Oral Communication Abstract – S.02

HETEROSIS IN MAIZE: FROM OTL ANALYSIS TO DEVELOPMENT AND **EVALUATION OF NEAR ISOGENIC LINES FOR HETEROTIC QTL**

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Heterosis, i.e., the superiority of hybrids over parental lines, is sizable for allogamous species, especially maize (Zea mays L.). Heterosis has been extensively exploited but, despite a century of investigations, its genetic basis is not completely understood, yet. To gain information on its genetic control, we undertook a long term research in maize, aimed at providing a framework of comprehensive quantitative trait locus (QTL) phenotyping, to be integrated with map based cloning.

As a first step, we jointly applied classical genetic and QTL analysis in a set of recombinant inbred lines (RILs), derived from the heterotic single cross B73 x H99. RILs were crossed to the three testers B73, H99 and B73 x H99, following a North Carolina III (NCIII) mating design and testcrosses were evaluated, together with the RILs, in three environments. Level of heterosis for several agronomic traits and underlying genetic effects (allelic and non-allelic interactions) were estimated. Several QTL with heterotic effects on agronomic traits were detected and most of them were characterized by dominant or overdominant gene action, whereas non-allelic interaction proved to be of minor importance.

We then developed genetic materials suitable for validation and precise estimate of the effects of six heterotic QTL chosen for their appreciable additive and dominance effects. For this purpose, we adopted a residual heterozygous lines (RHL)-based introgression program to produce pairs of near-isogenic lines (NILs) homozygous either for one or the other parental inbred allele (i.e. B73 or H99) at the selected heterotic QTL regions. In addition, during the process of NILs production, we were able to preliminarily validate the phenotypic effects of two major QTL for heterosis, mapped on chromosome 3 (bin 05) and 4 (bin 10).

Once NILs were obtained, we then approached a study aimed at verifying and characterizing QTL heterotic effects. The six pairs of NILs were crossed with the two parental inbred lines B73 and H99. The 24 testcrosses are now being evaluated in a multi-year research conducted over several environments at low and high plant densities (4.5 and 9.0 plants m^{-2} , respectively). This investigation is warranted because, in several studies, the level of heterosis has proven to be particularly important in coping with environmental stress.

Results obtained in the first year of testing allowed us to confirm additive and dominance effects of heterotic QTL for traits that showed strong heterosis in our previous studies. From nonstress to stress condition, for yield per plant and other agronomic traits the contribution of additive effects declined, while that of dominance increased. These preliminary findings thus confirm the importance of heterosis in coping with stress and its possible role in enhancing crop sustainability.

The ultimate objective of QTL mapping is to identify the causal genes that underlie these QTL. Starting from F_1 hybrids obtained by crossing contrasting NILs, we produced large F_2

populations, each segregating only for one QTL region. We limited our attention to the introgressed QTL mapped on chromosome 4 (bin 10) and 10 (bin 03) because of their sizable effects on yield and other traits. F_2 populations were genotyped at markers flanking the segregating QTL, and F_3 families are now being produced by selfing informative recombinant F_2 individuals. The so obtained F_3 families will be evaluated for agronomic traits in order to fine map the heterotic QTL.