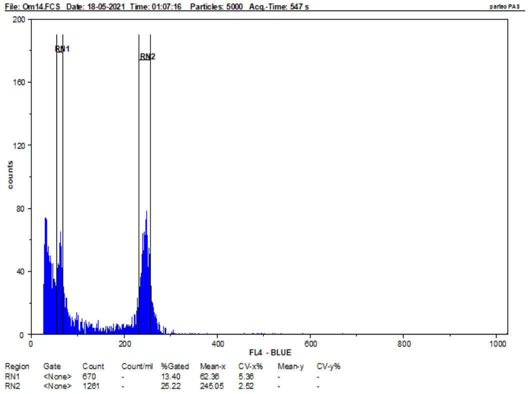

File: OM02 Date: 25-05-2022 Time: 14:39:23 Particles: 14836 Acq.-Time: 99 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	4043	-	27.25	30.65	12.25	-	-
RN2	<None>	4300	-	28.98	78.71	6.00	-	-

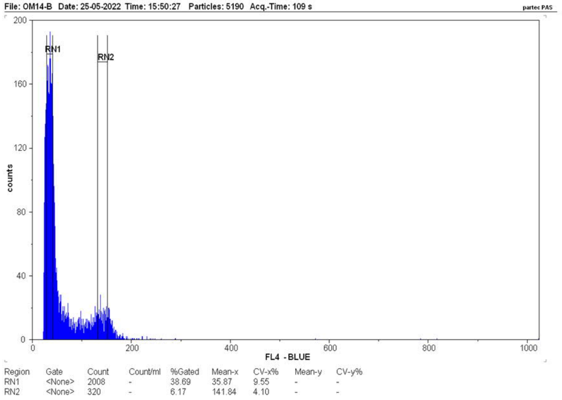
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM14	8*x*	*R. fortunei* (OM60)	fresh	62.33	6.37	250.59	2.84	23-02-2021 (left)
		8*x*	*R. fortunei* (OM60)	silica gel-dried	62.34	5.32	244.2	2.57	18-05-2021 (middle)
		2*x*? / 8*x*?	*R. fortunei* (OM60)	Herbarium	35.84	9.74	141.86	4.14	25-05-2022 (right)



Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1907	-	16.58	62.33	6.37	-	-
RN2	<None>	515	-	4.48	250.59	2.84	-	-

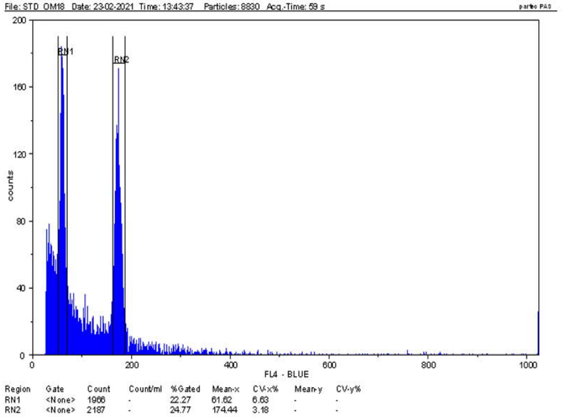


Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	670	-	13.40	62.36	5.36	-	-
RN2	<None>	1261	-	25.22	245.05	2.52	-	-

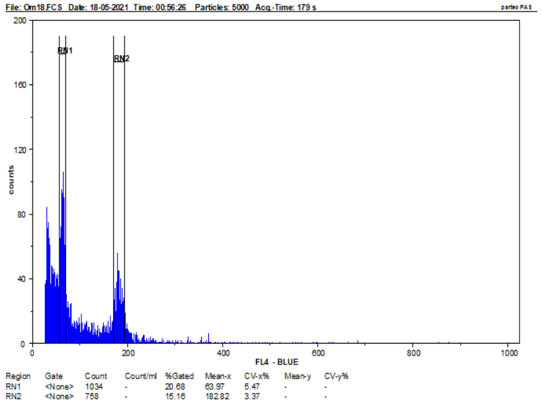


Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2008	-	38.69	35.87	9.55	-	-
RN2	<None>	320	-	6.17	141.84	4.10	-	-

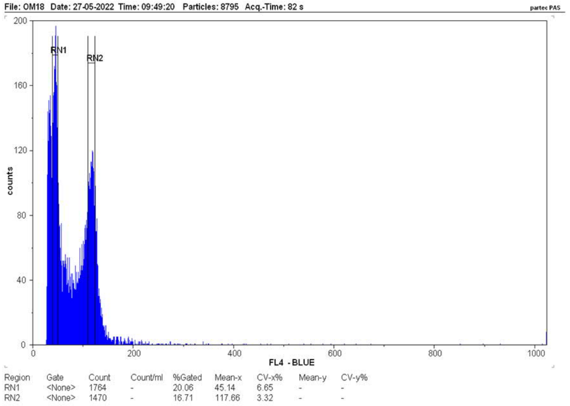
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM18	6*x*	*R. fortunei* (OM60)	fresh	61.73	6.62	174.45	3.19	23-02-2021 (left)
		6*x*	*R. fortunei* (OM60)	silica gel-dried	64.08	5.44	182.84	3.36	18-05-2021 (middle)
		5*x*	*R. fortunei* (OM60)	Herbarium	45.18	6.75	117.76	3.32	27-05-2022 (right)



Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1966	-	22.27	61.62	6.63	-	-
RN2	<None>	2187	-	24.77	174.44	3.18	-	-

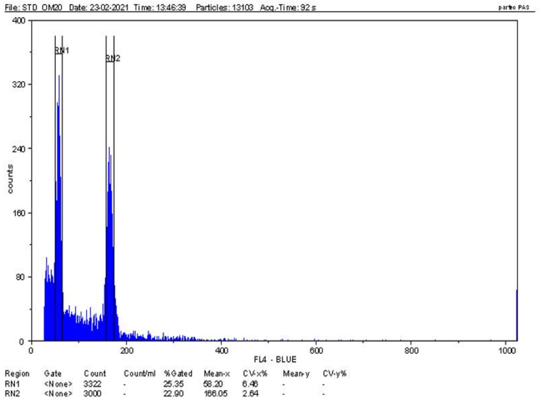


Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1034	-	20.68	63.97	5.47	-	-
RN2	<None>	758	-	15.16	182.82	3.37	-	-

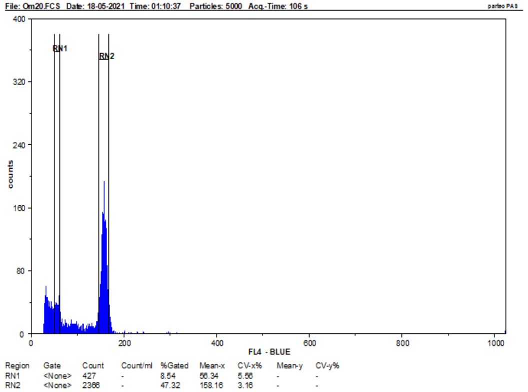


Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1764	-	20.06	45.14	6.65	-	-
RN2	<None>	1470	-	16.71	117.66	3.32	-	-

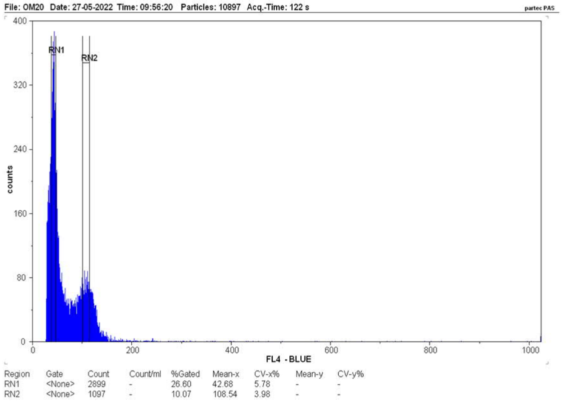
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM20	6*x*	*R. fortunei* (OM60)	fresh	58.28	6.42	166.06	2.64	23-02-2021 (left)
		6*x*	*R. fortunei* (OM60)	silica gel-dried	56.34	5.49	158.12	3.07	18-05-2021 (middle)
		5*x*	*R. fortunei* (OM60)	Herbarium	42.3	6.35	108.95	5.56	27-05-2022 (right)



```
File: STD_OM20   Date: 23-02-2021  Time: 13:46:39    Particles: 13103   Acq.-Time: 92 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   3322    -         25.35   58.20   6.46   -       -
RN2      <None>   3000    -         22.90   166.05  2.64   -       -
```

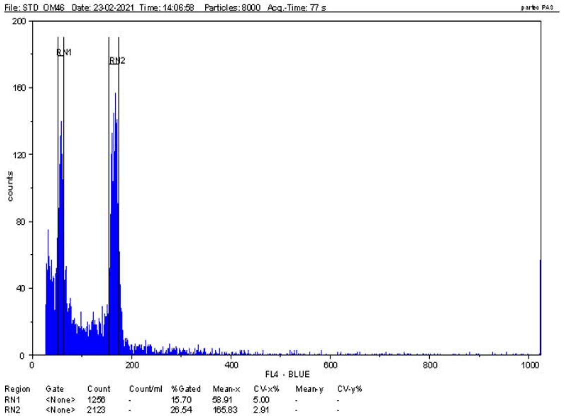


```
File: Om20.FCS   Date: 18-05-2021  Time: 01:10:37   Particles: 5000   Acq.-Time: 106 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   427     -         8.54    56.34   5.56   -       -
RN2      <None>   2366    -         47.32   158.16  3.16   -       -
```

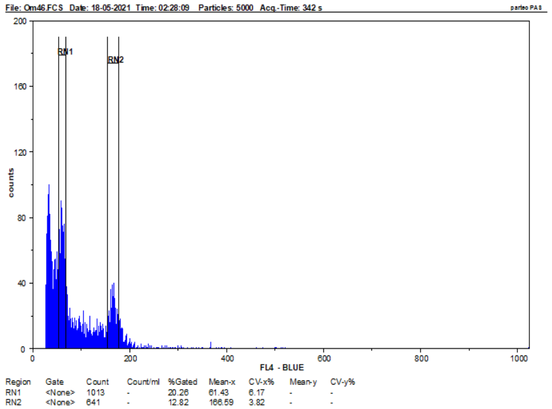


```
File: OM20   Date: 27-05-2022  Time: 09:56:20   Particles: 10897   Acq.-Time: 122 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   2899    -         26.60   42.68   5.78   -       -
RN2      <None>   1097    -         10.07   108.54  3.98   -       -
```

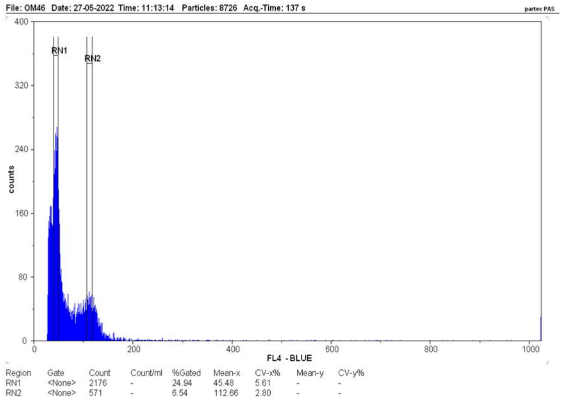
Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM46	6*x*	*R. fortunei* (OM60)	fresh	59.02	4.98	165.86	2.9	23-02-2021 (left)
		5-6*x*?	*R. fortunei* (OM60)	silica gel-dried	61.5	6.15	166.68	3.81	18-05-2021 (middle)
		5*x*	*R. fortunei* (OM60)	Herbarium	45.49	5.52	112.63	2.88	27-05-2022 (right)



```
File: STD_OM46   Date: 23-02-2021  Time: 14:06:58    Particles: 8000   Acq.-Time: 77 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   1256    -         15.70   58.91   5.00   -       -
RN2      <None>   2123    -         26.54   165.83  2.91   -       -
```

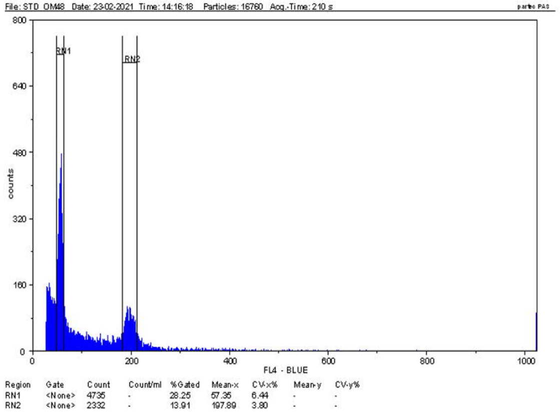


```
File: Om46.FCS   Date: 18-05-2021  Time: 02:28:09   Particles: 5000   Acq.-Time: 342 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   1013    -         20.26   61.43   6.17   -       -
RN2      <None>   641     -         12.82   166.59  3.82   -       -
```



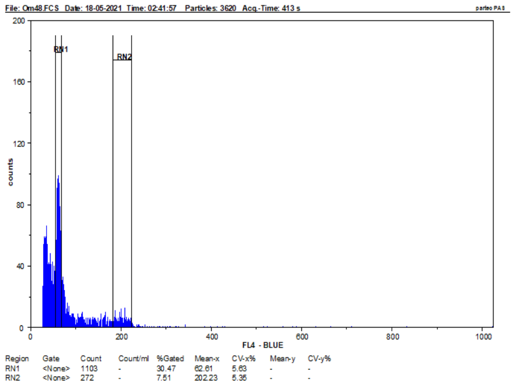
```
File: OM46   Date: 27-05-2022  Time: 11:13:14   Particles: 8726   Acq.-Time: 137 s

Region   Gate     Count   Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1      <None>   2176    -         24.94   45.48   5.61   -       -
RN2      <None>   571     -         6.54    112.66  2.80   -       -
```

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM48	7*x*	*R. fortunei* (OM60)	fresh	57.4	6.48	197.92	3.84	23-02-2021 (left)
		2x? / 7x?	*R. fortunei* (OM60)	silica gel-dried	62.64	5.62	202.26	5.32	18-05-2021 (middle)
		6-7x	*R. fortunei* (OM60)	Herbarium	37.05	9.41	125.97	2.87	27-05-2022 (right)



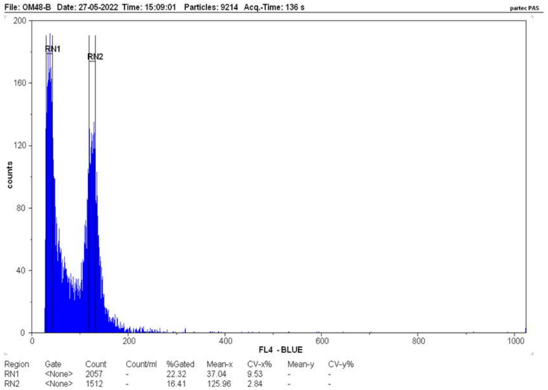
File: STD OM48 Date: 23-02-2021 Time: 14:16:18 Particles: 16760 Acq.-Time: 210 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	4735	-	28.25	57.35	6.44	-	-
RN2	<None>	2332	-	13.91	197.89	3.80	-	-



File: Om48.FCS Date: 18-05-2021 Time: 02:41:57 Particles: 3620 Acq.-Time: 413 s

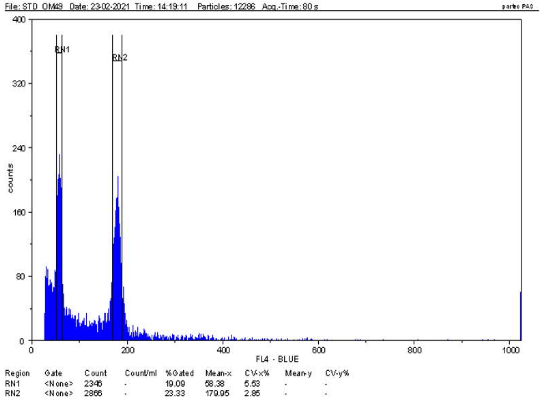
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1103	-	30.47	62.61	5.63	-	-
RN2	<None>	272	-	7.51	202.23	5.35	-	-



