tri peptide poly (Aspartyl-Phenylalanine-Lysine). These DNAs were cloned into expression vector pINIIIA3 plasmid. Clones containing genes coding up to 128 repeats of this tri peptide have been isolated and expressed as artificial proteins. These proteins were synthesized as insoluble aggregates. Artificial protein was purified and digested with trypsin, resulting in the production of tripeptide, Asp-Phe-Lys. For the preparation of peptide sweetner, α-L-aspartyl-L-phenylalanine methyl ester, this tripeptide was hydrolysed with carboxypeptidase B to produce dipeptide, Asp-Phe, and esterified with methanol in the presence of α-chymotrypsin in a water-methanol solvent system.

D–30. Expression of Tomato Proteinase Inhibitor I Gene Confers Tobacco Plants Resistance to Insects
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Plants have been considered to defend themselves from attacking pests by synthesizing proteinase inhibitors and storing them in storage organs such as seeds and tubers or by inducing their synthesis in leaves of tomato and potato when attacked by insects. In order to investigate its possibility, we tried to express a wound-inducible proteinase inhibitor I gene of tomato in tobacco plants constitutively. A chimeric gene between the promoter of the cauliflower mosaic virus 35S transcript and cDNA of the tomato inhibitor I (CaMV 35S-inhibitor I) gene was constructed in a binary vector derived from Ti-plasmid of Agrobacterium tumefaciens. The CaMV 35S-inhibitor I gene was introduced into tobacco cells by the method of Agrobacterium-mediated transformation. Transformed cells were regenerated to whole plants. Immunoassay of leaf extracts from the transgenic tobacco plants with anti-inhibitor I antibody confirmed the expression of the CaMV 35S-inhibitor I gene in the transgenic plants. Insect bioassay of transgenic plants indicated that the tobacco plants synthesizing the inhibitor I proteins were protected from insect attacks while control plants were not.

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In potato, proteinase inhibitor II proteins are encoded by a family of about 10 members. They are expressed developmentally in tubers and are induced in leaves upon attacks by insects or mechanical wounding. In order to elucidate the mechanisms of their differential expressions, an inhibitor II gene present in a 13.5 kb EcoRI fragment was isolated from a EcoRI-partial genomic library and characterized. The nucleotide
sequence revealed that the gene is complete and encodes an open reading frame of 146 amino acids which is interrupted by an intervening sequence of 113 bp, situated within the codon of amino acid 18. In addition to a promoter element, TATAAA, a sequence resembling a putative regulatory element involved in its wound induction, GCACATCTT, was found at the 5' flanking region. In order to investigate the mode of expression of this inhibitor II gene, chimeric genes between the inhibitor II gene and bacterial chloramphenicol acetyltransferase (CAT) and β-glucuronidase (GUS) genes were constructed in a binary vector derived from Ti-plasmid of Agrobacterium tumefaciens. Studies of plant transformation will shed light on the mechanism by which this inhibitor II gene is regulated, that is whether this gene is developmentally controlled or induced by environmental conditions or activated under both conditions.

D–32. RELPs and DNA Fingerprint from Human Hydatidiform Moles

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The chromosome constitution of complete hydatidiform moles (CHM) is known to be 46, XX with genetically 100% homozygosity, which is being derived by androgenetic mechanisms. The present study was undertaken to find a mechanism among three possible androgenetic derivations: 1) duplication of a haploid sperm after fertilization with anucleated egg, 2) fertilization of a diploid sperm due to nondisjunction at second meiotic division, 3) fertilization of two haploid sperm simultaneously. Our results obtained from RFLPs and DNA fingerprinting techniques showed that the genome of CHM is derived by duplication of a haploid sperm. This is in accord with the hypothesis proposed from the experimental results using cytogenetic banding techniques (Jacobs et al., 1978; Lawler et al., 1978, 1982, Vejerslev. et al., 1978) and polymorphic enzyme markers (Jacobs et al., 1980; Lawler et al., 1982; Vejerslev et al., 1987), and also using HLA typings &Yamashita et al., 1979; Coullins et al., 1985; Vejerslev et al., 1987).

D–33. Genetic characterization of OCT plasmid for crude-oil degradation
(원유분해 OCT plasmid의 유전자적 특성)

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Xanthomonas campestris M12나 Acinetobacter lwofii G1의 경우 OCT plasmid 위에만 C-C까지의 n-alkane을 분해하는 유전자가 있을음을 확인하였다. 또한 P. maltophilia N246 균주를 대상으로 검토한