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Genetic Basis of Sex Determination in Fishes: Searching for Master Key Regulator Genes in the Sex Determination Pathway of Tilapias*

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Abstract

Recent results show a striking similarity in the dynamics of expression of gonad differentiation regulators in zebrafish and mammals. Candidates for the role of master key regulators (MKRs) in tilapia were selected, based on three concepts established in the literature for non-mammal species. These three concepts are: (a) MKRs are DM-proteins or their close downstream/upstream partners in the sex determination pathway, (b) MKRs are genes working just upstream of aromatase in the sex determination pathway, or the aromatase itself, and (c) MKRs are homologs of mammal genes which are close partners of SRY ("missing" in non-mammal vertebrates), mostly belonging to the SOX family. Coding sequences of putative genes were searched in cichlid (TIGR) and general (NCBI) databases, and in the tilapia gonad EST library (RBEST). Primers in two adjacent exons were designed, based on predicted exon-intron boundaries for each of 11 selected genes. Amplified segments of the targeted genes in two purebred tilapia species were sequenced. Seven SSLP and four SNP-based markers were identified in the candidate genes for MKRs of sex determination and mapped to the tilapia genetic map using genotype data of 76-90 individuals of the F_2 mapping family. The mapping positions of the selected genes relative to previously reported QTL regions for sex determination are discussed.

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* The full paper: *Amh* and *Dmrta2* Genes Map to Tilapia (*Oreochromis* spp.) Linkage Group 23 within QTL Regions for Sex Determination, by Andrey Shirak, Eyal Seroussi, Avner Cnaani, Aimee E. Howe, Raisa Domokhovsky, Noam Zilberman, Thomas D. Kocher, Gideon Hulata and Micha Ron has been accepted for publication by *Genetics*.

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