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**Poster Abstract - C.18**

# CO-LOCATION OF QTLs FOR SILENT GENETIC VARIATION AND FOR HETEROSIS IN MAIZE

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Heat-shock protein 90 (Hsp90) is an abundant cytosolic protein that contributes to homeostasis under physiological and stress conditions (Buchner, 1995). Studies conducted on *Drosophila* and *Arabidopsis* showed that the use of Hsp90 inhibitors, such as geldanamycin (GDA), can reveal silent genetic variation (Queitsch *et al*, 2002) involved in adaptation to peculiar environmental conditions. Moreover, Hsp90 proved to chaperone the signalling proteins that control plant growth and development. Therefore, it appears that manipulating Hsp90's buffering capacity offers a tool for harnessing cryptic genetic variation and for elucidating the interplay between genotype and environment in the determination of phenotype (Sangster *et al*., 2004).

It has been proposed that the silent variability can be involved in hybrid vigour. Since $F_1$ hybrids are generally characterized by higher stability than their parents, challenging Hsp90 in genotypes with different levels of heterozygosity could reveal hidden genetic buffers, thus providing useful clues on the genetic control of heterosis. The exploitation of heterosis has been considered one of the most revolutionary advancements in plant improvement, but its genetic basis is not yet completely understood. In a previous study (Frascaroli *et al.*, 2004), the genetic control of heterosis in maize (*Zea mays* L.) has been investigated combining both classical and molecular methods. That study allowed the identification of important QTLs determining heterosis.

The aim of this work was to identify QTLs controlling the response to chemical compounds inactivating Hsp90 and to verify their possible co-location with the QTLs controlling heterosis.

The plant material utilized in this work derived from a mapping population of 142 RILs of the cross B73 x H99 already characterized for more than 200 SSRs and AFLPs markers. Each RIL was crossed to both parental inbreds to obtain two pseudo-backcross (YBC) families per RIL. All YBC families were tested both in absence and in presence of the Hsp90 inhibitor (GDA). Seeds were sterilized and left overnight in a solution containing distilled water and DMSO (control) or DMSO plus GDA (treated). Soaked seeds were transferred to Petri dishes then incubated at 20 °C for 21 days. The response to the treatment was evaluated as difference between control and treated for shoot length, primary root length and quality of root development (as a score of root curling, twining and abnormal hair production).

QTL analysis was performed on YBC data, by adopting a model allowing the estimation of additive and dominance effects. Several QTLs were detected for reaction to GDA in all traits. Most of them (on chromosome 2, 3, 6, 8 and 10) co-located with major QTLs controlling heterosis found in our previous work for grain yield and other agronomic traits. These preliminary findings can stimulate interesting new hypotheses regarding the explanation of the biochemical basis of heterosis.