

Microfungal community in sandy beaches located in Kedah, Pahang and Sabah, Malaysia

ABSTRACT

Microfungi are fundamental organisms help in balancing the ecosystem. The aims of this study are to identify microfungi isolated from sandy beaches based on internal transcribed spacers (ITS) sequence analysis and to determine the phylogenetic relationship among the locations of sampling areas. Fifty-seven isolates of microfungi were obtained from six beaches located in Kedah (Chenang Beach), Pahang (Balok Beach) and Sabah (Mamutik Island, Manukan Island, Sapi Island and Tanjung Aru Beach) to be used in this study. From the finding, the highest identified species were *Aspergillus* species (27 isolates) followed by *Trichoderma* species (12 isolates), *Penicillium* species (10 isolates), *Fusarium* species (6 isolates), *Bipolaris* species (1 isolate) and *Chaetomium* species (1 isolate). ITS fragment of all isolates was amplified in within the size range of 533–658 bp. A phylogenetic tree was constructed using maximum likelihood (ML) method; the isolates were grouped into three clades according to their classes. In conclusion, diverse microfungi isolated from sandy beach soil depicting 19 species were discovered. Future studies are highly recommended to focus on intra-and interspecies diversity based on microsatellite markers analysis, consequently the originality and distribution of the fungal isolates. The outcome of this study includes a baseline data on the occurrence and species-diversity as well as important information on the status of microfungi in Malaysia beaches located in Kedah, Melaka and Sabah. It can be used as a checklist for future studies related to fungi distribution in the tropical beaches.

Keyword: Ecology; Environmental mycology; Fungi; Identification; Microbial phylogenetics