

GENETIC CHARACTERIZATION OF ITALIAN ZEA MAYS L. LANDRACES, ORIGINALLY CULTIVATED IN LAZIO REGION – MAREVAL

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In the framework of the Research Collaboration Agreement between CREA and ARSIAL, project MAREVAL - Recupero e caratterizzazione di varietà tradizionali di *Zea mays L.* originarie della regione Lazio - aims at performing a morpho-physiological and genetic characterization of maize Italian accessions originally cultivated in Lazio Region and belonging to a collection of genetic resources already surveyed by ARSIAL (Regional Law N.15/2000). In 2022, a set of 50 accessions of maize landraces from the Lazio Region chosen respectively i) by ARSIAL collection (38) and ii) by CREA Research Centre for Cereal and Industrial Crops in Bergamo maize germplasm collection (12), was selected for phenotypical characterization in field trial performed at CREA Experimental Station, Bergamo. The following plant morpho-physiological descriptors were recorded in the field: plant height, ear height, female and male flowering time. After manual harvesting, morphological descriptors were collected for ears and seeds. The chemical composition of grains, in terms of protein, lipid, starch, ash and fiber contents was evaluated through Near-Infrared Spectroscopy (NIRS). However, due to the unusual climatic condition observed during 2022 maize season, characterized by a long period of drought and extremely high temperatures, and because of a heavy presence of pests (eg. *Diabrotica virgifera virgifera*) in CREA Bergamo field trials, it was not possible to multiply all the accessions, which were sown again in

2023.

Molecular characterization was carried out on the same set of accessions cultivated during 2022 at CREA Bergamo Experimental Station. Samples were collected at young leaf stage - a single plant per genotype - for genomic DNA extraction and ddRAD (double digest Restriction Associated DNA) – sequencing, aiming at identifying the genetic structure of the accessions from ARSIAL and/or CREA, and their diversity at inter and intra varietal level. The bioinformatic analysis of sequencing data is in progress.