ARTICLES

Combining ability of wheat genotypes in two models of diallel analyses

Igor Pirez Valério[1*], Fernando Irajá Félix de Carvalho[2], Antonio Costa de Oliveira[2], Velci Queiroz de Souza[3], Giovani Benin[4], Douglas André Malmann Schmidt[5], Guilherme Ribeiro[2], Rafael Nornberg[2], and Henrique Luch[2]

ABSTRACT – *Diallel analyses are commonly used for the estimate of population genetic effects. Different models can be used, with a direct effect on the inferences. The objective of this study was to determine and compare two diallel analysis models, fixed and random, regarding the combining effects among six wheat genotypes. The experiment was conducted in the county of Capão do Leão/RS in the year 2006. Six wheat genotypes were used that were used for artificial crosses according to a complete diallel model without reciprocals, resulting in 15 hybrid combinations. The data were subjected to diallel analyses according to model 2 of Griffing (fixed) and BLUP (random). The results show that both diallel models indicate similar general combining ability effects. On the other hand, for the specific combining ability, the data must be used with caution, considering the two models simultaneously.*

Key words: BLUP, Griffing, fixed, random, quantitative traits.

INTRODUCTION

The use of procedures that enable the selection of the best parents for crosses represents an excellent tool for the generation of elite populations to be targeted by selection. Therefore, diallel crosses are successfully used in plant breeding, since they allow the evaluation of combining ability and heterosis potential of lines or varieties when crossed, as well as basic studies on genetic structure of populations (Geraldi and Miranda Filho 1998).

Diallel analysis methods allow an estimate of the genetic effects. Such methods were proposed by Hayman (1954), Gardner and Eberhart (1966) and Griffing (1956), in which the effects and the square sum of effects of general and specific combining ability are estimated. Cruz et al. (2004) cite this last method as one of the most widely used in diallel analysis, which can also be subdivided in four different methods. Each method has a specific mathematical model for the analysis. This model can be analyzed as fixed, random or mixed, depending on the parental sampling nature and study

[1] OR Melhoramento de Sementes Ltda, 99050-120, Passo Fundo, RS, Brazil. *E-mail: igorvalerio@gmail.com
[2] Universidade Federal de Pelotas (UFPel), Centro de Genômica e Fitomelhoramento (CGF) - Faculdade de Agronomia "Eliseu Maciel" (FAEM), 96010-900, Pelotas, RS, Brazil
[3] Universidade Federal de Santa Maria, Departamento de Agronomia – CESNORS, Linha Sete de Setembro, s/n, BR 386, KM 40, Frederico Westphalen, RS, Brazil
[4] Universidade tecnológica Federal do Paraná (UTFPR), 85501-970, Pato Branco, PR, Brazil
[5] Brasmax Genética, 73802-4020, Formosa, Goiás, Brazil

objectives, but often the models are analyzed as fixed to simplify calculations (Resende 1999).

N the usual form of diallel analysis genetic values are assumed as fixed, which may distort evaluations and even bias the estimated genetic values (Henderson 1975). In many cases, the genetic effects can be considered random. However, the traditional analysis includes genetic effects in the fixed matrix using the method of ordinary least squares. In practical terms, this would not allow the use of mixed model techniques. Therefore, an approach using mixed model equations is used, developed by Henderson (1949).

When using the mixed linear model method, random effects are predicted by the Best Linear Unbiased Prediction (BLUP) and the fixed effects are estimated by the Best Linear Unbiased Estimator (BLUE) (Resende 1999). This method is adequate for the prediction of genetic values of each individual, and can be used to predict not-performed crosses (Bernardo 1996). The approach consists in considering genetic effects as random, adjusting them for the remaining fixed effects of the model. It is also appropriate for high unbalanced orders.

