

GEMMA: EXPLORING MAIZE BIODIVERSITY AND MICROBIOME IN ITALIAN LOCAL VARIETIES AS STRATEGIC TOOLS TO FACE ABIOTIC AND BIOTIC STRESSES IN CLIMATE CHANGE

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Italian maize local varieties represent an interesting source of agrobiodiversity. Brought to Italy in the 16th century, they were adapted to different zones of cultivation and maintained by farmers as open pollinated populations. Their main features include capability of adaptation to different local environments, seed pigmentation and nutritional quality. So, local varieties are a valuable source of genetic diversity for addressing challenges such as climate change and soil degradation that threaten food security and agricultural sustainability.

In the GEMMA project (GEnotipi di Mais lombardo e MicrobiomA – Regione Lombardia), four Italian maize varieties, maintained at CREA Bergamo Genebank, including Spinato di Gandino (VA 1304), Rostrato Rosso di Rovetta (VA 1306), Nero Spinoso Valcamonica (VA 1269) and Fiorine di Clusone (VA 33) and the control line B73 have been characterized i) to highlight novel phenotypic and microbiological diversity and ii) to examine their involvement in agronomic traits as well as the plant response to abiotic (water deficiency) and biotic (toxinogenic fungi) stresses, useful tools in organic farming systems. Data related to plant development, productivity, and seed nutritional quality (NIRS) of the four GEMMA genotypes cultivated in four different locations and in three seasons, will be presented. Data

about the response of the four Italian maize varieties to *Fusarium verticillioides* field artificial inoculation (Kernel Inoculation Assay, KIA), in three locations and in two seasons, will be also presented. Differences between inoculated materials and water inoculated controls and variability in response to *Fusarium* inoculation among genotypes grown in different locations, were recorded. Additionally, the response of Italian varieties under study to drought, measured in controlled conditions by growing plants in soils taken from the experimental sites, will be described also considering soil chemical and biological differences.

To analyze the microbial diversity, both cultivation and NGS characterization of the embryo bacterial microbiota were carried out. 100 bacterial strains were isolated from the embryos, among which 12 showed high *F. verticillioides* growth inhibition in vitro, and 2 greatly reduced the infection also in vivo. The NGS characterization showed low diversity, with Enterobacteriaceae contributing more than 90% of the total bacterial reads in most genotype/field combinations.

The dataset produced by the GEMMA project will include correlations among genotypic, phenotypic and microbiota diversity, thus providing a comprehensive picture of a sample of maize accessions that will constitute a model for future studies and exploitation of crop biodiversity to face environmental challenges.

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