

Analysis of genetic marker linked with a homozygous lethal condition in Olive flounder family

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Introduction

Skewed segregation ratios of genetic loci are often observed in the progeny of inter-and intra-specific hybrids and the phenomenon may be resulted from competition among gametes or from abortion of a gamete or zygotes. Deviations from the expected Mendelian segregation ratios of genetic markers have been reported in many plants and animals as well as in some of fishes. In the course of QTL analysis of the olive flounder back cross (BC) families, we observed significant segregation distortion at microsatellite marker, *Poli9-58TUF*.

Materials and methods

The random BC progenies derived from a cross between the F1 male genotype (A/B) and the F1's female parent genotype (A/C) were used in segregation analysis at day 25 and day 105 after fertilization. Genotype of individual samples at the microsatellite *Poli9-58TUF* locus were determined by Genotyper software and automatically exported to a database.

Results and summary

The segregation of alleles for this locus at day 25 after fertilization was concordant with the expected Mendelian segregation (A/A:A/B:A/C:B/C=48:23:10:19). However, the significant distortion in *Poli9-58TUF* locus was discovered and found out that it was caused by the elimination of homozygous A/A genotypes at day 105 after fertilization (A/A:A/B:A/C:B/C=0:19:30:51). This implies that the parent fishes of this family carried a recessive gene or genes hampering development at an early stage. From the double heterozygote parents, the reduction in frequency or elimination of one homozygous class in the progeny is an evidence for linkage between the genetic marker and gene(s) with recessive deleterious alleles. This data support a hypothesis that the region contains a recessive lethal gene or genes.

References

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