

Research Article

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Genetic parameters estimation in quantitative traits of a cross of triticale (*x Triticosecale* W.)

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Abstract: Triticale (*x Triticosecale* Wittmack) is a cereal used in Argentina as a winter seasonal pasture or feeding grain. Efforts made on breeding have led to varieties with potential grain yield similar or greater than with wheat. The aim of this study was to determine the gene effects, heritability, genetic gain, heterosis and inbreeding depression in various quantitative traits of a cross from contrasting lines of triticale using generation means analysis. The thousand kernel weight was adjusted to a model of additive-dominance, while the rest of the traits exhibited significant epistatic effects: additive x additive (i) for hectoliter weight, additive x dominance (j) for number grains per spike and grain yield per plant. Other traits showed a more complex as inheritance additive x additive (i) and additive x dominance (j) interactions effects for spike length or additive x dominance (j) and dominance x dominance (l) interactions effects for number of spikes per plant and number of spikelets per spike. High values of heritability and genetic gain were also detected for grain yield, spikelets per spike, spike per plant and hectoliter weight. All traits except spike per plant had positive relative mid-parent heterosis, but none resulted in positive heterobeltiosis, therefore this cross is not recommended for obtaining hybrids varieties. Selection in early generations by thousand kernel weight and hectoliter weight would be efficient, while the selection in advanced generations where segregation is minimal would be recommended for the remaining traits.

1 Introduction

Triticale (*x Triticosecale* Wittmack) in Argentina is potentially suitable to various uses, although the most frequent is direct grazing, it can also be used as a dual purpose and to supplement or include in rations. Triticale is in a free expansion period, especially in sub-humid and semi-arid areas where it successfully replaces the use of rye (Grassi et al. 2004). Its rusticity is similar to rye but with superior forage quality (Amigone and Kloster 1997). The selection of experimental line for grain yield registers varied antecedents in Argentina (Grassi et al. 2003, 2004; Cardozo et al. 2005; Castro et al. 2011; Ferreira et al. 2015).

Grain yield is a complex trait with multiple components and is strongly influenced by the environment, in which numerous morphological and physiological traits contribute in its expression. It would be necessary to know the inheritable and not inherited contribution with the help of genetic parameters (Singh and Chaudary 1985; Kahrizi et al. 2010; Maniee et al. 2009). The analysis of the nature and magnitude of the gene effects on quantitative traits helps the researcher to design an efficient improvement program and to provide information on the potential manifestation of heterosis (Shekhawat et al. 2000). Analysis of relative mid-parent heterosis (Mh%) and heterobeltiosis (Hh%) allows to define the breeding strategy (Yildirim et al. 2014). Recent studies in triticale suggest that hybrids performance are significantly higher than cultivated varieties (Oettler et al. 2003; 2005; Yildirim et al. 2014).

Generation mean analysis is a simple technique to estimate the genetic effects and to elucidate the nature of the epistasis, being useful to decide the procedure to be adopted in the improvement of quantitative traits (Abd El-Rahman and Hammad 2009). Joint-scaling test

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is a method used to determine the most appropriate genetic model and to partition the digenic epistatic effects (Ceballos 1996).

Although investigations on genetic effects and inheritance of quantitative traits in wheat are multiple, they are scarce in triticale and no one in using generation mean analysis. The purposes of this study were to provide information about genetic effects and heritability of yield and its components in a triticale cross, as to assess the heterosis and inbreeding depression in order to determine the strategy to be applied in an improvement program.

2 Materials and methods

The experimental materials analyzed in this study were obtained from the cross of the high yield genotype CIMMYT 820 (CTSS99BOO125S-0M-9Y-13M-1Y-4M-0Y, CIMMYT, Mexico) and cultivate feed Don Santiago INTA (6TH 131, Foundation Jenkins, USA), both parents were selected for presenting contrasting traits, CIMMYT 820 has short spike length, high hectoliter weight and excellent thousand kernel weight while Don Santiago INTA has high number of spikes per plant, high number of spikelets per spike and excellent number of grains per spike. Generations CIMMYT 820 (P_1), Don Santiago INTA (P_2), first and second filial generations (F_1 , F_2) and backcross $P_1 \times F_1$ (BC_1) and $P_2 \times F_1$ (BC_2) were sowed in a complete randomized blocks design with three replications in the experimental field of the Agronomy Faculty of the National University of La Pampa during the 2014 growing season. This field was located in Santa Rosa, La Pampa (Argentina), at south latitude $36^\circ 46'$, west longitude $64^\circ 17'$ and 210 meters above sea level, characterized by on a petrocalcic Paleustol soil and a semi-arid climate with an rainfall during growing season 2014 of 417 mm. The non-irrigated assay was conducted without nutritional limitations on plots of five rows of three meters of length and equidistant spacing of 15 cm between plants. The experimental unit consisted on the main tiller or the total value of each plant according to the trait analyzed. Seventy plants were analyzed in parents and F_1 , 170 plants in BC_1 and BC_2 and 230 plants in F_2 . The following traits were recorded:

