COMMUNICATIONS IN PLANT SCIENCES

RESEARCH ARTICLE

Dynamic characters involved in grain yield and variability of wheat segregating populations

Liamara Bahr Thurow, **Raíssa Martins da Silva**, **Henrique Pasquetti Carbonari**, **Cristiano Stülp**, **Ricardo Garcia Figueiredo**, **Luciano Carlos da Maia**, and **Antonio Costa de Oliveira***

Federal University of Pelotas, Faculty of Agronomy Eliseu Maciel,
Departament of Phytotechny, University, Campus Capão do Leão,
Pelotas, RS, Brazil.
*Author for correspondence: acostol@terra.com.br.

OPEN ACCESS

doi: 10.26814/cps2018005

Received on January 26, 2018
Accepted on April 13, 2018
Early View on April 13, 2018
Revised on April 17, 2018

Authors declare no conflict of interest

Wheat is the main source of carbohydrate for humanity, being the second most-produced cereal in the world. Brazil is not self-sufficient in this crop, and the Country needs to import wheat to supply the national demand. The objective of this study was to analyze the performance of agronomic traits in wheat segregating populations in the F_2 generation, and to estimate the genetic distance between the parents and the segregating populations. The populations 1 (Abalone x Fundacep Nova Era), 2 (Ônix x Fundacep Raízes), 3 (CD 104 x Fundacep Cristalino), 4 (Fundacep Cristalino x Fundacep Nova Era) and 5 (CD 104 x Fundacep Raízes) and parents (Abalone, CD 104, Fundacep Cristalino, Fundacep Nova Era, Ônix and Fundacep Raízes) were used. The traits Days from Emergency to flowering (DEF), plant height (PH), number of fertile tillers per plant (NFT), ear length (EL), ear mass (EM), number of grains per ear (NGE), grain mass per ear (GME), grain yield per plant (GYP) and ear harvest index (EHI) were measured. The population 5 showed the greatest stature and population 4 showed less variability for the trait. All populations showed averages of NFT and GYP higher than the parents, indicating the presence of transgressive segregants, or presence of dominance in these traits. The grain mass per ear is the trait that contributes most to the distance between the genotypes. There was the formation of four groups by Tocher's grouping method and the population 3 is the most different to the parents, when considering all traits.

Highlighted Conclusion
There is genetic variability for traits within wheat segregating populations.

In Brazil, wheat was the third most produced cereal, behind maize and rice. In the 2016 harvest season, it reached a production of 5.22 million tons. National demand is estimated at 11.4 million tons, requiring imports of 6.2 million tons (CONAB 2017). In order to overcome this deficit, breeding programs aim to obtain superior genotypes for grain yield, quantitative trait, with expression controlled by several genes of small effect, that are largely influenced by the environment (Cuthbert et al. 2008, Ali et al. 2011).

In order to increase genetic variability and to form initial populations of selection that contemplate yield and industrial quality, the most efficient way is to carry out artificial hybridizations between elite parents (Pandini et al. 1997). Subsequently, these should be evaluated with the aid of statistical analysis to describe the direction and magnitude of the variability of the data obtained. Thus, estimates of measures of asymmetry and kurtosis are considered as more in-depth analysis of the data (Coimbra et al. 2004, Lopes et al. 2015). The measure of asymmetry indicates the degree of separation from distribution of the unit of symmetry and informs the direction of the distribution followed by the data. The kurtosis estimate is the degree of flattening of the distribution of populations, allowing to estimate the degree of genetic variability for a given trait (O'Rourke et al. 2005).

The success of a breeding program depends on the genetic variability in the working populations. It is possible to estimate this distance through agronomic, morphological and molecular traits, where this range of information is expressed in measures of dissimilarity (Cruz 2006a). The grouping method is used to collect genotypes, by means of classification criteria, in groups that present homogeneity within the group and heterogeneity between the groups, being appropriate to identify the divergent genotypes, which may be successful in future hybridizations (Cargnelutti Filho et al. 2008). One of the grouping methods used in the breeding of plants is the hierarchical, in this method, the genotypes are grouped by processes that are repeated in several levels, establishing a dendrogram (Silva et al. 2011).

The objective of this work was to analyze the performance of segregating wheat populations in the F_2 generation, regarding agronomic traits and to estimate the genetic distance between the parents and segregating populations.

MATERIAL AND METHODS

The experiment was conducted in 2013, in the experimental field of Plant Genomics and Breeding Center (CGF), located in the Agricultural and Center of Palma (CAP), belonging to Federal University of Pelotas (UFPel), county of Capão do Leão – RS, located at 31º 52' 00'' of latitude south and 52º 21' 24'' of longitude west; at an altitude of 13.24 m, with an annual average rainfall of 1280.2 mm. The soil is described as Yellow-red Podzolic (PVA) from the Mapping Pelotas unit (Santos et al. 2006).

