

(312) Full Length cDNA Sequence of Pear (*Pyrus bretschneideri* Rehd.) S₂₉-RNase and S₂₉-Allele Identification

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Chinese white pear (*Pyrus bretschneideri* Rehd.) belongs to Rosaceae that exhibits characteristic gametophytic self-incompatibility. This type of self-incompatibility is controlled by S-locus which carries a series of multi-allelic alleles encoding S-RNases. To elucidate the function of S-allele and the possible molecular mechanism of gametophytic self-incompatibility in Chinese white pear, full length cDNA encoding S₂₉-RNase was cloned by rapid amplification of cDNA ends (RACE) approach from cultivars 'Mili' (S₁₉S₂₉) and 'Zaomi' (S₁₉S₂₉). The S₂₉-RNase gene contained an open reading frame of 684 nucleotides encoding 228 amino acid residues. S₂₉-RNase displayed typical sequence features of rosaceous S-RNases, i.e. five conserved regions (C1, C2, C3, RC4 and C5) and a hypervariable (HV) region. At the deduced amino acid level, S₂₉-RNase showed 30% to 92% similarities with other rosaceous S-RNases. Phylogenetic analysis revealed that rosaceous S-RNases occurred before divergence of species, but after divergence of subfamilies Maloideae and Amygdaloideae. Genomic PCR amplification with primer combination FTQQYQ and anti-(I/T)IWPNV followed by digestion with the restriction enzyme AccII allowed effectively distinguishing S₂₉-allele from other pear S-alleles.

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(313) Analysis of Seed-Expressed Sequence Tags in *Vernicia fordii*

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Tung-oil tree (*Vernicia fordii*) is one of the high-value industrial oil trees in China, whose seed has 52% to 64% oil-yields content. The tung oil is widely used in painting and chemical industry. Its principal

component is eleostearic acid (9,11,13-octadecatrienoic acid) that is a conjugated trienoic fatty acid. It is readily oxidized when exposed to air, which resulted in formation of the unique polymer. To isolate the genes related to tung oil synthesis and examine their expression patterns in *V. fordii*, we constructed a cDNA library using the developing seed tissues of *V. fordii* 'duiniantong' and picked out 3,107 clones randomly for sequencing on the 5'-end to construct the EST library. We then performed homology comparison with nucleic acid NR database. The results indicated that 2,205 cDNA sequences were highly homologous to these sequences of other plant species in database of NCBI. A total of 482 different genes had been identified preliminarily and 342 clones possibly represented genes with unknown function. The sequences related to tung oil synthesis had delta 12 oleic acid desaturase (FAD2), omega-3 fatty acid desaturase, 3-ketoacyl-CoA thiolase, beta-ketoacyl-ACP synthase I, enoyl-acyl-carrier-protein reductase, esterase/lipase/thioesterase family protein, polyunsaturated fatty acid synthase subunit B, enoyl-CoA hydratase/isomerase family protein, and etc. Seed storage protein had caleosin, oleosin, legumin, albumin, and etc. There are lots of ribosomal RNA and pollen allergen genes. Many sequences corresponded to transfer protein, gene expression, development regulation, resistance, growth substances and embryogenesis, and etc., while the sequences of 338 genes related to universal substances biochemical metabolism were expressed only once. The numbers and trends of expressed genes were at the phase of *V. fordii* seeds near to late embryogenesis. Establishing the EST library of *V. fordii* and researching the genes related to the tung oil synthesis have great significance to producing high-quality tung oil.

(314) SAD and FAD2 cDNA Genes Cloned from *Camellia oleifera* Abel

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Seeds of *Camellia oleifera* Abel produced high-quality edible oil, important cosmetic ingredients, and bio-fuel, such as poly unsaturated fatty acids (about 90%). Oleic acid transformed from saturated fatty acid in the process of grease biosynthesis catalyzed by stearyl-ACP desaturase (SAD), then transformed into linoleic acid and other poly unsaturated fatty acids catalyzed by fatty acid desaturase (FAD) family gradually. So the cloning SAD and FAD genes from *C. oleifera* are very important for revealing the lipids biosynthesis patterns and achieving molecular-aided breeding in *C. oleifera*. We constructed cDNA and EST libraries of *C. oleifera* and 3 copies of SAD gene and 3 copies of FAD gene were obtained from the EST library. One of three SAD EST clones was confirmed to be the full-length cDNA and named as *co-sad*, and 3 FAD2 EST clones were not full-length cDNA by BLAST with SAD and FAD genes from other plants via GenBank, DBJ and EMBL. Bioinformatics analysis showed that *co-sad* was 1579 bp in length and contained an 1188 bp open reading frame (ORF) encoding 396 amino acids. However, there was no obvious signal peptide and trans-membrane structure in the deduced protein sequence. BLAST results suggested that *co-sad* shared high homology with SAD genes