



## Genetic dissimilarity among wheat genotypes for lodging-associated traits

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Received 5 november 2003

Accepted 20 July 2004

**ABSTRACT** - Lodging-resistance is an important wheat trait; however there are few studies on genetic divergence of wheat genotypes concerning lodging-related traits. Therefore, the objectives of this study were to estimate the genetic dissimilarity of 14 wheat genotypes based on lodging-related traits, the relative contribution of the traits to the dissimilarity, and the most promising hybrid combinations. A total of 14 traits were evaluated and subjected to canonical variable analysis, Mahalanobis' distance, and Tocher's and UPGMA clustering algorithms. The high divergence detected among genotypes indicated the presence of genetic variability in the traits of interest. The genotypes TB951 and Rubi presented the greatest dissimilarity while Rubi and BR119 were the most similar. Best parents for controlled crosses based on the different analyses were TB951 and ORI for either crossing with each other or with the other tested genotypes.

**Key words:** *Triticum aestivum* L., dissimilarity measures, culm lodging-resistance coefficient.

### INTRODUCTION

Genetic variability is very important for the formation of segregating populations in plant breeding programs. This variability can be achieved through the choice of genetically dissimilar parents, associating high mean and variability for the target traits. The segregating population will therefore have a higher probability of presenting higher means for the target traits, thus reducing time and cost spent on the improvement.

Quantifying the genetic dissimilarity allows inferences about the specific combining ability and heterosis as an alternative to diallel crosses, which are complex and cumbersome (Cruz and Regazzi 1997). According to Ferreira et al. (1995) the

evaluation of genetic dissimilarity before performing any cross can help breeders concentrate their efforts on only the most promising combinations. The dissimilarity estimated with base on phenotypic information that takes physiological, morphological and agronomical differences among parents into account has been widely used for this purpose (Singh et al. 1981, Barbosa-Neto et al. 1996, Morais et al. 1998, Benin et al. 2003a, b). Such expectations are due to the fact that heterosis and specific combining ability depend on the existence of dominance controlling the trait and on the existing dissimilarity among genotypes.

A rise in the wheat yield level and its adaptation to marginal areas depends essentially on the development of lodging-resistant

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genotypes (Cruz et al. 2001). In Brazil, lodging-resistant wheat genotypes have become extremely desirable as a consequence of the higher nitrogen doses applied on farms, a now widespread technique. Breeding for lodging-resistance is quite difficult since it is a quantitative trait (controlled by many genes) and highly influenced by environmental effects (Keller et al. 1999). Despite the importance of lodging for wheat breeding, very few efforts have been undertaken to characterize different related characters in tolerant genotypes.

In this sense, the objectives of this study were: i) to estimate the genetic dissimilarity among 14 wheat genotypes based on 14 traits associated with lodging; ii) to estimate the relative contribution of lodging-related traits to the genetic dissimilarity; iii) to indicate potential parents for generating segregating populations with a high level of lodging-resistance.

## MATERIAL AND METHODS

This study was conducted at the Centro Experimental da Palma, which is part of the Faculdade de Agronomia "Eliseu

Maciel" (FAEM) of the Universidade Federal de Pelotas (UFPEL), Capão do Leão (RS). The county is located at 31° 52' 00" lat S and 52° 21' 24" long W, at an altitude of 13.24 m asl. According to Köppen, the climate is of the Cfa type with an annual rain precipitation of 1280.2 mm.

The field experiment was installed in June 15, 1999, in a randomized block design with four replications, in three row plots of three meter length. The spacing used was 0.3 m between rows and between plants in a row, with the goal of growing isolated plants without competition for an individual evaluation. This was done because the great majority of wheat breeding programs, including the one at UFPEL, advance their segregating populations through the pedigree method as spaced plants. Therefore, the development of a methodology for plant selection must use the same environment. Fertilization consisted in a base application of 300 kg ha<sup>-1</sup> of NPK (5-20-20) plus 60 kg ha<sup>-1</sup> applied at the beginning of the tillering phase. Weeding was performed manually and ants controlled by granulated bates. Pests and diseases were controlled according to the culture recommendations. The wheat genotypes used, year of release and their pedigrees are shown in Table 1.

