Evaluation of the breeding potential for height growth in *Acacia mangium* Willd.

Evaluación del potencial de mejoramiento genético en el crecimiento en altura de *Acacia mangium* Willd.

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Abstract

In 2009-10, in Ayapel, Planeta Rica and Tierralta, Córdoba (Colombia) the growth performance in overall height of 90 open-pollinated families of *Acacia mangium* was evaluated. In these municipalities the climate is classified, according to Holdridge, as tropical dry forest (TDF), except Tierralta that it is tropical moist forest (TMF). During the first year of growth, plants in each family were evaluated in progeny tests using a randomized complete block experimental design, with six blocks in each of the three locations. The experimental unit consisted of six open-pollinated plants per family, randomly distributed in three spatially separated pairs within each block. The prediction of genetic parameters of individuals and of families was conducted by the BLUP (best linear unbiased prediction) method and the variance components by REML (restricted maximum likelihood) procedure using the software SELEGEN. Heritability estimates ranged from <1 to 13%, and between 6 to 68%, for strictly individual heritability (h^2a) and family-mean heritability (h^2mp), respectively. Genetic ranking in height of the top 15 families indicates that those with the largest growth were also more stable and had greater adaptability to environments. Results suggest a high potential for improvement at the family level in growth and productivity of plantations of *A. mangium* in the department of Córdoba, Colombia. New measurements in next years are needed to achieve a better genetic selection.

Key words: Acacia, breeding, forest plantations, genetic parameters, progeny tests, Reml/Blup, Selegen, tree improvement.

Resumen

En el periodo 2009-10, en Ayapel, Planeta Rica y Tierralta, departamento Córdoba (Colombia) se evaluó el desempeño en crecimiento en altura total de 90 familias de polinización abierta de *Acacia mangium*. En estos municipios el clima se clasifica, de acuerdo con Holdridge, como bosque seco tropical (Bs-T), excepto Tierralta que es bosque húmedo tropical (Bh-T). Durante el primer año de crecimiento, las plantas en cada familia fueron evaluadas en ensayos de progenie mediante un diseño experimental de bloques completos al azar, con seis bloques en cada una de las tres localidades. La parcela o unidad experimental consistió en seis plantas de polinización abierta por familia, distribuidas aleatoriamente en tres parejas espacialmente separadas dentro de cada bloque. La predicción de parámetros genéticos individuales y de familias se efectuó por medio del procedimiento BLUP y los componentes de varianza por medio del procedimiento REML utilizando el software SELEGEN. Las estimaciones de heredabilidad variaron entre <1 y 13%, y entre 6 y 68%, para heredabilidad individual en sentido estricto (h^2a) y heredabilidad media de familias

(h^2mp), respectivamente. El ranking genético en altura de las 15 mejores familias indica que las de mayor crecimiento fueron también las más estables y de mayor adaptabilidad a los ambientes. Los resultados sugieren un alto potencial de mejoramiento al nivel de familia en crecimiento y productividad de plantaciones de *A. mangium* en el departamento de Córdoba, Colombia. Nuevas medidas en los próximos años son necesarias a fin de lograr una mejor selección genética.

Palabras clave: Acacia, ensayos de progenie, fitomejoramiento, mejoramiento genético, parámetros genéticos, plantaciones forestales, Reml/Blup, Selegen.

Introduction

Acacia mangium Willd. is one of the most cultivated forest species in Cordoba, Colombia (Rincon, 2009) and in the whole country. In 2009, the world market of wood and forestry products increased to US$188,805.2 million, from which 12.8% was sawnwood and 12.6% to wood pulp. In the same year, Colombia exported forestry products valued in US$263,5 million (Faostat, 2011). According to Ladrach (2010) *A. mangium* is one of the most used species in the world to produce pulp, together with numerous species and clonal hybrids of *Eucalyptus* spp. and *Pinus* spp. Nonetheless the importance of this forest species, some technological gaps have been identified, among them the lack of wood for sowing and genetic breeding (MADR, 2008), which is necessary to transform the forestry activity on a sustainable and safe productive process (Murillo and Badilla, 2004). Therefore, genetic breeding programs (GBP) for *A. mangium* have started in the last 5 years in the north of Costa Rica and in Cordoba, Colombia as efforts from the Cooperativa Internacional de Mejoramiento Genético Forestal (Genfores) (Espitia *et al.*, 2010; Murillo, 2011; Pavlotzky and Murillo, 2012).

