https://doi.org/10.1590/1678-4499.20190271

PLANT BREEDING
Article

A new proposal for the m + a methodology in segregating populations of cowpea

Renata Fernandes de Matos[1*], Antônio Moreira Barroso Neto[1], Júlio César DoVale[1], Cândida Hermínia Campos de Magalhães Bertini[1], Roberto Fritsche-Neto[2]

1. Universidade Federal do Ceará – Departamento de Fitotecnia – Fortaleza (CE), Brazil.
2. Universidade de São Paulo – Escola Superior de Agricultura “Luiz de Queiroz” – Departamento de Genética – Piracicaba (SP), Brazil.

ABSTRACT: The evaluation of segregating populations in plant breeding programs is an onerous and time-consuming process. Early identification of populations with genetic potential can be done by m + a methodology. However, the possibility of a modification in the traditional methodology in order to make it more efficient, that is, faster and cheaper, was envisaged. Thus, the objective of this study was to compare the genetic gains obtained by both methodologies, the traditional one and the proposed modification. For this, ten segregating bean-cowpea populations were evaluated at two distinct levels of homozygous $F_{3:4}$ and $F_{3:5}$. Genetic values were predicted by two different statistical genetic models. This was possible due to the methodology proposed here to present a much shorter execution time than the traditional methodology. Thus, with a shorter evaluation time, the breeding program manager can plan the evaluation of a larger number of populations in a short time.

Key words: genetical enhancement, precocity, selection.

Received:
Jul. 11, 2019

Accepted:
Feb. 3, 2020

Section Editor:
Freddy Mora

*Corresponding author:
renatafmatos@hotmail.com

INTRODUCTION

Conducting segregating populations is considered the most critical, laborious, and costly phase of an autogamous breeding program (Rocha et al. 2015; Pontes Júnior et al. 2016). Although there is a 50% reduction in the frequency of heterozygous loci for each generation of self-fertilization, the probability of selecting a genotype with a high concentration of favorable alleles in early generations is very low. It becomes difficult when polygenic traits are considered. Thus, populations should be conducted to more advanced generations to overcome this difficulty (Jinks and Pooni 1976; Abreu et al. 2002). Therefore, the previous knowledge about populations with potential for extraction of superior inbred lines can lead to a considerable reduction in costs, time, and demands in a breeding program.

A useful approach in this process is the m + a estimates (Vencovsky 1987), which allows the evaluation of the genetic potential of segregating populations with varying levels of homozygosity in early generations. The value of “m” refers to the mean of the population, while “a” is the contribution of the homozygous loci concerning that average. In this sense, the m + a estimates correspond to the mean of all the individuals that compose a population in a given generation. Thus, the greater the value of m + a, the greater the frequency of favorable alleles and, consequently, the more easily inbred lines of high breeding value can be extracted from a population (Carneiro et al. 2002). In order to achieve this aim, by the traditional methodology, simultaneous evaluation of the populations in two consecutive generations is necessary, and they must be subjected to the same trial conditions.

This method was adopted in some studies in the past to identify promising inbred lines to obtain single-crosses, mainly in maize. Some of these studies achieved less than satisfactory results (Nass and Miranda Filho 1995; Viana et al. 2009). It is likely due to the complexity of gene expression of a single-cross because, in addition to the additive genetic effects, there is also the considerable contribution of nonadditive genetic effects (dominance × additive and dominance × dominance). Theoretically, the methodology would be suggested to predict inbred lines in autogamous species, due to the predominance of the loci in homozygotes.

Nevertheless, there are almost no papers in the literature applying the m + a methodology neither to autogamous species, nor to breeding programs for cowpea. An explanation may be the slow process of this method, at least three growing seasons, since it requires two following populations (e.g., F_2 and F_3 or F_3 and F_4) only to be evaluated together. Thus, it makes this approach costly and time-consuming. However, the authors of this work believe that with a simple modification, it is possible to turn it into in a more attractive method, achieving greater methodological and flexibility, without significant losses of robustness.

Therefore, the proposal is to evaluate the potential of populations in segregating generations as they are normally obtained (continuously), where the effect given by the environment (which should be common to both trials) is estimated by the behavioral differential of checks in two consecutive generations. The hypothesis is that estimates are equivalent to those generated by the first m + a methodology, and that it will be possible to reduce time, cost, and area dedicated to evaluations. Hence, the objective of this study was to compare the genetic gains obtained by the original methodology m + a, which can be estimated by the expression $2F_2$-F_1 and the proposed modification.

