

Genome-wide methylation in the panmictic European eel (*Anguilla anguilla*)

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Abstract

The role of methylation in adaptive, developmental and speciation processes has attracted considerable interest, but interpretation of results is complicated by diffuse boundaries between genetic and non-genetic variation. We studied whole genome genetic and methylation variation in the European eel, distributed from subarctic to subtropical environments, but with panmixia precluding genetically based local adaptation beyond single-generation responses. Overall methylation was 70.9%, with hypomethylation predominantly found in promoters and first exons. Redundancy analyses involving juvenile glass eels showed 0.06% and 0.03% of the variance at SNPs to be explained by localities and environmental variables, respectively, with GO terms of genes associated with outliers primarily involving neural system functioning. For CpGs 2.98% and 1.36% of variance was explained by localities and environmental variables. Differentially methylated regions particularly included genes involved in developmental processes, with hox clusters featuring prominently. Life stage (adult versus glass eels) was the most important source of inter-individual variation in methylation, likely reflecting both ageing and developmental processes. Demethylation of transposable elements was observed in European X American eel hybrids, possibly representing postzygotic barriers in this system characterized by prolonged speciation and ongoing gene flow. Whereas the genetic data are consistent with a role of single-generation selective responses, the methylation results underpin the importance of epigenetics in the life cycle of eels and suggests interactions between local environments, development and phenotypic variation mediated by methylation variation. Eels are remarkable by having retained eight hox clusters, and the results suggest important roles of methylation at hox genes for adaptive processes.

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