Genetic diversity of commercial species of the tilapia genus *Oreochromis* in Mexico

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Introduction. Mexico is one of the most important tilapia producers in Latin America Ruiz *et al.,* (2007).Cichlids are cultured in almost all the country including Sinaloa state, where the interest for tilapia farming industry is increasing Rodríguez-González (2009). For instance, identified genes from four tilapia species inside the genetic pool of a commercial variety, pointed out that inbreeding increase organisms deformities, genetic damage, and promote heterogeneous size of fry in tilapia populations, and reduce feed conversion ratio, survival and growth of juvenile and adult fish. In Nowadays, molecular techniques such as the DNA markers are commonly used to examine inter and intra population variation among fish strains. Specifically, DNA markers have been used for mapping genetic information of *O. niloticus* Lee *et al*., (2004), to evaluate the genetic variability of two *O. niloticus* strains cultured, study the expected and obtained heterozygosity in several commercial tilapia varieties and to compare productive indices among different fish strains related to genetic information. Therefore, the objective of the present work was to assess the genetic diversity of three tilapia species (*Oreochromis aureus*, *O. mossambicus* and *O. niloticus*) cultured in Sinaloa, Mexico, using DNA markers.

Methods. Genetic variables measured were: size of each locus, number of alleles observed and expected allele frequency heterogeneity, Weimberg Hardy, polymorphic information content for each locus and locus combination and heterogeneity in allele frequencies. Used eight microsatellite markers (UNH145, UNH155, UNH160, UNH166, UNH190, UNH207, UNH208 And UNH211). We performed a DNA bank of 24 agencies (12 males and 12 females) for each species. Microsatellite markers were amplified for each of our DNA bank through the PCR and the products obtained were analyzed on polyacrylamide gels in 6.5% semi-automated sequencer LICOR.

Results.
A panel of microsatellites for joint typifying of the three Tilapia species most used in farming systems of Mexico was successfully optimized. Descriptive information of microsatellite panel optimized by Tilapia species is presented in Table 2. All microsatellite showed to be informative, except UNH190 for *O. mossambicus* with the lowest average number of alleles (A), and the unamplified UNH208 for *O. mossambicus* and *O aureus*. Individual identity exclusion probabilities for genotyped microsatellites ranged from 0.403 to 0.952 for *O. mossambicus*, 0.784 to 0.989 for *O. aureus*, and 0.716 to 0.982 for *O. niloticus*. Combined exclusion probabilities were 1.40^{-6}, 1.1^{-9} and 1.9^{-10}, for the three panels optimized for Tilapia species, respectively.For *O. mossambicus, O aureus* and *O. niloticus* the A obtained was 6.42, 11.71 and 11.25 alleles per loci, respectively; and estimated average Ae for all three species was 2.96, 6.42 and 5.70 alleles per loci. The standard diversity indices showed that *O. niloticus* was the observed most variable (average H_O= 0.541) followed by *O. aureus* (average H_O = 0.464) and *O. mossambicus* (mean He = 0.351). Similarly gene diversity (G) estimators were 0.868, 0.611 and 0.237 for *O. niloticus*, *O aureus* and *O. mossambicus*, respectively. For fixation index F_{IS} the highest average level was observed for *O. aureus* population (0.436) and the lowest for *O. niloticus*. Highly significant deviations ($P < 0.05$) from Hardy-Weinberg equilibrium were estimated for all loci and populations, with exception of UNH145 locus for all populations and UNH166 in *O. niloticus*. Fixation indices analysis by allele identity showed divergence in population structure, amongst the studied *Oreochromis* populations. Estimated pairwise F_{ST} was high between all species; with the higher estimate between *O. mossambicus and O niloticus* (0.2845) and lower between *O. aureus* and *O. niloticus* (0.1651).

Conclusions. The obtained results showed that the use of microsatellites is a powerful tool to evaluate the commercial tilapia populations cultured in Sinaloa, Mexico. It is concluded that genetic diversity of the tested species is low, promoted perhaps, by particular management practices and low genetic flow suggesting the progressive close of populations and inbreeding risk. These and periodical molecular data would aid decision making on convenient reproduction management of stocks, assuring the maintaining of low inbreeding levels and the highest productive response.

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