Selection gain and interrelations between agronomic traits in wheat F_5 genotypes

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ABSTRACT

This work aimed to estimate the variance components and genetic parameters, the selection gain, and the cause and effect relationships among traits in order to identify important traits for direct and indirect selection of wheat (*Triticum aestivum* L.) lines. Three strategies were used to obtain selection gains: direct and indirect selection, an index based on "ranks," and the Smith and Hazel index. In the 2017 crop season in Brazil, 420 wheat lines from the F_5 generation were conducted in families with intercalary controls. High heritability of spike weight, number of kernels, and total kernel weight resulted in the best direct selection gains. The selection of plants with a high number of tillers resulted in grain yield improvement. The use of selection indexes is important in advanced wheat lines; they promote genetic gains distributed among agronomic traits.

Keywords: correlation; genetic parameters; selection gains; *Triticum aestivum* L.

INTRODUCTION

Wheat breeding (*Triticum aestivum* L.) has evolved intensely over the last century. This is mainly because of the importance of wheat having a high grain yield and high quality of gluten proteins for use in the food industry in the production of breads, pastas, and cakes (Sun *et al.*, 2017). This evolution has been made possible by implementing precise experimental designs and sophisticated statistical methods and by understanding the concepts of quantitative and population genetics (Bassi *et al.*, 2016).

Selection indexes are among the most efficient statistical methods used for identifying the best crop lines and potential parents to be used for future crosses (Yao *et al.*, 2018). Among the indexes, Mulamba & Mock (1978), and Smith (1936) and Hazel (1943) are the most commonly used. The efficiency of using selection indexes for crop breeding has also been highlighted by Moreira *et al.* (2019) and Smiderle *et al.* (2019).

Among the analyses used to identify the association of traits, Pearson's linear correlation reveals the sense and degree of linear association between two traits (Pearson, 1920). However, to quantify and interpret trait associations based only on simple linear correlation may result in misunderstandings in the selection process; a third, or a group of traits may be acting in response to the selection of the main trait (Cruz *et al.*, 2014). Considering this, the path analysis developed by Wright (1921) has been an important tool in the evaluation of trait associations; it allows decomposition of the linear association of direct effects with the main trait and of indirect effects among other traits.

In order to select potentially high-yielding wheat lines in breeding programs, superior genotypes need to be selected for with greater accuracy. There is a large amount of information in the literature on selection in early generations, but knowledge of selection in advanced generations is lacking. Thus, the following hypotheses were formulated: (i) the selection gains in advanced generations are satisfactory for wheat and (ii) understanding the association among agronomic traits may help to obtain superior genotypes that meet market expectations for productivity. In this way, the aim of this work was to estimate the variance components, genetic parameters, selection gains, and the cause and effect relationships among traits in order to identify important traits for direct and indirect selection of wheat lines.

MATERIALS AND METHODS

Plant material

The study was performed in the 2017 crop season, at Frederico Westphalen (27°232 262 2 S, 53°252 432 2 W; 481 m above sea level). The soil was classified as typical dystrophic Red Latosol (Santos *et al.*, 2013) and the climate as Cfa according to Köppen (Alvares *et al.*, 2013).

We evaluated 420 lines descending from a biparental cross between the cultivars Mirante and Abalone. The crosses were performed in a greenhouse during the 2013 crop season. The generation advance was performed using the Single Seed Descent (SSD) method until the F_4 generation was obtained. In generation F_5, the lines were studied in families with intercalary controls. Six replicates of six cultivars (BRS 327, Quartzo, Mirante, Pampeano, Abalone, and Supera) were used as the intercalary controls.

The base fertilization consisted of 200 kg ha^{-1} of N-P_2O_5-K_2O (08-24-12). A supplementary fertilization with 90 kg ha^{-1} of N (urea form; 45% N) was applied in two stages: one in the tillering stage and the other in the elongation stage (Reunião, 2016). Weeds, pests, and diseases were controlled according to the technical recommendations for wheat.

Traits studied

For lines and cultivars, the traits measured were a) days from emergence to flowering (DF); b) plant height (PH; cm), measured from the soil to the spike of the main tiller; c) number of tillers (NT), obtained by counting fertile tillers; d) spike weight (SW; g), obtained by weighing the spike of the main tiller; e) spike length (SL; cm), from the spike insertion point to start of the awn; f) number of spikelets (NS), obtained by counting the spikelets of the main tiller spike; g) kernel weight (KW; g), obtained by weighing the main tiller spike; h) total number of kernels per plant (TNK); and i) total kernel weight per plant (TKW; g).

