

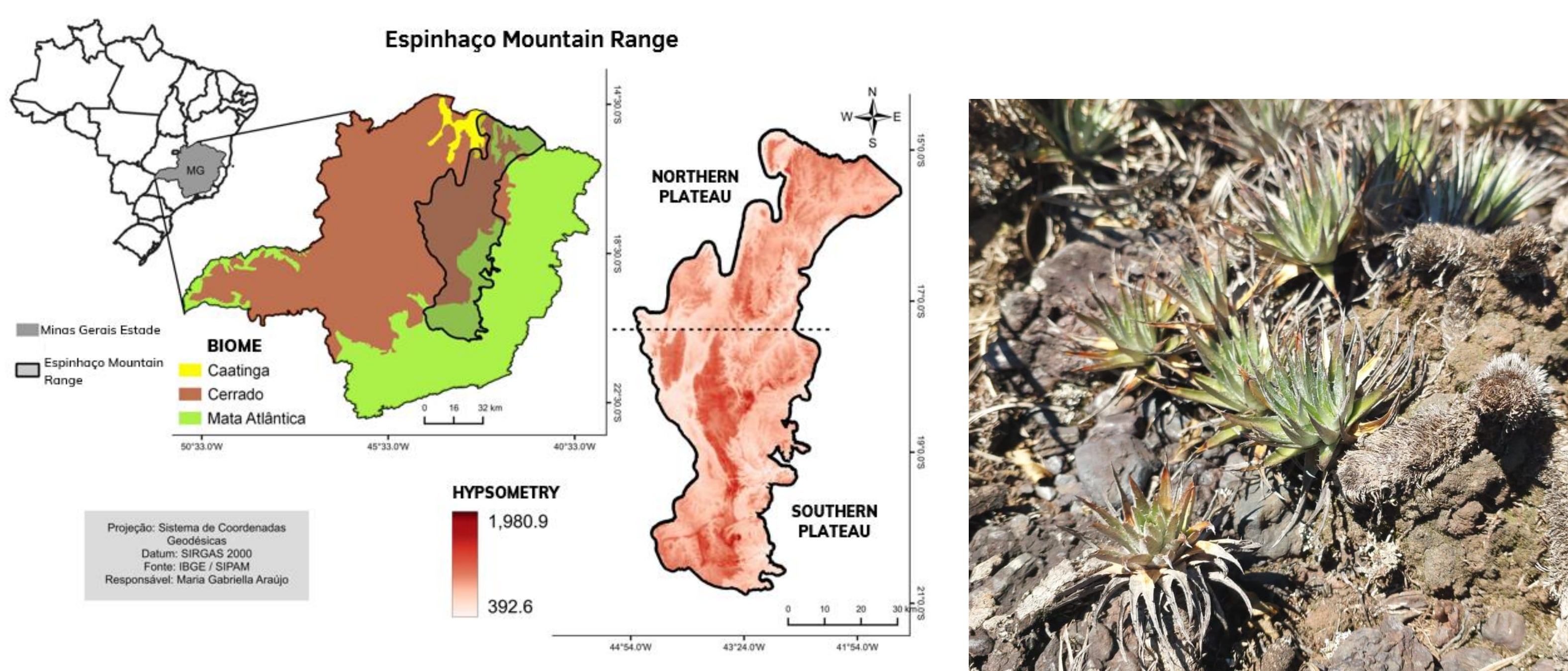
Phylogeny, structural patterns, and polymorphisms in *Dyckia* spp. from the Espinhaço Mountain range in Brazil, based on complete chloroplast genome

