

Identification and Characterization of the WUSCHEL-related homeobox (WOX) Genes Family in *Passiflora organensis*.

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Abstract

In model plants, such as *Arabidopsis thaliana*, changes in floral morphology, as well as in plant architecture, depend on the behavior of the stem meristem (vegetative, inflorescence and floral), whose control is directly related to the expression of the WUSCHEL (WUS) gene belonging to the WUSCHEL-related homeobox (WOX) gene group. The sequencing of *Passiflora organensis* genome will allow the identification and analysis of key genes expression in the development of this genus plants. The present work intends to identify and characterize the members of the WOX gene family in *Passiflora*, with a focus on investigating the role of the WUS gene in *P. organensis* by analyzing the gene expression by qRT-PCR and *in situ* hybridization.

Key words:

Plant development, WOX genes, WUSCHEL

Introduction

The superfamily of homeotic gene is characterized by a sequence called homeobox. These transcription factors are intimately related to organism development. In *Arabidopsis thaliana*, 15 homeobox genes, named WUSCHEL-related homeobox (WOX), were identified and have a wide variety of roles during the plant development¹. The WUSCHEL (WUS) homeobox is a member of the WOX family gene and it is expressed in the organizing-center cells of the shoot apical meristem (SAM) and axillary meristem, and operates to regulate and guarantee the stem cell maintenance². WOX genes can be classified in three different clades: WUS, Intermediate and Ancient¹. Different from what is observed in *A. thaliana*, where the conversion of the SAM in meristem of inflorescence produces the floral meristem, the plants of the genus *Passiflora* have a more complex architecture. As most *Passiflora* species are perennial, inflorescence meristems, which in turn produce floral meristems, are produced by axillary meristems. In *Passiflora*, however, there is a complication, which is the simultaneous formation of a tendril³. In this way, it would be extremely interesting to investigate the role of WOX family genes, specially WUS, in the behavior of the meristems in *Passiflora*, mainly its pattern of expression during the development of axillary buds and tendril. Therefore, this work seeks to identify and investigate the role of WOX genes, with emphasis on WUS, in *P. organensis*.

Results and Discussion

Using the genomic sequence of *P. organensis* (unpublished data) obtained by our research group as source for the identification of orthologs WOX genes, comparing to published sequences of *A. thaliana* using the BLAST algorithm. We have found 19 WOX genes in *P. organensis*, which are distributed in three clades, as well as in *A. thaliana* (Image 1).

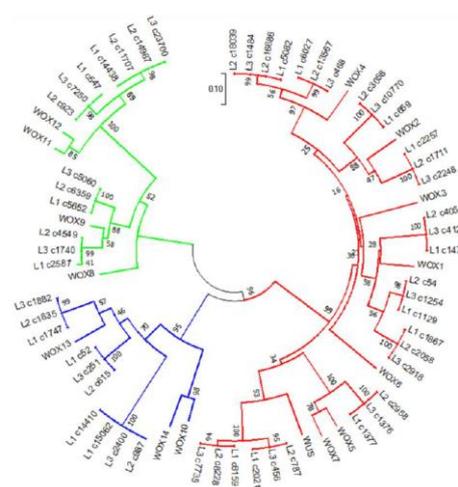


Image 1. Phylogenetic tree obtained by genomic sequence of *Passiflora organensis* and *A. thaliana* WOX sequences. L1, L2 and L3 represents three different individuals.

Conclusions

Were found 19 WOX genes in *P. organensis*, four more than what was described in *A. thaliana*. Further analyses of the gene expression by the use of qR-PCR and *in situ* hybridization will show us the validation of those genes.

Acknowledgement

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¹ van der Graaff, E.; Laux, T.; Rensing, S. A. *Genom Bio.* **2009**, 10: 248.

² Costanzo, E.; Trehin, C.; Vanderbusche, M. *Annals of Bot.* **2014**, 114: 1565 – 1553

³ Cutri, L.; Domelas, M. C.; *Comp. and Func. Genom.* **2012**, 2012: 510549