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Genetic parameters and productivity of quinoa in western Paraná State, Brazil

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ABSTRACT. Quinoa has been gaining attention because of its nutritional quality, low cholesterol and lack of gluten; in Brazil, the cultivation efforts in the different regions are mainly related to breeding. This study aimed to determine the genetic parameters and evaluate the productivity of the different genotypes of quinoa for detecting genotypes amenable to selection. The experiment was conducted in crop years 2010/11 and 2011/12 in environment 1 and environment 2, respectively. In environment 1, the evaluation of 61 genotypes was performed, and in environment 2, 31 genotypes were evaluated. The experimental design was a randomized block with two replications; each plot measured 2.0 x 5.0 m (10 m^2) and consisted of four rows spaced at 0.45 m. Data collected on the productivity, plant height at maturation and growth cycle were analyzed using an analysis of variance, average tests and estimates of the genetic parameters. The genotypes N24 and N08 were the only genotypes more productive than the other 46 genotypes, with values of productivity of 1,446.23 and 1,428.93 kg ha^{-1} and with a growth cycle of 117 and 111 days, respectively. The heritability values determined demonstrate the possibility of genetic gain using joint selection that involves two environments.

Keywords: *Chenopodium quinoa*, genotypic selection, agronomic performance.

Parâmetros genéticos e produtividade de quinoa no oeste do Estado do Paraná, Brasil

RESUMO. A quinoa possui destaque devido à sua qualidade nutricional, baixo colesterol e ausência de glúten; no Brasil, os esforços em seu cultivo, nas diferentes regiões, estão relacionados principalmente ao melhoramento. O presente trabalho objetivou determinar os parâmetros genéticos e avaliar a produtividade de diferentes genótipos de quinoa com o propósito de detectar genótipos passíveis de seleção. O experimento foi realizado nos anos agrícolas de 2010/11 e 2011/12, caracterizando ambientes 1 e 2, respectivamente. Dentro do ambiente 1, realizou-se a avaliação de 61 genótipos, no ambiente 2, foram avaliados 31 genótipos. O delineamento experimental adotado foi o de blocos casualizados com duas repetições, cada parcela medindo 2,0 x 5,0 m (10 m^2) sendo constituída de quatro linhas espaçadas de 0,45 m. Com os dados de produtividade, altura de plantas na maturação e ciclo, foram realizadas análise de variância, teste de média e estimado os parâmetros genéticos. Os genótipos N24 e N08 foram os únicos a superar a produtividade de outros 46 genótipos, apresentando valores de produtividade de 1.446,23 e 1.428,93 kg ha^{-1}, com ciclo de 117 e 111 dias, respectivamente. Os valores de herdabilidade determinados demonstram a possibilidade de ganho genético com a seleção conjunta, envolvendo os dois ambientes.

Palavras-chave: *Chenopodium quinoa*, seleção de genótipos, desempenho agronômico.

Introduction

Quinoa is an annual crop from the family Chenopodiaceae. It was introduced in Brazil during the 1990s as part of an effort to diversify the production system in the Cerrado. The first attempts to adapt it to the cultivation were made through selection in hybrid populations using descendant from Cambridge, England (Spehar, 2007).

For commercial production in Brazil, quinoa is desired that presents rapid growth, absence of lodging, photoperiod insensitivity, low ramification, perianth and seed indehiscence, an early cycle and uniform maturation. The genotypes must present various cycles, high yields of grains and biomass, seed protein quality, tolerance to saline conditions and 100-grain weight between 2.0 and 3.5 g (Adolf, Shabala, Andersen, Razzaghi, & Jacobsen, 2012; Gonzalez, Konishi, Bruno, Valoy, & Prado, 2012; Silva, Fuentes, Zamora, Jacobsen, & Schwember, 2014). Such characteristics have been the target of quinoa improvement programs, including for BRS

Piabiru (Spehar, 2007) and BRS Syetetuba (Spehar, Rocha, & Santos, 2011) Brazilian savannah and in southern Brazil (Vasconcelos, Egewarth, Oliveira, & Piano, 2013).

