New, Flexible Bayesian Approaches to Revolutionize Conservation Genetics

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The goal of the rapidly expanding field of conservation genetics is to combine genetic methods and theory to improve the management of species severely affected by human activities. Molecular biology and population genetics are the main components of this discipline, with the former yielding an impressive quantity of relevant data and the latter permitting detailed interpretations. Results can then be integrated with other conservation management tools to help define priorities for intervention (Frankham et al. 2002).

Recently, the explosion in development of new analytical tools in population genetics (mainly based on Monte Carlo algorithms now treatable with desktop computers) and the possibility of analyzing a large number of genetic markers simultaneously (the genomic approach) have had two major consequences: the array of both statistical and technical methods potentially useful to conservation genetics has undergone a quantum leap, while a substantial gap has been created between the theoretical and applied sciences in this field.

This gap was significantly narrowed at a recent workshop entitled "Population Genetics for Animal Conservation," where the splendid isolation of the conference site and evening software sessions encouraged lively discussion among the 18 invited speakers and 42 selected participants. (Abstracts available from http://web.unife.it/progetti/genetica/pgac2003/pgac2003.htm, Center for Alpine Ecology, Trento, Italy.)

As underlined by Phil Morin, Mike Bruford, and several other speakers, conservation genetics urgently requires flexible statistical methods tailored to address specific questions. It emerged early in the workshop that the plethora of recent Bayesian methods based on multilocus genotypes is the answer to these needs (Eric Anderson). This step change will be realized through the implementation of new, fast, and efficient approximations based on summary statistics and modified rejection-sampling algorithms (Mark Beaumont, Laurent Excoffier), and understanding of complex population dynamics will be possible through the simultaneous estimation of important parameters such as effective population size and its rate of variation, admixture proportions, migration rates, and selection coefficients. Moreover, Bayesian methods are suitable for questions concerning individuals (e.g., Who is the migrant? Who is the hybrid? Who is the most successful?) and can even allow the integration of a priori nongenetic information (Oscar Gaggiotti). These new methods represent an efficient alternative to sophisticated coalescent-based maximum-likelihood methods (Peter Beerli) or nested-clade analysis on intra-specific networks (David Posada). The bottom line is that all these sophisticated techniques have the potential to revolutionize statistical inference in conservation genetics.

A second hot point discussed at the workshop was the long-standing but increasingly fundamental question of the relationship between neutral and adaptive variation (Craig Primmer, Kathryn Rodríguez-Clark). It became obvious that genomic approaches have already begun to clarify this issue through direct analyses of selected genes, quantitative trait loci (QTL) mapping of selected phenotypes (Louis Bernatchez, Dave Coltman), and elucidation of gene expression patterns through microarray technology (Carlo Largiadèr). Once more, new statistical approaches appear to be the key to identifying candidate loci by focusing on markers with unusual patterns of genetic variance among populations (Mark Beaumont, Gordon Luikart).

Finally, the importance of interpreting ancient or historical DNA data for the conservation of extant species was emphasized by several speakers (Robert Fleischer, Peter Galbusera, Elizabeth Hadly, Carles Vilà, Peter

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Wandeler). The analysis of genetic data from both modern and ancient samples, in the light of environmental changes and threats, is the next challenge for the new statistical methods.

Literature Cited

Frankham, R., J. D. Ballou, and D. A. Briscoe. 2002. Introduction to conservation genetics. Cambridge University Press, Cambridge, United Kingdom.