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CROP BREEDING AND
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NOTE

Prediction of genotypic values of maize for the agricultural frontier region in northeastern Maranhão, Brazil

Emmanuel Arnhold[1]*, Freddy Mora[2], Cleso Antônio Patto Pacheco[3] and Hélio Wilson Lemos de Carvalho[3]

ABSTRACT – *Agricultural research, mainly focused on the evaluation of maize cultivars along agricultural frontiers, are scarce. This study assessed 128 maize genotypes in the agricultural frontier region of the State of Maranhão, between 2008 and 2009. The experiment was arranged in a lattice design with two replications. The genotypes were evaluated for grain yield in a mixed model, with fixed intercept and experimental effects. The random effects were genotype, genetic class (single-, double or triple-cross hybrid and variety), and incomplete block/replication/ environment. The genotype effect was significant by the likelihood ratio test in all models, highlighting the genotypic values of the single-cross hybrids DKB177, AG8088 and DKB390, the triple-cross PL6882, the double-cross BM502 and of the open-pollinated variety SHS3031.*

Key words: Zea mays *L., cultivar, grain yield, REML/BLUP*

INTRODUCTION

The commercial exploitation of maize in the northeastern cerrado region began in the 1980s, in western Bahia, South of Maranhão and in the developing region of Uruçuí- Gurguéia, in the state of Piauí. These areas are appropriate for maize cultivation, in view of the favorable soil conditions and a climate suited for rainfed grain production, aside from a topography that allows mechanized agriculture (Carvalho et al. 2000).

However, in the Brazilian Northeast, the high population density and increasing poultry and pork production have led to a considerable demand for maize. The production of the Brazilian Northeast is insufficient to meet this need, so that large grain quantities must be imported from other regions of the country and from abroad, to complement the regional need (Carvalho et al. 2002). This region has an extensive agricultural frontier where cultivation can be expanded to increase yields (Cardoso et al. 2003).

It is known that higher yields involve a number of factors, above all the correct choice of cultivars adapted to a particular region (Cruz et al. 2004). Every year, several maize cultivars are being released on the market by public and private companies.

These should be evaluated, to identify those with highest yield potential for the regional environmental conditions (Cardoso et al. 2003). Thus, considering the differences in environments and in production systems, the evaluation of maize cultivars seems interesting, as an orientation for farmers when choosing these materials (Carvalho et al. 2005).

In this context, it should be noted that the northeastern region of Maranhão (Lower Parnaíba Region), in the far north of the mid-north region of Brazil, is promising for agricultural expansion. The area is suitable for mechanized farming, and also located near the harbor of São Luis, whose location favors the grain export to countries in Europe and the USA. The region can also become a center of regional development and produce food for northern and northeastern Brazil. However, little scientific or technical data are available for this specific region that could serve as guidelines for producers who are often rely on empirical methods to search for new technologies and increase productivity (Arnhold et al. 2010).

Another important aspect to be taken into consideration is the statistical methodology used to evaluate the genotypes. For Resende and Duarte (2007), the estimators of Value for Cultivation and Use (VCU) should almost always be based

[1] Universidade Federal de Goiás, Campus Samambaia, C.P. 131, 74.001-970, Goiânia, GO, Brazil. *E-mail: earnhold@pq.cnpq.br
[2] Instituto de Biología Vegetal y Biotecnología, Universidad de Talca, 2 Norte 685, Talca, Chile
[3] Embrapa Tabuleiros Costeiros, Avenida Beira Mar, 3250, Jardins, C. P. 44, 49.025-040, Aracajú, Sergipe, Brazil

on random or mixed models with random effects of genetic treatments for the use of intergenotypic information derived from this assumption of randomness. In this context in plant breeding, the estimation of variance components and prediction of genetic values are key aspects in the quantitative genetic analysis of economically important traits. By the mixed linear model methodology, it is possible to calculate the BLUP (Best Linear Unbiased Prediction) of the random effects, in this case the genetic gain, by maximizing the combined density function considering the fixed and random effects of the mixed model. The prediction of random effects of the mixed model depends on the accuracy of the variance component estimates, which are preferably estimated by the REML (Restricted Maximum Likelihood) procedure. According to Borges et al. (2010), REML / BLUP methods are nowadays the most accurate methods for analyses in a wide range of applications, advantageously replacing the method of analysis of variance, especially in cases of experiments with a certain degrees of imbalance.