The concepts of the nature of effects present in a model have been refined, but generally deal with the same range of inferences to be performed. In case of fixed effects, conclusions are limited to the results, i.e., specific to locations and genotypes of the analysis. On the other hand, when considering the effects as random, conclusions can be extrapolated to a wider set of environments. The use of mixed models (Panter and Alten 1995) would also allow the extrapolation of inferences to other conducting environments. This would be useful for the indication of genotypes, especially when quantitative traits are analyzed, which are under strong environmental influence (Falconer and Mackay 1997).

Therefore, when information on combining ability of quantitative traits in breeding programs is required, it is essential that a wider range of genotype expressions can be obtained, since very often possible combinations are missing. The objective of this study was to evaluate two diallel analysis models, Griffing's (fixed) and BLUP (random), with regard to their combinatory effects for six wheat genotypes.

MATERIAL AND METHODS

The experiment was established in the year 2006 in an experimental field of the Centro de Genômica e Fitomelhoramento (CGF) from the Faculdade de Agronomia Eliseu Maciel (FAEM), Universidade Federal de Pelotas (UFPel), located at Capão do Leão County – RS (lat 31° 52' 00'' S; long 52° 21' 24'' W; 13.24 m asl). The climate classification is Cfa, with a mean annual precipitation of 1,280.2 mm (Moreno 1961). The soil is a clayey-texture Typic Hapludult with a hilly relief and the water table is close to the surface.

A total of six Brazilian wheat genotypes were selected because of their contrasting tillering capacity: FUNDACEP 29 (provided by the Fundação Centro de Experimentação e Pesquisa - FUNDACEP); IPR 85 (of the Instituto Agronômico do Paraná - IAPAR); OCEPAR 11-JURITI (from the Cooperativa Central de Pesquisa Agrícola – COODETEC); Safira (from OR Melhoramento de Sementes Ltda), BRS Figueira and BRS 177 (from Embrapa Trigo). The genotypes were artificially crossed according to the diallel model without reciprocals, consequently resulting in 15 hybrid combinations.

F_1 seeds from each combination were obtained in a greenhouse in the summer growing season of 2006. In July 2006, a field experiment was installed with parents and F_1 generations. Plants were grown in 3-m-long rows spaced 0.3 m apart in a completely randomized block design with three replications, where each individual plant was considered an observation unit.

The following traits were evaluated: i) number of tillers per plant (NT p^{-1}), by counting the number of tillers of each plant individually at flowering; ii) number of fertile tillers per plant (NFT p^{-1}) at maturation stage; iii) ear weight per plant (EW p^{-1}), by weighing the main ear in grams; iv) grain weight per plant (GW p^{-1}), by weighing the grains of the main ear, in grams; v) number of grains per plant (NG p^{-1}), by counting grains on the main ear of each plant and vi) grain yield (g) per plant (GY p^{-1}), by threshing each plant individually.

The data were subjected to analysis of variance and the sum of squares of treatments were partitioned into general (GCA) and specific combining ability (SCA), based on an a diallel analysis of variance. In the partitioning, Griffing method 2, model B (Griffing 1956) was used. The statistical model was, $Y_{ij} = m + g_i + g_j + s_{ij} + \varepsilon_{ij}$ where: Y_{ij} is the mean value of the combination ($i \neq j$) or parental ($i = j$); m is the general mean; g_i, g_j are the effects of the general combining ability of ith and j^{th} parent, respectively; S_{ij} is the specific combining ability effect for the crosses

between i and j parents; and $\bar{\varepsilon}_{ij}$ is the mean experimental error, considering the model fixed. These analyses were performed using software Genes (Cruz 2001).

For the diallel analysis based on random effects, Selegen-REML/BLUP was used, model number 36, using complete blocks and one plant per plot, considering unrelated parents (Resende 2002). The statistical model was $y = Xr + Za + Wf + e$, where: y is the data vector; r is the vector of replication effects (assumed as fixed) added to the general mean; a is the vector of individual additive genetic effects (assumed as random); f is the vector of full-sib line dominance effects (random); e is the vector of errors or residues (random) and capital letters represent incidence matrices for these effects.

