P1.18

In silico modeling of an interaction network of genes involved in the cell cycle progression during root morphogenesis in mono- and dicotyledonous plants

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The objective of the presented study is to reach a more comprehensive understanding of the cell cycle genes involvement in the root system development in monocotyledonous and dicotyledonous plants. The vast majority of studies on the genetic control of root system development are carried mainly on the well-studied dicotyledonous model species, such as *Arabidopsis thaliana*. The current state of knowledge on mechanisms of regulation of analogous processes in monocots, which include cereals, remains incomplete. Applied research strategy is based on a comparative *in silico* analysis of the course of genetically conserved cell cycle regulatory pathways that are also involved in the morphogenesis of the root system. It will allow for the verification of the convergence of these processes within mono-and dicotyledonous plants. Conducted *in silico* analyses were aimed at the identification of a defined set of genes that possess an overlapping function in cell cycle regulation and root system development. The initial screening of core regulating factors consisted in a database mining process. Determined subset of core genes was afterwards subjected to analysis of intra- and interindividual interaction with a use of bioinformatics tools and characterized among the biological context based on the Gene Ontology (GO) annotation. Target genes expression profiles regarding spatial and temporal expression during plant growth and development were evaluated depending on databases derived repository. Gathered data served as an input data for the construction of a conceptual model of key factors interaction within differential cell cycle progression during root system development of mono- and dicotyledonous plants. This will allow for a comparison of the function and redundancy of analyzed regulatory pathways involved in the course of morphogenesis of the root system, which architecture significantly differs between the analyzed groups. The idea behind the proposed study is to create an interactive model of the regulation of plant root system morphogenesis occurring in the course of cell cycle progression. The analyses enabled the assessment of redundancy and existing homology within processes of morphogenesis in plants root of mono- and dicotyledonous plants. Created model will provide a useful tool to support further detailed functional analysis of selected regulatory genes controlling investigated processes, with particular emphasis on the differences the advancement of the processes within mono- and dicotyledonous plants. Presented resources, can also be used in the selection of specific involved in the regulation of morphogenetic processes in the development of the root system of candidate genes for which the identification of new alleles would be highly desirable in breeding programs of cultivated plants.

P1.19

Enzymatic activity and arginase gene expression in *Arabidopsis* plants infected with a cyst-forming nematode

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The nematode *Heterodera schachtii* is a sedentary endoparasite of sugar beet and many Brassicaceous plants. Its second-stage juveniles penetrate host roots and induce permanent feeding site (a syncytium) being the sole source of nutrients for the developing nematode. Increased contents of many amino acids (including proline) in syncytia induced in *Arabidopsis thaliana* roots were found. Proline and polyamines are important for cell protection and repair processes. They are synthesized from ornithine, the product of arginase-catalyzed reaction. Arginase

(EC 3.5.3.1) is an important enzyme for nitrogen metabolism as it produces urea aside from ornithine. Recently, the role of arginase in plant defense has attracted attention, as the arginase gene expression is induced as a result of viral or microorganism infections, as well as after wounding. Because our experiments have shown an elevated activity of arginase in shoots of *A. thaliana* infected with *H. schachtii*, we studied arginase gene expression in syncytia, roots and shoots of the nematode-infected plants. Using semi-quantitative RT-PCR we showed the presence of arginase1 and arginase2 RNAs in shoots of *A. thaliana,* whereas only arginase 1 was expressed in roots. In plants collected on the third and seventh day after infection, expression of arginase1 both in roots and shoots was lower than in uninfected plants. Similarly, the arginase2 expression was strongly inhibited in shoots on the seventh day after nematode infection. However, fifteen days after infection, a higher expression of arginase1 was found in infected plants than in appropriate control shoots. Thus, we infer that cell wall damage and/or metabolic changes caused by invading nematodes influence the profile of arginase expression in *H. schachtii*-infected *Arabidopsis* plants.

P1.20

Molecular characterization and expression of a new calreticulin gene involved in pistil transmitting tract maturation and progamic phase in *Petunia hybrida*

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Calreticulin (CRT) is a highly conserved and ubiquitously expressed Ca^{2+}-binding protein in multicellular eukaryotes. In animals, CRT is involved in many different intra- and extracellular processes, such as Ca^{2+} storage and signaling, molecular chaperone activity in the endoplasmic reticulum (ER), regulation of gene expression, control of cell adhesion and migration, immune regulation, apoptosis, and pathogenesis. Plant CRT has the same molecular structure as the animal protein and shares its chaperone and Ca^{2+} binding activities. In higher plants, the CRT family consists of three members, which are classified into two distinct subclasses: CRT1/CRT2 (also designated CRT1a/CRT1b) and CRT3. Sequence homology of plant CRTs suggests that CRT1 and CRT2 are similar to each other, whereas the plant-specific *CRT3* genes are more highly conserved across species. *CRT's* expression pattern suggests that it could play a role in regulation of Ca^{2+} homeostasis during pollen-pistil interactions and thus contribute to successful fertilization. To address this possibility, we cloned and characterized the full-length cDNA of a new *CRT* gene (*PhCRT*) from *Petunia*. The deduced amino-acid sequence of *Ph*CRT shares homology with other known plant CRTs, and phylogenetic analysis indicates that the *PhCRT* cDNA clone belongs to the CRT1/CRT2 subclass. Northern blot analysis was used to assess *PhCRT* gene expression in different parts of the pistil before pollination and during subsequent stages of the progamic phase. The highest level of *PhCRT* mRNA was detected in the stigma-style part of the unpollinated pistil one day before anthesis and during the early stage of the progamic phase, when pollen is germinated and tubes outgrow on the stigma. In the ovary, *PhCRT* mRNA was most abundant after pollination and reached maximum at the late stage of the progamic phase, when pollen tubes grow into the ovules. From these results, we suggest that *PhCRT* is expressed during multiple steps of plant reproduction: pistil transmitting tract maturation, pollen germination and tube outgrowth, and pollen tube growth into the ovule. We speculate that CRT's molecular chaperone and Ca^{2+}-buffering activities facilitate these processes, which require high rates of protein synthesis and careful regulation of Ca^{2+} homeostasis. This project was supported by the Ministry of Science and Higher Education in Poland, grant N303 023 32/1034 (to ML) and founds provided by Nicolaus Copernicus University for the research program of the Laboratory of Developmental Biology.