

Genome-wide identification and expression analysis of lectins during cell development in elongation in maize root

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Motivation and Aim: Lectin domains are a group of different structural units of proteins capable to specifically recognize carbohydrate structures. They are found in combination with a wide variety of protein domains and are involved in various physiological processes. Although some lectin motifs are very similar in plants, animals and bacteria, most often they are associated with different domains and perform completely different functions. Plant lectins are quite divergent and can be localized in various cell compartments suggesting the differences in their function. In plants, lectins are quite numerous. The large proportion of lectins are transmembrane proteins; their lectin domains are oriented outside of plasma membrane and together with lectins fully located in apoplast have direct access to the cell wall polysaccharides. Several proteins with lectin domains from specific family of proteins with lectin domain were reported to be the possible elements to monitor the cell wall state and to evolve signals that regulate organ development [1, 3]. However, an involvement of proteins with lectin domains in the process of cell elongation that involves extensive cell wall rearrangements has not received yet the adequate and systemic attention. A renowned model to study plant growth is maize (*Zea mays* L.) primary root that is characterized by the presence of consecutive zones that differ by cell sizes and relative rates of their increase [2].

Methods and Algorithms: We performed a genome-wide screening for maize genes that encode proteins with lectin domains. The domain organization of proteins encoded by identified genes was characterized and amino acid sequences were checked both for the presence of a signal peptide and transmembrane domain. The putative subcellular localization of proteins with lectin domains was predicted. We also performed the multiple alignment of protein sequences and build phylogenetic trees for eight families of maize proteins with lectin domains. Using transcriptomic data obtained earlier [2] for 5 zones of the apical part of the primary maize root (before the root hairs initiation) we tried to relate the expression of these genes to certain stages of root cell development and peculiarities of cell wall metabolism.

Results: Screening of the maize genome revealed 307 genes that encode members of 15 different families of proteins with lectin domains. The half of these genes encode lectin receptor-like kinases (RLK). The largest maize families of lectin domain-containing proteins are GNA and legume, which is typical for plants. All members of maize RLKs were predicted to be membrane-bound with a lectin domain faced to the extracellular space. In addition to transmembrane proteins there are members of jacalin-related lectin, galactose-binding, hevein, RicinB and EUL families that are predicted as cell wall proteins.

In total, 70 % of all identified genes for proteins with lectin domains were expressed in the analyzed zones of maize root. For most part, genes within the same family have

diverse expression patterns. Each zone has its own set of specifically upregulated genes for proteins with lectin domains, both cell-wall related and non-related. The expression of most genes raised at the active elongation and the start of cell maturation and differentiation. Homologues of some characterized proteins with lectin domains of other species were identified in maize genome.

Conclusion: For the first time we revealed the genes for proteins with lectin domains that are specifically upregulated at initiation of cell elongation, are important in the course of active elongation or late elongation, opening the door for further studies on the molecular mechanisms of lectin involvement in plant morphogenesis.

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References

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