Data means were compared by the Scott & Knott test at 5% probability. Spearman's correlation analysis was used to estimate the association between the methods (fixed and random), considering the GCA and SCA effects in each treatment. The association between means was estimated by Pearson's correlation.

RESULTS AND DISCUSSION

The analysis of variance detected significance at 5% probability for the treatment mean squares (TMS) in all evaluated traits (Table 1). In this way, the square sum of treatments was partitioned into general (GCA) and specific (SCA) combining ability, according to Griffing's method 2 (Griffing 1956). The significance for TMS was expected since the parents were selected based on their high genetic dissimilarity for the evaluated traits, mainly tillering capacity. Likewise, GCA and SCA effects were significant (p<0.05) for all evaluated traits. The significance of effects indicated

the presence of variability among GCA effects (g_i), associated to additive gene effects and among SCA effects (S_{ij}), associated to non-additive gene effects (Cruz et al. 2004).

The higher GCA and SCA mean square values found in this study suggest that additive gene effects are more important, stabilizing the expression of these traits in the F_2 generation (Allard 1999), as Joshi et al. (2004) also observed for wheat . However, the predominance of non-additive and the presence of both, additive and non-additive gene effects were also observed in bread wheat (Menon and Sharna 1997). Other reports claim that GCA effects tend to persist in self-crossing generations, while SCA varies according to the population evaluated and is mainly determined by the type of gene action involved in the trait control (Masood and Kronstad 2000). The reason is that dominant and episthatic gene actions decrease when generations are advanced, due to a reduction in the fraction of heterozygous plants in the population.

The original means and the means attributed to genetic effects only (BLUP random model) were calculated for the populations and their respective parents (Table 2). Regarding the parental mean, the highest values for the traits number of tillers per plant (NT p^{-1}) and number of fertile tillers (NFT p^{-1}) were observed for genotype BRS Figueira. For ear weight per plant (EW p^{-1}) and grain weight per plant (GW p^{-1}), the individual performance of IPR 85 was best. For the traits number of grains per plant (NG p^{-1}) and grain yield per plant (GY p^{-1}), the best performance was observed for BRS 177. These results indicate the parents with greatest capacity to confer considerable genetic variability to the progenies. The values further indicate

Table 1. Diallel variance analysis mean squares by balanced fixed model of Griffing, for six wheat traits [*]

SV	df	Mean squares (MS)					
		NT p^{-1}	NFT p^{-1}	EW p^{-1}	NG p^{-1}	GW p^{-1}	GY p^{-1}
Treatment	20	135.30*	96.34*	0.29*	166.82*	0.18*	174.42*
GCA	5	493.37*	347.06*	0.67*	362.58*	0.36*	351.59*
SCA	15	15.94*	12.77*	0.17*	101.57*	0.12*	115.36*
Error	40	4.36	5.71	0.06	11.78	0.04	5.79
CV (%)	-	12.18	16.38	8.37	7.40	12.22	11.02

[*] Traits: NT p^{-1} (number of tillers per plant), NFT p^{-1} (number of fertile tillers per plant), EW p^{-1} (ear weight per plant), NG p^{-1} (number of grains per plant), GW p^{-1} (grain weight per plant) and GY p^{-1} (grain yield per plant). * Significant at 5% probability by the F test. CV (%) Coefficient of variation

that the mean performance (mean parameter) is preferable to the random genetic model (BLUP mean), since the results are consistent. The mean performance of each genotype regarding the combinations in which they participate as parents (Y_i), indicated BRS Figueira as a superior genotype for three of six traits (NT p^{-1}, NFT p^{-1} and GW p^{-1}), demonstrating the genetic potential of transferring favorable alleles to improve population performance, suggesting the hypothesis that the GCA of genotype BRS Figueira is higher than of the other genotypes for these traits. In this sense, the use of genotype BRS Figueira in breeding programs can represent a viable strategy for increasing tiller production and grain yield. Besides, no difference was detected in the evaluation of the trait number of tillers during flowering or maturity, when tested by the parameter of the mean of the best genotypes. On the other hand, it must be pointed out that the genotypes with the highest means were those with the highest differences between tiller production at flowering and at maturity. These phenomena could be attributed to a higher tiller senescence rate in genotypes with higher tillering capacity (Richards 1988) and should therefore be used with caution by breeders.