According to Maia et al. (2011), mixed models would be more realistic, with more accurate results. According to the same authors, more refined genetic-statistical procedures, e.g., the variance component estimation and mean component prediction by REML / BLUP are upcoming trends in plant breeding.

In fact, mixed models with prediction of genotypic values have been used in several studies, for perennial, semi-perennial as well as annual plants (Oliveira et al. 2005, Carbonnel et al. 2007, Bastos et al. 2007, Piepho et al. 2007, Pedrozo et al. 2008, Arnhold et al. 2009, Maia et al. 2009, Borges et al. 2010, Maia et al. 2011).

Piepho et al. (2007) discussed the usefulness of linear mixed models in the advanced stages of cultivar selection (i.e., in VCU trials, considering tests in multiple environments). The researchers demonstrated that the Restricted Maximum Likelihood was preferable to the Maximum Likelihood (ML; Maximum Likelihood), in the estimation of variance components. In turn, in the VCU trials, BLUP is preferable to the BLUE (Best Linear Unbiased Estimator), justifying the use of genotype as random effect.

Thus, this study was carried out to predict genotypic values (BLUPs) of maize genotypes in the region of the agricultural frontier in the northeastern state of Maranhão.

MATERIAL AND METHODS

Between 2008 and 2009, 128 different maize genotypes were evaluated in three experiments, divided into three environments, along the agricultural frontier in the northeastern state of Maranhão. Three trials were carried out: 1) a 6 x 7

lattice with single, triple and double-cross hybrids; 2) a 6 x 7 lattice with single, triple and double-cross hybrids and open-pollinated varieties and 3) a 7 x 8 lattice with single, triple and double-cross hybrids and open-pollinated varieties. The lattices were replicated twice and involved 12 common genotypes in at least two experiments.

Experiment 1 was evaluated in two environments, one beginning on February 14, 2008, in Anapurus and the other on February 18, 2008, in Brejo. Experiment 2 was evaluated in an environment, installed on February 15, 2008, in Anapurus. Experiment 3 was evaluated in an environment in Chapadinha, beginning on February 13, 2009. All three environments are located in the northeastern state of Maranhão, along the agricultural frontier of the region known as the Lower Parnaíba of Maranhão.

In all experiments, each plot consisted of four 5-m rows, spaced 0.90 m apart. Plants were thinned to 25 seedlings per row, corresponding to a population of approximately 55,555 plants ha^{-1}. Fertilization was tailored for each experiment according to the results of soil analyses for each experimental area. Each plot corresponded to the two complete central rows, totaling an evaluated area of 9.0 m^2. In this area, the threshed grain weight (kg plot^{-1}) and moisture (%) were determined. Prior to the statistical analyses, grain moisture was standardized at 15% and grain weight was transformed from kg plot^{-1} to kg ha^{-1}.

The genotypes were evaluated by the following mixed model, in which grain yield was a response variable (GY, kg ha^{-1}).

$$y_{ijkb(r)(a)} = \mu + \alpha_i + \beta_j + \gamma_k + (B/R/A)_{b(r)(a)} + e_{ijkb(r)(a)}$$

where:

- $y_{ijkb(r)(a)}$: is the observed value in experiment i(α:i = 1,2,3), of genotype j(β:j = 1,2,3, ... ,128), which belongs to gene class k(γ:k = 1,2,3,4), in the incomplete block b(B:b = 1,2,3, ... ,22), within replication r(R:r = 1,2), of environment a(A:a = 1,2,3);