MATERIAL AND METHODS

A complete diallel was conducted between the parent lines CE-542, CE-796, CE-945, CE-954, F4RC1, and MNC03-737E-5-10 and selection between and within them based on plant height, precocity, and grain yield. The ten best populations of cowpea were obtained in F_3: CE-542 X CE-796, CE-542 X CE-945, CE-542 X CE-954, CE-542 X MNC03-737E-5-10, EC-796 X CE-945, CE-796 X F4RC1, CE-796 X MNC03-737E-5-10, CE-954 X MNC03-737E-5-10, CE-796 X CE-954, and CE-945 X CE-954, which were used in this study. In addition, two checks were used, the cultivars Sempre Verde and BRS Tumucumaque.

Both the first ($F_{3:4}$ generation) and the second trial ($F_{3:5}$ generation) were conducted at the same site in the municipality of Marco, CE, Brazil (3° 4’ 60” S and 40° 4’ 51” W), more precisely in the irrigated perimeter of Baixo Acaraú. This location has a warm semiarid tropical climate, with average annual rainfall of 860 to 900 mm, 52 m altitude, and temperature ranging from 26 to 28 °C and a rainy season from February to May (SEPLAG and IPECE 2009). The first trial was conducted from March to July 2014 and the second from February to June 2015. A randomized complete block design with three replicates was used in both trials. The plots were composed of a 15.0 m row, with a spacing of 2.0 m between rows and 0.30 m between plants.

Although conducted in different years, both trials were implemented in the same climatic season and received the same crop treatments. Two seeds per hill were used, leaving only one plant after thinning, which occurred 21 days after sowing. Plants were irrigated by a conventional sprinkler system for 2 h in three days. In order to control invasive plants, manual weeding at germination and pod maturation were performed. The insecticide ACTARA 250 WG was applied to control the most common crop pests. Harvesting of pods occurred plant per plant, thus avoiding mixtures of seed genotypes between plants of the same population, as well as neighboring populations.

To obtain seed in the $F_{3:5}$ generation, the seeds of $F_{3:4}$ plants were harvested from the populations evaluated in the first trial. The single seed descent (SSD) method was used by randomly removing one seed per plant, generating a mixture that represented all the individuals of the population (absence of selection), providing for expression of existing genetic variability.

The following main traits related to reduction in plant height, precocity, and yield were considered in evaluation of the populations: plant height (PH); length of pod (LP); number of grains per pod (NGP); 100 grain weight (100GW) and grain yield (GY).

The data of each of the traits were subjected to analysis by restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) to obtain the variance components and estimates of genetic parameters, as described by Resende (2002). Analyses of deviance (ANADEVs) were performed with the comparison of the random effects of the model using the likelihood ratio test (LRT) and fixed effects using the Wald test (Resende 2007).

To this end, the traits data obtained in the sequential evaluations ($F_{3:4}$ and $F_{3:5}$) were analyzed *a priori* by the following genetic-statistical model Eq. 1:

$$y = Xr + Zg + e \tag{1}$$

where: *y* is the vector of the phenotypic means of the populations;
r is the vector of the repetition effect (assumed as fixed) added to the general mean;
g is the population effect vector (assumed to be random), *e* is the vector of errors;
and *X* and *Z* are incidence matrices that relate, respectively, the effects of *r* and *g* to vector y.

Subsequently, data from the individual trials were analyzed together and, for this, the following genetic-statistical model was considered Eq. 2:

$$y = Xr + Zg + Hk + Tc + e \tag{2}$$

where: *y* is the vector of phenotypic means of populations; *r* is the nested vector of repetition within generations (assumed as fixed) added to the general mean; *g* is the population effect vector (assumed to be random); *k* is the generation effect vector (assumed to be random); *c* is the vector of the nested effect of control within generations (assumed as fixed); and is the vector of errors; *X*, *Z*, *H* and *T* are incidence matrices that relate, respectively, to the effects of *r*, *g*, *k* and *c* to vector *y*.

