

POPULATION STRUCTURE, LINKAGE DISEQUILIBRIUM AND ASSOCIATION MAPPING FOR MORPHOLOGICAL TRAITS IN SUNFLOWER (*HELIANTHUS ANNUUS* L.)

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ABSTRACT

Sunflower is one of the most important oil crops worldwide. Agro-morphological traits are important for sunflower breeders in selection of genotypes with high performance and other traits. The objectives of this study were to determine the population structure and linkage disequilibrium among 106 dispersed sunflower genotypes and to identify the genomic regions associated with agro-morphological traits using the association mapping approach. High genetic variability was observed among the sunflower genotypes for the studied agro-morphological traits. In molecular experiments, the genetic variability among the genotypes was assessed by using simple sequence repeat (SSR, or microsatellite), inter-retrotransposon-amplified polymorphism (IRAP) and retrotransposon-microsatellite amplified polymorphism (REMAP) markers. In this study, 248 loci were detected using 28 IRAP and REMAP primers and also a total number of 67 alleles were detected using 30 SSR loci. The studied sunflower lines were divided into two subpopulations using IRAP+REMAP data and into five subpopulations using SSR data. By using a mixed linear model procedure, 224 loci showed significant association with quantitative trait loci (QTL) controlling the investigated traits. The identified and associated markers are expected to be useful in marker-aided selection in sunflower breeding programs

Key Words : Association Mapping, Linkage Disequilibrium, Microsatellite, Mixed Linear Model, Retrotransposon-Based Molecular Markers, Sunflower