

Conservation Biology: The Need for Multidisciplinary Approaches

Human impacts – anthropogenic climate warming, habitat loss and fragmentation – are likely to increase during the twenty-first century (Smith *et al.*, 2009). Thus, the challenges facing conservation biologists tasked with preserving biodiversity and evolutionary processes are likely to become more complex. One of the important challenges is how to determine conservation strategies without comparable biodiversity metrics (Bach *et al.*, 2012). Population and evolutionary genetics will become increasingly important both in theoretical and applied research. The description and quantification of species distributions and diversity patterns at the levels of genes, species, and ecosystems will be integrated within appropriate hypothesis-testing frameworks, with the aim of identifying the causal determinants of evolution (Guisan and Zimmermann, 2000; Allen *et al.*, 2002; Franklin, 2010). Notably, the role of geographic variation in environmental factors such as climate creates an important basis for predicting responses to future climate change (e.g. Thomas *et al.*, 2004; Kjærsgaard *et al.*, 2012; Kristensen *et al.*, 2012). Although evolutionary biologists and ecologists increasingly are turning to molecular genetics to study the demographic and genetic consequences of natural selection and evolution in the wild, a need for integrative approaches is apparent. Important topics include determining what limits the ability of species to adapt to selective pressures, thus helping us to understand the importance of genetic and environmental components on phenotypic variability; and the relative importance of genetic and ecological factors for the short- or long-term persistence of populations. Detailed knowledge on how past evolutionary pressures have shaped the genetic composition and the present geographic distribution of species can help us to better predict the future consequences of climate changes (Stamenković-Radak *et al.*, 2012; Faurby and Pertoldi, 2012). The biotic effects of Pleistocene glaciations exemplify how climate changes influence species distributions by alternately inducing southward range contractions with northward expansions (Pertoldi *et al.*, 2012a). The geographic patterns resulting from these processes differ with the varying dispersal abilities and ecological requirements of species (Avice, 1998). One central question emerges: namely, can we learn from historical reconstructions how to limit the detrimental consequences of ongoing climate changes on biodiversity?

Based on this perspective, there is a need for a deeper understanding of how genetic parameters can be used to evaluate causal processes, including the genetic signature of populations' decline or expansion (Mucci *et al.*, 2012) due to selective pressures that could be caused by climate-induced environmental changes. Selective pressures also change the patterns of biotic interactions between species, and their morphology. Greater emphasis should therefore be on integrating the wealth of genomic knowledge and phenotypic investigation, to understand complex and still largely unknown gene-phenotype connections, which can unravel ecological patterns that are undetectable using neutral molecular markers. Research projects are beginning to broaden in scope and impact by attempting to correlate genetic, demographic, and phenotypic properties of the same populations. Furthermore, recent progress in biostatistics and mathematics (e.g. theory of coalescence, Bayesian statistics, individual-based population dynamics, algorithms for

efficient simulation and sampling of complex processes) has improved our ability to infer population genetic processes of neutral and non-neutral genes via the development of novel theoretical models (Faurby and Pertoldi, 2012). Moving the genomic methodologies from laboratory model organisms to non-model organisms is now becoming possible, allowing genomic analysis in a population- and species-wide fashion (Mitchell-Olds *et al.*, 2008). The recent identification of functional genes and genes linked to quantitative traits is paving the way for the analysis of functional genes and components of genetic control of physiological processes, and is therefore expected to contribute to our understanding of local adaptation (Marsano *et al.*, 2010). Population genomics will very soon contribute to these issues, delivering large amounts of data on regulatory polymorphisms on a genomic scale. Moreover, we may address the question of whether the regulatory variation *per se* causes adaptation to local conditions. Quantitative genetic analyses are important in the assessment of extinction risk both at the individual and population level, since this approach can provide information on the amount of non-neutral genetic variability governing variation in given traits (Pertoldi *et al.*, 2012b). This information allows us to scrutinize fitness components on various genetic and environmental backgrounds, producing information on the fate of genetic diversity and the strength of selection acting on populations. This will in turn allow quantification of the importance of a given environmental stressor in the expression of functional genes. Such information is becoming extremely relevant in the field of evolutionary biology, as there is a need for detailed studies on how variation at the level of genes translates, through developmental and physiological processes, into phenotypic variation in ecologically important traits (Coulson *et al.*, 2006; Ludoški *et al.*, 2012). A combination of ecological genomics and quantitative genetics will therefore lead to a greatly increased understanding of ecological responses, ranging from genetic variation in natural populations to the description of shifts in phenotypes as a result of evolutionary responses to environmental changes (Luikart *et al.*, 2003).

