LETTER TO THE EDITOR

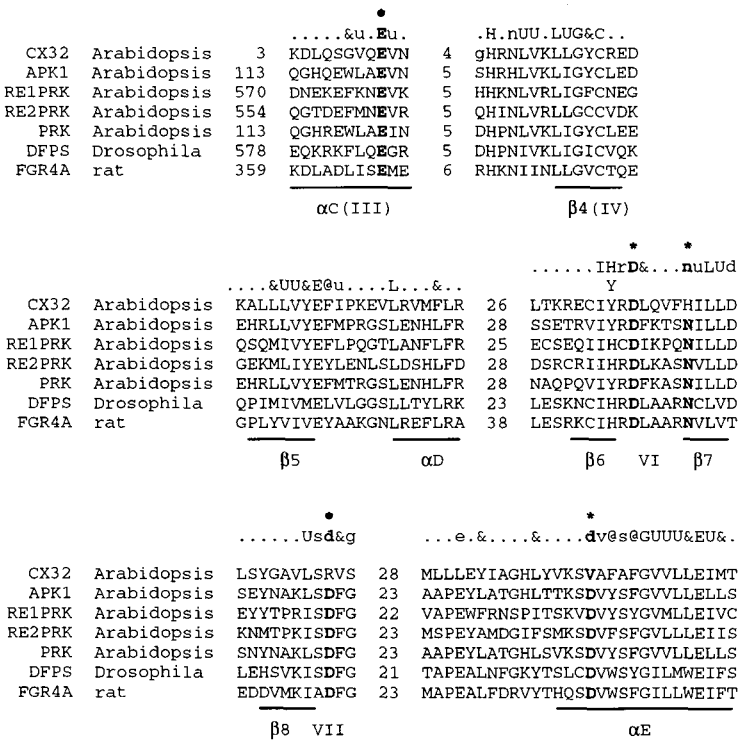

Figure 1. Multiple Alignment of the CX32 Protein Sequence with Selected Protein Kinase Sequences.

The alignment was generated using the MACAW program (Schuler et al., 1991). Only conserved blocks from the alignment are shown, with the distances between them and from the N-termini of the respective proteins indicated. The lower case g in the CX32 sequence indicates the position where one nucleotide was inserted to put the putative upstream conserved motif in frame. The consensus line shows amino acid residues conserved in all of the aligned sequences (shown in upper case) and in all sequences but one (shown in lower case). U indicates a bulky aliphatic residue (I, L, V, or M); @ indicates an aromatic residue (F, Y, or W); and & indicates a bulky aliphatic or aromatic residue. Asterisks indicate positions containing conserved amino acid residues in the majority of protein kinases that are directly implicated in catalysis (Taylor et al., 1992); in these positions, the residues conforming to the consensus are shown in bold type. Secondary structure elements derived from the crystal structure of the catalytic subunit of mouse cAMP-dependent protein kinase are indicated (after Taylor et al., 1992), as are motifs conserved in the protein kinase superfamily (Hanks et al., 1988). The data bases and accession numbers for the sequences are as follows: CX32, PIR accession number A39357; Arabidopsis protein tyrosine/serine/threonine kinase APK1, PIR S28615; putative Arabidopsis protein kinase PRK, GenBank L07248; two receptor-like protein kinases from Arabidopsis, RE1PRK and RE2PRK, GenBank M80238 and PIR S27754, respectively; Drosophila tyrosine kinase DFPS, SWISS-PROT P18106; and rat fibroblast growth factor receptor FGR4A, GenBank M91599.

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Reply

A number of research groups are now active in utilizing anti-connexin probes to localize and isolate plasmodesmata in an effort to characterize their polypeptide composition. These studies, in conjunction with reconstitution and functional assays, will clarify whether connexin-like epitopes in plant cell proteins are fortuitous or have functional significance for intercellular communication.

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