4. CONCLUSIONS

- Ancestral HyPRP evolved probably from a lipid transfer protein (LTP) relative that had acquired a sequence encoding a long proline-rich N-terminal domain. The origin of HyPRPs may be one of the evolutionary innovations of seed plants.

- Specific sequence is not probably important for formation of the functional 8 CM domain of HyPRPs with exception of eight conserved cysteine residues, which stabilize the tertiary structure of the domain.

- HyPRPs with long proline-rich N-terminal domains are relatively well-conserved and probably evolutionary more original. Proteins with atypical N-terminal domains (very short, glycine-rich) evolved apparently relatively recently and independently in different plant species possibly by means of shortening, loss or rearrangements of the ancestral longer proline-rich domains.

- Glycine-rich domains could originate from proline-rich ones by way of inversion in the coding sequence. This mechanism could have great impact in evolution of cell wall proteins in general, because they are often rich either in proline or glycine.

- N-terminal domains of angiosperm C-type HyPRPs remained relatively well conserved (long and hydrophobic), while the rest of angiosperm HyPRPs has been undergoing rapid and continuous diversification. However, in the gymnosperms the diversification took place predominantly within the C-type clade.

- The character and high-level variability of expression profiles of *HyPRP* genes from potato suggests that expression data for a single or few genes from the large family provide little useful information on the whole family of these proteins.
- C-type HyPRPs, which are more conserved and whose genes had broader expression patterns, are probably house-keeping proteins of this family.
- Expression patterns of several *HyPRP* genes from potato do not correlate with patterns of their *Arabidopsis* orthologues suggests that the knowledge gained by experiments in model plants need not be always applicable to other species.
- Variability of expression patterns in connection with diversity of HyPRP sequences suggests possible functional redundancy of HyPRPs and low degree of functional specialization of different proteins from this family.
- HyPRPs with any type of N-terminal domain are probably involved in cell wall expansion. The possible cause of the expansion might be enhancement of plasticity/loosening of the plant cell wall mediated by the 8 CM domains of HyPRPs.
- The missing phenotypic changes of transgenic potato plants with modified expression of *HyPRP* genes are most likely a consequence of complexity and plasticity of plant tissues and presumed functional redundancy of HyPRPs.