**Table 1.** Wheat genotypes evaluated, year of release, and pedigree

Genotypes	Year of release	Pedigree
BRS179	1999	BR 35/PF 8596/3/PF772003*2/PF 813//PF83899
EMB40	1995	PF 7650/NS18-78//CNT 8/PF7577
CEP24	1992	BR 3/ CEP7887//CEP 7775/CEP 11
IAC5	1966	Frontana/Kenya 58//PG 1
RUBÍ	1998	PF 869107/Klein H3450C3131
BRS177	1999	PF 83899/PF813//F27141
BRS120	1998	PF 83899/PF813//F27141
BRS119	1998	PF 82252/BR 35//IAPAR 17/PF8550
BR18	1986	Unknown
BRS49	1996	BR 35/PF 83619//PF858/PF 8550
BR23	1987	Corre Caminos/Alondra Sib/3/IAS 54 -20/Cotiporã//CNT 8
FCEP29	1997	BR 23/CEP8423//Buc Sib
OR1	1996	EMBRAPA 27 SIB/Bagula Sib
TB951*	-	TB 108 // BR 23 * 2/PF 869114

\*not yet in commercial use

Lodging-resistance (LR) was measured in the field for all the studied genotypes using Petrucci's methodology described by Souza (1998). Each genetic constitution received a grade as follows: grade 2 = lodging-sensitive; grade 2.5 = from moderately sensitive to lodging-sensitive; grade 3 = moderately sensitive; grade 4 = moderately lodging-resistant; grade 4.5 = from resistant to moderately lodging-resistant; grade 5 = lodging-resistant and grade 6 = highly lodging-resistant. Besides lodging, 14 additional traits that present association with lodging (Zuber et al. 1999, Cruz et al. 2001) were measured as follows: i) culm lodging-resistance coefficient (cLr), determined according to Grafius and Brown (1954) by the equation:  $cLr = F/b$ , where F = weight in grams of a suspended chain weighing 0.5g per link and composed of two links per cm, attached to the base of the spike. Also b =

culm height in cm, measured from the crown to the base of spike; ii) culm tension test (CTT) determined according to Watanabe (1997), by using a dynamometer with a capacity of three Newtons to measure the strength needed to bend the main culm to an angle of 45 degrees; iii) culm index (CI) determined according to Watanabe (1997), consisting of measuring the diameter of the second internode divided by b; iv) plant height in cm (PLH); v) length of the second internode in cm (L2I); vi) length of the last internode in cm (LLI); vii) length of the peduncle in cm (LP); viii) diameter of the second internode in mm (D2I); ix) diameter of last internode in mm (DLI); x) peduncle diameter in mm (PD); xi) weight of 1 cm from the basal culm end in mg cm<sup>-1</sup> (CBW); xii) spike length in cm (ESP); xiii) culm length in cm (CDC); xiv) total number of nodes (TNN) as described by Cruz et al. (2001).

Analysis of variance was performed for all traits, with exception of the lodging resistance (LR) which did not meet the analysis assumptions. The means of the variables were later compared by the Scott-Knott test (Scott and Knott 1974) at an error probability level of 5%. The distance between all genotype pairs was estimated using the generalized distance of Mahalanobis ( $D^2$ ) based on standardized means for all measured traits except for LR, using software Genes (Cruz 2001). The cluster analysis method of Tocher was applied to the generated genetic dissimilarity matrix and a dendrogram was obtained using the UPGMA clustering method.

The cophenetic correlation coefficient ( $r$ ) was calculated to estimate the adjustment between the dissimilarity matrix and the obtained dendrogram (Sokal and Rohlf 1962), using software NTSYS-pc 2.1 (Rohlf 2000). The relative importance of the evaluated traits concerning genetic dissimilarity was obtained by means of the contribution of  $D^2$  components, relative to each trait, to the total observed dissimilarity (Singh 1981). An analysis of canonical variables (based on standardized means) was also performed using software Genes (Cruz 2001), in order to obtain the genotype dispersion plot.

