

F829Molecular Cloning and Characterization of a cDNA Clone Encoding Metallothionein of *Petunia hybrida*

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Metallothioneins (MTs) are cystein-rich, low-molecular weight proteins that bind to heavy metals and are believed to play a role in their metabolism and detoxification. Genes encoding MT-like proteins have been isolated in a number of plants, however, their function remains to be elucidated. We identified a cDNA encoding a metallothionein-like protein from a petunia (*Petunia hybrida*) cDNA library derived from petal protoplast cultures. This cDNA (*PhMT*: *Petunia hybrida* Metallothionein) encoded an open reading frame of 74 amino acids whose molecular weight is about 7.5 kDa. The deduced amino acid sequences of *PhMT* is 57-81% identical with bean, Arabidopsis, and tomato. Northern blot analysis showed that the transcript levels were not significantly affected by treatment with Cu and Zn. The expression level of *PhMT* in mature petunia plants was extremely high in stems relative to roots, leaves, petals, and sepals. Also the transcript strongly expressed in senescence stage of flower development. These results indicate that gene expression clone are differentially regulated in various tissues and developmental stage.

F830Analysis of the STR Loci for *HUMSTRX1*, *HUMHPRTB*, *HUMARA*, *DYS390*, *DYS392* and *DYS393* in KoreanHye Won Seol^{1*}, Kyung Sook Park¹, Katsuya Honda², Zaw Tun², Shogo Misawa³
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Three STR loci (*HUMSTRX1*[AGAT]_n, *HUMHPRTB*[AGAT]_n and *HUMARA*[AGC]_n) on X chromosome and three STR loci (*DYS390*[CTG/AT]_n, *DYS392*[ATT]_n and *DYS393*[GATA]_n) on Y chromosome have been analyzed in 154 unrelated healthy Korean. Four loci (*HUMSTRX1*, *HUMHPRTB*, *DYS390* and *DYS393*) were amplified by quadruplex polymerase chain reaction (PCR) using fluorescently labeled primers (FLP) and *HUMARA* and *DYS392* were performed by single PCR, separately, also using FLP. Then they were run in automated DNA sequencer and were analyzed by using Genescan software. We found the 7 alleles (308-332bp) in *HUMSTRX1*, 7 alleles (275-299bp) in *HUMHPRTB*, 16 alleles (252-315bp) in *HUMARA*, 6 alleles (203-223bp) in *DYS390*, 7 alleles (245-263bp) in *DYS392* and 5 alleles (116-132bp) in *DYS393* and the *13(34%), *13(51%), *23(17%), *23(50%), *14(41%) and *13(40%) alleles were observed the highest in frequencies of *HUMSTRX1*, *HUMHPRTB*, *HUMARA*, *DYS390*, *DYS392* and *DYS393*, respectively. The heterozygosities and the polymorphism information content (PIC) values of three X-STRs were observed 0.73 and 0.68 in *HUMSTRX1*, 0.66 and 0.63 in *HUMHPRTB* and 0.87 and 0.90 in *HUMARA*, respectively, and the gene diversities of three Y-STRs were observed 0.64 in *DYS390*, 0.69 in *DYS392* and 0.66 in *DYS393*. Recently, STR on X and Y chromosomes as well as autosomal chromosome were described as highly polymorphic marker for population genetics studies and for forensic sciences because it is useful for determining of the sex and has genetic stability.