Genetic Diversity and Genomic Selection in Eucalyptus Benthamii

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Genetic diversity and genomic selection in *Eucalyptus benthamii*

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ABSTRACT

The study investigates the genetic diversity and the ability of genomic-wide selection to predict breeding genomic values of an *E. benthamii* trial. All individuals (115) of the breeding population were genotyped with 13 microsatellites loci. The diameter at breast height and total height were measured. The data analysis was carried using the softwares: Structure, Popgene, GDA, SPAGeDi1.5 and R. Predictive ability, heritability and standard errors markers were estimated using the RRblup method. The average number of alleles per locus was nine, and the polymorphism level for each locus varied from 3 to 17. The average expected heterozygosity (H_e=0.655) was very similar to observed heterozygosity and the estimated inbreeding (F = 0.02) was very low. These results corroborate that this population is in Hardy-Weinberg equilibrium for the most loci. The trial genetic diversity is considered high, once the trial sampling demonstrated similar values to the natural populations. The group coancestry (0.085) demonstrate that the trees, in general, related at the half-sib level in this population. By using the Evanno's method it is inferred that the individuals came from two original populations. The genetic distance calculated among the two groups was low (D=0.21). The heritability estimated from genomic selection for phenotypic traits was very low; however, the heritability estimated using the kinship coefficients was higher. The marker-based heritability using kinship coefficients probably is the more accurate than the one estimated using genomic selection, showing that the population samples can be used to establish breeding populations, hybrids and enriching the species germplasm bank.

Keywords: clustering method; coancestry; frost-tolerant; genome-wide selection; heritability

1. Introduction

Some *Eucalyptus* species are frost tolerant, showing good performance on subtropical areas with high probability of frost. This aspect and their performance in wood productivity have aroused the interest of the forestry sector in many countries. Currently, one of the major studied species which combines the frost tolerance ability with high wood productivity is *Eucalyptus benthamii* (Bush et al. 2016). Some companies have used this species to develop interspecific hybrids. International initiatives have verified a relation between cold tolerance established from field trials plantations in southeast Texas with frost-prone regions of southern Brazil (Hart et al. 2016). The species also has showed a good performance across different sites in China (Xie et al. 2017). Kellyson et al. (2013) noticed that the species is appropriate to be managed by breeding process, arguing that it shows quick progress through genetic selection. According to the authors

genetic gains can be obtained as much as in growth, as well in wood quality and in cold tolerance. In Brazil, *E. benthamii* is the most adapted eucalypt species to south region, where intense frosts usually occur (Santarosa et al. 2014). *E. benthamii* wood main use is in energetic products, such as charcoal and firewood. One of the limiting factors to development of the species use is lack of information about the genetic material introduced in the country hampering the progress of breeding programs.

The species natural occurrence is narrow being found only in a restricted area southwest of Sydney in Australia. Therefore, it makes the species vulnerable to extinction (Butcher et al. 2005). Currently, the efforts in the region have been to preserve and study the forest remnants (Baccarin et al. 2015). Small populations of tree species can have their genetic variability reduced. The low number of individual can lead to a loss of alleles, decreasing the adaptation capacity of the population. In the future, the high level of relatedness between the breeding individuals can increase inbreeding (Maxted et al. 2013). This situation can be worsen in advanced-generation of breeding. In this case it can hamper the genetic gains for the next generations. The genetic variability of a population can be estimated by parameters such as the number of alleles per locus (A) and genetic diversity estimated by expected heterozygosity (H_e) (Dungey et al 2018). Microsatellites markers or Single Sequence Repeats (SSR) have shown an efficient capacity to capture this information. The use of SSR markers has been frequent in tree population's studies (Mora et al. 2017; Kaur et al. 2018; Liu et al. 2018; Miranda et al. 2019; Chen et al. 2020; Lv et al. 2020)

The use of SSR allows the access of high-quality genetic information in a reduced period of time and can also be applied to drive the selection of individuals. On this path, a lot of works have been successful achieving this goal through genome-wide selection (SGW). The Genomic-wide Selection proposed by Meuwissen et al. (2001) is based on the analysis of a large number of markers wide distributed in the whole genome. The effects of the markers are estimated based on phenotypic data of an individual group called training population. This strategy can reduce the time between the selection cycles (Crossa et al., 2011), and makes it possible to select the best genotypes without the need of phenotyping at an early age. Several studies infer that the use of GWS can increase the genetic gains in eucalyptus cultures and other crops (Hayes et al. 2013; Desta and Ortiz 2014; Isik et al 2014, Liu et al 2015; Gois et al. 2016; Torres-Dini et al. 2016; Müller et al. 2017; Resende et al 2017; Laviola et al 2017)

Although, GSW it is still a relatively new technology, a deeper understanding of its mechanisms is required. The major questionings about the factors that influence its predictive quality are: minimum number of individuals in the training population, type and quantity of molecular markers that can be used and the importance level of relatedness among the individuals (Desta and Ortiz 2014; Crossa et al. 2017; Azodi et al. 2019; Sawitri et al. 2020). The objective of this study is to investigate the genetic diversity of an *E. benthamii* seed production area and to apply GWS to this population to estimate genomic breeding values and genetic gains.