In the forestry field, the GBP success is associated with the capacity of accuracy in selecting superior trees to be parentals of later generations (Barros *et al.*, 2006; Cruz and Carneiro, 2003; Apiolaza *et al.*, 2000) that, progressively, allow benefit increments by using higher yield materials in diverse environmental conditions.

The purpose to evaluate genetic assays is to determine breeding population parameters, by separating efficiently the genetic and environmental effects, and also by efficiently selecting the best genotypes based on their merits (Espitia *et al.*, 2010). In general, in uniform environments there is an efficient evaluation and selection of genetically superior trees (Talbert *et al.*, 1981). However, for perennial species these estimates should be obtained by more precise methods, because the information comes from timely measurements that usually make impossible the use of balanced data, which in turn, can generate mistakes in their analysis and interpretation (Resende *et al.*, 2007; Resende, 2000).

Barros *et al.* (2006) indicate that among the main procedures to estimate genetic parameter in progeny assays the analysis of variance (Anova) and the REML/BLUP (Restricted Maximum Likelihood / Best Lineal Unbiased Prediction) procedures are outstanding. However, Anova does not allow an efficient separation of the genetic and environmental effects (Resende *et al.*, 2007). Resende (2006) suggest that a suitable process for analysis and selection of forest genetic breeding experiments should: (1) favor selection based on genotypic values free of environmental effects, and (2) consider unbalance data in a suitable way. Therefore, according to this author (Resende, 2002) the most suitable procedure to predict genetic values in perennial plants and forestry species is the individual BLUP (Henderson and Quaas, 1976), while for genetic parameters estimation the recommendation is to use REML method, developed by Patterson and Thompson (1971). Thus, the optimal techniques for genetic evaluation involved, simultaneously, genetic values prediction and variance components estimation, therefore, the global procedure that allows a complete evaluation of the testing material is the REML/BLUP procedure (Resende *et al.*, 2007).

In forest research, selection of ‘plus’ trees for genetic breeding programs is primarly based on information generated on progeny assays, from which, the breeders use height growth data to compare development patterns between genotypes (Apiolaza *et al.*, 2000). In *Pinus taeda* L., for instance, tree height at early ages is used as selection criteria for the trait total volume (McKeand, 1988; Balocchi *et al.*, 1993), because it is a good predictor and is less affected by competence factors than stem diameter (Foster, 1986).

Selection of the best genotypes requires as well the estimation of its genetic stability through different environmental conditions; otherwise, it is not possible to use the best genetic material for extensive and diverse region as the department of Cordoba or in a large area of the Colombian Caribbean region (Espitia *et al.*, 2010). Therefore, this research estimated the first genetic parameters of behavior of *A. mangium* selected materials in various locations in the department of Cordoba, based on the use of mix models and REML/BLUP procedures with the SELEGEN software (Resende *et al.*, 2007).

Materials and methods

Research was done in the 2009 – 10 period in the towns of the department of Cordoba (Colombia): Ayapel (Site 1), Planeta Rica (Site 2) and Tierralta (Site 3). In these places the weather is classified, according to Holdridge (1967) as tropical dry forest (TDF), except Tierralta that it is tropical moist forest (TMF). Weather conditions in each site are shown in Table 1 (Palencia *et al.*, 2006).

In each site there were *A. mangium* progeny assays based on open pollination seeds (half-brothers families) from 90 plus trees (genotypically superior) (Vallejos *et al.*, 2010) as part of the Genetic Breeding Program on *A. mangium* in the department of Cordoba, Colombia, (Espitia *et al.*, 2010). Assays included commercial material available in the region as controls and, and they were established in May (Tierralta) and July (Ayapel and Tierra Rica) 2009 using 4 months old seedlings from nursery. Each assay had two lines of plants at the edges to protect the trees and void the edge effect on the evaluation. 30 days after the establishment of the assays, new plants where sowed to reduce unbalance in the assay caused by early plant mortality. Since at the end of the first year most of the trees were not higher than 1.3 m, only the total height could be used as responsive variable of interest for potential early selection; therefore, at this age total height (cm) with a metric scale was the only variable evaluated.

