Genetic variation in the mitochondrial genome of the giant grouper Epinephelus lanceolatus (Bloch, 1790) and its application for the identification of broodstock

Abstract

Mitochondrial DNA (mtDNA) markers are ideal for the validation of maternal inheritance and the identification of brood-stock in aquaculture breeding programs. The complete mitochondrial genomes of 11 species of grouper are currently available at the GenBank. This study was directed towards the characterization of mtDNA loci which can be applied for identification of interspecific F1 hybrids developed from Epinephelus fuscoguttatus and Epinephelus lanceolatus in aquaculture breeding programs. DNA was extracted from the fin clip of one specimen of E. lanceolatus which the source of sperm for the artificial spawning of the interspecific F1 hybrid E. fuscoguttatus \times E. lanceolatus. Specific primers were designed to amplify the DNA after comparative analysis of the mtDNA genomes available at the GenBank. The primers were applied to test for cross-amplification in F1 hybrids as well as in the maternal parent E. fuscoguttatus (Forsskål, 1775) and the genetically related species Epinephelus coioides and Epinephelus corallicola (Valenciennes, 1828). DNA sequence analysis revealed that the Malaysian variety of E. lanceolatus exhibited variation at 11 of the 13 ORFs when compared to the variety from Taiwan. A distinct segmented duplication was observed in the D-loop region which was determined to be unique to the E. lanceolatus specimen obtained from Sabah, Malaysia. Cross amplification of mtDNA loci in the groupers E. fuscoguttatus, E. coioides, E. corallicola and the F1 hybrid of E. fuscoguttatus × E. lanceolatus revealed distinct profiles for each of the species with a clear indication that mtDNA were inherited from the maternal parent of the F1 hybrid.. mtDNA loci can be applied by fish breeders to determine interspecific hybridization events.