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

**Mahboobeh Azarakhsh[1]***

[1] Cell and Molecular Biology Department, Faculty of Basic Sciences, Kosar University of Bojnord, Bojnord, Iran

## Abstract

*KNOX* (*KNOTTED-like homeobox*) genes play critical roles in plant growth and development. Recent studies have shown their involvement in stress responses, particularly under drought conditions. In this study we have investigated the expression of *KNOX* genes in *Medicago truncatula* under drought stress using transcriptomic data from Medicago Expression Atlas. The results showed that *KNOX2*, *KNOX5*, and *KNOX10* exhibited significant changes in their expression levels in response to drought stress.

## Introduction

*KNOX* (*KNOTTED-like homeobox*) genes are key transcription factors that regulate numerous developmental processes in plants. For example *SHOOTMERISTEMLESS (STM)* gene which belongs to KNOX subfamily is primarily involved in maintaining the shoot apical meristem (SAM). Moreover, *KNOX* genes are involved in symbiotic nodule development as demonstrated by the overexpression of *KNOX3* in *Medicago truncatula* which caused formation of spontaneous nodules in absence of bacteria (Azarakhsh et al., 2015). Beyond their well-established roles in growth and development, *KNOX* genes have recently been recognized for their involvement in plant responses to both biotic and abiotic stresses. In this study we have analyzed the expression of *KNOX* genes in *Medicago truncatula* symbiotic nodules in response to the drought conditions using available transcriptomic data (Rathour et al., 2022).

## Materials and methods

The data on gene expression in roots and nodules in normal watered and drought conditions (2 and 4 days drought conditions) were retrieved from available transcriptomic data from *Medicago truncatula* gene expression atlas (INRAE/CNRS Medicago Expression Atlas). In this experiment, *Medicago truncatula* cv. Jemalong A17 inoculated with *Sinorhizobium meliloti* strain Rm1021. RNA was extracted from two biological repeats. RNA samples were sequenced and the data were normalized and annotated. The results were considered as significant if FDR (false discovery rate) was less than 0.05.

## Results and discussion

In *Medicago truncatula* 10 *KNOX* genes were identified (*KNOX1-KNOX10*) (Azarakhsh et al., 2015). The expression levels of these *KNOX* genes in response to drought stress were evaluated in roots and in nodules under varying drought conditions. Among the *KNOX* genes examined, *KNOX5*, and *KNOX10* exhibited significant changes in expression levels under drought stress. the downregulation of *KNOX5* may reflect a resource-conservation strategy during stress. In contrast, the consistent upregulation of *KNOX10* under drought conditions points to a potential role in enhancing nodule resilience and maintaining essential symbiotic processes.

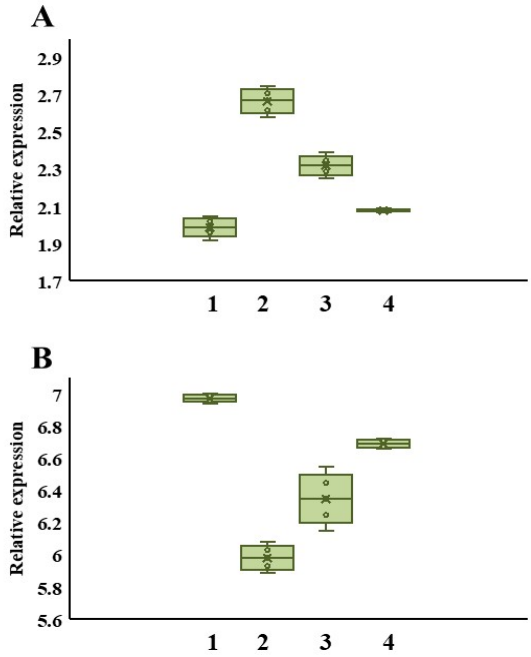


Figure 1- The relative expression of *KNOX5* (A) and *KNOX10* (B) in roots, in nodules in watered and water stopped conditions. 1: roots, 2: nodules in watered conditions, 3: nodules in water stopped conditions for two days, 4: nodules in water stopped conditions for four days.

## References

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