Genetics Features of Natural and Cultured Populations of Half-Smooth Tongue Sole (*Cynoglossus semilaevis*) Revealed by RAPD Markers

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Abstract

Randomly amplified polymorphism DNA (RAPD) was used to evaluate genetic diversity in natural and cultured populations of half-smooth tongue sole (*Cynoglossus semilaevis*). Two hundred genotypes from four natural populations (Laizhou, Weihai, Qingdao, Rizhao) and one cultured population (Mingbo) were screened with 18 RAPD primers. Of 101 loci in the five populations, 43.33%, 47.52%, 45.83%, 44.57%, and 42.86%, respectively, were polymorphic. The number of polymorphic loci detected by a single primer combination ranged 1-4. Average heterozygosity was 0.0735, 0.0893, 0.0871, 0.0847, and 0.0685, respectively. Weihai had greater genetic diversity than the other populations (*p*<0.05) including number of RAPD bands, number of polymorphic bands, average heterozygosity, and number of genotypes. Mingbo had the least genetic viability. Intentional or accidental release of cultured half-smooth tongue sole into natural sea areas may disrupt local gene pools and result in loss of genetic variability. Genetic variability of cultured populations should be monitored to conserve natural half-smooth tongue sole resources.

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