

Genetic diversity and genomic selection in *Eucalyptus benthamii*

Ananda Virginia De Aguiar ^{*† 1}, Bruno Souza ², Lucas Abreu ³, Marilia Pappas ⁴, Vânia Azevedo ⁴, Paulo Eduardo Santos ¹, Aparecida Sousa ¹, Rodrigo Santos ⁵

¹ Florestas (Embrapa) – Colombo, Paraná, Brazil

² Universidade Federal de São Carlos (UFSCar) – São Carlos - SP, Brazil

³ Universidade Federal do Parana (UFPR) – Curitiba, Brazil

⁴ Cenargen (Embrapa) – Brasília, DF, Brazil

⁵ University of Florida (UF) – Gainesville, FL 32611, United States

Cold and frost-tolerant Eucalypt species has been very interesting for the forestry sector in many countries. Currently, one of the main species which shows good development in subtropical areas is *Eucalyptus benthamii*. The aim of this study is to investigate genetic diversity and the ability of genomic-wide selection to predict breeding genomic values of a *E. benthamii* trial. The seeds were originated from a mix of 10 trees located at Wentworth Falls. The whole individuals (115) were genotyped with 13 microsatellite loci, and their diameter at breast height (DBH) and total height (HT) were measured. The data analysis was carried out by using the software: Structure, Popgene, GDA and R. Predictive ability, heritability and standard errors markers were estimated for 122 alleles originated from 13 microsatellite markers based on the RRblup method. The mean of alleles per locus was nine, and the polymorphism level for each locus varied from 3 to 17. The average expected heterozygosity (0.655) was very similar to observed heterozygosity, and these results corroborate this population is in Hardy-Weinberg equilibrium for the most locus. The inbreeding level estimated for this population ($F = 0.02$) was very low. The genetic diversity of trial can be considered elevated because the natural occurrence range was narrow and the trial sampling demonstrated values of diversity similar to the natural forests. By using Structure and the Evanno's method it is possible to infer that the individuals of the studied trial came from two original populations. So, considering the existence of two groups in the population, genetic values were performed considering separately the individual from each group. The genetic diversity levels calculated within populations are very similar, even when the genetic mean distance among them was elevated (0.81). The heritability estimated from genomic selection for phenotypic traits was very low, leading to a low predictive capacity. The trial suffered two selective thinning, which hampered the possibility to achieve higher genetic gains. However, some samples population should be used to improve variability in breeding populations. Moreover, the individuals showing more genomic breeding values should be used to established orchard seed and hybrids development.

*Speaker

†Corresponding author: ananda.aguiar@embrapa.br