## RESULTS AND DISCUSSION

The differences between the genotype means compared by the Scott-Knott test show the existence of variability for the analyzed traits (Table 2). A higher number of significant differences was detected for the traits cLr and LP, which present four groups "a", "b", "c", and "d". The traits with a lower mean stratification were DLI, PD, CDC, and TTN. For trait CTT, no difference was detected among the evaluated genotypes.

For a stronger explanation about the variability of the groups of evaluated genotypes it is necessary that the first two canonical variables explain at least 80% of the variance contained in the total set of analyzed traits (Cruz and Regazzi 1997). It can be observed in Table 3 that with the inclusion of all traits in the analysis, the first two canonical variables explain 68.94% of the total variation.

Thus, it was necessary to identify the redundant traits which contributed little or not at all to the genetic dissimilarity among the evaluated genotypes through the verification of loading coefficient (Table 4). This procedure is based on the principle that a given trait can be discarded if it is more important for a canonical variable that contributes little or not at all to the total variation. In other words, the traits that present the highest loading coefficients for the last canonical variables can be discarded (Cruz and Regazzi 1997).

The trait plant height (PLH) presented the highest loading coefficient for the 14<sup>th</sup> canonical variable (Table 4) although this

was not considered dispensable since it is a trait of easy measurement and routinely used in plant breeding programs. Besides, it is highly correlated to lodging-resistance (Zuber et al. 1999, Cruz et al. 2001) in spite of presenting a high genetic correlation with the trait culm length,  $r = 1.0$  (Cruz et al. 2001), which was excluded. Additionally, CDC presented the second-highest loading coefficient for the 14<sup>th</sup> canonical variable. The trait that presents high correlation with any other trait is considered redundant and can therefore be discarded, which makes it the one of easiest scoring or the one that presents highest variability.

It was observed that the traits that did not present significant correlations with the most important canonical variables. The highest loading coefficient for the last five canonical variables and therefore considered redundant were: culm length (CDC), culm index (CI), length of the second internode (L2I), length of the last internode (LLI), length of the peduncle (LP), and total number of nodes (TTN). With the exclusion of these six redundant traits, the first two canonical variables came to explain 84.50% of the total variation, as can be observed in Table 3, allowing the construction of a dispersal biplot (Figure 1).

The analysis of the graphical dispersal of canonical variable scores after the exclusion of redundant traits (Figure 1) showed that genotype TB951 was the most distant one, forming a distinct cluster. The second-highest degree of dissimilarity (Figure 1) was the distance between OR 1 and the group formed by genotypes BRS179 and CEP24. Likewise, the third degree of dissimilarity is found between OR1 and the group formed by genotypes FCEP 29, BRS120, and BR 23.

When looking at the clusters formed by Tocher's method (Table 5) and UPGMA (Figure 2), two characteristic groups were detected: the first composed by line TB951, and the second composed by the remaining genotypes. This fact reinforces the results obtained by the analysis of canonical variables, in which genotype TB951 presented great dissimilarity when compared to the remaining genotypes.

Line TB951 presents short height and high lodging-resistance (Table 2); this genotype was developed at Embrapa Clima Temperado in Pelotas, state of Rio Grande do Sul (RS). Its genetic dissimilarity to the other genotypes originated from Embrapa Trigo in Passo Fundo (RS) is striking, in spite of having cultivar BR23 as one of its parents (Table 1) to which it is dissimilar. This result agrees with the argumentation of Barbosa-Neto et al. (1996) who did not observe any significant correlation between the genetic dissimilarity and inbreeding coefficient.

It was observed that the most dissimilar genotypes were TB951 and Rubi and the most similar ones Rubi and BRS119 (Figures 1 and 2). The cophenetic correlation coefficient ( $r = 0.90$ ) evidenced a good adjustment of the dissimilarity matrix to the obtained dendrogram, indicating that the dendrogram reflects the dissimilarity matrix adequately.

