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Characterization of a cDNA Encoding a Proline-Rich 14 kDa Protein in Developing Cortical Cells of the Roots of Bean (*Phaseolus vulgaris*) Seedlings

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A cDNA clone, corresponding to mRNAs preferentially expressed in the roots of bean (*Phaseolus vulgaris* L.) seedlings, was isolated. This clone contains a 381 bp open reading frame encoding a polypeptide of 13.5 kDa, designated PVR5 (*Phaseolus vulgaris* root 5). The amino acid sequence of this clone is rich in proline (13.5%) and leucine (12.7%) and shares significant amino acid sequence homology with root-specific and proline-rich proteins from monocots (maize and rice), and proline-rich proteins from dicots (carrot, oilseed rape, and madagascar periwinkle). The precise biological roles of these polypeptides are unknown. PVR5 mRNA accumulation is developmentally regulated within the root, with high levels at the root apex and declining levels at distances further from the root tip. *In situ* hybridization shows that PVR5 mRNA specifically accumulates in the cortical ground meristem in which maximal cell division occurs. Southern blot analysis suggests that genomic DNA corresponding to PVR5 is encoded by a single gene or small gene family.

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The PCR/FLP Analysis of 3 STR Loci and Frequency Distribution in Korean Population

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We have analysed the allelic frequency distribution at the short tandem repeat(STR) to the CD4, TH01, vWA(vWA31A) loci in Human DNA by PCR/FLP techniques. In a sample of 200 unrelated Koreans, the CD4 locus demonstrated a heterozygosity of 43% with 5 alleles and 7 genotypes. The allelic diversity value and the PD of CD4 were found to be 0.44 and 0.61 respectively. The TH01 locus demonstrated a heterozygosity of 70.3% with 5 alleles and 14 genotypes. The allelic diversity value and the PD of TH01 were found to be 0.71 and 0.80 respectively. The vWA locus demonstrated a heterozygosity of 79.9% with 7 alleles and 23 genotypes. The allelic diversity value and the PD of vWA were found to be 0.799 and 0.97 respectively. Comparison of the result an allele frequencies with other published databases showed that their distributions were not similiar. Observed heterozygosity was similar to that reported in other population studies but significantly higher than expected. These population data will allow the use of the 3 STR marker in paternity determination and the analysis of individual identity in forensic samples