Six wheat cultivars were selected based on the agronomic performance (grain yield and industrial quality), which were: Abalone, CD 104, Fundacep Cristalino, Fundacep Nova Era, Ônix and Fundacep Raízes. At the end of the year 2011, the crosses between parents were made. The crosses between Abalone x Fundacep Nova Era (Population 1), Ônix x Fundacep Raízes (Population 2), CD 104 x Fundacep Cristalino (Population 3), Fundacep Cristalino x Fundacep Nova Era (Population 4) and CD 104 x Fundacep Raízes (Population 5). These crosses were chosen because of the industrial classification, where they obtained crosses between bread and soft, bread and bread, bread enhancer and bread enhancer, bread enhancer and soft, bread and bread. A bulk of F_1 seeds was formed, in which 50 seeds from each cross were randomly separated. In the field, the parents (P1 and P2) and the segregating population F_2 were evaluated. The experimental design was randomized blocks with two replicates, arranged in three rows of two meters, spaced 0.2 m between plants and between rows. A total of 26, 30, 25 and 28 plants were evaluated from Population 1, Population 2, Population 3 and Population 4, respectively.

Soil preparation of the experimental area was according to the recommendations of the crop, and corrections of acidity and fertilization were performed with macro nutrients (NPK) as a function of the levels observed in soil chemical analysis to meet the necessary demand of the crop. Sowing was performed manually. Cultural treatments, as well as the weed, disease and pest control were carried out according to the recommendations for the crop (Silva et al. 2017).

In the field, the following evaluations were performed: days from emergence to flowering (DEF), when the line presented 50% of the inflorescences released from the flag leaf; plant height (PH, in cm), obtained by measuring the individual plants using a graduated ruler, measuring the distance from the soil to the highest spikelet of the plant; number of fertile tillers per plant (NFT, in units), counting all the ears of each plant.

After the reproductive cycle, each plant was harvested individually. From the total of ears of each plant, one ear was chosen randomly and the following evaluations were performed: ear length (EL, in cm), in which length was measured using a graduated ruler; ear mass (EM, in g), obtained by weighing the ear; number of grains per ear (NGE, in units), the ears were manually trashed and counting of the grains was performed; grain mass per ear (GME, in g), obtained from weighing only the grains. Afterwards, all ears of the plant were harvested to obtain the grain yield per plant (GYP, in g). Based on this information, the ear harvest index (EHI, dimensionless) was estimated from the ratio between the grain mass per ear and the ear mass.

The results were analyzed using frequency distribution and univariate statistics that included position and dispersion measurements: mean, minimum and maximum values, coefficients of variation (CV), asymmetry (S) and kurtosis (K). The reference values adopted for the coefficient of asymmetry were $S < 0$, asymmetric distribution to the left and $S > 0$, asymmetric distribution to the right. Regarding the coefficient of kurtosis, the reference values were: $K = 0$, normal distribution (mesocurtic), $K > 0$, distribution more "sharp" than normal distribution (leptokurtic); and $K < 0$, a flatter distribution than normal (platykurtic) (O'Rourke et al. 2005). The analyzes were made using the statistical package SAS (Statistical Analysis System, version 9.3) (SAS 2002).

For DEF, a comparison of means between the parents and the segregating populations was performed, since this was an evaluation by lines, not individual plants as in the other traits. Tukey test was used at $p \leq 0.05$, using the SAS statistical program. Mahalanobis distance was used to estimate the genetic distance between the parents and the segregating populations, and the averages generated by the program were later grouped using the UPGMA method (mean linkage). To facilitate the visualization of the groups formed in the dendrogram the following formula was used: cutoff point = mean + (K.SD), where K presents a value of 1.25 and SD is the standard deviation (Cruz 2006b). The relative importance of the evaluated traits for the estimation of genetic dissimilarity was obtained through the participation of the D^2 components, related to each trait, in the total dissimilarity observed (Singh 1981).

RESULTS AND DISCUSSION

Tables 1 and 2 present the results of the descriptive statistical analysis of the agronomic components for five wheat segregating populations in the F_2 generation, as well as the average of the parents for each of the evaluated components.

Table 1. Results of the descriptive statistical analysis of the agronomic traits of wheat for the F_2 segregating populations, from the crosses between Abalone x Fundacep Nova Era (population 1), Ônix x Fundacep Raízes (population 2), CD 104 x Fundacep Cristalino (population 3) and Fundacep Cristalino x Fundacep Nova Era (population 4) and their parents for the mean content of these components.