To foster ongoing discussion in this field of research, the Section of Population and Evolutionary Genetics of the Serbian Genetic Society organized the Second Symposium of Population and Evolutionary Genetics (PEG2012), which was held in Belgrade, Serbia on 9–12 May 2012. The meeting was partly financed by the Serbian Ministry of Education, Science and Technological Development. The aim of the symposium was to bring together scientists from the research fields of population and evolutionary genetics and conservation genetics and genomics to present and discuss state-of-the-art research, and review the progress made across the fields of population and evolutionary genetics, from the theoretical and methodological points of view. We invited leading researchers in population genetics, evolutionary biology, conservation biology, ecology, taxonomy, systematics and genomics, working at various levels of biological organization, from molecules to populations and species. The wide variety of methodological approaches provided the template for inspiring discussions on cutting-edge approaches to studying population and evolutionary genetics problems in free-living as well as in model organisms.

The symposium sessions were organized according to selected topics, which covered many population and evolutionary genetic issues, including: (1) advances in our understanding of the evolution of quantitative traits, using nuclear and extra-nuclear genomic information on variation, evolution of genotype \times environment interactions, and plasticity; (2) interactions among individuals and between individuals and the environment, including the impact of anthropogenic factors on population fragmentation and genetic structure as well as evolutionary genetic responses to global and local environmental changes; (3) collection and analysis of field data from natural populations and their use in addressing

conservation genetics issues; (4) the evolutionary significance of host–parasite interactions and insight into short- and long-term co-evolutionary processes; (5) molecular data coupled with a population approach in human population genetics studies related to aspects of geographic structure of populations, human forensics, pharmacogenetics, and epidemiological studies.

We encouraged conference speakers to submit articles based on their work, and from among these we selected a group of papers appropriate for this special issue of *Evolutionary Ecology Research* entitled: ‘Conservation Biology: The Need for Multidisciplinary Approaches’. It focuses on biological adaptation to environmental change. Such adaptation depends on complex interactions between ecological and genetic mechanisms.

FUTURE DIRECTIONS

To test the robustness of the theoretical foundations of evolutionary and ecological genetics, three areas of research should be addressed using multidisciplinary approaches. (A) *Experimental population genetics furthers research*, including: (i) The evolutionary importance of phenotypic plasticity, environmental and genetic stressors. (ii) The consequences of inbreeding and outbreeding on population fitness and phenotypic plasticity. (iii) The selective effects of fluctuating selective regimes on plasticity genes. Model organisms including clonally reproducing strains may be well suited to improving our knowledge of these issues and a combination of quantitative genetics and molecular omics approaches will enable a deeper insight into the questions. (B) *The collection and analysis of empirical data based on molecular and quantitative genetics studies* should be derived from several species with different ecological characteristics and with different demographic history, such as recent and ancient population decline or expansion. Changes in population size and range are common consequences of climate-induced environmental change (CIEC), and examples include habitat fragmentation and rapid colonization or re-colonization processes. Extensive collections of several species provide the opportunity to analyse large numbers of samples on a temporal scale and directly document changes in genetic diversity. The results of these analyses will improve our understanding of the historical dimension of population change, and provide important data for the interpretation of genetic diversity studies in an ecological and evolutionary context.

The combination of ecological models of the distribution of the species investigated with both mitochondrial DNA (mtDNA) data and synthetic genetic maps constructed from multivariate analysis of microsatellites and morphometric data will allow us to discuss hypothesized historical biogeographic scenarios. By directly dating and quantifying changes in genetic diversity, these investigations will allow examination of postulated causes of population decline, including habitat loss and climate change. (C) *Computational population genetics* using stochastic simulation tools, based on a quantitative infinitesimal model, in which the size of N_e can be varied, should be developed. Using this approach, several topics can be addressed:

1. How different environmental scenarios can affect both genetic and demographic parameters.
2. How differences in life history between ecologically similar species can lead to substantial differences in N_e and σ_a^2 , and to what extent fluctuations in vital rate parameters induced by environmental change can alter N_e .

3. Quantify the interactions of each particular life-history parameter with other factors (sensitivity analysis).
4. Quantify the effects and the interactions that N_e , inbreeding, gametic phase disequilibrium, plasticity, and developmental homeostasis have on the speed at which a population can react to a selective pressure.

If the information obtained from the computational approach can be combined with empirical data, obtained from approaches (A) and (B), we will have a powerful tool for understanding complex dynamics and making predictions about the possible effects of selective pressures and their interactions with other factors.

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