Tocher's cluster analysis method only excludes an

**Table 2.** Means of the evaluated traits used to estimate the genetic dissimilarity among 14 wheat cultivars

Genotypes	Traits <sup>1</sup>														
	LR	cLr	CTT	PLH	L2I	LLI	LP	D2I	DLI	PD	CBW	CI	ESP	CDC	TNN
		cg cm <sup>-1</sup>	N	cm	cm	cm	cm	mm	mm	mm	mg cm <sup>-1</sup>	%	cm	cm	
BRS179	2.0	31 d*	0.4 a	85 a	8 b	15 b	44 a	3.6 c	4.1 a	3.4 a	268 b	4.8 c	10 b	75 b	4.1 b
EMB40	2.0	22 d	0.5 a	82 a	10 a	18 a	36 b	3.8 b	4.1 a	2.8 a	217 c	5.4 c	11 b	71 b	4.3 a
CEP24	2.5	30 d	0.5 a	92 a	10 a	19 a	42 a	3.7 c	4.0 b	3.2 a	287 b	4.5 c	10 b	82 a	4.3 a
IAC5	2.5	32 d	0.4 a	86 a	10 a	19 a	38 b	3.7 c	4.1 a	3.1 a	264 b	4.9 c	10 b	75 b	4.4 a
RUBÍ	3.0	30 d	0.5 a	75 b	10 a	18 a	32 c	3.6 c	3.8 b	2.8 b	197 c	5.4 c	9 c	66 b	4.3 a
BRS177	4.0	52 b	0.5 a	82 a	10 a	19 a	37 b	3.6 c	3.7 b	3.1 a	215 c	5.1 c	11 b	71 b	4.1 b
BRS120	4.0	37 c	0.5 a	81 a	10 a	18 a	36 b	3.6 c	3.7 b	3.1 a	244 c	5.2 c	11 b	70 b	4.2 b
BRS119	4.0	29 d	0.5 a	75 b	9 b	17 b	34 b	3.7 c	3.9 b	2.9 b	191 c	5.6 c	9 c	66 b	4.3 a
BR18	4.0	39 c	0.5 a	68 c	8 b	14 b	31 c	3.6 c	3.9 b	2.7 b	235 c	6.2 b	9 c	59 c	4.4 a
BRS49	4.5	32 d	0.5 a	84 a	10 a	20 a	33 c	3.6 c	4.0 b	2.9 b	294 b	4.9 c	9 c	75 b	4.5 a
BR23	4.5	41 c	0.5 a	78 a	9 b	18 a	35 b	4.2 a	4.3 a	3.1 a	225 c	6.2 b	11 b	68 b	4.2 a
FCEP29	5.0	56 b	0.4 a	72 b	8 b	15 b	35 b	4.1 a	4.3 a	3.3 a	233 c	6.5 b	9 c	63 b	4.1 b
OR1	6.0	43 c	0.5 a	60 d	8 b	15 b	23 d	3.9 b	4.1 a	2.3 b	168 c	7.6 a	9 c	51 b	4.0 b
TB951	6.0	73 a	0.6 a	69 c	6 c	12 c	30 c	3.9 b	4.3 a	3.3 a	370 a	7.2 a	14 a	55 b	4.1 b
CV(%)	-	15.59	21.51	6.88	10.4	10.34	8.04	5.73	6.07	7.21	17.57	12.23	8.84	7.65	4.67

<sup>1</sup>Lodging-resistance (LR), culm lodging-resistance coefficient (cLr), culm tension test (CTT), plant height (PLH), length of the second internode (L2I), length of the last internode (LLI), length of the peduncle (LP), diameter of the second internode (D2I), diameter of last internode (DLI), peduncle diameter (PD), weight of 1 cm from the basal culm end (CBW), culm index (CI), spike length (ESP), culm length (CDC) and total number of nodes (TNN)

\*Means followed by the same letter on the column do not differ by the Scott and Knott's test at 5% probability level

**Table 3.** Variances, variance in percent, and accumulated variances in relation to the first three canonical variables aiming to estimate the genetic dissimilarity among 14 wheat cultivars

