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A Novel Proline Rich Protein from Rice (*Oryza sativa* L.)

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We have isolated a full length cDNA clone (designated rPRP1) encoding a proline rich protein from Oryza sativa. Sequence analysis of coding region revealed that the open reading frame encodes a 28.8-kDa protein. The C terminal region of this protein is rich in proline residue. The amino acid sequence of this clone shows significant homology with known monocot and dicot PRP's and aligned with nine conserved proline residues. Unlike other proline rich proteins this protein contains more Alanine residue instead of Lysine residue. Southern blot analysis showed that rPRP1 is a member of a small gene family with in the Oryza sativa genome. Reverse transcription (RT)-PCR analysis showed that rPRP1 mRNAs were more abundant in flowers. Further studies aimed to localize the mRNA by in-situ hybridization and to investigate the function of rPRP1 gene we generated transgenic rice plants, the research is in progress.

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A Molecular Approach to Programmed Cell Death of Rice Tapetum

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Anther tapetum plays very important role in pollen development. This secretary tissue produces numerous nutritive proteins necessary for pollen maturation and undergoes programmed cell death (PCD) by the time that pollen fully mature. We have reported previously that thermosensitive genicmale-sterile rice is associated with premature programmed cell death of the tapetum. In this study, we have isolated and characterized a cDNA clone designated rFAF1 from the male-sterile rice. Sequence analysis revealed that the clone is homologous to hFAF1 of human. The hFAF1, a member of Fas-DISC, is known to be involved in Fas-induced apoptosis, interacting with FADD and caspase-8. Southern blot analysis revealed that rFAF1 gene exists as a single copy in the rice genome. Potential roles of the gene during PCD in rice are discussed.

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Genetic Diversity and Population Structure of *Kalopanax pictus*

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The study of genetic diversity was carried out in the *Kalopnax pictus* Nakai. Starch gel electrophoresis was used to investigate the allozyme variation and genetic structure of seven Korean populations of this species. Of the 14 genetic loci surveyed, nine (64.3%) was polymorphic in at least one population. Genetic diversity was high at the species level (Hes = 0.240), whereas, that of the population level was relatively low (Hep = 0.191). Nearly 79% of the total genetic diversity in *Kalopnax pictus* was apportioned within populations. The sexual and asexual reproductions, longevity, and colonization process are proposed as possible factors contributing to high genetic diversity. The indirect estimated of gene flow based on Gst was 0.95.

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The Biological Functions of *EuNOD-CHT1* and *EuNOD-CHT2*, Differentially Expressed Chitinases from *Elaeagnus umbellata*

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Previous study on two chitinases (*EuNOD-CHT1* and *EuNOD-CHT2*) from *Elaeagnus umbellata* showed that these two genes were differentially expressed in the root nodule and root meristem (Kim and An, 2001). In order to examine possible biological roles of these two chitinases distinct from each other, we made transgenic *Arabidopsis* plant ectopically expressing *EuNOD-CHT1* and *EuNOD-CHT2* and their phenotypes such as germination rates, number of secondary roots and weight of plants were observed. *EuNOD-CHT1* transgenic lines showed that more improved phenotype than wild type plants in normal growth conditions, however *EuNOD-CHT2* and double transgenic lines didn't. To investigate whether *EuNOD-CHTs* play a role in defense mechanisms against pathogens, we infected bacterial and fungal pathogens to transgenic plants, a few lines showed enhanced resistance. Also, to elucidate the function of *EuNOD-CHTs*, their promoter sequences from *E. umbellata* were analyzed.