Table 2. Analysis of means[*] for six traits[**] and mean genetic component effect based on the random model (BLUP)

Generations	NT p^{-1}		NFT p^{-1}		EW p^{-1}		NG p^{-1}		GW p^{-1}		GY p^{-1}	
	O.M.	BLUP	O.M.	BLUP	O.M.	BLUP	O.M.	BLUP	O.M.	BLUP	O.M.	BLUP
OCEPAR 11-JURITI	7.73e	7.39	6.56c	6.34	2.63b	2.77	35.25d	35.07	1.20b	1.23	10.67e	11.30
FUNDACEP 29	9.89e	10.07	8.39c	8.58	2.77b	2.88	46.89b	47.24	1.75b	1.79	14.50e	14.57
IPR 85	9.05e	9.41	8.21c	8.83	3.52a	3.49	42.67c	43.06	1.94a	1.95	12.71e	13.12
BRS 177	22.69b	22.42	18.82b	18.71	2.89b	2.93	55.07a	54.68	1.59b	1.63	35.33a	34.87
Safira	25.67b	25.17	17.89b	18.36	2.76b	2.79	51.89a	51.75	1.55b	1.59	18.06d	18.37
BRS Figueira	30.90a	30.33	25.33a	25.23	2.50b	2.58	40.67c	40.29	1.39b	1.44	24.20c	24.37
OCEPAR 11-JURITI/ FUNDACEP 29	8.52e	8.65	7.26c	7.42	3.27a	3.18	45.75b	45.79	1.82a	1.78	13.34e	13.48
OCEPAR 11-JURITI/IPR 85	9.80e	9.54	8.73c	8.40	3.23a	3.23	41.87c	42.12	1.65b	1.68	16.00d	16.12
OCEPAR 11-JURITI/BRS 177	12.64e	13.18	9.94c	11.10	3.11a	3.07	48.48b	48.30	1.74b	1.70	16.63d	16.87
OCEPAR 11-JURITI/Safira	17.34c	16.87	14.85b	13.86	3.25a	3.12	58.73a	57.33	1.92a	1.82	25.93c	25.63
OCEPAR 11-JURITI/ BRS Figueira	16.77c	17.15	14.92b	15.31	2.92b	2.89	37.80d	38.02	1.62b	1.59	24.19c	24.06
FUNDACEP 29/IPR 85	13.98d	12.99	11.04c	10.20	3.37a	3.33	53.67a	53.03	2.13a	2.07	19.12d	19.08
FUNDACEP 29/BRS 177	17.75c	17.30	14.87b	14.33	3.14a	3.10	57.55a	56.78	1.85a	1.83	17.58d	17.77
FUNDACEP 29/Safira	11.42e	13.03	8.99c	11.20	2.90b	2.92	48.46b	48.67	1.76b	1.77	12.36e	12.75
FUNDACEP 29/ BRS Figueira	21.33b	20.88	19.17b	18.16	3.24a	3.10	45.67b	45.44	1.95a	1.87	26.58c	26.33
IPR 85/BRS 177	14.43d	14.87	13.28c	13.64	3.51a	3.40	55.05a	54.35	2.29a	2.16	21.05d	21.17
IPR 85/Safira	18.08c	17.81	16.47b	15.46	3.31a	3.24	51.59a	51.23	1.96a	1.92	36.45a	35.73
IPR 85/BRS Figueira	17.47c	18.06	15.37b	16.26	2.96b	3.00	36.02d	36.67	1.67a	1.70	28.50c	28.27
BRS 177/Safira	23.73b	23.47	20.64a	19.78	2.61b	2.73	47.62b	48.02	1.62b	1.64	25.54c	25.53
BRS 177/BRS Figueira	25.08b	25.14	22.32a	22.11	2.93b	2.90	35.08d	36.13	1.59b	1.60	29.04c	28.93
Safira/BRS Figueira	26.00b	26.10	23.39a	22.77	2.50b	2.60	38.45d	39.07	1.52b	1.55	30.86b	30.60
OCEPAR 11-JURITI (Yi)*	12.13	12.13	10.38	10.40	3.07	3.04	44.65	44.43	1.66	1.63	17.79	17.91
FUNDACEP 29 (Yi)	13.81	13.82	11.62	11.64	3.11	3.08	49.66	49.49	1.88	1.85	17.25	17.33
IPR 85 (Yi)	13.80	13.78	12.18	12.13	3.32	3.28	46.81	46.74	1.94	1.91	22.32	22.24
BRS 177 (Yi)	19.39	19.39	16.64	16.61	3.03	3.02	49.81	49.71	1.78	1.76	24.20	24.19
Safira (Yi)	20.37	20.40	17.04	16.90	2.89	2.90	49.45	49.34	1.72	1.71	24.87	24.76
BRS Figueira (Yi)	22.92	22.94	20.08	19.97	2.84	2.84	38.95	39.27	1.62	1.62	27.23	27.09
Média Geral do Dialélo	17.16	17.13	14.59	14.57	3.02	3.01	46.39	46.33	1.74	1.73	21.84	21.85