Genotypes	Canonical variables <sup>1</sup>			Canonical variables <sup>2</sup>		
	1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>	1 <sup>st</sup>	2 <sup>nd</sup>	3 <sup>rd</sup>
BRS179	2.28	9.33	19.42	18.60	14.56	23.23
EMB40	2.87	2.85	21.92	28.20	13.00	24.59
CEP24	1.97	7.57	21.53	27.40	17.35	24.43
AC5	3.58	6.26	20.31	15.30	16.72	23.75
RUBÍ	4.18	4.35	17.71	14.50	15.43	25.05
BRS177	7.44	6.22	20.65	23.10	15.65	21.26
BRS120	5.22	5.57	20.35	15.30	14.92	24.34
BRS119	4.28	5.14	17.69	25.40	14.59	24.83
BR18	5.31	6.32	17.14	23.50	13.63	23.53
BRS49	3.58	6.17	19.17	29.40	14.53	24.37
BR23	7.17	5.44	19.90	21.20	14.56	26.28
FCEP29	9.28	9.37	16.67	17.20	13.27	21.87
OR1	9.59	1.72	17.51	22.50	9.63	23.53
TB951	16.39	6.97	21.78	15.50	11.85	25.37
Variance	14.91	4.48	3.24	4.54	3.90	0.83
Variance (%)	53.00	15.94	11.51	45.45	39.05	8.30
Accumulated						
Variance (%)	53.00	68.94	80.45	45.45	84.50	92.80

<sup>1</sup>Including all variables

<sup>2</sup>Discarding the redundant traits (CDC, CI, L2I, LLI, LP, and TNN)

individual from a given cluster in formation if its average distance to this group does not surpass a given pre-established value. In this case, this value was the highest value from the set of smallest distance estimates between each genotype in each cluster. Therefore, due to the large  $D^2$  estimates involving TB951 compared to the other evaluated genotypes, Tocher's cluster analysis method allowed the formation of only two groups, one consisting of TB951 and the other of the remaining genotypes.

In this context and to avoid the subjective effect of an arbitrary limit in Tocher's method, the analysis was performed anew, excluding line TB951 (Table 5). The result of Tocher's method without TB951 allowed the formation of three groups, of which one formed a one-element group with genotype OR1, quite distant from the others; a second intermediary group was composed by the genotypes BRS177 and FCEP29; and a third group contained the remaining genotypes. This fact can be explained by a decrease in the inter-group distance after excluding genotype TB951. This procedure allowed minimizing the influences of some characters which contrast strongly between TB951 and the other genotypes, such as the culm lodging-resistance coefficient (cLr) and spike length (ESP) (Table 2). This change contributed decisively to the large distances detected between TB951 and the remaining genotypes.

It was observed that the traits CDC, PLH, cLr, LP, ESP, CI and L2I contributed with 80% to the total dissimilarity. The seven remaining traits contributed little to the studied genetic dissimilarity, presenting minimal importance in an overall dissimilarity evaluation among the genotypes (Table 6). After excluding TB951 the importance for genotype differentiation of the character spike length (ESP) decreased from 9.2 to 1.3% among the remaining 13 genotypes (Table 6). This situation can be explained by the narrowing variability for this character with the exclusion of TB951, since the spike length of this genotype is considerably greater than the length of spikes of the remaining genotypes (Table 2). An inverse situation occurred for character CI, which increased from 7.3 to 13.2%.

Regarding the recommendation of crosses, the results show that a good alternative for parents are the genotypes TB951 and OR1, either for crossing with each other or with any evaluated genotype. This is due to the fact that these genotypes are highly dissimilar to each other and to the remaining genotypes and also have a short height and high lodging-resistance (LR= 6.0; Table 2). Cruz et al. (2001) had already pointed out that these genotypes would be good sources of lodging-resistance genes.

The presence of the genetic variability and dissimilarity is indicative that the set of evaluated genotypes can be exploited as a promising source of parents. In this sense Bhatt (1973) observed that genetic variance among  $F_{4,5}$  wheat lines was highly correlated with the multivariate distance estimated through quantitative characters. For barley, there are also reports on the possibility of obtaining transgressive individuals for lodging-

resistance from the cross of resistant and susceptible individuals, once both parents contributed positively and negatively with alleles to the trait resistance (Hayes et al. 1995). This point supports the expectation of obtaining transgressive individuals from the cross between highly lodging-resistant genotypes which are otherwise dissimilar for characters related to the target trait. This fact confirms the potential of TB951 and OR 1 even more to be useful as parents of segregating populations with high levels of lodging-resistance. Furthermore, Keller et al. (1999) found a narrow-sense heritability value for lodging-resistance of 0.90, indicating that there is an easy transmission of this trait and that selection pressure can be intensified in highly segregating populations.

