



Transcriptome analysis of the vegetative desiccation tolerance plant *Tripogonella spicata* (Nees) P.M.Peterson & Romasch.

Carolina Vianna Morgante¹; Agnaldo Rodrigues de Melo Chaves¹; Ana Paula Zotta Mota², Saulo de Tarso Aidar¹

¹ **Embrapa Semiárido, Petrolina, PE, Brazil**

² **Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil**

Contact E-mail: Carolina.morgante@embrapa.br

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ABSTRACT:

Tripogonella spicata is a wild grass that is geographically distributed from South Texas to Patagonia desert. In Brazil, this species occurs in a savannah from northeastern semiarid region and in seasonally flooded regions of Pantanal. In this work, we have confirmed the vegetative desiccation tolerance of *T. spicata*, by exploring ecophysiological, biochemical, and molecular aspects of plants during dehydration–rehydration cycle. The results showed that *T. spicata* rapidly recovered physiological functionality after a period of extreme dehydration, being a homoiochlorophyllous plant, as the photosynthetic apparatus was preserved during desiccation process. The role of nonenzymatic mechanisms in the redox state control was evidenced by the accumulation of carotenoids in leaves, as a form of heat dissipation, and no increasing of classical antioxidant enzymes activities in dehydrated leaves. Additionally, we performed an Illumina RNA-Seq 2500 analysis of roots and leaves of mild-, severely dehydrated, and rehydrated plants. A genome-guided strategy was conducted, using the closest available genome of *Oropetium thomaeum* as a reference to reconstruct the transcriptome. From the 785 millions reads generated, 67.88 % were mapped in the reference genome. A total of 27,299 non-redundant contigs was obtained, with completeness of 85%. The overall expression profile revealed that most differentially expressed genes in dehydrated plants were downregulated, confirming the tendency to an anabiose state and a quick recovery of metabolic functions after rehydration. It is a valuable database for the search of drought tolerance genes to be used in crop breeding.

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