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Profile analysis of expressed sequence tags from citrus 'Shiranuhi' peel cDNA libraries

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Objectives

1. To construct the cDNA libraries of citrus 'Shiranuhi' fruit peels.
2. To understand the profile of gene expression in the fruit peel of citrus 'Shiranuhi' .

Materials and Methods

1. Gene source: Fruit peels of citrus 'Shiranuhi' [(*C. unshiu* Marc. × *C. sinensis* Osb.) × *C. reticulata* Bla.].
2. cDNA library construction: ZAP-cDNA synthesis and ZAP-cDNA Gigapack III Gold Cloning Kit.
3. EST analysis: Blastx in NCBI

Results and Discussion

Three cDNA libraries were constructed from different type of fruit peels of 'Shiranuhi'. One was generated from immature fruit peel and the other two from normal and abnormal peels of mature fruits. The 1373 clones from immature fruit peel, 2037 clones from normal peel and 2217 clones from abnormal peel of mature fruits were randomly selected and their partial sequences were determined. By the assembling sequences, the numbers of 1095, 1472 and 1692 unigenes were identified in the ESTs of immature fruit peel, normal and abnormal peels of mature fruits, respectively. According to the homology search with Blastx against NCBI database, 826 unigenes from immature fruit peel were homologous with known protein and also 2399 unigenes of mature fruit peels including 1110 from normal peel and 1289 from abnormal peel were matched to known protein. The other unigenes had no homology with any peptide in GenBank. The most highly expressed genes of the immature fruit peel were germin-like proteins, peroxidase and chitinase precursors in the order. On the other hand, the most abundant gene of the mature fruit peels was metallothionein-like protein. Thiazole biosynthetic enzyme and late-embryogenesis protein were highly expressed only in normal peel and not in abnormal peel of mature fruit. The most abundant genes, germin-like proteins in immature and metallothionein-like protein in mature fruit peels were known to be responsible genes to biotic and abiotic stresses.

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