was identified from a human infection. Antifungal susceptibility tests of clinical isolates were carried out using disc diffusion and E-test methods. The detected antifungal susceptibility values were mostly within the value ranges determined previously for *A. flavus* isolates, although the *A. pseudotamarii* isolate proved to be more susceptible to amphotericin B than either *A. flavus* or *A. tamarii*. Aflatoxin producing abilities of the isolates were tested in YES culture media, and determined by HPLC analysis. Most of the examined *A. flavus* isolates carry the MAT1 mating-type gene.

Further investigations of the genetic variability of the *A. flavus* isolates by UP-PCR, microsatellite analysis and mating-type locus gene (MAT) analysis, and aflatoxin producing ability testing using an ELISA method are in progress.

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The role of glutathione transferases in the stress tolerance of different plant species

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Physiological processes involved in detoxification have important role in agriculture (and so in plant biology), because plants are exposed to disadvantageous environmental conditions. Abiotic stressors, e.g. xenobiotics, heavy metals presented in the soil, and drought are able to launch the production of toxic by-products of metabolic processes (such as lipid peroxides) and harmful amount of reactive oxygen species in stress-exposed plants, which can cause reduced growth and decreased yields.

Glutathione transferases (GSTs) are a divergent enzyme family with two major *in vivo* detoxification functions in plants: conjugating toxic compounds with a glutathione molecule, thereby making them less harmful and promoting their compartmentalisation to the vacuole, and the glutathione-dependent peroxidase activity, which plays a role in maintaining membrane integrity under stress conditions. To examine the role of GSTs in the abiotic stress tolerance of different plant species, we used two experimental set-up.

First, two inbred lines of the cereal model organism *Brachypodium distachyon,* Bd21 and Bd21-3 were grown hydroponically, and were exposed to osmotic stress treatment for modelling drought stress. We observed the effects of osmotic stress to growth parameters, water status, enzymatic responses, and gene expression pattern of the plants. As results, we concluded that root growth of the *Brachypodium* lines differed (Bd21 had increased root growth, while it was reduced in Bd21-3). The water homeostasis of the two line were similar: both showed isohydric strategy during our experiments. We observed higher guaiacol peroxidase and glutathione transferase activities in line Bd21, and all examined enzymes showed induced activities during the osmotic treatment. For quantitative real-time PCR, six GST genes were selected based on our previous studies on wheat cultivars, expression data published in literature, and promoter sequence analysis. In line Bd21 we observed the induction of a wider range of genes under the osmotic stress, which indicates the importance of the selected genes in the detoxification process, and also suggests (according to the other parameters) that line Bd21 may be more tolerant to the applied osmotic treatment. In addition, we may conclude that both lines are highly resistant, compared to cereals previously studied in our research, so using *Brachypodium* lines for experimental purposes may give important results for cereal breeding.

Our other experimental system was equipped to examine the detoxification processes of bred poplar clones. Poplars (*Populus spp.*) are widely cultivated plants for their rapid growth and high biomass, and are increasingly used in scientific research as model organism of trees, and for phytoremediation purposes. Stress adaptation processes against heavy metals and osmotic stress were examined on three outstanding biomass producer poplar lines. Cuttings were grown hydroponically, and treated by copper, zinc, and polyethylene-glycol. We described the water potential of plants, the malondialdehyde content of shoots and roots, enzyme activities (guaiacol peroxidase, glutathione peroxidase, and glutathione transferase activities), amount of reactive oxygen (total intracellular ROS, superoxid radical) and nitrogen species (nitrogen oxide, peroxynitrite). Furthermore, we quantified the induction of ten transcripts, which probable are fundamental parts of the poplars stress adaptation processes. Among these were four glutathione transferases, two ABC transporters, three metallothioneins, and a phytochelatine synthase. Our results shows, that all three poplar clones are efficient in stress adaptation, but this properties have different molecular backgrounds. *P. deltoides* clones B-229 and PE 19/66 showed slightly lower water potential during zinc and hyperosmotic treatment, and in all treatments, they have significantly lower glutathione transferase activities, than *P. x canadensis* clone M-1. By contrast, B-229 and PE 19/66 clones are more effective to induce the gene expression of various components of the detoxification process, such as the GSTs. Based on our research, *P. deltoides* clones may be well utilized for phytoremediation purposes on heavy metal contaminated sites with good water supply, but under osmotically inappropriate circumstances further research needed to understand acclimatization processes.

During our work, evidence was found for the important role of GSTs in the stress responses of *Brachypodium* and *Populus*.

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