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ARTICLE

Mixed model-based Jinks and Pooni method to predict segregating populations in wheat breeding

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Abstract: *The improvement of superior wheat cultivars depends on the identification of promising segregating populations to derive superior lines. A lattice model (8×8) involving 56 F_2 populations and eight parents was conducted in the 2020 cropping season, and grain yield per plant was evaluated for every F_2 population, with further analysis of the population potential by Jinks and Pooni method via REML/BLUP. A total of 5,410 F_2 plants were evaluated in this study. The results showed that the use of genetic variance associated with the individual genotypic value (BLUP) was superior compared with the use of variance and traditional phenotypic values. The F_2 populations, CD 1303/BRS 254, CD 1303/Tbio Duque, CD 1303/Tbio Ponteiro, BRS 264/Tbio Aton, Tbio Ponteiro/Tbio Aton, and Tbio Sossego/CD 1303 had the highest likelihood of deriving superior lines.*

Keywords: *Triticum aestivum L; quantitative genetics; plant selection*

INTRODUCTION

Brazil has a wheat deficit of approximately six million tons (CONAB 2021). However, the country has the potential to expand its wheat production, especially in the Brazilian Cerrado region (Pasinato et al. 2018); hence, cultivars adapted to the climatic conditions of that region need to be developed (Pereira et al. 2019).

One of the challenges of breeding programs is the formation of segregating populations with the potential to derive superior lines since they depend on the concentration of favorable alleles in the parents involved (Fasahat et al. 2016) and on the early evaluation of the populations obtained, which allows selection of those with potential and discarding the least promising populations, saving time and resources from the breeding program. The method by Jinks and Pooni (1976) is a possible tool for evaluating the potential of segregating populations in early generations in soy (Lima et al. 2012), beans (Rocha et al. 2013), and rice (Morais Júnior et al. 2015).

However, one of the challenges of the method proposed by Jinks and Pooni (1976) is that it estimates variances based on the evaluation of individual plants, which can culminate in negative variance estimates (Pimentel et al. 2013). Considering this problem, the restricted maximum likelihood (REML) method can be an alternative to the least-squares method. For variance component estimates, the REML method is translation-invariant; it does not provide

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variance component estimates outside the parametric space and does not provide biased estimates. Additionally, the best linear unbiased prediction (BLUP) method provides the genotypic value of individual plants even under unbalanced conditions, based on the mean performance of the population and their respective parents (Resende and Alves 2020).

In that context, the REML/BLUP method has been extensively used in studies of quantitative genetics (Silva et al. 2013), genetic diversity (Casagrande et al. 2020), and diallel analysis (Laviola et al. 2018), as well as the method by Jinks and Pooni (Morais Júnior 2014). However, the analysis and selection of promising segregating wheat populations using the variance components of REML and the genetic effects of BLUP using the methodology by Jinks and Pooni (1976) to derive superior lines has not been documented.

Therefore, the objectives of this study were to evaluate the genetic potential of 56 tropical wheat F_2 populations in 5,410 plants, derive superior lines, and select plants with superior performance through the method by Jinks and Pooni (1976) via REML/BLUP.

MATERIAL AND METHODS

Crossing of F_1 populations

To obtain the experimental material, eight tropical wheat cultivars were crossed in a complete diallel crossing scheme. Cultivars from three different breeding programs were selected for good agronomic performance variables, including grain yield, health, and plant architecture, combined with quality traits of wheat such as gluten strength, in addition to being adaptable to cultivation in the Brazilian Cerrado region. The cultivars used were: CD 1303 (Cooperativa Central de Pesquisa Agrícola-COODETEC), BRS 254, BRS 264, and BRS 394 (Empresa Brasileira de Pesquisa Agropecuária - EMBRAPA), and four cultivars from Biotrigo Genética (Tbio Aton, Tbio Duque, Tbio Ponteiro, and Tbio Sossego). Hybridization was conducted between August and October 2019. In February 2020, F_1 seeds obtained from each crossing were multiplied to generate the F_2 populations. Both activities were conducted in the greenhouse at the Department of Agronomy at the Federal University of Viçosa, Minas Gerais State, Brazil.

Field experiment

A total of 5,410 F_2 plants were evaluated in the field during the 2020 winter cropping season, in the field at the Department of Agronomy of the Federal University of Viçosa (lat 20º 45' 14" S, long 42º 52' 55" W, and altitude of 648 m), Viçosa, Minas Gerais State, Brazil. The 56 F_2 combinations and 8 parents were evaluated in the field using a lattice model (8 × 8) with 2 replicates. The experimental plot consisted of three rows of 3 m with an intra-row spacing of 0.2 m. Ten seeds were sown per meter following the pedigree method by McVetty and Evans (1980). In each plot, individual plants were harvested, threshed, and the grain yield per plant (g pl^{-1}) was determined.

The experiment was conducted under sprinkler irrigation. Basic and cover fertilization were applied for soil correction based on soil chemical analyses and according to the crop`s nutritional needs. Control of weeds, insects, and pests was done using chemicals according to the recommendations for wheat cultivation in Brazil (Embrapa 2020).

