transgenic *Arabidopsis*. This suggests that 1il might enhance GUS expression by Intron-Mediated Enhancement(IME). Further analysis will give more informations on regulation of *PhADF* genes.

F832 Genetic Polymorphism of Mitochondrial DNA in Jeju Native Horses Inferred from PCR-RFLP

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We analyzed the mitochondrial DNA in the three populations of Jeju native horses using PCR-RFLP. The partial region, about 2 kilo base pairs, including two mitochondrial polypeptide genes (NADH dehydrogenase subunit 6 gene; *ND6* and cytochrome B gene; *cyt*B) and two mitochondrial tRNA genes (tRNA-Glu gene and tRNA-Thr gene), was amplified by PCR. The RFLP analyses were performed with 10 kinds of restriction enzymes. We found polymorphisms in these digested with four of the 10 enzymes, *Bam*H?, *Hin*f?, *Msp*? and *Rsa*?. Three morph types were detected in those digested with *Msp*? and *Rsa*?, respectively; two morph types with *Bam*H? and *Hin*f?, respectively. They were classified into twelve types, and their frequencies were different among three populations. Also, the patterns of the heteroplasmic digestion were found in some animals. These results showed that mtDNAs, which are maternally inherited, of the Jeju native horses were highly polymorphic. This suggests that hybridization or/and introgression among the populations of the east Asian native horses occurred in the past. These results can be a useful parameter to verify the maternal lineages of the Jeju native horses.

F833 Identification and Characterization of Genes Overexpressed by Hypoxia in Human Synovial Fibroblasts of Rheumatoid Arthritis

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Rheumatoid arthritis (RA) is an immunologically mediated disease characterized by chronic articular inflammation that leads to the destruction of cartilage and bone in the affected joint. The rheumatoid synovium is known to be in hypoxic environment which may result in diverse cellular responses in rheumatoid synovium, especially in synovial fibroblasts which play a central role in the pathogenesis of RA. For this reason, screening of genes overexpressed in RA synovial fibroblasts under hypoxia was performed by suppression subtractive hybridization and differential hybridization with mRNAs extracted from primary cultured human RA or osteoarthritis synovial fibroblasts incubated under hypoxic or normoxic conditions. The procedure resulted in the selection of 38 clones overexpressed in RA synovial fibroblasts and 37 clones overexpressed in hypoxic RA synovial fibroblasts. The selected clones have genes identified as transglutaminase 2, reticulocalbin 1, proteasome 26S unit (n=2), matrin 3, kinesin family member 5B, mitochondrial cytochrome C oxidase subunit 2 (n=2), laminin receptor 1, BPTF, ILF2, BRF1, EF-1 (n=2), ferritin heavy polypeptide (n=3), acid ceramidase, annexin A1, cyclin C, endophilin B1, RAB11A (RAS oncogene family), complement 3 and CTCL tumor antigen se33-1. The present study suggests that hypoxia might influence to the pathogenesis of RA by regulating the expression of various genes in rheumatoid synovial fibroblasts.