Experimental design and genetic parameters

The variance analysis was performed according to families with intermediate witnesses controls experimental design (Cruz *et al.*, 2014). Thus, families were evaluated using the variance components of the controls as environmental effects.

The value of each observation for the controls was given by the regular treatment model evaluated with repetitions: $Y_{ij} = \mu + T_i + \varepsilon_{ij}$,

where Y_{ij} represents the value of the trait for i-th control in the j-th replicate; μ is the general controls average; T_i is the i-th controls effect (i = 1,2,...t); and ε_{ij} is the random error involving controls ($\varepsilon_{ij} \sim N (0, \sigma^2)$). For families submitted to non-regular treatments, without the use of repetitions: $y_i = \mu_f + F_i + \varepsilon_i$, where y_i represents the value of the trait for the i-th family; μ_f is the general genotypes average; F_i is the i-th genotype effect; and ε_i is the random error involving genotypes ($\sim N (0,)$).

Variance-covariance phenotypic and genotypic matrix was estimated to be used in selection indexes.

Linear correlation and path analysis

The linear correlation matrix containing nine explanatory traits (DF, PH, SL, NT, SW, TNK, KW, NS, and TKW) was evaluated for the level of multicollinearity. This was determined using the condition number, which is given by the ratio between the major and minor eigenvalues of the correlation matrix. Traits that caused multicollinearity problems were excluded from the analysis, as recommended by Olivoto *et al.* (2017). Subsequently, path analysis was performed using the matrix of genotypic correlations, considering TKW as a dependent trait and the other traits as explanatory.

The *t* test was used to evaluate whether the phenotypic correlation coefficient (r) was equal to zero, by means of the expression, , where *t* is associated with n-2 degrees of freedom and 1% probability, n is the number of pairs of observations (n = 420), and r is correlation coefficient (Steel & Torrie, 1980). The magnitudes of the correlation estimates were classified according to Carvalho *et al.* (2004).

Selection gain

The direct selection gains for traits were estimated using the equation, GS = (Xsi-Xoi) = DSi h², where Xsi is the mean value of individuals selected for trait i; Xoi is the original population mean; DSi is the differential selection performed in the population; and h² is heritability of trait i. The indirect gain in trait j, by selection in trait i, is given by GSj (i) = DSj (i) h², where DSj (i) is the indirect selection differential obtained as a function of the trait mean of superior individuals on which direct selection was performed (Cruz, 2006).

Superior individuals were indicated according to the genotypic values obtained from the selection index proposed by Smith (1936) and Hazel (1943), and on the sum of ranks index of Mulamba & Mock (1978). The classic index (Smith, 1936; Hazel, 1943) consists of the linear combination of several traits of economic importance, whose weighting coefficients were estimated by the genetic coefficient of variation of the experiment, in order to maximize the correlation between the index and the aggregate genotype. According to Cruz (2006), the economic weight may be estimated from the experimental data. In the index based on the sum of ranks, the genotypes were classified by the selection index, described as I = r1 + r2 + ... + rn, where I is the index value for a given genotype or family; rj is the rank of a progeny in relation to the jth trait; and n is the number of traits considered for performing the index described by Mulamba & Mock (1978).

The selection was aimed at increasing SL, NT, SW, KW, NS, TNK, and TKW, and reducing DF and PH. Selection was applied in order to select the 10 best genotypes. All statistical analyses were performed using the Genes software (Cruz, 2016).

RESULTS

Variance components and genetic parameters

There was genetic variability in the wheat lines and cultivar controls evaluated. This variability was affirmed by finding significative differences between DF, SW, SL, NS, KW, TNK, and TKW in different lines. For the controls, the observations were meaningful for PH, SW, SL, NS and TKW (Table 1). The wheat lines displayed a high potential for improving these agronomic traits via selection.

The wheat lines presented higher phenotypic variance for the PH, NT, and TNK traits, which was mostly attributed to the lower environmental variation (Table 2). It may be highlighted that the PH revealed higher values of variance for controls, suggesting that they were more influenced by the environmental variation than advanced generation wheat lines. The heritability, coefficient of genetic variation (CVg), and ratio between the coefficients of genetic and experimental variation (CVg/CVe), as a function of the environmental influence, revealed higher heritability values for SW, KW, and TKW, of more than 70%.