Statistical analysis

Initially, the 56 density plots were evaluated using the phenotypic data and considering each F_2 hybrid population to visualize the distribution behavior of the trait on grain yield per plant. The following statistical parameters were calculated from the data: number of observations (number of pl, count); maximum, minimum, and mean value in g pl^{-1}; standard deviation (SD); coefficient of skewness according to Bowley (1920) (SK); and kurtosis (K).

The data for individual plants from the 56 populations and 8 parents were submitted to mixed model analysis to estimate genetic parameters via restricted maximum likelihood (REML) and predict genotypic values through the best linear unbiased prediction (BLUP). Initially, the following model was used to estimate the parameters for each population:

$$y = X\beta + Z_1\mu_1 + Z_2\mu_2 + e_1 \quad (1)$$

where y is the vector of the phenotypic data observed, X and β are the incidence matrix and the corresponding vector of fixed effects, respectively (general mean of the crossing in each sub-block), Z_1 and Z_2 are the matrices of random effects, μ_1 is the vector of random effects of crossing $\mu_1 \sim N(0, I\sigma^2_{\mu_1})$, μ_2 is the vector of random effects of the plot $\mu_2 \sim$

$N(0, I\sigma^2_{\mu_2})$, and e_1 is the vector of residual random effects $e \sim N(0, I\sigma^2_e)$.

Subsequently, the following model was used to fit the parents:

$$y = X\beta + Z_3\mu_3 + Z_4\mu_4 + e_2 \quad (2)$$

where y is the vector of phenotypic data of the parents, β is the fixed effect vector of the general mean of the parents in each sub-block, μ_3 is the vector of random genetic effects of the parents $\mu_3 \sim N(0, I\sigma^2_{\mu 3})$ μ_4 is the vector of random effects of the plot $\mu_4 \sim N(0, I\sigma^2_{\mu 4})$, and e_2 is the vector of residual random effects $e \sim N(0, I\sigma^2_e)$. The terms X, Z_3, and Z_4 constitute the incidence matrices of the aforementioned effects.

Finally, the individual genetic values of plants (BLUP) were obtained using the following model:

$$y = X\beta + Z_5\mu_5 + Z_6\mu_6 + e_3 \quad (3)$$

where y is the vector of the phenotypic data observed, β is the vector of replicate effects (fixed), μ_5 is the vector of the genotypic random effects of genotypes (populations and parents) $\mu_5 \sim N(0, I\sigma^2_{\mu 5})$, μ_6 is the vector of the plot random effects and $\mu_6 \sim N(0, I\sigma^2_{\mu 6})$, and e_3 is the vector of residual random effects $e \sim N(0, I\sigma^2_e)$. X, Z_5 and Z_6 are the incidence matrices of the respective effects.

The mean genetic variance of the crossing ($\sigma^2_{\mu 1}$) obtained by Model 1 is given by

$$\hat{\sigma}^2_{\mu 1} = (1 - F_{ST})\hat{\sigma}^2_{a0} \quad (4)$$

where F_{ST} is the inbreeding coefficient for the generation of populations, and $\hat{\sigma}^2_{a0}$ is the original additive genetic variance of the parent population, given by $\hat{\sigma}^2_{a0} = \hat{\sigma}^2_p/2$, where $\hat{\sigma}^2_p$ is the genetic variance of the parents.

Heritability ($\hat{h}^2$) was estimated by the following equation:

$$\hat{h}^2 = \hat{\sigma}^2_{\mu 1} / \hat{\sigma}^2_{e1} \quad (5)$$

where, $\hat{\sigma}^2_e$ is the residual variance.

After obtaining the variance and genotypic values (BLUPs), the probability of extracting line (P) from each population was estimated using the method by Jinks and Pooni (1976), with the probability corresponding to the direct area of a given value of Z in the abscissa of the normal distribution. Then, measured through the Z table that contains the probabilities $P(Z \geq z)$ of the standard normal distribution, with Z being obtained by:

$$Z = \frac{\overline{L} - \overline{F}_{ni}}{\sqrt{\hat{\sigma}^2_g}} \quad (6)$$

where $\overline{L}$ corresponds to the standard genotypic value mean, corresponding to the mean grain yield per plant of the 56 F_2 populations evaluated plus 1.5 × σ_g, that is, 12.14 g pl^{-1}, obtained through equation (3); σ_g is the genotypic standard deviation of the 56 F_2 populations obtained through equation (3); $\overline{F}_{ni}$ is the mean grain yield per plant estimated for each F_2 population, which corresponds to the mean of all possible lines in the F_∞ generation in a model without dominance, as long as they are conducted without selection; and $\hat{\sigma}^2_g$ is the estimate of genetic variance between plants of the F_2 generation of each population individual, obtained through Equation (2).

In sequence, out of the F_2 populations that obtained a probability (P) equal to or greater than 45%, plants with a genotypic value higher than the mean of the populations previously selected were selected. Analyses were performed using the software Selegen (Resende 2016) and ggplot2 (Wickham 2016) package in the R (R Core Team 2020) environment.