2. Methods

2.1. Study population

The studied stand was the first known germplasm bank of *E. benthamii* introduced in Brazil. It was established by Embrapa Florestas in 1988 at the municipality of Colombo in state of Paraná, southern Brazil. The area has been managed as a seed production area, and has provided cuttings and seeds to be used in commercial planting. The seeds were provided by CSIRO[1](Australia), and were originated from a mix of 10 trees located at Wentworth Falls (NSW) (Graça et al. 1999). The initial number of individuals in the stand was 443 trees and this number was reduced to 199 by a selective thinning in 1995. Currently there are 115 remaining individuals occupying a total area of 0.5 ha.

The stand is located at an elevation of 1,027 m above the sea level in a climate Cfb clime, fully humid with warm temperature, according to Köppen. The average annual rainfall is 1,638 mm. The average maximum temperatures on the warmer and colder months are 28° C and 19° C, respectively. There is natural occurrence of frost in the colder days of the year. On the last 20 years temperatures around or below 0°C were registered in more than 30 days. (INMET 2018).

2.2. Plant material and genomic DNA extraction

All individuals of the referred stand had they diameter at breast height (dbh) and height measured in 2017. For the genetic analyses, cambium samples were collected from all the individuals. Genomic DNA was extracted using a CTAB-sorbitol based method (Inglis et al., 2018). Samples were quantified using Nanodrop (Thermo Fisher Scientific) and diluted to a final concentration of 5.0 $ng.\mu l^{-1}$ to run PCR reactions for

[1] The Commonwealth Scientific and Industrial Research Organization (CSIRO) is an independent agency of the Australian Federal Government responsible for scientific research in Australia

genotyping 13 microsatellite loci using primers previously reported (Butcher et al. 2005). PCR were carried out using 5.0 ng of DNA, 1 unit of Taq polymerase, buffer 1x, 0.25 mg bovine serum albumin, 0.28 μM of each primer in 8.0 μl reaction. PCR products were multiplexed in duplexes and triplexes according to fluorochrome labelling and size range for injection in 3730 DNA Analyzer (Thermo Fisher Scientific). Allele call was conducted using Gene Mapper software (Thermo Fisher Scientific).

2.3. Genetic analysis

Analyses of obtained data were performed using the GDA software (Lewis and Zaykin 2001). The following parameters were estimated: allele frequency (A), expected (H_e) and observed heterozygosis (H_o) and fixation index (H_o). The expected allele frequencies were calculated based on the observed frequencies, considering the Hardy-Weinberg equilibrium model. The observed heterozygosity was calculated based on Brown and Weir (1983): H_o= 1- $\sum p_{ii}$, where p_{ii} is the observed frequency of homozygotes on the *i* allele. The expected heterozygosity considering the Hardy-Weinberg equilibrium was estimated according to Nei (1978). The fixation index was estimated using the expected and the observed heterozygosity (Wright 1965).

The population structure was inferred by using a Bayesian model-based clustering method with software STRUCTURE version 2.3 (Pritchard et al. 2000). STRUCTURE uses genotypic data to determine the number of distinct genetic clusters (K) among the sample locations, and estimates individual assignment probability to each cluster. Twenty replicate runs (100,000 Markov Chain Monte Carlo step burn-in plus an additional 100,000 runs) were performed for each value of K. Results were summarized using STRUCTURE Harvester version 0.6.6 (Earl and vonHoldt 2012), which generated a plot of the mean value of L(K) (ln likelihood of data) at each *K*. With STRUCTURE Harvester analysis it was possible to infer the most likely number of clusters by identifying the highest L(K) value with relatively small variance

Later, further genetic analyses were performed using the software POPGENE 1.32 (Young et al. 2000), considering separately each group within the population. Allele frequency, expected and observed heterozygosity and fixation index were estimated for each group. The genetic distance between the groups was also calculated trough the Nei's standard genetic Distance (D) (Nei, 1972).

Coancestry coefficient (θ_{xy}) was calculated by the estimate of pairwise kinship coefficient describe by Loiselle et al. (1995). The estimates were calculated using Jackknife resampling among loci using SPAGeDi 1.5 software (Hardy and Vekemans 2015). The pairwise relatedness was also used to calculate individual

heritability ($\hat{h}_2$) using a marker-based method proposes by Ritland (1996). The calculation of $\hat{h}_2$ was given by the equation: $\hat{h}_2 = \frac{C_{ZR}}{2V_r}$, where, V_r is the actual variance of relatedness among all pairs i and R is the sample covariance between phenotypic similarity (Z_i) and estimated relatedness (R_i). Among related individuals the phenotypic similarity is written as: $Z_i = \frac{(Y_i - U)(Y'_i - U)}{V}$. For i pair, Y_i is the value of trait in the first individual, Y'_i the value of trait in the second individual, U is the mean of the trait and V the population variance (Ritland 1996).