Population	Traits	P1	P2	Average	MiV	MaV	CV(%)	S	K	σ^2	Q1	Q3
Abalone (P1) x Fundacep Nova Era (P2)	PH	47.78	54.77	50.69	24.00	81.00	23.70	0.28	0.70	144.38	44.00	60.00
	NFT	4.72	5.81	7.62	2.00	17.00	45.65	0.38	0.50	12.09	4.00	10.00
	EL	7.86	8.97	8.32	6.20	11.00	14.14	0.43	-0.13	13.84	7.50	9.00
	EM	1.12	1.57	1.43	0.49	2.64	43.07	0.32	-0.50	0.38	1.07	1.78
	NGE	34.44	41.73	36.73	4.00	78.00	41.14	0.31	1.67	228.36	27.00	45.00
	GME	0.71	1.07	0.93	0.14	1.83	50.98	0.03	-0.61	0.23	0.64	1.23
	GYP	1.80	4.33	5.29	0.38	11.39	60.14	0.34	-0.91	10.10	2.48	8.01
	EHI	0.62	0.68	0.62	0.28	0.74	21.75	-1.46	0.92	0.02	0.61	0.71
Ônix (P1) x Fundacep Raízes (P2)	PH	52.56	50.45	52.90	39.00	75.00	15.43	0.63	0.53	66.64	47.00	56.00
	NFT	5.09	5.24	5.83	1.00	16.00	55.15	0.91	2.05	10.35	4.00	7.00
	EL	8.13	7.19	8.39	5.00	11.00	14.87	-0.73	1.27	1.56	7.50	9.20
	EM	1.10	1.08	1.25	0.65	2.21	31.62	0.46	-0.17	0.16	0.98	1.54
	NGE	34.38	32.00	38.43	21.00	56.00	25.14	-0.12	-0.53	93.36	33.00	43.00
	GME	0.70	0.72	0.82	0.25	1.52	39.56	0.05	-0.57	0.10	0.58	1.06
	GYP	2.51	2.92	3.35	0.45	11.70	73.40	1.56	3.40	6.03	1.58	3.86
	EHI	0.64	0.66	0.63	0.32	0.75	14.79	-1.73	3.59	0.01	0.59	0.68
CD 104 (P1) x Fundacep Cristalino (P2)	PH	49.28	54.68	53.44	44.00	63.00	11.19	-0.13	-1.04	35.76	49.00	57.00
	NFT	4.68	4.48	5.80	2.00	13.00	41.34	1.16	2.19	5.75	4.00	7.00
	EL	8.10	7.29	8.33	6.90	10.00	10.35	0.30	-0.72	0.74	7.80	9.00
	EM	1.52	1.32	1.75	0.81	2.70	28.27	0.01	-0.67	0.25	1.41	2.11
	NGE	39.56	35.68	41.48	21.00	59.00	22.60	-0.16	-0.50	87.84	35.00	49.00
	GME	1.05	1.00	1.21	0.41	1.92	33.35	-0.35	-0.43	0.16	1.04	1.47
	GYP	3.02	3.83	4.62	0.43	10.96	55.81	0.78	0.52	6.65	2.65	5.45
	EHI	0.69	0.76	0.68	0.40	0.78	13.71	-1.67	1.52	0.01	0.67	0.73
Fundacep Cristalino (P1) x Fundacep Nova Era (P2)	PH	54.68	54.77	54.36	33.00	74	14.81	0.07	2.01	64.83	50.00	57.50
	NFT	4.48	5.81	7.25	3.00	12	33.29	0.18	-0.74	5.82	5.00	9.00
	EL	7.29	8.97	8.10	6.50	9.5	9.55	-0.06	-0.62	0.60	7.55	8.75
	EM	1.32	1.57	1.62	0.88	2.51	25.03	0.30	0.15	0.17	1.40	1.87
	NGE	35.68	41.73	39.36	17.00	56	25.74	-0.65	0.14	102.61	34.50	45.50
	GME	1.00	1.07	1.11	0.32	1.84	33.53	-0.11	-0.02	0.14	0.90	1.35
	GYP	3.83	4.33	5.91	1.15	13.61	50.56	0.51	0.23	8.92	3.90	7.94
	EHI	0.76	0.68	0.67	0.33	0.78	16.65	-1.96	4.09	0.01	0.63	0.74

PH= Plant height; NFT= Number of fertile tillers; EL= Ear length; EM= Ear mass; NGE= Number of grains per ear; GME= Grains mass per ear; GYP= Grain yield per plant; EHI= Ear harvest index; P1 = Average parent 1; P2 = Average parent 2; Average = average of F_2 segregating population; MiV= Minimum value; MaV= Maximum value; CV (%) = Coefficient of variation; S = Coefficient of asymmetry, K = Coefficient of kurtosis; σ2 = Variance of F_2; Q1 = first quartile; Q3 = third quartile.

For plant height (PH), it was observed that Population 5 presented higher F_2 mean, while in Population 4, it was possible to observe a reduction in the trait when compared to the parental average (Tables 1 and 2). It was possible to observe a great variation within the populations with values ranging from 24 to 81 cm. The observed short stature is due to the delay in sowing, caused by rainfall, that prevented sowing to be performed in the period indicated in the region. The coefficient of variation, relative dispersion, that infers the degree of concentration of the data around the mean (Carvalho et al. 2004) was considered high (23.70%) according to Pimentel Gomes (1985) for population 1. For the other populations, the CV was medium, corroborating with other studies carried out with this trait (Biudes and Camargo 2009, Gross et al. 2012).

Table 2. Results of the descriptive statistical analysis of wheat agronomic traits for the F_2 segregating population, from the cross between CD 104 x Fundacep Raízes (population 5) and their parents for the mean content of these components.

Population	Traits	P1	P2	Average	MiV	MaV	CV(%)	S	K	σ^2	Q1	Q3
CD 104 (P1) x Fundacep Raízes (P2)	PH	49.28	50.45	57.07	43.00	72.00	14.06	0.16	-0.92	64.38	50.00	63.00
	NFT	4.68	5.24	7.04	1.00	13.00	44.85	0.16	-0.82	9.96	4.00	10.00
	EL	8.10	7.19	8.19	6.20	11.00	13.03	0.97	1.27	1.14	7.40	8.50
	EM	1.52	1.08	1.52	0.78	2.30	23.08	-0.10	0.13	0.12	1.31	1.76
	NGE	39.56	32.00	38.11	12.00	56.00	28.26	-0.50	0.06	116.03	31.00	45.00
	GME	1.05	0.72	1,02	0.33	1.57	29.13	0.02	0.10	0.09	0.84	1.22
	GYP	3.02	2.92	4.97	0.92	11.75	60.92	0.67	-0.23	9.15	2.39	6.99
	EHI	0.69	0.66	0.66	0.42	0.79	11.97	-0.84	2.26	0.01	0.62	0.70

