Studi filogenetik dan analisis host specificity cercospora spp berdasarkan data sequence daerah its rdna gen elongation factor 1 dan gen calmodulin = Phylogenetic study and host specificity analysis of cercospora spp based on its region of rdna elongation factor 1 gene and calmodulin gene sequences / Floreta Fiska Yuliarni

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Abstrak

ABSTRAK
Penelitian bertujuan menganalisis hubungan kekerabatan spesies-spesies Cercospora berdasarkan data sequence daerah Internal Transcribed Spacers (ITS) rDNA, gen elongation factor 1- (EF), dan gen calmodulin (CAL); mengetahui lokus yang paling baik dalam memisahkan spesies-spesies Cercospora; dan menguji host specificity Cercospora spp. dengan tanaman inangnya. Pada penelitian ini telah dilakukan amplifikasi dan sequencing daerah ITS rDNA, gen EF, dan gen CAL pada 14 spesies dari 23 strain Cercospora yang berasal dari tiga famili tanaman inang (Asteraceae, Cucurbitaceae, dan Solanaceae). Pohon filogenetik dibangun menggunakan metode Neighbor-Joining, Maximum Parsimony, dan Bayesian. Hasil penelitian menunjukkan bahwa pohon filogenetik berdasarkan data sequence daerah ITS rDNA tidak dapat menjelaskan hubungan kekerabatan antarspesies pada genus Cercospora; sebagian besar Cercospora (57 dari 61 OTU) berada dalam satu kelompok besar yang jarak cabangnya berimpit satu dengan lainnya. Pohon filogenetik berdasarkan data sequence gen EF dapat menjelaskan hubungan kekerabatan beberapa spesies Cercospora, walaupun sebagian spesies Cercospora (24 OTU) berada dalam satu kelompok yang jarak cabangnya berimpit satu dengan lainnya. Pohon filogenetik berdasarkan data sequence gen CAL dapat menjelaskan hubungan kekerabatan sebagian besar spesies Cercospora, jarak cabang terlihat lebih panjang dibandingkan pada pohon filogenetik berdasarkan data sequence gen EF, walaupun beberapa spesies Cercospora (16 OTU) belum dapat dipisahkan. Hasil analisis filogenetik menunjukkan bahwa spesies-spesies Cercospora tidak dapat dipisahkan berdasarkan data sequence daerah ITS rDNA, akan tetapi sebagian spesies dapat dipisahkan berdasarkan data sequence gen EF dan gen CAL. Pohon filogenetik berdasarkan data sequence gen CAL menunjukkan bahwa gen tersebut dapat digunakan untuk memisahkan spesies-spesies Cercospora lebih baik daripada daerah ITS rDNA dan gen EF. Hasil analisis filogenetik berdasarkan data sequence multilokus menunjukkan bahwa 11 dari 14 spesies Cercospora yang digunakan dalam penelitian tidak host-specific, hanya tiga spesies yaitu C. zinniicola, C. cocciniae, dan C. mikaniicola yang spesifik terhadap inangnya.
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ABSTRACT

The aims of this study were to analyze the phylogenetic relationships of Cercospora spp. based on sequence data of the internal transcribed spacer (ITS) region of rDNA, elongation factor 1- (EF), and calmodulin (CAL) genes; to determine the best locus in separating Cercospora species; and to investigate the host specificity of Cercospora spp. In this study, the sequences of the ITS region of rDNA, EF, and CAL genes of 23 strains which belong to 14 species of Cercospora from three host plants families were amplified and sequenced. The phylogenetic trees of the Cercospora spp. were constructed by Neighbor-Joining, Maximum Parsimony, and Bayesian methods. Our result showed that phylogenetic relationship of Cercospora at the species level could not be resolved by ITS rDNA; most of Cercospora species (57 OTU) were grouped in one major clade with no branch length differences among species. The EF phylogenetic tree, showed that some species of Cercospora could be separated, although 24 OTU were grouped into one clade with no branch length differences. The CAL phylogenetic tree showed that the majority of Cercospora species could be separated with longer branch compared to the EF phylogenetic tree, although several species (16 OTU) could not be separated. The phylogenetic analyses showed that most of Cercospora species could not be separated in the ITS rDNA tree, however those species could be separated in the EF and CAL phylogenetic trees. The results showed that CAL gene was the best locus in separating Cercospora species compared to ITS rDNA and EF gene. Molecular phylogenetic analysis from multiloci (ITS regions of rDNA, EF gene, and CAL gene) revealed that 11 out of 14 species of Cercospora have no host specificity (have a wide host range) and only three species e.g., C. zinniicola, C. cocciniae, and C. mikaniicola showed host specificity.