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Identification and Pathogen Diversity of New Emerging Leaf Fall Disease on Rubber (Hevea brasiliensis (Willd. ex A.Juss.) MÃ¼ll.Arg.) in Indonesia
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Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

ABSTRACT

A new emerging leaf fall disease with distinctive circular spots is causing severe defoliation of rubber trees in Indonesia, but its etiology and pathogen diversity remain poorly understood. This study aimed to (i) confirm the causal agents, (ii) evaluate virulence and genetic diversity of the main pathogen groups, and (iii) compare the phyllosphere mycobiome across locations, seasons, and symptom levels. A total of 89 isolates of putative Sporocadaceae and *Colletotrichum* were obtained from symptomatic leaves in nine provinces and assessed using pathogenicity tests on detached leaflets, rep-PCR genotyping, multigene phylogeny, morphometrics, and ITS amplicon metabarcoding. Most isolates reproduced the characteristic circular spots, chlorosis, and necrosis, confirming their pathogenic role. Rep-PCR revealed high genotypic diversity and weak geographic or clone-based structuring within both *Colletotrichum gloeosporioides* sensu lato and Sporocadaceae populations, suggesting extensive gene flow and multiple cryptic lineages. Concatenated ITS and β-tubulin analyses of 20 representative isolates resolved at least five genera and eight species, including several *Neopestalotiopsis* species, *Pseudopestalotiopsis elaeidis*, *Pestalotiopsis diploclisiae*, *Colletotrichum siamense*, and *Lasiodiplodia theobromae*, demonstrating a multi-genus disease complex rather than a single pathogen. ITS metabarcoding of pooled leaf samples showed that Ascomycota, followed by Basidiomycota, dominated the phyllosphere, with *Phyllosticta* and *Colletotrichum* as abundant core taxa whose dominance differed among season–location combinations. Richness and phylogenetic diversity were consistently higher in South Sumatra than in Central Java and peaked in severely symptomatic leaves only in the rainy season, so the hypothesis that diversity rises with symptom severity was only partially supported. Beta diversity was driven mainly by location and season rather than symptom level, revealing a stable core mycobiome with context-dependent pathogen assemblages. These findings show that the new rubber leaf fall epidemic in Indonesia is driven by a diverse, seasonally modulated multi-pathogen complex, with important implications for diagnostics, resistance screening, and integrated disease management.

Colletotrichum; Fungal diversity; ITS amplicon metabarcoding; Multi-pathogen complex; Sporocadaceae

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INTISARI

Penyakit gugur daun baru dengan gejala bercak melingkar yang khas menyebabkan defoliasi berat pada tanaman karet di Indonesia, tetapi etiologi dan keragaman patogennya belum banyak dipahami. Penelitian ini bertujuan (i) mengonfirmasi patogennya, (ii) mengevaluasi virulensi dan keragaman genetik kelompok patogennya, dan (iii) membandingkan mikobioma filosfer antarlokasi, musim, dan tingkat gejala. Sebanyak 89 isolat yang diduga termasuk Sporocadaceae dan *Colletotrichum* diperoleh dari daun bergejala di sembilan provinsi. Isolat tersebut kemudian dianalisis melalui uji patogenisitas pada anak daun terpisah, genotiping rep-PCR, filogeni multigen, morfometri, dan metabarkoding amplikon ITS. Sebagian besar isolat mampu menghasilkan kembali gejala khas berupa bercak melingkar, klorosis, dan nekrosis, sehingga peran patogeniknya terkonfirmasi. Rep-PCR menunjukkan keragaman genotipe tinggi serta struktur geografis maupun klonal yang lemah, baik pada populasi *Colletotrichum gloeosporioides* sensu lato maupun Sporocadaceae. Hal ini mengindikasikan aliran gen luas dan keberadaan beberapa garis keturunan kriptik. Analisis gabungan ITS dan β-tubulin terhadap 20 isolat representatif mengidentifikasi sedikitnya lima genus dan delapan spesies. Spesies tersebut mencakup beberapa spesies *Neopestalotiopsis*, *Pseudopestalotiopsis elaeidis*, *Pestalotiopsis diploclisiae*, *Colletotrichum siamense*, dan *Lasiodiplodia theobromae*. Artinya, penyakit ini merupakan kompleks multigenus, bukan disebabkan oleh patogen tunggal. Metabarkoding ITS pada sampel daun gabungan menunjukkan bahwa filosfer didominasi Ascomycota, diikuti Basidiomycota. *Phyllosticta* dan *Colletotrichum* merupakan taksa inti melimpah yang dominansinya berbeda antarkombinasi musim–lokasi. Kekayaan dan keragaman filogenetik secara konsisten lebih tinggi di Sumatera Selatan dibandingkan Jawa Tengah. Puncaknya pada daun bergejala berat hanya terjadi pada musim hujan, sehingga hipotesis bahwa keragaman meningkat seiring keparahan gejala hanya terdukung sebagian. Keragaman beta terutama dipengaruhi lokasi dan musim, bukan tingkat gejala. Hal ini menunjukkan adanya mikobioma inti yang selalu hadir, sedangkan komposisi patogennya berubah mengikuti lokasi dan musim. Temuan ini menunjukkan bahwa epidemi penyakit gugur daun karet baru di Indonesia disebabkan oleh kompleks multipatogen yang beragam dan dipengaruhi musim. Temuan ini berimplikasi penting bagi diagnostik, penapisan ketahanan, dan pengelolaan penyakit terpadu.

Colletotrichum; keragaman fungi; kompleks multipatogen; metabarkoding amplikon ITS; Sporocadaceae