File: OM48-B Date: 27-05-2022 Time: 15:09:01 Particles: 9214 Acq.-Time: 136 s

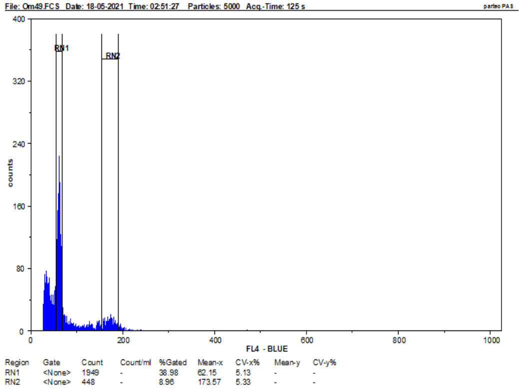
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2057	-	22.32	37.04	9.53	-	-
RN2	<None>	1512	-	16.41	125.96	2.84	-	-

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM49	6*x*	*R. fortunei* (OM60)	fresh	58.46	5.54	179.98	2.86	23-02-2021 (left)
		5-6*x*?	*R. fortunei* (OM60)	silica gel-dried	62.19	5.18	173.5	5.34	18-05-2021 (middle)
		6*x*	*R. fortunei* (OM60)	Herbarium	37.81	8	111.4	4.17	27-05-2022 (right)



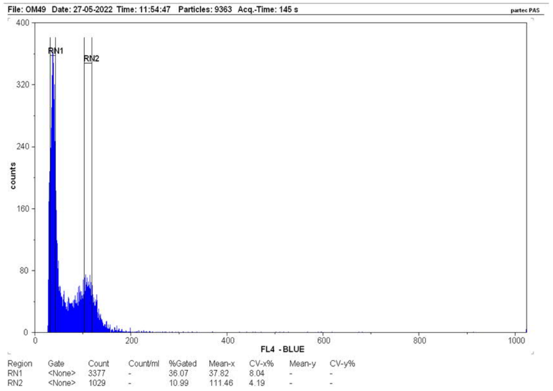
File: STD OM49 Date: 23-02-2021 Time: 14:19:11 Particles: 12286 Acq.-Time: 80 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2346	-	19.09	58.38	5.53	-	-
RN2	<None>	2866	-	23.33	179.95	2.85	-	-



File: Om49.FCS Date: 18-05-2021 Time: 02:51:27 Particles: 5000 Acq.-Time: 125 s

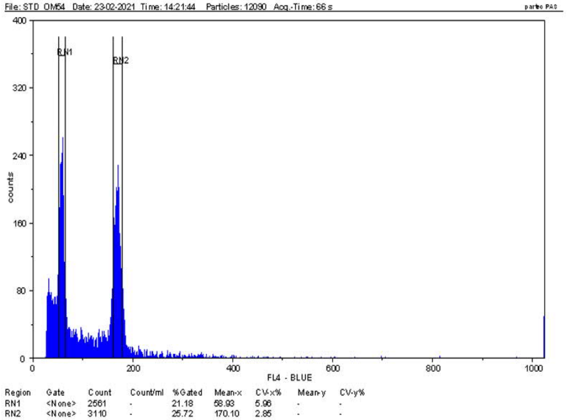
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1949	-	38.98	62.15	5.13	-	-
RN2	<None>	448	-	8.96	173.57	5.33	-	-



File: OM49 Date: 27-05-2022 Time: 11:54:47 Particles: 9363 Acq.-Time: 145 s

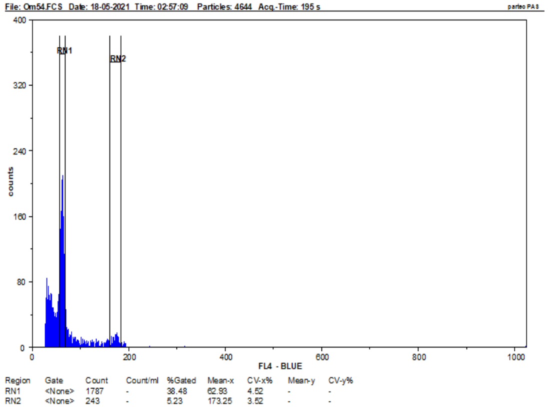
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	3377	-	36.07	37.82	8.04	-	-
RN2	<None>	1029	-	10.99	111.46	4.19	-	-

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	OM54	6*x*	*R. fortunei* (OM60)	fresh	58.98	5.97	170.11	2.87	23-02-2021 (left)
		5-6*x*?	*R. fortunei* (OM60)	silica gel-dried	63.03	4.5	173.35	3.52	18-05-2021 (middle)
		5*x*	*R. fortunei* (OM60)	Herbarium	44.71	6.32	117.89	2.63	27-05-2022 (right)



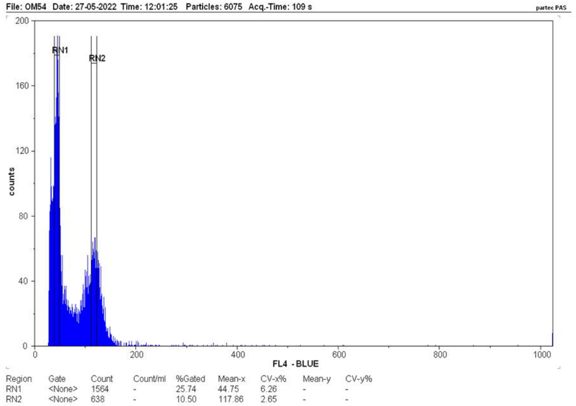
File: STD OM54 Date: 23-02-2021 Time: 14:21:44 Particles: 12090 Acq.-Time: 66 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2561	-	21.18	58.93	5.96	-	-
RN2	<None>	3110	-	25.72	170.10	2.85	-	-



File: Om54.FCS Date: 18-05-2021 Time: 02:57:09 Particles: 4644 Acq.-Time: 195 s

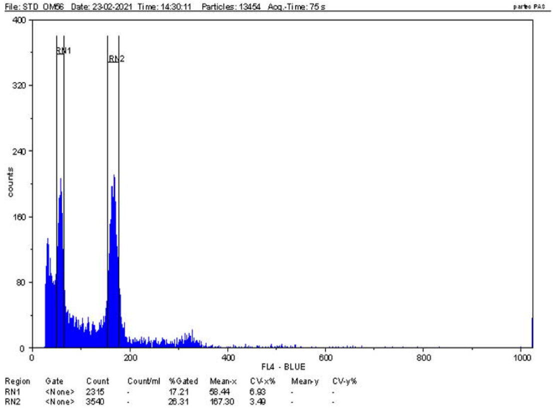
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1787	-	38.48	62.93	4.52	-	-
RN2	<None>	243	-	5.23	173.25	3.52	-	-



File: OM54 Date: 27-05-2022 Time: 12:01:25 Particles: 6075 Acq.-Time: 109 s

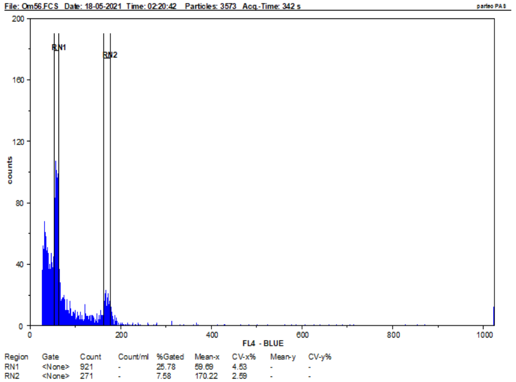
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1564	-	25.74	44.75	6.26	-	-
RN2	<None>	638	-	10.50	117.86	2.65	-	-

R. maddenii ssp. *maddenii*	OM56	6*x*	*R. fortunei* (OM60)	fresh	58.53	6.9	167.38	3.5	23-02-2021 (left)
		6*x*	*R. fortunei* (OM60)	silica gel-dried	59.76	4.54	170.32	2.59	18-05-2021 (middle)
		2*x*	*R. fortunei* (OM60)	Herbarium	34.88	9.43	n/a	n/a	27-05-2022 (right)



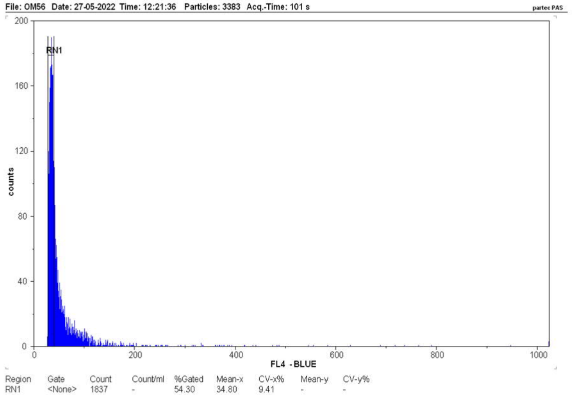
File: STD OM56 Date: 23-02-2021 Time: 14:30:11 Particles: 13454 Acq.-Time: 75 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2315	-	17.21	58.44	6.93	-	-
RN2	<None>	3540	-	26.31	167.30	3.49	-	-



File: Om56.FCS Date: 18-05-2021 Time: 02:20:42 Particles: 3573 Acq.-Time: 342 s

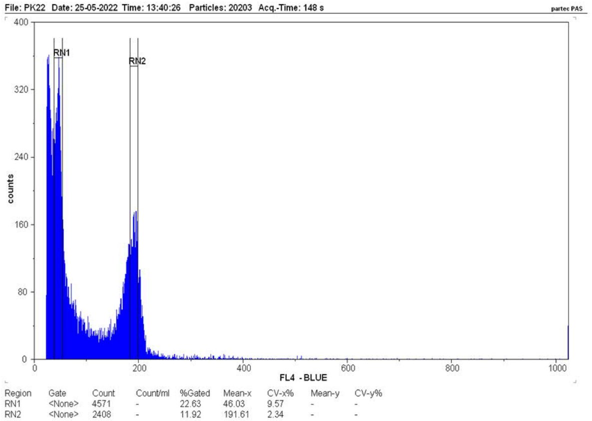
Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	921	-	25.78	59.69	4.53	-	-
RN2	<None>	271	-	7.58	170.22	2.59	-	-



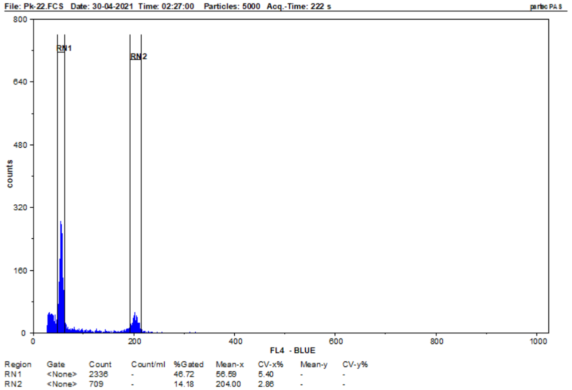
File: OM56 Date: 27-05-2022 Time: 12:21:36 Particles: 3383 Acq.-Time: 101 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1837	-	54.30	34.80	9.41	-	-

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *crassum*	PK22	8*x*	*R. fortunei*	fresh	46.09	9.6	191.62	2.36	25-05-2022 (left)
		7*x*	*R. parryae*	fresh	56.84	5.26	204.51	2.81	30-04-2021 (right)

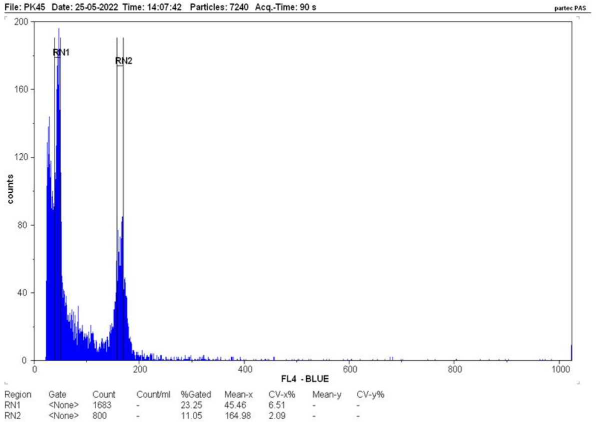


```
File: PK22   Date: 25-05-2022   Time: 13:40:26   Particles: 20203   Acq.-Time: 148 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   4571    -          22.63    46.03    9.57    -        -
RN2      <None>   2408    -          11.92    191.61   2.34    -        -
```

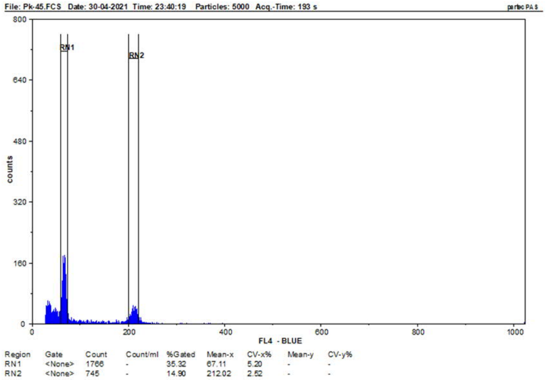


```
File: Pk-22.FCS   Date: 30-04-2021   Time: 02:27:00   Particles: 5000   Acq.-Time: 222 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   2336    -          46.72    56.59    5.40    -        -
RN2      <None>   709     -          14.18    204.00   2.86    -        -
```

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *crassum*	PK45	7*x*	*R. fortunei*	fresh	45.52	6.59	165.01	2.06	25-05-2022 (left)
		6*x*	*R. parryae*	fresh	67.11	4.97	212.12	2.47	30-04-2021 (right)

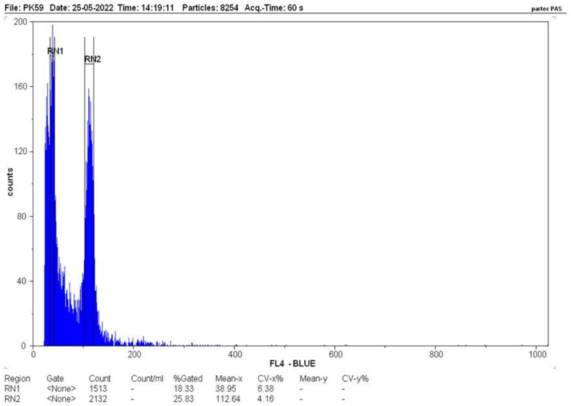


```
File: PK45   Date: 25-05-2022   Time: 14:07:42   Particles: 7240   Acq.-Time: 90 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1683    -          23.25    45.46    6.51    -        -
RN2      <None>   800     -          11.05    164.98   2.09    -        -
```

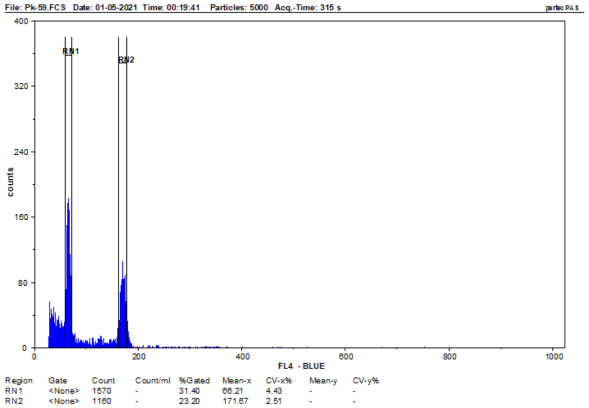


```
File: Pk-45.FCS   Date: 30-04-2021   Time: 23:40:19   Particles: 5000   Acq.-Time: 193 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1766    -          35.32    67.11    5.20    -        -
RN2      <None>   745     -          14.90    212.02   2.52    -        -
```

