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**Classification and Characterization of Putative Cytochrome P450 Genes from
“Panax ginseng C.A. Meyer”**

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Objectives

In plants, heme containing cytochrome P450 is a superfamily of monooxygenases, functions are attributed to chemical defensive mechanism under terrestrial environmental conditions; several are involved in secondary metabolite pathways. However, the evolutionary relationship of P450 genes in Panax ginseng remains largely unknown though P450 is considered to be an important candidate, catalyzing the final step in triterpenoid pathways. The study was aimed to group the known P450 from ginseng EST database into their respective families and subfamilies by following Nelson nomenclature and also to check the expression of selected P450s under biotic stress conditions.

Materials and Methods

o From EST database unique sequences were collected and phylogenetic tree was drawn using Mega 4 software.

o The Panax ginseng C.A. Meyer seedlings were obtained from Korean Ginseng Resource Bank, South Korea and grown for 4 week old ginseng seedlings with MS, 3% sucrose and supplemented with gibberellic acid (30mg/ml) at 25°C under a 16h photoperiod. The fungal strains such as Botrytis cinerea (KACC 41298), Colletotrichum gloeosporioides (KACC 40003), Rhizoctonia solani (KACC 40101), Phythium ultimum (KACC 41062) were obtained from Korean Agricultural Culture Collection (KACC), South Korea. Untreated seedlings were used as control. After fungal treatment, seedlings were harvested at 6, 24, 48 and 72 h intervals. We particularly focused on these strains because these fungal strains causes damping off, rusty rot, fruit and leaf blight diseases in ginseng.

Results and Discussion

We identified 116 putative P450 genes in P. ginseng by a similarity search, and confirmed the families of putative P450 by phylogenetic analysis. When comparing P. ginseng with other genomes like Arabidopsis, soybean, M. trunculata, and rice, 116 P450s sequences were identified in P. ginseng. These comparisons clearly showed that half of the cytochrome P450 genes were predicted in P. ginseng. In addition, using in silico and bioinformatic

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tools, we studied EST derived P450 expression profiles. Diverse expression patterns of all four P450 genes was observed under both biotic and abiotic stress treatments, interestingly P450 genes are seemed to be highly expressed under abiotic stress conditions compared to biotic stress conditions. Both types of conditions induce oxidative stress by following distinct cascade pathways. The present study clearly shows the up-regulation of defense related/ or secondary metabolite related P450s under biotic stress conditions.

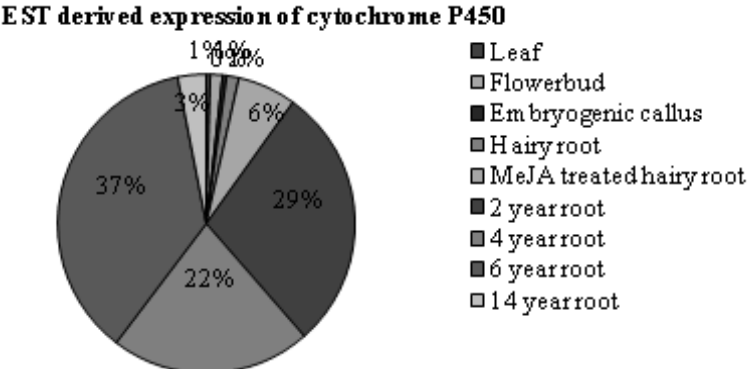


Fig 1: EST derived expression of P450 in *Panaxginseng* EST database

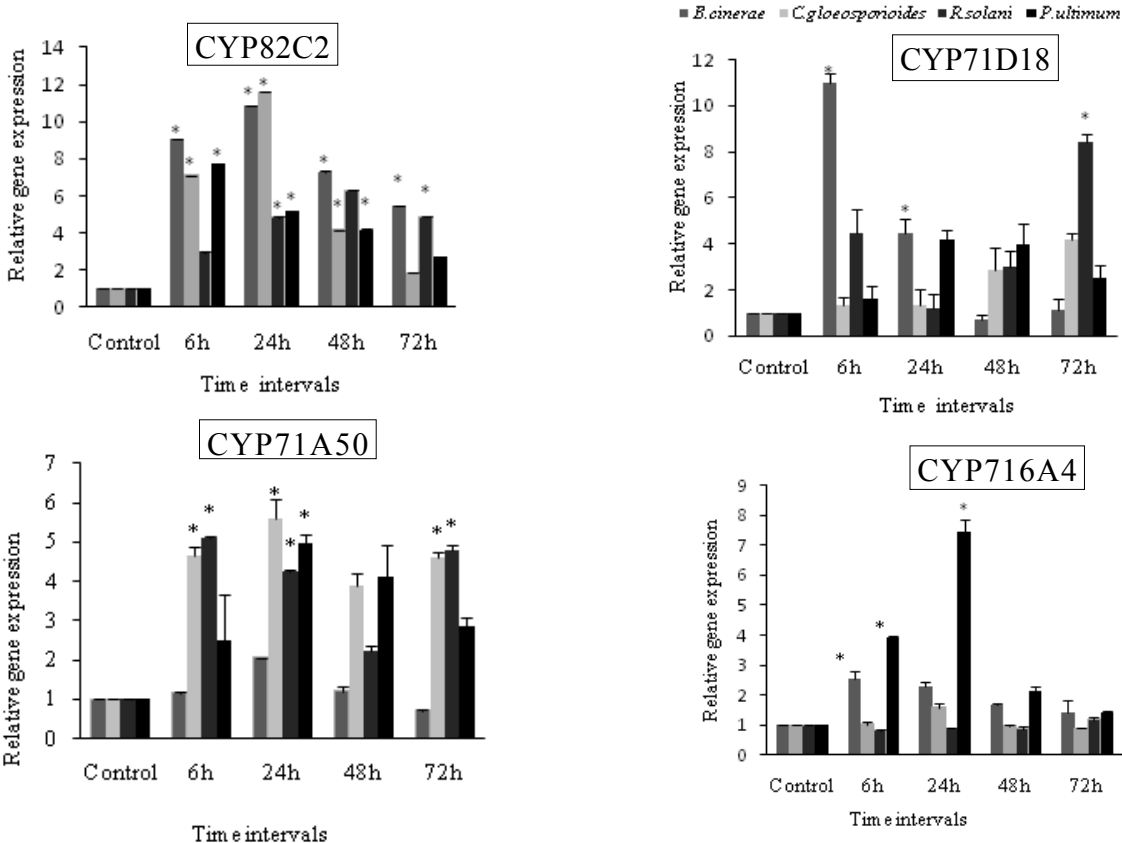


Fig 2: Effect of biotic stresses on the expression of cytochrome P450 genes. (A.CYP82C22, B.CYP71D184, C.CYP71A50U, D.CYP704G12 on fungal treatment.