



# Correlation and selection gains in F6 wheat genotypes<sup>1</sup>

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## ABSTRACT

The agronomic traits have complex quantitative inheritance, wheat breeding has a highly cost and time expending to achieve advanced lines, and new cultivars. The objective of this work was to estimate the phenotypic ( $r_p$ ), genotypic ( $r_g$ ) and environmental ( $r_e$ ) correlation coefficients and the genetic parameters, as well as to estimate the selection gains between agronomic traits in wheat using multivariate analysis. F<sub>6</sub> generation was carried out in a randomized block experimental design, with fifteen wheat genotypes arranged in three replications. The traits measured were days of emergence to flowering, plant height, number of tillers, spike length, number of spikelets, kernel weight and thousand kernel weight. Correlation coefficients, variance components, genetic parameters, selection gain, Euclidiana's distance, relative contribution of traits and canonical variables were estimated. Selection based on number of tillers, kernel weight and thousand kernel weight may result in expressive selection gains. The number of fertile tillers per plant showed a significant and positive intermediate association with kernel weight and positive correlation with number of spikelets. The cycle showed greater contribution to the genetic divergence among genotypes studied. Distinct groups highlighted the genetic variability among genotypes.

**Keywords:** Advanced generation; genetic divergence; *Triticum aestivum* L.

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal in the world, being a major commodity in the international grain market. It is used as a source of human and animal food (Ali *et al.*, 2016). Crop has been extensively searched in recent decades, with breeders' focus on increasing productivity. But as the agronomic traits have complex quantitative inheritance, thus, wheat breeding has a highly cost and time expending to achieve advanced lines, and new cultivars (Ni *et al.*, 2017).

The increase in wheat productivity is the result of two elements: improvement of the growing environment and the genetic gain (Xiao & Tao, 2014). Environmental improvement through agronomic practices is to provide the crop with an environment more favorable to the best development, providing adequate water supply, adequate fertility, and elimination of other biotic and abiotic stresses (Laidig *et al.*, 2017). Genetic gain refers to the increase in

performance that is achieved through plant breeding, in this context, a new breeding program should increase grain yield. Several authors have been reporting the genetic gain in wheat worldwide, in Brazil (Woyann *et al.*, 2019), Argentina (Lo Valvo *et al.*, 2018) and China (Yao *et al.*, 2012).

In plant breeding programs, the study of linear relationships among traits may provide important results, especially in identifying traits to be used in indirect selection (Falconer & Mackay, 1996). The correlation coefficient ( $r$ ) measures the intensity and sense of linear association between two random variables (Galton, 1888; Pearson, 1920) and has been used in association studies among traits in plant breeding trials (Olivoto *et al.*, 2017). Knowledge of the phenotypic, genetic, and environmental correlation among traits is essential for simultaneous selection of several traits, also it is important when target trait reveals low heritability or is difficult to measure (Falconer & Mackay, 1996).

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Selection of superior genotypes is easily proceeded when there are large differences in phenotypic expression, thus grouping analysis aims to gather classification criteria, so that there is high homogeneity within the group and heterogeneity between groups, according to criteria of similarity or dissimilarity (Cruz *et al.*, 2004). To select potentially high-yielding wheat lines in breeding programs, superior genotypes need to be selected for with greater accuracy.

The following hypotheses were formulated: (i) the selection gains in advanced generations are satisfactory for wheat and (ii) genetic deviations can be used to select superior genotypes. In this way, the objective of this work was to estimate the phenotypic ( $r_p$ ), genotypic ( $r_g$ ) and environment ( $r_e$ ) correlation coefficients and genetic parameters; as well as to estimate the selection gains between agronomic traits in wheat using multivariate statistics.

## MATERIAL AND METHODS

The study was performed in 2018 crop season, in Frederico Westphalen (27°23'26"S, 53°25'43"W, 481 m above the sea level). The soil was classified as ferric aluminum Hapludox type and the climate as Cfa according to Köppen (Alvares *et al.*, 2013).

