

KEYNOTE ADDRESS: CONSERVATION GENETICS OF FRESHWATER ORGANISMS



This manuscript serves as a summary of both the importance of genetics in conservation, and the range of methodological approaches available. Two somewhat distinct realms of conservation genetics are outlined. The first theoretically rests upon the field of population genetics, and primarily concerns itself with the conservation of genetic diversity within and among populations, both in the wild and captivity. Basic concepts such as heterozygosity, genetic drift, and effective population size are discussed in the framework of freshwater conservation interests. Most importantly, it is emphasized that only multi-locus data sets, with adequate sample sizes are appropriate for answering a range of conservation-oriented questions with such population genetic approaches. The second area of research rests upon the fields of phylogenetics and phylogeography and concerns itself with systematics and the designation of conservation units. The somewhat popularised role of using trees based on mitochondrial DNA sequences and phylogeographic structure to define conservation units is described, but also criticized. In its place, a pluralistic approach should be undertaken, which takes into consideration both the socio-economic and legislative framework within which conservation units can be managed. Finally, despite much attention to the varying definition of conservation units, both theoretical and practical considerations support that the unit most important to conservation is the population.

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