The m + a estimates were obtained by the difference between the genetic values of the $F_{3:5}$ and $F_{3:4}$ generations, as described by Vencovsky (1987), to obtain the contrasts for estimates by the traditional method. The predictions of the genetic values by the proposed modification in this study were obtained through the grouped analyzes, that is, considering the two trials in a single model. The equivalence between both methodologies was verified by correlation the BLUPs prediction of the traditional analyses (a) with the BLUPs predictions from the modified analyses (a'). Thus, if the ranking of the populations obtained by one methodology coincides with the rankings generated by the other method, high correlation coefficients will be achieved, showing that the new proposal is as efficient as the original methodology. For that purpose, the Spearman correlation coefficient ($r_{a,a'}$) was used, determined by the following expression Eq. 3:

$$r_{a,a'} = \frac{1\text{-}6\Sigma d_i^2}{n(n^2 - 1)}, \tag{3}$$

were: d_i^2 is the difference between the position of each corresponding value of *x* and *y*, and *n* is the number of pairs of values.

In order to compare the genetic progresses obtained by the two methodologies, gains were simulated with the selection of 20% of the best populations. To this end, the following expression was used: $GS=\overline{X}_S$, in which, *GS* corresponds to the gain with the selection; $\overline{X}_S$ the average of 20% of the best populations for each trait. As the genetic values of the populations were used, then this average will be obtained by Eq. 4:

$$\overline{X}_S = \frac{\Sigma\, genetic\ values}{2}. \tag{4}$$

In addition, the relative efficiencies of the genetic gains per unit time of the modification methodology of m + a proposed in this study will be obtained in relation to the traditional procedure. For this, the following expression will be used Eq. 4:

$$EF_{\text{mod}(\%)} = \left(\frac{GS_{\text{mod}} \times t_{trad}}{GS_{trad} \times t_{\text{mod}}}\right) \times 100 \tag{5}$$

where: $EF_{mod(\%)}$ is the relative efficiency of the gains per unit of time generated by the modification of the m + a methodology in relation to the gains generated by the traditional methodology; GS_{mod} and GS_{trad} are the selection gains generated by modifying the methodology and traditional methodology, respectively; t_{mod} and t_{trad} are the times demanded by the modified and traditional methodology, estimated at 7 and 18 months, respectively.

Genetic-statistical analyses were performed using the R statistical program (RDC 2014) and mixed model equations were solved using the ASReml-R package (Gilmour et al. 2009).

RESULTS AND DISCUSSION

The population effect was significant for the PH, NGP, and 100GW traits (Table 1). It indicates that the populations of cowpea used in this study showed genetic variability regarding the plant height and grain yield components, making it possible to obtain gains through selection. The effect of generation was significant in all the traits, showing variation in the additive effects from one generation to another due to an increase in homozygosity.

The effect of replicate within generation gives an idea of the homogeneity between the blocks present in the first and second sites. Therefore, the conditions were found to be quite similar to one trial and the other, except for PH and LP. On the other hand, the effect of checks within generations shows that the responses of the checks (genotyped-fixed) were different from one generation to another. It shows a variation in environmental conditions over the years, probably due to reduced rainfall in 2015 and, consequently, changes in temperature, humidity, and solar radiation. Moreover, it reveals that the performances of the populations from one year to the next must be adjusted/corrected by the behavior of the commercial checks.

The highest heritability coefficients were identified for the NGP and 100GW traits, directly involved with crop productivity, indicating greater efficiency in selection for these traits (Pimentel et al. 2014). Entry-mean heritabilities lead to more efficient selection because the environmental effects are weighted by the number of replicates and individuals per plot.

The mean estimate obtained for PH shows the proper choice of the parents used in the diallel since the individuals of the ten populations had an average of 30 cm height, which is usually characteristic of upright genotypes. There is considerable demand for upright cowpea cultivars because they facilitate manual and mechanized harvest, allow greater plant density, and, in general, have earlier maturation (Matos Filho et al. 2009). However, they tend to be lower yielding. Thus, the difficulty of selection is to identify individuals that are upright and at least reasonably productive.

Table 1. Estimates of the joint sums of squares of fixed effects, likelihood ratio test (LRT) random effects, heritability at the level of average, accuracy and coefficient of variation (CV) for the traits of plant height (PH), length of pod (LP), number of grains per pod (NGP), 100 grain weight (100GW), and grain yield (GY) in 10 $F_{3:4}$ and $F_{3:5}$ populations and two checks of cowpea.

