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Metamorphosis and transition between developmental stages in European eel (*Anguilla anguilla*, L.) involve epigenetic changes in DNA methylation patterns

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Abstract

The life history of the European eel (*Anguilla anguilla*, L.) is characterized by a series of metamorphoses and transitions that provoke drastic morphological changes. Most of these changes go along with the catadromous life cycle in eels, involving extensive physiological adaptations. In this study it was investigated whether these drastic changes have an epigenetic basis by analyzing global methylation patterns in liver, gill and brain tissue from glass eels caught at the British coast as well as yellow and silver eels from River Rhine using methylation-sensitive amplified polymorphisms (MSAP). Analysis of molecular variance (AMOVA) on MSAP data derived from liver tissue revealed only minor differences in methylation patterns between glass, yellow and silver eels, reflecting uniform functioning of the liver throughout the investigated lifespan. In brain and gill tissue, however, marked differences in methylation patterns were found. Principal coordinates analysis (PCoA) revealed yellow eels being partially clustered with silver eels and a more distinct cluster of glass eels based on the methylation patterns in the brain. According to results found in the gills, glass eels were more similar to silver eels whereas yellow eels were found to be clustered separately. From these results it can be concluded that epigenetic changes in gill tissue most likely reflect and

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