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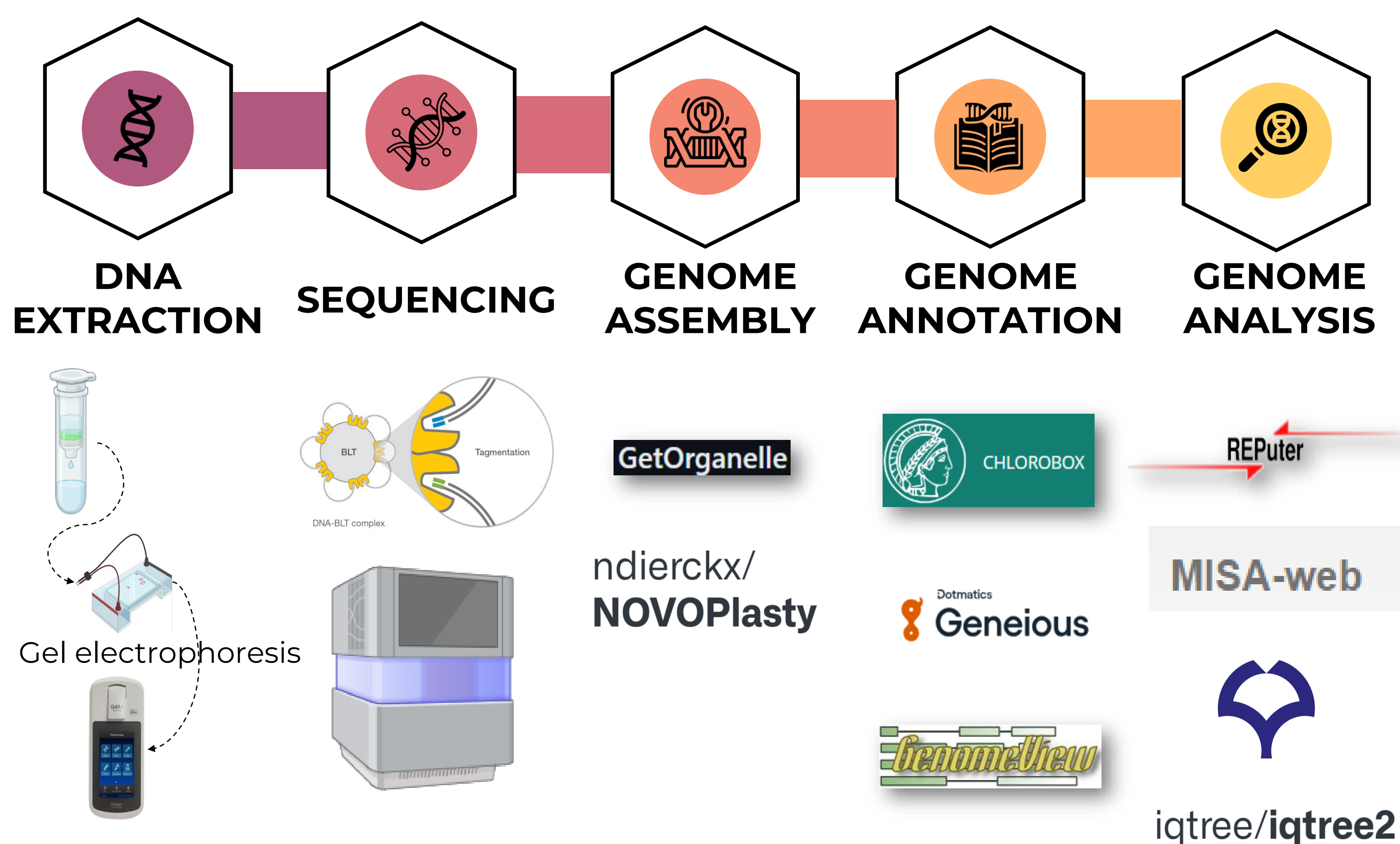
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INTRODUCTION