2.4. Genome-wide selection

To analyze the phenotype data the mixed linear model used was BLUP/RELM. The Predicted additive genetic values were deregressed and corrected for parents' effects to obtain the adjusted phenotypic values to be used for genomic predictions. To use information from the SSR markers in the GWS technique it was necessary to transform the genetic information into a binary code of 0 and 1. For each individual a "0" was added when it did not show the corresponding allele and one "1" when it presented the correspondent allele. This way each individual presents a code indicating the presence or absence of all observed alleles in the population. The markers had their effects estimated adjusting all the allelic effects simultaneously using the random regression best linear unbiased predictor (RR-BLUP). The method was performed using RR-BLUP package in R (Endelman 2011), as described previously (Resende et al. 2008; 2012). The RR–BLUP assumed that the markers effects were random. The variance parameters were assumed to be unknown and were estimated by restricted maximum likelihood (REML). The linear mixed model adjusted to estimate the effects of markers was: $y = X_b + W_m + e$. Where y is the vector of phenotypic data (deregressed additive genetic values), b is the vector of fixed effects, m is the vector of random effects of markers and e refers to the vector of random residues. X and W are the incidence matrices for b and m. The mixed model equations for genomic prediction of m via the RR-BLUP method is:

$$\begin{bmatrix} X'X & X'W \\ W'X & W'W + I\ \frac{\sigma_e^2}{\left(\sigma_g^2/n_Q\right)} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{m} \end{bmatrix} = \begin{bmatrix} X'y \\ W'y \end{bmatrix}$$

Where σ_g^2 is total genetic variation and n_Q is the number of loci. The σ_g^2 was estimated by REML from phenotype. The total genomic breeding value of individual j is given by VGG=$\hat{y}_j = \sum_i w_{ij}\hat{m}_i$, where W_i is equals to 0 corresponding to the genotype m, or 1 corresponding to the genotypes Mm and MM. The amount

of n_Q equals $n_Q = 2\sum_i^n p_i\,(1 - p_i)$ .The equations presented above assume a priori that all loci explain equal amounts of the genetic variation.

Predictive accuracy, heritability and standards errors were estimated by averaging the Jack-Knife (Quenouille 1949) cross-validation method. The approach used was the "leave-one-out". A single individual from the population was used as the validation set, and the remaining individuals as the estimation or training set. This was repeated such that each individual in the sample was used once as the validation data. This process was repeated 115 times, using each time a different set of individuals for estimation and one different individual for validation having all individuals their phenotypes predicted and validated.

3. Results

Analysis of 13 SSR loci resulted in a total of 122 alleles. The mean of alleles per locus was nine, ranging from three to 17 alleles (Table 1). The high variation in the numbers of alleles found per locus result in a diverse expected heterozygosity (H_e) by locus. It did not demonstrate a disparity compared to the observed one (H_o). The inbreeding levels estimated to this population were very low (Figure 1). The analysis also evidenced that the population is in Hardy-Weinberg equilibrium for most of the locus.

The clustering method inferred the most likely number of clusters by identifying the highest L(K) (L'(K)= 343,11) value with relatively small variance (Figure 2). It is possible to conclude that the stand individuals came from two Australian's original populations. Thus, the trees were gathered in two groups: one with 54 and the other with 61 individuals (Figure 3). So, considering the existence of two groups in this population, genetic values were performed considering separately the individual from each group (Table 2). The genetic diversity levels calculated within both populations were very similar. The genetic distance among them was 0.21.

This breeding population showed low prediction ability to dbh and height traits in GWS (Table 3). This means that the number of markers and population sizes were not enough to validate this methodology. The dbh trait indicates a high phenotypic variance.

The estimated pairwise kinship coefficient shows that the individuals in the population reveal a considerable relatedness (Table 3). And the marker-based heritability estimated was very disparate from that one found through GSW.

4. Discussion

The genetic diversity of the studied population was relatively elevated comparing the genetic parameters to those natural population. In the restricted natural area of this species occurrence, the number of alleles ($\bar{A}$= 10.4) and the indexes of heterozygosity (H_e = 0.739 and H_o=0.630) are very similar to those found in the stand (Butcher et al. 2005). Even though only ten adult trees were used as seed source for the population setting, the stand is representative of a significant part of the total species diversity. The study's observations address the high diversity levels for this population in relation to the gene flow of its original population. As we noticed, both populations are in Hardy-Weinberg equilibrium and demonstrate very low endogamy coefficients. This scenario suggests that this population was originated by random crossbreeding between unrelated parents (Randall et al. 2016). The stand reveal heterozygosity level similar to other tree breeding populations, like *E. meliodora* (Broadhurst 2013), *Acacia mangium* (Yuskiante and Isoda 2012), *Pinus taeda* (H_E: 0.659; Ai-rabab'ah and Willians 2002), and *Araucaria cunninghamii* (H_E: 0.61, Peakall et al. 2003). Costa et al. (2015) observed similar genetic diversity in populations of *Aracaucária Angustifolia* (H_e = 0.674, F = 0.062). This indicates that crossbreeding with different pollen donors occurred in the reproductive events that generate the studied population. Despite the existence of kinship with a high degree of relatedness (half-brothers and full siblings), there is also the presence of crosses with low levels of kinship in the population.

