The role of genetics in defining taxonomic boundaries and conservation units

David J. Coates[1], Margaret Byrne[1], Melissa A. Millar[1], Kelly A. Shepherd[2] and
Stephen J. van Leeuwen[1]

[1]Science Division, Department of Environment and Conservation,
Locked Bag 104, Bentley Delivery Centre, WA 6983
[2]Western Australian Herbarium, Science Division, Department of Environment and Conservation,
Locked Bag 104, Bentley Delivery Centre, WA 6983
Corresponding author email: Dave.Coates@dec.wa.gov.au

Identification of appropriate taxonomic and population units for protection and management is essential for the conservation of biological diversity. To be effective, conservation strategies should not only aim to preserve current levels of species diversity, but also consider intraspecific variation and the evolutionary and ecological processes associated with its generation and maintenance. Genetic principles and methods for species identification and classification are relatively well developed, although biologists and wildlife managers are still faced with ongoing debates concerning species and taxon delimitation. Within species the identification and characterisation of genetically distinct local populations or conservation units, based on population genetic structure and phylogeographic patterns, provides an important basis upon which more specific strategies can be developed for the conservation of genetic diversity and evolutionary processes. Furthermore, the local population is often considered the functional unit in ecosystems. However, like species delimitation, defining conservation units can be controversial, as is evident in the various views expressed when identifying Evolutionarily Significant Units (ESUs). These issues are discussed in the context of a number of Western Australian examples that highlight the use of molecular genetic approaches in assessing taxonomic boundaries and delimiting populations as conservation units.

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