The estimation of genetic and phenotypic parameters, such as heritability, genetic and phenotypic correlation and gains with selection, is important for genetic improvement programs because these estimates facilitate the choice of methods and characters used in the initial and advanced phases of improvement programs, thereby allowing the study of mechanisms, genetic values and variability for one character (Cruz, Regazzi, & Carneiro, 2012; Vasconcelos, Reis, Sediyama, & Cruz, 2012). However, characteristics related to the quinoa cultivation have not been studied with regard to genetic values for quantity.

From a genetic point of view, the improvement and evolution of wild or cultivated plants have many common features; they require variability, some type of selection and some degree or form of insulation to preserve the characteristics of the types that are cultivated. Studies are aimed at determining the degree of heterogeneity among the possible genotypes for selection to ensure that only the best genotypes stay in a breeding program (Silva, Chaves, Arnhold, & Cruz, 2009), particularly for quinoa.

The variability among cultivars reflects the heterogeneity of the genetic material, improves food security threatened by climate change and offers the possibility of identifying promising material for use in a breeding plant program (Ruiz et al., 2014). In the case of quinoa, Gonzalez, Konishi, Bruno, Valoy, and Prado (2012) showed that variability related to the cultivation area caused variation in yield and seed quality.

In the South of Brazil, the study of quinoa behavior to evaluate productive characteristics and the possibility of selecting genotypes with potential for a new cultivar is necessary. As a result, quinoa will be able to contribute to crop rotation and expand the spectrum of possibilities in regional agriculture (Vasconcelos et al., 2013).

The present study aimed to determine the genetic parameters and analyze the productivity of 61 quinoa genotypes (*Chenopodium quinoa* Willd) during the crop year of 2010/11 and 31 genotypes during the crop year of 2011/12 in the region of Marechal Cândido Rondon, Paraná State, Brazil.

Material and methods

The experiments were conducted in the crop years of 2010/11 and 2011/12 in Marechal Cândido Rondon, Paraná State, Brazil, where the average annual temperature varies between 22 and 23°C, the total normal average annual precipitation for the region is between 1,600 and 1,800 mm, and the local soil is classified as Eutoferric Red Latosol - ERL, with clay texture.

In the crop year 2010/11, which constitutes the first experiment, 61 genotypes derived from selections performed in the year 2009/10 were used, whereas in the second experiment, crop year 2011/12, the 31 genotypes analyzed were derived from selections made in the year of 2010/11; 10 genotypes were sown in both the first and second experiments to serve as common checks. The genotypes were selected for plant height between 1.00 and 1.20 m, with growth cycles between 110 and 125 days and panicle size greater than 15 cm.

The experimental design adopted was a randomized block with two replications because of the low number of available seeds, with each plot measuring 2.0 x 5.0 m (10 m^2) and formed by four 5.0 m long rows spaced at 0.45 m.

The implementation of the experiments was made by manual direct seeding in an area that previously had been used to cultivate corn in the first year and soybean in the second. The fertilization was based on a dose of 250 kg ha^{-1} of the formula 08 - 20 - 20 during the seeding, which was provided 5 cm below the seeds. The seeding of the first environment was performed on 19 October 2010, whereas the second environment was sown on 15 February 2011.

'Engeopleno' (Thiamethoxam) was applied at a dose of 150 mL ha^{-1} during flowering for pest control of the 'vaquita de San Antonio' (*Diabrotica speciosa*) and stink bug. Weed control was performed whenever necessary through manual weeding. The grain harvest and threshing was also performed manually with sieves.