Wheat genotypes in F6 generation developed from single crosses were evaluated: Mirante/Quartzo (UFSMFW1 01), Mirante/Fundacep Horizonte (UFSMFW 1 02), Supera/Quartzo (UFSMFW1 03), Supera/Quartzo (UFSMFW1 04), BRS 327/Fundacep Horizonte (UFSMFW1 05), Supera/Abalone (UFSMFW1 06), BRS 327/Fundacep Horizonte (UFSMFW1 07), Supera/Abalone (UFSMFW1 08), BRS 327/Fundacep Horizonte (UFSMFW1 09), Supera/Fundacep Horizonte (UFSMFW1 10), Mirante, Supera, Pampeano, Quartzo e TBIO Toruk. The last five cultivars were used in function of the variability among them. To obtain these lines, the crosses were realized in greenhouse and generation advance was performed using Single Seed Descent method (SSD). The experimental design was randomized complete blocks, with three replicates. The plots were composed by four rows 4-m long, spaced by 0.17m, in a density of 350 plants m<sup>-2</sup>. The sowing was performed on Jun 12<sup>nd</sup> 2018, in the no-tillage system; and pest, disease and weed control was done preventively.

The traits measured were: a) days of emergence to flowering (DF); b) plant height (PH, cm), measured from the soil to spike of main tiller; c) number of tillers (NT), obtained by count of fertile tillers; d) spike length (SL, cm), considering spike insertion point to start of awns; e) number of spikelets (NS), obtained by counting of spikelets of main tiller spike; f) kernel weight (KW, g) obtained by weight of main tiller spike; g) thousand kernel weight (TK, g). Except for days from emergence to flowering, the other traits were obtained at the time of harvest.

The meteorological data were obtained from the Instituto Nacional de Meteorologia (INMET), referring to automatic weather station of Frederico Westphalen - RS (A854), located about 350 m from experiment, for cultivation period of Jun 12<sup>th</sup>, 2018, to Oct 31<sup>st</sup>, 2018. For that, instantaneous, maximum, and minimum air temperature recorded every hour was used, obtaining average for instantaneous, maximum, and minimum temperature recorded for day. And for daily precipitation was carried out accumulation on a day.

Data were submitted to analysis of variance carried out at 5% significance level of test using the statistical model:  $Y_{ij} = \mu + g_i + b_j + \epsilon_{ij}$ , where  $\mu$  is the mean,  $g_i$  is the effect of  $i^{\text{th}}$  genotype,  $b_j$  is the effect of  $j^{\text{th}}$  block,  $\epsilon_{ij}$  is random error. Assuming treatments effects as random, the accuracy, was estimated (Resende & Duarte, 2007):

$$\hat{r} = \left[ \frac{1}{1 + (\sigma_e^2/b)/\sigma_g^2} \right]^{1/2}, \text{ where: } b \text{ is number of replicates or blocks.}$$

For genotypic, phenotypic, and environmental correlations between two traits (x and y) were estimated by analysis of variance. For it, the mean square associated with treatments (PMT) and residual (PMR) according the formulas:  $PMT_{xy} = \frac{MST_{x+y} - MST_x - MST_y}{2}$  and

$$PMR_{xy} = \frac{MSR_{x+y} - MSR_x - MSR_y}{2}, \text{ phenotypic correlation: } r_p = \frac{PMT_{xy}}{\sqrt{MST_x MST_y}}$$

$$r_a = \frac{PMR_{xy}}{\sqrt{MSR_x MSR_y}} \text{ and genotypic correlation:}$$

$$r_g = \frac{\hat{\sigma}_{gxy}}{\sqrt{\hat{\sigma}_{gx}^2 \hat{\sigma}_{gy}^2}}, \text{ being } \hat{\sigma}_{gxy} = \frac{PMT_{xy} - PMR_{xy}}{r}, \text{ where}$$

MQT is mean square of treatment, MSR is mean square of residue,  $\hat{\sigma}_{gxy}$  is genotypic covariance estimator,  $\hat{\sigma}_{gx}^2$  and  $\hat{\sigma}_{gy}^2$  are the genotypic variance of X and Y, respectively.

The significance test of the phenotypic and environmental correlations, the  $t$  test was used as described by Steel & Torrie (1980) according to equation:  $t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2}$ .

Genotypic correlations were submitted to bootstrap analysis with five thousand (5000) simulations to identify correlations with significance.