On the other hand, the diversity indicators in this study were lower than *Eucalyptus* species with a more widespread natural occurrence area. Breeding populations and seed orchards from *Eucalyptus* species such as *E. dunnii* (Marcucci Poltri et al. 2003), *E. globulus* (Jones et al. 2006), *E. grandis* (Chaix et al. 2003) and *E. urophylla* (Silva et al. 2018) showed higher expected heterozygosity. This occurs because the genetic diversity is associated with the environmental variability. If the species distribution occurs only in narrow area and similar environments, like *E. benthamii*, the genetic diversity tends not to be so elevated. Still, it is noticeable that the estimated values are higher than those verified for some conifers such as *Pinus pinaster* (Wshid et al. 2010), *Pinus tabulaeformis* (Di and Wang 2013), *Pinus resinosa* (H_E: 0.358; Ter-Mikaelian and Bowling 2014) and *Pinus dabeshanensis* (Xang et al. 2015). It indicates that the typical genetic diversity of *E. benthamii* is moderate among other tree species.

In general, Breeding stands composed of selected trees usually show a reduced genetic diversity. The trend is that for each new crosses generation the genetic diversity will be reduced (Jones et al. 2006), since

222 favorable alleles concentration increase in selection processes. The stand under study exhibited a high value
223 of diversity compared to natural stands of the same species. This assures the capacity of this stand c contribute
224 with the species conservation, helping as collection of accesses to a germoplasm bank. After two selective
225 thinnings the remaining trees represent selected elite regarding growth traits. Furthermore, the stand contains
226 a valuable material for breeding program aiming at frost tolerant fast growth trees, since more than 10 frosts
227 occurs annualy.

228 The clustering method showed that seeds originated in this stand came from two original populations.
229 Due to low genetic distance among populations it is possible that the genetic pools of both populations are
230 very similar (Nei 1972). The parent's original populations must have could originally occupied areas with
231 similar environments. Furthermore, they must belong to the same provenance, since the genetic distance
232 between them is very small. Also, these populations probably are not completely isolated from each other,
233 likely, they exchanged gametes maintaining a gene certain flow level (Vekemans and Hardy 2004). The
234 presence existence of two groups of individuals in the stand can contribute significantly to breeding strategies
235 as well as in conservation strategies for the species. Individuals from different groups can be used in
236 controlled pollinations or can be crossed with closer individuals to get a purer pedigree. In breeding programs,
237 it is common to get a high reduction on genetic variability which hampers the estimate of genetic gains. By
238 knowing how genetic groups are distributed within population, it is easier to manage the maintenance of
239 genetic variability (Schwartz and Mckelvey 2009), and to develop strategies for collecting, conserving, and
240 using these germplasm resources.

241 GWS is an adequate method to direct the selection process in breeding population, but for this particular
242 *E. benthamii* population it will not work. This approach shows a low predictive capacity for this small
243 population. Other studies involving GWS in tree breeding populations usually show a higher selective
244 accuracy ($\hat{r}_{\hat{y}y}$) and heritability. Grattapaglia et al. (2011) e Resende et al. (2012) found values for the $\hat{r}_{\hat{y}y}$ of
245 the 0.69 and 0.54 for dbh trait in eucalypt species. Duran et al. (2017) archived an even higher predict power
246 for volume with a clonal *E. globulus* (0.73). Tan et al. (2017) detected a more moderate average of 0.27 for a
247 hybrid generation of *E. grandis* x *E. urophylla*. For *Pinus taeda* Aguiar et al. (2015) estimated a $\hat{r}_{\hat{y}y}$ of 0.63
248 for dbh at age six years (14,000 markers). Considering crop species, such as grapes (*Vitis rupestris* × *Vitis*
249 *arizonica/girdiana*) and cassava (*Manihot esculenta*), respectively values of 0.67 and 0.50 were predicted for

growth traits (Viana et al. 2016; Silva et al. 2016). When we compare the cited studies and the present one, apparently the number of individuals sampled on the population and marker density is the main difference.

By comparison with different studies it is possible to point out which variables cause more difference at the GWS method results. Resende et al. (2012a) found lower accuracy in their results with a *Pinus taeda* population using 4,953 SNPs markers and 941 individuals in the training population that Zapata-Venezuela et al. (2012) using 3.406 SNPs and 526 individuals of the same species. On the other hand, a considerable increase in the number of SNP markers provoked a big difference in the results for *Picea abies* (up to 6,932 SNPs) (Beaulieu et al. 2014) and *Picea engelmannii* (from 8,868 to 55,618 SNPs) (El-dien et al. 2015). Considering *Eucalyptus grandis* x *Eucalyptus urophyla* hybrid Resende et al. (2012b) reached a good predictive power using DArT(>3,000), a dominant marker, as well Müller et al (2019) using 46,000 SNPs, a dominant/co-dominant marker, for the same hybrid. Marchal et al. (2016) using 313 SRR marker, similar as applied in this work, obtained high levels of accuracy in the predict genetic values of 478 crosses in an *Elaeis guineensis* (oil palm) population.

In comparing the cited studies to this one, the number of individuals sampled on the population and marker density is the main difference is observed. In this case it is presumable that the number of individuals in the training population and markers were insufficient to produce an accurate prediction. In consensus, the method accuracy tends to get higher as the individual of the training population gets larger (Jannink 2010). Torres-Dini et al. (2016), despite using a high number of markers (15,106 SNPs), obtained low accuracy results with a small population (78 individuals) of eucalyptus hybrids. And regarding the number of markers, papers show reliable results with trials using around eighty SRR markers (Fritsche-Neto et al. 2012).

