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There are 11 species in the genus *Rumex* in Korea. The shape of leaves are very similar but seed type and chromosome numbers are different. Analysis of genus *Rumex* in Korea have been carried out using chromosomal, RAPD and FISH techniques. There are two dioecious plants, *Rumex acetosa* and *R. acetocella*. The chromosome number of *R. acetosa* was 2n=14 in the female and 2n=15 in the male individuals and *R. acetocella* was 2n=42 and 43. The somatic chromosome numbers of *R. crispus* and *R. japonicus* were 2n=60 and that of *R. niponicus* were 2n=50, *R. obtusifolius* was 2n=40. The chromosomal locations of 45s rDNA genes using FISH technique were determined in *R. crispus*. One pair of 45s rDNA signals was detected with avidin-FITC conjugate. Key words : *Rumex*, FISH, RAPD

**F804 Functional roles of a Novel Zinc Finger Protein, FAX-ZFP in *Xenopus laevis***

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A subfamily of the many C2H2 type zinc finger protein (ZFP) in *Xenopus laevis* contains a highly conserved N-terminal nonfinger portion designated finger-associated box (FAX). Neither the biological roles for most of the FAX-containing ZFP (FAX-ZFP) have been yet to be discovered. We isolated a gene encoding a member of *Xenopus* FAX-ZFP

family protein that interacts with the *Xenopus* TATA-binding protein (xTBP) by employing yeast two-hybrid system. A chimeric construct encoding a fusion FAX protein with Gal4 DNA binding domain repressed the transcriptional activity of a heterologous promoter containing the Gal4-binding sequence in both A6 cells (*Xenopus* kidney) and NIH3T3 cells (mouse). xTBP was also shown to make a direct contact with the FAX-ZFP protein in vitro pull down assay. These data support that the FAX-ZFP family transcription factors may interact TBP in order to negatively regulate the expression of target gene(s). In order to elucidate eleven bp consensus sequence, GCGA(A/G)GGGGTG, was selected to bind strongly with FAX-ZFP.

**F805 Analysis of Anther-specific and -preferentially Expressed Genes from Lily**

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We have randomly selected 2,000 cDNA clones from an anther cDNA library of oriental lily. Using differential screening, 150 anther-specific clones and 400 anther-preferentially expressed clones were isolated. The selected clones were partially sequenced at the putative 5'-end of insert cDNAs. Among 150 anther-specific expressed sequence tags (ESTs), 139 cDNA clones were nonredundant. Twenty-two clones had sequence homologies with functionally defined genes at peptide level and only five clones encoded known anther/pollen-specific proteins. One hundred twenty-eight clones showed little or no similarity with previously reported genes. Using slot blot hybridization, expression patterns of the 150 ESTs were examined during anther development. Most of the genes (123 ESTs) were strongly expressed

in mature anther. RNA blot analyses of 32 genes revealed that 27 of them were also expressed at high level in mature pollen. From 400 anther-preferentially expressed ESTs, 359 ESTs were nonredundant. 50 ESTs out of them exhibited significant similarities at the nucleotide level with functionally defined genes and could be classified to 9 groups according to their putative function. The identified anther-specific and preferentially expressed ESTs indicate that most of them are related to pollen or anther development.

#### **F806** Chromosome D/B of Native Plants in Korea

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The first cytological investigation on plant chromosome in Korea was reported in 1958 by the late professor Woong-Jik Lee. Since then investigation of chromosome numbers and karyotype analysis have been the main subject in Korea by late 1980s. So far chromosome numbers has been examined from about 55 families, 182 genus and 474 species. C-banding technique has been successfully applied for the identification of chromosomes in *Lilium* and *Allium*. *Scilla scilloides* Complex is considered to be a model plant for cytogenetic studies in Korea. Recently molecular cytogenetic techniques such as FISH and GISH are prevailing in chromosome studies. The project titled "Establishment of Chromosome D/B from Korean Native Plants" supported by the Plant Diversity Research Center of 21st Frontier Research Program launched from 2001. The Web sites, [chromosomeworld.com](http://chromosomeworld.com) in English and [chromosomekorea.com](http://chromosomekorea.com) in Korean, will be available.

#### **F807** Polymorphisms of estrogen metabolizing genes, 2 CYP1B1, COMT, GSTP1, GSTM1, and GSTT1 in breast cancer

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Cytochrome P450 1B1 (CYP1B1) is responsible for the 4-hydroxylation of estradiol to catecholestrogens (CE), whereas catechol o-methyltransferase (COMT) and glutathione s-transferase (GSTs) are involved in detoxifying CE and reactive semiquinone/quinone in estrogen metabolism. Accumulation of CE participates in estrogen-induced carcinogenesis by DNA oxygenic damage. *CYP1B1* Leu432Val variant with increased activity, *COMT* Val158Met variant and *GSTP1* Ile105Val variant with reduced activity, *GSTM1* and *GSTT1* null allele with deficient activity may result in the accumulation of CE and its metabolites through high and low enzymatic activity for CE formation and conjugation, respectively. We investigated the association between *CYP1B1*, *COMT*, *GSTP1*, *GSTM1* and *GSTT1* genetic variations and breast cancer susceptibility. Genotyping analyses were PCR RFLP for *CYP1B1*, *COMT* and *GSTP1* gene, and multiplex PCR for *GSTM1* and *GSTT1* gene in 280 controls and 108 breast cancer patients. The *COMT*<sup>Met</sup>/<sup>Met</sup> genotype frequency was found to be higher in breast cancer than in controls (10.2% vs. 5.4%), and odds ratio (OR), 2.25; 95% confidence interval (CI), 0.98-5.23, but frequencies of other enzymatic genotypes were not different. Furthermore, the proportion of postmenopausal women with *COMT*<sup>Val</sup>/<sup>Val</sup> genotype encoding high activity was lower than premenopausal women (25.0% vs. 54.4%, p=0.04) in breast cancer patients, was indicated that the *COMT*<sup>Val</sup>/<sup>Val</sup> genotype was a decreasing risk factor for breast cancer in postmenopausal women. A significant increase in the *COMT*<sup>Met</sup>/<sup>Met</sup> genotype was observed and its combined