Comparative genomics of an adaptive radiation using two ecologically divergent Tillandsia species (Bromeliaceae)

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T. fasciculata vs T. leiboldiana Radiation of subgenus Tillandsia The expansion of Tillandsia (pineapple family) from South America (SA) into CA species with key ecological Central America (CA) resulted in a significant diversification event (300 and morphological differences: species in CA, 30 in SA). This diversification is marked by repeated evolution of key innovation traits - Photosynthetic strategy (CAM (e.g. CAM / C3 photosynthesis) and strong underlying genome dynamics. vs C3) - Trichome layer (dense vs Geographic expansion of subgenus Tillandsia¹ sparse) Gene loss and duplication dynamics in Tillandsia - Tank formation (absent vs Tillandsia CA T. fasciculata 2-3 mya present) juncea T. leiboldiana Jenus T. trauneri Subgenus Tillandsia propagulifera SA Comparatively explore the T. fasciculata and T. leiboldiana to 6 mya T. adpressiflora better understand the sources of variation fuelling adaptive radiations, and the role of genome evolution in driving divergent Duplications / unit branch length Losses / unit branch length Rapidly evolving families / unit branch length adaptation in *Tillandsia*. Assembly strategy I. Assembly 2. Polishing 3. Hi-C scaffolding 4. Final polish 5. TE annotation 6. Gene annotation Using PacBio reads Remove haplotigs in In collaboration with Using short-read With EDTA Using BRAKER and Down-DovetailTM (33 - 38 x) case of high H Illumina data (50 x) MAKER₂ stream TE library assessed analyses with RepeatMasker Base/indel correction Infer scaffolds based Base/indel correction A. comosus gene CANU assembler with Arrow on proximity **BUSCO** assesment & BUSCO models & mRNAseq data as evidence Gene count per 1 MB windows % repetitve content per I MB windows The *T. leiboldiana* genome is 1.4 times larger than *T*. fasciculata, due to an expansion in repetitive content largely localized around centromeres. Chromosome size distribution is wider in T. leiboldiana 31,898 gene models 33,971 gene models 89.6 % BUSCO score 85.3 % BUSCO score than T. fasciculata, suggesting both expansions and 65.5 % masked content 77 % masked content reductions in chromosome size. However, this may also be due to higher repetitive content in T. leiboldiana leading to a more fragmented assembly (~ 10,000 scaffolds). Conclusions Synteny and orthology ~ 24,000 orthologs, of which 12,700 one-to-one T. fasciculata and T. leiboldiana, two ecologically divergent species of the One-to-many Many-to-one T. fas to T. lei 1084 7371 a genomic level. T. lei to T. fas 2330 5717

Overall, large syntenic blocks exist between both species.

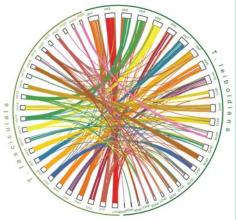
At the same time, rearrangements seem to have occurred (eg. Chr2 of T.fas).

Larger spacing between genes can be observed in T. leiboldiana compared to T. fasciculata, agreeing with its larger estimated repetitive content.

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Tillandsia radiation, vary substantially on

This genomic variation may have been a key source in driving the adaptive radiation of the subg. Tillandsia.

We will further elucidate this by studying differential gene expression and gene family evolution linked to key adaptive functions.

References

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