

Sasitorn Jindamorakot 2006: The Species Diversity of Yeasts in Some Natural Habitats of Thailand. Doctor of Philosophy (Microbiology), Major Field: Microbiology, Department of Microbiology. Thesis Advisor: Associate Professor Savitree Limtong, Dr.Eng. 229 pages. ISBN 974-16-1939-1

Two hundred and eighty-three strains of yeast were isolated from insect frass (144 strains), flowers (24 strains), leaves (54 strains), mosses (27 strains), mushrooms (28 strains), and some other habitats (6 strains), which were collected from various places in Thailand. Among 283 strains taxonomically studied, 194 strains belonged to ascomycetous yeasts and 89 strains belonged to basidiomycetous yeasts. Based on the sequence analysis of D1/D2 domain of 26S rDNA, 139 strains (49%) were assigned to 56 known species because their D1/D2 domain sequences differed by 0-1 nucleotide substitution from known species. Among the strains were assigned to be known species, 97 strains belonged to 39 species of 17 genera of ascomycetous yeasts and 42 strains belonged to 17 species of 9 genera of basidiomycetous yeasts. One hundred and sixteen strains (41%) were considered to represent 101 new species because their D1/D2 domain sequences differed by 4 nucleotide substitutions or more from closest species. Among the strains assigned to new species, 87 strains belonged to 76 species of 14 genera of ascomycetous yeasts and 29 strains belonged to 25 species of 7 genera of basidiomycetous yeasts. The remaining 28 strains (10%) are not yet identified because their D1/D2 domain sequences showed 2-3 nucleotide substitutions from known species.

Twenty-one new species were selected for precise taxonomic studies by considering phylogenetic clusters and nucleotide differences. These yeasts were studied by polyphasic approaches, including conventional taxonomy, chemotaxonomic study and molecular taxonomy and described as *Candida easanensis* sp. nov., *Candida flocculi* sp. nov., *Candida hasegawae* sp. nov., *Candida jaroonii* sp. nov., *Candida kazuoi* sp. nov., *Candida koratica* sp. nov., *Candida lignicola* sp. nov., *Candida nakhonratchasimensis* sp. nov., *Candida pattanina* sp. nov., *C. pattaniensis* sp. nov., *Candida songkhlaensis* sp. nov., *Candida thailandica* sp. nov., *Candida udonthanina* sp. nov., *Candida* sp. 1 (ST-331), *Hanseniaspora thailandica* sp. nov., *Kloeckera siamensis* sp. nov., *Kloeckera songkhlaensis* sp. nov., *Kloeckera tradensis* sp. nov., *Pichia koratensis* sp. nov., *Pichia nongratonensis* sp. nov., and *Trichosporon siamense* sp. nov.

The frequency of isolation of respective species showed that, *Candida tropicalis* (9 strains) and *Saccharomyces kluyveri* (8 strains) are the dominant species of ascomycetous yeasts and *Cryptococcus heveanensis* (8 strains) is the dominant species of basidiomycetous yeasts. Among 101 new species found in the present study, 93 species (92.1%) comprised one strain and the remaining 8 species (7.9%) comprised 2-5 strains. In contrast, 26 known species (44.8%) comprised one strain and 32 known species (55.2%) comprised 2-9 strains. This fact means that, in the natural environment, the number of yeast cells of known species is bigger than those of new species. Significantly, 14 species (14 strains) of undescribed yeasts differed in 60-110 nucleotide substitutions (10-18%) from closest known species. These species may represent new groups, probably new genera or families, of yeasts. It is concluded that hitherto unknown yeast are rich in the natural habitats of Thailand and many new groups, new genera or new families, will be found from these unknown yeasts.

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Thesis Advisor's signature