Due to seed inviability, 15 genotypes of the first experiment did not germinate, which made the analysis of those genotypes impractical. Because of these losses, the number of analyzed genotypes in the first environment was 35, in addition to the 10 genotypes that were used as common checks. For the second environment, 21 genotypes, plus the genotypes used for common checks, were analyzed, amounting to a combined analysis of 66 genotypes. The traits were initially corrected by the values obtained in the common checks, and these corrected values were then used in the analysis of variance (Cruz, 2006).

With the data on productivity, plant height and cycle, quantitative genetic analyses were performed with the aim of determining if, and how much, gain was accomplished with selection.

The variance analysis was performed for each of the experiments following the equation 1:

$$Y_{ijk} = m + G_i + T_j + GT_{ij} + B_k + \epsilon_{ijk} \qquad (1)$$

where:
Y_{iik} = the characteristic value,
m = the overall average of the experiments,
G_i = the effect of the ith genotype (i = 1, 2, ..., g),
T_i = the effect of the jth common checks (j = 1, 2, ..., r),
GT_{ii} = the effect of the interaction Genotype (i) x Common checks (j),
B_k= the effect of the kth block, and
ϵ_{iik} = random error.

The statistical model adopted for the combined analysis was as follows equation 2:

$$Y_{ijkl} = m + {}^{G}\!/_{A_{il}} + T_j + A_l + TA_{jl} + {}^{(G/T)}\!/_{A_{ijl}} + {}^{B}\!/_{A_{kl}} + \epsilon_{ijkl} \qquad (2)$$

where:
Y_{iikl} = the characteristic value,
m = the overall average of the experiments,
G A_{il}^{-1} = the effect of the ith genotype in the lth environment,
T_i = the effect of the jth common checks,
A_l = the effect of the lth environment,
TA_{jl} = the effect of the interaction between the jth common checks and the lth environment, (G T^{-1}) A_{iil}^{-1} = the effect of the G T^{-1} interaction in the lth environment,
B A_{kl}^{-1} = the effect of the kth block in the lth environment, and
ϵ_{ijkl} = the random error.

Based on the variance analysis of both experiments, we determined the following genetic parameters:

σ_g^2 = the genotypic variance, which was calculated based on the expectancy of the mean square genotypes (MSg), according as equation 3:

$$\sigma_g^2 = \frac{MS_g - MS_e}{b} \qquad (3)$$

where:
σ_e^2 = MS_e = the environmental variance;
σ_g^2 = the genetic variance;
b = the number of blocks, and
MS_e = the mean square residue.
h_r^2 = narrow sense heritability, which was calculated based on combined variance according as equation 4:

$$h_r^2 = \frac{\sigma_g^2}{\frac{2MS_g}{b}} \qquad (4)$$

where:
CVg = the coefficient of genetic variation, which was calculated according as equation 5:

$$h_r^2 = \frac{\sigma_g^2}{\frac{2MS_g}{b}} \qquad (5)$$

where:
m = the experiment general mean.
CVe = the coefficient of environmental variation, which was calculated according as equation 6:

$$CV_e = \frac{100 * \sqrt{MS_e}}{m} \qquad (6)$$

The ratio CVg CVe^{-1} corresponds to the ratio between the coefficients of genetic and environmental variation.

The variance analysis, genetics parameters and the comparison averages (Tukey's test at a 5% probability) were obtained with the aid of the computer application GENES (Cruz, 2013).

Results and discussion

In the variance analysis (Table 1), a significant difference was verified among genotypes, among common checks and among genotypes versus common checks (test F at 5%), for all analyzed characteristics. This result determines the existence of variability in the population, a basic condition that enables selection among these materials. The combined variance analysis of the productivity and cycle characteristics showed the existence of variability among the subjects of different populations analyzed in different years.

The overall average values found for productivity (1,155.08 kg ha^{-1} in environment 1, 288.33 kg ha^{-1} in environment 2 and 801.97 kg ha^{-1} in the combined analysis – Table 1) compared to the mean value found by Vasconcelos, Vasconcelos, Balan, and Silvério (2012) during an experiment performed with quinoa in the city of Campo Mourão, Paraná State, which was 846 kg ha^{-1}, demonstrates the need to perform a selection for this characteristic in west Paraná. According to Spehar (2007), quinoa can reach productivity averages up to 3,000 kg ha^{-1} under favorable conditions.

