O-020

Foxl2 and Foxl3 in teleosts: origin, regulation and role in reproduction

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Foxl2 is a forkhead transcription factor involved in many biological processes such as development and reproduction. The role of Foxl2 has been widely studied in mammals whereas information in teleosts is more limited. Moreover, processes that control its expression remain mainly unknown. Two *foxl2* teleost-specific paralogs, namely *foxl2a* and *foxl2b*, have been previously described in some fish species. We recently cloned these two Foxl family members in European sea bass (*Dicentrarchus labrax*). In contrast to the previously proposed origin, our phylogenetic and synteny analysis revealed that they originated before the teleost-specific whole genome duplication and therefore should be re-named as *foxl2* and *foxl3*. Tissue expression patterns show high sexual dimorphism that could indicate different roles for these two Foxl proteins in gonadal maturation and sexual identity. Foxl2 binding to both gonadal and brain aromatase promoters has been documented in several teleosts, herein, we describe new potential target genes for both Foxl2 and Foxl3. We have used both *in vitro* and *in silico* strategies to determine if activation of these genes is done directly through promoter binding or indirectly. Finally, we have inserted the promoter of sea bass *foxl2* in a luciferase expression plasmid to investigate potential ways of regulation by co-transfection with homo- and heterologous transcription factors. Supported by MICINN (AGL2011-28890, PhD-fellowship O.L-C-W), GV (REPROBASS-Prometeo, ACOMP/2013/085).