W633 Genomics of an ancient sex chromosome in Tilapia

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Jean-François Baroiller, CIRAD, Montpellier, France

Lucile Soler , CIRAD, Montpellier, France S. Bocs , CIRAD, Montpellier, France M. Conte , University of Maryland, College Park, MD A. D'Hont , CIRAD, Montpellier, France Thomas Kocher , University of Maryland, College Park, MD Ozouf Ozouf , Muséum National d'Histoire Naturelle, France

H. D'Cotta, CIRAD, Montpellier, France

We have developed important genomic tools and methods of comparative genomics in the Nile tilapia, Oreochromis niloticus. The physical comparative map generated with BACs allowed us to calculate that there were about one rearrangement of intra-chromosomal every 3 Mb. For most chromosomes (about 40-48 Mb) there were about 16 breakpoints with ie eight inversions per chromosome. When extrapolated to the large bivalent chromosome Chr 1-LG3 (about 100-120 Mb), we estimate probably 40 breakpoints and 20 inversions. Our work suggests that intrachromosomal rearrangements with 160 inversions have occurred since the divergence of tilapia with stickleback, the species found to be closely related to tilapia. We have also developed a high resolution RH map containing 1296 markers distributed over the 22 chromosomes, that are now identifiable by cytogenetic analysis. The linkage groups of the genetic map were anchored with 149 microsatellites to chromosomes. A inverted zone was found by BAC-FISH close to the centromere in one of the Chr1-LG3 chromosomes of XY males and in 2 Chr1-LG3 chromosomes of YY males, but absent in XX females. This inversion is not in the region where recombination is suppressed. These results suggest that the Chr1-LG3 chromosome is still acting as a sex chromosome. The Nile tilapia appears to be in the midst of a transition between ZW to XY systems. In the Chr1-LG3 chromosome, 515 protein-encoding genes were found with 152 being tilapia-specific, while in the inversed region 19 genes were found including the gene dmrtA1. Highly conserved and ordered syntenies have been identified with the genes of the inversion zone, not only with the stickleback (Chr 7 and Chr9) but also with the chicken Z chromosome, the platypus X5 Chr and also with human Chr9, in which genes involved in sex determination are located.

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