INVESTIGATING THE ROLE OF DRIFT AND SELECTION ON THE DIVERSIFICATION OF *Pitcairnia lanuginosa* complex (BROMELIACEAE) WITH RAD-SEQ MARKERS

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Filogeografia/Oral

The identification of the main mechanisms responsible for the diversification of intra and inter-specific lineages is a major question in evolutionary biology. Investigating these drivers can improve our understanding of why South America harbors extraordinarily high levels of plant diversity. In this study, we infer the evolutionary history and genetic structure of *Pitcairnia lanuginosa,* a morphologically homogeneous complex of bromeliads widely distributed throughout tropical South America. We sampled 19 populations (N=132) in the Brazilian Cerrado and Peruvian Yungas (Amazonia-Andes transition), and genotyped 688 SNP markers defined through double-digest restriction-site associated DNA sequencing (ddRAD-Seq). Our results point to extremely low genetic diversity and high levels of inbreeding in all populations, which is possibly related to ecological aspects such as high selfing rates and fragmented distribution. Phylogenetic reconstructions and a Bayesian clustering analysis indicate a remarkable differentiation between populations from the Brazilian Cerrado and the Peruvian Yungas, with a strong genetic differentiation among populations within the Cerrado cluster (F_{ST}=0.59). Bayesian generalized linear mixed models (GLMMs) revealed that genetic variation within the Cerrado biome is better explained by a combined effect of isolation by distance (IBD) and isolation by environment (IBE) rather than by IBD alone. F_{ST} outlier tests identified a small proportion of SNPs marker as putatively under balancing selection. The application of next-generation sequencing approaches to our model refined our previous understanding on the genetic structure within this complex achieved by traditional markers and revealed previously unresolved questions on the drivers of *Pitcairnia lanuginosa* diversification.

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