RESULTS AND DISCUSSION

Descriptive analysis

The descriptive statistics of the 5,410 plants of the F_2 populations based on phenotypic data are shown in Table 1. The number of plants evaluated ranged from 76 to 130, depending on the final stand of the plants at the end of the crop cycle. The highest yield (35.33 g pl^{-1}) was recorded in an F_2 plant originating from the crossing of BRS 254/Tbio Ponteiro. The phenotypic mean of the F_2 populations was 9.81 g pl^{-1}, which was higher than the 5.72 g pl^{-1} reported by Pimentel et al. (2010) when measuring yield in individual F_3 plants of tropical wheat.

Table 1. Descriptive analysis containing number of plants evaluated (nº of pl), maximum (Max), minimum (Min) and mean phenotypic values, standard deviation (SD), skewness and kurtosis for the production per plant (g pl^{-1}) of 56 F_2 populations of tropical wheat

Crossings	nº of pl	Max	Min	Mean	SD	Skewness	Kurtosis
CD 1303/BRS 254	97	29.330	3.200	12.150	5.700	0.226	-0.135
CD 1303/BRS 264	99	20.500	2.980	9.313	3.877	-0.009	-0.019
CD 1303/BRS 394	113	20.590	2.310	9.638	4.164	0.243	-0.535
CD 1303/Tbio Aton	98	31.520	1.270	11.417	5.263	0.125	1.474
CD 1303/Tbio Duque	81	32.270	3.380	12.516	6.025	0.193	1.008
CD 1303/Tbio Ponteiro	108	32.970	2.390	12.106	5.482	0.127	1.476
CD 1303/Tbio Sossego	108	29.410	2.910	11.200	5.385	-0.023	1.929
BRS 254/CD 1303	111	32.510	2.580	10.201	4.658	0.005	4.595
BRS 254/BRS 264	109	18.820	0.890	7.942	3.924	-0.199	-0.206
BRS 254/BRS 394	130	25.490	2.390	9.193	4.835	0.357	1.035
BRS 254/Tbio Aton	99	28.690	1.950	10.398	5.935	-0.062	0.302
BRS 254/Tbio Duque	110	23.690	3.120	9.675	4.098	0.107	0.469
BRS 254/Tbio Ponteiro	111	35.330	1.730	9.979	5.515	-0.133	4.208
BRS 254/Tbio Sossego	97	29.720	1.940	9.122	4.756	0.267	2.839
BRS 264/CD 1303	101	28.860	1.600	11.696	5.553	0.149	0.614
BRS 264/BRS 254	105	24.120	0.740	9.838	5.099	0.258	0.138
BRS 264/BRS 394	115	21.980	3.080	9.278	3.666	0.048	0.466
BRS 264/Tbio Aton	97	25.100	1.750	11.916	5.695	0.094	-0.610
BRS 264/Tbio Duque	87	28.710	2.960	10.052	5.681	0.255	1.569
BRS 264/Tbio Ponteiro	66	23.490	1.880	10.394	5.067	0.072	-0.272
BRS 264/Tbio Sossego	86	23.740	1.200	8.993	4.448	0.121	0.978
BRS 394/CD 1303	112	22.800	2.210	8.324	4.181	0.246	2.415
BRS 394/BRS 254	96	22.320	1.260	8.847	4.412	0.244	0.320
BRS 394/BRS 264	97	21.210	1.540	8.448	4.096	0.214	0.675
BRS 394/Tbio Aton	63	31.250	2.160	10.178	5.866	0.434	1.941
BRS 394/Tbio Duque	97	26.300	2.050	9.565	4.444	-0.105	1.382
BRS 394/Tbio Ponteiro	92	26.610	0.470	8.607	4.616	-0.057	2.027
BRS 394/Tbio Sossego	98	20.390	0.540	8.636	4.151	0.155	-0.102
Tbio Aton/CD 1303	113	26.970	1.750	10.811	5.262	-0.117	0.311
Tbio Aton/BRS 254	102	24.050	1.470	10.872	5.469	0.108	-0.381
Tbio Aton/BRS 264	101	28.320	1.050	8.966	4.840	0.022	2.491
Tbio Aton/BRS 394	100	28.030	0.670	7.744	5.275	0.227	1.938
Tbio Aton/Tbio Duque	49	29.960	1.870	14.111	7.238	0.020	-0.782
Tbio Aton/Tbio Ponteiro	110	26.630	2.990	9.920	4.466	0.264	0.789
Tbio Aton/Tbio Sossego	67	27.170	2.590	11.507	4.866	0.070	0.574
Tbio Duque/CD 1303	116	24.590	1.270	8.515	4.826	0.080	0.928
Tbio Duque/BRS 254	111	30.070	1.310	8.965	4.733	0.063	2.875
Tbio Duque/BRS 254	118	19.710	1.640	8.840	4.227	0.287	-0.208
Tbio Duque/BRS 394	64	24.720	2.760	11.158	5.178	-0.167	-0.052
Tbio Duque/Tbio Aton	108	27.090	1.810	9.256	4.306	0.194	1.478
Tbio Duque/Tbio Ponteiro	98	24.320	0.810	9.181	4.429	0.100	0.387
Tbio Duque/Tbio Sossego	105	21.340	2.100	9.291	3.930	0.027	0.024
Tbio Ponteiro/CD 1303	110	29.750	0.460	11.467	6.271	0.169	0.335
Tbio Ponteiro/BRS 254	26	12.350	0.200	4.846	3.815	0.543	-1.164
Tbio Ponteiro/BRS 264	113	20.730	1.580	9.069	4.021	-0.117	0.558
Tbio Ponteiro/BRS 394	99	26.250	2.060	9.252	5.509	0.243	0.296
Tbio Ponteiro/Tbio Aton	81	36.380	0.230	11.770	7.419	0.116	1.779
Tbio Ponteiro/Tbio Duque	95	22.070	1.410	9.464	4.856	0.244	-0.078
Tbio Ponteiro/Tbio Sossego	93	34.410	2.210	10.225	5.932	0.176	2.239
Tbio Sossego/CD 1303	103	31.820	0.750	11.977	5.680	-0.072	0.765
Tbio Sossego/BRS 254	103	21.060	1.380	8.971	4.427	0.124	0.128
Tbio Sossego/BRS 264	90	32.220	1.630	9.584	5.431	0.037	3.500
Tbio Sossego/BRS 394	89	25.120	1.120	7.944	4.515	0.137	2.140
Tbio Sossego/Tbio Aton	85	26.220	1.080	8.707	4.875	0.077	0.840
Tbio Sossego/Tbio Duque	102	27.000	0.840	8.958	5.387	0.216	1.041
Tbio Sossego/Tbio Ponteiro	76	28.490	1.600	8.616	5.234	0.033	2.120

