The gene flow between Araucaria angustifolia populations through coalescent theory

T1.12 Forest genetics tools to improve forest resilience to climate change and forest health

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Abstract: *Araucaria angustifolia* (Brazilian-pine, araucaria) is a conifer tree of high ecological and social value in Brazilian subtropical region due to its high-quality wood and pine nuts production used for feeding. However, the species have been heavily exploited. The remaining populations are isolated and may encounter difficulties adapting to climate change. So, this study examined the gene flow between populations of araucaria across its geographical natural range through a coalescent approach. Genomic DNA samples were collected from 185 trees in a provenance and progeny test sampled from 15 natural populations. The genotyping was performed using a 3K Axiom SNP array (2022 SNPs) and 28 microsatellites. Gene flow demographic models among the populations were tested to verify the direction (North or South) of the migratory flow between neighboring populations. All models were run at MIGRATE-N software. The migration rate, the effective number of migrants per generation (xNimij), and the effective population size (Ne) were estimated. The mean Ne observed using the SNPs markers for populations further north (959.02) is slightly higher than that southern (893.61). We identified neighboring populations with more intense migratory flows than the others and the general tendency of migratory flow between these populations. Thus, we identified populations that stand out as the main sources of migrant individuals showing a negative migration balance; and the ones that receive a high migration flow. We also noticed populations that stand out for their weak connection with others. By correlating the migration parameters with climatic variables, we observed that the minimum average temperature in the coldest month, and the amount of rain in the driest month present a high and significant correlation with xNimij. A negative correlation was observed between the rainfall regime and xNimij. So, the greater the amount of rain in drought period smaller the number of migrant individuals. About temperature, we observe a positive correlation between migration and average minimum temperature up to a specific temperature, after which the regression curve inflects. In general, the observed gene flow suggests a connection between the remained populations, being the greatest sources of genetic diversity of the species found in southern Brazil.