1. Number of spikes per plant (SP).
2. Spike length of main tiller (SL).
3. Number of spikelets per spike of main tiller (SS).
4. Number of grains per spike of main tiller (SG).
5. Thousand kernel weight (TKW).
6. Hectoliter weight (HW).
7. Grain yield per plant (GY).

2.1 Statistical analysis

Analysis of variance (ANOVA) and Fisher LSD test ($\alpha \leq 0.05$) were performed to detect significant differences among generation means using InfoStat software (Di Renzo et al. 2008).

Generation mean analysis of the six generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) was performed using Mather and Jinks (1982) method. The mean of each trait is indicated as follows:

$$Y = m + \alpha[d] + \beta[h] + \alpha^2[i] + 2\alpha\beta[j] + \beta^2[l]$$

where Y = the mean of one generation; m = the mean of all generation; d = the sum of additive effects; h = the sum of dominance effects; i = the sum of additive x additive interaction; j = the sum additive x dominance interactions; l = the sum of dominance x dominance interactions and α , β , α^2 , $2\alpha\beta$ and β^2 are the coefficients of genetic parameters.

To estimate the parameters and to select the most suitable model, the Joint-scaling test (Cavalli 1952; Mather and Jinks 1982; Ceballos 1996) was employed. Genetic coefficients and the generation means were sequentially adjusted to the model via weighted least-squares and the best fit was determined with the simplest model that found no significance in Chi-Square χ^2 test. The significance of genetic effects was estimated using the “t” of Student test. The type of epistasis was considered only when dominance (h) and dominance x dominance (l) effects were significant. When these effects had the opposite signs, the type of epistasis was duplicate (Kearsey and Pooni 1996).

The components of variation were calculated according to Mather and Jinks (1982):

$$\begin{aligned} E &= 1/3 (\text{variance of } P_1 + \text{variance of } P_2 + \text{variance of } F_1) \\ D &= 4 * \text{variance of } F_2 - 2 (\text{variance of } BC_1 + \text{variance of } BC_2) \\ H &= 4 (\text{variance of } F_2 - 1/2 * \text{dominance variance} - \\ &\quad \text{environmental component of variance}) \end{aligned}$$

where:

E = environmental component of variance

D = additive genetic variance

H = dominance variance (was set to zero when estimated variance turned out to be negative).

The narrow-sense heritability (h^2) was estimated according to the formula proposed by Warner (1952):

$$h^2 = [2 * \text{variance of } F_2 - (\text{variance of } BC_1 + \text{variance of } BC_2)] / \text{variance of } F_2$$

Relative mid-parent heterosis (Mh%), heterobeltiosis (Hh%) and inbreeding depression (ID%) were determined as: $Mh\% = [(F_1 - (P_1 + P_2)/2) / ((P_1 + P_2)/2)] \times 100$; $Hh\% = [(F_1 - P_{max}) / P_{max}] \times 100$; $ID = [(F_1 - F_2) / F_1] \times 100$, where P_{max} refers to the higher performing parent.

Ethical approval: The conducted research is not related to either human or animals use.

3 Results and discussion

The analysis of variance revealed significant differences for all the traits. The mean value, standard error and comparison of means for each generation are presented in Table 1. CIMMYT 820 and Don Santiago INTA showed significant differences in all the traits, except for GY. CIMMYT 820 exhibited the highest values of TKW and HW while Don Santiago INTA in SP, SL, SS and SG. These genetic variations were suitable to perform a genetic parameters analysis.