Effect	Traits				
	PH	LP	NGP	100GW	GY
Population[1]	3.87^{++}	0.00^{ns}	17.68^{+++}	20.29^{+++}	1.04^{ns}
Generation[2]	153.76^{***}	0.02^{***}	21.70^{***}	59.80^{***}	0.46^{**}
Generation/replication[2]	300.31^{***}	0.07^{***}	1.40^{ns}	3.90^{ns}	0.23^{ns}
Generation/check[2]	1747.09^{***}	0.09^{***}	38.90^{***}	69.30^{***}	0.93^{***}
Adjusted error	98.18	0.00	1.00	1.50	0.07
h^2m	0.15	0.09	0.71	0.73	0.24
Accuracy	0.49	0.53	0.79	0.82	0.48
Means	30.6	19.4	14.1	17.5	29.8
CV(%)	8.8	4.0	7.7	6.5	31.5

[1] Likelihood ratio test (LRT), tested by chi-square with 1 degree of freedom. $^{+++}$ and $^{++}$, significant at $p < 0.01$ and at $p < 0.05$, respectively. NS - Nonsignificant.
[2] Wald test *** and **, significant at $p < 0.001$ and at $0 < 0.01$, respectively. .

Table 2. Genetic values of populations for the traits of plant height (PH), length of pod (LP), number of grains per pod (NGP), 100 grain weight (100GW), and grain yield (GY) in 10 $F_{3:4}$ and $F_{3:5}$ populations and two checks of cowpea.

Population	PH		LP		NGP		100GW		GY	
	$F_{3:4}$	$F_{3:5}$	$F_{3:4}$	$F_{3:5}$	$F_{3:4}$	$F_{3:5}$	$F_{3:4}$	$F_{3:5}$	$F_{3:4}$	$F_{3:5}$
Pop 1	3.541	0.778	-0.744	-0.204	-0.748	-0.221	-0.670	-0.087	-1.806	-0.750
Pop 2	2.127	0.455	0.466	-0.774	-0.321	0.267	-2.455	-2.082	0.904	-0.384
Pop 3	1.752	2.802	1.223	0.738	1.805	1.311	1.360	0.927	2.197	3.527
Pop 4	-1.241	-2.091	-0.649	-0.952	-0.903	-0.849	-0.019	-0.310	-0.736	-0.729
Pop 5	5.955	-0.019	0.040	0.387	0.281	0.469	0.892	0.676	3.067	-0.099
Pop 6	5.903	0.119	-0.162	-0.314	-0.305	-0.118	-0.236	0.273	-0.871	0.443
Pop 7	1.688	-3.244	-0.653	-1.179	-0.652	-1.335	-1.040	-0.652	-0.507	-3.158
Pop 8	3.605	-0.307	-0.288	-0.326	-0.428	-0.254	1.153	0.477	-0.853	-0.768
Pop 9	1.419	0.889	0.094	-0.095	-0.157	0.219	-0.312	0.618	0.420	1.478
Pop 10	4.359	-0.334	-0.165	-0.470	0.741	0.305	-1.304	-0.737	0.901	0.264
Check 1	-13.921	1.993	-0.525	0.249	1.774	1.319	-1.158	-0.894	1.376	1.614
Check 2	-15.188	-1.041	2.296	2.942	-1.084	-1.115	3.789	1.512	-4.094	-1.439

Population 1 = CE-542 × CE-796; Population 2 = CE-542 × CE-945; Population 3 = CE-542 × CE-954; Population 4 = CE-542 × MNC03-737E-5-10; Population 5 = CE-796 × CE-945; Population 6 = CE-796 × F4RC1; Population 7 = CE-796 × MNC03-737E-5-10; Population 8 = CE-954 × MNC03-737E-5-10; Population 9 = CE-796 × CE-954; Population 10 = CE-945 × CE-954; Check 1 = 'Sempre Verde'; Check 2 = 'BRS Tumucumaque'.

In general, the genetic values of the populations decreased from $F_{3:4}$ to $F_{3:5}$ (Table 2). Thus, two suppositions are possible: 1) the increase in homozygosity was detrimental to the performance of the individuals belonging to the segregating populations studied, and 2) the environment in the second year was less favorable to growth. The first assumption can be ruled out by the fact that the commercial checks, genotypically fixed, had much smaller genetic values in the second year. It was probably due to differential expression of gene blocks, i.e., genes expressed in the first year may not have been expressed in the second year, or if they were expressed, it was at a lower intensity. Therefore, this leads the authors of this work to believe that the second supposition must be the one that best explains these results.