[*] Means: O.M. (original mean of the trait, where: treatments followed by the same letter do not statistically differ by the Scot Knot test at 5% probability). [**]Traits: NT p^{-1} (number of tillers per plant), NFT p^{-1} (number of fertile tillers per plant), EW p^{-1} (ear weight per plant), NG p^{-1} (number of grains per plant), GW p^{-1} (grain weight per plant) and GY p^{-1} (grain yield per plant). * Mean performance of each genotype regarding the parental combinations in crosses (Yi)

The analysis of GCA effects for the six parents evaluated in this study in the two models (fixed and random) facilitates the identification of highly promising genotypes for use in crosses targeting higher grain yields. By Griffing's method, high positive or negative gi (GCA) estimates indicate that the parent analyzed performs better or worse than the others included in the diallel design (Cruz et al. 2004). In this sense, the GCA performance of the cultivars BRS Figueira, Safira and BRS 177, with high and positive values for the traits NT p^{-1}, NFT p^{-1} and GY p^{-1}, indicate the potential of these genotypes for use in crosses targeting these traits.

The use of genotypes with high number of tillers (BRS Figueira, Safira and BRS 177) in crossing blocks, with the goal of increasing grain yield and ear number in wheat is based on gene complements. This suggests that these genotypes will determine a wider range of selection classes, with a high probability of forming superior progenies. The same is true for genotypes with a low tiller number, such as IPR 85 and FUNDACEP 29, regarding the traits EW p^{-1} and GW p^{-1}, with high and positive GCA values. However, the use of these genotypes in breeding programs with the goal of increasing grain yield, based on GCA only, should only be used in the selection targeting the traits EW p^{-1} and GW p^{-1}, since the effects on the other traits were negative. Regarding the trait NG p^{-1}, the genotypes with high GCA values were FUNDACEP 29, BRS 177 and Safira (Table 3).

The variability of results regarding the GCA gene effects was high for the tested genotypes, and the range of classes of selection was wide in different traits. GCA estimates with similar sign and value for both diallel models were also observed. This demonstrates a stable prediction of GCA performance, despite the environmental influence. The importance of GCA is related to the high effectiveness and easiness of selection due to predominant additive effects involved in the trait expression. This feature is most pronounced in self-pollinating plants, since they are fixed after successive generations of selfing.

