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***Petunia axillaris* ssp. *parodii* HIGH DENSITY GENOME ANALYSIS REVEALS POPULATION DIFFERENTIATION CORRELATED WITH DIFFERENT ECOREGIONS**

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Understand the genetic structure and diversity distribution of natural populations enable comprehend processes involved in diversification. This remains an important challenge, especially for species widely distributed in heterogeneous environments. Advances in genome scanning using high-throughput sequencing methods allow the analysis of genome-wide SNPs and the understanding of species evolutionary history and adaptive methods. *Petunia axillaris* ssp. *parodii* is a widely distributed taxon in Pampa and Chaco, two distinct ecoregions in Neotropical grasslands areas marked by strong seasonality and that present geological discontinuity and distinct physiographic and soil conditions. Here, we analyzed 80 individuals distributed in 18 populations using population genetic methods for genotyping-by-sequencing data to assess genetic structure of ssp. *parodii* in all its geographical distribution. A total of 4511 filtered SNPs were analyzed and we found an average of 3 SNPs/Mb. To identify the genetic structure, we used a distance matrix of the filtered SNPs based on Endelman-Jannink method to run a cluster dendrogram and a Principal Component Analysis (PCA). Our preliminary results provide strong evidence for two main distinct groups in ssp. *parodii* related to geographical distribution in Pampa e Chaco ecoregions. We will perform analysis of genetic diversity and differentiation, and to assess the genomic signature of adaptation, we will test for outlier SNPs. Those results indicate that ssp. *parodii* is a useful model to understand grassland plants speciation and diversification in South America.

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