The selection process must be conducted in a balanced way most of the time. It suggests that a population with a favorable expression for all traits will hardly ever be attained. Moreover, it is noteworthy that the intention is to increase expression for some traits (e.g., NGP, 100GW, and GY), because they are related to production, and to reduce expression for others (e.g., PH) favoring the mechanized cultivation. In this context, it was observed that populations 3 and 5 showed a more desirable combination of genetic values in $F_{3:4}$ and $F_{3:5}$. In fact, these values were, in most cases, higher than those observed in commercial checks. These results show that both populations should have individuals (selection within) with potential for evaluation in final tests of the cowpea breeding program in the Northeast of Brazil.

The BLUPs of populations of the individual analyses (a) reflect the differential (accumulation) of the additive genetic effects of generation $F_{3:4}$ for $F_{3:5}$. The BLUPs generated in the joint analysis (a') reflects the proposal of this work and would show the same differential if the populations were evaluated together in the same year (Table 3). In this more detailed approach, the potential of population 3, previously indicated by genetic values (Table 2), is confirmed. With exception of PH trait, population 3 has always stood out in the other traits, either by the predictions of the traditional or by the modified methodology. Furthermore, the population 3 stood out for expression of smaller upright plants, bigger grain size, and higher grain yield. Undoubtedly, this merits attention, as well as populations 5 and 9, since what is observed is that genotypes of reduced size (upright) tend to be lower yielding (Matos Filho et al. 2009). The authors of this work believe that genotypes with these characteristics may be very useful for cultivation in the Northeast of Brazil, but also in the Cerrado (Brazilian tropical savanna) region, which exhibits considerable expansion in the area of cowpea production under high technology cultivation.

By simulating the genetic gain with the selection of 20% of the best populations for each trait, it was observed that, in general, the gains were greater with the predictions obtained by the traditional method, except NGP

Table 3. Estimates m + a considering the BLUPs of the joint analyses (a'), contrasts of BLUPS between individual analyses (a), BLUPs plus the fixed effect of the mean and Spearman correlation coefficients ($r_{a,a'}$) between a and a' for the traits of plant height (PH), length of pod (LP), number of grains per pod (NGP), 100 grain weight (100GW), and grain yield (GY) in 10 $F_{3:4}$ and $F_{3:5}$ populations and two checks of cowpea.

Population	PH		LP		NGP		100GW		GY	
	a'	a	a'	a	a'	a	a'	a	a'	a
Pop 1	1.519	-1.985	-8.30×10^{-6}	0.335	-0.485	0.307	-0.219	0.497	-0.058	0.305
Pop 2	-6.176	-1.217	-1.21×10^{-5}	-1.081	0.031	0.855	-2.255	-1.708	0.009	-1.673
Pop 3	3.689	3.852	4.16×10^{-5}	0.251	1.792	0.816	1.382	0.494	0.099	4.857
Pop 4	-7.262	-2.941	-2.27×10^{-5}	-1.254	-0.935	-0.795	0.141	-0.043	-0.027	-0.722
Pop 5	3.450	-5.995	1.56×10^{-5}	0.732	0.476	0.659	1.002	0.459	0.036	-3.267
Pop 6	3.782	-5.664	2.16×10^{-6}	-0.465	-0.185	0.070	0.204	0.782	-0.010	1.756
Pop 7	-5.949	-8.175	-2.57×10^{-5}	-1.704	-1.082	-2.017	-0.728	-0.264	-0.079	-5.801
Pop 8	3.254	-4.218	$-1.42\times1^{0-}5$	-0.365	-0.331	-0.079	1.020	-0.198	-0.029	-0.682
Pop 9	2.789	0.359	1.20×10^{-5}	-0.285	0.092	0.595	0.363	1.548	0.034	2.536
Pop 10	7.865	-5.027	-1.17×10^{-6}	-0.774	0.628	-0.130	-0.909	-0.170	0.023	-0.371
Check 1	-	17.908	-	1.023	-	0.865	-	-0.630	-	1.853
Check 2	-	13.105	-	3.587	-	-1.145	-	-0.766	-	1.214
$r_{a,d}$	-0.08^{ns}		0.39^{ns}							

Population 1 = CE-542 × CE-796; Population 2 = CE-542 × CE-945; Population 3 = CE-542 × CE-954; Population 4 = CE-542 × MNC03-737E-5-10; Population 5 = CE-796 × CE-945; Population 6 = CE-796 × F4RC1; Population 7 = CE-796 × MNC03-737E-5-10; Population 8 = CE-954 × MNC03-737E-5-10; Population 9 = CE-796 × CE-954; Population 10 = CE-945 × CE-954; Check 1 = 'Sempre Verde'; Check 2 = 'BRS Tumucumaque'. ^{ns} nonsignificant at test t.

