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Poster Abstract – A.46

PRODUCTION AND FINE CHARACTERIZATION OF NEAR ISOGENIC LINES FOR HETEROTIC QTL IN MAIZE

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Although heterosis is largely exploited for crop improvement and breeding, its genetic basis is still poorly understood. Integrating biometrical and molecular marker approaches can produce useful information to elucidate the genetic basis of complex traits and, therefore, be particularly advantageous for studying heterosis. This approach was originally applied on materials developed from the maize single cross B73 x H99 in order to: (i) study the level of heterosis for traits of agronomic importance; (ii) detect the genetic effects involved (i.e., allelic and non-allelic interactions) by following procedures of both classical and neoclassical (i.e. QTL) genetic analyses; (iii) investigate the relationships between the level of molecular marker heterozygosity and the phenotypic performance; (iv) identify the genomic regions most involved in heterosis (i.e. showing overlaps among QTLs for the most heterotic traits). The mapping population is represented by 142 Recombinant Inbred Lines (RILs) genotyped for almost 200 molecular markers. Several QTLs for heterosis were identified, and both biometrical and QTL analyses indicated that heterosis was mainly due to overdominance and/or pseudo-overdominance, whereas epistasis was negligible.

Here we present the advancements of the subsequent introgression program aimed at the production of sets of Near Isogenic Lines (NIL) for a subset of selected QTLs for heterosis, carried out with the purpose of obtaining a more accurate estimate of their effects on hybrid vigor and eventually isolating the implicated genetic factors. Where possible, two sets of NIL were produced starting from different RILs. Our "short-cut" strategy adopted for NILs production and preliminary results of fine mapping for the selected QTL intervals are here described.