Taxon	**Sample**	**FCM ploidy**	**Diploid standard**	**Leaf sample**	**Mean-x (RN1)**	**CV-x% (RN1)**	**Mean-x (RN2)**	**CV-x% (RN2)**	**FCM date**
R. maddenii ssp. *crassum*	PK59	6*x*	*R. fortunei*	fresh	38.99	6.36	112.66	4.16	25-05-2022 (left)
		5*x*	*R. parryae*	fresh	66.14	4.43	171.57	2.52	01-05-2021 (right)

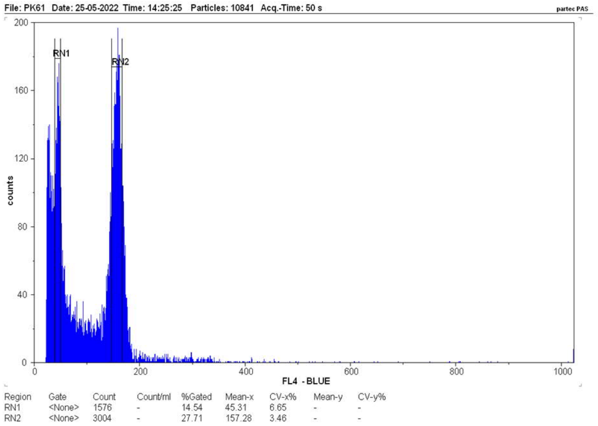


```
File: PK59   Date: 25-05-2022  Time: 14:19:11   Particles: 8254   Acq.-Time: 60 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1513    -          18.33    38.95    6.38    -        -
RN2      <None>   2132    -          25.83    112.64   4.16    -        -
```

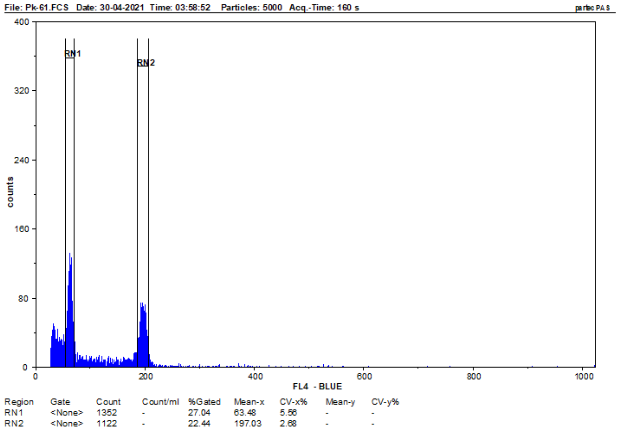


```
File: Pk-59.FCS   Date: 01-05-2021  Time: 00:19:41   Particles: 5000   Acq.-Time: 315 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1570    -          31.40    66.21    4.43    -        -
RN2      <None>   1160    -          23.20    171.67   2.51    -        -
```

R. maddenii ssp. *crassum*	PK61	7*x*	*R. fortunei*	fresh	45.34	6.78	157.25	3.48	25-05-2022 (left)
		6*x*	*R. parryae*	fresh	63.57	5.48	197.26	2.68	30-04-2021 (right)

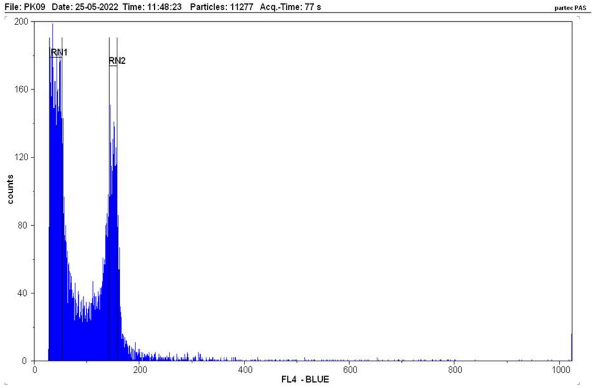


```
File: PK61   Date: 25-05-2022  Time: 14:25:25   Particles: 10841   Acq.-Time: 50 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1576    -          14.54    45.31    6.65    -        -
RN2      <None>   3004    -          27.71    157.28   3.46    -        -
```



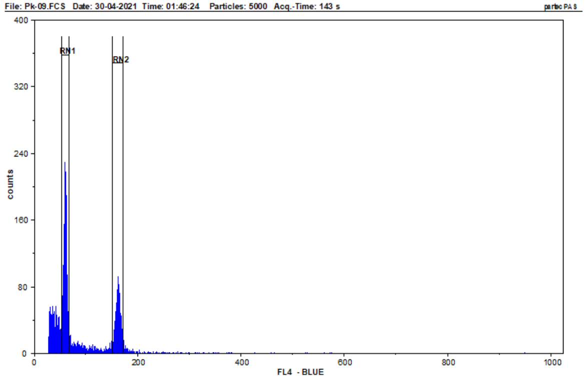
```
File: Pk-61.FCS   Date: 30-04-2021  Time: 03:58:52   Particles: 5000   Acq.-Time: 160 s

Region   Gate     Count   Count/ml   %Gated   Mean-x   CV-x%   Mean-y   CV-y%
RN1      <None>   1352    -          27.04    63.48    5.56    -        -
RN2      <None>   1122    -          22.44    197.03   2.68    -        -
```

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	PK09	7*x*	*R. fortunei*	fresh	41.41	16.62	151.06	2.91	25-05-2022 (left)
		5*x*	*R. parryae*	fresh	61.12	5.09	163.18	2.74	30-04-2021 (right)



File: PK09 Date: 25-05-2022 Time: 11:48:23 Particles: 11277 Acq.-Time: 77 s

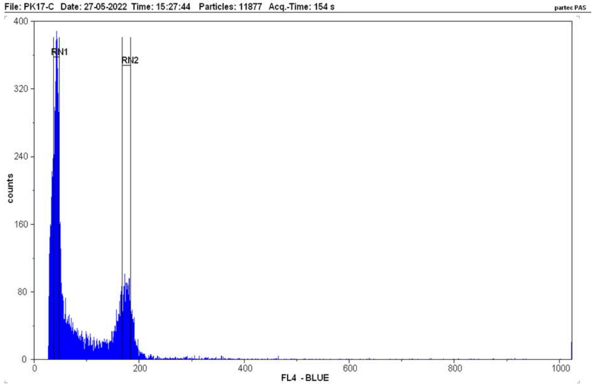
```
Region  Gate    Count  Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1     <None>  3886   -         34.46   41.47   16.58  -       -
RN2     <None>  1851   -         16.41   151.01  2.89   -       -
```



File: Pk-09.FCS Date: 30-04-2021 Time: 01:46:24 Particles: 5000 Acq.-Time: 143 s

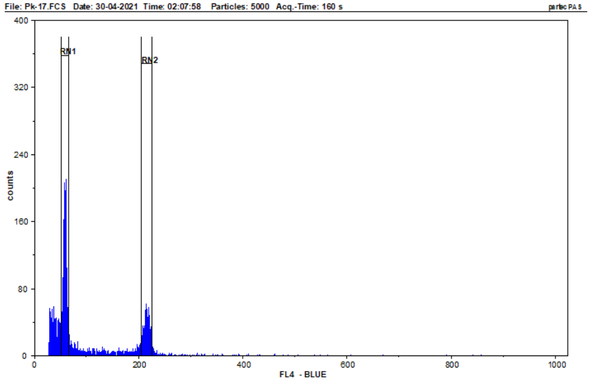
```
Region  Gate    Count  Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1     <None>  1862   -         37.24   60.93   5.19   -       -
RN2     <None>  1015   -         20.30   162.81  2.83   -       -
```

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	PK17	8*x*	*R. fortunei*	fresh	43	7.02	176.66	2.57	27-05-2022 (left)
		7*x*	*R. parryae*	fresh	59.74	5.13	216.78	2.24	30-04-2021 (right)



File: PK17-C Date: 27-05-2022 Time: 15:27:44 Particles: 11877 Acq.-Time: 154 s

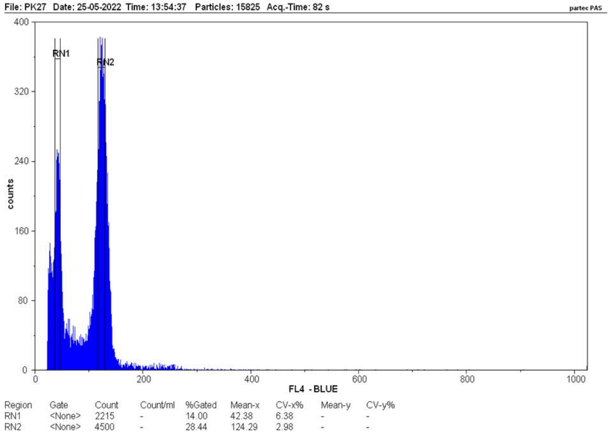
```
Region  Gate    Count  Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1     <None>  3553   -         29.91   42.92   7.05   -       -
RN2     <None>  1325   -         11.16   176.59  2.57   -       -
```



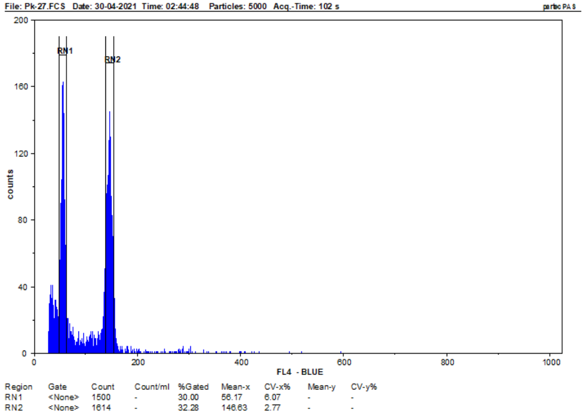
File: Pk-17.FCS Date: 30-04-2021 Time: 02:07:58 Particles: 5000 Acq.-Time: 160 s

```
Region  Gate    Count  Count/ml  %Gated  Mean-x  CV-x%  Mean-y  CV-y%
RN1     <None>  1750   -         35.00   59.54   5.14   -       -
RN2     <None>  920    -         18.40   216.52  2.28   -       -
```

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	PK27	6*x*	*R. fortunei*	fresh	42.39	6.3	124.27	3	25-05-2021 (left)
		5*x*	*R. parryae*	fresh	56.24	6.01	146.7	2.75	30-04-2021 (right)

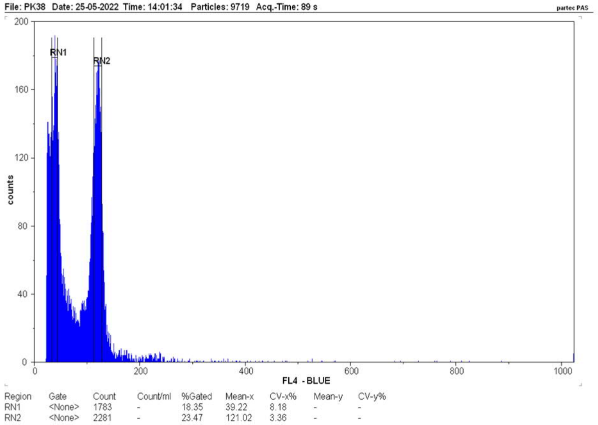

File: PK27 Date: 25-05-2022 Time: 13:54:37 Particles: 15825 Acq.-Time: 82 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	2215	-	14.00	42.38	6.38	-	-
RN2	<None>	4500	-	28.44	124.29	2.98	-	-

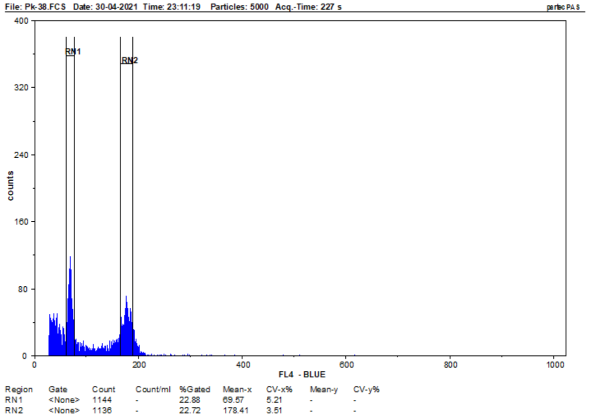

File: Pk-27.FCS Date: 30-04-2021 Time: 02:44:48 Particles: 5000 Acq.-Time: 102 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1500	-	30.00	56.17	6.07	-	-
RN2	<None>	1614	-	32.28	146.63	2.77	-	-

R. maddenii ssp. *maddenii*	PK38	6*x*	*R. fortunei*	fresh	39.29	8.12	121.05	3.38	25-05-2021 (left)
		5*x*	*R. parryae*	fresh	69.55	5.22	178.2	3.52	30-04-2021 (right)

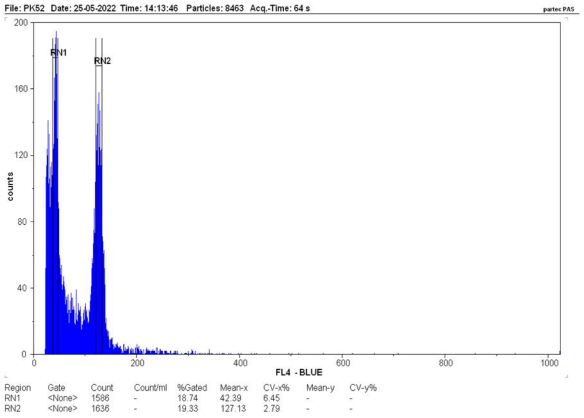

File: PK38 Date: 25-05-2022 Time: 14:01:34 Particles: 9719 Acq.-Time: 89 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1783	-	18.35	39.22	8.18	-	-
RN2	<None>	2281	-	23.47	121.02	3.36	-	-

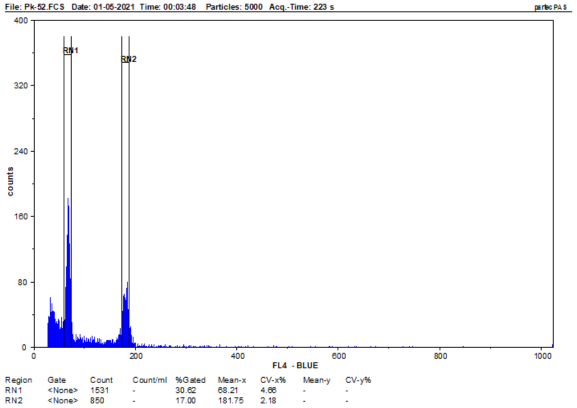

File: Pk-38.FCS Date: 30-04-2021 Time: 23:11:19 Particles: 5000 Acq.-Time: 227 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1144	-	22.88	69.57	5.21	-	-
RN2	<None>	1136	-	22.72	178.41	3.51	-	-

Taxon	Sample	FCM ploidy	Diploid standard	Leaf sample	Mean-x (RN1)	CV-x% (RN1)	Mean-x (RN2)	CV-x% (RN2)	FCM date
R. maddenii ssp. *maddenii*	PK52	6*x*	*R. fortunei*	fresh	42.35	6.31	127.2	2.77	25-05-2022 (left)
		5*x*	*R. parryae*	fresh	68.34	4.53	181.49	2.13	01-05-2021 (right)

