

## INTRODUCTION

# Special Issue on Gene Conservation: Identification and Management of Genetic Diversity

TIM L. KING\* and TERRY BURKE†

\*Biological Resources Division, U.S. Geological Survey, Leetown Science Center, 1700 Leetown Road, Kearneysville, WV 25430, USA, †Department of Animal & Plant Sciences, University of Sheffield, Sheffield, S10 2TN, UK

Effective programmes for conserving threatened species require the identification of unambiguous units of management that reflect evolutionarily important lineages (Avice 1994). Heritable genetic information offers an objective means to delineate conservation units, and provides an evolutionary framework from which to develop and evaluate conservation priorities. The value of molecular markers in delineating breeding structures and evolutionarily important lineages is well established (Avice 1994; Hillis *et al.* 1996; Kocher & Stepien 1997). There is, however, much contention as to whether phylogenetic systematics, a more phenetic approach to evolutionary genetics, or some combination of each is most suitable for identifying appropriate units of management (Amato *et al.* 1998). The primary disagreement centres on the level of the evolutionary continuum, from distinct population segment to species, at which conservation units should be defined (Moritz *et al.* 1995; Waples 1998). In the United States, the Endangered Species Act (US ESA) legislates for the protection of identifiable Distinct Population Segments (DPSs) in vertebrate species. A strict application of the phylogenetic species concept allows only consistently diagnosable population units to have biological or, apparently, political meaning. The populations that can be diagnosed consistently using this concept are generally larger than the smallest DPSs that can be identified using genetic variation that is not population specific. A phenetic approach to population genetics accepts quantitatively identifiable population structure, such as variation in frequency or associations among alleles that are spatially and/or temporally stable, as a means of identifying distinct population segments.

For example, the use of the DPS concept for the management of anadromous Pacific salmonids, when defined as the evolutionarily significant unit (ESU; Ryder 1986), has proven extraordinarily contentious (Pennock & Dimmick 1997; Waples 1998). An ESU is defined as a population or aggregation of populations that is substantially reproductively isolated from other conspecific groups, and represents an important component in the evolutionary

legacy of a species (Waples 1991, 1995). A strict phylogenetic perspective would disallow the ESU interpretation of a DPS because it would argue that unambiguous genetic evidence of evolutionary separation between populations should be taken as evidence that they are distinct species (see synthesis by Mayden & Wood 1995). A phenetic approach to genetic population structure allows finer levels of differentiation to provide insight into the evolutionary processes that shape the individual–population–species continuum and, consequently, which DPSs warrant recognition and preservation. In an attempt to find a middle ground, Moritz (1994) proposed the management unit as a population with significant, but not necessarily diagnostic, allelic divergence at nuclear or mitochondrial loci between populations. Management units are not afforded the mandated protection accompanying ESUs (i.e. DPSs) under the US ESA.

To further the debate of this often contentious issue, a symposium entitled 'Gene Conservation: Identification and Management of Genetic Diversity' was held during the VII International Congress of Ecology (INTECOL) at Florence, Italy in July 1998. Conservation geneticists from research groups on five continents convened to discuss empirical and theoretical insights into the appropriate application of genetic variation in conservation. This supplemental Special Issue of *Molecular Ecology* contains 14 invited or contributed papers arising from the symposium: 11 Original Articles, one Review Article, and two Opinion pieces. The papers represent most of those presented at the symposium and clearly illustrate the breadth of conservation genetics problems that are currently being addressed and the variety of molecular techniques at the disposal of contemporary researchers. The central theme of the symposium was the identification of genetic variation using molecular techniques and the use of this variation to define conservation units. The appropriate application of molecular genetic data in resource management was a secondary theme.

In *Molecular Ecology's* 1994 Special Issue on Conservation Genetics, one of us (T.B.) predicted that conservation

geneticists would soon give more attention to species other than the 'charismatic megafauna' that attracted most attention at that time. However, conservation genetics does still seem to be directed mostly towards large charismatic vertebrates, here including the harbour porpoise (Rosel *et al.*), South American cats (Johnson *et al.*), lemurs (Wyner *et al.*), the Komodo dragon (Coifi & Bruford), and Eurasian sturgeons (Doukakis *et al.*). A couple of smaller vertebrate species discussed here have also been the focus of considerable attention from conservation agencies and attracted much public attention (redband trout, Nielsen *et al.*, and red squirrel, Barratt *et al.*). However, organisms involved more subtly in the function of their ecosystem such as the eulachon (McLean *et al.*), a freshwater bivalve (King *et al.*) and a geranium (Martin *et al.*) also make an impact on this collection of papers. In addition, there are two papers on the interactions of agricultural plants with their wild relatives: on barley (Marmioli *et al.*) and an extensive review of the general topic (Jarvis & Hodgkin).

