**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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Rec.: 14.10.11 Acept.: 08.06.12

**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 (h2a) and family-mean heritability (h2mp), 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 (h2a) y heredabilidad media de familias (h2mp), respectivamente. El rankinggenético 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.

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| **Table 1.** Location and weather characteristics of the progenie experimental sites of *Acacia mangium* in Cordoba, Colombia. |
| **Town** | **Coordinates** | **PPA****(mm)** | **HR****(%)** | **Temp.****(°C)** | **BS****(Horas)** |
| ***Latitude (N)*** | **Longitude (O)** |
| 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. |

**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:

**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, $\hat{Y}$ *Ŷ* 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: *Vâ*: additive genetic variance, *V*$\hat{parc}$: environmental vari­ance between plots, *V*$\hat{int}$: interaction genotype x environment variance, *Vê:* residual variance (environmental plus no-additive). From these components of variance another genetic pa­rameters were generated *h2â = h2*: individual heritability in strict sense, it means, from the additive effects, *h2*$\hat{aj}$*:* individual heritability in strict sense, adjusted for the plot effects, , *c2parc = c2*: determination coefficient of the plot effects, *c2int = c21*: determination coeffi­cient of the interaction genotype x environ­ment effects, *h2*$\hat{mp}$*:* 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, *h2*$\hat{ad}$*:* 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), ***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 + â*).

**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 (*h2a*) 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 *h2â*. This can explain the fact that the site combi­nations 1-2 and 2-3 got very low estimates for *h2â* (<1%), because the variance components of the interactions (V$\hat{int }$y V$\hat{parc}$) were between 3 to 15 times higher than the variance for the additive effects (*Vâ*), reducing the estimate for individual heritability in a direct way. $\hat{int }\hat{parc}$However, it is worth to note that at the age of 1 year, the genetic variation between families (*Vâ*) was still low, which can explain the low estimates for general heritability.

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| **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 â | 20.31 | 33.43 | 704.57 | 254.64 |
| V$\hat{parc}$ | 320.74 | 125.59 | 320.45 | 249.75 |
| V$\hat{int}$ | 132.39 | 169.37 | 133.32 | 147.19 |
| *Vê* | 3457.94 | 3059.52 | 4113.11 | 3586.59 |
| V$\hat{f}$ | 3931.38 | 3387.90 | 5271.44 | 4238.17 |
| *h2â* | 0.01 | 0.0099 | 0.13 | 0.06 |
| *c2parc* | 0.08 | 0.0371 | 0.06 | 0.06 |
| *c2int* | 0.03 | 0.0500 | 0.03 | 0.03 |
| *h2*$\hat{mp}$ | 0.06 | 0.0820 | 0.68 | 0.52 |
| *Acprog* | 0.24 | 0.2864 | 0.83 | 0.72 |
| *h2*$\hat{ad}$ | 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 |

In recent researches with *A. mangium* in Costa Rica, for traits as diameter in the year 1 and 4, there are *h2â* 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, *h2â* 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 (*Vê*) 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 *h2â* values of 0.09 for height. Lokmal (1994) found *h2â* va­lues of 0.07 for *Gmelina arborea* Roxb. Nava­rro and Hernández (2004) found for progenies of *Swietenia macrophylla* from different ori­gins *h2â* 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 (h2$\hat{mp}$) 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 h2$\hat{mp} $values that are over 90%. However, Rosales *et al.* (1999) found h2$\hat{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*.

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| **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. |

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.

**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 (h2$\hat{mp}$) is high, which indicates a good po­tential for selection at this level based on initial growth in height.
* $\hat{mp}$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 ob­tain 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

**Acknowledgements**

Authors are thankful to the Universidad de Córdoba, Kanguroid-3F company and to the Ministry of Agriculture and Rural Develop­ment (MADR) for financing the macro project Selection of Plus Trees and Creation of Seed Sources of Teca (*Tectona Grandis* L.), Melina (*Gmelina Arborea* Roxb.) and Acacia (*Acacia mangium* Willd.) in the Department of Cordoba, in which this research was framed.

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