Selection gains were estimated through heritability and the proportion of the additive variance explored (Cruz *et al.*, 2004), and it was estimated by:  $GS = ip\hat{\sigma}_g$  where  $i$  is the selection intensity;  $p$  parental control;  $\hat{\sigma}_g$  genetic standard deviation;  $h$  square of heritability, for the selection unit considered.

The relative contribution of each trait was estimated by Singh (1981) methodology. After, for canonical variables analysis, only traits with relative contribution up to 10% were used. Statistical software Genes (Cruz,

2016) and R (R Development Core Team, 2016) was used to perform the analysis.

To study genetic diversity of populations genetic distance matrix was estimated by Euclidian's distance, and clustering analysis was done using the UPGMA (Unweighted Pair Group Method with Arithmetic Averages), and it was represented on a dendrogram. The cut level in the dendrogram, which separates populations into distinct groups, was determined by the Mojena's method (Mojena, 1977), and adjusted by cophenetic correlation. The clusters analysis were performed using "HDMD" (McFerrin, 2013) and "cluster" (Maechler *et al.*, 2018) package in R (R Development Core Team, 2016).

## RESULTS AND DISCUSSION

The analysis of variance (Table 1) showed significant difference for days of emergence to flowering, plant height, number of tillers and kernel weight by F test ( $p < 0.05$ ) genotypes. The data presented low accuracy (spike length), moderate (number of tillers) and high magnitudes (days of emergence to flowering, plant height, number of tillers, kernel weight, thousand kernel weight) (Resende & Duarte, 2007). The genotypes studied presented greater phenotypic variance for the plant height and days of emergence to flowering, and it is worth to mentioning that the environment had large influence (Table 2). It stands out the plant height traits, which revealed higher values of variance being the most influenced by environment.

Regarding the heritability, the higher estimates were observed for days of emergence to flowering (0.99), plant height (0.91), number of tillers (0.71) and kernel weight (0.73). Other researchers have obtained high heritability values for heading (0.94), plant height (0.93) and kernel weight (0.87) (Wiersma *et al.*, 2001). For plant height (0.97) and number of tillers per plant (0.95) (Mangi *et al.*, 2010). For days to 75% heading/flowering (0.87) and plant height (0.85) (Kefale & Menzir, 2019).

The results reveal a favorable condition for genetic gains with selection through these traits. Thus, these high heritability estimates indicated genetic control over evaluated traits. Therefore, it is possible to infer that traits studied in this set of genotypes may be used to evaluate genetic variability and they are efficient for prediction of selection.

The highest selection gains of wheat genotypes were evidenced for thousand kernel weight (40.56%), plant height (15.84%), number of tillers (13.25%), kernel weight (13.64%), followed by days of emergence to flowering (4.91%), spike length (1.91%) and number of tillers (5.50%) that had low estimates of selection gain among the genotypes. Therefore, selection for number of tillers and thousand kernel weight may increase selection gains since these traits response to more easily to selection due to high heritability coefficients. Fellahi *et al.* (2018), obtained selection gains of 27.14% for thousand kernel weight and 12.98% for plant height. Meira *et al.* (2019), in the study of black oat populations the selection strategy

**Table 1:** Summary of variance analysis mean ( $\bar{x}$ ) and selective accuracy ( $\hat{r}_{gg}$ ) for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TK)

Source of variation	Degrees of freedom	Mean square						
		DF	PH	SL	NT	NS	KW	TK
Block	2	3.75	62.15	1.75	0.28	1.68	0.05	0.90
Genotypes	14	34.92*	364.03*	1.80	2.4	2.56*	0.09*	1.32
Residue	28	0.08	33.67	1.46	1.5	0.73	0.03	0.48
Total	44							
$\bar{x}$		75.57	68.77	8.15	2.75	13.04	1.03	33.02
$\hat{r}_{gg}$		0.98	0.95	0.40	0.64	0.88	0.87	0.66

\*Significative to F test ( $p < 0.05$ ).