Table 1. Resume of the analysis of individual variance and combined variance of the variables Productivity, Cycle and Plant Height, evaluated in Marechal Cândido Rondon, in the crop years 2010/2011 and 2011/2012.

			Mean Square		
Environment	F.V.	GL	Productivity	Cycle	Plant Height
1	Treatments	44	453959.87*	35.49*	224.44*
	Genotypes	34	402971.91*	23.66*	174.43*
	Common checks	9	474789.82*	67.80*	337.09*
	G X Witn.	1	2000081.15*	146.75*	911.03*
	Residue	44	17811.28	5.55	34.92
	Overall Average		1155,08	133.69	54.98
	CV%		11.55	1.76	10.75
2	Treatments	30	41214.74*	7.99*	82.16^{NS}
	Genotypes	20	43049.34*	7.72*	97.40^{NS}
	Common checks	9	22849.37^{NS}	9.47*	55.52^{NS}
	G x Witn.	1	169810.89*	0.24^{NS}	16.95^{NS}
	Residue	30	12632.87	0.61	50.70
	Overall Average		288,33	100.71	39.72
	CV%		38.98	0.78	17.93
Combined	Environment	1	27626408.65*	39927.41*	8550.90*
	Common checks	9	239672.30*	50.04*	252.01*
	Witn x Envir.	9	257966.90*	27.22*	140.60^{NS}
	Genot/Envir	54	269667.25*	17.75*	145.90*
	(W vs G)/Envir	2	1084946.02*	73.49*	463.99^{NS}
	Residue	74	15711.92	3.55	41.32
	Overall Average		801.97	120.24	48.75
	CV%		15.63	1.57	13.18

*Significant by test F at a 5% probability level; ^{NS}Nonsignificant by test F at a 5% probability level.

The variable cycle averaged 134, 101 and 120 days, for environment 1, environment 2 and combined analysis, respectively (Table 1). The results were found within the variable average of the crop, determined by Spehar (2007), which lies between 80 and 150 days in Brazilian conditions. The height averages found in the present experiment were 54.98 cm, 39.72 cm and 48.75 cm for environment 1, environment 2 and the combined analysis, respectively (Table 1), showing higher results in environment 1, which was sown on 19 October 2010 in the normal harvest period. The sowing date for which Vasconcelos, Vasconselos et al. (2012) obtained the greater plant height was 18 March, a period currently referred to as interim harvest, where an average plant height of 65 cm was observed in the city of Campo Mourão, Paraná State. In contrast to the great variation observed between environments 1 and 2, the averages obtained for the combined analysis presented results of mean productive performance, growth cycle and plant height closer to the results obtained for the most productive environment (environment 1), characterizing greater possibility of selection for the two environments combined, than if selection was performed in only one of the environments.

The coefficient of variation (CV) represents the residual standard deviation expressed as a percentage of the overall average. The distribution of the CV values of a response variable allows researchers to establish limits of values, which indicate the validity of study results, with low CV values suggesting higher precision. Pimentel-Gomes (2009), studying the coefficients of variation obtained in agricultural assays, classifies these CVs as follows: low (CV below 10%), medium (CV between 10 and 20%), high (CV between 20 and 30%), very high (CV values above 30%). Based on this classification, the coefficients of variation found for the productivity variable presented medium indexes (11.54 and 15.63%) for environment 1 and the combined analysis, respectively, and a very high index (38.98%) for environment 2 (Table 1). The CV values observed for plant height (10.75% in environment 1, 17.93% in environment 2 and 13.19% in the combined analysis - Table 1), coincide with the CV values obtained by Vasconcelos, Vasconselos et al. (2012), which are classified as medium values, showing the reliability of data, as well as the precision of the experiments.