The SCA effects are interpreted as deviations of a hybrid compared to the value expected based on the parental GCA. Therefore, reduced S_{ij} values indicate that hybrids have a similar performance to what would be expected based on GCA values, while high absolute S_{ij} values indicate a better or worse performance than the expected based on the GCA (Cruz et al. 2004). The SCA estimates (S_{ij}) revealed either positive or negative values for both analysis models. A predominance of negative values on S_{ij} effects of parents indicates that both contribute to increase the progeny potential for most of the studied traits. In this sense, the genotypes IPR 85 (with -7.55 and -7.38 for Griffing's fixed model and BLUP, respectively) and Safira (with -7.38 and -5.87 for Griffing's fixed model and BLUP, respectively) lead to the highest positive heterosis in hybrids, regarding GY p^{-1} in both analysis models (Table 4).

To detect the most promising populations to be used in breeding programs, one must consider the positive S_{ij} values plus at least one parental with a high GCA effect (Cruz et al. 2004). In this sense, the highest SCA effect for trait GY p^{-1} was observed in populations derived from IPR 85 x Safira ($\overline{x}$ = 36.45) and OCEPAR 11-JURITI x Safira ($\overline{x}$ = 25.93) crosses. This is due to a high mean performance of genotypes with reduced tiller numbers for the other yield components, as observed in IPR 85 for EW p^{-1} ($\overline{x}$ = 3.52) and GW p^{-1} ($\overline{x}$ = 1.94). This performance is attributed to a buffering effect of genotypes with low tillering capacity, to compensate for the low number of tillers (Scheeren et al. 1995).

Table 3. General combining ability (g_i) of six wheat parents, considering fixed (Griffing) and random (BLUP) models, for six traits*

Genotypes	NT p^{-1}		NFT p^{-1}		EW p^{-1}		NG p^{-1}		GW p^{-1}		PG p^{-1}	
	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random
OCEPAR 11 - JURITI	-4.94	-9.71	-4.16	-8.14	-0.008	-0.011	-2.7	-4.2	-0.12	-0.198	-4.43	-5.82
FUNDACEP 29	-3.41	-6.58	-3	-5.76	0.044	0.064	2.51	3.68	0.1	0.146	-4.36	-5.85
IPR 85	-3.52	-6.79	-2.6	-4.99	0.289	0.43	-0.15	-0.15	0.17	0.243	-0.79	-1.08
BRS 177	2.36	4.6	2.06	4	-0.003	-0.004	3.64	5.3	0.01	0.019	3.45	4.59
Safira	3.47	6.75	2.24	4.35	-0.127	-0.188	2.98	4.35	-0.03	-0.042	1.79	2.38
BRS Figueira	6.04	11.73	5.46	10.54	-0.194	-0.29	-6.29	-8.98	-0.13	-0.168	4.33	5.78

*Traits: NT p^{-1} (number of tillers per plant), NFT p^{-1} (number of fertile tillers per plant), EW p^{-1} (ear weight per plant), NG p^{-1} (number of grains per plant), GW p^{-1} (grain weight per plant), GY p^{-1} (grain yield per plant)

Table 4. Specific combining ability (s_{ij} and s_{ij}) of 21 treatments, considering fixed (Griffing) and random (BLUP) models, for six traits

