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EXPLORING THE BIODIVERSITY OF PLANT TRAITS AND MICROBIOME IN MAIZE LOCAL VARIETIES AS NOVEL TOOLS TO FACE ENVIRONMENTAL CHALLENGES

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The valorization of germplasm collections is a theme of considerable importance both in global and in local scales. Their intrinsic agrobiodiversity will contrast the progressive loss of species and accessions occurred in the last decades, beyond providing novel tools to enhance plant adaptability and resilience to environmental changes.

In this context, Italian maize local varieties represent an interesting source. Brought to Italy in the 16th century, they were adapted to climatic zones of cultivation and maintained by farmers as open pollinated populations, are now preserved in *ex-situ* collections. The capability of adaptation to local environments is a distinct feature of these genotypes along with other interesting traits including seed pigmentation, endosperm texture and nutritional quality.

In the GEMMA project (GEnotipi di Mais lombardo e MicrobiomA: nuove prospettive per il controllo di funghi tossinogeni e l’adattamento ai cambiamenti climatici – Regione Lombardia), a set of varieties, maintained at CREA Bergamo Maize 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 in depth. Aim of the project is to highlight novel genetic and microbiological diversity involved in traits of agronomic importance as well as plant response to abiotic (water deficiency) and biotic

(toxinogenic fungi) stresses, useful tools in organic farming systems.

The five GEMMA genotypes have been cultivated in four locations and analyzed for their agronomic performance. Data related to plant development, productivity and seed nutritional quality (NIRS) will be presented. Differences in the response to *Fusarium verticillioides* infection, have been investigated in mature ears previously subjected to field experimental inoculations with a fungus suspension, and the response to drought has been measured in controlled conditions, by growing plants to the six-leaf stage in soils taken from the experimental sites.

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

Since including correlations among genotypic, phenotypic and microbiota diversity, the dataset produced by this project will constitute a comprehensive picture of a sample of maize accessions and provide a model for future studies and usage of crop biodiversity.