

Linking epigenetics and biological conservation: Toward a conservation epigenetics perspective

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Conservation biology is a multidisciplinary field aiming at maintaining and restoring biodiversity from genes ecosystems. In the last decades, genomic tools were integrated into conservation biology to estimate demographic parameters and adaptive potential, characterize population structure, delimitate taxonomic groups and *evolutionary significant units* (ESUs; i.e. groups of individuals that have been ideally characterized ecologically and genetically to guide conservation efforts for preserving adaptive genetic variance within species), and manage population rescue strategies. However, genetic approaches give generally poor information on the short term interaction between individuals and their environment because genetics mainly represents the long term history of populations. Moreover, the evolutionary potential relies on functional diversity that is inherited, but the non-genetic molecular mechanisms of inheritance are still little considered. Finally the upscaling from genetics (i.e. the study of some targeted genomic regions) to genomics (i.e. the study of the overall genomes) has not yet filled the gap to identify rapid molecular responses to be used in modern conservation.

We here argue that epigenetics; i.e. the study of reversible chemical changes involved in the regulation phenotypes without, modifying the nucleotide sequence of the DNA, constitute a promising complementary disciplinary field for conservation biology as it allows documenting the ecological background of organisms. Epigenetic marks are sensitive



to the environment, and they are involved in organisms' short term adaptive responses to changing environments. As such they affect ecological and evolutionary processes at all biological levels, from individuals to the ecosystems. Among the identified epigenetic components, DNA methylation is the most studied mechanism in ecology. In this study we illustrate the relevance of DNA methylation for i) developing biomarkers of past and present environmental stress events as well as biomarkers of physiological conditions of individuals; ii) documenting the ecological structuring/clustering of wild populations and hence refining the delimitation of ESUs; iii) improving conservation translocations and iv) studying landscape functional connectivity.

Based on the theoretical and practical aspects developed in this study, we propose that epigenetics constitute a promising field that should be integrated in the toolbox currently available for biological conservation.