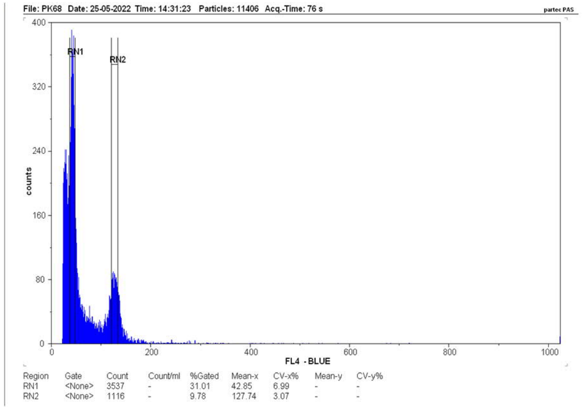

File: PK52 Date: 25-05-2022 Time: 14:13:46 Particles: 8463 Acq.-Time: 64 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1586	-	18.74	42.39	6.45	-	-
RN2	<None>	1636	-	19.33	127.13	2.79	-	-

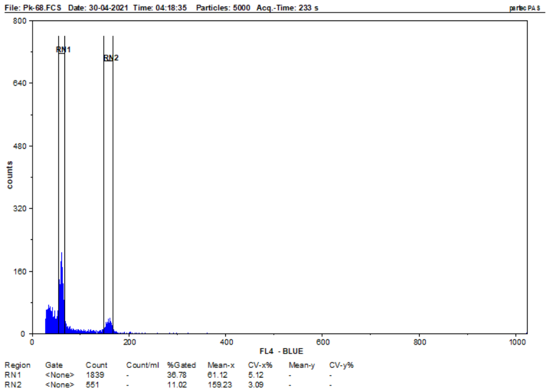

File: Pk-52.FCS Date: 01-05-2021 Time: 00:03:48 Particles: 5000 Acq.-Time: 223 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1531	-	30.62	68.21	4.66	-	-
RN2	<None>	850	-	17.00	181.75	2.18	-	-

R. maddenii ssp. *maddenii*	PK68	6*x*	*R. fortunei*	fresh	42.92	6.96	127.69	3	25-05-2022 (left)
		5*x*	*R. parryae*	fresh	60.92	5.05	158.64	3.14	30-04-2021 (right)

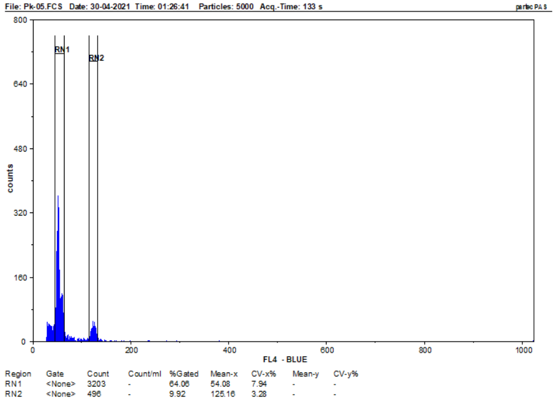

File: PK68 Date: 25-05-2022 Time: 14:31:23 Particles: 11406 Acq.-Time: 76 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	3537	-	31.01	42.85	6.99	-	-
RN2	<None>	1116	-	9.78	127.74	3.07	-	-

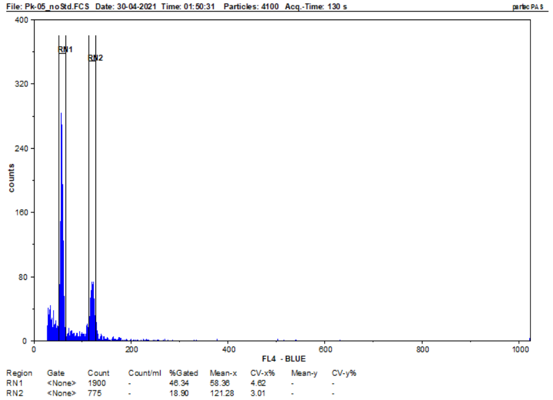

File: Pk-68.FCS Date: 30-04-2021 Time: 04:18:35 Particles: 5000 Acq.-Time: 233 s

Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1839	-	36.78	61.12	5.12	-	-
RN2	<None>	551	-	11.02	159.23	3.09	-	-

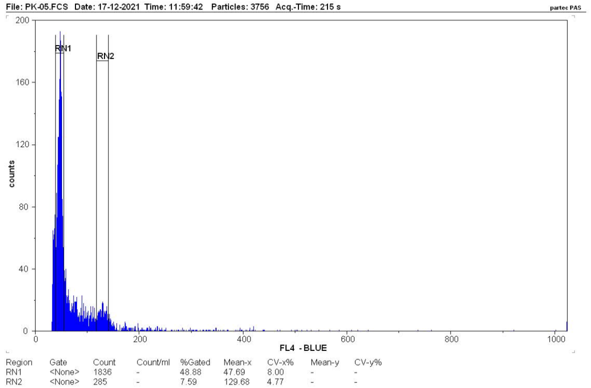
Taxon	**Sample**	**FCM ploidy**	**Diploid standard**	**Leaf sample**	**Mean-x (RN1)**	**CV-x% (RN1)**	**Mean-x (RN2)**	**CV-x% (RN2)**	**FCM date**
R. taggianum	PK05	2*x*?	*R. parryae*	fresh	54.11	7.93	n/a	n/a	30-04-2021 (left)
			no standard co-shopped	fresh	58.45	4.6	121.35	3.03	30-04-2021 (middle)*
		5*x*?	*R. fortunei*	fresh	47.74	8.04	129.79	4.77	17-12-2021 (right)
		PK 05 conclusion: 2*x* looks the most reasonable according to ploidy of sample chopped without standard. *showing polyploidy even with no standard material, suspected to be cell cyle of the sample.							



Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	3203	-	64.06	54.08	7.94	-	-
RN2	<None>	496	-	9.92	125.16	3.28	-	-



Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1900	-	46.34	58.36	4.62	-	-
RN2	<None>	775	-	18.90	121.28	3.01	-	-



Region	Gate	Count	Count/ml	%Gated	Mean-x	CV-x%	Mean-y	CV-y%
RN1	<None>	1836	-	48.88	47.69	8.00	-	-
RN2	<None>	285	-	7.59	129.68	4.77	-	-

Table S3.4 Genome size measurements of *R. fortunei* Lindl. and *R. parryae* Hutch.

$$\text{"2C} - \text{Tax"} = \frac{\text{"Tax}-\text{Mean}-\text{x"}}{\text{"Std}-\text{Mean}-\text{x"}} \times \text{"2C} - \text{Std"}$$

Taxon	Standard	Flow Code	Tax-Mean-x	Std-Mean-x	Ratio	2C-Std (pg)	2C-Tax (pg)
Rhododendron parryae Hutch.	*Pisum sativum* L.	RP-PS-1	71.47	377.29	0.189429882	8.8	1.666982957
Rhododendron parryae Hutch.	*Pisum sativum* L.	RP-PS-2	98.36	488.55	0.201330468	8.8	1.771708116
Rhododendron parryae Hutch.	*Pisum sativum* L.	RP-PS-3	113.82	549.49	0.207137528	8.8	1.822810242
***Rhododendron parryae* Hutch.**							**1.75 (Average)**
Rhododendron parryae Hutch.	*Zea mays* L.	RP-ZM-1	66.16	219.54	0.301357384	5.33	1.606234855
Rhododendron parryae Hutch.	*Zea mays* L.	RP-ZM-2	104.41	316.29	0.330108445	5.33	1.759478011
Rhododendron parryae Hutch.	*Zea mays* L.	RP-ZM-3	103.61	317.11	0.326732049	5.33	1.74148182
***Rhododendron parryae* Hutch.**							**1.70 (Average)**
Rhododendron fortunei Lindl. (OM60)	*Pisum sativum* L.	RFOM60-PS-1	88.15	493.78	0.178520799	8.8	1.570983029
Rhododendron fortunei Lindl. (OM60)	*Pisum sativum* L.	RFOM60-PS-2	85.97	503.91	0.170605862	8.8	1.501331587
Rhododendron fortunei Lindl. (OM60)	*Pisum sativum* L.	RFOM60-PS-3	88.48	518.9	0.17051455	8.8	1.50052804
***Rhododendron fortunei* Lindl. (OM60)**							**1.52 (Average)**
Rhododendron fortunei Lindl. (OM60)	*Zea mays* L.	RFOM60-ZM-1	90.71	319.99	0.283477609	5.33	1.510935654
Rhododendron fortunei Lindl. (OM60)	*Zea mays* L.	RFOM60-ZM-2	90	304.61	0.295459768	5.33	1.574800565
Rhododendron fortunei Lindl. (OM60)	*Zea mays* L.	RFOM60-ZM-3	92.52	305.96	0.30239247	5.33	1.611751863
***Rhododendron fortunei* Lindl. (OM60)**							**1.57 (Average)**

Appendix III: Supplementary Files – Chapter 4

Figure S4.1 BLAST results of the blueberry 3K DArTag baits against *Rhododendron* genomes

Figure S4.2 Recovered loci for each of the 203 samples in the full dataset

Figure S4.3 A) Maximum likelihood vs. B) Bayesian trees of the full dataset

Figure S4.4 A) Maximum likelihood vs. B) Bayesian trees of samples in the *R. maddenii* complex

Figure S4.5 A) Maximum likelihood vs. B) Bayesian trees of all diploids including the two diploid samples of *R. maddenii*

Table S4.1 Specimen information for the accessions sampled for phylogenetic study

Figure S4.1 BLAST results of the blueberry 3K DArTag baits against *Rhododendron* genomes

Percentage of identity threshold is 90%. 'chr' or 'LG' represents each of the 13 chromosomes in a haploid. A) *R. simsii* B) *R. williamsianum.*

Figure S4.1 A)

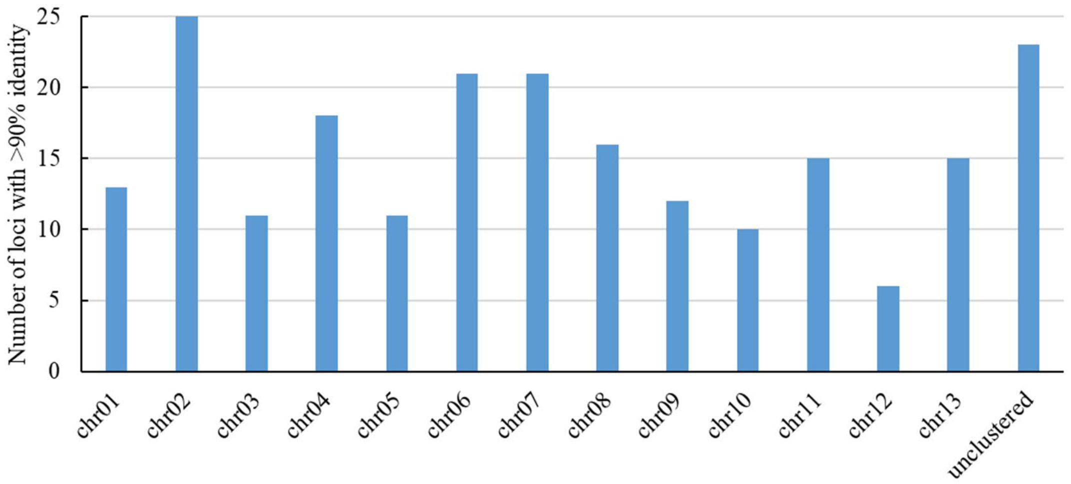


Figure S4.1 B)

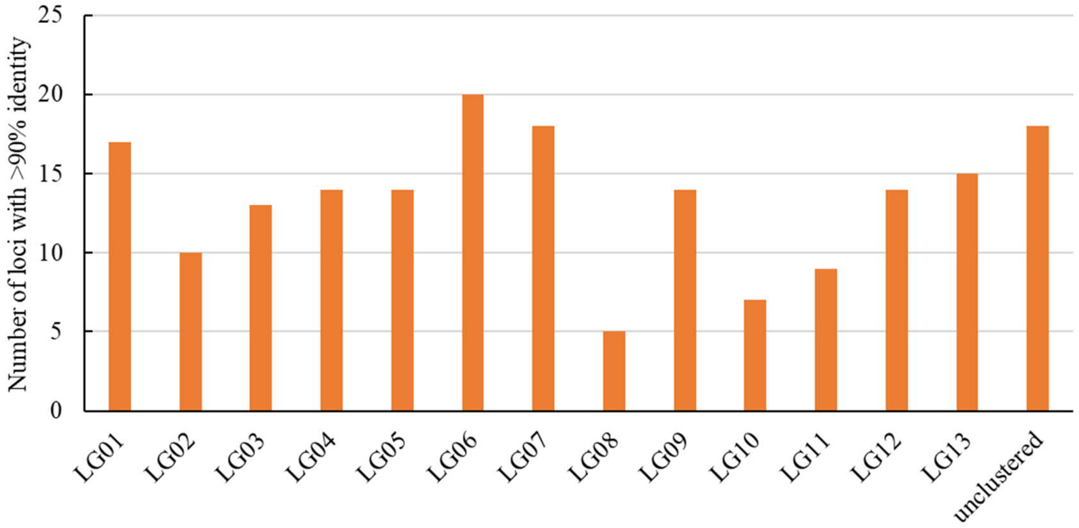
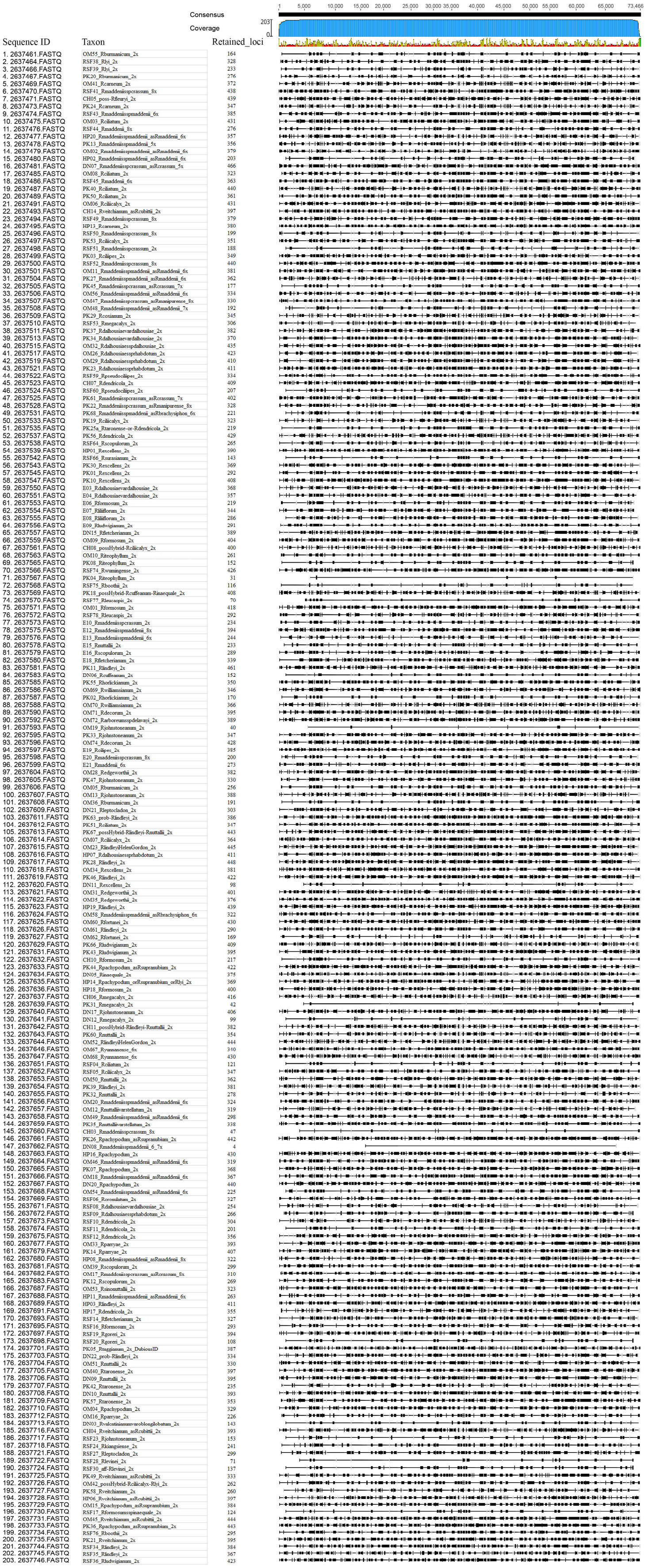


Figure S4.2 Recovered loci for each of the 203 samples in the full dataset

This figure shows the consensus loci as presented in Geneious 9.1.8, at identify threshold 85%. Gaps are ignored. For each sample, the loci of gray sites show agreements to the consensus using *R. simsii* genome as the reference (a total of 1,176 loci captured after reads filtering using ipyrad). The disagreements to the consensus are highlighted in black. The number of recovered loci is shown in the 'Retained_loci' column. The name string in the 'Taxon' column represents '(sample ID)_(taxon name)_(ploidy level)'.

