

Agronomic performance of bread wheat (*Triticum aestivum* L.) and hexaploid triticale (*X Triticosecale* Wittmack) based on the use of a selection index.

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Summary

The objective of this research was to evaluate the actual agronomic performance in bread wheat (*Triticum aestivum* L.) and hexaploid triticale (*X Triticosecale* Wittmack) based on the use of a selection index constituted by eleven traits measured at plot level. Two samples of 142 S_0 hexaploid triticale progenies and 89 S_0 bread wheat progenies were sown under rainfed conditions and a selection index was constituted using the following traits: spikes ($n^\circ \text{ plant}^{-1}$ and $n^\circ \text{ plot}^{-1}$), grain and biological yield (g plot^{-1}), harvest index (%), 1000 grain weight (g), grain ($n^\circ \text{ plot}^{-1}$), grain and biomass yield (g spike^{-1}), harvest index spike^{-1} (%) and straw yield (g spike^{-1}). A disruptive selection intensity of 7.0 % (triticale) and 11.2% (bread wheat) was applied in both directions of the frequency distributions for the selection index. The 20 S_1 triticale families (ten per group) and 20 S_1 bread wheat families (ten per group) were evaluated during 2003. Grain and biological yield (g m^{-2}), spikes ($n^\circ \text{ m}^{-2}$), 1000 grain weight (g), harvest index (%) and grain ($n^\circ \text{ m}^{-2}$) were measured and the differential and the response to selection were estimated from the S_0 progenies and S_1 derived families, respectively. A higher number of significant differences between the higher and lower index group mean values were observed for the bread wheat germplasm. In both species and for all measured traits, the mean values corresponding to the higher group were greater than those observed in the lower one. These results confirm that using a selection index it is possible to get a harmonic yield improvement in both species.

Index words: Selection index, grain yield, yield components, bread wheat, hexaploid triticale

Introduction

The primary objective of most plant breeding programs is to identify genotypes superior in grain yield. When a selection scheme is applied to improve grain yield, changes in this character are often accompanied by changes in other characters. These are the grain yield components and, taking into account that some of them (e. g. grain number) are also co-responsive to selection, it would be useful to take them as selection criteria.

Yield component breeding and the modification of plant architecture offer possibilities in developing more efficient systems leading to an increase in grain yield potential (Sidwell *et al.*, 1976). It is reasonable to think that it is possible to combine grain yield and its components in an index, and to apply a selection scheme using this index (as a single character) with the aim to achieve the above mentioned goal in a short time (Falconer, 1984). Moreover, it would be expected to improve all of them simultaneously, which is difficult to accomplish through selection for a individual trait at a time. With a selection index the superior segregant and recombinant multiple trait families are maintained and the inferior ones are excluded from the selected group (Simmonds, 1981).

Despite the advantages of the selection indexes, they have not been frequently used in winter cereal breeding programs mainly because a complex equation has to be developed with appropriate relative economic or a genetic weightings for all traits.

Among the recently published reports, the work carried out by Sharma and Duveiller (2003) should be mentioned. They used a selection index in wheat including the traits Helminthosporium blight (HLB) resistance, maturity and kernel weight, and found that it was possible to select for HLB resistance and early maturity simultaneously. Moreover, they demonstrated that it was possible to detect desirable correlated responses in biomass yield, grain yield and harvest index, suggesting that the selection index could be used as an indirect selection criterion to improve grain yield.

On the other hand, Maich *et al.* (2002) evaluated the agronomic performance in bread wheat and hexaploid triticale with the use of a selection index constituted by eighteen characters. Twelve out of eighteen of the traits included in this selection index were measured at sample level (5 spikes per sample) and six of eighteen were measured at a plot level. Spike characteristics represented 50% of all traits included in the index. The experimental material of this study consisted of two samples of 131 S_0 (triticale) and 121 S_0 (bread wheat) progenies derived from the second and fifth cycle respectively of two recurrent selection programs performed under rainfed conditions. They observed that not all traits included in the selection index responded in the expected manner. In wheat, for example, a differential of selection (ds) of 51.9% (lower selection index group mean=100) was calculated for grain number m^{-2} ; however, the response to selection (RS) was slightly negative (-0.7%). The same tendency was observed in triticale, where a ds of 60.6 % was applied and a RS of -11.6 % was obtained. In summary, fourteen of eighteen (bread wheat) and ten of eighteen (triticale) RS and ds coincidences were observed with respect to the direction of selection applied.

