

Induction of endogenous mechanisms contributes to engineering metal accumulation and tolerance

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Metal-homeostasis genes are expressed in plants to modify metal uptake, accumulation and tolerance for phytoremediation and biofortification purposes. However, the phenotype generated in transgenic plants has often been far from expected. In addition, the expression of a transgene failed to yield one set pattern of metal/s accumulation/distribution in plant organs at varying medium composition. Our study performed on wild-type and transgenic tobacco and tomato expressing various Zn and Cd transporters (including *HMA4* from *Arabidopsis thaliana* and *Arabidopsis halleri*) indicates that expression of the introduced gene deregulates a metal/s balance in a host plant and changes metal status at a cellular/tissue/organ level. To counteract, endogenous metal homeostasis mechanisms are activated which contribute to generation of characteristic features of transgenic plants. To understand underlying molecular mechanisms, comparative analysis was performed at the organ level with the use of microarray and Suppression Subtractive Hybridization (SSH), and at the tissue level applying Laser Capture Microdissection (LCM) followed by microarray and Real Time-qPCR analysis. These studies were accompanied by physiological and biochemical analysis. Key genes involved in the regulation of the phenomenon of Zn/Cd supply-dependent of Zn/Cd root/shoot partitioning in wild-type plants, and in modifications resulting from expression of *HMA4* have been identified. Modification of the expression level of endogenous metal-homeostasis genes in transgenic plants were highly tissue-specific (in examined roots and leaves) and involved ethylene pathway and ethylene-dependent metal transport genes. Thus, secondary effects induced by a transgene expression are an integral part of the mechanism involved in engineering of metal-related desired traits in plants.

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Metabolomic approach to resistance of Avena species to *Fusarium* head blight (FHB)Igor G Loskutov^{1,2}¹N I Vavilov Institute of Plant Genetic Resources, Russia²St-Petersburg State University, Russia

Creation of new agricultural crop cultivars possessing a complex of important traits, high yielding ability and product quality under different environmental conditions requires the well-studied initial material. A potentially high grain yield of agricultural crops should be combined with other economically important traits and resistance to biotic and abiotic factors. Diseases not only suppress plants and reduce the size of grains and yields per unit area, but also deteriorate the yield quality through the accumulation of pathogens waste products. Mycotoxins decrease the cost and consumption properties of oat grain and adversely influence human and animal health. Complex field and laboratory evaluation of accessions of cultivated and wild species of *Avena* collection VIR showed these results. Infection of *Fusarium* fungi was detected in analyzed oat accessions. Average grain infestation ranged from 6.1 to 18.7%, the maximum value was 64.0%. The group of relatively resistant genotypes to *Fusarium* infection and to accumulation mycotoxins was found. The assessment of large genetic diversity of wild *Avena* species by using DNA testing was shown. These indicators were linked to each other and to grain infection with *Fusarium* head blight. Metabolomics spectra of seeds of wild and cultivated oat species were investigated. The kernels of wild and cultivated species displayed the highest values for protein, for oil and for other biochemical components. Content and composition of organic and fatty acids, amino acids, polyatomic alcohols and sugar were analyzed. Positive correlations have been found to reliably exist between the studied kernel metabolomics spectra, *Fusarium* head blight resistance and mycotoxins accumulation.

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