One hundred and sixteen strains (41%) demonstrated 4 or more nucleotide substitutions from respective nearest species in the D1/D2 domain of 26S rDNA sequences (Table 13). These strains are considered to represent new species as discussed by Kurtzman and Robnett (1998). They were classified into 101 species belonged to 76 species (87 strains) of ascomycetous yeasts and 25 species (29 strains) of basidiomycetous yeasts. The frequencies of isolateion of new species are very high in respective habitats collected in various places in Thailand; flowers (11 strains, 46%), insect frass (56 strains, 41%), leaves (26 strains, 48%), mosses (6 strains, 26%), and mushrooms (14 strains, 50%). The places where new species were found are shown in Fig. 3. The remaining 28 strains (10%) out of 283 strains may be known or new species because 2-3 nucleotides were different from respective nearest species (Table 14). As mentioned above, these species are conspecific or sister species from each other. DNA-DNA reassociation experiment is required to identify these strains.

In the present study, 283 strains isolated from various kinds of natural habitat collected in Thailand were identified as 56 known species of 26 genera, 101 species of hitherto undescribed species and 28 unidentified species, based on the D1/D2 sequences. Namely, 41.0% of isolates belong to undescribed species. This frequency is much higher than that of fermented foods and related substrates, which were reported by Saito *et al.* (1983), Suzuki *et al.* (1987), Suzuki *et al.* (1994), Jindamorakot (2000) and ballistoconidium-forming yeasts from Bangkok and southern seacoast from Bangkok to Pattaya (Nakase *et al.*, 2001) and resembles the case of ballistoconidium-forming yeasts from Sakaerat (Fungsin, 2003). It is considered that yeasts in the natural habitats of Thailand, especially in protected forests, are very rich in biodivesity, not only in ballistoconidium-forming yeasts other than ballistoconidium-forming yeasts.