The phenotypic distribution patterns were verified for skewness and kurtosis (Table 1). F_2 populations showed almost normal patterns; the distributions showed weak skewness both on the right (0 < SK < 1) and left (−1 < SK < 0), although with stronger skewness to the right, that is, with a longer tail on the right, with values concentrated on the left of the mean. The highest skewness value on the right was observed in the BRS 394/Tbio Aton population (0.43). Most populations presented kurtosis characterized as platykurtic (K < 3), that is, the phenotypic data of the populations were less concentrated around the mean. Only the BRS 254/CD 1303, BRS 254/Tbio Ponteiro, and Tbio Sossego/BRS 264 presented leptokurtosis (K > 3). With the aim of genetic improvement, populations with asymmetric curves to the left (concentration of individuals above the average) were sought to increase the probability of deriving superior lines, highlighting populations with higher values of asymmetry on the left, including BRS 254/BRS264, BRS 254/Tbio Ponteiro, Tbio Aton/CD 1303, and Tbio Duque/BRS 394.

Based on Figure 1, it is possible to visualize the variability of the distribution patterns of F_2 populations of tropical wheat between the F_2 generations and their reciprocals. The visualized variability indicates that the distribution pattern

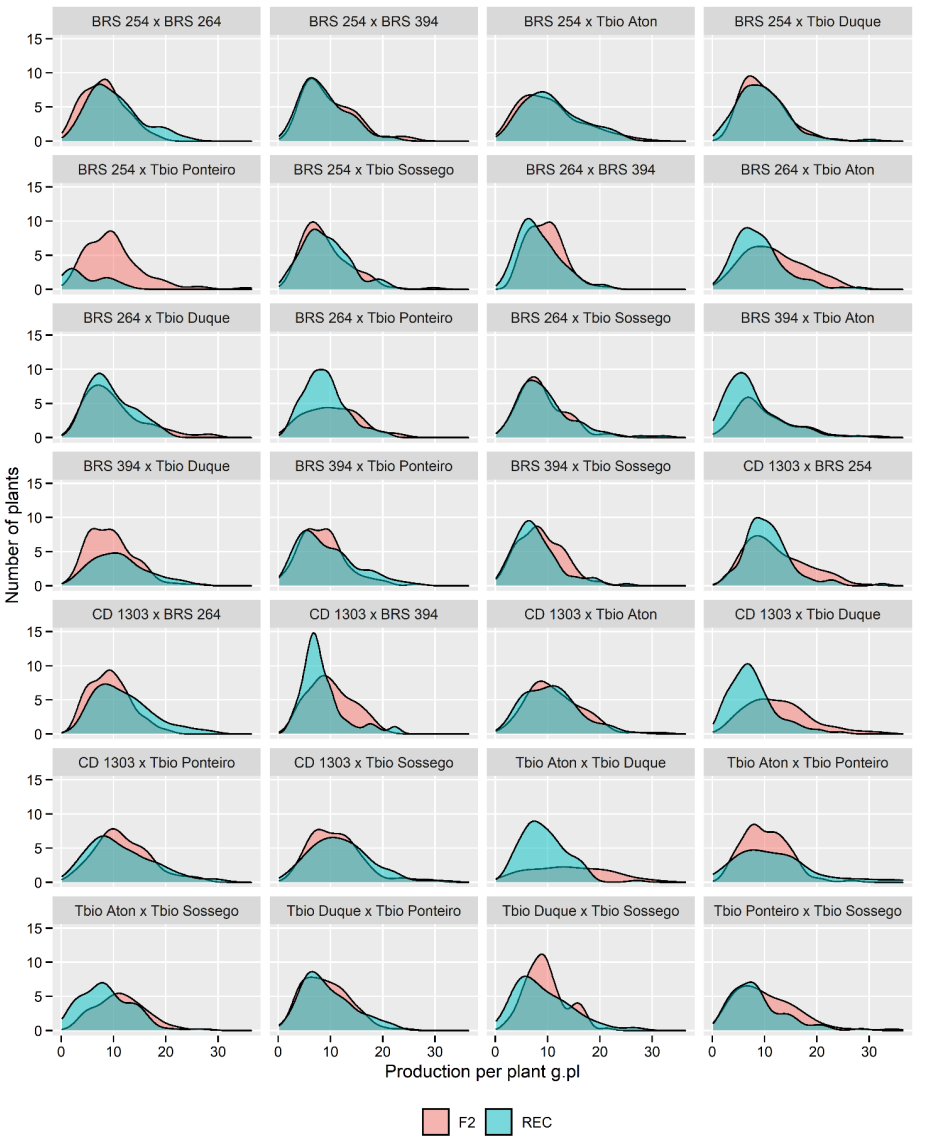

Figure 1. Pattern of density distribution of grain yield per plant in 56 tropical wheat F_2 populations. F_2: crosses and REC: reciprocal.

between F_2 populations and their respective reciprocals are similar, with greater visual discrepancies present in the BRS 254/Tbio Ponteiro, BRS 264/Tbio Aton, BRS 394/Tbio Duque, CD 1303/BRS 394, CD 1303/Tbio Duque, and Tbio Aton/Tbio Ponteiro populations. Such variation in performance can be indicative of a reciprocal effect, with the consequence for the adoption of the cultivar to be used as the maternal or paternal parent (Rocha et al. 2014); however, it is based on visual verification of performance through graphical analysis, requiring a significance test for the reciprocal effect. These effects may be due to the nuclear genes (maternal effect) and cytoplasmic genes (non-maternal effect) (Barata et al. 2019). Easterly et al. (2020), who studied 650 F_1 combinations of wheat, reported an insignificant reciprocal effect in grain yield. Pelegrin et al. (2020), who studied F_2 populations of wheat with a partial diallel crossing design (5 × 5), reported a significant reciprocal effect for the trait grain weight per plant.

Jinks and Pooni methodology

The probability of extracting superior lines was calculated using the method by Jinks and Pooni (1976) (Table 2). The probability ranged from 0.00 (Tbio Ponteiro/BRS 254) to 49.64 (CD 1303/Tbio Ponteiro). Six populations (CD 1303/BRS 254, CD 1303/Tbio Duque, CD 1303/Tbio Ponteiro, BRS 264/Tbio Aton, Tbio Ponteiro/Tbio Aton, and Tbio Sossego/CD 1303) recorded probabilities greater than 45%. These populations stood out for the extraction of superior lines with productive potential. The Jinks and Pooni (1976) method has proven its efficiency in other studies involving grain crops, such as rice (Morais Júnior et al. 2015) and beans (Rocha et al. 2013).