The growth cycle character presented low coefficients for all environments: 1.76% in environment 1, 0.78% in environment 2 and 1.57% in the combined analysis. The highest coefficients of variation were found in environment 2 for productivity (38.98%), and for plant height (17.93%) (Table 1).

In the test of averages, the productivity averages were weighted by the common checks according to Cruz (2006), and genotypes N24 and N08 surpassed the averages of the 46 other genotypes, presenting productivity mean values of 1,446.2 and 1,428.9 kg ha^{-1}, respectively. The real productivity values are presented in Table 2, where it is possible to observe that the maximum productivity average (2,501.3 kg ha^{-1}) was achieved by genotype N08. Vasconcelos, Vasconselos et al. (2012), who analyzed the effect of different sowing periods in quinoa genotypes in the city of Campo Mourão, observed a superior maximum average value of 1,884.4 kg ha^{-1}.

The genotypes N13, N14, N25, P08 and Preta 06 presented cycle averages that surpassed 13 other genotypes, having a higher number of days when compared to the others (Table 2). Possibly, the averages of those genotypes that are superior to others exhibit the longest growth cycles. The plant height variable, on the other hand, presented a single genotype (genotype N19) that surpassed 22 other genotypes, and this genotype had an average height of 68.27 cm (Table 2).

Table 2. Mean values of weighted productivity, real productivity, growth cycle and plant height for quinoa genotypes cultivated in the crop years 2010/11 and 2011/12.

