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Gypsy retrotransposon-derived maize IncRNA GARR2 modulates gibberellin response

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Abstract: Long non-coding RNAs (lncRNAs) mediate diverse biological events mainly through the modulation of transcriptional hierarchy. The phytohormone gibberellin (GA) is essential for various aspects of plant growth and development. However, the roles of lncRNAs in the regulation of the GA response remain largely unknown. Through sequencing multiple strand-specific and ribosomal-depleted RNA libraries, we delineated the landscape of lncRNAs in maize (Zea mays). Out of identified lncRNAs, 445 GIBBERELLIN-RESPONSIVE lncRNAs (GARRs) were differentially expressed upon GA application. By the intersection of GARRs from normal-height and dwarf plants from an advanced backcross population, four shared GARRs (GARR1 to GARR4) were identified. Out of these four shared GARRs, GARR2 was derived from a Gypsy LTR retrotransposon. GA-responsive element P-boxes were identified upstream of GARR2. GARR2-edited lines exhibited a GA-induced phenotype. Editing of GARR2 resulted in changes in the transcriptional abundance of GA pathway components and endogenous GA contents. Besides GA, GARR2 affected the primary auxin response. An RNA pull-down assay revealed the HECT ubiquitin—protein ligase family member ZmUPL1 as a potential interaction target of GARR2. GARR2 influenced the abundance of ZmUPL1 in the GA response. Our study uncovers lncRNA players involved in the modulation of the GA response and guides the development of plant height ideotype driven by knowledge of the phytohormone GA.

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