Pimentel et al. (2013) highlighted that when estimates of genetic components are obtained through evaluations in individual plants, the results are biased due to the high volume of errors associated with negative genetic variance estimates being possible. Furthermore, errors associated with measurements on individual plants are inevitable as they are not homogeneous at the time of sampling, and each plant can interact exclusively with the environment (Westneat et al. 2015). In this context, techniques such as the REML/BLUP method that estimate the genetic values of individual plants and minimize tendencies should be adopted.

The REML/BLUP method stands out for its ability to provide the genetic value (BLUP) of each plant even under unbalanced conditions by assuming central estimates of genetic value, that is, normally distributed with the true genetic value being central, making it an unbiased predictor. Thus, selection between and within populations is allowed to increase the prediction success. REML, in turn, is translation-invariant, besides being iterative, providing estimates of non-negative variance components for restricting the parametric space, which is an unbiased method once a sufficient number of observations are used (Resende and Alves 2020). Thus, the REML/BLUP methodology is ideal for estimating genetic parameters and predicting genetic values. The genetic variance estimated in the present study did not present negative values (Table 2), that is, within the parametric space, differently from what occurs in contrast to the methodology by Jinks and Pooni (1976), based on phenotypic data using the least-squares technique. Previous studies have reported the superiority of biometric techniques based on the REML/BLUP methodology compared to those based on least squares, such as selection indexes (Entringer et al. 2016), diallel analysis (Laviola et al. 2018), and genetic diversity (Casagrande et al. 2020).

Selection of superior plants

The genotypic value (BLUP) of plants above the mean of six F_2 populations of tropical wheat selected by the method by Jinks and Pooni (1976) (P > 45%) are shown in Figures 2 and 3. The mean of genetic values of the six selected populations was 12.81 g pl^{-1} which was 30.05% more than the means of the other F_2 populations and 87.83% more than the means of the parents. The CD 1303/Tbio Duque population had 55 plants with means higher than 12.81 g pl^{-1}, with the population with the highest number of individuals above the mean, followed by the CD 1303/Tbio Ponteiro population with 40 individuals with values above the mean. The other populations had 39 (CD 1303/BRS 254) and 31 (Tbio Ponteiro/Tbio Aton) individuals above the mean. Although the selection of segregating populations in the F_2 generation should be treated sparingly because of previously reported heterosis effects on productivity (Bailey et al. 1980, Jiang et al. 2017), these populations have promising performances when analyzing the Jinks and Pooni probability (P%) value together with their genotypic means. The greater number of selected populations in which the cultivar CD 1303 (four populations) participated as parents regardless of the large number of descendants selected in these populations are indications that this parent has a high number of favorable alleles for the grain yield trait;

