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EXPRESSION PATTERNS OF DNA METHYLTRANSFERASE GENES DURING GAMETOGENESIS AND EARLY DEVELOPMENT IN RAINBOW TROUT *Oncorhynchus mykiss*

Jingwei Liu*, Huihua Hu, Stephane Panserat, Lucie Marandel

INRA, Univ Pau & Pays de l'Adour, UMR1419 Nutrition Metabolism and Aquaculture, Aquapôle, F-64310 Saint-Pée-sur-Nivelle, France

E-mail : jingwei.liu@inra.fr

DNA methylation is one of the most extensively studied epigenetic mechanisms that modulate gene expression and cellular differentiation. It plays critical roles during gametogenesis and early development of vertebrates. Previous studies in mammals demonstrated that DNA methylation is accomplished through the activities of DNA methyltransferases (Dnmts). Dnmt1 is associated with the maintenance of methylation status, whereas Dnmt3a and Dnmt3b are essential for *de novo* methylation. The present study aimed at investigating the dynamic transcription pattern of *dnmt* genes during gametogenesis and early development for the first time in rainbow trout (*Oncorhynchus mykiss*), an economically important fish species.

Due to the fact that the teleost experienced a third round of whole genome duplication (WGD) apart from the two round of WGD that occurred at the root of the vertebrate lineage, the evolutionary of *dnmt* genes remains unclear. Indeed, there are three common fates for the duplicated genes after WGD: loss one of the duplicate gene, sub- or neo-functionalisation. In the present study, two ohnologs of *dnmt1* (*dnmt1a* and *dnmt1b*) and eight paralogs of *dnmt3* (including 3 paralogs of *dnmt3a*: *dnmt3aa*, *dnmt3ab1*, *dnmt3ab2*, and 5 paralogs of *dnmt3b*: *dnmt3ba1*, *dnmt3ba2*, *dnmt3bba1*, *dnmt3bba2* and *dnmt3bbb*) were identified in rainbow trout. Spatial expression patterns of *dnmt* genes were analysed using the PhyloFish database to identify the main expression territories of these genes. Results showed that, both *dnmt1* ohnologs were preferentially expressed in unfertilised eggs. *dnmt3a* paralogs were highly expressed in brain, whereas *dnmt3ba1*, *dnmt3ba2*, *dnmt3bbb* were predominantly expressed in skin, head kidney and ovary, respectively, which could be possibly linked to a sub- or neo-functionalisation after WGD.

The dynamic expression patterns of *dnmt* genes were analysed in trout gonads during gametogenesis (between two spawn). Our results showed that there was a remarkable increase in the mRNA levels of *dnmt1a* and three of the five *dnmt3b* paralogs in oocytes compared with ovaries in females. In males, we observed the highest mRNA level of *dnmt1a* together with the lowest mRNA levels of *dnmt3ab1* and *dnmt3bba1* at the late-spermatogenesis stage. Besides, mRNA levels of *dnmt* genes were also analysed during early development of trout from stage 0 (oocyte) to stage 36 (alevin). All *dnmt* genes displayed a similar expression pattern, with no or low mRNA levels from stage 0 up to 15, followed by a sharp increase at the setting up of the most of the vital organs (stage 22/23) and then decreased after hatching. By contrast, there was relatively high transcript abundance of *dnmt3bbb* from the beginning of embryogenesis, suggesting its functionally importance during early development.

In conclusion, the dynamic expression patterns of *dnmt* genes during gametogenesis and early development suggested that epigenetic mechanisms actively participated in these physiological processes in trout. The distinct transcription patterns of *dnmt3b* paralogs indicated that they may subject to sub- or neo-functionalisation after WGD.

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