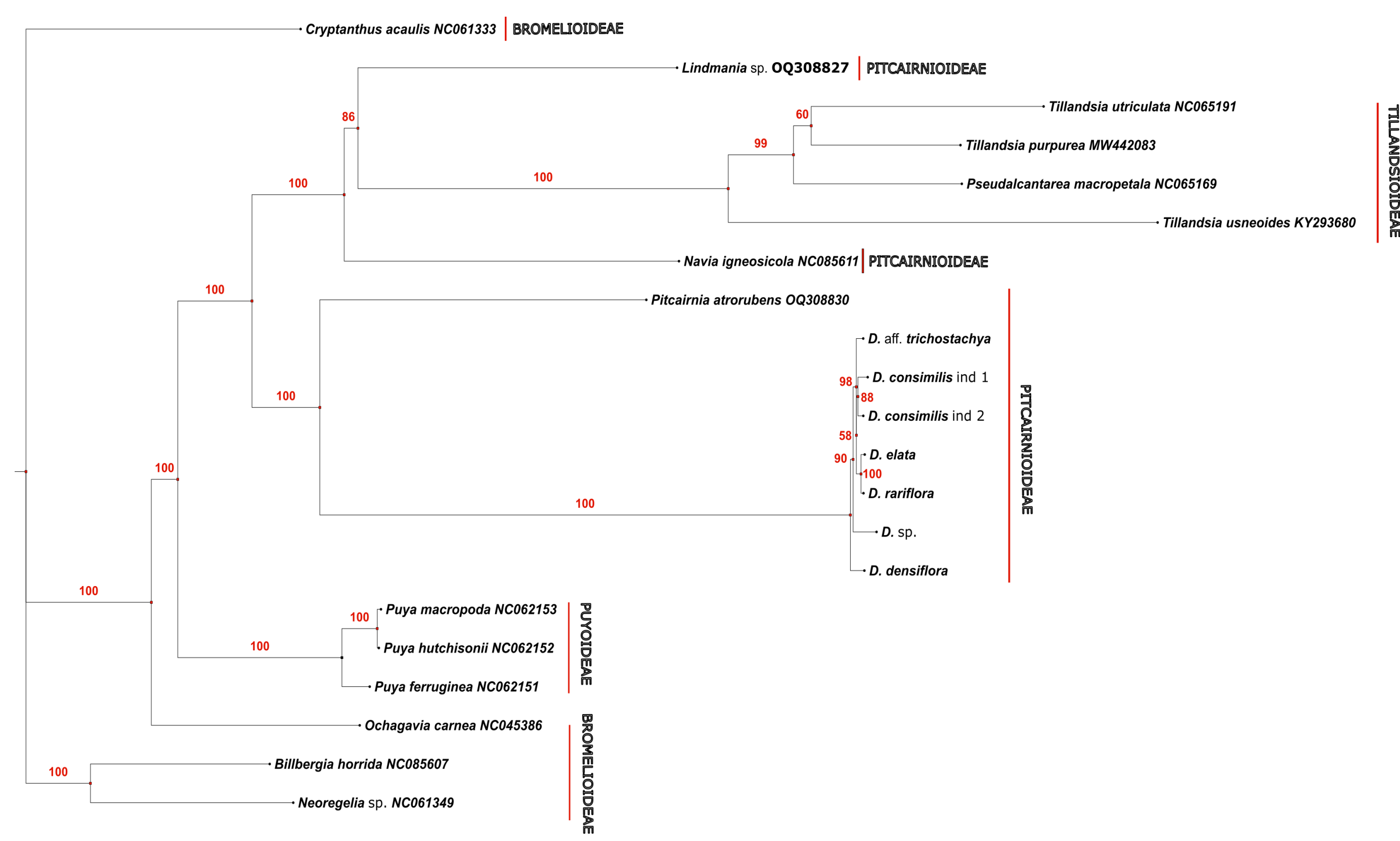
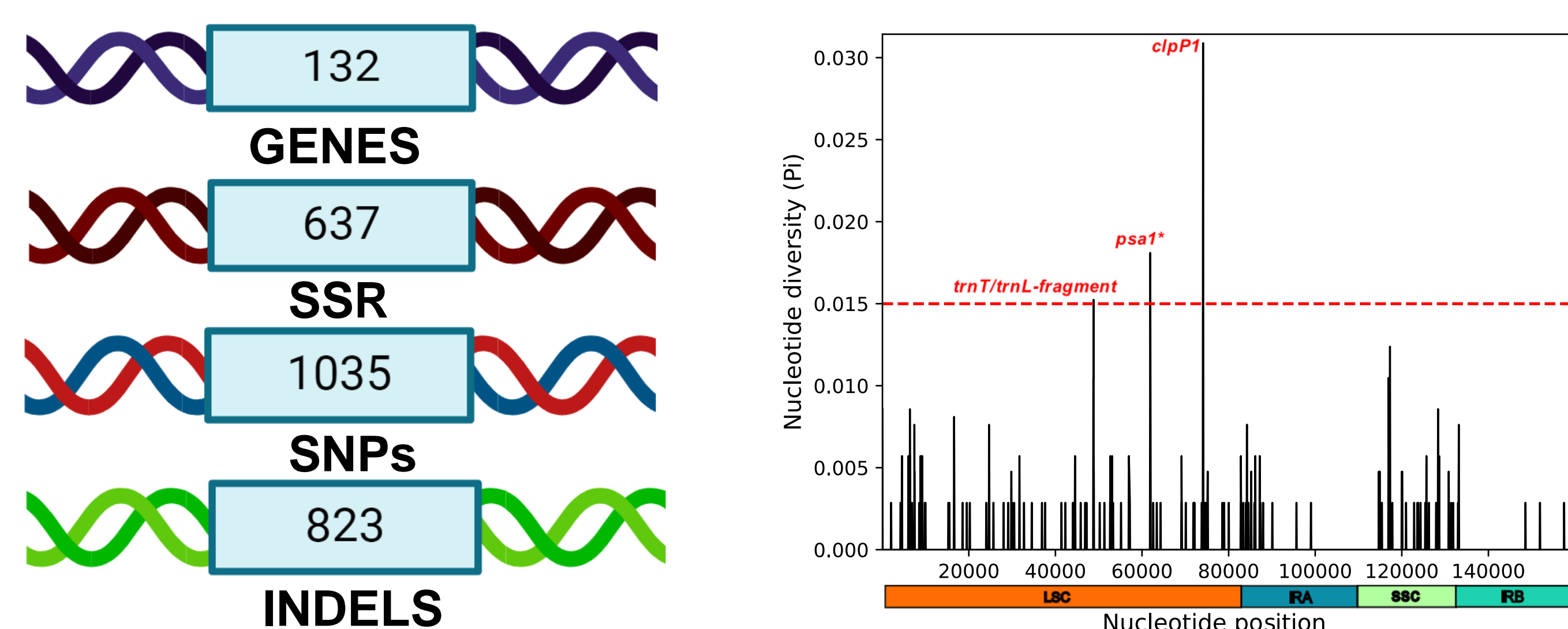
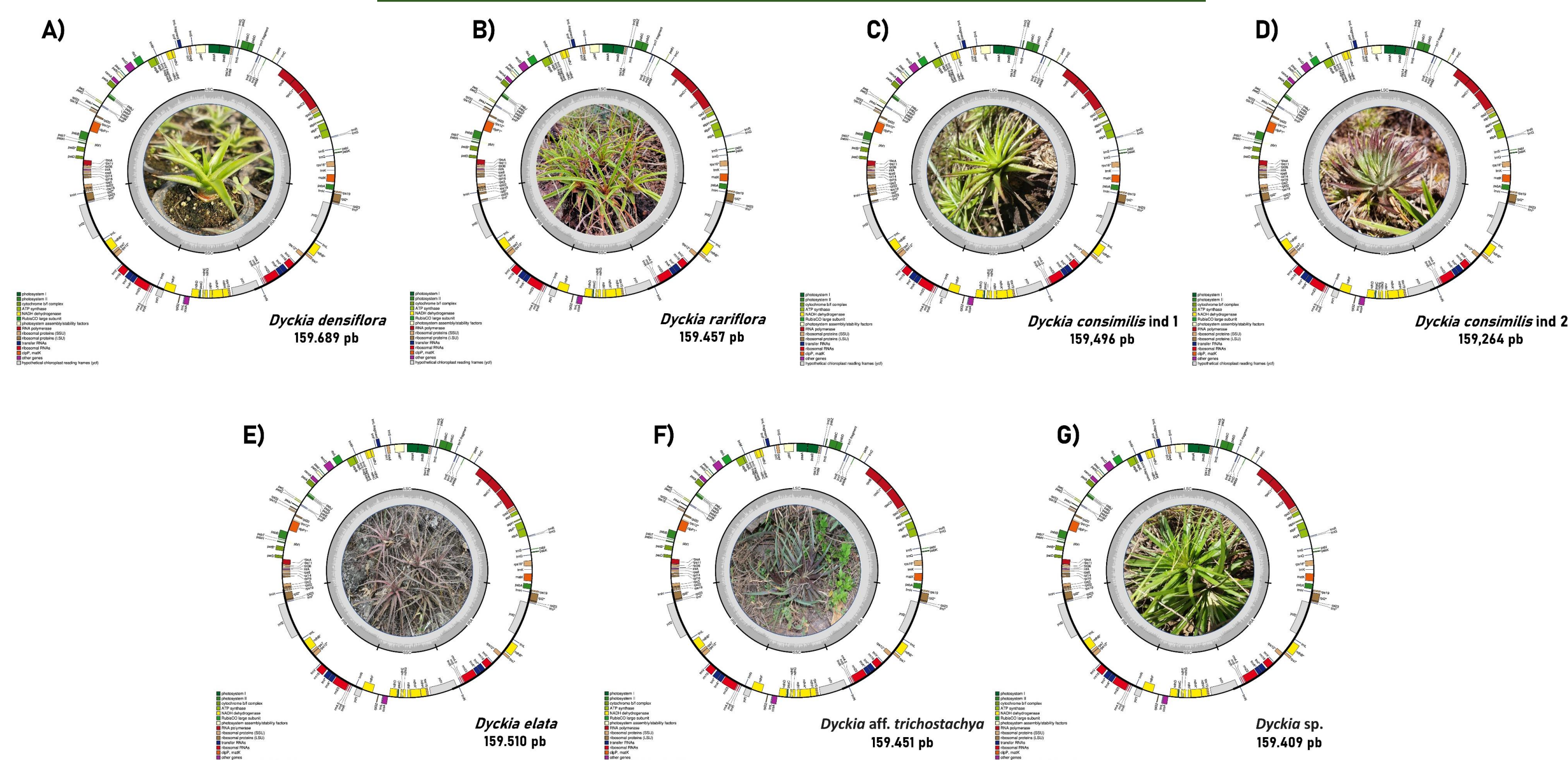


Dyckia spp. are predominantly xeromorphic bromeliads, with their diversity concentrated in the ferruginous rocky outcrops of the Espinhaço mountain range within the Brazilian savanna. Despite their richness, a significant portion of species in this region are microendemic and threatened by human activities. Estimates based on plastid markers suggest that *Dyckia* underwent a substantial radiation process between 4.6 to 2.9 million years ago, still within the Pliocene epoch. This recent radiation, combined with the species' phenotypic plasticity and limited herbarium records, presents challenges for their identification and the development of robust phylogenetic hypotheses. We sequenced the complete chloroplast genomes of six rare *Dyckia* species to identify molecular diversity hotspots that may serve as markers for distinguishing species and elucidating phylogenetic relationships within the genus.

MATERIAL & METHODS



KEY RESULTS



CONCLUSION

Phylogenetic analyses using whole plastid genomes showed low variability among species, associating them with their geographic distribution. These findings provide essential molecular tools for species identification and phylogenetic analysis, crucial for developing effective conservation strategies for these rare and vulnerable bromeliads in Brazil.

ACKNOWLEDGEMENTS



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