



Population Genetics for Animal Conservation

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evolutionary origin of the only extant tortoises in the Indian Ocean, the Aldabra tortoise, *Geochelone dussumerii*, an trying to evaluate levels of genetic diversity and its evolutionary relationships to other extant and extinct tortoises from the Indian Ocean. These data have been used to understand the history of the group but also to help develop conservation strategies. I will present several examples of how genetic data are used in these giant reptiles to develop management strategies for captive and wild populations based on a multidisciplinary approach.

A10

TBA

Michel Milinkovitch

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A11

Genetic methods and avian conservation: bottlenecks, fragmentation and conservation units

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Genetic methods can be applied to issues of avian conservation in a variety of ways. Neutral genetic markers can be used to assess inbreeding levels, genetic variation, population structure and phylogenetic or conservation units. Non-neutral genetic systems can be useful for assessing the potential adaptability of a population to environmental change or translocation. Birds are thought to be more coarse-grained in associations with their environment, and so local adaptation may not be considered as much of a factor as with invertebrates or plants. Endangered bird populations can become highly fragmented and decrease to very low levels, and ensuing genetic bottlenecks could impact fitness. However, flight provides most birds with greater powers of dispersal and thus gene flow is higher and may mitigate these impacts. Interactions with infectious disease may be one of the greatest conservation problems facing birds, as evidenced by introduced pathogens (malaria, pox) in Hawaii and West Nile Virus in the U.S. I discuss how genetic analyses may be used to provide information relevant to conservation and management, and provide several case studies for illustration.

A12

Patterns of genetic variation at micro-geographic scales in five mammals in the Italian Alps, with management implications

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Using sequence variation at the mitochondrial control region (D-loop) and allele frequencies at ten microsatellite nuclear markers, we analyzed patterns of genetic variation in five mammals species in the Autonomous Province of Trento (Italy): chamois (*Rupicapra rupicapra*), roe deer (*Capreolus capreolus*), red deer (*Cervus elaphus*), European brown hare (*Lepus europaeus*) and mountain hare (*Lepus timidus*). All these game species are presently widespread throughout the Province; however, they suffered a strong size reduction in the last century as a result of a remarkable transformation in land use and over-exploitation. Subsequent, uncontrolled restocking have probably also affected the native populations and their genetic composition. For all five species, at least four different samples were considered, each consisting of about 25 specimens, collected from populations separated by geographic distances of between 20 and 100 kilometers. Genetic divergence can be observed even at this micro-geographic scale. The relationship between the

patterns of genetic variation, the ecological characteristics of the different species, and the estimated levels of anthropogenic impact in the sampling areas, is discussed.

A13

TBA

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A14

The use of cDNA microarrays for studying local adaptation in natural animal populations

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The cDNA microarray technology has been emerging as a powerful tool to monitor gene expression of thousands of genes simultaneously. The technology has been indeed developed as a search tool for candidate genes rather than to investigate the evolutionary significance of gene expression diversity itself. In particular, individual gene expression diversity has been so far considered as a nuisance parameter that has often been ignored, for instance by pooling RNA-samples of several individuals. However, the fundamental unit of the evolutionary process is the individual. Any selection process acting on levels of gene expression is thus fuelled by inter-individual differences, which are therefore of central importance for studying local adaptation. We shall discuss how to take into account gene expression variability at the level of individuals in experimental design and in statistical analyses in general, showing that already existing statistical methodologies can be adapted to analyze cDNA microarray data. These methodologies will be applied to the particular case of investigating possible genetic determinants of local adaptation in freshwater fish populations of brown trout (*Salmo trutta*).

A15

Using molecular markers to study quantitative genetic variation in the wild

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Traits underlying fitness and adaptation to changing environmental conditions are generally quantitative in nature. A quantitative genetic approach is therefore the most direct avenue towards a better understanding of the adaptive potential of populations that are under conservation threat. Inferences about genetic variances can be made using either analytical methods based on molecular pedigrees or through marker-regression techniques that consider the covariance of trait similarity and inferred relatedness. The relative merits of these approaches are compared using empirical data from two wild ungulate populations. We estimated the heritabilities of life-history and morphometric traits related to fitness using microsatellite based pedigree and relatedness estimates from bighorn sheep (*Ovis canadensis*; Ram Mountain, Canada) and alpine ibex (*Capra ibex*; Parco Gran Paradiso, Italy). Pedigree-based analyses using an “animal model” approach generated significant heritability estimates with considerably less error than regression-based estimators.

A16

MHC genes on the history and conservation of the rare porpoise Vaquita

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