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## **Oral Communication Abstract – S.03**

## **HETEROSIS IN MAIZE: NEW TOOLS AND COMPLEXITIES**

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Heterosis is the phenomenon whereby the progeny of particular inbred lines have enhanced agronomic performance relative to both parents. Although several hypotheses have been proposed to explain this fundamental biological phenomenon, the responsible molecular mechanisms have not been determined. The maize inbred lines B73 and Mo17 produce a heterotic  $F_1$  hybrid that is being used as a model to study heterosis.

The regulation of gene expression levels in hybrid combinations can be studied via eQTL mapping, a combination of traditional QTL mapping and global expression profiling. The maize IBM population of recombinant inbred lines (RILs) was developed from a cross between the inbred lines B73 and Mo17. Each RIL is mosaic and homozygous for either the B73 or the Mo17 allele at each locus. A genetic map based on the IBM RILs containing over 9,000 markers (ISU\_IBM Map7) was used in conjunction with eQTL analyses to gain insight into the regulation and mechanisms related to heterosis. As a first step, 30 IBM RILs were crossed onto both B73 and Mo17. In combination with the RILs *per se*, the resulting cross-types provide a contrast of gene expression for the heterozygous genotype and both homozygous genotypes across all loci polymorphic between B73 and Mo17.

Four replications of each RIL, B73xRIL, and Mo17xRIL genotype were hybridized to a custom cDNA microarray using a loop design that included all pair-wise comparisons between each RIL and its crosses with B73 and Mo17. In each cross-type hundreds of significant associations were identified between genetic markers and gene expression levels. Although many of these eQTLs exhibit additive gene action, large numbers exhibit dominant gene action. Substantial numbers of the eQTLs act *in trans*.

Natural Antisense Transcripts (NATs) can regulate gene expression by virtue of their ability to form double-stranded RNA duplexes. Both sense and antisense transcripts accumulate to detectable levels for over 70% of a random set of maize genes. Significantly, these sense and antisense transcripts exhibit significantly different expression patterns between the B73 and Mo17 inbreds. To investigate the genetic mechanisms that regulate the accumulation of antisense transcripts, two replications of each of the 90 genotypes (30 RILs, 30 B73xRIL, and 30 Mo17xRIL) described above were hybridized to a custom, strand-specific, oligonucleotide microarray. Many eQTLs that regulate both the absolute levels of sense and antisense transcripts as well as those that regulate the *ratios* of complementary sense and antisense transcripts were identified. We hypothesize that the complex genetic interactions identified in this study contribute to heterosis.