The results of the joint-scaling test are presented in Table 2. The trait TKW was fitted to the three-parameter (additive-dominance) model, which showed that the effect of epistasis was not involved in its inheritance. The additive (d) and dominance (h) effects were positive and significant, with the additive effect being the major contribution. Similar results were reported in wheat (Grzesik 2000; Erkul et al. 2010; Tonk et al. 2011). Despite the adjustment to the additive-dominance model, the lack of detection of epistasis does not exclude the presence of inter-allelic interactions. According to Moroni et al. (2013)

a balance of positive and negative epistatic effects could result in a non-significant epistasis estimate. Significant epistatic effects for this trait were reported in wheat (Dvojković et al. 2010; Hassan and El-Said 2014).

For the rest of the traits, the additive-dominance model was not adequate to interpret the existent variability; therefore, more complex models were necessary to detect the presence of epistasis. The trait SL, SG and GY behaved in a similar way, adjusting to a four-parameter model with additive (d), dominance (h) and dominance x dominance (l) effects, with additive effects of little relative importance. With regard to the trait GY the additive (d) effect was not significant and dominance (h) and dominance x dominance (l) effects had the higher contribution. Like SL, SG and GY showed a duplicate type epistasis, indicating a predominance of dispersed alleles at the interacting loci. The presence of duplicate epistasis type in quantitative trait might limit the range of variability and the selection success in the early generations could be negatively affected (Ljubičić et al. 2016). Different models and magnitude of the epistatic genetic effects for the SL, SG and GY have been published in wheat (Ali et al. 2014; Bnejdi and El Gazzah 2010; Grzesik 2000; Dvojković et al. 2010; Tonk et al. 2011; Hassan and El-Said 2014; Darwish and El-Nahas 2015).

In the same way, HW fitted to a four-parameter model with additive x additive (i) epistatic effect. Effects (d), (h) and (i) were positive, with predominance of components (h) and (i). This situation is more favorable than the presence of dominance x dominance (l) effects or duplicate epistasis type, because it is possible to fix additive x additive effects in selecting at early segregating

Table 1: Mean \pm standard error in quantitative traits in six generations from a triticale cross

Generation	Traits ¹						
	SP	SL (cm)	SS	SG	TKW (g)	HW (kg hl ⁻¹)	GY (g)
P ₁ CIMMYT 820	2.19 \pm 1.07 b	7.21 \pm 0.41 c	16.6 \pm 0.27 e	39.7 \pm 1.32 c	39.4 \pm 0.63 a	65.2 \pm 0.46 a	2.23 \pm 0.23 b
P ₂ Don Santiago INTA	2.57 \pm 0.92 a	9.64 \pm 0.12 ab	21.9 \pm 0.28 a	51.8 \pm 1.12 ab	28.9 \pm 0.51 d	63.3 \pm 0.43 bc	3.41 \pm 0.16 ab
F ₁	2.13 \pm 0.96 b	9.12 \pm 0.14 b	20.0 \pm 0.31 cd	48.0 \pm 1.22 b	35.8 \pm 0.52 b	65.0 \pm 0.33 ab	3.43 \pm 0.21 ab
F ₂	2.59 \pm 1.16 a	9.35 \pm 0.09 ab	20.7 \pm 0.21 bc	50.9 \pm 0.81 ab	35.8 \pm 0.41 b	61.7 \pm 0.27 c	4.23 \pm 0.15 a
BC ₁	2.60 \pm 1.05 a	8.98 \pm 0.08 b	19.8 \pm 0.18 a	48.9 \pm 0.81 ab	37.9 \pm 0.46 ab	64.7 \pm 0.28 ab	4.25 \pm 0.15 a
BC ₂	2.46 \pm 0.98 ab	9.90 \pm 0.11 a	21.1 \pm 0.22 ab	53.4 \pm 0.96 a	32.3 \pm 0.43 c	62.1 \pm 0.28 c	3.83 \pm 0.15 ab

¹Traits: SP = spikes per plant, SL = spike length, SS = spikelets per spike, SG = number of grain per spike, TKW = thousand kernel weight, HW = hectoliter weight, GY = grain yield.

Means within a column followed by the same letter are not significantly different at the 0.05 probability level

generations and thus increase the chances of success in the improvement (Novoselović et al. 2004; Ljubičić et al. 2016).

