IV International Congress on APOMIXIS

December 3 - 7, 2023 • Rosario, Argentina

Book of Abstracts

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Expression atlas of Eragrostis curvula reproductive tissues

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Eragrostis curvula, commonly known as weeping lovegrass, is a perennial grass native to Southern Africa naturalized in semi-arid regions of Argentina. The species has garnered attention not only for its adaptive qualities but also for its significance as a model organism for the study of apomixis (diplospory). Within the context of diplosporous apomixis research our group has developed several genetic and epigenetic approaches aimed at elucidating this particular reproductive mode. In the last few years, small RNAs and mRNAs were sequenced covering reproductive tissues of genotypes with contrasting reproductive modes. Due to the small size of weeping lovegrass flowers and the specific requirements for RNA extraction, in our previous works we used whole spikelet tissue instead of pistils for transcriptomic studies. However, the use of whole spikelet carries certain inherent complications, such as the presence of male sexual processes and other non-target tissues. In this work, a protocol for the identification of female tissue in different reproductive stages as well as the steps to obtain high-quality RNA from pistils samples alone was developed in order to perform comparative transcriptomic studies. Three developmental stages have been chosen from two contrasting genotypes, a fully apomictic (Tanganyika, USDA) and a fully sexual (OTA-S, USDA): Stage 1: Megaspore mother cell (MMC, pre-apomeiotic/pre-meiotic), Stage 2: post-apomeiotic/post-meiotic and Stage 3: mature embryo sac. RNA from three biological replicates (three different plants from each genotype) was extracted using NucleoSpin RNA XS kit and successfully sequence with the Illumina platform (Novogene). As expected, PCA analysis showed that replicates and samples cluster according to the stages. Differential expression analyses showed distinctive gene expression patterns between the fully apomictic and fully sexual *E. curvula* genotypes across the stages 1, 2 and 3. A total of 4986 genes were exclusively expressed in the apomictic genotype, while 5452 genes were exclusive to the sexual one. The strategy used here enables us to capture the intricate interplay of genes throughout the reproductive processes of *E. curvula*. As a result, it elucidates the complex molecular panorama that governs the species reproductive biology, providing a deeper understanding of its mechanisms. Even more, samples from a facultative cultivar will be included to disclose the quantitative regulation of the trait. Finally, the assay will be completed adding post anthesis stages in order to characterize both, meiotic and parthenogenic regulation and disclose the apomictic mechanism in *E. curvula*.

Keywords: female tissue, diplospory, Eragrostis curvula.