Root system architecture and rhizosphere microbiota of winter wheat: responses to dynamic and realistic air and soil warming profiles

Andong Shi (1,2), Robert Koller (1), Arnd Kuhn (1), Katharina Frindte (3), Christian Kuppe (1), Dagmar van Dusschoten (1), Daniel Pflugfelder (1), Claudia Knief (3), and Michelle Watt (1)

(1) Institute of Bio- and Geosciences (IBG-2), Plant Sciences, Forschungszentrum Jülich GmbH, 52425 Jülich, Germany, (2) Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, 100081 Beijing, China, (3) Institute of Crop Science and Resource Conservation (INRES) – Molecular Biology of the Rhizosphere, University of Bonn, 53115 Bonn, Germany

Abstract:
A large number of studies have been conducted to predict how plants are influenced by warmer temperatures. In a review of 76 such studies[1], we found considerable variation in the responses of shoot and root biomass to warming. Contrasting results may be attributed to the fact that most warming treatments were either above or below ground, and lacked the temporal dynamics of outdoor environments. To better understand the responses of plants to warmer temperatures, we are conducting a series of experiments using custom-made, temperature-controlled systems[2] that realistically mimic the diurnal fluctuations of temperatures of cropping systems. Winter wheat plants were exposed to air and topsoil temperatures profiles nearly-identical to those measured in situ in an agricultural field in North Rhine-Westphalia, Germany during the typical planting time between late fall and early winter. Winter wheat (Triticum aestivum cv.) was sown directly into pots with soil and grown to two fully-expanded leaves, experiencing temperatures of “today” (‘Control’ treatment) and “future” (‘Warming’ treatment, 5°C warmer) in air and soil conditions. To quantify root architecture responses, plants were repeatedly measured with Magnetic Resonance Imaging (MRI)[3]. At harvest, tightly-bound (TB) and loosely-bound (LB) rhizosphere microorganisms [4] of roots from surface (0-5 cm) and deeper (5-25 cm) soil layers were sampled for bacterial community composition and measured by 16S rRNA gene amplicon sequencing. When comparing treatments based on growing days, we found that shoot dry weight, leaf area and total root length were 4-, 6- and 5-fold lower in control conditions than warmer conditions. In contrast, when plants were compared at the same phenological stage (2 leaves), the cooler-treated control plants had 7% greater root penetration rate, greater maximum rooting depth, greater root length density depending on soil layer, and allocated a greater ratio of biomass to roots than shoots, than warmer-treated plants.

Bacterial community composition differed between LB and TB fractions: Acidobacteria was notably greater in the LB than TB fraction although relative abundance in both fractions (Proteobacteria>Actinobacteria>Bacteroidetes) was similar. Non-metric multidimensional scaling showed that warming influenced the bacterial community in the LB fraction, but not in the TB fraction that was tightly bound to the roots. We speculate that bacterial communities may be influenced by extent of binding within root and rhizosphere, with temperature modulating root system functions and root exudates. These are being tested with follow up experiments.