

EVOLUTION OF RHIZOSPHERE MICROBIAL COMMUNITIES' COMPOSITION AND ACTIVITY DURING PERENNIAL WHEAT CROPS CULTIVATION

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Cultivation of perennial grain cropping systems has been proposed as an innovative method to face climate changes and restore soil health. Indeed, growing perennial crops can reduce soil erosion, ensure more efficient use of nutrients and water due to a massive root system, and increase soil carbon sequestration, providing fundamental advantages for climate change mitigation/adaptation. Moreover, the permanent soil cover, reduced soil disturbance and the allocation of belowground carbon (C), in term of root exudates and root debris, support highly structured and complex food webs as well as stimulate microbial biomass and activity and shape microbial community composition over time. However, few studies monitored shifts of microbial communities under perennial grain crops cultivation for multiple years. In this study, we examined the evolution of rhizosphere microbial communities' composition and activity of four perennial wheat lines derived from different hybridization between common wheat cultivars and *Thinopyrum spp.* These four genotypes have been selected from a wider group of nine wheat x wheatgrass derivatives with a relatively high post-harvest regrowth capacity and for their higher nutritional and technological quality.

Rhizosphere microbial communities were evaluated on the first and fourth year of growth of the perennial wheat lines and compared with the rhizosphere microbial communities of an annual common wheat cultivar and the parental species *Thinopyrum intermedium*. In particular, we analyzed: i) the variations in biochemical activity of a broad range of hydrolytic enzymes, ii) the 16S rDNA and ITS based bacterial and fungal community composition in the rhizospheres by NGS techniques and iii) the variation in metabolites and lipids associated to the root system. In the first year of cultivation, the rhizosphere bacterial and fungal communities associated to perennial wheat lines were close to those of the annual common wheat cultivar, while after 4 years of cultivation, the microbial communities significantly evolved and were more similar to those of the parental species *Thinopyrum intermedium* which was present in the soil since 2011. No significant differences were detected among the four different perennial wheat lines in term of bacterial and fungal biodiversity. Untargeted GC-MS and LC-MS metabolomic analyses revealed a strong effect of the year in shaping the soil metabolites associated to the rhizosphere, while differences in soil enzymes between years and genotypes were less pronounced. Therefore, perenniality more than plant varieties influenced microbial community composition and activity. Our findings demonstrate that established perennial grain crops selected specific bacterial and fungal taxa, affecting also the physiological interaction between plant and soil.