Table 2. Average genetic value per plant (g pl^{-1}), genetic variance ($\hat{\sigma}^2_g$), heritability ($\hat{h}^2$), Z value for $\bar{L}$ = 12.14 g pl^{-1} and their respective probabilities of extraction of superior lines (P, %), for the grain production trait per plant of tropical wheat F_2 populations

Parents	nº of pl	Mean	$\hat{\sigma}^2_g$	$\hat{h}^2$	Z	P (%)[1]
CD 1303	15	9.198	1.137	-	-	-
BRS 254	15	5.707	1.290	-	-	-
BRS 264	15	8.781	0.990	-	-	-
BRS 394	15	4.004	0.494	-	-	-
Tbio Aton	15	6.141	1.650	-	-	-
Tbio Duque	15	7.189	8.104	-	-	-
Tbio Ponteiro	15	7.664	1.332	-	-	-
Tbio Sossego	15	5.893	0.734	-	-	-
Mean	15	6.822	-	-	-	-

Crossings	Mean	$\hat{\sigma}^2_g$	$\hat{h}^2$	Z	P (%)[1]
CD 1303/BRS 254	12.108	3.938	0.125	0.020	49.202
CD 1303/BRS 264	8.717	1.976	0.125	2.440	0.734
CD 1303/BRS 394	9.619	2.266	0.125	1.680	4.648
CD 1303/Tbio Aton	11.417	3.594	0.125	0.380	35.197
CD 1303/Tbio Duque	12.239	4.725	0.125	-0.050	48.006
CD 1303/Tbio Ponteiro	12.307	3.699	0.119	-0.090	49.642
CD 1303/Tbio Sossego	11.073	3.636	0.125	0.560	27.877
BRS 254/CD 1303	10.243	2.836	0.124	1.130	12.924
BRS 254/BRS 264	7.908	2.071	0.124	2.940	0.164
BRS 254/BRS 394	9.177	3.033	0.125	1.700	4.457
BRS 254/Tbio Aton	10.837	4.081	0.125	0.650	25.785
BRS 254/Tbio Duque	9.621	2.683	0.124	1.540	6.178
BRS 254/Tbio Ponteiro	10.082	3.836	0.125	1.050	14.686
BRS 254/Tbio Sossego	9.130	2.836	0.125	1.790	3.673
BRS 264/CD 1303	11.673	3.908	0.125	0.240	40.517
BRS 264/BRS 254	9.820	3.294	0.125	1.280	10.027
BRS 264/BRS 394	9.276	1.774	0.125	2.150	11.578
BRS 264/Tbio Aton	11.912	4.146	0.125	0.110	45.621
BRS 264/Tbio Duque	10.638	4.186	0.125	0.730	23.270
BRS 264/Tbio Ponteiro	10.394	3.171	0.113	0.980	16.354
BRS 264/Tbio Sossego	8.909	2.341	0.125	2.110	1.743
BRS 394/CD 1303	8.422	2.182	0.125	2.520	10.587
BRS 394/BRS 254	8.938	2.420	0.125	2.060	1.970
BRS 394/BRS 264	8.380	2.131	0.125	2.580	0.494
BRS 394/Tbio Aton	10.104	4.116	0.125	1.000	15.866
BRS 394/Tbio Duque	9.671	2.982	0.124	1.430	7.636
BRS 394/Tbio Ponteiro	8.617	2.669	0.090	2.160	1.539
BRS 394/Tbio Sossego	8.523	2.100	0.125	2.500	0.621
Tbio Aton/CD 1303	10.797	3.626	0.125	0.710	23.885
Tbio Aton/BRS 254	10.872	3.489	0.125	0.680	24.825
Tbio Aton/BRS 264	8.994	2.970	0.125	1.830	3.363
Tbio Aton/BRS 394	7.913	3.394	0.125	2.290	1.101
Tbio Aton/Tbio Duque	13.842	4.688	0.125	-0.790	21.476
Tbio Aton/Tbio Ponteiro	9.916	2.691	0.122	1.360	8.692
Tbio Aton/Tbio Sossego	12.474	2.822	0.125	-0.200	42.074
Tbio Duque/CD 1303	8.670	2.845	0.125	2.060	1.970
Tbio Duque/BRS 254	9.202	3.241	0.125	1.630	5.155
Tbio Duque/BRS 254	8.858	2.769	0.125	1.970	2.442
Tbio Duque/BRS 394	11.694	3.544	0.125	0.240	40.517
Tbio Duque/Tbio Aton	9.265	2.905	0.125	1.690	4.551
Tbio Duque/Tbio Ponteiro	9.034	2.700	0.105	1.890	2.938
Tbio Duque/Tbio Sossego	9.283	2.487	0.125	1.810	3.515
Tbio Ponteiro/CD 1303	11.459	5.083	0.124	0.300	38.209
Tbio Ponteiro/BRS 254	4.675	1.370	0.107	6.380	0.001
Tbio Ponteiro/BRS 264	9.066	2.167	0.102	2.090	1.831
Tbio Ponteiro/BRS 394	9.325	3.625	0.106	1.480	6.944
Tbio Ponteiro/Tbio Aton	11.974	6.685	0.125	0.060	47.608
Tbio Ponteiro/Tbio Duque	9.642	2.878	0.107	1.470	7.078
Tbio Ponteiro/Tbio Sossego	10.099	4.377	0.117	0.980	16.354
Tbio Sossego/CD 1303	11.963	4.107	0.125	0.090	46.414
Tbio Sossego/BRS 254	9.155	2.361	0.125	1.940	2.619
Tbio Sossego/BRS 264	9.689	3.532	0.125	1.300	9.680
Tbio Sossego/BRS 394	7.928	2.531	0.125	2.650	0.403
Tbio Sossego/Tbio Aton	8.747	3.008	0.125	1.960	2.500
Tbio Sossego/Tbio Duque	8.849	4.112	0.125	1.620	5.262
Tbio Sossego/Tbio Ponteiro	8.646	3.165	0.125	1.960	2.500
Mean	9.853				

