

*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*\*1) 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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Enzyme electrophoresis was used to estimate genetic diversity and population structure of maize, *Zea mays* L.(Graminales) in Korea. In thirteen populations, fourteen of the 24 loci (58.3%) showed detectable polymorphism. Genetic diversity (0.130) was lower than average values for species with similar life history traits. The recent cultivated populations were found to have fewer alleles per locus (1.39 vs. 1.61), fewer alleles per polymorphic locus (2.28 vs. 2.41), lower percent polymorphic locus (23.4% vs. 35.8%), and lower diversity (0.122 vs. 0.168) than primitive cultivated populations. These genetic diversity parameters indicated that the recent cultivated populations were genetically depauperate relative to primitive cultivated populations. Analysis of fixation indices showed a substantial deficiency of heterozygotes relative to Hardy-Weinberg expectations suggesting inbreeding in maize. The  $G_{ST}$  value of 13 cultivated populations was 0.151. Nearly 85% of the total the genetic diversity in *Zea mays* was apportioned within populations. The indirect estimate of gene flow based on mean  $G_{ST}$  was moderate ( $Nm = 1.41$ ).

### F811 Genetic Diversity and Population Structure of Maize, *Zea mays* in Both Primitive Cultivated and Cultivated Populations

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### F812 Development of Expression vector using insulin-like growth factor- $\alpha$ & epidermal growth factor

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Many attempts have been done on various essential protein production by using transformed *E. coli* system. However, prokaryote system does not equipped the protein maturation mechanisms which are necessary for eukaryotic proteins. In this sense, among the eukaryotes, silkworms have two major merits in overcoming the difficulties. First, the protein maturation mechanisms are available in silkworm. Second, the silkworms have fibroin promoter known as the most powerful and effective promoter which controls the expression of fibroin, one member of silk protein. Insulin-like growth factor-I (IGF-I) and epidermal growth factor (EGF) play roles in neonatal growth, cell reproduction and cell proliferation. In this study, the production of recombinant human IGF-I and