This figure is shown on the next page.

Figure S4.2 (caption on the previous page)



Sequence ID	Taxon	Retained_loci
1. 2637461.FASTQ	OM55_Rburmanicum_2x	164
2. 2637464.FASTQ	RSF38_Rlyi_2x	328
3. 2637466.FASTQ	RSF39_Rlyi_2x	233
4. 2637467.FASTQ	PK20_Rburmanicum_2x	276
5. 2637469.FASTQ	OM41_Rcarneum_2x	372
6. 2637470.FASTQ	RSF41_Rmaddeniisspcrassum_8x	438
7. 2637471.FASTQ	CH05_poss-Rfleuryi_2x	439
8. 2637473.FASTQ	PK24_Rcarneum_2x	347
9. 2637474.FASTQ	RSF43_Rmaddeniisspmaddenii_6x	385
10. 2637475.FASTQ	OM03_Rciliatum_2x	431
11. 2637476.FASTQ	RSF44_Rmaddenii_8x	276
12. 2637477.FASTQ	HP20_Rmaddeniisspmaddenii_asRmaddenii_6x	357
13. 2637478.FASTQ	PK13_Rmaddeniisspmaddenii_5x	356
14. 2637479.FASTQ	OM02_Rmaddeniisspmaddenii_asRmaddenii_6x	379
15. 2637480.FASTQ	HP02_Rmaddeniisspmaddenii_asRmaddenii_6x	203
16. 2637481.FASTQ	DN07_Rmaddeniisspcrassum_asRcrassum_5x	466
17. 2637485.FASTQ	OM08_Rciliatum_2x	323
18. 2637486.FASTQ	RSF45_Rmaddenii_6x	363
19. 2637487.FASTQ	PK40_Rciliatum_2x	440
20. 2637489.FASTQ	PK50_Rciliatum_2x	361
21. 2637491.FASTQ	OM06_Rciliicalyx_2x	431
22. 2637493.FASTQ	CH14_Rveitchianum_asRcubittii_2x	397
23. 2637494.FASTQ	RSF49_Rmaddeniisspcrassum_8x	379
24. 2637495.FASTQ	HP13_Rcarneum_2x	380
25. 2637496.FASTQ	RSF50_Rmaddeniisspcrassum_8x	199
26. 2637497.FASTQ	PK53_Rciliicalyx_2x	351
27. 2637498.FASTQ	RSF51_Rmaddeniisspcrassum_2x	188
28. 2637499.FASTQ	PK03_Rciliipes_2x	349
29. 2637500.FASTQ	RSF52_Rmaddeniisspcrassum_8x	440
30. 2637501.FASTQ	OM11_Rmaddeniisspmaddenii_asRmaddenii_6x	381
31. 2637504.FASTQ	PK27_Rmaddeniisspmaddenii_asRmaddenii_6x	362
32. 2637505.FASTQ	PK45_Rmaddeniisspcrassum_asRcrassum_7x	177
33. 2637506.FASTQ	OM56_Rmaddeniisspmaddenii_asRmaddenii_6x	334
34. 2637507.FASTQ	OM47_Rmaddeniisspcrassum_asRmanipurense_8x	330
35. 2637508.FASTQ	OM48_Rmaddeniisspmaddenii_asRmaddenii_7x	192
36. 2637509.FASTQ	PK29_Rcoxianum_2x	345
37. 2637510.FASTQ	RSF53_Rmegacalyx_2x	306
38. 2637511.FASTQ	PK37_Rdalhousiaevardalhousiae_2x	382
39. 2637513.FASTQ	PK34_Rdalhousiaevardalhousiae_2x	370
40. 2637515.FASTQ	OM32_Rdalhousiaesspdalhousiae_2x	435
41. 2637517.FASTQ	OM26_Rdalhousiaessprhabdotum_2x	423
42. 2637519.FASTQ	OM29_Rdalhousiaessprhabdotum_2x	410
43. 2637521.FASTQ	PK23_Rdalhousiaessprhabdotum_2x	411
44. 2637522.FASTQ	RSF59_Rpseudociliipes_2x	334
45. 2637523.FASTQ	CH07_Rdendricola_2x	409
46. 2637524.FASTQ	RSF60_Rpseudociliipes_2x	207
47. 2637525.FASTQ	PK61_Rmaddeniisspcrassum_asRcrassum_7x	402
48. 2637528.FASTQ	PK22_Rmaddeniisspcrassum_asRmanipurense_8x	328
49. 2637531.FASTQ	PK68_Rmaddeniisspmaddenii_asRbrachysiphon_6x	221
50. 2637533.FASTQ	PK19_Rciliicalyx_2x	323
51. 2637535.FASTQ	PK25a_Rtaronense-or-Rdendricola_2x	219
52. 2637537.FASTQ	PK56_Rdendricola_2x	429
53. 2637538.FASTQ	RSF64_Rscopulorum_2x	265
54. 2637539.FASTQ	HP01_Rexcellens_2x	390
55. 2637542.FASTQ	RSF66_Rsurasianum_2x	143
56. 2637543.FASTQ	PK30_Rexcellens_2x	369
57. 2637545.FASTQ	PK01_Rexcellens_2x	292
58. 2637547.FASTQ	PK10_Rexcellens_2x	408
59. 2637550.FASTQ	E03_Rdalhousiaevardalhousiae_2x	368
60. 2637551.FASTQ	E04_Rdalhousiaevardalhousiae_2x	357
61. 2637553.FASTQ	E06_Rformosum_2x	219
62. 2637554.FASTQ	E07_Rliliiflorum_2x	344
63. 2637555.FASTQ	E08_Rliliiflorum_2x	286
64. 2637556.FASTQ	E09_Rludwigianum_2x	291
65. 2637557.FASTQ	DN15_Rfletcherianum_2x	389
66. 2637559.FASTQ	OM09_Rformosum_2x	404
67. 2637561.FASTQ	CH08_possHybrid-Rciliicalyx_2x	400
68. 2637563.FASTQ	OM10_Riteophyllum_2x	261
69. 2637565.FASTQ	PK08_Riteophyllum_2x	152
70. 2637566.FASTQ	RSF74_Rwumingense_2x	426
71. 2637567.FASTQ	PK04_Riteophyllum_2x	31
72. 2637568.FASTQ	RSF75_Rboothii_2x	116
73. 2637569.FASTQ	PK18_possHybrid-Rcuffeanum-Rinaequale_2x	408
74. 2637570.FASTQ	RSF77_Rleucaspis_2x	70
75. 2637571.FASTQ	OM01_Rformosum_2x	418
76. 2637572.FASTQ	RSF78_Rleucaspis_2x	292
77. 2637573.FASTQ	E10_Rmaddeniisspcrassum_2x	234
78. 2637575.FASTQ	E12_Rmaddeniisspmaddenii_8x	394
79. 2637576.FASTQ	E13_Rmaddeniisspmaddenii_6x	244
80. 2637578.FASTQ	E15_Rnuttallii_2x	233
81. 2637579.FASTQ	E16_Rscopulorum_2x	289
82. 2637580.FASTQ	E18_Rfletcherianum_2x	339
83. 2637581.FASTQ	PK11_Rlindleyi_2x	461
84. 2637583.FASTQ	DN06_Rcuffeanum_2x	152
85. 2637585.FASTQ	PK55_Rhorlickianum_2x	350
86. 2637586.FASTQ	OM69_Rwilliamsianum_2x	346
87. 2637587.FASTQ	PK02_Rhorlickianum_2x	170
88. 2637588.FASTQ	OM70_Rwilliamsianum_2x	366
89. 2637590.FASTQ	OM71_Rdecorum_2x	395
90. 2637592.FASTQ	OM72_Rarboreumsspdelavayi_2x	389
91. 2637593.FASTQ	OM19_Rjohnstoneanum_2x	40
92. 2637595.FASTQ	PK33_Rjohnstoneanum_2x	347
93. 2637596.FASTQ	OM74_Rdecorum_2x	428
94. 2637597.FASTQ	E19_Rcilipes_2x	385
95. 2637598.FASTQ	E20_Rmaddeniisspcrassum_8x	200
96. 2637599.FASTQ	E21_Rmaddenii_6x	273
97. 2637604.FASTQ	OM28_Redgeworthii_2x	382
98. 2637605.FASTQ	PK47_Rjohnstoneanum_2x	330
99. 2637606.FASTQ	OM05_Rburmanicum_2x	256
100. 2637607.FASTQ	OM13_Rjohnstoneanum_2x	388
101. 2637608.FASTQ	OM36_Rburmanicum_2x	191
102. 2637609.FASTQ	DN21_Rleptocladon_2x	303
103. 2637611.FASTQ	PK63_prob-Rlindleyi_2x	386
104. 2637612.FASTQ	PK51_Rciliatum_2x	347
105. 2637613.FASTQ	PK67_possHybrid-Rlindleyi-Rnuttallii_2x	443
106. 2637614.FASTQ	OM07_Rciliicalyx_2x	364
107. 2637615.FASTQ	OM23_RlindleyiHelenGordon_2x	445
108. 2637616.FASTQ	HP07_Rdalhousiaessprhabdotum_2x	411
109. 2637617.FASTQ	PK28_Rlindleyi_2x	448
110. 2637618.FASTQ	OM34_Rexcellens_2x	381
111. 2637619.FASTQ	PK46_Rlindleyi_2x	422
112. 2637620.FASTQ	DN11_Rexcellens_2x	98
113. 2637621.FASTQ	OM31_Redgeworthii_2x	401
114. 2637622.FASTQ	OM35_Redgeworthii_2x	376
115. 2637623.FASTQ	HP19_Rlindleyi_2x	439
116. 2637624.FASTQ	OM58_Rmaddeniisspmaddenii_asRbrachysiphon_6x	322
117. 2637625.FASTQ	OM60_Rfortunei_2x	430
118. 2637626.FASTQ	OM61_Rlindleyi_2x	290
119. 2637627.FASTQ	OM62_Rfortunei_2x	169
120. 2637629.FASTQ	PK66_Rludwigianum_2x	409
121. 2637631.FASTQ	PK43_Rludwigianum_2x	395
122. 2637632.FASTQ	CH10_Rformosum_2x	217
123. 2637633.FASTQ	PK44_Rpachypodum_asRsupranubium_2x	422
124. 2637634.FASTQ	DN05_Rinaequale_2x	375
125. 2637635.FASTQ	HP14_Rpachypodum_orRsupranubium_orRlyi_2x	369
126. 2637636.FASTQ	HP18_Rformosum_2x	400
127. 2637637.FASTQ	CH06_Rmegacalyx_2x	416
128. 2637639.FASTQ	PK31_Rmegacalyx_2x	42
129. 2637640.FASTQ	DN17_Rjohnstoneanum_2x	406
130. 2637641.FASTQ	DN12_Rmegacalyx_2x	99
131. 2637642.FASTQ	CH11_possHybrid-Rlindleyi-Rnuttallii_2x	382
132. 2637643.FASTQ	PK60_Rnuttallii_2x	354
133. 2637644.FASTQ	OM52_RlindleyiHelenGordon_2x	444
134. 2637646.FASTQ	OM67_Ryunnanense_6x	340
135. 2637647.FASTQ	OM68_Ryunnanense_6x	430
136. 2637651.FASTQ	RSF04_Rciliatum_2x	121
137. 2637652.FASTQ	RSF05_Rciliicalyx_2x	347
138. 2637653.FASTQ	OM50_Rnuttallii_2x	362
139. 2637654.FASTQ	PK39_Rlindleyi_2x	381
140. 2637655.FASTQ	PK32_Rnuttallii_2x	278
141. 2637656.FASTQ	OM20_Rmaddeniisspmaddenii_asRmaddenii_6x	324
142. 2637657.FASTQ	OM12_Rnuttalliivarstellatum_2x	319
143. 2637658.FASTQ	OM49_Rmaddeniisspmaddenii_asRmaddenii_6x	298
144. 2637659.FASTQ	PK35_Rnuttalliivarstellatum_2x	338
145. 2637660.FASTQ	CH03_Rmaddeniisspcrassum_8x	47
146. 2637661.FASTQ	PK26_Rpachypodum_asRsupranubium_2x	442
147. 2637662.FASTQ	DN08_Rmaddeniisspmaddenii_6_7x	4
148. 2637663.FASTQ	HP16_Rpachypodum_2x	430
149. 2637664.FASTQ	OM46_Rmaddeniisspmaddenii_asRmaddenii_6x	319
150. 2637665.FASTQ	PK07_Rpachypodum_2x	368
151. 2637666.FASTQ	OM18_Rmaddeniisspmaddenii_asRmaddenii_6x	367
152. 2637667.FASTQ	DN20_Rpachypodum_2x	440
153. 2637668.FASTQ	OM54_Rmaddeniisspmaddenii_asRmaddenii_6x	225
154. 2637669.FASTQ	RSF06_Rcrenulatum_2x	327
155. 2637671.FASTQ	RSF08_Rdalhousiaevardalhousiae_2x	254
156. 2637672.FASTQ	RSF09_Rdalhousiaessprhabdotum_2x	266
157. 2637673.FASTQ	RSF10_Rdendricola_2x	304
158. 2637674.FASTQ	RSF11_Rdendricola_2x	201
159. 2637675.FASTQ	RSF12_Rdendricola_2x	356
160. 2637677.FASTQ	OM33_Rparryae_2x	393
161. 2637679.FASTQ	PK14_Rparryae_2x	407
162. 2637680.FASTQ	HP08_Rmaddeniisspmaddenii_asRmaddenii_8x	322
163. 2637681.FASTQ	OM39_Rscopulorum_2x	299
164. 2637682.FASTQ	OM17_Rmaddeniisspcrassum_asRcrassum_8x	310
165. 2637683.FASTQ	PK12_Rscopulorum_2x	269
166. 2637687.FASTQ	OM53_Rsinonuttallii_2x	323
167. 2637688.FASTQ	HP11_Rmaddeniisspmaddenii_asRmaddenii_6x	263
168. 2637689.FASTQ	HP03_Rlindleyi_2x	411
169. 2637691.FASTQ	HP17_Rdendricola_2x	355
170. 2637693.FASTQ	RSF14_Rfletcherianum_2x	327
171. 2637695.FASTQ	RSF16_Rformosum_2x	293
172. 2637697.FASTQ	RSF19_Rgoreri_2x	394
173. 2637698.FASTQ	RSF20_Rgoreri_2x	108
174. 2637701.FASTQ	PK05_Rtaggianum_2x_DubiousID	387
175. 2637703.FASTQ	DN22_prob-Rlindleyi_2x	334
176. 2637704.FASTQ	OM51_Rnuttallii_2x	330
177. 2637705.FASTQ	OM40_Rtaronense_2x	397
178. 2637706.FASTQ	DN09_Rnuttallii_2x	395
179. 2637707.FASTQ	PK42_Rtaronense_2x	235
180. 2637708.FASTQ	DN10_Rnuttallii_2x	393
181. 2637709.FASTQ	PK57_Rtaronense_2x	353
182. 2637710.FASTQ	OM04_Rpachypodum_2x	329
183. 2637712.FASTQ	OM16_Rparryae_2x	226
184. 2637713.FASTQ	DN03_Rvalentinianumvaroblongilobatum_2x	143
185. 2637716.FASTQ	CH04_Rveitchianum_asRcubittii_2x	393
186. 2637717.FASTQ	RSF23_Rjohnstoneanum_2x	153
187. 2637718.FASTQ	RSF24_Rkiangsiense_2x	241
188. 2637721.FASTQ	RSF27_Rleptocladon_2x	299
189. 2637722.FASTQ	RSF28_Rlevinei_2x	71
190. 2637724.FASTQ	RSF30_aff-Rlevinei_2x	137
191. 2637725.FASTQ	PK49_Rveitchianum_asRcubittii_2x	333
192. 2637726.FASTQ	OM42_possHybrid-Rciliicalyx-Rlyi_2x	262
193. 2637727.FASTQ	PK58_Rveitchianum_2x	260
194. 2637728.FASTQ	HP06_Rveitchianum_asRcubittii_2x	397
195. 2637729.FASTQ	OM15_Rpachypodum_asRsupranubium_2x	384
196. 2637730.FASTQ	RSF17_Rformosumsspinaequale_2x	124
197. 2637731.FASTQ	OM45_Rveitchianum_asRcubittii_2x	444
198. 2637733.FASTQ	PK36_Rpachypodum_asRsupranubium_2x	443
199. 2637734.FASTQ	RSF76_Rboothii_2x	295
200. 2637735.FASTQ	PK21_Rveitchianum_2x	395
201. 2637744.FASTQ	RSF34_Rlindleyi_2x	384
202. 2637745.FASTQ	RSF35_Rlindleyi_2x	367
203. 2637746.FASTQ	RSF36_Rludwigianum_2x	423

