

GENETIC DIVERSITY WITHIN A COLLECTION OF ITALIAN MAIZE INBRED LINES: A RESOURCE FOR MAIZE GENOMICS AND BREEDING

MASTRANGELO A. M.*, **, HARTINGS H.***, LANZANOVA C.***, BALCONI C.***, LOCATELLI S.***, VALOTI P.***, PETRUZZINO G.*, PECCHIONI N.*, **

*) CREA-Centro di ricerca Cerealicoltura e Colture Industriali/Research Centre for Cereal and Industrial Crops SS 673 km 25,200 - 71122 Foggia, Italy

***) CREA-Centro di ricerca Cerealicoltura e Colture Industriali/Research Centre for Cereal and Industrial Crops Via Stezzano 24 - 24126 Bergamo, Italy

maize, germplasm collection, genetic diversity

Genetic diversity is of paramount importance to understand the architecture of loci controlling traits of agronomic importance, and core collections are an essential tool to dissect and analyse genetic diversity in crops. In particular, knowledge of genetic diversity in maize lines is a key information for breeders to decide which sources of diversity to integrate in their programs to achieve specific goals. Moreover, favourable alleles for traits of interest can be identified through association mapping in such collections. A panel of 384 lines, a subset of a larger collection preserved at CREA Bergamo Genebank, which includes inbred lines derived from traditional Italian maize varieties and advanced breeding ones (Elite Inbred Lines) was grown during 2018 in Bergamo and subject to extensive SNP search through the tGBS® Genotyping by Sequencing technology conducted with the restriction enzyme Bsp1286I (Freedom Markers). A set of 797,368 SNP sites was produced by the initial analysis. Following an imputation and filtering process based on the percentage of missing data, redundant markers and the frequency of the rarest allele, a final dataset of 15,872 SNP markers that were physically mapped was defined for further analyses. In particular, the inbred lines panel was characterized for linkage disequilibrium (LD), genetic diversity, population structure and genetic relationships. LD decay at genome wide level was evaluated and it was of 12.3 kb for r^2 0.1, indicating the collection as a valuable resource for genome wide association mapping. The pattern of LD was depending on the chromosomal regions and showed some variations across the ten maize chromosomes. The analysis of the population structure, carried out with ADMIXTURE, was performed on a set of non-redundant markers following a pruning with r^2 thresholds of 0.8 and 0.5, and showed that grouping statistics stabilized at K 4, with a certain differentiation between inbred lines derived from the same cultivar. In particular, a prevalence of the Nostrano dell'Isola and Isola Basso lines was observed in the groups 1 and 4, "Insubria" and "microsperma" lines were abundant in group 2, while the majority of elite and other lines derived from American breeding genepool were present in group 3. The genotypic information allowed us to characterise the panel for genetic diversity, in the whole panel and in the groups identified by the analysis of the population structure. Based on these data, the CREA Italian maize collection once genetically characterized represents an important tool for the identification and study of useful traits/alleles and for their use in maize breeding.