Statistical design and data analysis

In order to reduce the size of the blocks in the genetic assays and to reduce the risk of enhancing variability within the blocks, the 90 families collection was subdivided in two subpopulations with less than 50 families each and with 5 families in common in both subpopulations. However, in each experimental site the two complementary assays were established. The progeny of the 90 selected trees (plus) were planted in a completely random block design, where the plot or experimental unit (treatment) was the family conformed by six progenies, randomly distributed in three pairs within each block. Sowing density was 3 x 3 m. Random distribution of each pair from each family in each block was done using the software Excel developed by the Cooperative of Forest Genetic Breeding, Genfores (Murillo, 2011). Data analysis of the progeny assays was done with SELEGEN REML/BLUP software (Resende, 2006) and the models used are described below:

Table 1. Location and weather characteristics of the progenie experimental sites of *Acacia mangium* in Cordoba, Colombia.

Town	**Coordinates**		**PPA**	**HR**	**Temp.**	**BS**
	Latitude (N)	**Longitude (O)**	**(mm)**	**(%)**	**(°C)**	**(Horas)**
Tierralta	8°02’05.5”	76°12’01.2”	2674.6	82	27.6	1806.6
Planeta Rica	8°24’47.6”	75°36’16.9”	1564.3	80	27.6	1801.7
Ayapel	8°12’33.0”	75°05’07.6”	3487.8	85	26.9	1406.8

PPA: Annual average precipitation; HR: Relative humidity; Temp.: Annual average temperature; BS: Solar brightness.

Combined analysis

Statistical analysis of each one of the combinations of the evaluated sites was performed using the following statistical model:

$$\hat{Y} = Xr + Za + Wp + Ti + e$$

where, $\hat{Y}$ $\hat{Y}$ is the data vector, a common parameter among all the evaluated families, r corresponds to the repetition effects (assumed as fixed) summed to the general average, a corresponds to the individual additive genetic effects (assumed as random), p corresponds to the plot effects (assumed as random), i correspond to the interaction genotype x environment effects (random), and e correspond to experimental error effects (random).

Variance components were obtained by the REML Individual procedure in SELEGEN, from where it was determined: $V\hat{a}$: additive genetic variance, $V\widehat{parc}$: environmental variance between plots, $V\widehat{int}$: interaction genotype x environment variance, $V\hat{e}$: residual variance (environmental plus no-additive). From these components of variance another genetic parameters were generated $h^2\hat{a} = h^2$: individual heritability in strict sense, it means, from the additive effects, $h^2\hat{a}j$: individual heritability in strict sense, adjusted for the plot effects, , $c^2parc = c^2$: determination coefficient of the plot effects, $c^2int = c^2 1$: determination coefficient of the interaction genotype x environment effects, $h^2\widehat{mp}$: average family heritability, assuming complete survival, *Acprog*: precision of the genetic parameters estimates, assuming total survival, *rgloc*: genotypic correlation between family performance through the three sites, $h^2\widehat{ad}$: additive heritability within the family, *PEV*: variance of the prediction error of the family genotypic values, assuming complete survival, *SEP*: standard deviation of the predicted family genotypic value and, *general mean* of the experiment.

Stability, adaptability and phenotypic production analysis

The stability (MHVG) was obtained using the calculus on the harmonic mean of the predicted genetic values; adaptability (PRVG) was obtained from the ratio between the relative yield of the predicted genetic values and the mean for each environment and, based on the harmonic mean of the predicted genotypic values relative yield, the phenotypic productivity (MHPRVG) was obtained. Estimation of these parameters in the three environments evaluated was done with SELEGEN software based on the model:

$$\hat{Y} = Xr + Zg + Wp + Ti + e$$

Where, Y is the data vector, r is the vector for repetition effects (assumed as fixed) summed to the general mean, g is the vector for the genotypic effects (assumed as random), p is the vector for the plot effects (random), $\boldsymbol{i}$ is the vector for the genotype x environment interactions (random) and e is the vector for errors or residuals (random).