Nevertheless, even in small populations with 100 or 200 samples, Grattapaglia & Resende (2011) simulated that the GWS would have a better accuracy (about 0.7 for N = 100) using SNPs markers at density of 2 per centiMorgans(cM). Muller (2017) employing GWS technique for *E. benthamii* breeding population argues that the most influential factor in predictive power is the relatedness among individuals, followed by the amount of genetic addictive variance of population. It is also noticeable that this population has an expressive phenotypic variance in relation to dbh trait. Due to the low accuracy of the estimation, the values regarding to heritability are probably underestimated. The true value of population's addictive genetic

277 variance should be higher than that estimated (Callus 2010). Due to the narrow origin of its genitors, besides
278 the low genetic variance, the individuals show an expressive relatedness as was demonstrated by the
279 population coancestry coefficient. The θ_{xy} of the population get closer to the half-sib number (θ_{xy}=0.125)
280 (Cockerham 1967), this indicates that part of individuals in the population share at least one parental in
281 common. As the seeds that originated this population were collect from only 10 trees of the same provenance;
282 part of them probably share a common mother and different fathers.

283 The GWS and the marker-based procedures (using kinship coefficients) should estimate similar
284 values for heritability. On this particular study, the marker-based heritability must be the closest to real one.
285 The GWS methods for this test reveal low predict ability. That leads to inaccurate genetic values estimative
286 and, consequently, to one underrated heritability. Genetic markers provide information about relatedness
287 between individuals of unknown pedigree making it possible to estimate a kinship matrix based on average
288 values of relatedness (Ritland 1996). Da Silva et al. (2015) compared the results obtained for heritability
289 based on the kinship coefficients of Lynch and Ritland (1999), Queller and Goodnight (1989) and Wang
290 (2002) and conclude that the Ritland (1996) method is the most robust. The authors argued that the method
291 allows a greater adequacy of the data in the model used. However, the GWS procedure is more accurate than
292 that one based on relatedness, this because it effectively captures the actual kinship matrix performed and not
293 an average kinship matrix associated with the pedigree, like the second procedure (Arcia et al. 2011).
294 According to Munoz (2014), GWS is the method that best explores the mendelian sampling segregation
295 occurring during the gamete origin, once it directly evaluates the associated DNA at each locus of all
296 polygenic traits. Thereby, it captures the exactly kinship matrix and not a pedigree-matched relatedness
297 matrix. The GWS allows the obtaining of information that produces more accurate estimates of the genetic
298 values at the individual level. Although the trial had already submitted to two selective thinning, the
299 heritability estimated trough markers show a potential to achieve considerable genetic gain using short-term
300 selection methods.

301 **5. Conclusion**

302 The *E. benthamiii* population presents considerable genetic diversity, and has potential to contribute to
303 species genetic breeding. The individuals with more genomic breeding values can be used to established seed

orchard aiming at breeding (frost tolerant stands, for hybrid production,) and conservation (enriching germplasm bank of the species, as the only collection with replica in Brazil). Still, regarding the continuity of future breeding or conservation programs using this population as base, it is indicated the introduction of more individual to improve the germplasm collection. Considering the natural narrow occurrence of the species, is proposed to cross the selected individuals with trees from the most distant provenances as possible from this population genitors' origin region.

Genome-wide section method was not effective to provide high genetic gains through selection for this particular population and marker density. A significant level of relatedness among the individuals was found, being possible to assume that with a larger number of individuals the GWS could reach acceptable precision level. It can be more efficient and less costly that the phenotypic selection. So, for further generations of this population, as well for stands with similar genetic characteristics, the SGW could reach the aimed goals.

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6. **Data archiving statement**

The genotypes of the115 individuals for 13 loci are available on Mendeley website, doi: 10.17632/yxjddg3cff.1 (Marchetti de Souza et al. 2020).

7. Disclosure statement

The authors declare no conflict of interest to disclosure with respect to this paper.

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Table 1- Descriptive genetics of the microsatellite loci used for individuals of *Eucalyptus benthamii* in Colombo, state of Paraná, Brazil. With number alleles (n), expected heterozygosity (H_e), observed heterozygosity (H_o) and Fixation index (F).

Locus	n	$\mathbf{H_o}$	$\mathbf{H_e}$	**F**
eg61	6	0.342	0.352	0.023
embra06	14	0.613	0.834	0.262
embra10	12	0.567	0.734	0.225
embra11	14	0.790	0.653	-0.214
eg126	5	0.664	0.575	-0.159
eg67	17	0.785	0.859	0.082
es157	7	0.624	0.726	0.137
eg91	8	0.670	0.692	0.028
en06	9	0.761	0.681	-0.123
eg99	10	0.781	0.790	0.006
es140	8	0.455	0.448	-0.023
eg128	3	0.639	0.650	0.011
eg84	9	0.700	0.732	0.038
Mean	9.38	0.645	0.671	0.023

Figure 1. Descriptive genetics of the microsatellite loci used for individuals of *E. benthamii* in municipality Colombo, state of Paraná, Brazil. The red horizon line corresponds to the mean value of the parameter across all loci.

