



Expression of *BELL* genes in symbiotic nodules of *Medicago truncatula* under drought stress

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Abstract

Drought is one of the main environmental stresses affecting plant growth. Transcription factors of the BEL1-like homeodomain (BELL/BLH) family are known to participate in plant development and stress responses. One of the developmental processes involving *BELL* genes is symbiotic nodule formation. The behavior of *BELL* genes in symbiotic nodules under drought conditions is still not well understood. In this study, we examined the expression patterns of *BELL* genes in *Medicago truncatula* roots and nodules under normal watering and drought stress conditions using publicly available transcriptomic data. Out of fourteen identified *BELL* genes, two genes *Medtr1g057790* and *Medtr1g023050* have demonstrated changes in their expression.

Introduction

Abiotic stress, particularly drought, is a major factor affecting plant growth and reducing economic value in agricultural systems. Transcription factors (TFs) are key molecular switches in stress signaling pathways, and the BEL1-like homeodomain (BELL/BLH) TFs, plays a critical role in mediating these responses (Chen et al., 2025). In legume plants, a critical biological process is the formation of symbiotic nitrogen-fixing nodules. It was shown that BELL transcription factors are involved in nodule initiation and development in legumes (Dolgikh et al., 2020). This study aims to elucidate the expression profiles of *BELL* genes within symbiotic nodules in response to drought stress using available transcriptomic data.

Materials and methods

The gene expression data for roots and nodules under well-watered and drought conditions (2 and 4 days of drought) were obtained from the *Medicago truncatula* gene expression atlas (INRAE/CNRS *Medicago* Expression Atlas). In this study, *Medicago truncatula* cv. Jemalong A17 plants were inoculated with *Sinorhizobium meliloti* strain Rm1021. RNA was extracted from two biological replicates, followed by sequencing. The resulting data were normalized and annotated, and differential gene expression was considered statistically significant at a false discovery rate (FDR) of less than 0.05.

Results and discussion

In *Medicago truncatula* 14 *BELL* genes were identified (Dolgikh et al., 2020). The expression levels of these *BELL* genes in response to drought stress were evaluated in roots and in nodules under varying drought conditions. Among the *BELL* genes examined, only *Medtr1g023050* and *Medtr1g057790* (*BELL1-3*) exhibited significant changes in expression levels under drought stress. The *BELL* gene *Medtr1g057790* are involved in nodule organogenesis, besides its expression is activated in response to the drought conditions. Furthermore, the expression of *BELL* gene *Medtr1g023050* appear to be predominantly stress-inducible whose activity is normally suppressed in the nodule but restored under extreme environmental pressure.

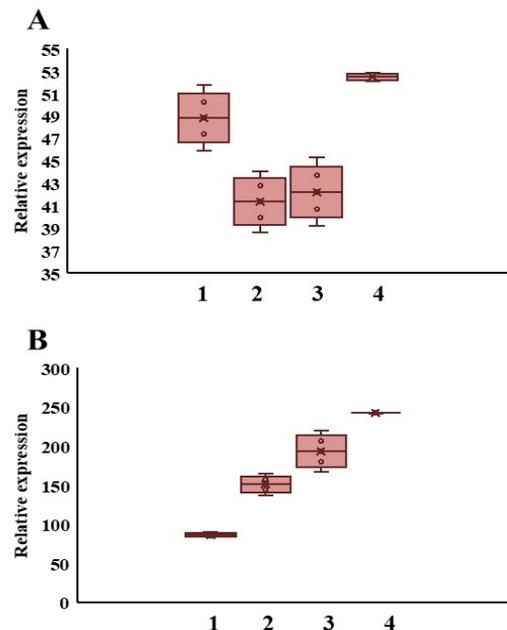


Figure 1- The relative expression of *Medtr1g023050*(A) and *Medtr1g057790*(B) in roots, in nodules in watered and water stopped conditions. 1: roots, 2: nodules in watered conditions, 3: nodules in water stopped conditions for two days, 4: nodules in water stopped conditions for four days.

References

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