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KNOX LOST THE MEINOX: ALTERNATIVE SPLICING OF THE ARABIDOPSIS *KNAT1/BP* GENE PRODUCES AN ISOFORM THAT LACKS THE PROTEIN-PROTEIN INTERACTION DOMAIN

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Knotted1-like homeobox (KNOX1) transcription factors belong to the three amino acid loop extension (TALE) superclass of homeodomain proteins in higher plants and are essential for proper formation and maintenance of the shoot apical meristem (SAM). Within the TALE, KNOX proteins are closely related to myeloid ecotropic viral integration site (MEIS) proteins in humans, owing to a conserved N-terminus region. This domain, called MEINOX after KNOX and MEIS, defines this subclass of the TALE family. Protein-protein interactions with a second group of TALE proteins, the BEL-like homeodomain (BLH) family, modulates KNOX1 nuclear localization and target selection. These interactions depend on the KNOX MEINOX domain, and each homeodomain of the two proteins binds to target DNA as a protein heterodimer. Such regulatory interactions are reminiscent of those between different TALE proteins in animals, indicating that they might have an ancient origin.

KNOX1 transcription factors exert their role in maintaining indeterminate cell fate through the modification of multiple hormonal pathways to integrate developmental signals at the SAM. *KNOX1* transcription factors are also expressed in the stem where they regulate plant architecture and lignin deposition. Mutations in *KNAT1/BREVIPEDICELLUS* (*KNAT1/BP*), one of the four Arabidopsis *KNOX1* genes, result in plants with shorter internodes, downward pointing siliques, altered intra-bundle cell identity and altered lignin deposition. Recently, *KNATM*, a novel Arabidopsis *KNOX1* gene that encodes a MEINOX domain but lacks the homeodomain was identified and shown to regulate KNAT1/BP.

In this study, we identify and characterize a novel isoform of the KNAT1/BP transcription factor that arises from an event of alternative splicing and produces a novel protein (BPhox) that encodes a homeodomain but lacks the MEINOX domain. Expression patterns, intracellular localization, protein-protein interactions of this novel isoform have been characterized. Overexpression of the two isoforms under the control of constitutive/inducible promoters and complementation analyses were carried out to unravel the function of BPhox in plant development.