In this case the same variance components and genetic parameters described were obtained in the site combination analysis using REML. To this analysis were added: *CVgi%* = coefficient of individual genetic variation, *CVe%* = coefficient of residual variance and the *general* mean of the experiment. In the models described previously, capital letters represent the incidence matrix for the referred effects. From the genetic parameters estimates, SELEGEN generated a ranking of the best families based on their average genetic value and the additive genetic value ($u + \hat{a}$).

Results and discussion

It can be considered that at the age of 1 year, the phenotypic variability observes is highly influenced by the environmental effects (Table 2). It is observed than in the combinations where the site 2 is involved (1-2 and 2-3) present low estimated genetic values, however it increases as when the 1-3 site combination is evaluated, these represent the best climatic conditions for the development of plants (Table 1).

Individual heritability in the strict sense (h^2a) registered low values in general, including the combined analysis for the three sites (6%). The highest value is obtained in the site combination 1-3 (13%). Lokmal (1994) and Murillo (2001) mentioned that high values in the interactions (mainly, genotype x environment) sensibly reduce the estimates for $h^2\hat{a}$. This can explain the fact that the site combi

Table 2. Estimated genetic parameters and analysis of the genotype x environment interaction for total height in the first year of *Acacia mangium* families, evaluated on progeny assays of the genetic breeding program of this species in Cordoba (Colombia).

Genetic parameter	Site 1-2	Site 2-3	Site 1-3	Site 1-2-3
$V\ \hat{a}$	20.31	33.43	704.57	254.64
$V\widehat{parc}$	320.74	125.59	320.45	249.75
$V\widehat{int}$	132.39	169.37	133.32	147.19
$V\hat{e}$	3457.94	3059.52	4113.11	3586.59
$V\hat{f}$	3931.38	3387.90	5271.44	4238.17
$h^2\hat{a}$	0.01	0.0099	0.13	0.06
c^2parc	0.08	0.0371	0.06	0.06
c^2int	0.03	0.0500	0.03	0.03
$h^2\widehat{mp}$	0.06	0.0820	0.68	0.52
Acprog	0.24	0.2864	0.83	0.72
$h^2\widehat{ad}$	0.00	0.008	0.11	0.05
Rgloc	0.04	0.047	0.57	0.30
PEV	4.78	7.672	55.90	30.47
SEP	2.19	2.770	7.48	5.52
Average height (cm)	273.03	269.87	394.80	313.71

nations 1-2 and 2-3 got very low estimates for $h^2\hat{a}$ (<1%), because the variance components of the interactions ($V\widehat{int}$ y $V\widehat{parc}$) were between 3 to 15 times higher than the variance for the additive effects ($V\hat{a}$), reducing the estimate for individual heritability in a direct way. $\widehat{\imath nt}$ $\widehat{parc}$However, it is worth to note that at the age of 1 year, the genetic variation between families ($V\hat{a}$) was still low, which can explain the low estimates for general heritability.

In recent researches with *A. mangium* in Costa Rica, for traits as diameter in the year 1 and 4, there are $h^2\hat{a}$ values over 50% (Pavlotzky and Murillo, 2012) and values between 40 and 50% when two sites were analyzed simultaneously (Pavlotzky, 2012). In *A. mearnsii*, evaluated on a progeny assay with 1 year old plants of different subpopulations, $h^2\hat{a}$ varied between 0.04 and 0.63, which is explained, among other factors, as a consequence of the high environmental influence due to the early age of evaluation (Dunlop *et al.*, 2005) and, as genetic influence from the progenies, as it was found in *Pinus oaxacana* Mirov. (Zitácuaro and Aparicio, 2004) and in *Pseudotsuga menziessi* Mirb. (Gutiérrez, 2007), which had high variation between progenies evaluated in the first year of growth. This is in agreement with the findings in *A. mangium* in this research, where the environmental variance ($V\hat{e}$) represented from 78% (Site) till 90% (Site 2-3) of the total phenotypic variation. Thus, it is suggested that 1 year of establishment is not enough to achieve trustable genetic estimates, in particular if the evaluation is done on sites with highly contrasting environments