**Table 2:** Estimates of phenotypic variance ( $\hat{\sigma}_p^2$ ), genetic variance ( $\hat{\sigma}_g^2$ ), environmental variance ( $\hat{\sigma}_e^2$ ), heritability ( $h^2$ ), genetic gain ( $G_s$ ), for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TK)

Estimates	DF	PH	SL	NT	NS	KW	TK
$\hat{\sigma}_p^2$	11.64	121.34	0.60	0.80	0.85	0.03	0.44
$\hat{\sigma}_g^2$	11.61	110.11	0.11	0.30	0.60	0.02	0.17
$\hat{\sigma}_e^2$	0.03	11.23	0.49	0.50	0.25	0.01	0.26
$h^2$ (%)	99.74	90.74	18.48	37.45	71.28	73.15	40.56
$G_s$ (%)	4.91	15.84	1.91	13.25	5.50	13.64	40.56

is to reduce variability within families and to increase variability among families. This is to combine selection between and within populations to achieve high efficiency in the selection gain.

Around 90% of the correlations showed higher genotypic coefficient than phenotypic (Table 3). These results favor the selection strategy for breeding programs, since phenotypic correlations have genetic and environmental interactions, but only associations of a genetic nature are inheritable.

Spike length showed a significant and positive genetic correlation (0.43) with kernel weight and negative (-0.44) with thousand kernel weight. When a genotype has a long spike, it will usually produce a higher kernel weight and consequently will have a reduction in thousand kernel weight. Following this trend, Ahmad *et al.* (2010) found a positive genetic correlation (0.87 and 0.97) between spike length and kernel weight, studying two different populations. Mohammadi *et al.* (2011), found correlation (-0.32) between spike length and thousand kernel weight, in researches with durum wheat.

The number of tillers showed a significant and positive genetic correlation (0.52) with the kernel weight, this correlation is expected, since as we have a greater number of tillers, we have a greater number of ears and, consequently, greater weight of grains per plant. Elhani *et al.* (2007), verified simple correlations ranging from 0.42 to 0.91 between number of tillers and kernel weight, under

different management conditions. The results indicated that at the genotypic level there was a positive correlation between number of tillers and kernel weight (0.63) (Table 3). The increased number of spikelets per spike is an efficient strategy to improve grain yield of wheat, since this trait is associated to the increase in the number of grains per spike, considered an important wheat yield component (Fioreze & Rodrigues, 2012).

The negative correlation coefficients were observed between days of emergence to flowering and number of tillers (-0.55). In wheat, the shorter the vegetative period of a genotype, the lower its tillering potential. Compensatory potential of wheat tillering is modified according to development cycle and determine the number of spikes per plant (Carvalho *et al.*, 2015). In this way, photosynthetically active tillers tend to increase grain yield (Fioreze & Rodrigues, 2012).

The plant height showed a strong correlation with kernel weight (0.60), this association suggests that tall plants had greater accumulation of photosynthates for the grains, with a longer reproductive period resulting in higher grain weight (Khan *et al.*, 2013; Rigatti *et al.*, 2019).

The number of fertile tillers per plant showed a significant and positive intermediate association with kernel weight (0.52) and positive correlation with number of tillers (0.46) for genotypic correlation indicating that this trait may be used in indirect selection aiming for to increment grain yield in wheat.

**Table 3:** Estimates of phenotypic ( $r_p$ ), genotypic ( $r_g$ ) and environmental ( $r_e$ ) correlation between agronomic traits, for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TK) for wheat genotypes

Trait		PH	SL	NT	NS	KW	TK
DF	$r_p$	0.31*	0.08	-0.55*	-0.07	0.35	0.28
	$r_g$	0.46	0.45	-0.59 <sup>++</sup>	-0.42	0.51	0.46
	$r_e$	-0.23	-0.24	0.18	0.34*	-0.26	0.15
PH	$r_p$	-	0.34	-0.30	0.32	0.48	0.47
	$r_g$	-	0.55	-0.49 <sup>++</sup>	0.49	0.60	0.57
	$r_e$	-	0.37*	-0.16	-0.24	-0.19	-0.01
SL	$r_p$	-	-	0.04	0.03	0.04	-0.24
	$r_g$	-	-	0.43 <sup>++</sup>	0.46	0.49	-0.44 <sup>++</sup>
	$r_e$	-	-	-0.28	-0.22	-0.29	0.04
NT	$r_p$	-	-	-	0.18	0.35	0.13
	$r_g$	-	-	-	0.46	0.52 <sup>++</sup>	0.39 <sup>++</sup>
	$r_e$	-	-	-	0.20	0.45*	-0.19
NS	$r_p$	-	-	-	-	0.57*	-0.11
	$r_g$	-	-	-	-	0.63	-0.48
	$r_e$	-	-	-	-	0.14	-0.01
KW	$r_p$	-	-	-	-	-	0.17
	$r_g$	-	-	-	-	-	0.48
	$r_e$	-	-	-	-	-	-0.37

