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Conservation of the critically endangered frog

*Telmatobufo bullocki* in fragmented temperate forests of Chile

A thesis presented in partial fulfilment of the requirements for the degree of

Doctor of Philosophy

in

Conservation Biology

at Massey University, Albany, New Zealand

Virginia Moreno-Puig

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Abstract

Amphibians are currently facing several threats and are suffering severe population declines and extinction worldwide. *Telmatoberofo bullocki* (Anura: Calyptocephalellidae) is one of the rarest and most endangered amphibian species in Chile’s temperate forests. It is the fifth most evolutionarily distinct and globally endangered (EDGE) amphibian in the world, and one of the world’s top 100 priority species for conservation (Zoological Society of London, 2011). This stream-breeding frog is micro-endemic to the coastal Nahuelbuta mountain range in central-south Chile (37°-38°50' S), a hot-spot for conservation. This area has suffered severe loss and fragmentation of native forest, which has been replaced by extensive commercial plantations of exotic pines and eucalyptus. Despite its potential detrimental effects, the impact of native forest loss on this species has not been studied before. Furthermore, few historical observations exist, and the ecology and behaviour of the species is poorly known. In addition, current status and location of extant populations are uncertain, which makes conservation and targeted habitat protection difficult.

Through the use of different approaches and modern conservation tools this thesis aims to make a significant contribution to the conservation of *T. bullocki* and its habitat. Historical and new locations were surveyed to identify extant populations. A distribution modeling approach (i.e. Maxent) was used to infer the species’ distribution within Nahuelbuta, generate a predictive habitat suitability map, identify important environmental associations, and assess the impact of main environmental threats (i.e. native forest loss, climate change). Field-based research (e.g. surveys, radio-tracking) was done to extend the
ecological and behavioural knowledge of the species (e.g. movement patterns and habitat use), and identify critical aquatic and terrestrial habitat for protection (i.e. core habitat). Mitochondrial and specifically developed microsatellite genetic markers were used to measure levels of intra-specific genetic variability, define genetic population structure and connectivity, infer evolutionary history (phylogeography), estimate effective population size and detect demographic changes (e.g. bottlenecks). Finally, a landscape genetics approach was used to relate landscape characteristics to contemporary patterns of gene flow, and identify important landscape features facilitating (i.e. corridors) or hindering (i.e. barriers) genetic connectivity between populations.

_Telmatoctopus bullocki_ was found in nine basins within Nahuelbuta, including historic and new locations. Presence of _T. bullocki_ was positively related to the amount of native forests in the landscape. However, some populations persist in areas dominated by exotic plantations. Some frogs were found living under mature pine plantation adjacent to native forest, but no frogs were found in core plantation areas. _T. bullocki_ makes extensive use of terrestrial habitat adjacent to breeding streams during the post-breeding season, moving up to 500 m away from streams. A core terrestrial habitat of at least 220 m from streams is proposed for the protection of populations. Population genetics and phylogeography revealed significant population structure. The northernmost and disjunct population of Chivilingo is geographically and genetically isolated from all other sampled populations and was identified as a separate evolutionary significant unit (ESU). The population of Los Lleulles was also identified as a separate management unit, while the remaining populations were grouped into two clusters forming a larger and more connected metapopulation. Connectivity within groups was high, suggesting individuals are able to
disperse between neighbouring basins. Levels of genetic diversity were not homogeneous, and were lowest at Los Lleulles and highest at Caramávida. Results suggest disjunct populations are at highest risk and should be prioritised for restoration and habitat protection, while management of meta-populations should aim at maintaining and improving connectivity among basins. Landscape genetic results identified streams and riparian habitat as dispersal pathways, and least-cost-path analysis was used to identify a potential connectivity network.
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<th>Meaning</th>
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<tbody>
<tr>
<td>AIC</td>
<td>Akaike Information Criterion</td>
</tr>
<tr>
<td>Bd</td>
<td><em>Batrachochytrium dendrobatidis</em></td>
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<tr>
<td>BI</td>
<td>Bayesian Inference</td>
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<td>CH</td>
<td>Chivilingo</td>
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<td>CL</td>
<td>Calebu</td>
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<tr>
<td>COI</td>
<td>Cytochrome c oxidase subunit 1</td>
</tr>
<tr>
<td>CONAF</td>
<td>Corporacion Nacional Forestal de Chile</td>
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<tr>
<td>CR</td>
<td>Critically endangered (IUCN threat category)</td>
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<td>Cayucupil</td>
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<td>Evolutionarily distinct and globally endangered</td>
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<td>EM</td>
<td>Expectation maximization algorithm</td>
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<td>ESS</td>
<td>Effective sample size</td>
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<td>Abbr.</td>
<td>Description</td>
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<td>ESU</td>
<td>Evolutionarily significant unit</td>
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<td>HCVA</td>
<td>High Conservation Value Area</td>
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<td>HKY+I</td>
<td>Hasegawa, Kishino and Yano model of DNA substitution with invariable sites</td>
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<td>HPD</td>
<td>Highest posterior density</td>
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<td>Infinite Allele Model</td>
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<td>Isolation by distance</td>
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<td>IBR</td>
<td>Isolation by resistance</td>
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<td>IUCN</td>
<td>International Union for Conservation of Nature</td>
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<td>Los Lleulles</td>
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<td>ML</td>
<td>Maximum likelihood</td>
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<td>Mega Watt</td>
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<td>mya</td>
<td>Million years ago</td>
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<td>Ne</td>
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<td>Snout-to-vent length</td>
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<td>Time to most recent common ancestor</td>
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<td>Visual encounter surveying</td>
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