Identifikasi Khamir dari Saluran Pencernaan Lebah Pekerja Pengumpul Polen Apis mellifera L. Berdasarkan Data Sequence Daerah ITS rDNA = Identification of Yeasts Isolated from Digestive Tract of Pollen Collecting Bees Apis mellifera L. Based on ITS Region rDNA Sequence Data

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Abstrak

Penelitian bertujuan mengetahui identitas khamir dari saluran pencernaan lebah pekerja pengumpul polen (pollen collecting bees, PCB) Apis mellifera. Sebanyak 12 isolat khamir dari saluran pencernaan PCB yang mengunjungi bunga kapuk Ceiba pentandra di Jepara, Jawa Tengah, diidentifikasi berdasarkan data sequence daerah internal transcribed spacer (ITS) rDNA. Amplifikasi daerah ITS rDNA menggunakan primer forward ITS1 dan primer reverse ITS4. Elektroforesis produk PCR menunjukkan bahwa daerah ITS rDNA khamir-khamir tersebut berukuran antara 400--900 pb. Berdasarkan hasil pencarian homologi sequence menggunakan program basic local alignment search tool (BLAST), analisis filogenetik menggunakan metode Neighbor Joining (NJ), dan karakterisasi morfologi, 12 isolat khamir tersebut terdiri dari tujuh spesies yang termasuk dalam lima genus. Secara taksonomi, seluruh khamir tersebut termasuk phylum Ascomycota, class Hemiascomycetes, dan order Saccharomycetales. Isolat-isolat tersebut diidentifikasi sebagai Candida magnoliae (isolat JZ002), Candida orthopsilosis (isolat JZ003, JZ008, JZ011, dan JZ034), Candida rugosa (isolat JZ010); Debaryomyces hansenii (isolat JZ001); Meyerozyma caribbica (isolat JZ013 dan JZ014), Pichia guilliermondii (isolat JZ015), dan Zygosaccharomyces siamensis (isolat JZ005 dan JZ006).

.....The aim of this study was to obtain the identity of yeasts from digestive tracts of pollen collecting bees (PCB) Apis mellifera. A total of 12 yeast isolates obtained from digestive tract of PCB foraging on flowers Ceiba pentandra in Jepara, Central Java, were identified based on sequence data of internal transcribed spacer of ribosomal DNA (ITS rDNA). The primer set of ITS1 (forward primer) and ITS4 (reverse primer) were used to amplify the ITS region rDNA. Gel electrophoresis result showed that the size of ITS rDNA of those yeast were varied between 400--900 base pairs. Based on sequence homology search using basic local alignment search tool (BLAST) program, phylogenetic analysis by Neighbor Joining method, and morphological characterization, those 12 isolates belong to five genera and seven species. Taxonomically, all of those isolates belong to order Saccharomycetales, class Hemiascomycetes from the phylum Ascomycota. Those 12 isolates were identified as species Candida magnoliae (isolate JZ002); Candida orthopsilosis (isolates JZ003, JZ008, JZ011, and JZ034); Candida rugosa (isolate JZ010); Debaryomyces hansenii (isolate JZ001); Meyerozyma caribbica (isolates JZ013 and JZ014); Pichia guilliermondii (isolate JZ015); and Zygosaccharomyces siamensis (isolates JZ005 and JZ006).