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Genotype of Km using Polymerase Chain Reation -Allele Specific Oligonucleotide in Korean

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The human immunoglobulin kappa light chain (IgK) gene is located on chromosome 2p12 and consists of a single constant gene (C_k), five joining genes (J_k) and a number of variable genes (V_k). Three alleles for C_k have been defined by serological assy or PCR-ASO method. These alleles involve single amino acid changes at positions 153 and 191. The allotypes of the Kappa constant region were designated as follows : Km^1 has valine (GTC) at position 153 and leucine (CTC) at 191 ; $Km^{1,2}$ has Ala^{153}(GCC) and Leu^{191}(CTC) ; Km^3 has Ala^{153}(GCC) and Val^{191}(GTC). This study used the PCR-ASO to provide specific allelic typing system for Km at the IgK gene. The Km was typed in 131 normal Korean. For Km genotyping, 354 bp sequence was amplified by primers (BA05 5′ ACT GTG GCT GCA CCA TCT G 3′ and BA06 5′ GAA CTG AGG AGC AGG TGG G 3′). Amplified gene was hybridized with Km ASO probes and detected using colorimetric detection method. The frequencies of Km genotypes Km^3,$Km^{3;1,2}$ and $Km^{1,2}$ were 35.1%, 45.1% and 19.8%, respectively. The estimated allele frequencies for Km^3 and $Km^{1,2}$ were 0.58 and 0.42, respectively. The Km^3 frequencies were in the range of 0.9 in the caucasoid populations (Europeans, Polish Jews) and close to 0.5 in the mongoloid (Chinese, Japenese, Melanesians) and African (Zaire Pygmies).

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Detection of Genetic Variation and Gene Introgression in Potato Dihaploids Using Randomly Amplified Polymorphic DNA Markers

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Randomly amplified polymorphic DNAs were employed to study the genetic variation and gene introgression in potato dihaploids generated after interspecific pollination of tetraploid cultivars (2n=4X=48, *Solanum tuberosum* cvs. Irish Cobbler, Superior, and Dejima) by haploid inducer clones (2n=2X=24, *Solanum phureja*, 1.22, Hes-5 and Hes-6). Genetic variation and DNA marker segregation among dihaploids were observed. Most dihaploids contain *tuberosum* specific RAPD markers but haploid inducer-specific RAPD markers were also found in some dihaploids. Of fourteen different arbitrary 10-mer oligonucleotide primers which showed polymorphism between tetraploid cultivars and haploid inducers used, seven generated amplification products which seemed to be derived from the *S. phureja* parent. Our results clearly indicate that chromosomes of dihaploids produced by haploid inducers are not pure *S. tuberosum* and the presence of alien DNA segments would complicate segregation analyses of crosses. However, the introgression of inducer-specific markers into *S. tuberosum* genome may offer an way to introduce useful traits directly from haploid-inducer into *S. tuberosum* dihaploid genome.