Identifikasi khamir dari saluran pencernaan lebah pekerja pengumpul nektar apis mellifera l berdasarkan data sequence daerah its rDNA = Identification of yeasts from the digestive tracts of nectar collecting bees of apis mellifera l based on its region of rDNA sequence data

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Abstrak

Penelitian bertujuan mengetahui identitas khamir dari saluran pencernaan lebah pekerja pengumpul nektar (nectar collecting bee, NCB) Apis mellifera yang mengunjungi bunga kapuk (Ceiba pentandra) di Jepara. Sebanyak 12 isolat khamir diidentifikasi berdasarkan data sequence daerah Internal Transcribed Spacers (ITS) rDNA. Primer forward ITS1 dan primer reverse ITS4 digunakan untuk amplifikasi daerah ITS rDNA. Hasil elektroforesis produk PCR menunjukkan ukuran daerah ITS rDNA isolat khamir-khamir tersebut bervariasi antara 400 pb hingga 800 pb. Berdasarkan hasil pencarian homologi sequence daerah ITS rDNA m2elalui program Basic Local Alignment Search Tool (BLAST), analisis filogenetik dengan metode Neighbor Joining, dan pengamatan karakter morfologi, 12 isolat khamir tersebut diidentifikasi ke dalam empat genus dan lima spesies. Berdasarkan taksonomi, 11 isolat khamir termasuk ke dalam anggota order Sacharomycetales, class Hemiascomycetes dari phylum Ascomycota dan satu isolat termasuk ke dalam anggota order Ustilaginales, class Ustilaginomycetes dari phylum Basidiomycota. Isolat-isolat tersebut diidentifikasi sebagai Candida parapsilosis (JZ102, JZ105, JZ116, dan JZ121), Candida rugosa (JZ117, JZ121), Debaryomyces hansenii (JZ100, JZ113, JZ118), Meyerozyma caribbica (JZ124, JZ125), dan Pseudozyma sp. (JZ104).

.....The aim of this study was to identify the yeast isolates from the digestive tracts of nectar collecting bees (NCB) of Apis mellifera. A total of 12 yeast isolates from the digestive tracts of NCB foraging on flowers of Ceiba pentandra in Jepara, Central Java, were identified based on sequence data of Internal Transcribed Spacers Regions of ribosomal DNA (ITS rDNA). The primer set of ITS1 (forward primer) and ITS4 (reverse primer) were used to amplify the ITS rDNA of the isolates. Gel electrophoresis results showed that the size of ITS region rDNA of the isolates were varied on the range of 400 bp -- 800 bp. Based on sequence homology search results by Basic Local Alignment Search Tool (BLAST) program, phylogenetic analysis by Neighbor Joining method, and morphological characterization, those 12 isolates were identified into four genera and five species. Taxonomically, 11 isolates belong to order Sacharomycetales, class Hemiascomycetes from the phylum Ascomycota and 1 isolate belongs to order Ustilaginales, class Ustilaginomycetes from the phylum Basidiomycota. Those isolates were identified as Candida parapsilosis (JZ102, JZ105, JZ116, and JZ121), Candida rugosa (JZ117, JZ121), Debaryomyces hansenii (JZ100, JZ113, JZ118), Meyerozyma caribbica (JZ124, JZ125), and Pseudozyma sp. (JZ104).