

## Identification of the TCP (Teosinte Branched1/Cycloidea/Proliferating Cell Factor) gene family in *Passiflora organensis*.

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### Abstract

Plant development is generally controlled by a balance between hormonal influences and the action of transcription factors. Knowing the expression pattern of key genes is essential for the understanding of plant development. The TCP gene family members are thought to be involved in key events of plant development. There are reports in the literature that variations in the expression patterns of TCP genes contributed to the emergence of evolutionary novelties such as zigomorphic flowers and tendrils. The genome of *Passiflora organensis* is completely sequenced and allows the identification and analysis of genes potentially involved in the control of the development of plants from the genus *Passiflora*.

### Key words:

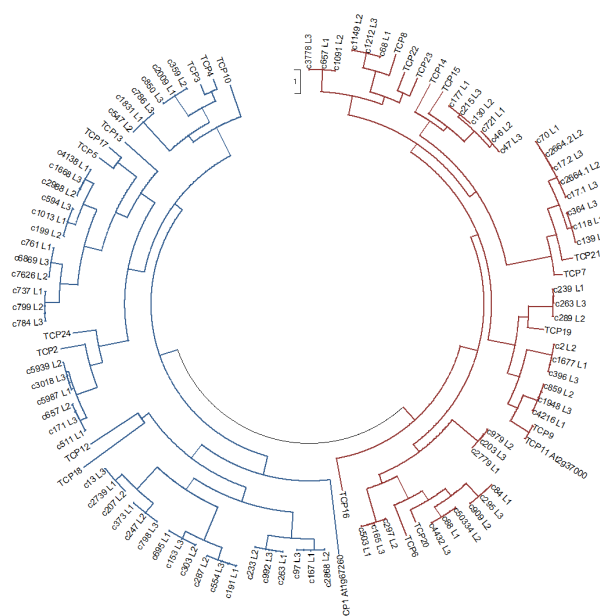
*Passiflora organensis*, TCP, Development.

### Introduction

The TCP gene family is responsible for encoding transcription factors that are tightly linked to processes of development of the plant body, such as the regulation of growth and differentiation in the meristems or in the formation of organ structures (1). Recently, it was found that members of this family are essential in the formation of tendrils (2; 3). In cucumber, studying the mutants in which the tendrils are absent, it was found that in a isogenic lineage carrying the ten (tendrillless) mutation affected a locus that encodes a member of the TCP family that is specifically expressed in tendrils (3). An almost simultaneous publication of another group (2) confirms the conservation of the expression of this ortholog in melon. In this case, the mutant lineage *ctl* (Chiba Tendril-Less) has no tendrils, while heterozygous plants for this mutation have intermediate structures between tendrils and lateral branches. Although the quantity and function of TCP family members in *Passiflora organensis* is unknown, the family comprises 24 members in *Arabidopsis thaliana* divided into two different classes. Thus, the objective of this work is to identify the TCP genes in *Passiflora organensis*.

### Results and Discussion

Our research group has the assembly sequence of genomic fragments of *P. organensis*, from three organisms, in the process of notation (unpublished data). These sequences served as a source for the identification of putative genes, by comparison with the known *Arabidopsis* sequences using the BLAST algorithm. In this process, 27 putative gene sequences were found. The amino acid sequences obtained were exported and aligned with the known sequences of *Arabidopsis*, making possible the construction of a phylogenetic tree (Image 1).



**Image 1.** Maximum likelihood phylogenetic tree from the amino acid sequences obtained in conjunction with the known *Arabidopsis* sequences. The genes starting with TCP in the name are genes from *Arabidopsis*, while the others were obtained from the genome of *Passiflora organensis*. The names are encoded as CxLy, where X represents the fragment in which the gene sequence was obtained and Y represents the organism.

### Conclusions

We found 27 putative genes belonging to the TCP family in *P. organensis*, in contrast to the 24 known genes in *Arabidopsis*. Future phases of the project are validation of gene expression via qRT-PCR and via *in situ* hybridization.

### Acknowledgement

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