Genotypes	NT p^{-1}		NFT p^{-1}		EW p^{-1}		NG p^{-1}		GW p^{-1}		PG p^{-1}	
	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random	Fixed	Random
OCEPAR 11-JURITI	0.46	-0.03	0.30	-0.09	-0.37	-0.23	-5.74	-7.06	-0.28	-0.30	-2.31	-4.73
FUNDACEP 29	-0.44	-0.48	-0.19	-0.23	-0.33	-0.19	-4.54	-2.78	-0.20	-0.09	1.39	-1.43
IPR 85	-1.05	-0.93	-1.17	-0.75	-0.07	0.05	-3.42	-3.12	-0.15	-0.02	-7.55	-7.65
BRS 177	0.80	0.68	0.09	0.13	-0.12	-0.07	1.38	3.04	-0.17	-0.12	6.59	8.42
Safira	1.56	1.28	-1.20	-0.57	0.00	-0.04	-0.47	1.06	-0.12	-0.10	-7.38	-5.87
BRS Figueira	1.65	1.46	-0.18	0.11	-0.13	-0.14	6.87	2.94	-0.09	-0.12	-6.31	-3.26
OCEPAR 11-JURITI / FUNDACEP 29	-0.28	-0.34	-0.16	-0.20	0.22	0.14	-0.46	-0.29	0.10	0.08	0.29	-2.54
OCEPAR 11-JURITI / IPR 85	1.12	0.66	0.91	0.39	-0.07	0.00	-1.67	-2.04	-0.14	-0.07	-0.62	-2.28
OCEPAR 11-JURITI / BRS 177	-1.94	-1.40	-2.55	-1.41	0.11	0.06	1.14	1.41	0.12	0.06	-4.23	-4.38
OCEPAR 11-JURITI / Safira	1.65	1.21	2.18	1.18	0.37	0.21	12.05	10.92	0.35	0.21	6.72	5.50
OCEPAR 11-JURITI / BRS Figueira	-1.49	-1.00	-0.97	-0.47	0.11	0.03	0.41	-1.73	0.14	0.05	2.45	2.23
FUNDACEP 29 / IPR 85	3.77	2.55	2.06	1.01	0.02	0.07	4.91	4.94	0.11	0.14	2.44	0.69
FUNDACEP 29 / BRS 177	1.64	1.15	1.21	0.64	0.08	0.06	4.99	5.96	-0.01	0.02	-3.35	-3.46
FUNDACEP 29 / Safira	-5.80	-4.19	-4.84	-2.67	-0.03	-0.03	-3.43	-1.68	-0.05	-0.02	-6.92	-7.36
FUNDACEP 29 / BRS Figueira	1.54	1.17	2.12	1.20	0.38	0.21	3.06	1.76	0.24	0.16	4.77	4.52
IPR 85 / BRS 177	-1.56	-1.16	-0.78	-0.44	0.21	0.17	5.16	5.44	0.36	0.29	-3.45	-2.44
IPR 85 / Safira	0.98	0.69	2.24	1.21	0.13	0.10	2.36	2.79	0.08	0.09	13.61	13.22
IPR 85 / BRS Figueira	-2.20	-1.54	-2.08	-1.09	-0.15	-0.08	-3.92	-5.10	-0.11	-0.07	3.12	4.07
BRS 177 / Safira	0.73	0.66	1.73	1.03	-0.27	-0.19	-5.40	-3.15	-0.09	-0.07	-1.55	0.18
BRS 177 / BRS Figueira	-0.49	-0.17	0.20	0.26	0.11	0.04	-8.66	-8.36	-0.03	-0.05	-0.59	1.89
Safira / BRS Figueira	-0.68	-0.28	1.09	0.74	-0.19	-0.17	-4.63	-4.95	-0.05	-0.07	2.89	4.67

[+]Traits: NT p^{-1} (number of tillers per plant), NFT p^{-1} (number of fertile tillers per plant), EW p^{-1} (ear weight per plant), NG p^{-1} (number of grains per plant), GW p^{-1} (grain weight per plant) and GY p^{-1} (grain yield per plant)

An indirect increase was seen in GY p^{-1} via a higher GW p^{-1} for the cross OCEPAR 11-JURITI x Safira ($\overline{x}=$ 1.92) and IPR 85 x BRS 177 ($\overline{x}=2.29$), with high positive values. Likewise, the selection of plants from the population FUNDACEP 29 x BRS Figueira ($\overline{x}=3.24$) and OCEPAR 11-JURITI x Safira ($\overline{x}=3.25$), with high positive SCA values for trait EW p^{-1}, suggests a strong genetic gain potential. The results for these traits also agree in the two diallel analysis models.