SP and SS traits were fitted to a five-parameter model with effects (m), (d), (h), (j) and (l). The additive effect was relatively low and a greater contribution of the effects of dominance and non-allelic interaction with duplicated epistasis type was detected. The low effects of additive and the duplicate epistasis determine that selection in the early segregating generation is not efficient. The presence of significant epistatic effects for these traits were reported by several authors in wheat (Bnejdi and El Gazzah 2010; Tonk et al. 2011; Ali et al. 2014; Hassan and El-Said 2014; Darwish and El-Nahas 2015). However, many publications indicated that the results depend on the parents used and the evaluation site or environment. In this regard, Bnejdi and El Gazzah (2010) and Erkul et al. (2010) reported fit to the three-parameter model.

For the traits GY, SS, SP and HW were observed high heritability and genetic gain indicating that genetic variation is largely explained by additive variation (Table 3). These results suggest that genotypes can be detected from their phenotypic expression, and that selection in the F_2 generation be effective to improve these yield components. In spite of this, the presence of epistatic effects of the duplicate type in the GY, SS and SP traits limits selection in early segregating generation. The traits SL, SG and TKW showed low heritability values,

indicating little additive variation and also that the genetic effects of dominance and epistatic interactions had a significant influence, adding to an important component of environmental variation. These results are in accordance with reports published by other authors in wheat (Bnejdi and El Gazzah 2010; Erkul et al. 2010; Dvojković et al. 2010; Sultan et al. 2011; Abd El-Rahman 2013; Amin 2013). The negative dominance variance for SP, SS, HW and GY may be due to micro-environmental variations, sampling errors and / or the fact that the basic generations are inefficient to determine the variance of dominance in the analysis (Novoselović et al. 2004; Dvojković et al. 2010).

Snape (1987) points out that it is common to find non-significant additive effects and significant effects of dominance for yield and its components, as it occurs in the present study with the GY, SS, HW and SP. Estimates of slight additive effects would be due to the fact that the parents had a high degree of dispersion of contributing alleles. This might explain why additive genetic component of variance (V_A) was significant (Dvojković et al. 2010).

The percentage of relative mid-parent heterosis (Mh%), heterobeltiosis (Hh%) and inbreeding depression (ID) can be observed in Fig. 1. The trait GY was the only one presenting positive Hh% (0.59), although the superiority of the hybrid (F_1) was not statistically different from the best parent (P_2), (Table 1). On the other

Table 2: The estimates of gene effects for quantitative traits in CIMMYT 820 x Don Santiago INTA x triticale cross

Genetic effects ³	Traits ¹						
	SP	SL	SS	SG	TKW	HW	GY
	Parameter ²						
	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE	Mean±SE
m	2.38±0.08**	8.42±0.08**	19.2±0.19**	45.8±0.86**	34.3±0.35**	58.7±0.96**	3.37±0.13**
d	0.19±0.08*	1.12±0.07**	2.61±0.19**	5.55±0.71**	5.33±0.34**	2.07±0.36**	-0.06±0.11
h	0.93±0.31**	3.32±0.36**	4.43±0.81**	18.8±3.49**	1.76±0.64*	6.07±1.59**	2.84±0.57**
i	-	-	-	-	-	6.61±1.06**	-
j	-0.66±0.27*	-	-2.51±0.69**	-	-	-	-
l	-1.18±0.31*	-2.62±0.39**	-3.66±0.87**	-16.7±3.58**	-	-	-2.78±0.60**
χ^2 (GL) ⁴	0.41 (1)	4.40 (2)	0.59 (1)	1.09 (2)	2.60 (3)	2.47 (2)	5.31 (2)
Type of epistasis	duplicate	duplicate	duplicate	duplicate	-	-	duplicate

¹Quantitative traits. SP=spikes per plant, SL= spike length, SS= spikelets per spike, SG= number of grain per spike, TKW= thousand grain weight, HW= hectoliter weight, GY= grain yield.

²Mean±SE (standard error)

³ Mean (m), additive (d), dominance (h), additive × additive (i), additive × dominance (j) dominance × dominance (l) genetic effects.

