F810 Genetic Variation at VNTR Locus YNZ22(D17S5) in Korean

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The human genome contains a great number of DNA segments of variable number of tandem repeats (VNTR) loci. The VNTR locus detected by probe YNZ22 (D17S5) on chromosome 17q13.3 is considered to be a highly useful genetic marker. In the present study, genetic variation for the YNZ22 locus were analyzed in 161 unrelated koreans using the PCR method. We observed 14 alleles and 55 phenotypes from this study. The distribution of phenotypes was significantly deviated from Hardy-Weinberg equilibrium (χ^2 =23.683, df=10, 0.005<P<0.01). The observed heterozygosity was 91.93%. When the power of discrimination (PD), power of exclusion (CE) and polymorphism information content (PIC) were calculated, the obtained values were 0.973, 0.759 and 0.856, respectively. The values showed a high efficiency of forensic science and population genetics.

F811 Phylogenetic Relationship Among Some *Prunus* species in Mt. Halla and Cultivated *Prunus yedoensis* by RAPD Analysis

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We analyzed the phylogenetic relationship among eight species (*P. pendula* for. *asendens* Ohwi, *P. yedoensis* Matsumura, *P. sargentii* Rehder, *P. serrulata* var. *quelpaertensis* Uyeki, *P. maximowiczii* Rupr., *P. serrulata* var. *pubescens* Nakai, *P. buergeriana* Miquel, *P. serrulata* var. *spontanea* Wils.) of genus *Prunus* in Mt. Halla and cultivated *P. yedoensis* Matsumura using random amplified polymorphic DNA(RAPD) analysis. RAPDs were identified in nine species by amplification using single 10-mer primers of arbitrary sequence. Nine species were clearly classified with 8 arbitrary random primers which generated 76 polymorphic amplified DNAs or RAPDs. The phylogenetic tree was constructed from the RAPD fragments patterns by neighbor-joining method. The genetic distance between *Prunus sargentii* Rehder and *P. serrulata var. quelpaertensis* Uyeki was 0.3036 and was the lowest than those of any other pairs, the other side, between *P. yedoensis* Matsumura and *P. yedoensis* Matsumura-Cultivar was 0.4297. These results showed that RAPD analysis is a useful tool or elucidating phylogenetic relationship among 9 species of cherry trees.