The results did not reveal a total agreement in the best performance combination rankings, when comparing SCA data for the fixed model of Griffing and BLUP. For trait NFT p^{-1}, the best three performances changed according to the model used. The best crosses for the fixed model (Griffing) were IPR 85 x Safira (2.24); OCEPAR 11-JURITI x Safira (2.18) and FUNDACEP 29 x BRS Figueira (2.12). For the random model (BLUP), best performances were observed for IPR 85 x Safira (1.21), FUNDACEP 29 x BRS Figueira (1.20) e OCEPAR 11-JURITI x Safira (1.18). Likewise, regarding the ranking of best genotypes the SCA of trait NG p^{-1} was not coincident in both models. This indicates that inferences for this trait should be considered cautiously.

The association of SCA estimates for both models did not reveal a complete agreement, as can be observed by the correlation estimates, even when the values were high and positive (Table 5). The two models must therefore be evaluated jointly, to obtain a more precise estimate of quantitative traits, contributing to the identification of the best hybrid combinations. For the parameters performance and GCA effect, the results of fixed and random models show are highly correlated, with a coefficient close to 1.0. This indicates a high reliability in the identification of genotypes for crossing blocks, suggesting the predictability of additive effects for inferences related to homozygous genotype performances, i.e., related to mean and GCA effect parameters.

Table 5. Spearman's correlation coefficients (*r*) between the two evaluation models (fixed and random), for the general and specific combining ability parameters (GCA and SCA) and Pearson's correlation (*r*) between the performance parameter (population and parental means), for six wheat traits

Traits[+]	Parameters		
	Performance	GCA	SCA
NT p[-1]	0.99*	1*	0.97*
NFT p[-1]	0.99*	1*	0.98*
EW p[-1]	0.98*	1*	0.94*
NG p[-1]	0.99*	1*	0.94*
GW p[-1]	0.98*	0.94*	0.89*
GY p[-1]	0.99*	0.94*	0.94*

(+)Traits: NT p[-1] (number of tillers per plant), NFT p[-1] (number of fertile tillers per plant), EW p[-1] (ear weight per plant), NG p[-1] (number of grains per plant), GW p[-1] (grain weight per plant) and GY p[-1] (grain yield per plant). * Significant at 5% probability by the *t* test

CONCLUSIONS

Both diallel models agree for general combining ability effects. On the other hand, for the specific combining ability, analyses should be preformed with caution and simultaneous use of fixed and random data.

Specific combinations, such as IPR 85 x Safira, are favorable for genetic gains, particularly for quantitative traits.

Capacidade combinatória de genótipos de trigo sob dois modelos de análise dialélica

RESUMO - As metodologias de análise dialélica permitem estimar os efeitos genéticos de uma população por diferentes modelos, com influência direta nas inferências de análise. Desta forma, o objetivo deste trabalho foi determinar e comparar dois modelos de análise dialélica, fixo e aleatório, quanto aos efeitos combinatórios entre seis genótipos de trigo. O experimento foi conduzido no município de Capão do Leão/RS no ano de 2006. Foram utilizados seis genótipos de trigo, os quais foram submetidos a cruzamentos artificiais conforme modelo dialélico completo sem os recíprocos, resultando em quinze combinações híbridas. Os dados foram submetidos à análise dialélica pelos modelos dois de Griffing considerando o modelo fixo e de BLUP ao considerar aleatório. Os resultados evidenciam que os dois modelos dialélicos, revelam concordância com os efeitos de capacidade geral de combinação. Por outro lado, para capacidade especifica de combinação, os dados devem ser utilizados com cautela, considerando os modelos simultaneamente.

Palavras-chave: BLUP, Griffing, fixo, aleatório, caracteres quantitativos.

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