

Poster 1.

Genetic and environmental influences on the epigenetic component of sexual development in a teleost fish, the European sea bass

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In many reptilian and piscine species, sex is a phenotypically plastic trait that can be influenced by temperature. In the European sea bass (*Dicentrarchus labrax*), the sex is determined by both genetic and environmental factors and the parental generation may produce more or less male-prone offspring. The response to temperature is mediated by the inhibition of gonadal aromatase (*cyp19a1a*) expression, the enzyme that converts androgens into estrogens, by increased DNA methylation in the gene promoter. However, the methylation levels of other genes related to sexual development and the parental effects on the epigenetically-mediated response to temperature may influence the phenotypic outcome. In this study, the offspring of four sires known to produce male- or female-prone progeny was reared at low or high temperature during the thermosensitive period. Then, in the gonads of adult fish, the methylation levels of the putative regulatory regions of 7 genes related to sexual development were measured by a custom-made multiplexed targeted bisulfite sequencing approach. We showed that the methylation of the two of the most important genes for sexual development, *cyp19a1a* and *dmrt1*, is both genetically and environmentally regulated in opposite directions according to sex. Furthermore, when we focused on the genetic component by including only the fish reared at low temperature, we observed that the CpGs of *er-β2*, *foxl2* and *nr3c1* presented unfluctuating methylation levels between sires and offspring. This result indicates a potential transmission of the methylation states across generations. On the other hand, the methylation levels of some CpGs were highly responsive to temperature. Using a combination of these CpGs we were able to achieve the first prediction of sex in a vertebrate with high accuracy based on analysis of DNA methylation pattern of a suite of selected CpGs. These results suggest a panel of CpG candidates to be used as biomarkers for sex prediction and multigenerational transmission of the methylation status. *Supported by MINECO grant AGL2016-78710-R "Epimark" to FP.*