

RINGKASAN

Pagrus major (Temminck & Schlegel, 1843) atau *red seabream* merupakan spesies ikan dari Family Sparidae yang umumnya ditemukan di perairan Jepang dan Korea. Penelitian ini bertujuan untuk mengetahui keragaman lokus, gen, polimorfisme dan juga struktur populasi *P. major* menggunakan metode *Random Amplified Polymorphic DNA* (RAPD). Dilatarbelakangi oleh pentingnya keragaman genetik sebagai dasar adaptasi dan ketahanan populasi, catatan awal *P. major* di perairan Indonesia menjadikan studi keragaman genetik ini penting untuk dilakukan.

Penelitian dilaksanakan antara bulan Agustus hingga Oktober 2025 di Laboratorium Genetika Fakultas Biologi Universitas Jenderal Soedirman. Bagian tubuh ikan yang digunakan adalah sirip yang kemudian diekstraksi DNA-nya menggunakan kit Zymo Research. Amplifikasi DNA dilakukan dengan PCR-RAPD menggunakan primer OPA 01, OPA 02, OPA 04, OPA 07, dan OPA 10. Produk PCR kemudian divisualisasi melalui elektroforesis gel agarosa dan dianalisis berdasarkan pola pita DNA. Parameter yang diamati mencakup keragaman lokus, keragaman gen, polimorfisme serta struktur populasi dengan bantuan *software* Arlequin.

Hasil analisis keragaman genetik menunjukkan bahwa tingkat polimorfisme mencapai 100%, menandakan adanya variasi genetik tinggi antar individu *P. major* di Laut Selatan Jawa. Keragaman gen sebesar 0,9964 dimana hampir semua individu memiliki kombinasi pita DNA berbeda, mencerminkan heterozigositas tinggi. Adapun keragaman lokus sebesar 0,396394 termasuk dalam kategori tinggi, menunjukkan bahwa sekitar 39,6% posisi nukleotida berbeda antar individu, sehingga populasi ini memiliki variasi genetik yang luas dan penting bagi keberlanjutan populasi. Analisis AMOVA memperlihatkan 26,70% variasi antar subpopulasi dan 73,30% variasi dalam populasi, dengan $F_{ST} = 0,26701$ ($P < 0,001$) yang mengindikasikan diferensiasi genetik sedang hingga tinggi berupa struktur populasi yang nyata serta terbatasnya aliran gen antar subpopulasi ($N_m = 0,686$). Perbedaan kondisi geografis dan oseanografi di pesisir selatan Jawa diduga berperan dalam membentuk pola struktur genetik tersebut.

Kata kunci : Keragaman genetik, *Pagrus major*, polimorfisme, struktur populasi

SUMMARY

Pagrus major (Temminck & Schlegel, 1843) or red seabream is a species of fish from the Family of Sparidae commonly found in Japanese and Korean waters. This study aims to determine the diversity of loci, genes, polymorphisms, and population structure of *P. major* using the Random Amplified Polymorphic DNA (RAPD) method. Given the importance of genetic diversity as the basis for adaptation and population resilience, the initial records of *P. major* in Indonesian waters make this genetic diversity study important to conduct.

The research was conducted between August and October 2025 at the Genetics Laboratory of the Faculty of Biology, Jenderal Soedirman University. The part of the fish used was the fin, from which DNA was extracted using a Zymo Research kit. DNA amplification was performed by PCR-RAPD using primers OPA 01, OPA 02, OPA 04, OPA 07, and OPA 10. The PCR products were then visualized through agarose gel electrophoresis and analyzed based on DNA band patterns. The parameters observed included locus diversity, gene diversity, polymorphism, and population structure with the help of Arlequin software.

The results of genetic diversity analysis show that the level of polymorphism reached 100%, indicating high genetic variation among *P. major* individuals in the Southern Java Sea. Gene diversity was 0.9964, with almost all individuals having different DNA band combinations, reflecting high heterozygosity. Locus diversity of 0.396394 is classified as high, indicating that approximately 39.6% of nucleotide positions differ between individuals, meaning that this population has broad genetic variation that is important for population sustainability. AMOVA analysis showed 26.70% variation between subpopulations and 73.30% variation within populations, with $F_{ST} = 0.26701$ ($P < 0.001$), indicating moderate to high genetic differentiation in the form of a distinct population structure and limited gene flow between subpopulations ($N_m = 0.686$). Differences in geographical and oceanographic conditions on the southern coast of Java are thought to play a role in shaping this genetic structure pattern.

Keywords: Genetic diversity, *Pagrus major*, polymorphism, population structure