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M. Adolfi, Anabel Martinez-Bengochea, A.S. Roco, V. Kottler, - Du, K., S. Kneitz, Qiaowei Pan, Romain Feron, Elodie Jouanno, Ming Wen, et al.

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## LECTURE 1

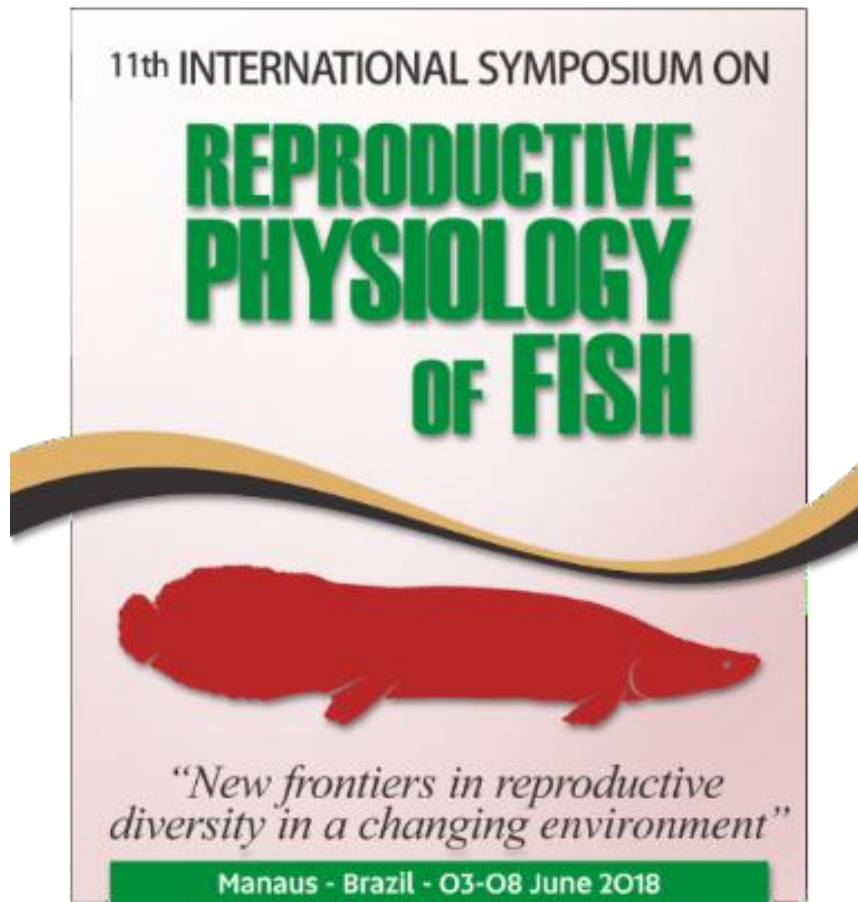
### SEX DETERMINATION DIVERSITY IN FISH

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Fish show the greatest plasticity of sex determination (SD) mechanisms amongst vertebrates. In the case of genetic SD this is linked to a similarly high variability of sex chromosome differentiation. While in a handful of species with genetic SD the master SD genes have been identified, their molecular function in directing the development of the bipotential gonad primordium towards testis or ovary is unclear in many cases or incompletely known in the others. To obtain a better understanding of the biological meaning of this diversity we need a deeper understanding of the molecular basis of SD mechanisms and the structure and genetic organization of sex chromosomes across a broad diversity of actinopterygian fish. To identify primary SD genes we used high throughput RAD-tag marker mapping in >40 species as well as transcriptomics, Pool-Seq and genome sequencing to identify sex-specific chromosomal regions and candidate SD genes. This led to the identification of sex-specific markers, allowing to delineate the extent of recombination suppression, which turned out to be highly variable between species. We identified several species with clear cut XX/XY or ZZ/ZW monofactorial systems but also species with more complex sex-determination systems including species with a mix of GSD and ESD and species with potential polygenic systems. In species with available genomic resources, sex-specific markers could be used to assign scaffolds to regions that are supposed to contain the primary SD gene. We identified candidate genes in several species and find that most of them belong to already known factors of the primary SD regulatory network including candidate genes that have not been found so far as being SD genes. We also find that many species harbor very poorly differentiated sex-chromosomes. While the variety of SD genes that can trigger the male or female SD regulatory network and the differentiation of the gonads is now well established, it is only emerging that also the whole system downstream of the primary SD factors is subject to evolutionary change and - like the top SD genes - can vary even between closely related species. Transcriptome profiling of gonads during male and female development and of mature ovaries and testes uncovered an unexpected extent of differential gene expressions in contrast to an obviously striking morphological and physiological conservation of the reproductive organ system.

# PROGRAM AND ABSTRACTS



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