Genotypic correlation index “+++” and “++++” significant to t test ( $p < 0.05$  and  $p < 0.01$ ). Phenotypic and environmental correlation index, “\*” and “\*\*\*” significant to t test ( $p < 0.05$  and  $p < 0.01$ ).

Spike length showed a significant negative genotypic association with thousand kernel weight (-0.442), indicating that larger spikes tend to increase yield. In this way, these traits are important to be considered in the cereals breeding, due to being closely related to the yield components and define wheat productivity (Silva *et al.*, 2010).

For canonical variables, two variables explained more than 90% of the genetic variation among the genotypes (Table 4).

In this way, a two-dimensional graph was used to represent canonical variables (Figure 1). There is large distance among the wheat genotypes, emphasizing the genotypes Pampeano, UFSMFW1 14, UFSMFW1 03 and UFSMFW1 07 (Figure 1). Based on the graphic dispersion of the populations it is possible to direct the crosses between divergent parents to the desired traits, to promote

**Table 4:** Variance (eigenvalues), percentage variance and accumulated variance of canonical variance, aiming to estimate the dissimilarity between ten wheat genotypes, for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TK)

Trait	Variance (eigenvalues)	Percentage variance (%)	Accumulated variances (%)
DF	63.16	89.06	89.06
PH	4.98	7.02	96.08
SL	1.27	1.79	97.87
NT	0.70	0.99	98.86
NS	0.43	0.61	99.47
KW	0.26	0.36	99.84
TK	0.12	0.16	100.00

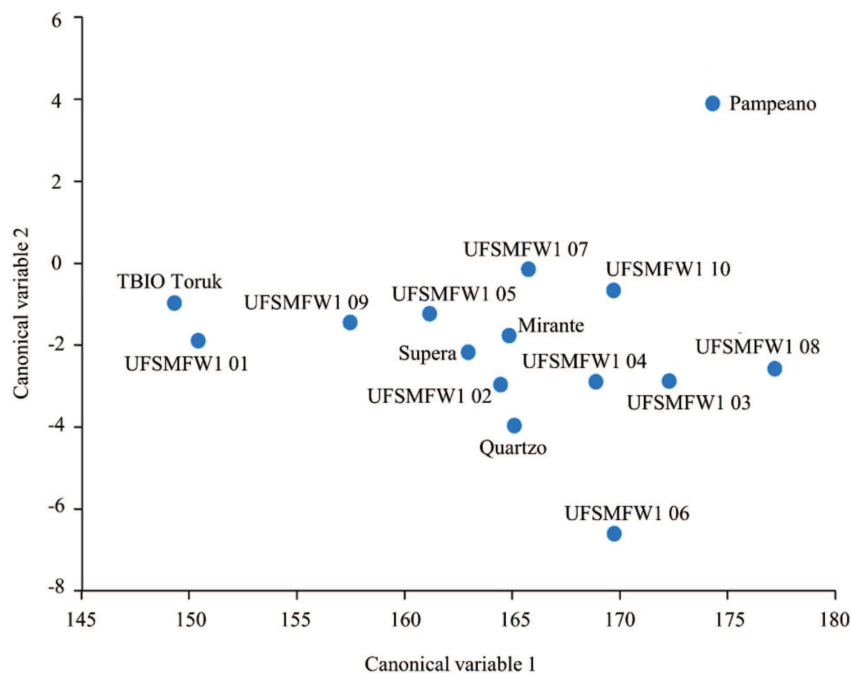
genetic recombination. In this case, hybridizations could be programmed, for example, between genotypes Pampeano with UFSMFW1 06, TBIO Toruk with Pampeano, UFSMFW1 01 with UFSMFW1 08.