Figure S4.3 A) Maximum likelihood vs. B) Bayesian trees of the full dataset

Trees are rooted with OM70 (*R. williamsianum*, 2*x*), with support values (bootstrap and posterior probability, respectively). Background highlight colours indicate the Davidian (1982) series: yellow – Ciliatum Series; purple – Maddenii Series Ciliicalyx Subseries; ocean blue – Maddenii Series Megacalyx Subseries; pink – Maddenii Series Maddenii Subseries. Annotated names in navy blue are outgroup. Names in red are samples from species that are threatened, at risk or lacking data following the Red List assessments summarised in List S2.3 (Chapter 2). Scale bar represents substitutions per site.

This figure is shown on the next two pages.

Figure S4.3 A) (caption on the previous page)

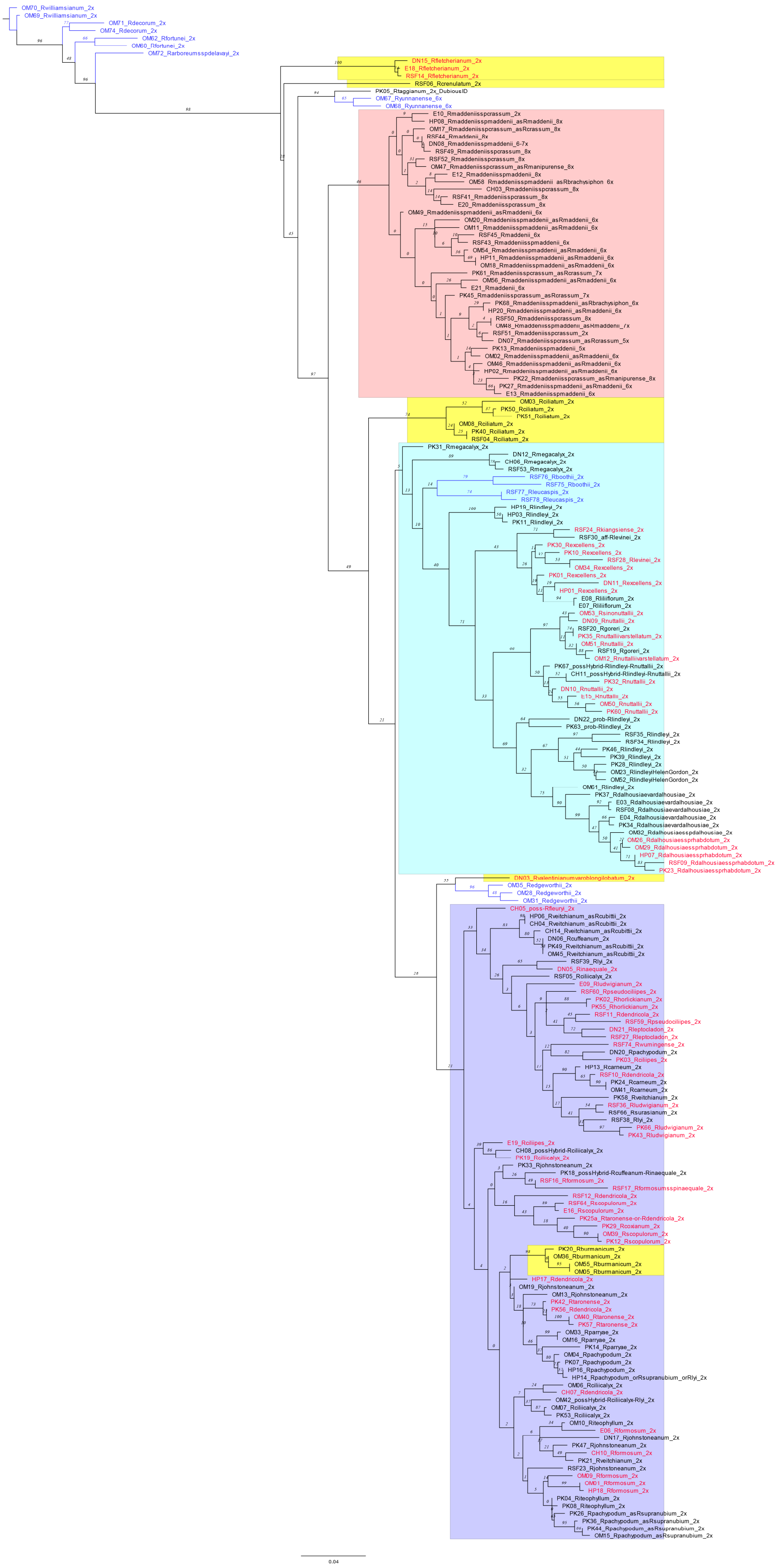


Figure S4.3 B) (caption on the page prior Figure S4.3 A)

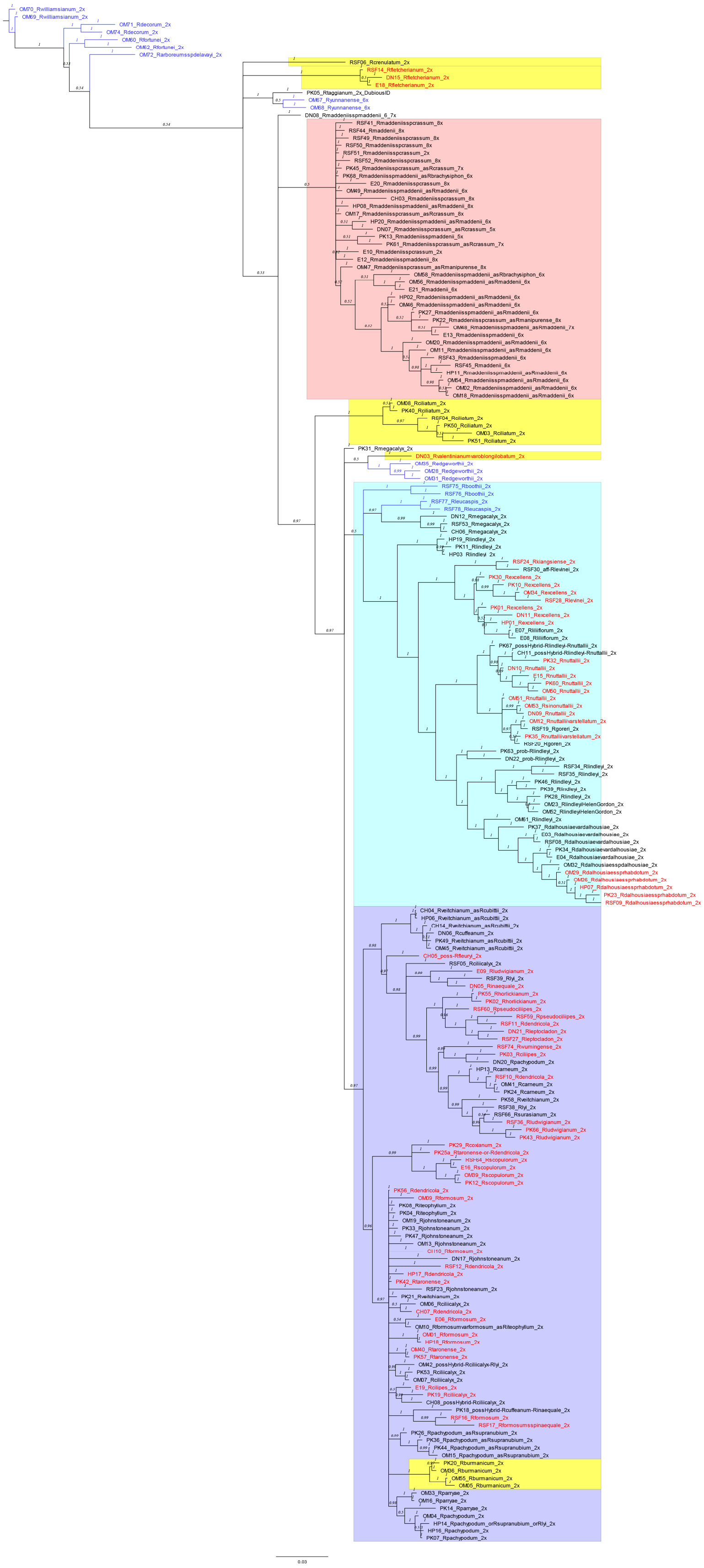


Figure S4.4 A) Maximum likelihood vs. B) Bayesian trees of samples in the *R. maddenii* complex

Trees are not rooted with OM58 (*R. maddenii* ssp. *maddenii* as the synonym *R. brachysiphon*, 6*x*). Scale bar represents substitutions per site.

This figure is shown on the next page.

(caption on the previous page)

Figure S4.4 A)

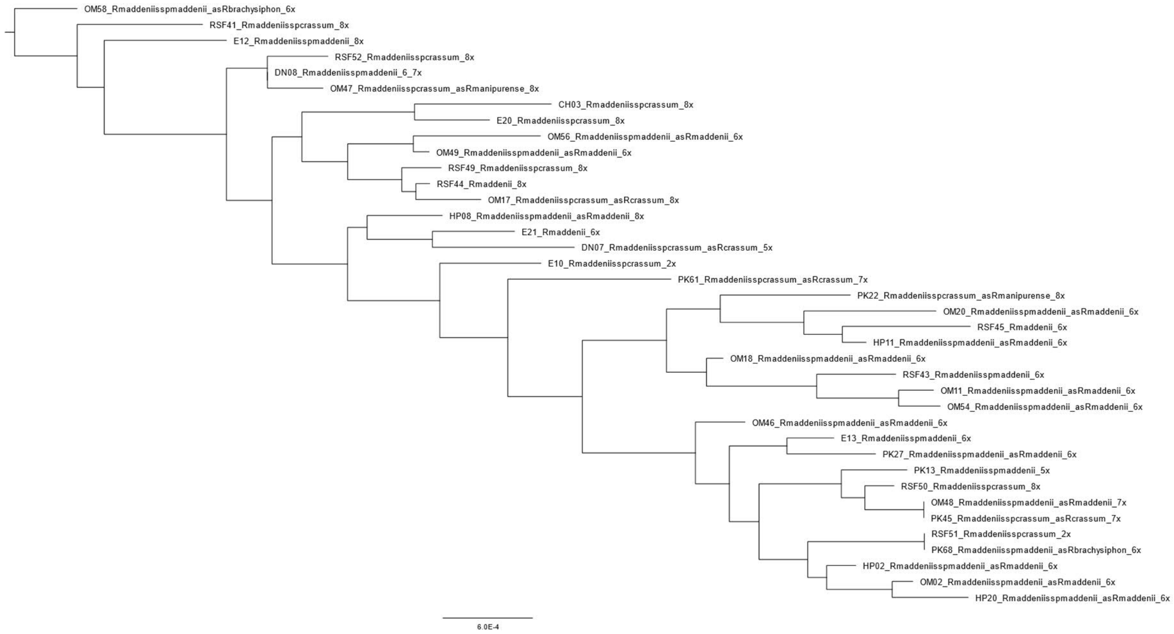


Figure S4.4 B)

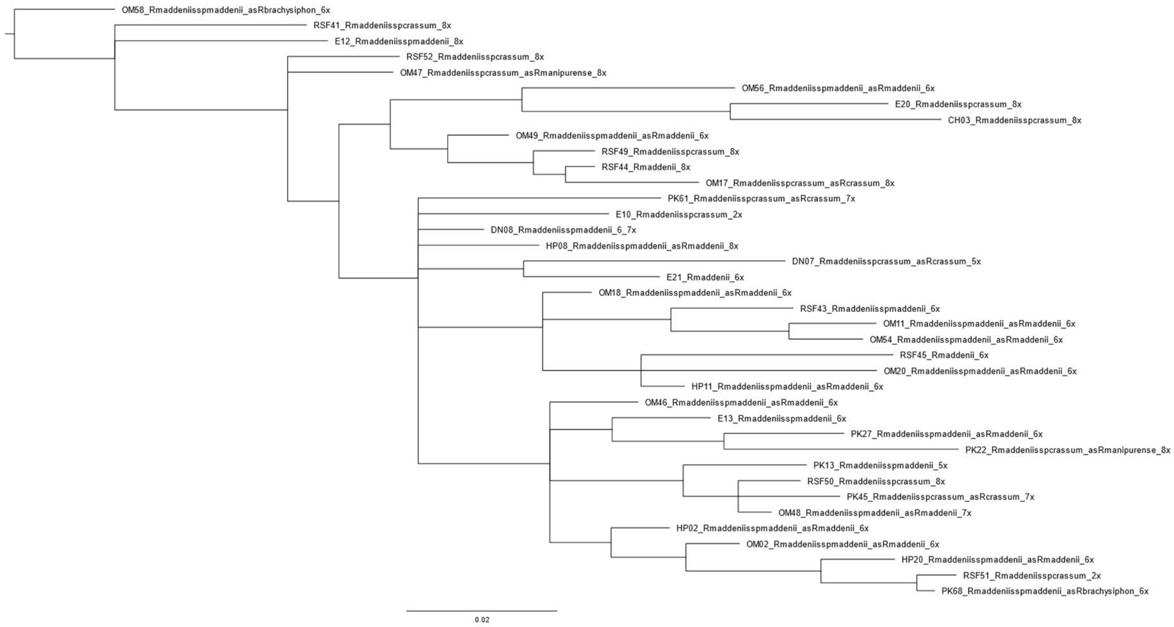


Figure S4.5 A) Maximum likelihood vs. B) Bayesian trees of all diploids including the two diploid samples of *R. maddenii*

Trees are rooted with OM70 (*R. williamsianum*, 2*x*). Scale bar represents substitutions per site.

This figure is shown on the next two pages.