In other forest species similar responses have been found in the first year of evaluation, as it is for *Pinus radiata* (Apiolaza *et al.*, 2000) and *Schizolobium parahybum* (Vell) Blake (Rosales *et al.*, 1999) with $h^2\hat{a}$ values of 0.09 for height. Lokmal (1994) found $h^2\hat{a}$ values of 0.07 for *Gmelina arborea* Roxb. Navarro and Hernández (2004) found for progenies of *Swietenia macrophylla* from different origins $h^2\hat{a}$ values of 0.55, 0.57 and 0.60 for ages of 1.70, 0.70 and 2.70 years, respectively, which are high when compared to the ones found in this study for *A. mangium.*

Genotype x environment interaction explains between 3% and 5% of the proportion of the total phenotypic variability for all the site combinations, however, the low estimated genetic variance does not allow good estimates of genotypic correlations (Rgloc) through the environments (Table 2). There is a high variability in the genetic response of the evaluated progenies in the studied environments. Only the correlation involving the 1-3 sites has a moderate estimate with a value of 0.57. This result implies that the genetic ranking between both sites starts to show similar results. Contrary, combinations with site 2 generate very low genotypic correlations, which mean that the best families in height are different within sites. Meanwhile, the correlation implying the three sites had a 0.30 coefficient indicating that the interaction can have a complex nature (Vencovsky and Barriga, 1992), nonetheless, the early evaluation of the progenies can supposed that these values will improve as the plant growth stabilizes and the differences tend to be less affected by the environments.

The average family heritability ($h^2\widehat{mp}$) and the accuracy of the selection estimates (Acprog) in the combined analyses show good values that allow predicting the efficiency of the general selection, even when the three sites are involved. Pavlotzky and Murillo (2012) found in the year 1 and 4 diameters in *A. mangium* families with $h^2\widehat{mp}$ values that are over 90%. However, Rosales *et al.* (1999) found $h^2\widehat{mp}$ values of 0.45 for *Schizolobium parahybum* (Vell) Blake, in the evaluation of progenies from different origins at 1 year age; these estimates are low respect to the ones obtained in this study with *A. mangium.*

In the Table 3 is shown the ranking of the best 15 families for total height according to the selection criteria given by the 4 and 51 models of SELEGEN REML/BLUP. It is observed that for *MHVG*, *PRVG* y *MHPRVG* seven of the 15 families are also in the genetic ranking for height in the combine analysis of sites. These results revealed that already in the first year, the families with larger height are also the ones with more stability and adaptability to different environments; this suggest their possible use at a commercial scale in all the regions of Cordoba, with low risk of reducing their yield despite of the environmental variability around.

Table 3. Genetic ranking for total height, stability (MHVG), adaptability (PRVG) and productivity (MHPRVG) of the best 15 families of *Acacia mangium*, in three sites in Cordoba, Colombia.

Order	Three sites*	MHVG	PRVG	MHPRVG
1	52	88	47	47
2	47	5	52	52
3	37	86	23	23
4	23	89	83	83
5	17	2	45	45
6	83	87	17	17
7	53	90	37	37
8	48	47	57	57
9	57	83	21	21
10	45	23	38	38
11	50	52	8	8
12	8	45	6	6
13	21	6	53	53
14	38	21	48	48
15	82	17	50	50

* Underlined values: common families in the genetic ranking through sites and analysis of adaptability, stability and phenotypic productivity.

Conclusions

- In the first year of *A. mangium* growth there is still a high environmental influence over the observed phenotypic variability for total height of trees. Genetic parameters estimates for total height increase when the site combination 1 and 3 is evaluated.
- Genotypic x environment effects are significantly superiors to the additive genetic effects at the individual level, this reduced the heritability values obtained in this research. However, the genetic control with respect to the familiar heritability ($h^2\widehat{mp}$) is high, which indicates a good potential for selection at this level based on initial growth in height.
- $\widehat{mp}$The estimates of the genetic parameters obtained at the individual level in the first year of age are not enough to accurately perform a selection of materials nor to estimate expected genetic gains. Therefore, it is convenient to follow successive evaluations of height on these assays to ob-

tain better genetic parameter estimates and be able to determine the best selection age.

- A group of families within the best 15 families genetic ranking for height registered also high stability, adaptability and productivity at the first year of growth; this suggests their possible use at commercial scale in Cordoba, with low risk of losing productivity

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