

PATHWAY APPROACHES TO DISSECTING THE INHERITANCE
OF MAIZE (*ZEA MAYS* L.) SHOOT-BORNE ROOTS

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ABSTRACT

Shoot-borne roots are essential plant components. Two pathway-based approaches were pursued to increase our understanding of genetic mechanisms controlling shoot-borne root patterning. The first pathway approach characterized the contribution of gibberellic acid-related genes in shoot-borne root patterning. Quantitative trait loci mapping in the Intermated B73xMo17 linkage mapping population identified chromosome regions controlling shoot-borne root patterning which also contained gibberellic acid biosynthetic and response genes. Phenotyping of mutants with altered gibberellic acid production and response validated these genes as potentially underlying the identified quantitative trait loci. Association analysis was conducted in a set of 260 diverse maize inbred lines. The association analysis identified significant polymorphisms in the catalytic domain of the gibberellic acid biosynthetic gene *dwarf3* and in the promoter region of the gibberellic acid response regulator *Dwarf8*. These results confirmed the previous hypothesis that gibberellic acid production is involved in shoot-borne root patterning and expanded it to include DELLA-mediated gibberellic acid response. In the second pathway-based approach a multivariate phenotypic analysis was conducted on 25 diverse maize inbred lines that were phenotyped for 23 developmental traits along with three shoot-borne root traits to define novel hypotheses about pathways involved in shoot-borne root patterning. Evidence for a light-signaling component in root development was found. Further support for the involvement of light-signaling was provided by mutant phenotyping and field experiments which confirmed the predictions of the multivariate analysis. The two pathways were integrated into one model where light-mediated redistribution of gibberellic acid dictates shoot-borne root patterning.