Figure S4.5 A) (caption on the previous page)

Figure S4.5 B) (caption on the previous page prior Figure S4.5 A)

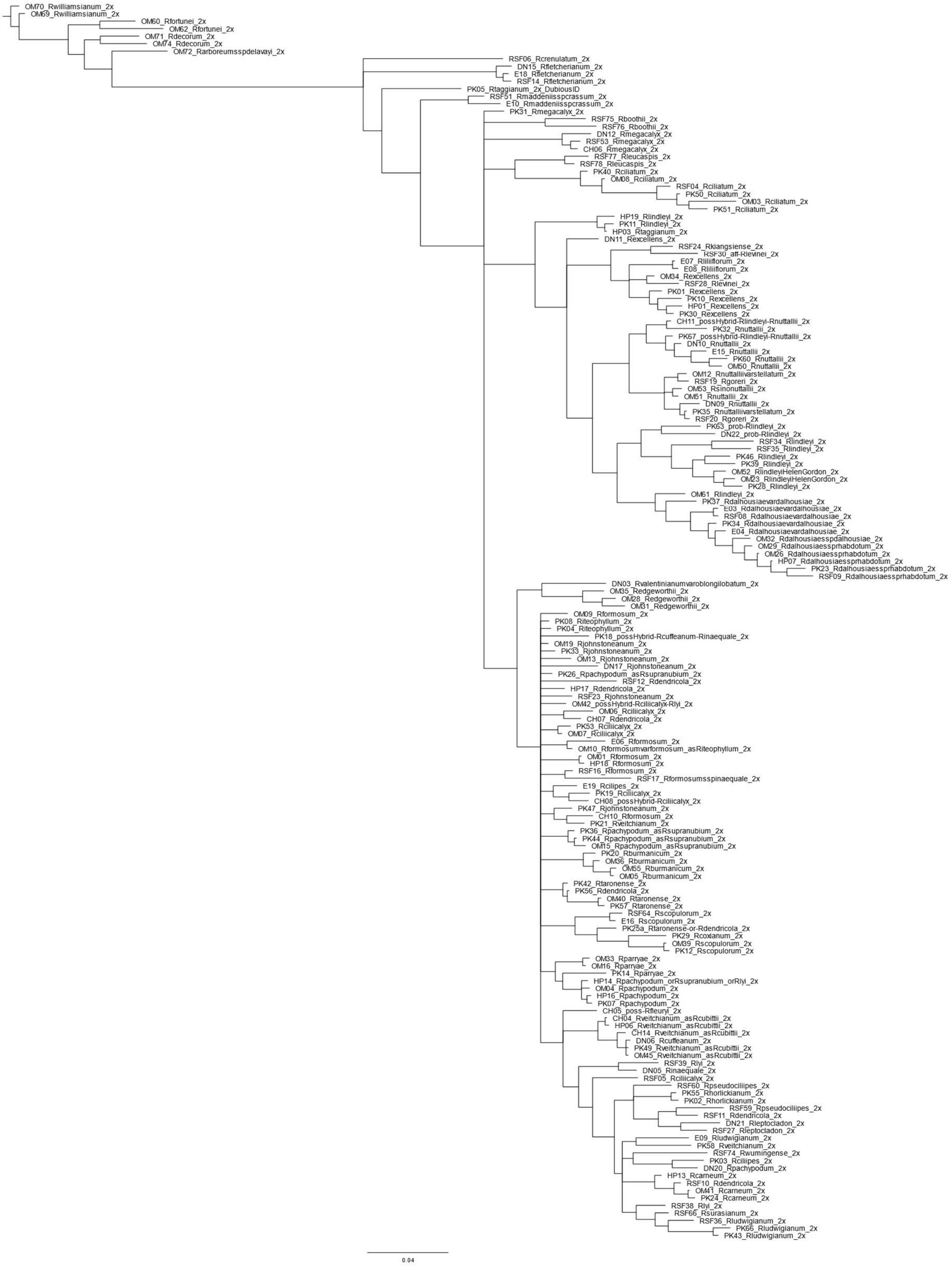


Table S4.1 Specimen information for the accessions sampled for phylogenetic study

Voucher specimens of New Zealand accessions are deposited in the Dame Ella Campbell Herbarium (MPN) at Massey University, Palmerston North, New Zealand; Living accessions are cultivated in Royal Botanic Garden Edinburgh (RBGE), UK, or Rhododendron Species Botanical Garden (RSBG), Washington, USA. 'FCM' in the heading stands for flow cytometry, with which the ploidy estimations are published in Hu et al. (2023) (Chapter 3).

Target seq ID	Sample	Taxon	FCM ploidy	Wild accession	Labelled as	Specimen
2637660	CH03	*R. maddenii* ssp. *crassum*	8*x*		*R. maddenii*	MPN52754; MPN52755; MPN52756; MPN52757
2637716	CH04	*R. veitchianum*	2*x*		*R. cubittii*	MPN52758
2637471	CH05	possibly *R. fleuryi*	2*x*		*R. carneum*	MPN52759; MPN52760
2637637	CH06	*R. megacalyx*	2*x*		*R. megacalyx*	MPN52761; MPN52762
2637523	CH07	*R. dendricola*	2*x*		*R. dendricola*	MPN52763; MPN53021
2637561	CH08	possibly hybrid of *R. ciliicalyx*	2*x*		*R. assamicum*	MPN52764
2637632	CH10	*R. formosum*	2*x*		*R. formosum*	MPN52766; MPN53014
2637642	CH11	possibly hybrid of *R. lindleyi* and *R. nuttallii*	2*x*		*R. lindleyi*	MPN52767
2637493	CH14	*R. veitchianum*	2*x*		*R. ciliicalyx*	MPN52770; MPN52771
2637638	DN02	*R. formosum* var. *formosum*	2*x*		*R. formosum*	MPN52953
2637713	DN03	*R. valentinianum* var. *oblongilobatum*	2*x*		*R. valentinianum* var. *oblongilobatum*	MPN52954
2637634	DN05	*R. inaequale*	2*x*		*R. formosum* var. *formosum*	MPN52956
2637583	DN06	*R. cuffeanum*	2*x*		*R. formosum* var. *inaequale*	MPN52957; MPN53007
2637481	DN07	*R. maddenii* ssp. *crassum*	5*x*?		*R. maddenii* (*R. polyandrum*)	MPN52958; MPN52959; MPN52999

Target seq ID	Sample	Taxon	FCM ploidy	Wild accession	Labelled as	Specimen
2637662	DN08	*R. maddenii* ssp. *maddenii*	6-7*x*?		*R. maddenii* (*R. polyandrum*)	MPN52960
2637706	DN09	*R. nuttallii*	2*x*		*R. nuttallii*	MPN52961
2637708	DN10	*R. nuttallii*	2*x*		*R. nuttallii*	MPN52962
2637620	DN11	*R. excellens*	2*x*		*R. excellens*	MPN52963
2637641	DN12	*R. megacalyx*	2*x*		*R. megacalyx*	MPN52964
2637557	DN15	*R. fletcherianum*	2*x*		*R. fletcherianum*	MPN52967
2637640	DN17	*R. johnstoneanum*	2*x*		*R. johnstoneanum*	MPN52969
2637667	DN20	*R. pachypodum*	2*x*	wild	*R. pachypodum* AC 1993	MPN52970
2637609	DN21	*R. leptocladon*	2*x*	wild	*R. leptocladon* (H.P. Cox) ex Murdoch	MPN52971
2637703	DN22	probably *R. lindleyi*	2*x*	wild	*R. taggianum* CCHH 108 ex Murdoch	MPN52972
2637550	E03	*R. dalhousiae* var. *dalhousiae*	2*x*	wild: India: W Bengal	*R. dalhousiae*	RBGE #19722633*F
2637551	E04	*R. dalhousiae* var. *dalhousiae*	2*x*	wild: India: Sikkim	*R. dalhousiae*	RBGE #19880631*F
2637553	E06	*R. formosum*	2*x*	wild: India: Meghalaya	*R. formosum*	RBGE #19751328*G
2637554	E07	*R. liliiflorum*	2*x*	wild: China: Guizhou	*R. liliiflorum*	RBGE #19911969*B
2637555	E08	*R. liliiflorum*	2*x*	wild: China: Guizhou	*R. liliiflorum*	RBGE #19861177*A
2637556	E09	*R. ludwigianum*	2*x*	wild: Thailand: Chiang Mai	*R. ludwigianum*	RBGE #19850478*D
2637573	E10	*R. maddenii* ssp. *crassum*	2*x*	wild: China: Yunnan	*R. maddenii* ssp. *crassum*	RBGE #19391033*N
2637575	E12	*R. maddenii* ssp. *maddenii*	8*x*	wild: Bhutan: Thimphu Dist.	*R. maddenii* ssp. *maddenii*	RBGE #19150028*L
2637576	E13	*R. maddenii* ssp. *maddenii*	6*x*	wild: Bhutan: Tashigang Dist.	*R. maddenii* ssp. *maddenii*	RBGE #19754068*I

Target seq ID	**Sample**	**Taxon**	**FCM ploidy**	**Wild accession**	**Labelled as**	**Specimen**
2637578	E15	*R. nuttallii*	2*x*	wild: China: Yunnan - Gaoligong Shan	*R. nuttallii*	RBGE #20042030*E
2637579	E16	*R. scopulorum*	2*x*	wild: China: Xizang (Tibet) Aut. Reg.	*R. scopulorum*	RBGE #19730921*P
2637580	E18	*R. fletcherianum*	2*x*	wild: Xizang (Tibet) Aut. Reg.	*R. fletcherianum*	RBGE #19754070*J
2637597	E19	*R. ciliipes*	2*x*	wild: China: Yunnan	*R. ciliipes*	RBGE #19991313*B
2637598	E20	*R. maddenii* ssp. *crassum*	8*x*	wild: China: Xizang (Tibet) Aut. Reg. - Yunnan border	*R. maddenii* ssp. *crassum*	RBGE #19491022*B
2637599	E21	*R. maddenii*	6*x*	wild: Bhutan: Thimphu Dist.	*R. maddenii*	RBGE #19831844*B
2637539	HP01	*R. excellens*	2*x*	wild	*R. excellens* DT307/98	MPN52703; MPN52704
2637480	HP02	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* (as *R. polyandrum*)	MPN52705; MPN52706; MPN52707
2637689	HP03	*R. lindleyi*	2*x*		*R. taggianum*	MPN52708; MPN52709
2637728	HP06	*R. veitchianum*	2*x*		*R. veitchianum*? (*as R. cubittii*)	MPN52715
2637616	HP07	*R. dalhousiae* ssp. *rhabdotum*	2*x*		*R. dalhousiae* var. *rhabdotum*	MPN52716; MPN52717; MPN52718
2637680	HP08	*R. maddenii* ssp. *maddenii*	8*x*		*R. maddenii* No. 1, ex Cullinane	MPN52719; MPN52720
2637688	HP11	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *crassum* Jury Selection (as *R. polyandrum*)?	MPN52726; MPN52727
2637495	HP13	*R. carneum*	2*x*		*R. ciliipes*	MPN52730; MPN52731; MPN52732; MPN52733
2637635	HP14	*R. pachypodum*	2*x*		*R. ciliicalyx* ssp. *lyi* Gigha form (as *R. lyi*)	MPN52734; MPN52735
2637663	HP16	*R. pachypodum*	2*x*		*R. pachypodum* (as *R. supranubium*)	MPN52738; MPN52739
2637691	HP17	*R. dendricola*	2*x*		*R. taggianum*	MPN52740; MPN52741

Target seq ID	**Sample**	**Taxon**	**FCM ploidy**	**Wild accession**	**Labelled as**	**Specimen**
2637636	HP18	*R. formosum*	2*x*		*R. inaequale*	MPN52742
2637623	HP19	*R. lindleyi*	2*x*		*R. taggianum*	MPN52743; MPN52744; MPN53025
2637477	HP20	*R. maddenii* ssp. *maddenii*	6*x*		*R. polyandrum*	MPN52745; MPN52998
2637571	OM01	*R. formosum*	2*x*		*R. inaequale*	MPN52583; MPN52584
2637479	OM02	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *crassum*	MPN52585; MPN52586
2637475	OM03	*R. ciliatum*	2*x*		*R. ciliatum*	MPN52587; MPN52588
2637710	OM04	*R. pachypodum*	2*x*		*R. pachypodum* (as *R. supranubium*)	MPN52589; MPN52590; MPN52591
2637606	OM05	*R. burmanicum*	2*x*		*R. burmanicum*	MPN52592; MPN52592
2637491	OM06	*R. ciliicalyx*	2*x*		*R. ciliicalyx*	MPN52594; MPN52595
2637614	OM07	*R. ciliicalyx*	2*x*		*R. ciliicalyx* ‘Charisma’	MPN52596; MPN52597
2637485	OM08	*R. ciliatum*	2*x*		*R. ciliatum*	MPN52598; MPN52599
2637559	OM09	*R. formosum*	2*x*		*R. formosum* (as *R. assamicum*)	MPN52600; MPN52601
2637563	OM10	*R. formosum* var. *formosum*	2*x*		*R. formosum* (as *R. iteophyllum*)	MPN52602; MPN52603
2637501	OM11	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii*	MPN52604; MPN52605
2637657	OM12	*R. nuttallii* var. *stellatum*	2*x*		*R. nuttallii* 'Stellata'	MPN52606; MPN52607
2637607	OM13	*R. johnstoneanum*	2*x*		*R. johnstoneanum* KB form	MPN52608; MPN52609
2637729	OM15	*R. pachypodum*	2*x*		*R. veitchianum* (as *R. cubittii*)	MPN52612; MPN52613
2637712	OM16	*R. parryae*	2*x*		*R. parryae*	MPN52614; MPN52615
2637682	OM17	*R. maddenii* ssp. *crassum*	8*x*		*R. maddenii* ssp. *crassum*	MPN52616; MPN52617
2637666	OM18	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* late pink	MPN52618; MPN52619
2637593	OM19	*R. johnstoneanum*	2*x*		*R. johnstoneanum*	MPN52620; MPN52621
2637656	OM20	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii*	MPN52622; MPN52623
2637615	OM23	*R. lindleyi* 'Helen Gordon'	2*x*		*R. lindleyi* ‘Helen Gordon’	MPN52679; MPN52680 (accession is a clone of OM52)
2637517	OM26	*R. dalhousiae* ssp. *rhabdotum*	2*x*		*R. dalhousiae* var. *rhabdotum*	MPN52626

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2637604	OM28	*R. edgeworthii*	2*x*		*R. edgeworthii*	MPN52629
2637519	OM29	*R. dalhousiae* ssp. *rhabdotum*	2*x*		*R. dalhousiae* var. *rhabdotum*	MPN52630
2637621	OM31	*R. edgeworthii*	2*x*		*R. edgeworthii*	MPN52633
2637515	OM32	*R. dalhousiae* ssp. *dalhousiae*	2*x*		*R. dalhousiae* var. *dalhousiae*	MPN52634; MPN52635
2637677	OM33	*R. parryae*	2*x*		*R. parryae*	MPN52636; MPN52637
2637618	OM34	*R. excellens*	2*x*		*R. excellens*	MPN52638; MPN52639
2637622	OM35	*R. edgeworthii*	2*x*		*R. edgeworthii*	MPN52640; MPN52641; MPN52642
2637608	OM36	*R. burmanicum*	2*x*		*R. burmanicum*	MPN52643; MPN52644
2637681	OM39	*R. scopulorum*	2*x*		*R. scopulorum*	MPN52649; MPN52650
2637705	OM40	*R. taronense*	2*x*		*R. taronense*	MPN52651; MPN52652
2637469	OM41	*R. carneum*	2*x*		*R. carneum*	MPN52653; MPN52654
2637726	OM42	possibly hybrid of *R. ciliicalyx* and *R. lyi*	2*x*		*R. veitchianum* (as *R. cubittii*)	MPN52655; MPN52656
2637731	OM45	*R. veitchianum*	2*x*		*R. veitchianum*? (*as R. cubittii*)	MPN52661; MPN52662
2637664	OM46	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* Jury selection	MPN52663; MPN52664
2637507	OM47	*R. maddenii* ssp. *crassum*	8*x*		*R. maddenii* ssp. *crassum*	MPN52665; MPN52666
2637508	OM48	*R. maddenii* ssp. *maddenii*	7*x*		*R. maddenii* ssp. *crassum*	MPN52667; MPN52668; MPN52669
2637658	OM49	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii*	MPN52670; MPN52671
2637653	OM50	*R. nuttallii*	2*x*	wild: Nth Vietnam	*R. nuttallii*	MPN52672; MPN52673; MPN52674; MPN52675
2637704	OM51	*R. nuttallii*	2*x*	wild: China	*R. nuttallii*	MPN52676; MPN52677; MPN52678; MPN53018
2637644	OM52	*R. lindleyi* 'Helen Gordon'	2*x*		*R. lindleyi* 'Helen Gordon'	MPN52679; MPN52680
2637687	OM53	*R. sinonuttallii*	2*x*		*R. sinonuttallii* (possibly a hybrid, L. Davies pers comm)	MPN52681; MPN52682; MPN52683
2637668	OM54	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* 'Virginalis'	MPN52684; MPN52685
2637461	OM55	*R. burmanicum*	2*x*		*R. burmanicum*	MPN52686
2637506	OM56	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *crassum*	MPN52687

