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Influence of miRNA on brace root patterning in *Zea mays* L.

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Brace roots reduce lodging by providing support and represent the majority of the root system in adult plants. Previous quantitative trait locus mapping results showed that Teopod1 (Tp1), Teopod2 (Tp2), and Corngrass1 (Cg1), all mapped in chromosome regions which influence brace root patterning. Tp1 and Tp2 are semi-dominant mutants and Cg1 is a dominant mutant that result in delayed-phase-change and overlap between the juvenile and reproductive phases. Gibberellic acid (GA) promotes phase change and exogenous GA alters Tp1 and Tp2 phenotype. Prior analysis of GA mutants in our laboratory and others indicates that GA affects brace root patterning. We performed a means comparison between Tp1 and Tp2 and their wild-type siblings and identified significant differences in brace roots traits, specifically, mutants exhibited more nodes with brace roots and more brace roots at a node than their wild-type counterparts. Cg1 encode a member of the miR156 family which is known to target squamosa promoter-binding (SPB)-like proteins. Tp1 and Tp2 have also been suggested to encode members of the miR156 family. To further validate the role of miRNA156 in brace root patterning, we performed association analysis with available sequence from the parents of the nested association mapping (NAM) population and brace root trait data. Preliminary analysis supports the involvement of miRNA156 family members in brace root patterning. Additional sequencing of miRNA156 in a larger group of maize lines is underway to provide a more robust dataset for association analysis.