



Tuesday 12 September 2017 at 13:00 - 14:00

Meeting room 2, AU conference center, Fredrik Nielsens Vej 4 (Building 1421)

Dr Anna Malolepszy

Gregor Mendel Institute (GMI), Austrian Academy of Sciences, Vienna Biocentre (VBC)

Using association genetics to identify common and species-specific mechanisms of nitrate dependent root growth responses

Nitrogen availability is one of the most limiting factors for most organisms. While nitrogen gas is the most abundant constituent of the Earth's atmosphere, it isn't available as nitrogen source for most organisms, including plants. Legumes evolved the mechanisms to cope with a low level of nitrate by establishing the beneficial interaction with rhizobia bacteria, which ensure the fixation of atmospheric nitrogen to a plant-usable form. This unique adaptation strategy enables them to grow in the nitrate-limiting condition. The formation of nodulation pathway clearly impacted the nitrate homeostasis and signaling networks in legumes. We would like to understand how nitrate signaling and homeostasis were modified to accommodate the evolutionary distinct way of obtaining nitrate via nodules. To get insights into this adaptation we investigate the root plasticity of natural accessions of the model legumes Lotus japonicus and Medicago truncatula under low and high nitrate conditions with and without rhizobia inoculation. The root traits are quantified via an automated pipeline for high-throughput phenotyping (BRAT) and are then used to conduct genome wide association studies (GWAS). Using a comparative approach and analyzing GWAS data from Lotus japonicus, Medicago truncatula as well as Arabidopsis thaliana, we can determine whether genetic variation underlying root growth responses to nitrate abundance is located in the same or different sets of genes. Overall, using this multi-species comparison we aim to shed light on the molecular basis of the nitrate economy in different species.

