Genetic structure of (sub)adult European eel (Anguilla anguilla L.) based on allozyme markers

Maes G. and F. Volckaert

Katholieke Universiteit Leuven, Laboratory of Aquatic Ecology Ch. De Beriotstraat, 32, B-3000 Leuven, Belgium E-mail: gregory.maes@student.kuleuven.ac.be

The life history of the European eel remains somewhat of a mystery. Adult eels are thought to spawn in the Sargasso Sea, where the newly hatched larvae start their journey to the European continent along the North Atlantic Current. They spend most of their life in the rivers until they metamorphose after about 10 years into silver eels and then return to their spawning grounds. Most studies on European eel considered the species as panmictic and highly homogeneous. However, some elements point to the heterogeneity of European eel.

In this study 309 (sub)adult European eels were examined at 18 different allozyme loci at 7 localities dispersed throughout the natural continental range. The aim was to determine (1) the genetic diversity and structure of the European eel across Europe, (2) if the genetic structure is in agreement with the results on glass eel and with literature, and finally if there is any evidence of selection forces comparable to those in American and Japanese eel.

We show that the 7 European eel populations are poorly differentiated, which is not surprising considering the impressive spawning migration and because the analyses were made outside the spawning grounds of the Sargasso Sea. A significant genetic difference was observed between the male and the female silver eel from the Dutch populations, which may indicate a relation between sexual differentiation and genetic structure. The longer impact of selection on female individuals could be one explanation. Unusual alleles were discovered in several individuals of the Irish and second Dutch population, which might be linked to introgression of American eel in the European eel species. Finally, we describe a significant geographical cline for three alleles at two loci. Such results have also been observed in the American and Japanese eel. This might point to the selection hypothesis, because so far there is no knowledge on genetic isolation among the European eel.

Keywords: Population Genetics; clinal variation; European eel, allozymes.