

THE INFLUENCE OF DIFFERENT WHEAT GENOTYPES AND SPECIES ON RHIZOSPHERIC AND ENDOSPHERIC BACTERIAL COMMUNITIES

SHAHPARI A.*, CAMPANA M.*, BAFFONI L.*, DI GIOIA D.*, ALBERONI D.*,
DE VITA P.***, GADALETA A.***, TUBEROSA R.*, MACCAFERRI M.*, SALVI S.*

*) Department of Agriculture and Food Sciences (DISTAL) Alma Mater
Studiorum - University of Bologna, Viale Fanin 44, 40127 Bologna, Italy

**) Council for Agricultural Research and Economics, Research Centre for
Cereal and Industrial Crops, S.S. 673, Km 25,200, 71122 Foggia, Italy

***) Department of Agricultural and Environmental Science (DiSAAT),
University of Bari Aldo Moro, Via G. Amendola 165/A Bari 70126, Italy

wheat, microbiome, sustainable farming

The expansion of the world population and the ongoing climate change require urgent improvements in our agricultural systems, including the development of new agronomic tools and genetically improved cultivars. Plant-associated microbiomes are critical for plant health, crop yield and many agroecosystem processes, thus they are increasingly viewed as critical mediators towards more sustainable agricultural production systems. An important question is to assess to what extent different plant genotypes, environments and their interactions affect the bacterial communities and which is the role of bacteria in plant resilience to environmental/nutritional stresses. The aim herein is to unravel rhizobiota and endophytic bacterial colonization in diverse wheat genotypes using metagenomics and evaluation of different locations and wheat varietal effects on microbiota compositions. Hence, 30 highly diverse wheat genotypes belonging to six species (*Triticum aestivum*, *T. durum*, *T. dicoccoides*, *T. dicoccum*, *T. monococcum* and *triticales*) were grown in three biological replicates in two fields in northern and southern Italy that have different environments for wheat growth, in which the northern environment is typical of bread wheat production whilst the southern climate is a commonplace for durum wheat cultivation. Both fields followed by a minimum-tillage management, and a total of 800 samples (rhizospheric and bulk soil and endophytic tissue samples) were collected at two plant

developmental stages (first node and beginning of ripening). Genomic DNA from soil and root samples was analysed using 16S rRNA high-throughput amplicon sequencing (V3-V4 hypervariable regions) to explore bacterial communities using QIIME (v.2.9.1). Results will be presented including the comparison of rhizospheric and endospheric bacterial compositions in different taxonomic levels for different genotypes and locations in both first node and beginning of ripening developmental stages. Furthermore, the alpha diversity using Shannon, Simpson and chao1 indices will be reported. Moreover, the beta diversity will be presented and compared using bray-curtis, weighted and unweighted UniFrac dissimilarity matrices.

Acknowledgements: This research has been supported by the project “CerealMed”- Enhancing diversity in Mediterranean cereal farming systems, funded by PRIMA2019-Section 2 and by the H2020 FP7.