CONCLUSION

As already discussed, 116 strains (41.0%) out of 283 isolated from some natural habitats of Thailand were predicted to represent hitherto undescribed species of yeasts based on the D1/D2 sequences of 26S rDNA. This is quite different from yeasts found in fermented foods and related materials and resemble ballistoconidium forming yeasts found in the phyllosphere of Thailand.

In the present study, 283 strains isolated from various kinds of natural habitats collected in Thailand were identified as 58 known species of 26 genera, 76 species of 21 genera of hitherto undescribed species, based on the D1/D2 sequences. The result showed that 41.0% (116 strains out of 283 strains) of isolates belong to undescribed species. This frequency is much higher than that of fermented foods and related substrates and ballistoconidium-forming yeasts from Bangkok and southern seacoast from Bangkok to Pattaya and resembles the case of ballistoconidium-forming yeasts from Sakaerat. It is considered that yeasts in the natural environment of Thailand, especially in protected forests, are very rich in biodivesity, not only in ballistoconidium-forming yeasts previous reported but also in ascomycetous yeasts and basidiomycetous yeasts other than ballistoconidium-forming yeasts.

Almost all the undescribed species predicted based on D1/D2 sequences are considered to represent new species with high possibilities though detailed taxonomic studies are required before the description of new species. As discussed in the text, the detailed taxonomic studies were carried out on 21 species. They were described as *Candida easanensis* sp. nov., *Candida flosculi* 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. (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.

It is interesting that the number of strains isolated per species is low in undescribed species in the present study and in 92.1% of species only 1 strain was isolated. It is assumed that the cell populations of these species are small in the natural habitats. In contrast, two or more strains were often isolated in the case of known species. The number of strains is high in popular known species such as *Candida tropicalis, Saccharomyces cerevisiae* and *Cryptococcus heveanensis*. It is considered that these popular species were described in the early history of yeast taxonomy since many cells are living in the natural environment in these species and researchers have many chances to find these species.

In D1/D2 domain sequences, 14 species of undescribed yeasts showed nucleotide substitutions more than 60 (10 %) from closest known species. These species may represent new groups, probably new genera or families, of yeasts. It is concluded that so many hitherto unknown yeast species are living in the natural environment of Thailand and many new groups, new genera or new families, will be found from these unknown yeasts. The study of these yeasts will much contribute to the progress of yeast science and technology, not only to the yeast systematics but also to the yeast technologies such as the production of useful substances and treatment of wastes because various kinds of new genes will be found.