[1] highlighted probabilities: selected populations.

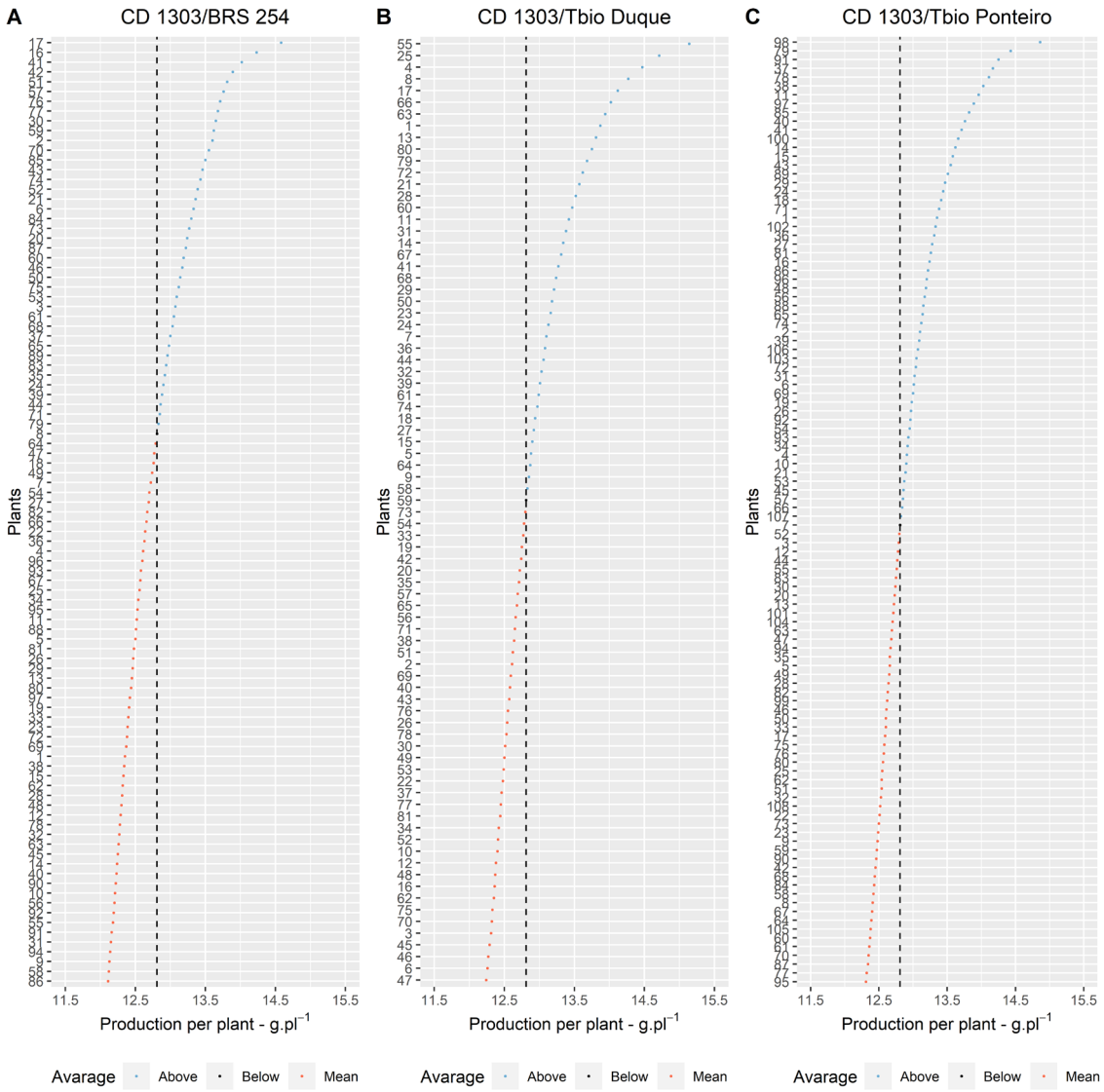

Figure 2. Genotypic value (BLUP) of plants above the mean of three F_2 populations of tropical wheat selected by the method of Jinks and Pooni (1976).

thus, lines from these plants have a high potential for use in tropical wheat breeding programs. For the selection of individuals based on the genetic value in this study, the individual BLUP is more reliable than the selection based on phenotypic values. This is because BLUP depends on the genetic merit of the population to predict the individual genetic value (Cowling 2013).