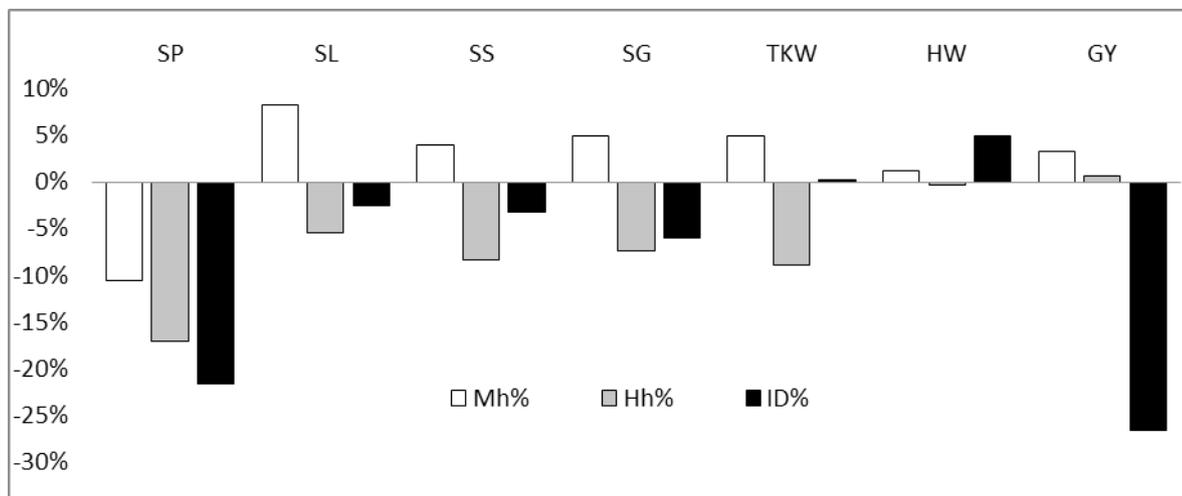
⁴ GL= degree of freedom, calculated as number of generations minus number of genetic effects estimated.

*P < 0.05, **P < 0.001.

Table 3: Variance components, narrow-sense heritability and expected genetic gain of quantitative traits in CIMMYT 820 x Don Santiago INTA triticale cross

	Traits 1						
	SP	SL	SS	SG	TKW	HW	GY
Phenotypic variance (V_p)	1.34	1.89	10.01	152.70	38.33	17.42	5.36
Environmental variance (V_e)	0.96	1.27	6.54	116.60	23.77	12.48	3.11
Additive variance (V_a)	0.61	0.30	5.07	22.49	4.77	7.70	3.17
Dominance variance (V_d)	0.00	0.32	0.00	13.63	9.78	0.00	0.00
Heritability ($h^2\%$)	45.50	15.80	50.60	14.70	12.44	44.50	59.10
Genetic Gain (GA)	1.15	0.40	3.30	3.70	1.58	3.80	2.80

¹Quantitative traits. SP: spikes per plant, SL: spike length, SS = spikelets per spike, SG = number of grain per spike, TKW= thousand kernel weight, HW= hectoliter weight, GY= grain yield

**Figure 1:** Percentage of relative heterosis (Mh%), heterobeltiosis (Hh%) and inbreeding depression (ID%) from CIMMYT 820 x Don Santiago INTA triticale cross. Traits: SP: spikes per plant, SL: spike length, SS: spikelets per spike, SG: number of grains per spike, TKW: thousand kernel weight, HW: hectoliter weight, GY: grain yield

hand, SL (8.25), SS (4.02), SG (4.89), TKW (4.9) and HW (1.21) stood out for their positive Mh%, but not SP (-10.5) that was lower than the average of parents. These results are not very promising to develop commercial hybrids. Fischer et al. (2010) mention that the prediction of the heterosis based on the parents averages of a single cross result in low precision, and in such a case, it would be advisable to carry out a general and specific combining ability analysis. Other authors (Oettler et al. 2001; 2003; 2005; Cifci and Yagdi 2007; Yildirim et al. 2014) have reported similar values of heterosis and heterobeltiosis in triticale. Traits that presented inbreeding depression were SP (-21.6), SL (-2.52), SS (-3.29), SG (-5.99) and GY (-26.64). On the other hand, HW (4.97) and TKW (0.16) did not show it, which would facilitate their genetic improvement.

4 Conclusions

The cross analysis did not show heterobeltiosis for grain yield and therefore it would not be promising to develop commercial hybrids, however, the results are an interesting contribution which ensures better insight in genetic action and gene effects and modes of inheritance of studied traits in triticale. Generation means analysis revealed that all traits analyzed have shown complex genetic behavior except thousand kernel weight. Number of spikelets per spike, spike length, number of spike per plant, number of grains per spike and grain yield per plant presented epistasis of the duplicate type or low additive effects, therefore it would be advisable to relegate the selection to more advanced generations, while in the early generations could be recommended to select for thousand kernel weight and hectoliter weight.

Conflict of interest: Authors state no conflict of interest.

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