Table 4. Genetics gains with selection and relative efficiency (RE) in percentage of populations for the traits of number of plant height (PH), length of pod (LP), number of grains per pod (NGP), 100 grain weight (100GW), and grain yield (GY) in 10 $F_{3:4}$ and $F_{3:5}$ populations and two checks of cowpea.

Methodology	Genetics gains with selection				
	PH	LP	NGP	100GW	GY
$(m + a)_{\text{modified}}$	-6.719	2.86×10^{-5}	1.210	1.201	0.035
$(m + a)_{\text{traditional}}$	-7.085	0.534	0.836	1.165	3.697
RE (%)	243.9	0.014	372.4	265.1	2.4

and 100GW traits (Table 4). However, relative efficiencies (RE) were estimated to compare both methodologies. Based on these, it can be seen that the methodology proposed in the present study surpassed the traditional methodology for all the traits, except LP, which should be considered differently. Probably this is due to the fact that the populations did not present genetic variability regarding this trait (Table 1), since in the selection of the parents, LP was not considered.

It is worth mentioning that the ER of the modified methodology exceeded by more than 200% for most of the traits. But how can this be possible if the predictions of the genetic gains were inferior by the methodology proposed in the present study? This was possible due to the methodology proposed here to present a much shorter execution time than the traditional methodology (about 1/3 of the time required by the traditional methodology). Thus, with a shorter evaluation time, the breeding program manager can plan the evaluation of a larger number of populations in a short time.

The original methodology requires that populations be advanced by two consecutive generations of homozygotes, thus, when the complete homozygosity is obtained, the average of the lines will be m + a, canceling the effects of the homozygotes, depending on the means of the lineages only of the loci that are fixed in the parents (Vencovsky 1987). Only after this, the assessment of these populations should be made under the same environmental conditions. The original proposal, while attractive, creates some obstacles to implementation. For example, depending on the cycle and location where the breeding program is located, a long time will be necessary for this evaluation to occur. In addition, larger areas are necessary for evaluation, since the number of populations evaluated is twice as large. In this proposal, populations will be assessed as the level of homozygosity progresses. For this reason, the effect of the environment (year to year or one crop season to another, etc.) is determined by the performance of the checks, common to the trials. Consequently, the performance of the populations must be corrected by the control effect. It makes possible to reduce the time required to identify populations with potential for higher extraction of inbred lines, reduce the financial and human resources spent in this process and, above all, reduce the area demanded population assessment.

According to Maia et al. (2011), genetic variability is minimized by the variation provided by the environment, especially under suboptimal growing conditions. In this sense, the proposal is considered useful, but its accuracy was compromised by the adversities in the second trial. However, it is important to test it on other crops and, if possible, in more than one environment and with more checks.

CONCLUSION

The progenies of cowpea show a different behavior in terms of size, precocity and production components. They have the potential to extract superior strains in the $F_{3:4}$ generation, with the progeny obtained from the crossing between CE-796 and MNC03-737E-5-10 being the one with the greatest potential for the selection of small strains.

The progeny with the greatest potential for the selection of early strains is obtained from the crossing between CE-796 and CE-954. The progenies obtained from the crossings between CE-796 and CE-945; and CE-796 and F4RC1 are promising for the selection of strains with high genetic potential.

The m + a estimate is shown to be feasible for identifying populations with genetic potential for the early selection of strains in the cowpea culture.

AUTHORS' CONTRIBUTION

Conceptualization, R. F. Matos, J. C. DoVale and C. H. C. M. Bertini; Methodology, R.F. Matos, A. M. Barroso Neto and J. C. DoVale; Investigation, J. C. Vale and R. Fritsche-Neto; Writing – Original Draft: R. F. Matos and J. C. Vale; Writing – Review and Editing, J. C. DoVale, C. H. C. M. Bertini and R. Fritsche-Neto; Funding Acquisition, J. C. DoVale and C. H. C. M. Bertini; Resources, J. C. DoVale and C. H. C. M. Bertini; Supervision, J. C. DoVale.