The objective of this research was to evaluate the actual agronomic performance in bread wheat and hexaploid triticale from the use of a new selection index constituted by eleven traits measured at plot level.

Material and methods

The experimental material consisted in two samples of 142 S_0 hexaploid triticale (*X Triticosecale* Wittmack) progenies and 89 S_0 bread wheat (*Triticum aestivum* L.) progenies derived from the third (C_3) and the sixth (C_6) cycle, respectively, of the two above mentioned recurrent selection programs (Maich *et al.*, 2002). The triticale germplasm was developed by crossing two genotypes, whereas sixteen commercial genotypes were used to created the initial population of bread wheat.

The triticale and bread wheat S_0 progenies samples were sown under rainfed conditions on May 22, 2002, at the Experimental Farm of the College of Agriculture (Córdoba National University), Córdoba, Argentina (31° 29' S; 64° 00' W). The experimental unit consisted of one-row plots without replications, 1.3 m in length, spaced at 0.20m and with a seeding rate of 100 grains m^{-2} . Systematic controls every nine experimental plots were used.

A selection index was constructed including the following traits: spikes (n° plant $^{-1}$ and n° plot $^{-1}$), grain and biological yield (g plot $^{-1}$), harvest index (%), 1000 grain weight (g), grain (n° plot $^{-1}$), grain and biomass yield (g spike $^{-1}$), harvest index spike $^{-1}$ (%) and straw yield (g spike $^{-1}$). For each trait measured, the progeny mean value was compared to the corresponding 142 C_3S_0 (hexaploid triticale) or 89 C_6S_0 (bread wheat) sample mean values (=100). The score per S_0 progeny was obtained as the sum of the eleven percentages (positives and negatives). A disruptive selection intensity of 7.0 % (triticale) and 11.2% (bread wheat) was applied in both directions of the frequency distributions for the selection index variable.

The 20 S_1 triticale families (ten per group) and 20 S_1 bread wheat families (ten per group) were evaluated during 2003 in the same location. One-row plots 5 m long spaced 0.20 m apart at a seeding rate of 250 grains m^{-2} were used. For each species, a completely randomized design with two replications was used.

The S_1 family traits measured on a plot basis were: grain and biological yield ($g\ m^{-2}$), spikes ($n^\circ\ m^{-2}$), 1000 grain weight (g), harvest index (%) and grain ($n^\circ\ m^{-2}$). For each trait, the ds and the RS were estimated from the S_0 progenies and S_1 derived families, respectively, as the differences (in percent) between higher and lower (=100) selection index group mean values. The estimation of the realized heritabilities pondered in the index (h^2r^*) was obtained by dividing the RS by ds per 100.

Data were submitted to an analysis of variance and the differences between mean values were determined by the DGC test (Di Rienzo *et al.*, 2001).

Results

Table 1 shows mean values, ds, RS and h^2r^* for six traits in bread wheat and hexaploid triticale germplasms.

Table 1: Mean values (lower and higher index groups), differentials (ds) and responses to selection (RS) and realized heritabilities (h^2r^*) for six traits of S_0 progenies and S_1 families in bread wheat and hexaploid triticale germplasms.

Bread wheat germplasm									
		S_0 progenies				S_1 families			
		Lower Group	Higher Group	ds (%)		Lower Group	Higher Group	RS (%)	h^2r^* (%)
GY	($g\ plot^{-1}$)	29.1	112.1	285.2	($g\ m^{-2}$)	215.1 *	259.9	20.8	7.3
BY	($g\ plot^{-1}$)	144.9	412.4	184.6	($g\ m^{-2}$)	840.6 *	975.8	16.1	8.7
SpN	($n^\circ\ plot^{-1}$)	57.8	124.4	115.2	($n^\circ\ m^{-2}$)	306.8 *	357.4	16.5	14.3
1000 GW	(g)	29.6	34.0	14.9	(g)	36.0 ns	37.3	3.6	25.3
HI	(%)	20.7	27.2	31.4	(%)	25.4 *	26.6	4.7	15.0
GN	($n^\circ\ plot^{-1}$)	982.3	3292.7	235.2	($n^\circ\ m^{-2}$)	5968.4 *	6957.2	16.6	7.0
Hexaploid triticale germplasm									
		S_0 progenies				S_1 families			
		Lower Group	Higher Group	ds (%)		Lower Group	Higher Group	RS (%)	h^2r^* (%)
GY	($g\ plot^{-1}$)	47.6	130.7	174.6	($g\ m^{-2}$)	331.5 ns	368.4	11.1	6.4
BY	($g\ plot^{-1}$)	227.1	506.3	122.9	($g\ m^{-2}$)	1256.4 ns	1357.3	8.0	6.5
SpN	($n^\circ\ plot^{-1}$)	41.5	81.7	96.9	($n^\circ\ m^{-2}$)	206.2 *	229.1	11.1	11.5
1000 GW	(g)	36.4	39.2	7.7	(g)	39.9 ns	40.7	2.0	25.7
HI	(%)	21.2	25.9	22.2	(%)	26.4 ns	27.2	3.0	13.7
GN	($n^\circ\ plot^{-1}$)	1311.9	3338.3	154.5	($n^\circ\ m^{-2}$)	8266.3 ns	9090.8	10.0	6.5