Regarding the relative contribution of traits Singh (1981), days of emergence to flowering expressed the largest contribution (81%) to genetic divergence among genotypes (Table 5). Showing the important genetic variability between the genotypes for the vegetative cycle. The traits kernel weight, number of tillers and number of tillers contributed with 5%, 2% and 2%, respectively, such results agree with Gurjar & Marker (2018).

The cluster analysis verified two distinct groups, expressing genetic differences, according to evaluated traits (Figure 2). Group I: composed by genotype Pampeano. Pampeano has a longer period for days of emergence to flowering, higher plant height and longer spike length than the other genotypes. Group II: genotypes

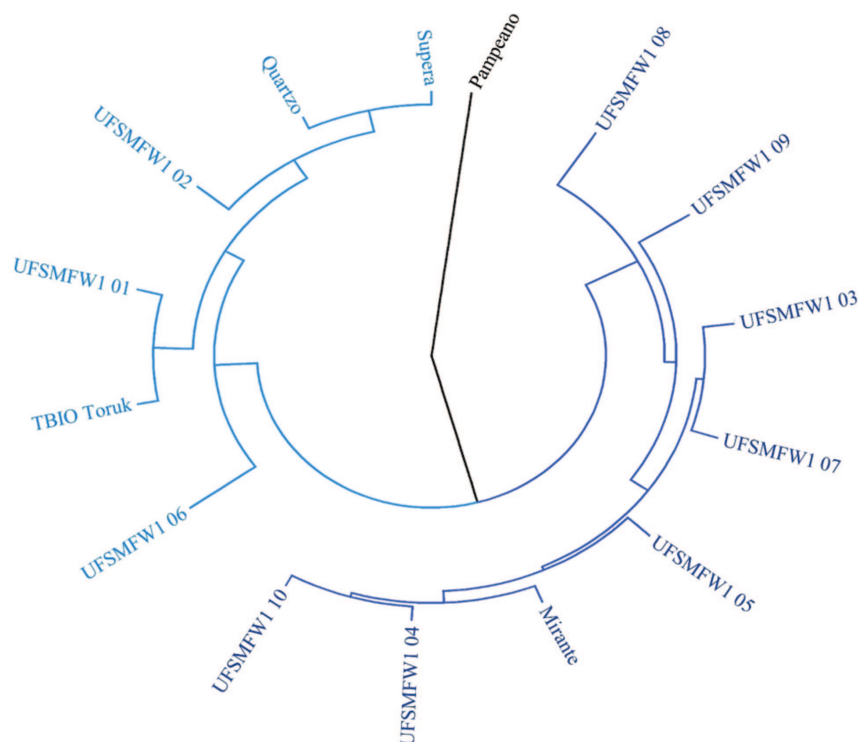
**Table 5:** Relative contribution of traits to divergence to Singh method for days of emergence to flowering (DF), plant height (PH), spike length (SL), number of tillers (NT), number of spikelets (NS), kernel weight (KW), thousand kernel weight (TK)

Trait	S.j	Value (%)
DF	12089.94	81.18
PH	1089.92	7.32
SL	105.72	0.71
NT	306.31	2.06
NS	302.60	2.03
KW	856.88	5.75
TK	141.48	0.95



**Figure 1:** Graphic dispersion of first score (canonical variable 1) and second score (canonical variable 2) for wheat genotypes.





**Figure 2:** Dendrogram using unweighted pair group method with arithmetic mean (UPGMA) from Euclidian's distance matrix for wheat genotypes. Cophenetic correlation coefficient ( $r$ ): 0.73.

UFSMFW1 01 to UFSMFW1 10, Mirante, Quartzo, Supera and TBIO Toruk in exception of Pampeano, the other genotypes have similarity among agronomic traits, being plant height and days of emergence to flowering the traits that more contribution to the divergence. The highest plant height for the genotype Pampeano, corroborated to results obtained by Bornhofen *et al.* (2013) studying the best genotypes for general combining ability.