Linear associations

Evaluating the linear associations among the traits studied (Figure 1), DF showed a moderate negative association with PH, SW, KW, and TKW. This demonstrated that precocity in wheat is promising for breeding programs owing to the positive association with total kernel weight.

The number of tillers showed a positive and strong association with TNK (0.952) and TKW (0.742) and a moderate association with other variables. The NT was directly associated with grain yield increase; considering this, the NT is an efficient trait to use for indirect selection for increasing grain yield.

The SW displayed a positive and strong correlation with KW (0.958) and a moderate correlation with TKW (0.543) and NS (0.479). Important associations were found between NG and TKW (0.746) on that the increase in the number of kernels maximizes grain yield.

Direct and indirect effects

According to the coefficient of determination, the analyzed traits may explain 78% of the total grain weight per plant (Table 3). The NT displayed a linear correlation of positive and moderate magnitude with TKW (r = 0.606).

Table 1: Summary of variance analysis, means, and heritability for wheat lines and controls studied in Frederico Westphalen, Brazil

Source of variation	GL	MS								
		DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Lines	419	40.44*	77.04^{ns}	66.35^{ns}	0.31**	2.26*	4.30*	0.21**	924.99*	53.51**
Control	5	30.51^{ns}	655.21**	65.88^{ns}	0.20**	6.37**	9.43**	0.11^{ns}	999.71^{ns}	25.83**
Residue	24	20.13	50.39	39.22	0.05	1.19	2.16	0.05	465.91	4.70
General mean		80.45	61.75	22.55	1.69	10.29	15.87	1.17	727.10	13.03
Lines mean		80.38	60.28	22.65	1.69	10.28	15.85	1.18	729.90	13.26
Controls mean		81.44	68.25	18.17	1.63	10.48	16.20	1.08	687.79	9.83
CV (%)		5.58	11.50	27.77	12.82	10.58	9.25	19.25	29.66	16.64
CV (%) Line		5.58	11.58	27.65	12.79	10.59	9.27	19.15	29.55	16.35
CV (%) Control		5.51	10.40	29.58	13.27	10.39	9.06	20.87	31.36	22.06
Heritability (%)		50.20	34.60	40.89	84.37	47.50	49.91	74.17	49.67	91.21

* and ** represent significance at p < 0.05 and p < 0.01, respectively, as determined by *t* test, ^{ns} not significative, GL, degrees of freedom, MS, mean square; CV, coefficient of variation; DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers; SW, spike weight; NS, number of spikelets; KW, kernel weight; TNK, total number of kernels per plant; TKW, total kernel weight per plant.

The DF had a direct negative effect on TKW, indicating that selecting for plants with a long flowering cycle is not advantageous for potentially increasing the grain yield. The KW had a positive direct effect on TKW and an indirect effect on NT. These associations may have been observed owing to the plant spacing implemented in the experiment.

Selection gains

The selection gain results revealed variation in gains for evaluated traits and methods used (Table 4). Direct and indirect selection showed gains from -23.82% for DF to 301.85% for TKW. The gains recorded for TKW, TNK, KW, and SW were overall positive. However, higher DF and PH values resulted in negative gains. Although direct selection resulted in high gains, indirect selection gains were also significant, in particular for NT and TNK. Selection for NT resulted in indirect gains of 45.38% and 100% for TNK and TKW, respectively, and a direct gain of 35.83% (Table 4). Selection for TNK resulted in direct gains of 53.34% and indirect gains in TKW of 96.12%.

