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Expression Of *Bat-3* And Phosphate Stress Induced Genes In Maize And Sorghum

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Phosphate unavailability is a growth-limiting factor for plants in many natural ecosystems. To thrive under Pi limited conditions plants have developed efficient mechanisms of phosphate acquisition and utilization of absorbed phosphorus in plant tissue. In order to decipher molecular determinants which could have a potential role in phosphorus acquisition and utilization efficiency, further studies on expression profiles of some of the phosphate responsive genes identified through microarray analysis were done. The advent of DNA microarray technology has made possible the analysis of global patterns of gene expression and revealed unexpected networks of coordinated regulation (Lockhart et al., 1996). The evaluation of expression of thousands of genes by microarray analyses in parallel has become an important tool in functional genomics. Recently, Girke et al. (2000) have identified genes which are transcriptionally regulated by different concentrations of phosphate. In collaboration with Pioneer HiBred Co. we have conducted a microarray analysis of a subset of genes expressed in maize. The microarray chips used were referred to as metabolic chips and transcription factor chips. Analysis was done with RNA isolated from P+ and P- roots and cobs. A set of genes were selected for expression analysis and further characterization. Based on the results of RNA blot experiments, Bat-3 gene was selected for further maize and sorghum analyses described in this study.