Identifikasi kapang dari manuskrip Cina lama yang mengalami deteriorasi asal plot 1 Perpustakaan Pusat UI berdasarkan daerah ITS rDNA = Moulds identification from deteriorated old Chinese manuscripts from plot 1 Central Library UI based on ITS rDNA region

Madinna Rahmadewi, author

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Abstrak

Penelitian ini bertujuan untuk mengidentifikasi kapang dari dua manuskrip Cina lama yang mengalami deteriorasi asal plot 1 Ruang Naskah PP-UI Depok berdasarkan data sekuens daerah internal transcribed spacers ribosomal DNA ITS rDNA . Pengambilan sampel kapang dari manuskrip dengan metode swab dan isolasi kapang dengan metode culture-dependent. Amplifikasi daerah ITS rDNA dan DNA sequencing menggunakan primer forward ITS5 dan primer reverse ITS4.

Pencarian homologi sekuens daerah ITS rDNA menggunakan program basic local alignment search tool BLAST. Pembuatan pohon filogenetik menggunakan metode Neighbor Joining, model dua parameter Kimura dan bootstrap sebanyak 1.000 kali replikasi. Lima isolat kapang terpilih diperoleh berdasarkan tipe morfologi yang berbeda dengan kapang dari manuskrip Cina lama asal plot 2, 4, 5, dan 6.

Hasil elektroforesis gel produk PCR daerah ITS rDNA menunjukkan lima strain memiliki ukuran fragmen ITS rDNA dengan kisaran 500--700 pb dan DNA sequencing menunjukkan panjang daerah ITS rDNA berkisar 579--610 pb. Lima strain UICC merupakan anggota dari dua kelas Class Eurotiomycetes dan Dothideomycetes , dua ordo Order Eurotiales dan Capnodiales serta tiga famili Family Aspergillaceae, Cladosporiaceae dan Trichocomaceae.

Strain UICC 1099 dan UICC 1102 memiliki homologi 99,4 dan 99,8 dengan type strain Aspergillus pseudodeflectus NRRL 6135T. Strain UICC 1103 memiliki homologi 99,7 dengan type strain Cladosporium colocasiae ATCC 200944 T. Strain UICC 1101 memiliki homologi 99,8 dengan type strain Penicillium coffeae NRRL 35363T. Strain UICC 1100 memiliki homologi 99,4 dengan type strain Penicillium mallochii DAOM 239917T. Lima strain UICC merupakan fungi anamorf dan bersifat xerofilik.

......The objective of this study was to identify moulds isolated from two deteriorated old Chinese manuscripts from plot 1 Ruang Naskah Central Library Universitas Indonesia Depok based on sequence data of internal transcribed spacer regions of ribosomal DNA ITS rDNA . Sterile cotton swab was used to obtain samples and culture dependent method was used to isolate moulds. Forward primer ITS5 and reverse primer ITS4 were used to amplify ITS rDNA region and sequencing the DNA.

Basic Local Alignment Search Tool BLAST program was used to determine the sequence homology of ITS rDNA region. A phylogenetic tree was constructed by Neighbor Joining method with Kimura rsquo s two parameter model and bootstrap with 1,000 replicates. Five selected mould isolates were obtained based on the morphological type differences compared to moulds from old Chinese manuscripts from plot 2, 4, 5, and 6.

Gel electrophoresis showed that the fragment lengths of ITS rDNA region from five strains were on the range of 500 700 bp and DNA sequencing showed that the length variations of ITS DNA fragments were 579 to 610 bp. The five UICC strains belonged to two classes Class Eurotiomycetes and Dothideomycetes , two orders Order Eurotiales and Capnodiales and three families Family Aspergillaceae, Cladosporiaceae and

Trichocomaceae.
UICC 1099 and UICC 1102 strains showed 99.4 and 99.8 homologies with their type strain Aspergillus pseudodeflectus NRRL 6135T. UICC 1103 strain has 99.7 homology with its type strain Cladosporium clocasiae ATCC 200944T. UICC 1101 strain has 99.8 homology with its type strain Penicillium coffeae NRRL 35363T. UICC 1100 strain has 99.4 homology with its type strain Penicillium mallochii DAOM 239917T. The five UICC strains are anamorphic and xerophilic fungi.