Selection gains obtained by the Smith (1936) and Hazel (1943) selection index, for the main trait, were similar among the methods studied (Table 4). The higher gains were observed for TKW, KW, NK, SW, and NT. The wheat lines rank for the Mulamba & Mock (1978) index had a 90% coincidence with the direct selection (Table 5), while the coincidence of the Smith (1936) and Hazel (1943) index was lower. The superior lines selected from the selection indexes (145, 183, 189, 193, and 299) are promising lines, mainly for improving grain yield.
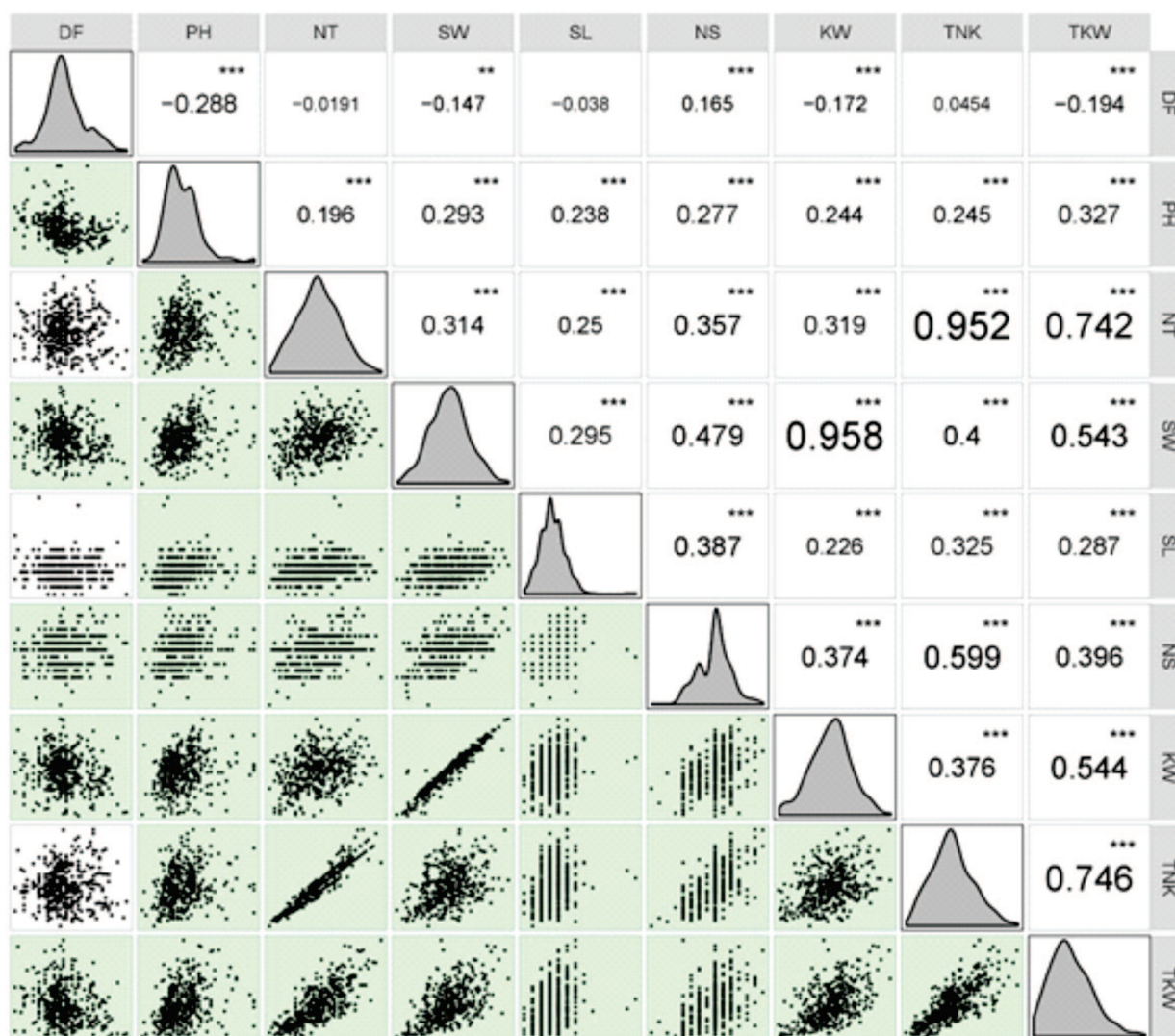
Figure 1: Pearson's linear correlation among agronomic traits of 420 wheat lines. *, **, and ***, which represent Pearson linear correlation coefficient (n = 420) significance levels at p < 0.05, 0.01, and 0.001, respectively, are highlighted in green. DF, days from emergence to flowering; PH, plant height; NT, number of tillers; SW, spike weight; SL, spike length; TNK, total number of kernels per plant; NS, number of spikelets; KW, kernel weight; TKW, total kernel weight per plant.