Thus, there is an expectation that the dissimilar genotypes identified here will originate genetically variable segregating populations for the character lodging-resistance when used in artificial crosses, achieving a maximization of genetic gain. Also, according to Cruz et al. (2001), the indirect selection of lodging-resistant genotypes can be performed through the lodging-resistance coefficient (cLr), plant height (PLH), peduncle length (LP), and culm index (IC) due to the high correlation between these traits and lodging-resistance.

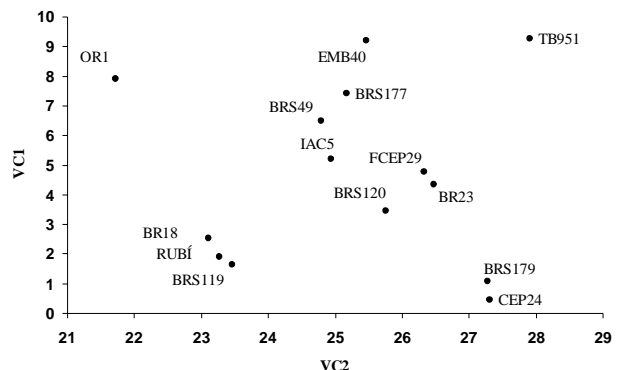


Figure 1. Dispersion biplot of 14 wheat cultivar scores in relation to the first two canonical variables

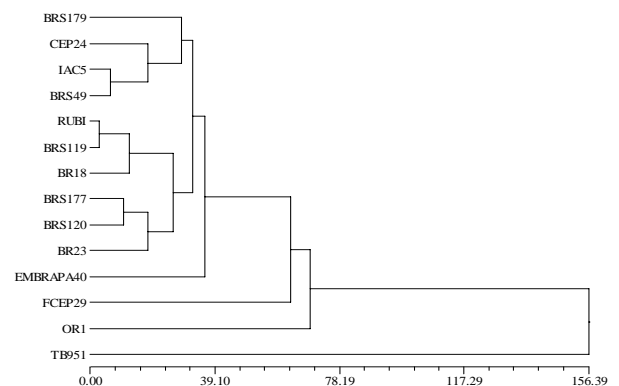


Figure 2. UPGMA dendrogram for 14 wheat cultivars applied to Mahalanobis' distance matrix. The value of the cophenetic correlation coefficient is 0.90

**Table 4.** Loading coefficient for the 14 traits to obtain the canonical variables (CV) and the indication of discarded traits

