

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 in English and 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*^{Met}/^{Met} 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*^{Val}/^{Val} 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*^{Val}/^{Val} genotype was a decreasing risk factor for breast cancer in postmenopausal women. A significant increase in the *COMT*^{Met}/^{Met} genotype was observed and its combined

*CYP1B1***Leu*/*Leu* genotype was observed in breast cancer, which was theoretically lead to higher CE exposure (OR=2.45, CI=1.0-6.21). And *COMT***Met*/*Met* genotype was observed trending to positive lymphnode metastasis. These results suggest that the *COMT***Met* allele may contribute to increased risk for breast cancer.

F808 C>T single nucleotide polymorphisms at -511 and 3953 of IL-1 beta and variable numbers of an 86 bp tandem repeat of IL-1ra in Koreans

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The cytokine interleukin-1 (IL-1) as the prototypic multifunctional cytokine is heavily involved in the enhancement of inflammation and host defense. There are 3 known IL-1 genes in a cluster on 2p13. Two of the genes encode pro-inflammatory proteins, *IL1A* for IL-1 and *IL1B* for IL-1, while the third gene (*IL1RN*) encodes a protein, it acts as a receptor antagonist (IL-1ra) by competing for receptor binding. And some of the polymorphisms may contribute to the recognized stable interindividual variation in cytokine production rates. In this study, we analyzed *Ava*I RFLP at -511 in 5' flanking region, *Taq*I RFLP at 3953 in exon 5 of *IL1B* and VNTR polymorphism in intron 2 of *IL1RN* is caused by the variable copy number of an 86bp sequence from unrelated 325 Koreans. The genotype frequencies of **C*/*C*, **C*/*T* and **T*/*T* at -511 nucleotide position of *IL1B* were 23.6%, 49.5% and 24.3%, respectively, and **C* allele frequency was 50.9%. The **C*/*C* and **C*/*T* frequencies at 3953 of *IL1B* were 93.8% and 6.2%, respectively, and **C* allele frequencies was 96.9%. VNTR polymorphism of *IL1RN* has four alleles, comparison between two and five repeats of an 86 bp sequence. The four repeat (*IL1RN**4) is most common (90.2%). No deviation from the expectation according to the Hardy-Weinberg equilibrium was found in three sites.

F809 -34 C>T single nucleotide polymorphism and variable number of tandem repeat polymorphism of Interleukine 4 in Koreans

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Interleukine-4 (IL4) is a pleiotropic cytokine which plays a key role in IgE-dependent inflammatory reactions. It is produced by T cells, mast cells, and eosinophils and is central to B cells switching to IgE antibody production and to the maturation of T helper cells to the Th2 phenotype. Although the initial trigger for IL-4 production remains unknown, genetic variation is likely to play a role because the polymorphisms in IL4 may result in an altered level of expression. We analyzed C>T SNP at -34 nucleotide position by *Mn*I RFLP and 70bp tandem repeat polymorphism in intron 3 from 325 Koreans. The genotype frequencies of *IL4***T*/*T*, *IL4***T*/*C* and *IL4***C*/*C* at -34 nucleotide position were 63.7%, 32.3% and 4.0%, respectively. And the *IL4***T* allele frequency was 79.8%. VNTR polymorphism in intron 3 of *IL4* was shown between one and three repeats of a 70 bp sequence and *IL4**1 with 2 repeats was the most frequent allele (77.7%). No deviation from the expectation according to the Hardy-Weinberg equilibrium were found in both sites. The *IL4***T* frequency at -34 in Koreans (79.8%) are similar to that of the Japanese (71.0%). Although VNTR polymorphism in intron 3 was shown 3 types of repeats in Koreans, there was shown only 2 types of repeats in Japanese and French. The frequency of *IL4**1 in Koreans (77.7%) was similar to that of the Japanese (73.0%).

F810 Genetic Diversity of Maize, *Zea mays* in Korea using AFLP Markers

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