## CONCLUSIONS

Selection based on number of tillers, kernel weight and thousand kernel weight may result in expressive selection gains. The higher significant positive genotypic correlations were verified between number of fertile tillers associated to days of emergence to flowering and kernel weight. The increased number of spikelets per spike is an efficient strategy to improve grain yield of wheat. The cycle showed greater contribution to the genetic divergence among genotypes studied. Distinct groups highlighted the genetic variability among genotypes.

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## REFERENCES

- Ahmad B, Khalil IH, Iqbal M & Rahman HU (2010) Genotypic and phenotypic correlation among yield components in bread wheat under normal and late plantings. *Sarhad Journal of Agriculture*, 26:259-265.
- Alvares CA, Stape JL, Sentelhas PC, Gonçalves JLM & Sparovek G (2013) Köppen's climate classification map for Brazil. *Meteorologische Zeitschrift*, 22:711-728.
- Bornhofen E, Benin G, Matei G, Silva CL, Beche E, Pagliosa ES, Hagemann TR & Pinnow C (2013) Combining ability of wheat parents in two generations. *Semina: Ciências Agrárias*, 34:3129-3140.
- Carvalho IR, Souza VQD, Nardino M, Follmann DN, Schmidt D & Baretta D (2015) Correlações canônicas entre caracteres morfológicos e componentes de produção em trigo de duplo propósito. *Pesquisa Agropecuária Brasileira*, 50:690-697.
- Cruz CD (2016) Genes Software - extended and integrated with the R, Matlab and Selegen. *Acta Scientiarum Agronomy*, 38:547-552.
- Cruz CD, Regazzi AJ & Carneiro PCS (2004) Modelos biométricos aplicados ao melhoramento genético. 4ª ed. Viçosa, Editora UFV. 480p.
- Elhani S, Martos V, Rharrabti Y, Royo C & García del Moral LF (2007) Contribution of main stem and tillers to durum wheat (*Triticum turgidum* L. var. durum) grain yield and its components grown in Mediterranean environments. *Field Crops Research*, 103:25-35.
- Falconer DS & Mackay TFC (1996) Introduction to quantitative genetics. London, Longman Malaysia. 463p.
- Fellahi ZEA, Hannachi A & Bouzerzour H (2018) Analysis of Direct and Indirect Selection and Indices in Bread Wheat (*Triticum aestivum* L.) Segregating Progeny. *International Journal of Agronomy*, 2018:01-11.
- Fioreze SL & Rodrigues JD (2012) Perfilamento do trigo em função da aplicação de regulador vegetal. *Revista Brasileira de Ciências Agrárias*, 7:750-755.
- Galton F (1888) Co-relations and their measurement, chiefly from anthropometric data. *Proceedings of the Royal Society of London*, 45:135-145.

