Intisari

DETEKSI MOLEKULER *Ralstonia syzygii* subsp. *syzygii* PENYEBAB PENYAKIT SUMATRA PADA SERANGGA VEKTOR *Hindola striata*

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Cengkih telah banyak dimanfaatkan baik sebagai rempah hingga obat. Meskipun demikian, produksi cengkih nasional di Indonesia masih tergolong rendah. Penyakit Sumatera (*Sumatra Disease)* merupakan salah satu penyebab rendahnya produksi cengkih di Indonesia. Serangga *Hindola fulva* Baker di Sumatra dan *H. striata* Maa di Jawa diduga memiliki peran penting terhadap penyebaran penyakit Sumatra. Penelitian ini bertujuan untuk mendeteksi keberadaan bakteri *Ralstonia syzygii* subsp. *syzygii* melalui teknik *Polymerase Chain Reaction* (PCR) menggunakan primer spesifik UGMRss pada serangga vektor *H. striata* dan melakukan identifikasi molekuler menggunakan gen mitokondria sitokrom oksidase subunit 1 (COI) pada serangga vektor *H. striata.* Metode yang digunakan meliputi koleksi serangga, identifikasi morfologi *H. striata,* ekstraksi DNA *H. striata,* amplifikasi DNA menggunakan primer UGMRss, amplifikasi gen COI, sekuensing, dan analisis filogenetik gen COI. Hasil penelitian menunjukan amplifikasi DNA *H. striata* menggunakan primer spesifik UGMRss mampu menghasilkan pita yang setara dengan kontrol positif berupa sampel ranting tanaman cengkih yang terinfeksi penyakit Sumatra, sehingga diduga bakteri *R. syzygii* subsp. *syzygii* berada dalam tubuh *H. striata*. Hasil amplifikasi dan sekuense gen COI pada sampel *H. striata* menunjukan pita sepanjang 709 bp, dengan komposisi nukleotida yang terdiri atas A 33.57%, C 16.08%, G 14.81%, T 35.54%, A+T 69.11% dan G+C 30.89%. Penelusuran sekuens dengan Blast-N menunjukan nilai *query coverage* gen COI *H. striata* dan *H. geisha* sebesar 63%, sementara presentase identitas sebesar 84.73%.

Kata kunci : deteksi molekuler, *Hindola striata*, penyakit Sumatra, *Ralstonia syzygii* subsp. *syzygii*.

Abstract

MOLECULAR DETECTION OF *Ralstonia syzygii* subsp. *syzygii* IN INSECT VECTOR *Hindola striata*

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Cloves have been widely used both as a spice to medicine. However, Indonesia national clove production is still relatively low. Sumatra disease is one of the causes of the low production of cloves in Indonesia. *Hindola fulva* Baker in Sumatra and *H. striata* Maa in Java are known to have an important role as insecet vectors of Sumatran disease. This study aims to detect the presence of the bacterium *Ralstonia syzygii* subsp. *syzygi* through Polymerase Chain Reaction (PCR) technique using specific primers UGMRss on insect vector *H. striata* and carrying out the molecular identification of *H. striata* using mitochondrial cytochrome oxidase subunit 1 (COI) gene. The methods used include insect collection, morphology identification of *H. striata*, DNA extraction of *H. striata*, DNA amplification using UGMRss primers, COI gene amplification, sequencing, and phylogenetic analysis of COI genes. The results showed that DNA amplification of *H. striata* using UGMRss was able to produce bands equivalent to positive control, so it was suspected that there was *R. syzygii* subsp. *syzygii* in the body of *H. striata*. The results of amplification and COI gene sequences in the sample showed a band of 709 bp long, with a nucleotide composition consisting of A 33.57%, C 16.08%, G 14.81%, T 35.54%, A+T 69.11 %, and G+C 30.89%. Sequence tracing with Blast-N showed the query coverage of the COI genes of *H. striata* and *H. geisha* was 63%, while the percentage of identity was 84.73%.

Key words : molecular detection, *Hindola striata*, Sumatra disease, *Ralstonia syzygii* subsp. *syzygii*.