Genotypes	Productivity (Kg ha^{-1})		Real productivity (Kg ha^{-1})	Cycle (days)		Plants Height (cm)	
N24	1,446.23	a	1,981.50	117.25	abcd	53.82	abc
N08	1,428.93	a	2,045.03	111.50	d	52.62	abc
N31	1,130.43	ab	1,665.70	117.75	abcd	54.97	abc
N33	1,115.53	abc	1,650.80	118.25	abcd	58.22	ab
P47	1,084.45	abc	549.18	117.75	abcd	56.49	abc
N03	1,053.79	abc	1,053.79	111.25	d	43.25	bcd
N10	1,053.48	abcd	1,588.75	111.25	d	48.12	abc
N19	1,035.97	abcd	1,035.97	121.25	abc	68.28	a
N13	1,024.23	abcd	1,559.50	124.25	a	33.92	bcd
P56	1,010.35	abcde	475.08	116.75	abcd	55.50	abc
N42	990.47	abcde	990.47	114.50	cd	46.56	abc
N23	978.23	abcde	1,513.50	122.75	ab	50.77	abc
P52	976.05	abcde	440.77	117.75	abcd	55.71	abc
N06	924.92	abcde	924.92	117.00	abcd	54.15	abc
P48	920.14	abcdef	384.87	116.75	abcd	52.43	abc
P32	907.29	abcdef	372.02	117.75	abcd	56.57	abc
P50	894.92	abcdef	359.65	116.25	abcd	43.35	bcd
P05	870.88	abcdef	335.60	118.25	abcd	50.89	abc
N20	843.40	abcdef	308.13	116.25	abcd	50.09	abc
P58	835.27	abcdef	300.00	116.25	abcd	45.90	abcd
N05	807.96	bcdef	807.96	115.25	bcd	42.91	bcd
P37	792.58	bcdef	257.31	116.75	abcd	53.38	abc
N32	790.98	bcdef	1,326.25	120.75	abc	45.32	abcd
P62	782.10	bcdef	246.82	112.75	cd	54.19	abc
N39	781.38	bcdef	1,316.65	117.75	abcd	45.92	abcd
N44	763.08	bcdef	1,298.35	119.75	abc	43.67	abcd
Real	757.00	bcdef	757.00	121.25	abc	43.45	bcd
P3	750.18	bcdef	1,285.45	119.75	abc	51.07	abc
Casa + aberta	747.93	bcdef	1,283.20	121.25	abc	46.62	abc
P61	746.41	bcdef	211.14	113.25	cd	53.24	abc
N29	744.83	bcdef	1,280.10	119.75	abc	46.07	abcd
Casa	743.78	bcdef	1,279.05	117.75	abcd	47.62	abc
Casa + fechada	743.05	bcdef	743.04	113.50	cd	47.43	abc
N34	739.08	bcdef	1,274.35	117.75	abcd	50.47	abc
P60	719.61	bcdef	184.33	111.25	d	58.66	ab
P54	715.26	bcdef	179.98	115.75	abcd	47.12	abc
N30	704.68	bcdef	1,239.95	119.75	abc	50.17	abc
P34	704.43	bcdef	169.15	116.75	abcd	38.27	bcd
P15	693.62	bcdef	158.35	112.75	cd	60.13	ab
N11	676.19	bcdef	676.19	117.75	abcd	50.91	abc
N36	675.28	bcdef	140.00	116.25	abcd	47.94	abc
N14	672.93	bcdef	1,208.20	124.25	a	48.92	abc
P21	654.43	bcdef	119.15	117.75	abcd	37.69	bcd
N 09	644.13	bcdef	1,179.40	121.25	abc	52.62	abc
N41	631.13	bcdef	1,166.40	119.75	abc	32.67	bcd
P57	606.52	bcdefg	71.25	116.75	abcd	43.83	abcd
N22	576.11	cdefg	576.11	117.25	abcd	57.48	ab
N 01	561.38	cdefgh	1,096.65	118.25	abcd	47.52	abc
P38	558.62	cdefgh	23.34	116.75	abcd	39.02	bcd
N35	553.18	cdefgh	1,088.45	119.75	abc	28.57	bcd
P14	545.57	cdefgh	10.29	113.75	cd	40.82	bcd
N15	533.53	cdefgh	1,068.80	110.75	d	46.17	abcd
N43	503.58	cdefgh	1,038.85	116.25	abcd	39.57	bcd
N 07	493.23	cdefgh	1,028.50	119.75	abc	38.97	bcd
N38	492.33	cdefgh	1,027.60	119.75	abc	30.62	bcd
N45	439.88	defgh	975.15	118.25	abcd	50.42	abc
N21	382.88	efghi	918.15	117.75	abcd	45.97	abcd
N25	382.63	efghi	917.90	124.25	a	41.92	bcd
N27	380.28	efghi	915.55	116.25	abcd	35.97	bcd
Guara 15	314.78	fghi	850.05	119.75	abc	40.87	bcd
Preta 06	-4.12	ghij	531.15	124.25	a	13.92	d
Orange 01	-51.52	hij	483.75	110.75	d	35.92	bcd
N12	-198.12	ij	337.15	119.75	abc	38.82	bcd
Orange 02 & 07	-372.87	j	162.40	121.25	abc	25.62	cd
P8	-445.42	j	89.85	124.25	a	35.92	bcd
P7	-497.52	j	37.75	117.25	abcd	48.92	abc

The same letters used in a column indicate that there is no significant difference by Tukey's Test at 5% significance.

The coefficient of genetic variation, which corresponds to the deviation of the genetic pattern and is expressed as a percentage of the average, is an indicator of the relative magnitude of change in a character, which can be obtained through selection in an improvement program. The relation CVg CVe^{-1} and the heritability coefficient in the narrow sense (h_r^2) are parameters that measure the reliability of the data and the success in the selection of superior genotypes. The estimations of high coefficients of heritability are associated with a greater genetic variability, greater selective accuracy (Cargnelutti Filho, Storck, & Ribeiro, 2009) and greater possibilities for success in selecting lineages with higher productivity of grain. The relations among the coefficient of genetic variation, the coefficient of environmental variation (CVg CVe^{-1}) and the heritability coefficient (h^2) are measures of environmental influence on the expression of phenotypes (Faluba et al., 2010).