- Gurjar D & Marker S (2018) Evaluation of genetic divergence in wheat (*Triticum aestivum* L.) germplasm. *Electronic Journal of Plant Breeding*, 91:361-367.
- Kefale H & Menzir A (2019) Genetic Variation of Bread Wheat (*Triticum aestivum* L.) Varieties Based on Phenological, Morphological and Quality Traits at Guay Kebele in Debre Elias District, East Gojjam Zone, Northwestern Ethiopia. *Journal of Biology, Agriculture and Healthcare*, 4:45-55.
- Khan A, Alam A, Alam MK, Alam MJ & Sarker ZI (2013) Genotypic and phenotypic correlation and path analysis in durum wheat (*Triticum turgidum* L. var. *durum*). *Bangladesh Journal of Agricultural Research*, 38:219-225.
- Laidig F, Piepho HP, Drobek T & Meyer U (2017) Breeding progress, variation, and correlation of grain and quality traits in winter rye hybrid and population varieties and national on-farm progress in Germany over 26 years. *Theoretical and Applied Genetics*, 130:981-998.
- Lo Valvo PJ, Miralles DJ & Serrago RA (2018) Genetic progress in Argentine bread wheat varieties released between 1918 and 2011: Changes in physiological and numerical yield components. *Field Crops Research*, 221:314-321.
- Mangi AS, Sial MA, Ansari BA, Arain MA, Laghari KA & Mirbahar AA (2010) heritability studies for grain yield and yield components in f3 segregating generation of spring wheat. *Pakistan Journal of Botany*, 42:1807-1813.
- Maechler M, Rousseeuw P, Struyf A, Hubert M & Hornik K (2018) Cluster: Cluster Analysis Basics and Extensions. Version 2.0.7-1. Available at: <https://svn.r-project.org/R/packages/trunk/cluster>. Accessed on: June 14<sup>th</sup>, 2020.
- McFerrin L (2013) HDMD: Statistical Analysis Tools for High Dimension Molecular Data (HDMD). Version 1.2. Available at: <https://CRAN.R-project.org/package=HDMD>. Accessed on: May 20<sup>th</sup>, 2020.
- Meira D, Meier C, Olivoto T, Nardino M, Klein LA, Moro ED, Fassini F, Marchioro VS & Souza VQD (2019) Estimates of genetic parameters between and within black oat populations. *Bragantia*, 78:43-51.
- Mohammadi M, Karimizadeh R, Shefazadeh MK & Sadeghzadeh B (2011) Statistical analysis of durum wheat yield under semi-warm dryland condition. *Australian Journal of Crop Science*, 5:1292-1297.
- Mojena R (1977) Hierarchical grouping methods and stopping rules: an evaluation. *The Computer Journal*, 20:359-363.
- Ni F, Qi J, Hao Q, Lyu B, Luo MC, Wang Y, Chen F, Wang S, Zhang C, Epstein L, Zhao X, Wang H, Zhang X, Chen C, Sun L & Fu D (2017) Wheat Ms2 encodes for an orphan protein that confers male sterility in grass species. *Nature Communications*, 8:15121.
- Olivoto T, Souza VQ, Nardino M, Carvalho IR, Ferrari M, Pelegrin AJ, Szareski VJ & Schmidt D (2017) Multicollinearity in Path Analysis: A Simple Method to Reduce Its Effects. *Agronomy journal*, 109:131-142.
- Pearson K (1920) Notes on the History of Correlation. *Biometrika*, 13:25-45.
- R Development Core Team (2016) R: A language and environment for statistical computing. Available at: <https://www.R-project.org/>. Accessed on: July 11<sup>th</sup>, 2020.
- Resende MDVD & Duarte JB (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. *Pesquisa Agropecuária Tropical*, 37:182-194.
- Rigatti A, Meira D, Olivoto T, Meier C, Nardino M, Lunkes A, Klein LA, Fassini F, Moro ED, Marchioro VS & Souza VQ (2019) Grain Yield and Its Associations With Pre-harvest Sprouting in Wheat. *Journal of Agricultural Science*, 11:142-150.
- Silva AHD, Camargo CEDO & Júnior EUR (2010) Potencial de genótipos de trigo duro para produtividade e caracteres agrônômicos no Estado de São Paulo. *Bragantia*, 69:535-546.
- Singh D (1981) The relative importance of characters affecting genetic divergence. *The Indian Journal of Genetic and Plant Breeding*, 41:237-245.
- Ali T, Singh MK, Bharadwaj DN & Singh L (2016) Analysis of genetic divergence in wheat (*Triticum aestivum* L.). *Environment and Ecology*, 35:2081-2083.
- Steel RGD & Torrie JH (1980) Principles and procedures of statistics: A biometrical approach. 2<sup>o</sup> ed. New York, McGraw-Hill. p.20-90.
- Wiersma JJ, Busch RH, Fulcher GG & Hareland GA (2001) Recurrent Selection for Kernel Weight in Spring Wheat. *Crop Science*, 41:999-1005.
- Woyann LG, Zdziarski AD, Zanella R, Rosa AC, Castro RL, Caierão E, Toigo MC, Storck L, Wu J & Benin G (2019) Genetic gain over 30 years of spring wheat breeding in Brazil. *Crop Science*, 59:2036-2045.
- Xiao D & Tao F (2014) Contributions of cultivars, management and climate change to winter wheat yield in the North China Plain in the past three decades. *European Journal of Agronomy*, 52:112-122.
- Yao Y, Lv L, Zhang L, Yao H, Dong Z, Zhang J, Ji J, Jia X & Wang H (2012) Genetic gains in grain yield and physiological traits of winter wheat in Hebei Province of China, from 1964 to 2007. *Field Crops Research*, 239:114-123.