

**E232** Isolation and Characterization of Lipid Transfer Protein Gene and Its Relation to Environmental Changes

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Lipid transfer proteins (LTP) are small, basic or acid proteins that participate in membrane biogenesis and regulation of the intracellular fatty acid pools. A cDNA clone, nonspecific *LTP* encoding a lipid transfer protein was isolated from cDNA library prepared from mRNA of hot pepper (*Capsicum annuum* L.) pericarp. It had an open reading frame of 354 bp which encoded a polypeptide with a predicted molecular weight of 13.5 kD. Nucleotide sequence of *LTP* has 77-89% identity with the *LTP* cDNA of tomato, potato, and watermelon. Amino acid sequence analysis shows high identity with the known LTP proteins. It was specifically expressed in floral organs of hot pepper. We also studied on the relationship between environmental changes and LTP gene induction in the hot pepper plant.

**E233** A New  $\varphi, \psi$  Representation of Protein Tertiary Structure and Specific Location of Amino Acid Residues in Secondary Structure

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Protein tertiary structure is constructed from a variety of secondary structure units such as helices,  $\beta$ -strands, and  $\beta$ -turns. They are built up from secondary structure elements assigned to amino acid residues in protein sequences.  $\varphi, \psi$  Representation of three-dimensional structures of 125 globular proteins were depicted for analyzing conformational details in their secondary structures. They can be drawn in the form of two-dimensional diagram. It is powerful for precise comparison of the relationship of primary and tertiary structures of homologous proteins. This representation is useful in readily recognizing all the secondary structures and particular positions in secondary structures as one progresses along the chain. A combination of intersegments hydrogen bonds among  $\beta$ -strands was also shown in the diagram. Using both dihedral angles and hydrogen bond definitions, 225 type-I  $\alpha$ -turns were extracted from 125 analyzed proteins. The  $\alpha$ -turns extracted are built up from 5%(1125) of total amino acid residues(23286) found in the proteins. Single amino acid preferences for specific locations at type-I  $\alpha$ -turns are compared to those at type-I  $\beta$ -turns and the ends of helices, and similarity of these single amino acid preferences is demonstrated.