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HIGHLIGHTING ADAPTIVE POTENTIAL TO INCREASE SUSTAINABILITY OF MAIZE CROP THROUGH LANDSCAPE GENOMICS

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Modern agriculture's greatest challenge lies in climate change, as the latter has significant impacts on agricultural systems through global warming, altered rainfall patterns, and increased frequency and intensity of extreme events. Maize, as a globally significant crop, is projected to be highly susceptible to climate change across Europe. To establish a more effective cropping system and develop resilient genotypes, existing market hybrids are inadequate due to their limited genetic diversity. In contrast, maize landraces - adapted to diverse agroecological conditions - can offer invaluable indigenous germplasm as a promising foundation for future genetic enhancements.

The present research aims to achieve two objectives: a comprehensive study and genotyping of 28 Italian landraces, and the identification of genetic markers likely to be associated with environmental variables. Selected landraces from Lombardia, Emilia Romagna, Trentino-Alto Adige, Veneto, Toscana, Valle d'Aosta and Friuli Venezia Giulia were analysed using the GBS technique. Subsequent population studies were conducted based on the sequencing data, revealing 12 ancestral populations in the admixture analysis. Together with prominent and well-defined populations, including Nostrano Val Tidone, Châtillon and Entrebin, there are completely admixed groups comprising varieties from Trentino, Emilia Romagna, and Toscana, making it challenging to identify a singular reference population. The high degree of genetic fragmentation is reflected in the phylogenetic tree,

which does not follow regional patterns but clearly distinguishes individual varieties. Notably, the Ottofile Mantovano variety stands out as the most distinct from all others, aligning with its unique field phenotype. In the PCA analysis as well, individual populations exhibit clear differentiation, although specific varietal groups are not discernible. Subsequently, a comprehensive analysis was conducted to investigate local adaptation in relation to the environment, using climatic variables spanning a 30-year period (1970-2000). Preliminary findings have revealed the identification of SNPs that exhibit strong correlations with environmental factors, indicating the presence of valuable traits for potential genetic improvement.

In conclusion, the analyses are consistent and indicate the presence of significant intra-population variability in the germplasm under study. Additionally, this collection comprises unique populations derived from ancestral lineages that have not interbred with others. The presence of admixed materials aligns with historical cultivation practices prior to hybridization, where farmers would migrate and cultivate diverse maize varieties under territorial continuity, thus facilitating easier cross-pollination between distinct materials.