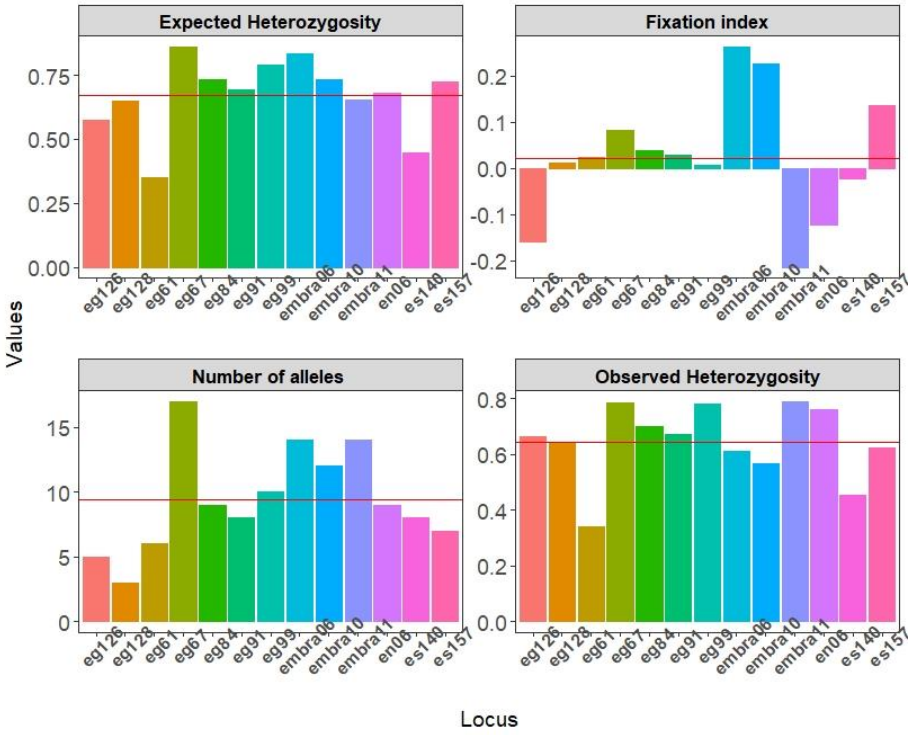


Figure 2. Values of delta K corresponding to each number of groupings simulated in a population of *E.benthamii* in municipality Colombo, state of Paraná, Brazil. $Delta\ K = mean\ (|L''(K)|)/sd\ (L(K))$

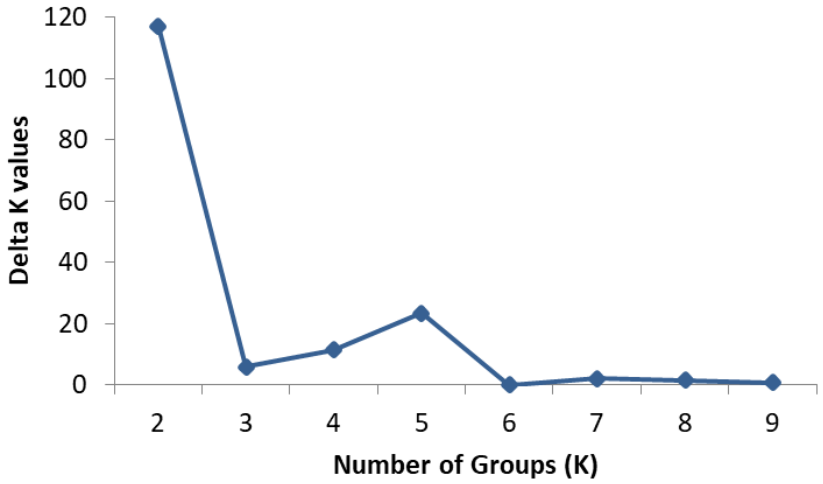
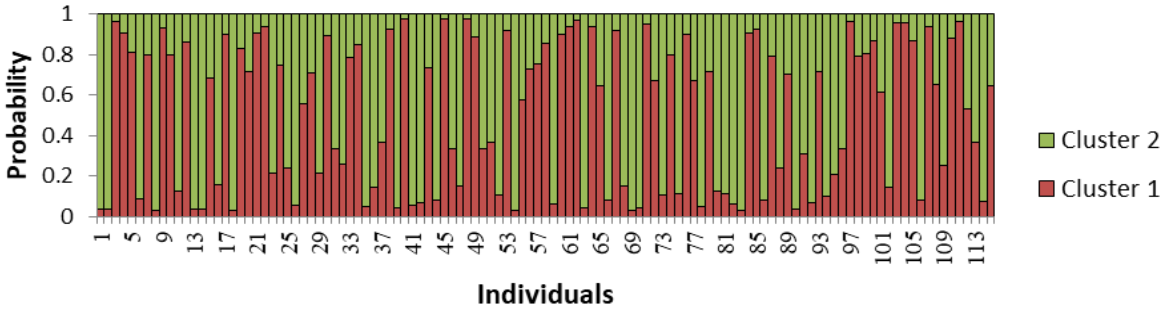


Figure 3. Bayesian-bases analysis of population structure for $K = 2$, L'(K)= 343,11 and ΔK= 117,20 in municipality Colombo, state of Paraná, Brazil.



