Studi Taksonomi Candida spp. dari Apis cerana Fabricius dan dari Bunga-bunga yang Dikunjunginya di Ciburial, Jawa Barat = Taxonomical Study of Candida spp. from Apis cerana Fabricius and Their Visiting Flowers in Ciburial, West Java

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Abstrak

Pada penelitian sebelumnya, diperoleh 18 strain Candida spp. dari Apis cerana dan bunga-bunga yang dikunjunginya di Ciburial, Jawa Barat. Hasil identifikasi berdasarkan data sequence daerah ITS rDNA menggunakan primer reverse ITS4, menunjukkan bahwa 18 strain tersebut memiliki homologi rendah (85--98%) terhadap spesies terdekatnya Candida spp. Dengan demikian belum diperoleh identitas yang akurat dari 18 strain Candida spp. tersebut.

Penelitian bertujuan untuk memperoleh identitas yang akurat dari 18 strain tersebut melalui identifikasi molekuler, analisis filogenetik, dan pengamatan karakter fenotipik (morfologi, fisiologi, dan biokimia). Identifikasi dilakukan melalui sequencing pada daerah ITS rDNA dan D1/D2 LSU rDNA. Analisis filogenetik dilakukan berdasarkan data sequence daerah ITS rDNA dan D1/D2 LSU rDNA, menggunakan metode neighbor-joining.

Berdasarkan hasil identifikasi molekuler, analisis filogenetik, dan pengamatan karakter fenotipik, 10 strain diidentifikasi ke dalam 5 spesies, yaitu C. parapsilosis (Candida sp. CR033, CR034, dan CR038), C. orthopsilosis (Candida sp. CR015 dan CR151), C. metapsilosis (Candida sp. CR047 dan CR053), Debaryomyces hansenii (Candida sp. CR065), dan Wickerhamomyces anomalus (Candida sp. CR070 dan CR105). Sebanyak 8 strain (Candida sp. CR004, CR007, CR013, CR014, CR018, CR023, CR027, dan CR035) belum dapat ditentukan nama penunjuk (epithet) spesiesnya. Berdasarkan sequence ITS rDNA 8 strain tersebut memiliki homologi yang rendah (97%) terhadap kerabat terdekatnya C. hawaiiana.

Pohon filogenetik berdasarkan sequence ITS rDNA menunjukkan 8 strain tersebut berada pada clade yang terpisah dengan C. hawaiiana dengan dukungan nilai bootstrap yang sangat tinggi, 99%. Delapan strain Candida tersebut termasuk dalam satu spesies yang memiliki perbedaan sequence 1% antara satu strain Candida dengan strain Candida lainnya atau disebut conspecific. Karakter fisiologi dan biokimia menunjukkan 8 strain tersebut memiliki perbedaan dengan C. hawaiiana CBS 9146T pada kemampuannya mengasimilasi sumber karbon - methyl -D-glucoside, dan ketidakmampuannya mengasimilasi ribosa. Hasil identifikasi penelitian menunjukkan bahwa 8 strain Candida tersebut merupakan spesies yang berbeda dengan C. hawaiiana.

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In the previous study, 18 strains of Candida spp. were obtained from Apis cerana and their visiting flowers in Ciburial, West Java. Based on sequence data of ITS rDNA using ITS4 reverse primer, these strains showed low homology (85--98%) to their closest relatives Candida spp. Therefore, the identity of these 18 strains were not established yet.

The purpose of this study was to establish the identities of the 18 strains of Candida spp. by conducting molecular identification, phylogenetic analysis, and phenotypic characterization (morphological, physiological, and biochemical characters). Identification and phylogenetic analysis was carried out by

sequencing the ITS rDNA and D1/D2 of LSU rDNA. Phylogenetic tree was constructed using neighbor-joining method.

Based on molecular identification, phylogenetic analysis, and phenotypic characterization, 10 strains were identified into 5 species. Those 10 strains were identified as C. parapsilosis (Candida sp. CR033, CR034, and CR038), C. orthopsilosis (Candida sp. CR015 and CR151), C. metapsilosis (Candida sp. CR047 and CR053), Debaryomyces hansenii (Candida sp. CR065), and Wickerhamomyces anomalus (Candida sp. CR070 and CR105). The identities of eight strains (Candida sp. CR004, CR007, CR013, CR014, CR018, CR023, CR027, and CR035) were not established yet. Based on sequence data of ITS rDNA they have low degree of homology (97%) to their closest related species, C. hawaiiana.

Phylogenetic tree based on sequence data of ITS rDNA showed they were separated from C. hawaiiana by 99% bootstrap value. Multiple alignment of their sequences of ITS and D1/D2 showed that they have 1% differences, which indicate that these strains are conspecific (same species). Their morphological, physiological and biochemical characteristics showed that these strains differed from C. hawaiiana CBS 9146T by their ability to assimilate -methyl-D-glucoside and their inability to assimilate ribose as carbon sources. Our data suggest that these strains were distinct species from C. hawaiiana.