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RAPD Variation and Taxonimic Relationships in Nine Populations of Five Species of Bamboo

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The phylogenetic relationships among one mystery and eight populations of four bamboo species were investigated at the population level by constructing tree based on RAPD markers. RAPD analysis was conducted to estimate and population structure of bamboo species. The mystery population was found to have fewer alleles per locus(1.171), fewer effective alleles per locus, lower percent polymorphic locus(17.1%), and lower gene diversity(0.073) than other populations. The mystery population was genetically depauperate relative to its related species and colonization process, vegetative reproduction, and small population size are proposed as possible factors contributing to low genetic diversity. Mystery population is closed related to *Pseudosasa japonica* and *Sasa borealis*.

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Genomic Organization and Expression of *parkin* in *Drosophila melanogaster*

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We have isolated the *D. melanogaster* homolog of human *parkin*and determined its genomic structure and expression. The 2,122 bp parkin gene sequence contains six exons that form a 1449 bp transcript encoding a protein of 482 amino acids. The 5′ UTR contains three transcription initiation sites. Neithera classical TATA or a CAAT box was found in the putative promoter sequence. However, binding sites for AhR-Arnt, AP4, NF1 and GATA transcription factors were identified. Transient transfection analysis of the 5′ UTR confirmed its promoter activity in HEK 293 cells and SH-SY5Y neuronal cells using a dual luciferase reporting system. The amino acid sequence of *D. melanogaster* Parkin exhibits 42%, 43% and 43% identity to that of human, mouse and rat, respectively, representing a 54 kDa protein band via western blot analysis. It shows a high degree of conservation in the Ubiquitin-like domain at the N-terminus (34%), the In-Between RING finger domains (IBR, 65-69%), and the RING finger domains at the C-terminus (56-57%). The expression pattern of *D. melanogaster parkin* differed among the developmental stages, with the highest expression in the adult stage as measured by competitive RT-PCR. From immunostainings of the embryo, *D. melanogaster parkin* was shown to be expressed slightly higher in the central nervous system (brain and nerve cord) during the late embryonic stage.

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Arabidopsis Functional Genomics Using Activation Tagging Mutagenesis

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The only way to discern *in planta* function of a gene is to isolate and characterize mutant.To elucidate the function of 25,000 genes in Arabidopsis genome, activation tagging mutagenesis has been performed. A primary goal of this study is to collect 20,000 activation tagging mutants individually. In addition, among 20,000 mutants, we will screen mutants with abnormal phytochrome signaling, abnormal morphology, hypersensitive or insensitive to vernalization, and mutants with abnormal seed size. The corresponding gene from each mutant will be cloned and characterized by molecular genetic methods. Eventually, the function of each gene will be elucidated. Such an effort will contribute to the understanding of molecular mechanisms of plant developmental process.

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Searching for Novel Components of "Flowering Clock" in *Arabidopsis*: Mutagenesis of Plants Overexpressing *SOC1*

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*Arabidopsis*flowering time is influenced by environmental and endogenous cues, and several genes are involved in the regulation. Genetic dissections of *SOC1*have shown that it promotes the transition to flowering of Arabidopsis and plays a role as an integrator of flowering signals. Flowering signals including autonomous, vernalization, photoperiod and gibberellinare converged to *SOC1* and induce flower identity genes like*LEAFY*.In this study, we expect to find genes required for *SOC1* to promote flowering. We adopted forward genetics and performed EMS mutagenesis of fsu1-1D, which is a transgenic plant overexpressing *SOC1*. Through the mutations masking or enhancing the effect of *35S::SOC1*, we are able to discover novel components relating flowering time. Finally, It will elucidates the regulatory networks of *Arabidopsis* flowering.