For grain productivity, the estimation of the ratio CVg CVe^{-1} was 3.29 and 1.1, and the estimated heritability coefficient was 95.58 and 70.65%, for the individual analyses of environment 1 and environment 2, respectively. For the combined analysis, estimated values of 2.97 (ratio CVg CVe^{-1}) and 94.17% (h_r^2) were observed for grain productivity (Table 3). These observations suggest that the quinoa from the combined selection shows better condition because the situation is favorable once the relationship CVg CVe^{-1} achieves values close to or superior to 1.00 (Faluba et al., 2010).

Table 3. Genetic parameters estimated from the individual and combined analysis of the data obtained for productivity, growth cycle and plant height in experiments performed in Marechal Cândido Rondon, Paraná State, in the crop years 2010/11 and 2011/12.

Variable	Condition	σ^2g	h_r^2	CVg	Ratio CVg CVe^{-1}
Productivity	Envir. 1	192,580.30	95.58	40.78	3.29
	Envir. 2	15,208.24	70.65	48.90	1.10
	Comb.	126,977.70	94.17	46.45	2.97
Cycle	Envir. 1	9.05	76.74	2.24	1.28
	Envir. 2	3.55	92.04	1.87	2.41
	Comb.	7.10	80.01	2.19	1.40
Plants Height	Envir. 1	69.75	79.98	15.68	1.41
	Envir. 2	23.35	47.95	12.28	0.68
	Comb.	52.29	71.68	15.05	1.14

σ^2g: genotypic variance; h_r^2: heritability coefficient in narrow sense (%); CVg: coefficient of genetic variation (%); CVe: coefficient of experimental variation (%).

The observed results differ from the ones obtained by Vasconselos et al. (2012), who, in an experiment performed with soybean genotypes, aimed at choosing the best genotypes for selection, found greater values of the coefficient of genotypic determination (H^2) for each environment (varying from 49 to 66% in the tests performed for germination in each environment individually) than the value obtained by the combined variance analysis (43%), indicating a better possibility of gain if the selection is performed for each environment, separately.

The estimation of the heritability coefficient in the narrow sense (h_r^2) is a very useful parameter for breeders because it allows one to predict the possibility of success with the selection, as it reflects the proportion of phenotypic variation that can be inherited; in other words, the heritability coefficient measures the reliability of the phenotypic value as an indicator of genotypic value (Vasconcelos et al., 2012).

The obtained data for coefficient of heritability (h_r^2) within the growth cycle character were of 76.74 and 92.04%, and the ratio CVg CVe^{-1} reached results of 1.28 and 2.41 for environment 1 and environment 2, respectively. The estimation of the coefficient of heritability (h_r^2) for the combined analysis (80.01%), as well as the value obtained for the ratio CVg CVe^{-1} (1.4), showed a result closer to the one obtained for environment 1 (Table 3).

As cited by Spehar and Santos (2005), the plant height variable is directly related to the obtained grain yield. In contrast with this affirmation and the observed results, the pattern of values for the coefficient of heritability is similar to the one observed for the productivity variable; thus, the h_r^2 value resulting m the combined analysis is closer to the highest h_r^2 value that belongs to the first environment (Table 3).

When it is desirable to maximize the gains for a series of environments, it is appropriate to acquire estimates using the components of genetic variance from the combined analysis. The estimation of genetic variance was greater than the estimation of environmental variance, which is reflected in the higher estimation of heritability (Table 3).

Conclusion

The N24 and N08 genotypes were the only ones to surpass the productivity of the 46 other genotypes, presenting productivity values of 1446,23 and 1428,93 kg ha^{-1}, with a growth cycle of 117 and 111 days, respectively.

For the productivity and plant height variables, the selection of quinoa genotypes in which both environments are considered together, based on the results obtained for the heritability per place, may produce greater gains when compared to the selection in individual environments.

The determined heritability values demonstrate the possibility of genetic gain with the combined selection that involved both environments.

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