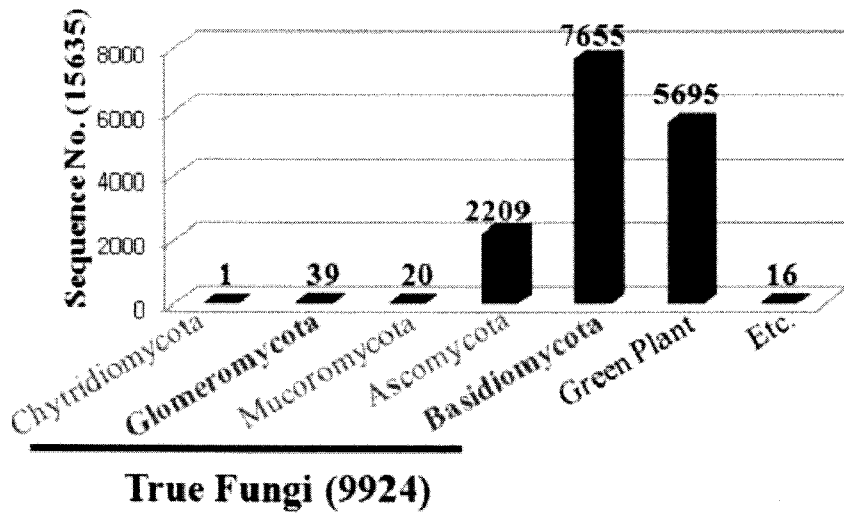


## Fungal diversity associated with oaks in Korea

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Eleven species of oak trees are common in Korean forests in association with evergreen pines. Although they have great economic value, oak trees have been received little attention. Since Korean oak forests have been attacked by the pathogenic fungus, *Raffaelea* vectored by the beetle *Platypus koryoensis*, awareness of their value has increased. With the goal to manage oak forests effectively, we investigated the diversity of decay-causing fungi and ectomycorrhizal (EM) fungi from the eight species of oak trees. Through examination of the specimens deposited in the Seoul National University Fungus Collection (SFC) and the National Institute of Biological Resources (NIBR) of the Ministry of Environment, a total of 523 decay fungi (104 species) associated with oak trees were identified and listed. No host specificity of decay fungi was evident. However, many decay fungi preferentially attacked the specific sites within oak trees, e.g. thin branch, trunk, bark, barkless heart wood, etc. To investigate the diversity of the ectomycorrhizal fungi, genomic DNA samples were extracted from the roots of healthy oak trees. Thirty colonies were chosen from each of eight root samples and used for the RFLP analysis and the cloning. Four to 12 different band patterns were detected by RFLP and 6 to 18 phlotypes were found from the clone sequencing. Through the sequence analysis of 243 clones, 67 sequences were identified as the plant and 176 sequences (62 phlotypes) were the fungi (Basidiomycota-142 (43), Ascomycota-34 (19)). Major phlotypes were ectomycorrhizal fungi such as *Russula* and *Lactarius*, and the others were litter/decay rotters and dark septate endophytes. A total of 17,694 sequence reads were obtained from pyrosequencing, where 9,951 were fungi and 5,597 were plant. Compared with RFLP and cloning, the pyrosequencing approach yielded more diverse results.



<그림 1> Pyrosequencing GS-FLX로부터 얻은 염기서열의 분석 결과