Identifikasi kapang dari manuskrip cina lama yang mengalami deteriorasi asal plot 5 Perpustakaan Pusat UI berdasarkan daerah ITS RDNA = moulds identification from deteriorated old chinese manuscripts from plot 5 central library ui based on ITS region of RDNA

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Abstrak

 ABSTRAK
 Penelitian ini bertujuan untuk memperoleh identitas spesies kapang dari dua manuskrip Cina lama yang mengalami deteriorasi asal plot 5 Ruang Naskah Perpustakaan Pusat Universitas Indonesia PP-UI , Depok berdasarkan data sekuens daerah internal transcribed spacers ribosomal DNA ITS rDNA . Pengambilan sampel pada manuskrip menggunakan metode swab dengan cotton bud steril. Isolasi kapang menggunakan metode culture-dependent. Polymerase chain reaction PCR 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 dan pembuatan pohon filogenetik menggunakan metode Neighbor Joining, model dua parameter Kimura, serta bootstrap sebanyak 1.000 kali replikasi. Penentuan spesies terdekat dan posisi taksonomi menggunakan analisis filogenetik dan didukung oleh data morfologi. Isolasi kapang menghasilkan enam isolat kapang terpilih berdasarkan tipe morfologi yang berbeda dengan kapang dari manuskrip Cina lama asal plot 1, 2, 4, dan 6 Ruang Naskah PP-UI, Depok. Berdasarkan elektroforesis gel, panjang fragmen daerah ITS rDNA dari enam isolat kapang bervariasi antara 600--700 pb. Hasil DNA sequencing lengkap menunjukkan panjang daerah ITS rDNA enam isolat berkisar 582--625 pb. Enam strain UICC merupakan anggota dari tiga kelas Dothideomycetes, Eurotiomycetes dan Sordariomycetes , tiga ordo Capnodiales, Eurotiales dan Hypocreales , dan empat famili Cladosporiaceae, Nectriaceae, Ophiocordycipitaceae, dan Pleosporaceae . Strain UICC 1107 memiliki homologi 99,32 dengan type strain Purpureocillium lilacinum sin. Paecilomyces lilacinus ATCC 10114T. Lima strain UICC tidak dapat ditentukan spesiesnya. Strain UICC 1106 adalah Cladosporium sp. dengan homologi 100 terhadap type strain Cladosporium oxysporum CBS 125991T dan Cla. tenuissimum CPC 14235T. Strain UICC 1105 adalah Curvularia sp.1 dengan homologi 93,80 dan strain UICC 1108 adalah Curvularia sp.2 dengan homologi 94,70 terhadap type strain Curvularia carica-papayae CBS 135941T. Strain UICC 1109 adalah Rectifusarium sp. dengan homologi 85,87 terhadap type strain Rectifusarium robinianum CBS 430.91T. Strain UICC 1104 adalah Sarocladium sp. dengan homologi 97,13 terhadap type strain Sarocladium bifurcatum UTHSC 05-3311T. Enam strain UICC merupakan fungi anamorf dan bersifat xerofilik.<hr> ABSTRACT<b> The aim of this study was to determine the species identity of moulds from two deteriorated old Chinese manuscripts from plot 5 Ruang Naskah Central Library Universitas Indonesia, Depok based on internal transcribed spacers region of ribosomal DNA ITS rDNA . Samples from the manuscripts were collected by using swab method with sterile cotton swabs. Mould isolates were obtained by culture dependent method. Polymerase chain reaction PCR and DNA sequencing were performed using forward primer ITS5 and reverse primer ITS4. Homology search of ITS rDNA sequences was carried out using basic local alignment search tool BLAST program and phylogenetic tree construction was performed using Neighbor Joining method, Kimura rsquo s two parameter model, and bootstrap 1,000 replicates. The closest species and taxonomic position were obtained by phylogenetic analysis and supported by

morphological data. Six mould isolates were selected based on morphological type differences compared to mould isolates from old Chinese manuscripts from plot 1, 2, 4, and 6 Ruang Naskah Central Library UI, Depok. Based on gel electrophoresis, the lengths of ITS rDNA fragments of six mould isolates varied between 600 700 bp. Full sequence data of ITS rDNA of six isolates showed that the lengths of their ITS rDNA varied between 582 625 bp. Six UICC strains belonged to three classes Dothideomycetes, Eurotiomycetes and Sordariomycetes , three orders Capnodiales, Eurotiales and Hypocreales , and four families Cladosporiaceae, Nectriaceae, Ophiocordycipitaceae, and Pleosporaceae . UICC 1107 strain showed 99.32 homology to the type strain, Purpureocillium lilacinum syn. Paecilomyces lilacinus ATCC 10114T. Five UICC strains were not able to be determined to the species level. UICC 1106 strain was identified as Cladosporium sp., with 100 homology to the type strains, Cladosporium oxysporum CBS 125991T and Cla. tenuissimum CPC 14235T. UICC 1105 strain was identified as Curvularia sp.1, with 93.80 homology and UICC 1108 strain was identified as Curvularia sp.2, with 94.70 homology to the type strain, Curvularia carica papayae CBS 135941T. Strain UICC 1109 was identified as Rectifusarium sp., with 85.87 homology to the type strain, Rectifusarium robinianum CBS 430.91T. Strain UICC 1104 was identified as Sarocladium sp., with 97.13 homology to the type strain, Sarocladium bifurcatum UTHSC 05 3311T. Six UICC strains were anamorphic and xerophilic fungi.