

Screening wheat microbiota isolates for mycotoxin control leads to the identification of potential new species.

Irene Valenti^{1,2}, Fatima Aqeel¹, Louis Carles², Florence Richard-Forget², Marco Saracchi¹, Daniela Bulgari¹, Andrea Kunova¹, Paolo Cortesi¹ and Matias Pasquali¹

¹ Department of Food, Environmental and Nutritional Sciences, University of Milan, Milan, Italy

² INRAE, MycSA, 33883, Villenave d'Ornon, France

The co-occurrence of different mycotoxins in the same cereal field is very common. Particularly, the combination deoxynivalenol (DON) – enniatin B (ENB) obtained a significant attention due to its potential synergistic effects on different biological systems [1]. The wheat microbiota may host microorganisms able to promote plant health contrasting pathogens and their secondary metabolites, like mycotoxins. This work aimed to screen strains isolated from wheat, to select new sustainable candidates able to contrast DON-ENB accumulation in grains.

Approximately 50 microorganisms, both bacteria and fungi, were isolated in selective media with the purpose of collecting the widest microbial diversity. The microorganisms were isolated from wheat spikes (i) affected by Fusarium head blight in experimental field sites and (ii) treated with DON and ENB in laboratory. Subsequently, genomic DNA was extracted and sequenced by Illumina NovaSeq X and only non-pathogens were retained for screening. Whole genomes were assembled using Galaxy platforms while Microscope or Helixer and EggNog Mapper, were used to annotate bacterial and fungal strains, respectively. Bacterial phylogenetic was based on whole-genome data by combining TYGS, PubMLST and ANI results. Fungal classification combined ANI with MLST analysis based on concatenated strain-specific nucleotide sequences.

This study revealed a total of 34 species, with different ecological roles, including pathogens (*Pantoea agglomerans*), novel potential plant-growth-promoting bacteria (*Kosakonia cowanii*), and saprophytic species like *Peniophora lycii* and *Trametes versicolor*. We identified both rare taxa (*Acrodontium* sp.) and ubiquitous genera (*Penicillium* spp.), and 3 new potential species belonging to the genera *Clavibacter*, *Achromobacter* and *Mortierella*. Considering the new species, genome completeness is estimated at 99.5% for bacteria (CheckM) and 96.5% for *Mortierella* (BUSCO). To fill the remaining gaps in the fungal genome, integration of long-read sequencing data is scheduled. Overall, these results highlight the complexity of plant microbiota and suggest the presence of still unexplored biodiversity, with potential implications for future research.

[1] Valenti, I., Tini, F., Sevarika, M., Agazzi, A., Beccari, G., Bellezza, I., Ederli, L., Grottelli, S., Pasquali, M., Romani, R., Saracchi, M., & Covarelli, L. (2023). Impact of Enniatin and Deoxynivalenol Co-Occurrence on Plant, Microbial, Insect, Animal and Human Systems: Current Knowledge and Future Perspectives. *Toxins*, 15(4), 271. <https://doi.org/10.3390/toxins15040271>