Metabolic Response of *Lolium Perenne* to Drought Stress

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The XXI International Grassland Congress / VIII International Rangeland Congress took place in Hohhot, China from June 29 through July 5, 2008.

Proceedings edited by Organizing Committee of 2008 IGC/IRC Conference

Published by Guangdong People's Publishing House

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Key words: *Lolium perenne*, drought, metabolic profiling

Introduction Under the predicted climate change scenarios plant growth will be increasingly affected by drought stress. A better understanding of biochemical and physiological responses on drought stress is necessary to design grasses capable of withstanding these climate perturbations. Despite response to drought stress is a complex process of multigenic nature, little is known about the whole-system response of biochemical reactions. Metabolomics is a useful approach to reflect the dynamic response of such metabolic networks to environmental changes (Nikiforova et al., 2005). The aim of our work was to use metabolic profiling to get insight in the response of *Lolium perenne* on drought stress. As grasses are often infected with fungal endophytes, *Neotyphodium lolii/L. perenne* associations were involved in our study to elucidate endophyte-induced changes in the response to drought.

Material and methods Endophyte-infected (E+) and endophyte-free (E-) clones of two *L. perenne* genotypes were grown under sufficient water supply (control) and increasing levels of water deficit (stress) in a controlled environment (Hahn et al., 2008). Above-ground biomass was harvested after the water stress period (first harvest) and after a subsequent re-watering period (second harvest). Metabolic profiling using gas-chromatography mass spectrometry was performed for samples of the first and second harvest ($n=10$ for each combination of genotype x endophyte x water supply). In total, 243 metabolites representing both known and unknown compounds were analyzed. Results of ANOVAs for each metabolite were used for comparisons between control and stress as well as between E+ and E-. To investigate entire metabolite profiles an independent component analysis (ICA) was performed.

Results and discussion Considering metabolic profiles of the water stress period and the rewatering period, ICA reveals drought as the major differentiating factor at the end of the water stress period whereas the genotype has a higher impact after rewatering. ANOVAs show that almost all metabolites occur in significantly different quantities in the dry mass of control and drought stressed plants. Particularly large effects of drought stress were observed for mannitol, proline, pipecolic acid and oxalic acid for both genotypes investigated. However, the amount of xylose and 2-hydroxyadipic acid was influenced by drought stress in opposite direction, depending on genotype. Interestingly, these observed effects were influenced by endophyte infection for one of the tested genotypes, but not for the other one.

As recovery and regrowth after drought is a key problem for agricultural practice, metabolic response after rewatering was analyzed. In contrast to the first harvest, the genotype has a higher impact than drought. Furthermore, the effect of endophyte infection was increased and showed a strong interaction with the grass genotype.

Conclusion As expected, drought stress induced in *L. perenne* a remarkable effect on metabolites that are indicative for drought stress, e.g. proline. Furthermore, a global effect of drought on almost all investigated metabolites was detectable showing changes in metabolic profiles that were dependent on grass genotype. Metabolic response of grass plants under drought may be affected by endophyte infection. Rewatering induced a higher impact of the genotype than of the drought stress imposed to *L. perenne* plants before.

References

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