

Poster 8.

DNA methylation levels of sex-related genes involved in the gonadal development of zebrafish (*Danio rerio*)

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Abstract

Fish exhibit all types of reproduction systems known in vertebrates. In fish, gonadal fate is the combined result of genetic and environmental influences and some evidence indicates that epigenetic processes such as DNA methylation may have an important role. However, little is known regarding the relationship between DNA methylation and the expression of key genes involved in sexual development. In this study, we analyzed the DNA methylation of the promoter regions of canonical reproduction-related genes (*dmrt1*, *dmrt3a*, *amh*, *cyp19a1a*, *fshr*, *foxl2*, *ar*, *sf1* and *fanc1*) and its association with sex in 90-day-old adults of two different AB zebrafish families. DNA was extracted from their gonads and NGS libraries were prepared and sequenced using a targeted bisulfite sequencing approach. Results showed that there were significantly higher DNA methylation levels in the promoter of *amh*, *cyp19a1a*, and *foxl2* of males compared to females, while *dmrt1* and *dmrt3a* exhibited the opposite pattern. Principal Component Analysis (PCA) showed that gonadal samples could be resolved according to sex. However, a subset of males was grouped closer to females than to the rest of males, suggesting that these males were neomales (genetic females developing as phenotypic males) produced spontaneously by perturbations of the process of sexual differentiation with a yet unknown etiology. In order to further analyze these findings, we are currently analyzing the expression levels of key genes related with male and female differentiation. This study contributes to our understanding of the role of DNA methylation in gene expression regulation during critical steps of gonadal development in a vertebrate model. *Supported by MINECO grant AGL2016-787107-R "Epimark" to FP.*