DISCUSSION

The phenotypic variance is related to the genotypic and environmental variance. In this study, the lines that presented higher plant heights were highly influenced by the environment. This trend was also observed by Keser *et al.* (2017), who found that the mean plant height decreased from 140.7 cm to 79.5 cm, from the oldest to the most current wheat cultivar. This reduction was associated with the introduction of the *Rht1* gene. Reducing plant height is an important factor to be considered in breeding programs as it is an essential and desirable trait (Yao *et al.*, 2018).

The heritability of DF found in the experiment was similar to that found in the studies conducted by Bind *et al.* (2016). These authors showed that the white oat cycle had a low heritability. Cargnelutti *et al.* (2009) observed that high heritability is linked to greater genetic variability, and therefore, greater accuracy in selection.

In relation to the association of traits, most (91%) of the coefficients revealed significance even with low magnitudes (Figure 1). This may be explained by the high degrees of freedom (n = 418) included in the *t* test (Steel & Torrie, 1980). The association of NT with TNK and TKW is an important consideration for wheat breeding, since the NT can be easily measured.

Table 2: Variance components and genetic parameters estimated for wheat lines and controls studied in Frederico Westphalen, Brazil

Parameter	Line								
	DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Phenotypic variance	40.44	77.05	66.35	0.30	2.26	4.30	0.20	92.99	53.51
Environmental variance	20.14	50.39	39.22	0.05	1.19	2.16	0.05	46.91	4.70
Genotypic variance	20.30	26.66	27.13	0.25	1.07	2.15	0.15	45.08	48.81
Heritability (%)	50.20	34.60	40.89	84.37	47.50	49.91	74.17	49.67	91.21
CVg (%)	5.61	8.42	23.00	29.71	10.08	9.25	32.44	29.35	52.68
Ratio CVg CVe^{-1}	1.04	0.73	0.83	2.32	0.95	0.98	1.69	0.99	3.22
Parameter	Control								
	DF	PH	NT	SW	SL	NS	KW	TNK	TKW
Phenotypic variance	6.10	131.04	13.18	0.04	1.28	1.89	0.02	95.54	5.17
Environmental variance	4.03	10.08	7.84	0.01	0.24	0.43	0.01	93.98	0.94
Genotypic variance	2.07	120.97	5.33	0.03	1.04	1.45	0.01	10691.56	4.23
CVgt (%)	1.77	16.11	10.91	10.78	9.72	7.45	10.06	15.03	20.91
Ratio CVg CVe^{-1}	0.32	1.55	0.37	0.81	0.94	0.82	0.48	0.48	0.95

DF, days from emergence to flowering; PH, plant height; NT, number of tillers; SW, spike weight; SL, spike length; NS, number of spikelets; KW, kernel weight; TNK, total number of kernels per plant; TKW, total kernel weight per plant. CVg, coefficient of genetic variation; CVe, coefficient of experimental variation; CVgt, coefficient of the controls' genetic variation.

Table 3: Estimates of direct (main diagonal) and indirect effects of eight agronomic traits on total kernel weight per plant (TKW) evaluated in 420 wheat lines, Frederico Westphalen, Brazil

	Explanatory traits					
	DF	PH	NT	SL	NS	KW
DF	**-0.120**	0.034	0.002	0.005	-0.020	0.021
PH	-0.024	**0.082**	0.016	0.019	0.023	0.02
NT	-0.012	0.119	**0.606**	0.151	0.216	0.193
SL	-0.001	0.006	0.006	**0.025**	0.010	0.006
NS	0.01	0.017	0.022	0.024	**0.062**	0.023
KW	-0.048	0.069	0.090	0.064	0.105	**0.282**
Linear	-0.194	0.327	0.742	0.287	0.544	0.396
Determination coefficient						0.784
Residual effect of variable						0.561
Number Condition						5.111
Determining variable						0.424

DF, days from emergence to flowering; PH, plant height; NT, number of tillers; SL, spike length; NS, number of spikelets; KW, kernel weight; bold values correspond to direct effects.

