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TRANSCRIPTIONAL HETEROSIS IN MAIZE

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The genetic and molecular mechanisms underlying heterosis are still unclear. Recent data suggest that regulation of gene expression might play an important role in determining hybrid vigor. As a contribution to uncover regulatory mechanisms possibly causing or being influenced by heterosis, here we present data on the transcription profiling in immature ears between inbred lines B73 and H99, and their corresponding F1 heterotic hybrid using cDNA microarray technology and Real Time PCR. Relative expression of 4,905 ESTs represented in triplicate on each slide, corresponding to about 1,900 maize genes, was investigated simultaneously on five replicated hybridizations per comparison. Relative variation of gene expression generally did not exceed a ± 1.5 -fold value. However, using appropriate statistical approaches, we were able to identify genes expressed at a significantly different level between both inbred lines and their hybrid and between inbreds. Both up and down regulated genes in inbred vs. hybrid were found, B73 vs. F1 comparison showing a higher number of differentially expressed genes than H99 vs. F1. No particular molecular functions were associated to significantly regulated ESTs between inbred lines and their heterotic hybrid, suggesting that a wide range of regulatory and metabolic pattern might be affected at the investigated stage of ear development. Regulatory hierarchies of expression levels for regulated genes were also estimated, allowing the establishment of a conceptual bridge between the molecular regulation events and the quantitative genetics models generally employed for illustrating heterosis. In fact, both dominance and over-dominance components were found affecting gene expression variation in the hybrid.

We discuss the possibility that the heterotic phenomena we observed at the molecular level might reflect the general mechanisms of hybrid vigor establishment in maize. Validation of microarray data by means of real time RT-PCR is also discussed.