PH= Plant height; NFT= Number of fertile tillers; EL= Ear length; EM= Ear mass; NGE= Number of grains per ear; GME= Grains mass per ear; GYP= Grain yield per plant; EHI= Ear harvest index; P1 = Average parent 1; P2 = Average parent 2; Average = average of F_2 segregating population; MiV= Minimum value; MaV= Maximum value; CV (%)= Coefficient of variation; S= Coefficient of asymmetry, K = Coefficient of kurtosis; σ2 = Variance of F_2; Q1= first quartile; Q3= third quartile.

The asymmetry coefficient indicates the distribution of individuals in classes. For all populations, except for 3, the asymmetry coefficient was positive, representing a higher concentration of individuals with smaller stature to the left of the arithmetic mean. The measure of kurtosis is related to the degree of concentration of the observations in the center and the tails of the distribution. For populations 1, 2 and 4, the kurtosis measure was above zero, fitting into a leptokurtic distribution, with a higher concentration of data around the mean. Population 4, because of a high asymmetry value (2.01), reveals a lower genetic variability among segregating individuals, due to a lower genetic base of the parents for this trait, since both are from the same research institution. For populations 3 and 5, the kurtosis measurement was lower than zero (-1.04 and -0.92), fitting the distributions as platykurtic. These populations have a larger number of individuals in each class. The first quartile, which corresponds to the minimum value at which 75% of the population is higher, presented a value of 44 to 50 cm. For the 3rd quartile, which establishes the minimum value in which 25% of the population is superior, it exhibited values of 56 to 63 cm. Populations 1, 2, and 4 presented 11 individuals of shorter stature than both parents (Table 3). These individuals are interesting in a breeding program, since smaller plants are less prone to lodging, avoiding losses in grain yield and industrial quality (Curtis and Halford 2014).

Table 3. Number of individuals from segregating populations with superior performance to the best parent and segregating individuals below the worst performing parent in the five segregant populations for each of the agronomic traits evaluated.

	Population 1			Population 2			Population 3			Population 4			Population 5		
Traits	A	B	T	A	B	T	A	B	T	A	B	T	A	B	T
PH	10	11	26	16	11	30	12	6	25	12	11	28	19	4	27
NFT	18	7	26	16	12	30	17	3	25	20	1	28	17	7	27
EL	7	9	26	20	3	30	14	3	25	7	4	28	13	2	27
EM	10	8	26	18	10	30	15	5	25	16	6	28	12	3	27
NGE	12	6	26	22	6	30	14	6	25	13	8	28	15	7	27
GME	11	8	26	18	12	30	16	6	25	14	11	28	11	4	27
GYP	15	11	26	15	12	30	15	7	25	19	7	28	19	8	27
EHI	13	8	26	12	12	30	2	9	25	5	11	28	8	14	27

Population 1: Abalone x Fundacep Nova Era; Population 2: Ônix x Fundacep Raízes; Population 3: CD 104 x Fundacep Cristalino; Population 4: Fundacep Cristalino x Fundacep Nova Era; Population 5: CD 104 x Fundacep Raízes; PH= Plant height; NFT= Number of fertile tillers; EL= Ear length; EM= Ear mass; NGE= Number of grains per ear; GME= Grains mass per ear; GYP= Grains yield per plant; EHI= Ear harvest index; A = number of individuals in the segregating population with performance above the best parent; B = number of individuals from the segregating population with inferior performance to the worst parent; T = total of individuals evaluated by population.

For the number of fertile tillers per plant (NFT), there was a superiority of the average of all F_2 populations when compared to the parents, suggesting a greater complementarity between the alleles, or dominance for the trait (Tables 1 and 2). Among the populations studied, the variation was from 1 to 17 fertile tillers per plant, showing the existence of transgressive segregating individuals for this trait, possibly due to the existence of complementary genes, a factor that is of extreme importance in genetic improvement (Lorencetti et al. 2006). The coefficient of variation was classified as very high for the five populations, corroborating with the results of other studies, which also found very high CV for this trait (Souza et al. 2013).

All populations were asymmetric positive, representing a greater number of individuals with NFT below the arithmetic mean of the population. Populations 1, 2 and 3 were in a leptokurtic distribution. Populations 4 and 5 presented platykurtic distributions. Population 4 showed the greatest variability, due to the distance between the parents for this trait. The other populations have parents with a lower genetic base for this trait. The first quartile showed values of 4 and 5, and in the 3rd quartile values ranged from 7 to 10 fertile tillers per plant (Table 1 and 2).

Populations 3 and 4 presented more than 70% of the individuals with more NFT when compared to the best performing parent (Table 3), making these crosses interesting in breeding programs because they have a greater possibility of obtaining transgressive positive segregating individuals for the trait.

