P. yedoensis from Jeju were clearly distinguished from the cultivar plants. On the other hand, the analyses of the ITS and *rbc*L gene sequences showed that *P. pendular* for. *ascendens* was more closely related to the population of *P. yedoensis*, making the latter one of the putative parents of *P. yedoensis*. These results suggest that ITS and *rbc*L gene sequences analyses are useful approaches for inferring molecular phylogeny and evolution between *P. yedoensis* and its related species.

A804 Comparison of genus Polgonatum using ITS(Internal Transcribed Spacers)and rbcL gene

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The genus *Polgonatum* belongs to Polygonatae of Liliaceae, which contains about 58 species in the world. In Korea 14 species and 2 varieties have been reported in this genus. The phylogeny of the genus *Polgonatum* is still in debate, because these are many different opinions on their morphological characters. We studied phylogenetic relationship of korea 14 *Polgonatum* species analysing ITS sequence of rDNA and *rbc*L gene. About 650~680base pairs of rDNA region were PCR-amplified and sequenced. The data obtained was compared with GenBank data base. The comparison of ITS sequences in the species through multiple alignments had homology with the known sequences. In addition same method was applied to *rbc*L gene.

A805 DNA Fingerprinting and Identification of Three Angelica Species using AFLP(amplified fragment length polymorphism) Markers

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This study was conducted to investigate genetic variability of herb medicine, to develop the three Angelica species-specific DNA marker and to estimate phylogenetic relationships among *Angelica gigas* Nakai, *A. sinensis*(Oliv.) Diels., *A. acutiloba* Kitagawa using AFLP(amplified fragment length polymorhism) markers as a fingerprinting technique. Two EcoRI and two MseI primers used in 8 primer combinations generated a total 262 bands, of which 25 were clearly polymorphic among the accessions. Three primer combinations were selected according to their reproducibility, number of polymorphic bands and polymorphism detected between three Angelica species. we propose that genomic fingerprinting techniques such as AFLP can be used as rapid, highly discriminatory screening techniques to determine the herb medicine.

A806 Identification and Phylogeny of Long Terminal Repeat Elements of Human Endogenous Retrovirus HERV-S

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A new human endogenous retroviral family (HERV-S) has recently been identified from human X chromosome. It is 6.7 kb in length and has a typical retroviral structure with LTR-gag-pol-env-LTR. Using the PCR and sequencing approach, we investigated LTR elements of the HERV-S family from a human genomic DNA. Four LTR elements (HSL-1, HSL-5, HSL-10, HSL-11) were identified and have a high degree of sequence similarity (96-99%) with

that of the HERV-S. Phylogenetic analysis from the HERV-S family indicated that the LTR elements were mainly divided into 2 groups through evolutionary divergence in the primate evolution. Further investigation of the HERV-S LTR elements in primates may cast light on the integration timing into the primate genome and understanding of human evolution.

A807 Identification and Phylogeny of the Human Endogenous Retrovirus HERV-W LTR Family in Human Brain cDNA Library and Xq21.3 Region

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Human endogenous retroviral long terminal repeats (LTRs) have been found to be coexpressed with sequences of genes located nearby. It has been suggested that the LTR elements have contributed to the structural change or genetic variation of human genome connected to various diseases. HERV-W family has been identified in the cerebrospinal fluids and brains of individuals with schizophrenia. Using cDNA library derived from human brain, we examined the HERV-W LTR elements and identified five new LTR elements. We also examined such elements using YAC clone panel from the Xq21.3 region linked to psychosis that was replicated on the Y chromosome after the separation of the chimpanzee and human lineages. Fourteen elements of the HERV-W LTR were identified in that region. Those LTR elements showed a high degree of sequence similarity (91.8 99.5%) with HERV-W LTR. A phylogenetic tree obtained by the neighbor-joining method revealed that new HERV-W LTR elements were closely related to the AX000960, AF072504, and AF072506 from GenBank database. The data indicates that several copy numbers of the HERV-W LTR elements exist on Xq21.3 region and are also expressed in human brain. These LTR elements deserve further investigation as potential leads to neuropsychiatric diseases.

A808 Wheat evolution : Polyphyletic origin of the B genomes and differences of the B genomes between *Triticum turgidum* and *T. aestivum*

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Common bread wheat (*Triticum aestivum*, AABBDD, 2n=2x=42) had evolved relatively recently. *Triticum monococcum* and *T. tauchii* (*Aegilops squarossa*) were to be the donors of A and D genomes in polyploid wheat by several lines of evidences. However, the B genomes in polyploid wheats had not been resolved for their genome donors. Either one or several diploid B genome plants should have donated their chromosomes to the polyploid wheats. The putative B genome donor plants are *T. searsii, T. speltoides, T. sharonensis, T. bicornis*, and *T. longissima*. We are not sure that there were a single or multiple events of hybridization between Einkorn A genome plant with Emmer B genome plants. Monophyletic or polyphyletic origins of the B genome chromosomes are not clear. As well. identity of the B genome chromosomes in *T. turgidum* (AABB) and *T. aestivum* (AABBDD) was not clear either. We have isolated a fungal microsatellite DNA which can hybridize in selective chromosomes in wheat species. With this DNA as a probe, we sought the B genome donors to polyploid wheats and the identity of the B genome chromosomes between *T. turgidum* and *T. aestivum*.