Introduction

Hybrid proline rich proteins (HyPRPs) create a subgroup of structural cell wall protein rich in proline (PRP). HyPRPs are composed of a hydrophobic N-terminal domain and two distinct domains: proline-rich domain and C-terminal domain. Repetition proline-rich domains are very variable in respect to the length and amino acid composition. Hydrophobic C-terminal domains have similar length and are characterized by characteristic pattern of eight cystein residues. Similar arrangement of cysteins is in sequences of structurally conserved non-specific lipid transfer proteins (ns-LTPs), whose structure has been described in detail. Four disulfide bridges created between eight cystein residues stabilize four (β)ββ−ββββ dimers. A hydrophobic pocket occurs inside this structure (Kader, 1987). Such disulfide bridges are important for stabilization of three-dimensional structure of proteins, the specific pattern of cysteines usually gives evidence of structural similarity (Josè-Estanyol and Puigdomènech, 2000).

Here we present analysis of all available sequences of HyPRPs from seven plant species and characterization of expression profiles of HyPRP genes in potato.

Methodology

Phylogenetic analysis of C-terminal domains of HyPRPs from seven plant species

HyPRPs create wide families in all studied plant species (approximately 10-30 members) with very variable proline rich domains.

Conclusions

Functional specialization of C-terminal domains was not confirmed

• Sequences of C-terminal domains developed most likely by random changes of amino acid residues limited by requirement of structure conservation. Proline-rich domains developed independently.

• Concurrent expression of HyPRP genes with all different types of proline-rich domains might be essential for structure or function of every vegetative potato organ.

• Sequences of LTPs and C-terminal domains of HyPRPs belong to separate branches of the phylogenetic tree, documenting different function of these proteins families.