There is a diversity of research goals as well as a diversity of study organisms. Six papers attempt to define units of conservation or management (porpoise, sturgeons, lemurs, cats, freshwater bivalve, geranium), three papers report measures of genetic variation as a basis for eventual discussion of management units (Komodo dragon, eulachon, red squirrel), and three papers discuss differences in wild and captive populations (trout, barley, cultivar introgression review). A diversity of techniques is also apparent. Four papers use mtDNA sequences (red squirrel, freshwater bivalve, lemurs and sturgeons), one paper each uses RAPDs and mtDNA RFLPs (geranium and eulachon, respectively), and two papers use microsatellites (redband trout and Komodo dragon). Perhaps indicative of a future trend, four papers use multiple molecular markers in combination (cats, porpoise, barley and cultivar introgression review). This is significant because neutral genetic markers are assumed to reflect adaptive genetic variation that is meaningful to the evolutionary prospects of the species of interest. The greater the number of independent markers and marker classes used, the greater the likelihood that useful genetic variation will be reflected in the management units that are identified.

A range of molecular genetic techniques is now available to document natural hybridization and introgression. These techniques have shown that introgression between crop cultivars and their wild relatives is an ongoing process affecting the genetic diversity of crops today. Jarvis & Hodgkin review the relationships between wild relatives and crop cultivars in the light of natural introgression and farmer-mediated selective processes. Marmioli *et al.* use multiple genetic markers and the study of structure and function of multiple complex genomes to compare genetic variation with phenotypic variation in the form of local adaptation. This search for quantitative differences

among genotypes in barley is at the frontier of a new field. The many current genome mapping projects will lead to the identification and quantification of numerous quantitative trait loci that should, in some cases, prove of value to the evaluation of the fitness of endangered populations.

Most of the papers in this issue apply a phenetic analysis in estimating population structure. However, two papers apply an interpretation to mtDNA sequence data that has been informed by the phylogenetic species concept (Wyner *et al.* and Doukakis *et al.*). These authors limit their interpretation to clear-cut phylogenetic reconstruction using parsimony, with only minimal reference to variation occurring across populations. This approach has the benefit of using stringent criteria for the designation of management units, minimizing the level of interpretation required by managers.

Brian Bowen has contributed a thoughtful essay on the contentious debate among conflicting approaches to defining conservation units. Bowen further refines the issues in terms of a triangular framework of systematic, ecological, and evolutionary perspectives. High-profile species are used to illustrate the differences among the three positions and their unique contribution to conservation. Because each field tends to employ a distinct set of molecular tools, it seems unlikely that a general consensus will be reached. Bowen also predicts a reduced role of any single technique in applying management or conservation designations to populations.

Another somewhat sobering theme that emerged during the symposium and in these papers was that molecular data do not always provide an absolute picture of differentiation within a species. Mike Bruford, in his presentation, noted a tendency for conservation organizations to view a molecular approach as a panacea. Molecular data have proven crucial to the shaping of management strategies and have been successfully applied to the identification of units for conservation. Bruford cautioned, however, that the potential consequences of misinterpretation are extremely serious. Molecular data in conservation biology are usually produced with a specific application in mind, with management action to follow. Problems such as the lack of congruence among data produced using different marker types, neutrality, and limitations in our ability to interpret data potentially hamper the effectiveness of molecular ecology in conservation.

This last concern was a driving force behind the second opinion paper, by Taylor and Dizon. The authors take exception to the stated goal of the symposium and remind us that conservation genetics is interconnected with public policy. When science is divorced from policy, inappropriate advice to managers can have unfortunate consequences. Taylor and Dizon suggest that at no level are strictly genetic criteria appropriate for determining management or conservation units.

Discussions in the well-attended symposium were spirited, due in part to fundamental philosophical differences between phylogenetic systematists and phenetic population geneticists. While both camps share the goal of measuring historical lineages, this is where the commonalities end. Although it is unlikely that many minds were changed (perhaps more heat was produced than light), the participants in the symposium did exhibit further appreciation for the counter argument. However, resource managers who disseminate a research report among conservation geneticists may be surprised to find two or three conflicting interpretations of the findings. Mixed responses to managers' enquiries may cause undue consternation that will not serve the future of threatened taxa well. Resource managers need to be informed about this disciplinary schism. In the absence of sufficient communication, conservation genetics may lose credibility with cooperating managers. Unfortunately, it seems that a consensus will not be achieved while the US ESA and laws similar to it (e.g. Australia's EPA) remain vaguely worded and offer insufficient operational evolutionary framework or guidance (Wayne 1992; Vogler & DeSalle 1994; Mayden & Wood 1995; Pennock & Dimmick 1997; Waples 1998).

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