- μ: constant (intercept) inherent to all observations;

- α: fixed effect of experiment i (α:i = 1, 2, 3);

- β: random effect of genotype j(β:j = 1,2,3, ... ,128), assuming ~NID(0, σ_g^2);

- γ: genetic random effect of class k(γ:k = 1,2,3,4), assuming ~NID(0, σ_c^2);

- $(B/R/A)_{b(r)(a)}$: effect of incomplete block b(B:b = 1,2,3, ... ,22), within the replication r(R:r = 1,2), within the environment a(A:a = 1,2,3), assuming ~NID(0, σ_b^2);

- $e_{ijkb(r)(a)}$: effect of the random errors associated with the observation $y_{ijkb(r)(a)}$, assuming ~NID(0, σ_e^2);

- and also assuming that β_j, γ_k, $(B/R/A)_{b(r)(a)}$: and $e_{ijkb(r)(a)}$ are independent.

The component "genetic class" was included in the model to correct the imbalance between experiments in relation to the number of single, double and triple-cross hybrids and varieties, which would be confused with the environmental effect.

The genetic class was considered random, for representing a sample of each assessed genetic class. The same applies to the use of incomplete blocks, considered random. But the genotypes were considered random according to the observations of Resende and Duarte (2007). For these authors, the effects of genetic treatments should be considered random when the number of treatments is greater than 10, to minimize the mean square error in the estimation of the true genetic values.

Fritsche-Neto et al. (2010) concluded that the prediction of genotypic values is little affected by an imbalance of up to 20% for genotypes. Despite the severe imbalance observed in this study, it was understood that this way of estimating the genotypic values, using REML/BLUP was the best to evaluate this genotype set, since in animal breeding, BLUPs are estimated with very severe imbalances. The genotype x environment interaction was not investigated since the differences between environments in the region were small and the imbalance considerable, which could generate imprecise estimates.

The significance of the effects of genotypes and of other random components of the model were checked by the likelihood ratio test (Arnhold et al. 2009). The Spearman correlation was used to evaluate the correlations between the genotype ranking based on their genotypic and phenotypic means.

These analyses were performed using software R (R Development Core Team 2011) and the package for analysis of mixed models called lme4 (Bates and Bolker 2011). In the lme4 package, the lmer function was used, with variance component estimation by REML.

RESULTS AND DISCUSSION

The overall mean of 128 genotypes was 4892 kg ha^{-1}, which is still low in view of the potential yield of maize, but is similar to the averages found in experiments with maize in northeastern Brazil, as reported by Souza et al. (2002), Cardoso et al. (2003), Carvalho et al. (2000), Carvalho et al. (2002), Carvalho et al. (2005) and Arnhold et al. (2010). In a study with hybrids only, Arnhold et al. (2010) recorded an average of 5593 kg ha^{-1}, while in this study open-pollinated varieties were evaluated as well.

In the Lower Parnaíba region of Maranhão, maximum yields reported by producers are around 6000 kg ha^{-1} on mechanized farms using modern hybrids. The difficulty of increasing yields is caused mainly by the adverse conditions of climate and soil and the lack of genotypes adapted to these conditions. In this context, the high night temperatures (minimum frequently above 24 ^{0}C) are particularly injurious, aside from heavy rainfalls that facilitate nutrient leaching, which is especially problematic because of the excessively sandy soils of the region. According to Galon et al. (2010), high night temperatures and nitrogen deficiency are among two of the main factors affecting maize production.

The genotypic variance, together with the other random components, was statistically significant (p < 0.05) by the likelihood ratio test, indicating the possibility of effective selection based on BLUPs of the genotype effect.

