

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

Floreta Fiska Yuliarni, author

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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. zinnicola*, *C. cocciniae*, dan *C. mikaniicola* yang spesifik terhadap inangnya.

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## <b>ABSTRACT</b><br>

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. zinnicola*, *C. cocciniae*, and *C. mikaniicola* showed host specificity.