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Morphotype characterization and PacBio amplicon sequencing of ribosomal DNA of fungi associated with shallow corals in the Western Gulf of Thailand

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Corals are conduits to numerous microorganisms, including zooxanthellae, protist, prokaryotes (bacteria and archaea) and viruses.

Purpose: The goal of this study is to investigate the species diversity and community structure of fungi associated with shallow corals in the western Gulf of Thailand (focusing on a robust coral and susceptible coral species to bleaching), using metagenomics approaches from PacBio SMRT sequencing system together with bioinformatic analysis.

Methods: The samples of three shallow coral *Porites lutea*, *Pavona decussata* and *Pocillopora damicornis* in the Western Gulf, southern Thailand (Chumphon, Prachuap Khiri Khan and Surat Thani provinces) were collected by scuba diving. The fungal communities as inferred by PacBio ribosomal amplicon sequencing for unculturable fungi, and the principle components analysis (PCA) for the occurrence of culturable fungi were explored.

Results and conclusions: Eighty-seven fungal strains isolated were found to belong to 18 orders in the Phyla Ascomycota and Basidiomycota. The Capnodiales was predominant fungi analysed by ribosomal DNA sequence and PacBio analyses. Principal component analysis showed an effect of the provinces on the fungal communities along the first and second components, but no significant effect of coral species. The community composition of fungi associated with shallow corals in Surat Thani province was different from the other provinces. The community composition of Prachuap Khiri Khan was slightly different to that of Chumphon which overlapped with the other provinces. The result from this study inferred that the diversity of fungi associated with shallow corals in the Western Gulf of Thailand is abundant.