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Evolutionary Dynamics in Taro **(*Colocasia esculenta* L.)**

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ABSTRACT

Understanding domestication is fundamental to understanding crop history and one of the most significant advancements in human history – the emergence of agriculture. Taro (*Colocasia esculenta*; family Araceae) is a root crop of importance to hundreds of millions of people in tropical to sub-tropical and temperate regions of the world. Despite its cultural and historical significance, the origins, domestication and worldwide distribution of this crop have been the focus of only a few phylogenetic and phylogeographic studies. This gap in understanding the history of taro can be partly attributed to the non-suitability of available molecular markers, and the scale of targeted plant sampling required. In this study, chloroplast genome sequences were determined for two morphotypes of taro (var. RR and var. GP) using an Illumina sequencing protocol and bioinformatic analyses. These genomes were compared to each other as well as to four publicly available aroid chloroplast genomes. Such comparisons enabled an analysis of the extent of genome-wide correlations between oligonucleotide repeats, substitutions and insertion – deletion mutations (indels). Recent studies have suggested such correlations in eukaryotic and prokaryotic genomes, but genome-wide studies on organelles have not been undertaken. The finding of a significant correlation among different kinds of mutational events in the chloroplast genomes of aroids led to a further hypothesis being proposed that the distribution of oligonucleotide repeat sequences in a single representative chloroplast genome could be used to predict mutational hotspot loci suitable for population genetic, phylogenetic and phylogeographic studies in other closely related plant species. To test this hypothesis, 30 primer pairs were designed to amplify and sequence loci predicted to be mutational hotspots in the chloroplast genome of taro. The phylogenetic and phylogeographic usefulness of these loci was then determined in a range of intra-specific to inter-generic analyses, which included samples from taro (*Colocasia esculenta*), four other *Colocasia* species (*C. affinis*, *C. fallax*, *C. formosana*, *C. gigantea*), and species from three other aroid genera (*Remusatia vivipara*, *Alocasia brisbanensis* and *Amorphophallus konjac*). Six of the 30 chloroplast DNA loci were sequenced from 170 wild and cultivated taro accessions from 20 Asian and Oceanic countries, and 35 accessions from closely related out-group species. This study provided further evaluation of novel markers that can be used to elucidate the origins, domestication and dispersal history of taro. The results provided a number of insights on the history of taro. Taro as a species most likely originated in

South to Southeast Asia during the Miocene to Pliocene period, and reached Australia and New Guinea separately in wild and possibly cultivated forms. Neighbor-Net and maximum likelihood analyses of the chloroplast DNA loci revealed the existence of three main super-clades in the wider taro germplasm. These super-clades were identified as: (i) a subtropical to tropical Indo-Pacific (IP) super-clade consisting of wild and cultivated, as well as diploid and triploid taros, (ii) a temperate to subtropical Himalayan (H) super-clade consisting of triploid cultivars, and (iii) a tropical Southeast Asian – Australian (SEAA) super-clade consisting of wild diploid taros. The current study does not support the prevailing hypothesis of taro domestication in New Guinea, but suggests that the domestication might have taken place independently for taros belonging to the IP and H super-clades. Hybridization of taro with other sympatric species in northern Vietnam was indicated by analysing sequences from six chloroplast and two nuclear DNA loci (Phytochrome C and internal transcribed spacer) in a subset of taro and other sympatric *Colocasia* species. This observation suggests that in taro as in many other plant species, hybridization has been a significant feature of their evolution. In total, this study significantly advances our understanding of the history of taro. The inferred phylogenetic relationships also have relevance for developing future taro breeding strategies.

DEDICATION

I dedicate this thesis to my late mother, who always encouraged me to seek and spread knowledge.

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