Canonical variables	cLr <sup>1</sup>	CTT	PLH	L2I	LLI	LP	D2I	DLI	PD	CBW	CI	ESP	CDC	TNN
1	0.91	0.12	-2.94	-1.19	0.56	-1.19	-0.19	0.03	0.56	-0.56	0.96	1.09	4.08	-0.55
2	0.48	-0.09	1.53	-0.42	-0.43	0.30	0.39	-0.12	0.71	0.68	-0.56	-1.26	-1.19	0.05
3	0.02	0.23	-1.61	0.34	0.35	1.21	-0.01	-0.12	-1.46	0.30	0.63	1.56	1.46	-0.05
4	0.02	-0.15	-0.76	-0.45	0.92	-0.74	0.79	0.05	0.92	-0.36	0.34	-0.12	1.60	-0.17
5	-0.03	0.01	-4.46	-0.23	0.29	-0.63	-0.18	0.53	0.17	0.59	-0.21	0.49	4.58	0.45
6	-0.08	-0.07	0.59	0.35	-0.30	-0.31	1.56	0.10	0.40	-0.20	-3.78	0.29	-3.32	0.86
7	0.29	0.00	-3.90	0.39	0.53	1.02	0.36	-1.23	-0.49	0.56	0.19	0.41	2.66	0.03
8	0.07	-0.23	-10.05	0.40	-0.47	0.92	0.85	-0.39	-0.88	0.16	-0.34	1.81	9.03	0.21
9	-0.15	0.67	-4.17	-0.47	-0.85	-0.87	0.42	-0.74	0.21	-0.29	0.67	0.70	6.26	-0.54
10	0.16	0.58	3.04	0.73	-0.40	<b>0.75</b>	0.33	0.02	-0.61	0.22	-0.15	-0.56	-3.72	0.40
11	-0.25	-0.26	0.49	-0.52	<b>0.79</b>	0.56	0.45	-0.77	-0.12	0.58	0.61	-0.16	-0.99	0.03
12	-0.13	-0.24	0.56	<b>1.76</b>	-1.41	-0.29	0.17	-0.34	0.39	0.37	0.12	-0.20	-0.71	0.13
13	-0.11	0.21	-2.29	0.15	0.92	0.68	-1.04	0.30	0.62	-0.23	<b>1.41</b>	0.34	1.59	0.23
14	0.09	-0.38	4.01	0.41	-0.86	-0.44	-0.13	-0.17	0.03	-0.31	0.67	-0.45	<b>-2.83</b>	<b>0.74</b>
Discarded traits				▲%	▲%	▲%					▲%		▲%	▲%

<sup>1</sup>coded as in Table 2

**Table 5.** Clustering of studied genotypes using Tocher's optimization method applied to the generalized distance of Mahalanobis

Clusters	Analysis including line TB951
I	RUBÍ, BRS119, BR18, BRS120, IAC5, BRS49, BR23, BRS177, EMB40, CEP24, BRS179, FCEP29 and OR1
II	TB951
Clusters	Analysis excluding line TB951
I	RUBÍ, BRS119, BR18, BRS120, IAC5, BRS49, CEP24, EMB40, BRS179 and BR23
II	BRS177 and FCEP29
III	OR1

**Table 6.** Relative contribution (RC) of each trait to the dissimilarity among genotypes based on Singh's statistics

Traits <sup>1</sup>	RC (%) including TB951	RC (%) excluding TB951
cLr	12.7	14.5
CTT	0.4	0.1
PLH	17.6	18.1
L2I	6.7	2.7
LLI	0.3	2.4
LP	11.8	13.7
D2I	0.4	1.3
DLI	1.1	1.2
PD	1.2	0.5
CBW	1.5	4.4
CI	7.3	13.2
ESP	9.2	1.3
CDC	27.5	24.5
TNN	2.1	2.3

<sup>1</sup>coded as in Table 2

**ACKNOWLEDGMENTS**

The authors acknowledge FAPERGS, CNPq, and CAPES for the financial support through grants and fellowships.

## Dissimilaridade genética entre genótipos de trigo para caracteres associados com o acamamento

**RESUMO** - A resistência ao acamamento é um caráter importante para o trigo; porém existem poucos estudos a respeito da divergência genética entre genótipos quanto aos caracteres relacionados ao acamamento. Os objetivos deste estudo foram estimar, com base em caracteres associados ao acamamento, a dissimilaridade genética entre 14 genótipos de trigo, a contribuição relativa dos caracteres para a dissimilaridade e apontar as combinações híbridas mais promissoras. Foram avaliados 14 caracteres associados ao acamamento e aplicadas análises de variáveis canônicas, distância de Mahalanobis e agrupamento pelos algoritmos de Tocher e UPGMA. Foi detectada grande divergência genética entre os genótipos, indicando a presença de variabilidade para os caracteres de interesse. Os genótipos TB951 e Rubi apresentaram a maior divergência, enquanto que os mais similares foram Rubi e BRS119. Para a recomendação de cruzamentos, as melhores alternativas foram os genótipos TB951 e ORI, tanto para cruzamento entre si bem como com qualquer dos outros genótipos avaliados.

**Palavras-chave:** *Triticum aestivum* L., medidas de dissimilaridade, coeficiente de resistência do colmo ao acamamento.

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