

CHARACTERIZING HETEROSIS IN A SET OF RECOMBINANT INTERCROSSES (RIXS) DEVELOPED FROM A MULTIPARENTAL MAIZE POPULATION

NEUPANE S. P.*, STAGNATI L.***, CAPRONI L.*, BUSCONI M.***, BATTILANI P.***, LANUBILE A.***, MAROCCO A.***, DELL'ACQUA M.*, PÈ M. E.*

*) Institute of Life Sciences, Scuola Superiore Sant'Anna, Pisa, Italy

***) Dipartimento di Scienze delle Produzioni Vegetali Sostenibili, Università Cattolica del Sacro Cuore, via Emilia Parmense 84, 29122 Piacenza

heterosis, multiparental maize population, QTL mapping, agronomic traits, Fusarium Ear Rot resistance

The exploitation of heterosis is key in modern maize breeding to capture the superior performance of heterozygous genotypes. Here, we developed a recombinant intercross (RIX) population in maize by crossing pairs of multiparental MAGIC recombinant inbred lines (RILs) to evaluate the heterosis across mosaics of eight maize haplotypes. Field phenotyping was performed on 400 RIX genotypes considering 11 agronomic traits as well as the resistance to Fusarium Ear Rot (FER), caused by *Fusarium verticillioides* (Sacc.) Nirenberg, in 2018 and 2019 in Piacenza, northern Italy. Phenotypic data showed a broad range of diversity in production and phenology traits thanks to the high level of allelic diversity available in parental genomes. The heterotic response of agronomic traits was computed based on RIL values as mid parent heterosis (MPH) and best parent heterosis (BPH). Both heterosis measures showed different magnitudes for different traits, with higher level of heterosis in yield and lower in flowering time, suggesting effects from partial dominance to over-dominance. No correlation was observed between phenotypic performance and heterozygosity level of RIXs for most of the agronomic traits. A preliminary quantitative trait locus (QTL) mapping detected a number of significant associations with agronomic traits across all chromosomes. The RIX collection showed a moderate heritability of FER resistance, and QTL were associated to this trait as well. The allelic effect estimates by our mapping model indicated the presence of minor effect QTL with relatively small additive effects on disease resistance in both years. Our findings confirm the usefulness of

the RIX population to decipher heterotic loci in maize and support utilizing this resource in future to accelerate crop improvement.