The NFT is indicated for use in the indirect selection of wheat populations because it has a direct association with grain yield (Kavalco et al. 2014), emphasizing that it is the main trait to be evaluated for grain yield per plant (Hartwig et al. 2007). Some reports described a negative correlation between NFT and NGE and GME traits. This performance is explained by a plant compensatory mechanism, where a large number of ears per plant causes a competition for photoassimilates, reflecting on the reduction of grain weight (Deng et al. 2011, Naruoka et al. 2011). In addition, a smaller number of ears can lead to a more efficient use of photoassimilates, compensating the reduced number of ears with a larger grain mass (Sramková et al. 2009).

The means of F_2 in populations 1 and 4 assumed values intermediate to the parental means for ear length (EL). Populations 2, 3 and 5 showed an average F_2 higher than the average of the parents, indicative of good allelic complementarity. The smallest range between the minimum and maximum values was observed in population 4, and the largest in Population 2 (6.0). The coefficient of variation was average for all populations, except for Population 4, which was classified as low (9.55%) (Table 1 and 2). Similar results were obtained for this trait in other reports (Silva et al. 2015).

Populations 1, 3 and 5 were classified as positively asymmetric. Populations 2 and 4 fitted into a negative asymmetric distribution, although Population 4 is very close to a normal distribution. For Population 2, it is more likely to obtain above-average individuals. Populations 1, 3 and 4 were classified as platykurtic, Population 1 being very close to a normal distribution. In contrast, Populations 2 and 5 were in leptokurtic distributions. In the first quartile, values were observed from 4.0 to 7.55 and in the 3rd quartile, values of 8.50 to 9.20 cm in length (Tables 1 and 2).

Population 2 presented a larger number of individuals (20) with EL greater than the best parent (Table 3), this may have been due to the fact that this population presented a lower NFT, and by a compensation mechanism these plants produced ears with a larger size, because there is not so much competition for photoassimilates.

Studies regarding the EL identified a direct effect (-0.205) on the number of spikelets per ear, and an even greater indirect effect (-0.393) on NGE. Therefore, if the selection for EL is performed, even without increasing grain yield, it tends to reduce NGE by its negative effect (Silva et al. 2006).

For ear mass (EM), Populations 1, 3 and 4, obtained higher values than the average of the parents, which makes them interesting for future selections. The range of value for the character was from 0.49 to 2.70, population 1 and 3, respectively. The coefficient of variation was very high for Populations 1 and 2 (43.07 and 31.62) and for the other populations it was classified as high. Population 2 presented the lowest value of the 1st and 3rd quartiles with values of 0.98 and 1.54 g, respectively (Tables 1 and 2).

All populations except 5 had positive asymmetry coefficients, with most of the values to the left of the arithmetic mean. However, Population 3 being very close to zero (0.01) can be considered as normal distribution. For the coefficient of kurtosis, Populations 1, 2 and 3 were classified as platykurtic, the others were classified as leptokurtic.

Populations 2 and 3 obtained 60% of the individuals with superior performance to the best parent. Population 1 was the one that presented the highest number of individuals with lower EM performance to the lowest performance parent. The EM trait can be used as an indirect selection, aiming at an increase in grain yield (Kavalco et al. 2014). Studies by Hartwig et al. (2007) found a high correlation with NGE, thus, if a selection for EM is performed, indirectly gains are obtained in both EM components (NGE and GME).

For the number of grains per ear (NGE), only Populations 2 and 3 presented a mean F_2 higher than the average of the parents, and the Population 2 presented 22 individuals superior to the best parent (Table 3), which suggests the occurrence of dominance in this trait. The greatest range of values was found in Population 1 with a value of 74, and the smallest range was in Population 2 with 35 grains per ear (Table 1 and 2). In this study, it was observed that an increase in the number of grains per ear caused by increased nitrogen doses (Cazetta et al. 2007, Boschini et al. 2011).

The coefficient of variation for the trait was classified as high for all populations, because it is highly influenced by the environment. The greatest range between the value of the 1st and 3rd quartiles was found in Population 1, and the lowest range in Population 2 with a value of 10. Population 1 presented a positive asymmetry coefficient, and the other populations showed negative asymmetry coefficients. For the coefficient of kurtosis, Populations 1, 4 and 5 were classified as leptokurtic, although Population 5 is very close to a normal (mesocurtic) distribution. The Populations 2 and 3 presented a platykurtic distribution.

For the grain mass per ear (GME), the F_2 segregating populations presented the means with a performance very similar to the NGE trait, being again the Population 2, followed by the Population 3, which presented a greater number of individuals with a performance superior to the best parent (Table 3). The range of values in the populations was from 0.14 to 1.92 g per ear. The Population 5 presented high CV and the others had very high CV (Table 1 and 2).

The asymmetry coefficient was positive for Populations 1, 2 and 5. However, it was very close to normal, which may have been influenced by population size. Populations 3 and 4 presented negative asymmetry. Only Population 5 was classified as leptokurtic, the other populations were classified as platykurtic distributions. The value of the 1st quartile ranged from 0.58 to 1.04 g (Population 2 and 3, respectively), and for the 3rd quartile, the same populations were repeated with values of 1.06 to 1.47 g.

