P-038: NMR-based metabolomic profiling reveals distinct metabolic recovery responses in shoots and roots of temporarily drought-stressed sugar beets

Rita Wedeking[1], Mickael Maucourt[2,3], Catherine Deborde[2,3], Annick Moing[2,3], Yves Gibon[2], Heiner E. Goldbach[4], Monika Wimmer[5]

[1]*Environmental Safety – Ecotoxicolgy, Bayer AG Crop Science Div., Monheim, Germany*
[2]*UMR1332 Biologie du Fruit et Pathologie, INRA, Université Bordeaux, France*
[3]*Plateforme Métabolome Bordeaux-MetaboHUB, IBVM, Villenave d'Ornon, France*
[4]*University of Bonn, Dpt. of Plant Nutrition, Bonn, Germany*
[5]*University of Hohenheim, Quality of Plant Products, Stuttgart, Germany*
E-mail: m.wimmer@uni-hohenheim.de

Drought stress is one of the major environmental factors responsible for yield and quality losses in sugar beet production. In view of a predicted increase in early season drought periods, the ability of the plants to recover from a stress event will become increasingly important for sustained yield.

The present study aimed at the identification and characterization of major metabolites of the primary metabolism to uncover leaf- and root-specific metabolic recovery of transiently drought-stressed sugar beets. We integrated a metabolomic strategy, non-targeted proton nuclear magnetic resonance spectroscopy (^{1}H NMR), targeted enzyme-based metabolite assays, and physiological measurements to identify crucial components of the metabolic response [1].

Sugar beet cultivar Pauletta was grown under controlled conditions at 24°C day / 18°C night, 75±10% relative humidity and a photoperiod of 16 h light (>250 µmol m^2 s^{-1}). When 4-5 leaves were visible, plants were subjected to drought for 13 days followed by gradual rewatering for 12 days. Control plants were kept well-watered throughout the experiment. At one to two-day intervals during drought and recovery, the youngest fully expanded leaf pair (YEL) and the root part 1.5 cm below the crown were harvested 2 h after the onset of the photoperiod. Materials were immediately frozen in liquid nitrogen, lyophilised and stored at -80°C until analysis.

Drought triggered changes in primary metabolism, especially increases in amino acid levels in both organs, accumulation of compatible solutes such as proline and glycine betaine in leaves, and of raffinose and glucose in roots. Upon rewatering, leaves and roots responded with different dynamics. While most metabolites returned to control levels within 5 days in leaves, amino acids recovered more slowly, but consistently in roots. Surprisingly, a second accumulation of amino acids and a strong increase in starch was observed after 8 days of recovery in leaves, while at the same time serine accumulated in roots. Both effects might indicate a stress imprint beneficial in upcoming drought events.

With respect to metabolism, drought and recovery are two distinct processes subject to different regulatory mechanisms actively driven by the plant. Organ specific metabolic recovery responses might be related to distinct functions and concomitant disparate stress levels in above- and belowground organs.

References

[1] WEDEKING, R., MAUCOURT, M., DEBORDE, C., MOING, A., GIBON, Y., GOLDBACH, H.E., and M.A. WIMMER, 2018: PLoS ONE, **13**, e0196102. doi: 10.1371/journal.pone.0196102.

Acknowledgments

We would like to thank Duyên Prodhomme (UMR1332 Biologie du Fruit et Pathologie, INRA, Bordeaux) and Katrin Kemmerling (INRES Plant Nutrition, University of Bonn) for their valuable contributions. This study was financially supported by INRA and MetaboHUB project (ANR-11-INBS-0010), as well as the German Federal Ministry of Education and Research (BMBF 0315529) and the European Union for regional development (EFRE z1011bc001a), and is part of CROPSENSe.net, the competence network for phenotyping research.