Analisis Keragaman Genetik Dan Struktur Populasi Hirschmanniella oryzae Berdasarkan Data Sekuens Di
Indonesia Dan GenBank
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INTISARI

ANALISIS KERAGAMAN GENETIK DAN STRUKTUR POPULASI *Hirschmanniella oryzae* BERDASARKAN DATA SEKUENS DI INDONESIA DAN GENBANK

Hirschmanniella oryzae merupakan nematoda endoparasit migratori yang menjadi kendala utama budidaya padi (*Oryza sativa*), namun kontribusi data genetik Indonesia terhadap pemahaman keragaman spesies ini di tingkat regional masih sangat terbatas dibandingkan negara produsen padi lain seperti Vietnam dan Filipina. Berdasarkan kajian penanda molekuler D2-D3 ekspansi segmen 28S rRNA yang bersifat konservatid namun peka membedakan taksa pada level genus dan spesies, penelitian ini menganalisis keragaman genetik, merekonstruksi pohon filogenetik terintegrasi, serta menganalisis struktur populasi *H.oryzae* asal Indonesia, Asia Tenggara, dan Asia Timur. Data dihimpun melalui perakitan sekuens konsensus dari isolat lokal Gunung Kidul dan Kulon Progo serta *data mining* sekuens GenBank, kemudian dilakukan analisis *alignment*, perhitungan p-distance, rekonstruksi pohon Maximum Likelihood (MEGA 11), dan analisis indeks fiksasi (FST) dengan DnaSP v6. Hasil menunjukkan divergensi nukleotida antarpopulasi *ingroup* sangat rendah (0,6-2,1%) dan seluruh isolat mengelompok dalam satu klad monofiletik tanpa struktur tegas berdasarkan negara asal, namun nilai FsT konsisten tinggi dan signifikan antarwilayah geografis (0,29-0,75), mengindikasikan diferensiasi genetik kuat meski jarak genetik rendah. Penelitian ini menyimpulkan bahwa marka D2-D3 28S rRNA valid untuk identifikasi molekuler *H.oryzae* namun kurang efektif untuk struktur populasi, sehingga aliran gen antarwilayah geografis sangat terbatas.

Kata kunci**:** *Hirschmanniella oryzae*; keragaman genetik; filogenetik; struktur populasi; 28S rRNA; GenBank.

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ABSTRACT

ANALYSIS OF GENETIC DIVERSITY AND POPULATIONS STRUCTURE OF *HIRSCHMANNIELLA ORYZAE* BASED ON SEQUENCE DATA IN INDONESIA AND GENBANK

Hirschmanniella oryzae is a migratory endoparasitic nematode that is the main obstacle to rice cultivation (*Oryza sativa*), but the contribution of Indonesian genetic data to the understanding of the diversity of this species at the regional level is still very limited compared to other rice-producing countries such as Vietnam and the Philippines. Based on the study of the D2-D3 molecular marker of 28S rRNA segment expansion which is conservative but sensitive to differentiating taxa at the genus and species levels, this study analyzes genetic diversity, reconstructs an integrated phylogenetic tree, and analyzes the population structure of *H. oryzae* from Indonesia, Southeast Asia, and East Asia. Data were collected through consensus sequence assembly from local isolates of Gunungkidul and Kulon Progo as well as *GenBank sequence data mining*, then aligment analysis is carried out, , *p-distance calculation*, Maximum Likelihood *tree reconstruction* (MEGA 11), and fixation index analysis (FST) with DnaSP v6. The results showed that nucleotide divergence between *ingroup populations* was very low (0.6-2.1%) and that all isolates were grouped in a monophyletic clade without a firm structure based on country of origin, but FST values were consistently high and significant across geographic regions (0.29-0.75), indicating strong genetic differentiation despite low genetic distance. This study concluded that the D2-D3 28S rRNA markings are valid for the molecular identification *of H. oryzae* but are less resolvable for population structure, so gene flow between geographic regions is very limited.

Keywords**:** *Hirschmanniella oryzae*; genetic diversity; phylogenetics; population structure; 28S rRNA; GenBank.