For grain yield per plant (GYP), one of the most sought traits in breeding programs, all F_2 populations had a mean higher than the average of the parents, the highest being of the Population 4 (5.91), indicating that the use of these parents could originate populations with positive transgressive segregants for the trait. Population 4 presented 19 plants, out of 28 evaluated, with an average higher than the best parent (Table 3). The lowest F_2 mean was observed in Population 2, even though this was higher than its parents. The greatest distance observed between the parents was in Population 1, where the parents produced 1.80 and 4.33, originating a population with production of 5.29 g per plant, presenting 15 individuals, out of the 26 evaluated, higher than the average of the best parent. This suggests a good allelic complementarity (Tables 1 and 2).

The CV for GYP of all populations was classified as very high. Other studies report a similar problem (Li et al. 2012). As the CV value is usually associated with the number of evaluated plants, one way to reduce it would be to use a larger population. The smallest range between the minimum and maximum values was seen in the Population 3 with 10.53, while the largest range was seen in the Population 4 with a value of 12.46. This was one of the traits that presented the smallest variance among individuals. The lowest value of the 1st and 3rd quartiles was seen in the Population 2, while the highest value of the 1st quartile was seen in the Population 4. For the third quartile, the highest value was seen in the Population 1 (Tables 1 and 2).

All populations presented positive asymmetry. The coefficient of kurtosis was higher than zero in Populations 2, 3 and 4 (leptokurtic). Population 2 showed a high positive asymmetry value and a high coefficient of kurtosis, which is indicative of a lower genetic variability, since parents with a narrow genetic base were used because of the great selection made on this trait. Populations 1 and 5 presented platykurtic distributions.

The ear harvest index (EHI) is an important production estimate, resulting from the straw ratio, to be used to calculate the relationship between GME and EM. None of the populations under study present an F_2 higher than the parental average. However, Population 1 presented 13 of the 26 individuals evaluated, with a performance higher than the best parent, while the Population 3 presented the highest number of individuals (9 of the 25 individuals evaluated) with inferior performance to the lower parent (Table 3). The greatest range between the minimum value and the maximum value was observed in Population 1. The smallest range was seen in Population 5 (Tables 1 and 2).

The CV of the Population 1 was classified as high (21.75%). For the other populations, the CV was classified as medium. The first quartile was represented by values ranging from 0.59 to 0.67 and the third quartile presented values ranging from 0.68 to 0.74. The asymmetry coefficient was negative for all populations. All populations were classified as leptokurtic (Tables 1 and 2). It is worth mentioning that the asymmetry coefficient is influenced by the size of the population, which may have influenced the results found.

Table 4 shows the average days of the emergence to flowering (DEF), where it can be observed that both F_2 populations and the parents differ statistically for this trait. Population 2 presented the shortest interval between emergence and flowering, and Population 5 had the highest DEF value. The earliest parents were Abalone and Fundacep Nova Era and the latest was Fundacep Raízes. This trait is controlled by the response to photoperiod genes accelerate or delay flowering in response to environmental stimulate to ensure that the onset of flowering occurs at optimal temperatures (Kamran et al. 2014).

Population 1, from the cross between Abalone and Fundacep Nova Era, both with the shortest DEF interval, presented the later cycle. Population 2, from the cross between Ônix x Fundacep Raízes, both from the long cycle to the trait, was the population with the most precocious cycle. Although both are interesting examples of transgressive segregants, plants with a smaller range of DEF are sought in breeding programs because they have a shorter cycle, which favors the implantation of summer crops. According to Vieira et al. (2007), the DEF trait provides a small direct effect on the GY trait, and a positive and high secondary direct effect on the NGE trait (the primary trait with the greatest direct effect on GY). However, this trait presents the problem of directly interfering with the increase of the culture cycle.

Table 4. Average performance of the five F_2 populations and the parents for the trait days of emergence to flowering.

Genotypes	DEF
Population 5	80.63 a
Population 1	77.00 b
Population 3	77.00 b
Population 4	77.00 b
Population 2	74.00 cd
Fundacep Raízes	79.90 a
Ônix	76.06 bc
CD 104	74.60 cd
Fundacep Cristalino	73.90 cd
Abalone	73.81 cd
Fundacep Nova Era	73.54 d

DEF = days of emergence to flowering. Population 1 (Abalone x Fundacep Nova Era); Population 2 (Ônix x Fundacep Raízes); Population 3 (CD 104 x Fundacep Cristalino); Population 4 (Fundacep Cristalino x Fundacep Nova Era); Population 5 (CD 104 x Fundacep Raízes).

In the analysis of relative contribution of the traits, presented in Table 5, it is possible to observe that the trait of greater relative contribution was GME (54.65%), followed by SM (26.26%) and NGE (10.21%). Together these three traits contributed more than 90% to the genetic distances between the evaluated genotypes.

Table 5. Summary of the relative contribution analysis of the traits evaluated for genetic dissimilarity of parents and F_2 segregant populations in wheat, according to method proposed by Singh (1981).

Traits	S.J	Value (%)
PH	394.91	0.26
NFT	2014.83	1.05
EL	7531.79	3.85
EM	51360.88	26.26
NGE	19891.93	10.21
GME	106901.94	54.65
GYP	2245.75	1.14
EHI	5030.35	2.57

PH= Plant height; NFT= Number of fertile tillers; EL= Ear length; EM= Ear mass; NGE= Number of grains per ear; GME= Grains mass per ear; GYP= Grain yield per plant; EHI= Ear harvest index.

