

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

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Radiation of subgenus *Tillandsia*

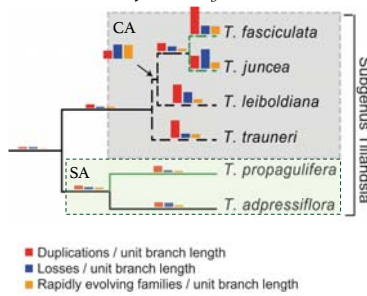
The expansion of *Tillandsia* (pineapple family) from South America (SA) into Central America (CA) resulted in a **significant diversification event** (300 species in CA, 30 in SA).

This diversification is marked by **repeated evolution of key innovation traits** (e.g. CAM / C₃ photosynthesis) and **strong underlying genome dynamics**.

Geographic expansion of subgenus *Tillandsia*



Gene loss and duplication dynamics in *Tillandsia*²



T. fasciculata vs *T. leiboldiana*

CA species with **key ecological and morphological differences**:

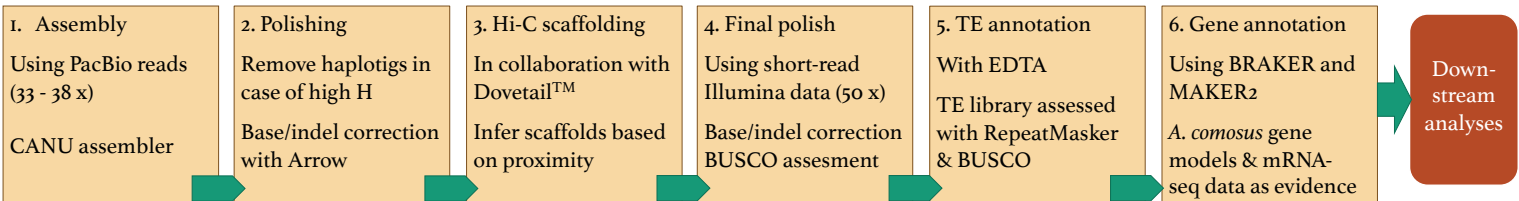
- Photosynthetic strategy (CAM vs C₃)
- Trichome layer (dense vs sparse)
- Tank formation (absent vs present)



Aims

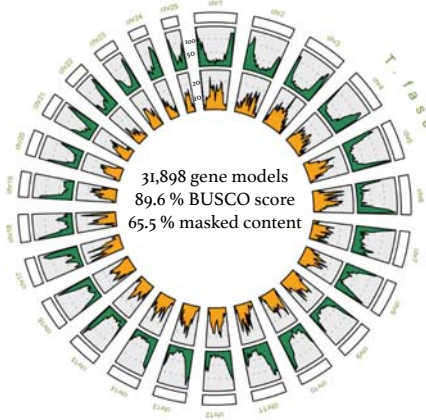
Comparatively explore the *T. fasciculata* and *T. leiboldiana* to better understand the **sources of variation** fuelling adaptive radiations, and the role of genome evolution in driving divergent adaptation in *Tillandsia*.

Assembly strategy



Genome overview

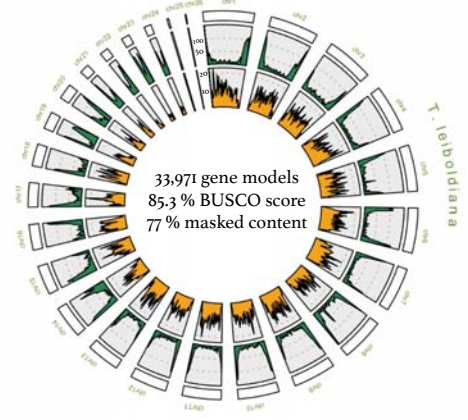
■ Gene count per 1 MB windows ■ % repetitive content per 1 MB windows



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* than *T. fasciculata*, suggesting both expansions and 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).



Synteny and orthology

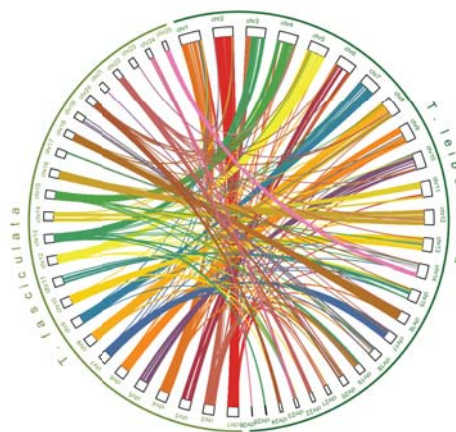
~ 24,000 orthologs, of which 12,700 one-to-one

	One-to-many	Many-to-one
T. fas to T. lei	1084	7371
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.



Conclusions

T. fasciculata and *T. leiboldiana*, two ecologically divergent species of the *Tillandsia* radiation, vary substantially on a **genomic level**.

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.