The estimated Spearman correlation of the BLUP ranking based on the genotype means was 0.75 (p < 0.05 by the t test). This result demonstrates that the selection based on the phenotypic means would not select the same genotypes. However, most selected genotypes would be common to a selection based on BLUP ranking. The variance components, determined by REML, also play an important role in the context of mixed models. In fact, according to Resende and Duarte (2007), the precise estimation of variance components is fundamental since it can enhance the accuracy of the genetic values of genotypes and, consequently, the identification of genetically superior plants. Therefore, when information from the agronomic data set is lost, the REML method is preferable.

The best 15 genotypes according to BLUP (Table 1) show that the single-cross hybrids are superior. This fact was expected, since single-cross generally performs better than triple-cross hybrids, which are generally better than the double-cross, which are in turn generally superior to the open-pollinated varieties (Alves et al. 2006, Emygdio et al. 2007, Arnhold et al. 2010). In this study, the yield means of the single, triple and double-cross hybrids and open-pollinated varieties were 5742, 4933, 4634, and 3322 kg ha^{-1}, respectively, while the BLUPs of the genetic class of the same were 917, 255, 29, and -1201, respectively.

The best-performing of the large number of assessed genotypes were the single-cross hybrids DKB177, AG8088 and DKB390, the triple-cross hybrids PL6882, the double-cross hybrids BM502, and the open-pollinated variety SHS3031 (Table 1). The genotypes DKB177, AG8088 and

Table 1. The 15 best genotypes by their respective BLUPs, with their respective genetic classes

Genotypes	BLUPs	Genetic Classes
DKB177	691	HS
AG8088	690	HS
BM502	667	HD
DKB390	640	HS
SHS3031	548	V
AS1567	543	HS
P30P70	520	HS
XB8030	505	HD
Balu761	501	HD
BRS3025	455	HS
PL6882	439	HT
GNZ9501	413	HS
P30F35	392	HS
ALVORADA	375	V
CD308	370	HT

* HS: single-cross hybrid; HT: triple-cross hybrid; HD: double-cross hybrid; V: open-pollinated variety.

DKB390 are single-cross hybrids sold by their companies as high yielding for vast growing regions of Brazil. These are the most indicated genotypes for exploitation on the mechanized farms of the region. The hybrids PL6882 and BM502 and the open-pollinated variety SHS3031 can be used on less mechanized, smaller farms. All these genotypes can be utilized in crosses with local varieties to obtain lines for the development of hybrids with a high regional performance.

Considering that the means of some of the genotypes were above 7000 kg ha^{-1}, it is concluded that the use of these lines can contribute very significantly to the intensification of maize cultivation in this region.

CONCLUSIONS

The likelihood ratio test indicated a significant genotype effect, and highest genotypic values of the single-cross hybrids DKB177, AG8088 and DKB390, the triple-cross hybrid PL6882, double cross hybrid BM502 and the open-pollinated variety SHS3031. These genotypes are recommended for direct use in planting or in breeding programs for the development of hybrids and varieties for the region.

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Predição de valores genotípicos de milho para região de fronteira agrícola no nordeste do Maranhão

Resumo - *É escassa a realização de pesquisas agronômicas com o milho em fronteiras agrícolas, principalmente quanto à avaliação de cultivares. Assim, objetivou-se avaliar 128 genótipos entre 2008 e 2009 em região de fronteira agrícola no Estado do Maranhão. Os experimentos foram delineados em láticas com duas repetições. Os genótipos foram avaliados pela produção de grãos em modelo misto, tendo como efeitos fixos o intercepto e o efeito de experimento. Os efeitos aleatórios foram os de genótipos, classe genética (híbrido simples, triplo ou duplo e variedade) e bloco incompleto/repetição/ambiente. O efeito de genótipo foi significativo pelo teste da razão da verossimilhança em todos os modelos, destacando-se os valores genotípicos dos híbridos simples DKB177, AG8088 e DKB390, o híbrido triplo PL6882, o híbrido duplo BM502 e a variedade de polinização aberta SHS3031.*

Palavras-chave: Zea mays *L., cultivar, rendimento de grãos, REML/BLUP.*

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