In the dendrogram (Figure 1) we can observe the hierarchical grouping of the genotypes, based on the dissimilarity matrix. The cutoff point was performed following the mean formula + (K.SD), indicating which genotypes would constitute the different groups. There were two groups, where the first group was formed by the parents (Abalone, Ônix, Fundacep Raízes and Fundacep Cristalino) and Population 2, who presented the lowest mean GME values, ranging from 0.70 to 0.99. The second group was the largest, formed by six genotypes, with averages from 0.93 to 1.21. It grouped the CD 104, Fundacep Nova Era and Populations 5, 4, 1 and 3. It can be seen that the F_2 segregating populations were in the same group as one of the parents. Population 5 was closer to the parent CD 104 and populations 4 and 1 were closer to Fundacep Nova Era.

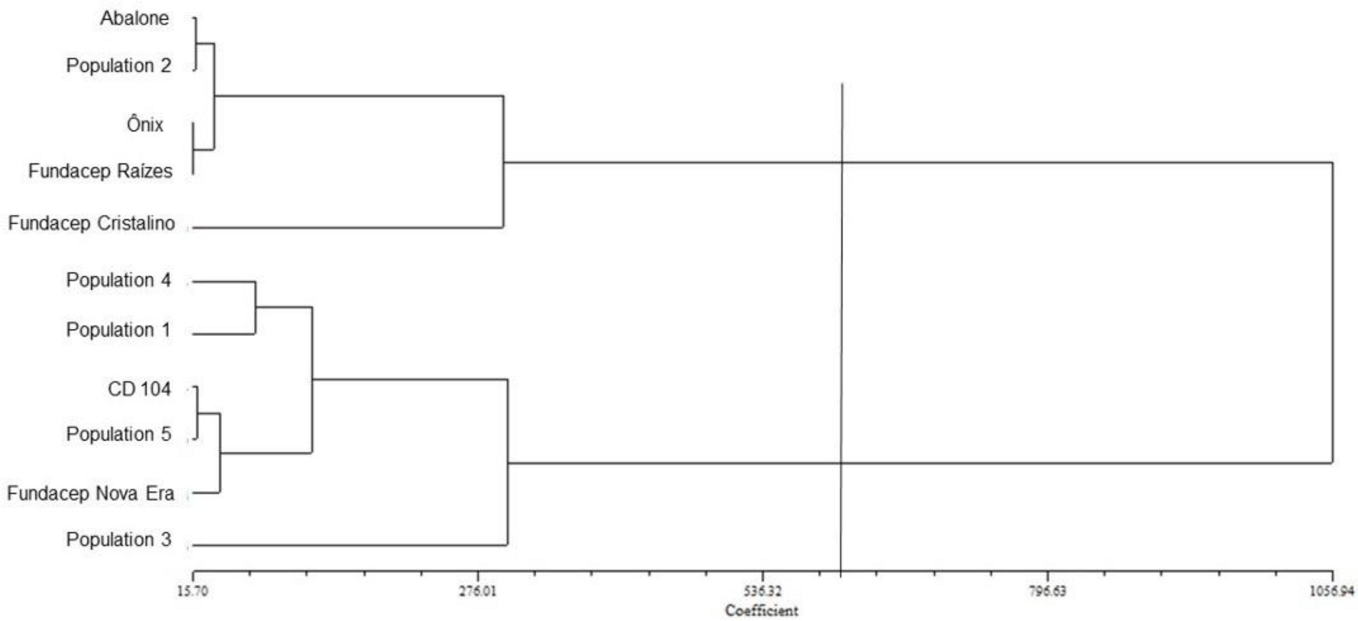

Figure 1. Dendrogram representative of genetic dissimilarity between parents and F_2 segregating populations of wheat grown in Capão do Leão - RS, using the Mahalanobis generalized distance, generated based on the average performance of traits of agronomic interest (plant height, fertile tillers per plant, ear length, ear mass, number of grain per ear, grain mass per ear, grain yield per plant and ear harvest index). The vertical line was calculated by the formula cut-off = mean + (K.SD). Population 1 (Abalone x Fundacep Nova Era); Population 2 (Ônix x Fundacep Raízes); Population 3 (CD 104 x Fundacep Cristalino); Population 4 (Fundacep Cristalino x Fundacep Nova Era); Population 5 (CD 104 x Fundacep Raízes).

In conclusion, all populations present an average superior to the parents for the number of fertile tillers per plant and grain yield per plant, indicating presence of dominance in these traits. The populations Abalone x Fundacep Nova Era, Fundacep Cristalino x Fundacep Nova Era and CD 104 x Fundacep Raízes present the highest number of individuals with values above average for the number of fertile tillers per plant and grain yield per plant. Grain mass per ear is the trait that most contributes to distance between genotypes. The population CD 104 x Fundacep Cristalino is the most distant of the parents when considered all the evaluated traits.

References

Ali ML et al. 2011. Mapping QTL for agronomic traits on wheat chromosome 3A and a comparison of recombinant inbred chromosome line populations. Crop Science 51: 553-566.

Biudes GB and Camargo CEO 2009. Genótipos de trigo: características agronômicas em dois locais do estado de São Paulo. Bragantia 68: 873-884.

Boschini APM et al. 2011. Aspectos quantitativos e qualitativos do grão de trigo influenciados por nitrogênio e lâminas de água. Revista Brasileira de Engenharia Agrícola e Ambiental 15: 450-457.