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2637624	OM58	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *maddenii*	MPN52689
2637625	OM60	*R. fortunei*	2*x*		*R. fortunei*	MPN52690
2637626	OM61	*R. lindleyi*	2*x*		*R. lindleyi*	MPN52691
2637627	OM62	*R. fortunei*	2*x*		*R. fortunei*	MPN52692
2637646	OM67	*R. yunnanense*	6*x*		*R. yunnanense*	MPN52695
2637647	OM68	*R. yunnanense*	6*x*		*R. yunnanense*	MPN52696
2637586	OM69	*R. williamsianum*	2*x*		*R. williamsianum*	MPN52697
2637588	OM70	*R. williamsianum*	2*x*		*R. williamsianum*	MPN52698
2637590	OM71	*R. decorum*	2*x*	wild: Yunnan, China	*R. decorum*	MPN52699
2637592	OM72	*R. arboreum* ssp. *delavayi*	2*x*		*R. arboreum* ssp. *delavayi*	MPN52700
2637594	OM73	*R. arboreum* ssp. *delavayi*	2*x*	wild: Yunnan, China	*R. arboreum* ssp. *delavayi*	MPN52701
2637596	OM74	*R. decorum*	2*x*	wild: Yunnan, China	*R. decorum*	MPN52702
2637545	PK01	*R. excellens*	2*x*	wild	*R. excellens* KR2998	MPN52774; MPN52775
2637587	PK02	*R. horlickianum*	2*x*		*R. horlickianum* Gwavas	MPN52776
2637499	PK03	*R. ciliipes*	2*x*	wild	*R. ciliipes* K56	MPN52777; MPN52778; MPN52779; MPN52780
2637567	PK04	*R. iteophyllum*	2*x*		*R. iteophyllum* Gigha form	MPN52781; MPN52782; MPN52783; MPN52784
2637701	PK05	*R. taggianum* (Dubious ID)	2*x*		*R. taggianum*	plant dead
2637665	PK07	*R. pachypodum*	2*x*		*R. pachypodum* (as *R. supranubium*)	MPN52787; MPN52788; MPN52789; MPN52790
2637565	PK08	*R. iteophyllum*	2*x*		*R. iteophyllum* Brodick (*R. formosum* var. *formosum* on the tag)	MPN52791; MPN52792; MPN52793
2637547	PK10	*R. excellens*	2*x*	wild	*R. excellens* TVO 064	MPN52798; MPN52799; MPN52800
2637581	PK11	*R. lindleyi*	2*x*	wild	*R. formosum* var. *inaequale* KW16029	MPN52801; MPN52802; MPN52803

Target seq ID	Sample	Taxon	FCM ploidy	Wild accession	Labelled as	Specimen
2637683	PK12	*R. scopulorum*	2*x*		*R. scopulorum*	MPN52804; MPN52805; MPN52806; MPN52807; MPN52808
2637478	PK13	*R. maddenii* ssp. *maddenii*	5*x*		*R. maddenia* ssp. *maddenii* (as *R. polyandrum*)	MPN52809; MPN52810
2637679	PK14	*R. parryae*	2*x*	wild	*R. parryae* RBGE146 Fischer form	MPN52811; MPN52812
2637569	PK18	possbly hybrid between *R. cuffeanum* and *R. inaequale*	2*x*	wild	*R. formosum* ‘Ten Tashi’	MPN52821; MPN52822; MPN52823
2637533	PK19	*R. ciliicalyx*	2*x*		*R. dendricola*	MPN52824; MPN52825; MPN52826; MPN52827; MPN52828
2637467	PK20	*R. burmanicum*	2*x*		*R. burmanicum* ‘Deep Yellow’	MPN52829; MPN52830; MPN52831
2637735	PK21	*R. veitchianum*	2*x*	wild: Thailand	*R. veitchianum* ‘Ice White’	MPN52832; MPN52833; MPN52834
2637528	PK22	*R. maddenii* ssp. *crassum*	8*x*		*R. maddenii* ssp. *maddenii*	MPN52836; MPN52837; MPN52838
2637521	PK23	*R. dalhousiae* ssp. *rhabdotum*	2*x*		*R. dalhousiae* var. *rhabdotum*	MPN52839; MPN52840
2637473	PK24	*R. carneum*	2*x*		*R. carneum*	MPN52841; MPN52842; MPN52843
2637535	PK25a	*R. taronense* or *R. dendricola*	2*x*		*R. dendricola*	MPN52844; MPN52845; MPN52846
2637661	PK26	*R. pachypodum*	2*x*		*R. pachypodum*	MPN52847; MPN52848; MPN52849; MPN52850
2637504	PK27	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *crassum*	MPN52851; MPN52852; MPN52853
2637617	PK28	*R. lindleyi*	2*x*	wild	*R. lindleyi* KW8546 ex Gwavas	MPN52854; MPN52855
2637509	PK29	*R. coxianum*	2*x*	wild	*R. coxianum* 1984-443, Glendoick?	MPN52856; MPN52857
2637543	PK30	*R. excellens*	2*x*	wild: Ban Khoang, Vietnam	*R. excellens* AC5630	MPN52860; MPN52861; MPN52862
2637639	PK31	*R. megacalyx*	2*x*		*R. megacalyx*	MPN52863; MPN52864; MPN52865; MPN52866
2637655	PK32	*R. nuttallii*	2*x*		*R. nuttallii*	MPN52867; MPN52868; MPN52869; MPN52870

Target seq ID	Sample	Taxon	FCM ploidy	Wild accession	Labelled as	Specimen
2637595	PK33	*R. johnstoneanum*	2*x*	wild	*R. johnstoneanum* KW20305	MPN52871; MPN52872
2637513	PK34	*R. dalhousiae* var. *dalhousiae*	2*x*	wild: Solu Khumbu, Nepal	*R. dalhousiae*	MPN52873; MPN52874
2637659	PK35	*R. nuttallii* var. *stellatum*	2*x*		*R. nuttallii* ‘Stellata’	MPN52875; MPN52876; MPN52877; MPN53024
2637733	PK36	*R. pachypodum*	2*x*		*R. veitchianum* ‘Ashcombe’	MPN52878; MPN52879
2637511	PK37	*R. dalhousiae* var. *dalhousiae*	2*x*		*R. dalhousiae*	MPN52880; MPN52881
2637654	PK39	*R. lindleyi*	2*x*		*R. lindleyi* Hollard form	MPN52884; MPN52885
2637487	PK40	*R. ciliatum*	2*x*		*R. ciliatum*	MPN52886; MPN52887; MPN52888; MPN52889
2637707	PK42	*R. taronense*	2*x*		*R. taronense*	MPN52892; MPN52893; MPN52894
2637631	PK43	*R. ludwigianum*	2*x*	wild	*R. ludwigianum* Doi Ang Kang, Thailand	MPN52895; MPN52896; MPN52897
2637633	PK44	*R. pachypodum*	2*x*		*R. lyi*	MPN52898; MPN52899
2637505	PK45	*R. maddenii* ssp. *crassum*	7*x*		*R. maddenii* ssp. *crassum*	MPN52900; MPN52901; MPN52902
2637619	PK46	*R. lindleyi*	2*x*		*R. lindleyi*	MPN52903; MPN52904; MPN52905
2637605	PK47	*R. johnstoneanum*	2*x*	wild	*R. johnstoneanum* AC5532	MPN52906; MPN52907
2637725	PK49	*R. veitchianum*	2*x*		*R. veitchianum*	MPN52911
2637489	PK50	*R. ciliatum*	2*x*		*R. ciliatum*	MPN52912; MPN52913; MPN52914
2637612	PK51	*R. ciliatum*	2*x*		*R. ciliatum*	MPN52915; MPN52916
2637497	PK53	*R. ciliicalyx*	2*x*	wild	*R. ciliicalyx* ‘Charisma’ KW20280	MPN52922; MPN52923
2637585	PK55	*R. horlickianum*	2*x*		*R. horlickianum*	MPN52925; MPN52926; MPN52927
2637537	PK56	*R. dendricola*	2*x*		*R. dendricola*	MPN52928; MPN52929
2637709	PK57	*R. taronense*	2*x*		*R. taronense*	MPN52930; MPN52931
2637727	PK58	*R. veitchianum*	2*x*	wild: Thailand	*R. veitchianum* Os Blumhardt collection	MPN52932; MPN52933

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2637643	PK60	*R. nuttallii*	2*x*	wild: China	*R. nuttallii*	MPN52936; MPN52937; MPN52938
2637525	PK61	*R. maddenii* ssp. *crassum*	7*x*		*R. maddenii* ssp. *crassum*	MPN52939; MPN52940
2637611	PK63	probably *R. lindleyi*	2*x*		*R. lindleyi*	MPN52942
2637629	PK66	*R. ludwigianum*	2*x*		*R. ludwigianum*	MPN52948; MPN52949
2637613	PK67	possibly hybrid of *R. lindleyi* and *R. nuttallii*	2*x*		*R. lindleyi*	MPN52950
2637531	PK68	*R. maddenii* ssp. *maddenii*	6*x*		*R. maddenii* ssp. *maddenii*	MPN52951
2637651	RSF04	*R. ciliatum*	2*x*	wild: Sikkim	*R. ciliatum* SEH 545	RSBG #2000/094
2637652	RSF05	*R. ciliicalyx*	2*x*	wild	*R. ciliicalyx* TH#1276 2013/113	RSBG
2637669	RSF06	*R. crenulatum*	2*x*	wild	*R. crenulatum* NV#072	RSBG
2637671	RSF08	*R. dalhousiae* var. *dalhousiae*	2*x*	wild	*R. dalhousiae* var. *dalhousiae* SEH 522	RSBG #99/153
2637672	RSF09	*R. dalhousiae* ssp. *rhabdotum*	2*x*	wild: India	*R. dalhousiae* var. *rhabdotum* KCSH 0310	RSBG #2006/046
2637673	RSF10	*R. dendricola*	2*x*	wild: Himalaya	*R. dendricola* F 17227	RSBG #1998/021
2637674	RSF11	*R. dendricola*	2*x*	wild: China	*R. dendricola* SEH 25037	RSBG #2007/246
2637675	RSF12	*R. dendricola*	2*x*	wild	*R. dendricola* DGEY#046 2013/490	RSBG
2637693	RSF14	*R. fletcherianum*	2*x*	wild	*R. fletcherianum*	RSBG #65/355
2637695	RSF16	*R. formosum*	2*x*	wild: Khasia, India	*R. formosum* C&H 320	RSBG #1998/012
2637730	RSF17	*R. formosum* ssp. *inaequale*	2*x*	wild: India	*R. formosum* var. *inaequale* C&H 301	RSBG #1998/002
2637697	RSF19	*R. goreri*	2*x*	wild: China	*R. goreri* KR 6027	RSBG #2003/188
2637698	RSF20	*R. goreri*	2*x*	wild: China	*R. goreri* RR 112	RSBG #2005/249
2637717	RSF23	*R. johnstoneanum*	2*x*	wild: India&Bhutan	*R. johnstoneanum* NAPE 024	RSBG
2637718	RSF24	*R. kiangsiense*	2*x*	wild	*R. kiangsiense* EN	RSBG #2013/269
2637721	RSF27	*R. leptocladon*	2*x*	wild	*R. leptocladon* HWJ#99688	RSBG #2005/035
2637722	RSF28	*R. levinei*	2*x*	wild	*R. levinei* CGG#14162	RSBG #2020/142
2637724	RSF30	aff. *R. levinei*	2*x*	wild	*R. levinei* aff.TH#2805	RSBG #2013/244

Target seq ID	Sample	Taxon	FCM ploidy	Wild accession	Labelled as	Specimen
2637744	RSF34	*R. lindleyi*	2*x*	wild: India	*R. lindleyi* KR 8074	RSBG #2008/100
2637745	RSF35	*R. lindleyi*	2*x*	wild	*R. lindleyi* SEH#534	RSBG #2001/239
2637746	RSF36	*R. ludwigianum*	2*x*	wild	*R. ludwigianum*	RSBG #2004/030
2637464	RSF38	*R. lyi*	2*x*	wild: Vietnam (? probably Thailand)	*R. lyi* KR Valder#	RSBG #2001/146
2637466	RSF39	*R. lyi*	2*x*	wild	*R. lyi* FMWJ#13042	RSBG #2015/018
2637470	RSF41	*R. maddenii* ssp. *crassum*	8*x*	wild	*R. maddenii* ssp. *crassum*	RSBG #2011/120
2637474	RSF43	*R. maddenii* ssp. *maddenii*	6*x*	wild: Sikkim, India	*R. maddenii* ssp. *maddenii* SEH#599	RSBG #2001/192
2637476	RSF44	*R. maddenii*	8*x*	wild	*R. maddenii*	RSBG #2005/237
2637486	RSF45	*R. maddenii*	6*x*	wild	*R. maddenii*	RSBG #2006/153
2637494	RSF49	*R. maddenii* ssp. *crassum*	8*x*	wild	*R. maddenii* ssp. *crassum*	RSBG #2007/273
2637496	RSF50	*R. maddenii* ssp. *crassum*	8*x*	wild: China	*R. maddenii* ssp. *crassum* BASE#9539	RSBG #2009/017
2637498	RSF51	*R. maddenii* ssp. *crassum*	2*x*	wild: Vietnam	*R. maddenii* ssp. *crassum* KR#3116	RSBG #1996/027
2637500	RSF52	*R. maddenii* ssp. *crassum*	8*x*	wild: Burma	*R. maddenii* ssp. *crassum* DJHM#13057	RSBG
2637510	RSF53	*R. megacalyx*	2*x*	wild: China	*R. megacalyx* BASE 9544	RSBG #2005/243
2637522	RSF59	*R. pseudociliipes*	2*x*	wild: China	*R. pseudociliipes* BASE 9697	RSBG #2005/132
2637524	RSF60	*R. pseudociliipes*	2*x*	wild: Vietnam	*R. pseudociliipes*	RSBG #2018/162
2637538	RSF64	*R. scopulorum*	2*x*	wild: Tibet & Bhutan	*R. scopulorum* KW 6354	RSBG #1998/014
2637542	RSF66	*R. surasianum*	2*x*	wild	*R. surasianum* (no detail)	RSBG #2003/177
2637566	RSF74	*R. wumingense*	2*x*	wild	*R. wumingense* CGG 14150	RSBG #2014/111
2637568	RSF75	*R. boothii*	2*x*	wild (GR#0868)	*R. boothii*	RSBG
2637734	RSF76	*R. boothii*	2*x*	wild	*R. boothii*	RSBG #2017/034
2637570	RSF77	*R. leucaspis*	2*x*	wild	*R. leucaspis*	RSBG #2008/323
2637572	RSF78	*R. leucaspis*	2*x*	wild	*R. leucaspis*	RSBG #2008/366