GENETIC DIVERSITY STUDY FOCUSED ON THE ENDANGERED
Chascolytrum scabrum (NEES EX STEUD.) MATTHEI (POACEAE; POEAE):
IMPLICATIONS FOR CONSERVATION

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Chascolytrum scabrum (Nees ex Steud.) Matthei is considered endangered due to several factors, such as small populations, fragmentation, overgrazing and loss of habitat for silviculture and invasive species. Furthermore, it is endemic to the highlands in Southern Brazil (Atlantic Forest) and only four wild populations are known in Rio Grande do Sul. As genetic diversity plays an important role in plant populations, it may be used as a guide to the establishment of conservation plans. To estimate the genetic diversity and population structure in C. scabrum, a genetic survey using the chloroplast intergenic region rpoB-trnC and Amplified Fragment Length Polymorphism (AFLP) markers was carried out. Four populations comprising 58 individuals were included in the analysis. Genetic diversity was calculated using ARLEQUIN 3.5.1.2 for cpDNA and POPGENE 1.32 for AFLP. A cpDNA neighbor-joining haplotype network was constructed using NETWORK v.5 and an analysis of molecular variance (AMOVA) was conducted in ARLEQUIN. To verify the possible clustering (K) between the accessions, a Bayesian analysis was performed in STRUCTURE 2.3.4 using AFLP data. The final cpDNA alignment consisted in 1032 sites, which 14 were variable. The three AFLP primers combination produced 495 fragments, which 494 were polymorphic (99.8%). Genetic diversity was considered high at species level (H=0.8440 in cpDNA and 0.2239 in AFLP). At population level, H ranged from 0 to 0.8603 in cpDNA and from 0.0640 to 0.1915 in AFLP. Population SCA4 exhibit the lowest genetic diversity values and population SCA1 the highest values. 14 haplotypes were obtained and their distribution ranged from 1 (SCA4) to 8 (SCA1). Any haplotype was found to be shared, indicating high phylogeographic differentiation between populations. High population structure was revealed by cpDNA (FST= 0.78099) and AFLP (0.43945) and no correlation between genetic and geographic distance was found. Simulations performed in STRUCTURE identified two genetic clusters (K=2). The most outstanding pattern recovered by the joint use of different markers was the recognition of SCA3 and SCA4 as a different lineage from the remaining SCA1 and SCA2 populations, a pattern recovered by the two inferred clusters and haplotype network. Since each population can be considered as an evolutionarily significant unit (ESU), we suggest the conservation of all populations of C. scabrum included in this study. (CNPq)

Keywords: phylogeography; AFLP; cpDNA.