550

551 Table 2- Comparative of descriptive genetics parameters between two populations of *E. benthamii* in
552 municipality Colombo, state of Paraná, Brazil.

553

Parameters	Population 1	Population 2
Sample Size	54	61
N. of alelles	8.31	7.39
Expct. heterozygosity	0.67	0.61
Fix. Ind.	0.01	0.02
Mean DBH	56 cm	54 cm

554 Table 3: Parameters estimated by pairwise kinship and genomic wide selection in a *E. benthamii* population in
555 Colombo, state of Paraná, Brazil.

556

Trait	r_{gy}	σ_a^2	σ_y^2	σ_e^2	h_2	θ_{xy}	$h_2{}'$
Dbh	-0.037	3.17	104.02	100.85	0.03		0.13
Height	-0.078	0.35	23.00	22.00	0.02		
Population						0.085	

557 Predictive ability (r_{gy}), additive variance (σ_a^2), phenotypic variance (σ_y^2), error variance (σ_e^2),heritability (h_2), pairwise
558 kinship coefficient (θ_{xy}) and heritability estimated using pairwise kinship coefficient ($h_2{}'$).
559
560

Figures

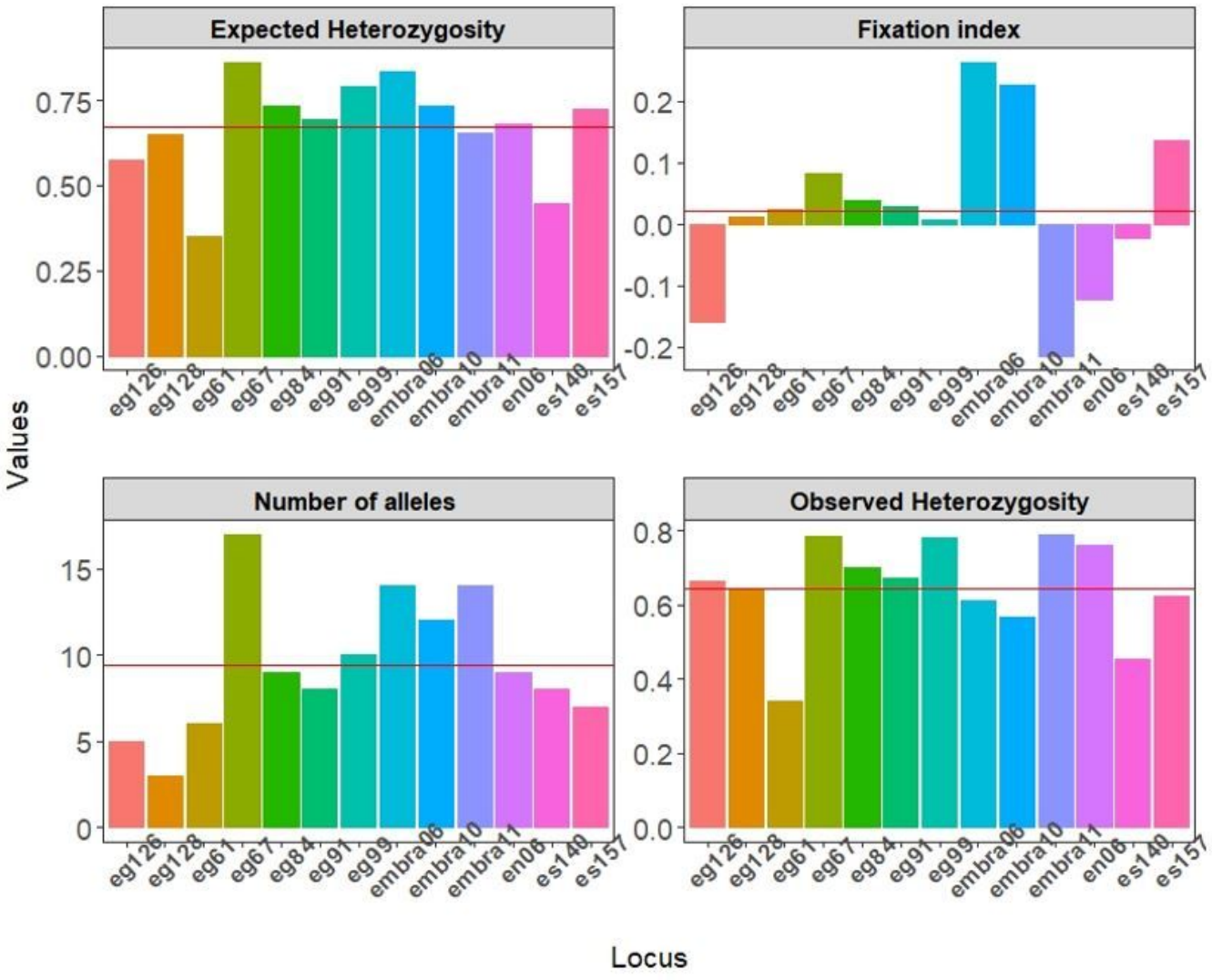


Figure 1

Descriptive genetics of the microsatellite loci used for individuals of E. benthamii in municipality Colombo, state of Paraná, Brazil. The red horizon line corresponds to the mean value of the parameter across all loci.

