# NTERNATIONAL CONFERENCE

# **FROM SEED TO PASTA IV**

A Sustainable Durum Wheat Chain for Food Security and Healthy Lives

# The influence of different wheat genotypes and species on rhizospheric and endospheric bacterial communities

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# BACKGROUND

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. OBJECTIVE. The aim herein is to unravel rhizobiota and endophytic bacterial colonization in diverse wheat genotypes using amplicon sequencing and evaluation of different locations and wheat varietal effects on microbiota compositions.

Table 1. wheat accession of which 2 Bread Wheat (BW), 6 Wild Emmer Wheat (WEW), 6 Domesticated Emmer Wheat (DEW), 6 Durum Wheat Landraces (DWL), 6 Durum Wheat Cultivars (DWC), 2 monococcum and 2 triticale.

Genotype	Subspecies	Category	Country of Origin	Mega Environment
Mentana	aestivum	BW	ITALY	Southern_Europe
Bologna	aestivum	BW	ITALY	Southern_Europe
TDS 281	dicoccoides	WEW	TURKEY	Western_Asia
TDS 283	dicoccoides	WEW	TURKEY	Western_Asia
TDS 289	dicoccoides	WEW	LEBANON	Western_Asia
TDS 263	dicoccoides	WEW	LEBANON	Western_Asia
TDS 310	dicoccoides	WEW	SYRIA	Western_Asia
TDS 239	dicoccoides	WEW	LEBANON	Western_Asia
Molise Colli	dicoccum	DEW	ITALY	Southern_Europe
DIC UNIBO-008	dicoccum	DEW	ITALY	Southern_Europe
DIC UNIBO-22	dicoccum	DEW	UK	Northern_Europe
TDS 231	dicoccum	DEW	SYRIA	Western_Asia
DIC UNIBO 54	dicoccum	DEW	GERMANY	Western_Europe
DIC UNIBO 49	dicoccum	DEW	IRAN	Southern_Asia
Russello SG7	durum	DWL	ITALY	Southern_Europe
Kyperounda L28	durum	DWL	CYPRUS	Western_Asia
Menceki	durum	DWL	TURKEY	Western_Asia
Tetra-IPK 251	durum	DWL	ETHIOPIA	Eastern_Africa
EP 4	durum	DWL	ETHIOPIA	Eastern_Africa
Cappelli	durum	DWL	ITALY	Southern_Europe
Altar 84	durum	DWC	CIMMYT	Central_America
Simeto	durum	DWC	ITALY	Southern_Europe
Saragolla	durum	DWC	ITALY	Southern_Europe
Lloyd	durum	DWC	USA	Northern_America
Svevo	durum	DWC	ITALY	Southern_Europe
Monastir	durum	DWC	FRANCE	Southern_Europe
Monlis	monococcum	monococcum	ITALY	Southern_Europe
DV-92	monococcum	monococcum	ITALY	Southern_Europe
Quirinale	triticale	triticale	ITALY	Southern_Europe
Trica	triticale	triticale	ITALY	Southern_Europe

#### **PROJECT RATIONALE**

- In order to reach our aim, we: 1) selected a list of wheat genotypes belonging to different origins and mega environment; 2) identified two very different locations in Northern and Southern Italy (Fig. 1); 3) used amplicon sequencing and targeting V3-V4 regions for exploiting both rhizospheric and endospheric bacterial communities.
- Figure 2 shows the statistical schematic for downstream analysis for microbiome feature table as following: alpha/beta diversity (A/B), taxonomic composition (C), difference comparison (D), correlation analysis (E), network analysis (F), classification of machine learning (G), and phylogenetic tree (H).



Fig 2. Overviews of statistical and

microbiome feature table:

visualization

downstream

methods

analysis

for

for





Fig 1. The two sites of the experimental fields in Northern and Southern Italy

# **MATERIALS AND METHODS**

- 30 highly diverse wheat genotypes belonging to six species (Triticum aestivum, T. durum, T. dicoccoides, T. *dicoccum, T. monococcum* and *triticale*) (Table 1)
- Three biological replicates in two fields in northern and followed southern by a minimum-tillage Italy management.
- A total of 800 samples (rhizospheric soil and endophytic collected samples) were tissue at plant two developmental stages (Figure 3)
- Sequencing (V3-V4 hypervariable regions) of the samples were carried out on a NovaSeq 6000

Fig.3 a) Foggia field, b) Bologna field

### **SUMMARY AND CONCLUSIONS**

- The first and second sampling (soil/root) have been done in April and June 2021, respectively.
- The genomic DNA of 800 soil and root samples have been extracted in the spring of 2022 and they have sent for NGS. Analysis of results is in progress.

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