REFERENCES

Abreu, A. F. B., Ramalho, M. A. P. and Santos, J. B. (2002). Prediction of seed-yield potential of common bean populations. Genetics and Molecular Biology, 25, 323-327. https://doi.org/10.1590/S1415-47572002000300013

Carneiro, J. E. S., Ramalho, M. A. P., Abreu, A. F. B. and Gonçalves, F. M. A. (2002). Breeding potential of single, double and multiple crosses in common bean. Crop Breeding and Applied Biotechnology, 2, 515-524.

Gilmour, A. R., Gogel, B. J., Cullis, B. R. and Thompson, R. (2009). ASRelm user guide release 3.0. Hemel Hempstead: VSN International.

Jinks, J. L. and Pooni, H. S. (1976). Predicting the properties of recombinant inbreed lines derived by single seed descent. Heredity, Oxford, 36, 243-26.

Maia, C., DoVale, J. C., Frische-Neto, R., Cavate, P. C. and Miranda, G. V. (2011). The difference between breeding for nutrient use efficiency and for nutrient stress tolerance. Crop Breeding and Applied Biotechnology, 11, 270-275. https://doi.org/10.1590/S1984-70332011000300010

Matos Filho, C. H. A., Gomes, R. L. F., Rocha, M. M., Freire Filho, F. R. and Lopes, A. C. A. (2009). Potencial produtivo de progênies de feijão-caupi com arquitetura ereta de planta. Ciência Rural, 39, 348-354. https://doi.org/10.1590/S0103-84782009000200006

Nass, L. L. and Miranda Filho, J. B. (1995). Inbreeding depression rates of semi-exotic maize (*Zea mays* L.) populations. Revista Brasileira de Genética, 18, 585-592.

Pimentel, A. J. B., Guimarães, J. F. R., Souza, M. A., Resende, M. D. V., Moura, L. M. and Ribeiro, G. (2014). Estimação de parâmetros genéticos e predição de valor genético aditivo de trigo utilizando modelos mistos. Pesquisa Agropecuária Brasileira, 49, 882-890. https://doi.org/10.1590/S0100-204X2014001100007

Pontes Júnior, V. A., Melo, P. G. S., Pereira, H. S. and Melo, L. C. (2016). Genetic potential of common bean progenies obtained by different breeding methods evaluated in various environments. Genetics and Molecular Research, 15, 1-12. https://doi.org/10.4238/gmr.15038622

Resende, M. D. V. (2002). Genética biométrica e estatística no melhoramento de plantas perenes. Embrapa Informação Tecnológica. Colombo: Embrapa Florestas.

Resende, M. D. V. (2007). Selegen-reml/blup: statistical system and computerized genetic selection by linear mixed models = Selegen-reml/blup. Colombo: Embrapa Florestas.

Rocha, G. S., Carneiro, J. E. S., Carneiro, P. C. S., Poersch, N. L., Lima, M. S. and Silva, L. C. (2015). Estratégias de predição e efeitos de ambientes na avaliação de populações segregantes de feijão. Revista Ceres, 62, 438-445. https://doi.org/10.1590/0034-737X201562050003

[RDC] R Development Core Team (2014). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. [Accessed Dec. 17, 2017]. Available at: http://www.r-project.org

[SEPLAG] Secretaria do Planejamento e Gestão, Governo do Estado do Ceará and [IPECE] Instituto de Pesquisa e Estratégia Econômica do Ceará (2009). Perfil básico municipal: Marco. Fortaleza: Instituto de Pesquisa e Estratégia Econômica do Ceará. [Accessed Dec. 17, 2017]. Available at: https://www.ipece.ce.gov.br/wp-content/uploads/sites/45/2018/09/Marco_2009.pdf

Vencovsky, R. (1987). Herança quantitativa. In Paterniani, E. (Ed). Melhoramento e produção do milho no Brasil (p. 122-201). Piracicaba: Editora ESALQ/USP.

Viana, L. F., Souza, J. C., Machado, J. C. and Lima, J. L. (2009). Predição de médias de linhagens obtidas de híbridos simples de milho (*Zea mays* L). Ciência e Agrotecnologia, 33, n. spec., 1999-2004. https://doi.org/10.1590/S1413-70542009000700051