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Conclusion: Effects of genetic erosion are poorly understood. Amphibians' populations often naturally occur as highly inbred. These represent the perfect possibility to measure the impacts of contaminant-driven genetic erosion.

Amphibian biodiversity in an alpine region: a multi-level approach. Patterns, processes and conservation implications

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The present study aims at investigating the patterns and processes affecting the different levels of amphibian biodiversity (genes, species and ecosystems), focusing on a South-Eastern Alps region (Trentino, Italy). Worldwide biodiversity is threatened by an ongoing crisis, caused directly or indirectly by human activities. Global change continuously stresses populations, ecological communities and natural environments, exposing them to new adaptive challenges. Amphibians are particularly sensitive to perturbations due to their complex life histories, susceptible physiology and low dispersal abilities. Since the '80s they are facing a dramatic decline, known as Global Amphibian Decline. Numerous studies have been carried out in order to monitor the conservation status of populations, their genetic diversity levels, as well as the availability and integrity of amphibian habitats. A growing body of evidence is showing that the different levels in which biological diversity may be divided are broadly linked and ecological processes results from the complex interactions between these parts. Despite of these intrinsic connections, the different aspects of biological diversity have so far been confined to separate lines of research, corresponding to the different fields of evolutionary biology and ecology. To overtake this limitation, modern conservation biology is now increasingly recognizing the need for an integrative approach in the study of the structural and functional components of biodiversity, with the ultimate goal of developing effective strategies to counteract its loss. With this study we made a general attempt in this direction, trying to investigate the evolutionary and ecological processes affecting amphibians populations and communities within a systemic perspective. We chose a widespread amphibian, the common frog (Rana temporaria), as target species for the evaluation of genetic diversity be tween and among populations. Genetic diversity provides the evolutionary potential for populations to adapt to environmental changes, and its preservation is of crucial importance in the context of a widespread amphibian decline. Species distribution records of amphibians species were collected for the whole study area. In addition, accurate information about amphibian communities composition for several selected sites belonging to the Natura2000 network were acquired, together with habitat heterogeneity data. Our goal is to shed light on the interactions between habitat heterogeneity (a proxy for ecosystem diversity) and amphibian diversity, both at the species and genetic level. It is generally accepted that habitat heterogeneity acts as a diversifying force and species richness and genetic diversity are hypothesised to co-vary with a positive correlation. Nevertheless, it is not always clear whether habitat heterogeneity affects the species and genetic level in similar or different patterns, and empirical data are sometimes contradictory. The described research is currently at its initial stage and we presented here some preliminary findings, together with possible conservation outcomes. In addition, some examples (taken from the recent literature) of the effects of one level of biodiversity on the others via several mechanisms are illustrated, with the aim of highlighting their consequences in terms of ecosystem stability and ecosystem services. Lastly, important conservation implications of a good/bad understanding of the nature of these interactions are discussed.

Evidence of recombination on the "speciation island" X-chromosome centromeric region between the malaria mosquitoes *Anopheles gambiae* and *An. coluzzii*

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Anopheles gambiae sensu stricto (Giles) and *An. coluzzii* (Coetzee & Wilkerson sp.n.) are two of the most important mosquito species transmitting malaria in sub-Saharan Africa. The two species are morphological identical, but can be