Using the REML/BLUP methodology proved to be efficient in generating genetic variances within the proposed parametric space with consequent reliable individual genetic effects (BLUPi) for the selection of wheat plants in the F_2 generation, considering that the individual evaluation of plants undergoes strong environmental influence, distorting the results of previous studies using least squares. Thus, the use of the methodology by Jinks and Pooni (1976) associated with the REML/BLUP methodology demonstrates the potential for use in improving wheat, intending to select superior individual plants in early generations.

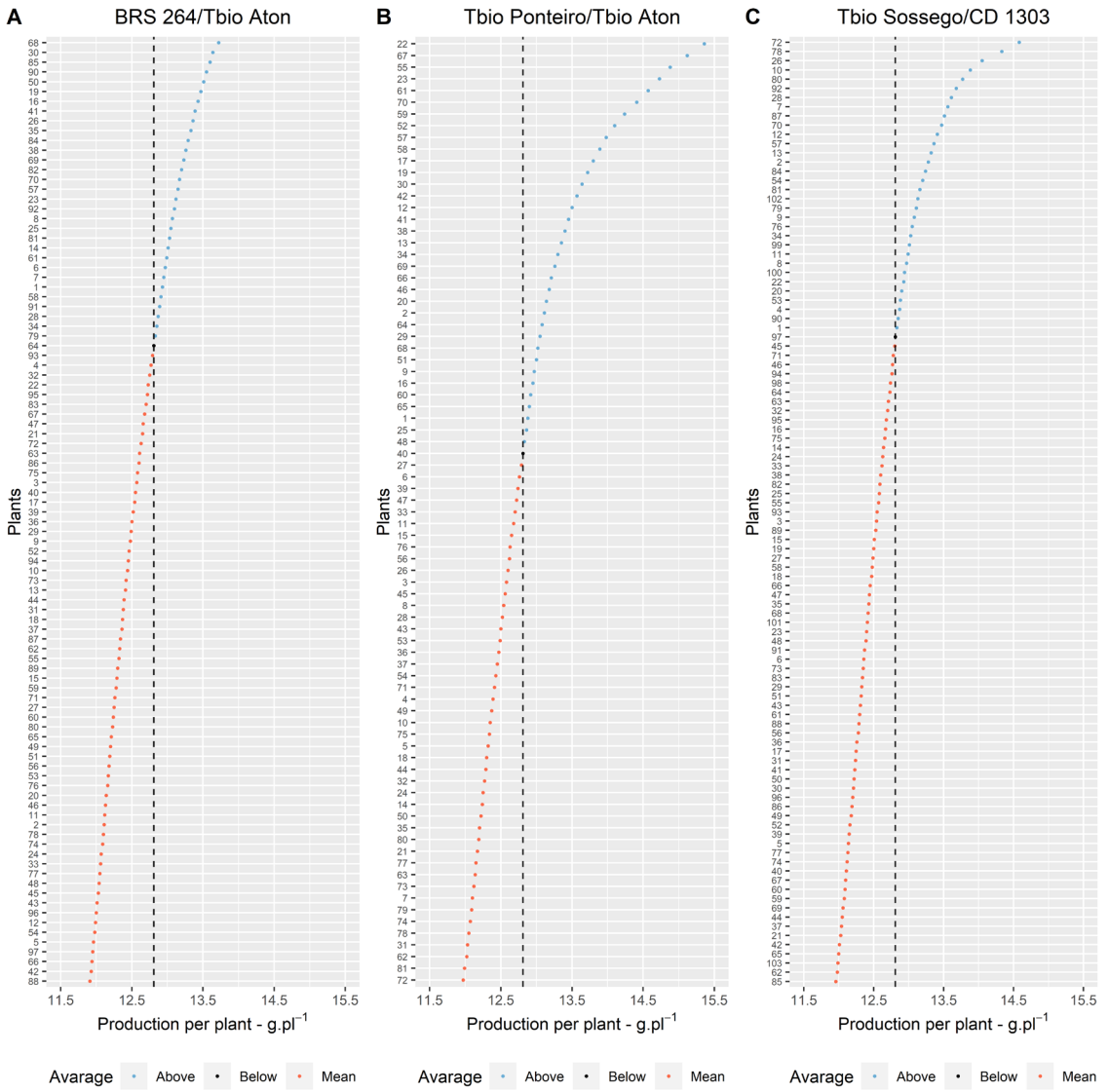

Figure 3. Genotypic value (BLUP) of plants above the mean of three F_2 populations of tropical wheat selected by the method of Jinks and Pooni (1976).

CONCLUSIONS

The method by Jinks and Pooni (1976), when using the genetic variance of REML with the individual genotypic value (BLUP), is an efficient alternative for selecting the most promising populations in tropical wheat.

The F_2 populations CD 1303/BRS 254, CD 1303/Tbio Duque, CD 1303/Tbio Ponteiro, BRS 264/Tbio Aton, Tbio Ponteiro/Tbio Aton, and Tbio Sossego/CD 1303 have the potential to derive superior lines of tropical wheat.

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