Cargnelutti Filho A et al. 2008. Comparação de métodos de agrupamento para o estudo da divergência genética em cultivares de feijão. Ciência Rural 38: 2138-2145.

Carvalho FIF et al. 2004. Estimativas e implicações da correlação no melhoramento vegetal. Pelotas: UFPel, 142p.

Cazetta DA et al. 2007. Resposta de cultivares de trigo e triticale ao nitrogênio no sistema de plantio direto. Científica 35: 155-165.

Coimbra JLM et al. 2004. Criação de variabilidade genética no caráter ciclo vegetativo em aveia: hibridação artificial x mutação induzida. Revista Brasileira Agrociência 10 :159-166.

CONAB – Companhia Nacional de Abastecimento. 2017. Levantamento de safra. Disponível em: http://www.conab.gov.br/OlalaCMS/uploads/arquivos/17_05_12_10_37_57_boletim_graos_outubro_2017.pdf. Acesso em 12 de outubro de 2017.

Cruz CD. 2006a. Programa Genes: Análise Multivariada e Simulação Viçosa: Universidade Federal de Viçosa, 382p.

Cruz CD. 2006b. Programa Genes: Biometria. Viçosa: Universidade Federal de Viçosa, 382p.

Curtis T and Halford NG. 2014. Food security: the challenge of increasing wheat yield and the importance of not compromising food safety. The Annals of Applied Biology 164:354-372.

Cuthbert JL et al. 2008. Molecular mapping of quantitative trait loci for yield and yield components in spring wheat (*Triticum aestivum* L.). Theoretical Applied and Genetics 11: 595-608.

Deng S et al. 2011. Characterization and precise mapping of a QTL increasing spike number with pleiotropic effects in wheat. Theoretical and Applied Genetics 122: 281-289.

Gross TF et al. 2012. Comportamento produtivo do trigo em diferentes métodos e densidades de semeadura. Scientia Agraria Paranaensis 11: 50-60.

Hartwig I et al. 2007. Estimativa de coeficientes de correlação e trilha em gerações segregantes de trigo hexaplóide. Bragantia 66: 203-218.

Kamran A. et al. 2014. Flowering time in wheat (*Triticum aestivum* L.): a key factor for global adaptability. Euphytica 197: 1-26.

Kavalco SAF et al. 2014. Análise de trilha em genótipos de trigo submetidos ao estresse por encharcamento. Semina: Ciências Agrárias 35: 1683-1696.

Li S et al. 2012. Genetic dissection of developmental behavior of grain weight in wheat under diverse temperature and water regimes. Genetica 140: 393-405.

Lopes MS et al. 2015. Exploiting genetic diversity from landraces in wheat breeding for adaptation to climate change. Journal of Experimental Botany 66: 3477-3486.

Lorencetti C et al. 2006. Retrocruzamentos como uma estratégia de identificar genótipos e desenvolver populações segregantes promissores em aveia. Ciência Rural 36: 1118-1125.

Naruoka Y et al. 2011. Identification of quantitative trait loci for productive tiller number and its relationship to agronomic traits in spring wheat. Theoretical and Applied Genetics 123:1043-1053.

O'Rourke N et al. 2005. A step-by-step approach to using SAS for univariate & multivariate statistics. SAS Institute, Cary, NC, USA.

Pandini F et al. 1997 Plant height reduction in populations of triticale (*X. triticosecale* Wittmack) by induced mutations and artificial crosses. Brazilian Journal of Genetics 20: 483-488.

Pimentel Gomes F. 1985. Curso de estatística experimental. 11 ed., Piracicaba. 466p.

Santos HG et al. 2006. Sistema brasileiro de classificação de solos. Rio de Janeiro: Embrapa Solos, 306p.

SAS - Statistical Analysis System. 2002. Sas Learning Edition, SAS Program - Getting started with the SAS Learning Edition, North Carolina: Cary, SAS Publishing, 200 p.

Silva JAG et al. 2006. Correlação de acamamento com rendimento de grãos e outros caracteres de interesse agronômico em plantas de trigo. Ciência Rural 36: 756-764.

Silva GC et al. 2011. Divergência genética entre genótipos de cana-de-açúcar. Revista Brasileira de Ciências Agrárias 6: 52-58.

Silva JAG et al. 2015. A expressão dos componentes de produtividade do trigo pela classe tecnológica e aproveitamento do nitrogênio. Brasileira Engenharia Agrícola Ambiental 19: 27-33.

Silva SR et al. 2017. Informações técnicas para trigo e triticale - safra 2017. X Reunião da Comissão Brasileira de Pesquisa de Trigo e Triticale (Londrina – PR). Brasília, DF: Embrapa.

Singh D. 1981. The relative importance of characters affecting genetic divergence. The Indian Journal of Genetics & Plant Breeding 41: 237-245.

Souza VQ et al. 2013. Desfolha em diferentes estádios fenológicos sobre características agronômicas em trigo. Bioscience Journal 29: 1905-1911.

Sramková Z et al. 2009. Chemical composition and nutritional quality of wheat grain. Acta Chimica Slovaca 2: 115 -138.

Vieira EA et al. 2007 Análise de trilha entre os componentes primários e secundários do rendimento de grãos em trigo. Revista Brasileira de Agrociência 13: 169-174.