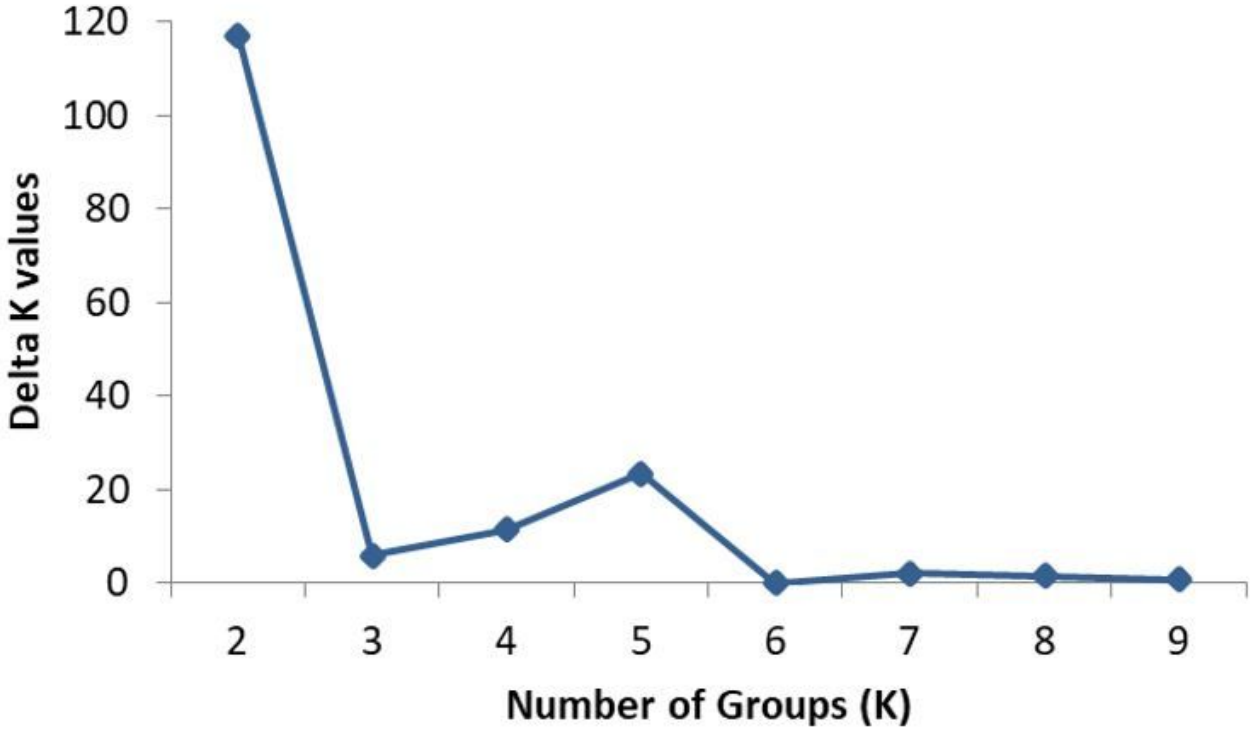


Figure 2

Values of delta K corresponding to each number of groupings simulated in a population of E.benthamii in municipality Colombo, state of Paraná, Brazil. Delta K=mean ((|L"(K)|))/(sd (L(K)))

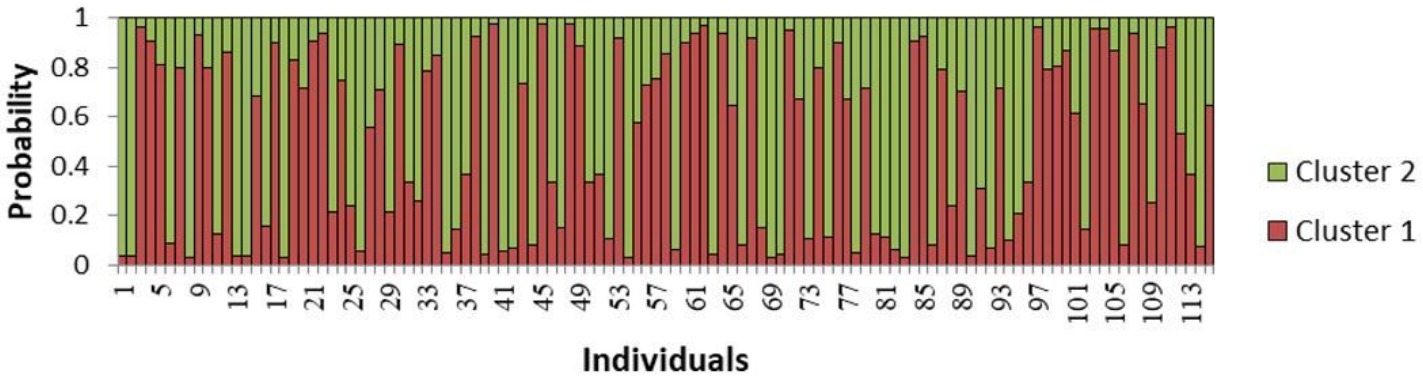


Figure 3

Bayesian-bases analysis of population structure for K = 2 , L'(K)= 343,11 and ΔK= 117,20 in municipality Colombo, state of Paraná, Brazil.