Table 4: Selection gains in wheat lines (GS%) determined using three methods: direct and indirect selection, and Mulamba & Mock and Smith & Hazel selection indexes

Traits	X0	XS	GS%									
			DF	PH	SL	NT	TNK	SW	KW	NS	TKW	Total
DF	80.37	65.70	**-9.17**	2.78	2.41	-1.18	-2.99	-8.17	-7.42	-1.09	1.01	-23.82
PH	61.28	45.60	1.76	**-8.85**	-4.98	-10.57	-17.06	-20.89	-18.67	-7.39	-45.84	-132.49
SL	10.27	14.80	-1.23	4.3	**20.89**	1.71	6.36	23.25	17.28	4.58	18.06	95.2
NT	22.65	42.50	1.51	4.24	2.41	**35.83**	45.38	11.53	14.71	2.06	100.62	218.29
TNK	729.91	1513.89	2.33	2.15	3.8	30.78	**53.34**	33.82	33.69	10.57	96.12	266.6
SW	1.69	3.03	-0.23	5.26	7.03	6.4	17.81	**66.78**	61.72	8.99	79.72	253.48
KW	1.18	2.21	-1.05	5.15	5.64	8.03	17.19	63.29	**65.24**	6.79	87.78	258.06
NS	15.84	21.10	4.39	2.38	7.49	12.72	35.93	38.7	32.56	**16.55**	43.1	193.82
TKW	13.26	34.03	-1.55	4.24	5.64	27.16	38.21	39.5	41.23	4.58	**142.84**	301.85
Smith & Hazel			-0.61	3.34	23.37	41.05	6.16	35.67	40.23	137.77	6.57	293.55
Mulamba & Mock			1.39	3.96	22.65	51.22	11.51	43.72	51.29	106.73	8.42	300.89

Bold values correspond to direct gains. DF, days from emergence to flowering; PH, plant height; SL, spike length; NT, number of tillers; TNK, total number of kernels per plant; SW, spike weight; KW, kernel weight; NS, number of spikelets; TKW, total kernel weight per plant.

In this study, the NS was associated with TNK. Thus, a higher sowing density provides an increase in the number of kernels per spikelet. In accordance with the results of this study, Board & Maricherla (2008) found a high ratio between the number of kernels and kernel weight per area. Spike size is an important agronomic trait for breeding, especially as it is positively associated with grain yield. Results from a previous study have shown that a larger spike resulted in a greater number of spikelets (Silva *et al.*, 2010).

Agronomic traits with high magnitudes of correlation must be considered in selection strategies (Vale *et al.*, 2014). Thus, based on our results for the experimental design used, the strategy adopted could be positive indirect selection. The traits suggested by the analysis for selection are the number of kernels and tillers, in front of the correlations among traits. However, it is important to highlight that a greater spacing of plants leads to a greater number of tillers per plant; this diverges from commercial sowing conditions, which involve high planting densities.

In order to improve our knowledge of the association of traits, path analysis is an important technique as it provides information on the direct and indirect effects on the main trait. Studies carried out by Entringer *et al.* (2014) and Carvalho *et al.* (2017) found satisfactory gains using both direct and indirect selection, since the traits showed favorable correlation. Falconer (1987) highlighted that indirect selection may promote greater gains; the same was evidenced by Pereira *et al.* (2017), who studied the genus *Paspalum*.

The selection gains obtained infer that all methods may be used for wheat line selection. The direct and indirect selection showed the best selection gains. The Mulamba & Mock sum of ranks index presented higher gains when compared to the Smith and Hazel index. The efficiency of using selection indexes has also been observed in silage maize (Crevelari *et al.*, 2019), soybean (Teixeira *et al.*, 2017), and wheat (Fellahi *et al.*, 2018). Almeida *et al.* (2019) showed concordance between indexes with regards to the ranking of the best genotypes; the magnitude of the expected gain must be considered.

CONCLUSIONS

The heritability of the spike weight, total number of kernels, and total kernel weight per plant reveals that selection of these traits may result in greater direct selection gains.

Selection of plants with a higher number of tillers resulted in more productive lines. Selection indexes are advantageous for breeding advanced generations of wheat, since they provide the gains, distributed among all the evaluated traits. The selection index based on the sum of ranks (Mulamba & Mock) was more efficient in the selection of productive wheat lines.

Table 5: Wheat lines selected by direct and indirect selection, Mulamba & Mock and Smith & Hazel selection indexes, Frederico Westphalen, Brazil

Selection Index	Lines
Direct selection	145, 183, 189, 193, 242, 299, 303, 310, 404, 413
Smith & Hazel	81, 145, 183, 189, 193, 299, 372, 396, 408, 412
Mulamba & Mock	145, 183, 189, 193, 242, 299, 303, 310, 385, 404

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