GY: grain yield; BY: biological yield; SpN: spike number; 1000 GW: thousand grain weight; HI: harvest index; GN: grain number; * significant differences at $P>0.05$ level; ns: non significant differences

In wheat as well as in triticale germplasm the higher ds were estimated for grain yield, grain number and biological yield, while the lower one corresponded to 1000 grain weight. The triticale's ds were lower than those estimated for the bread wheat germplasm.

With respect to the S_1 family performances, a higher number of significant differences between the higher and lower index group mean values were observed for the bread wheat germplasm. However, in both species and for all measured traits, the mean values corresponding to the higher group were greater than those observed in the lower one.

In both species similar values of h^2r^* per trait were observed. Grain yield, grain number and biological yield had the lowest estimations: 7% to 8% in bread wheat and 6.4% to 6.5% in triticale, whereas the highest value was observed for 1000 grain weight (25.3% for bread wheat and 25.7% for triticale). The intermediate estimation values corresponded to spike number and harvest index.

Discussion

Although for some of the triticale germplasm measured traits the mean values corresponding to the higher and lower index groups did not differ significantly between them; with respect to the selection index utilized by Maich *et al.* (2002), the superior performance of the former group shows an increase in the efficiency to discriminate the superior material through the use of this new index constituted by eleven variables, measured exclusively at plot level. Particularly in wheat germplasm, we make sure to recombine agronomic superior materials at the moment of constituting the next cycle of recurrent selection. In this context, the significant responses to disruptive selection observed after six cycles of recurrent selection were guaranteed by the utilization of sixteen cultivars as parents. Moreover, in order to maintain a high genetic variability, the optimal minimum number of recombinants recommended to constitute every new cycle is of about 30 and 45 families (Hallauer, 1985). In our case, the number of recombinants used to obtain every cycle was between 10 and 15 progenies; despite this, the genetic variability did not seem to be affected.

In the triticale germplasm the general absence of significant differences between higher and lower group mean values after three cycles of recurrent selection, may be due to the use of only two parents at the moment of constitution of the base population. This initial narrow genetic platform must be enhanced in order to show significant differences between germplasm selected disruptively.

With respect to the heritability estimations (pondered in the selection index), the lower realized heritabilities observed for grain yield and grain number suggest that, although grain number is the trait that better explains the increase in grain yield, it is at the same time a trait as complex, variable and unpredictable as grain yield itself (Slafer *et al.*, 2003). Because grain number is one of the main yield components, it may be taken as an alternative selection criterion to improve grain yield, but this would be an error due to the fact that any alternative trait must meet two requisites to be used as an indirect selection criterion: i) to be related to the main trait and ii) to have higher heritability than it has (Falconer, 1984). Grain number is related to grain yield but their heritabilities are similar. The same situation was observed for biological yield which is one of the main physiological yield components and also showed a low heritability estimation. In summary, neither grain number nor biological yield would be more efficient selection criteria than grain yield itself. On the other hand, the highest heritabilities estimated for 1000 grain weight and harvest index may lead us to think that selecting by any of these two traits, we can get an increase in grain yield. But, the compensatory effects that exist between some of these traits, e. g., an increase in the grain number is often accompanied by a decrease in 1000 grain weight, are well known.

Regardless of the relationship between grain yield and yield components and their heritabilities, our results confirm that using this selection index it is possible to get a harmonic yield improvement in both species. Moreover, comparing these results with those obtained by Maich *et al.* (2002), we conclude that a selection index is more efficient when the traits included in it are measured or estimated at plot level, because we can avoid subjectivity at the moment the sample is taken.

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