



Genetic variability in common wheat germplasm based on coefficients of parentage

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Abstract

The characterization of genetic variability and an estimate of the genetic relationship among varieties are essential to any breeding program, because artificial crosses among less similar parents allow a larger segregation and the combination of different favorable alleles. Genetic variability can be evaluated in different ways, including the Coefficient of Parentage (COP), which estimates the probability of two alleles in two different individuals being identical by descent. In this study, we evaluated the degree of genetic relationship among 53 wheat genotypes, and identified the ancestor genotypes which contributed the most to the current wheat germplasm, as a prediction of the width of the genetic base of this cereal. The results revealed a mean COP of 0.07 and the formation of 22 similarity groups. The ancestor genotypes Ciano 67 and Mentana were those which contributed the most to the current wheat germplasm. According to the COP analyses, the genetic base of wheat rests on a small number of ancestral genotypes.

Key words: COP, genetic base, gene pool, *Triticum aestivum* L.

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Introduction

Genetic variability is required to achieve genetic gains in a breeding program. Estimation of genetic variability among genotypes can be based on qualitative and quantitative traits (Spagnoletti-Zeuli and Qualset, 1987; Souza and Sorrells, 1991; van Beuningen and Busch, 1997b), molecular markers (Smith and Smith, 1988; Barbosa-Neto *et al.*, 1996; Cao *et al.*, 1998; Fahima *et al.*, 1999), and coefficient of parentage (Martin *et al.*, 1991; Barbosa-Neto *et al.*, 1996; Mercado *et al.*, 1996; van Beuningen and Busch, 1997a; Burkhamer *et al.*, 1998). The coefficient of parentage (COP) measures the probability that alleles of two individuals are identical by descent, and has been used extensively to indirectly assess variability within gene pools (Burkhamer *et al.*, 1998). A pair of individuals with a high COP probably share a greater number of identical alleles. A cross between them will probably produce a F₂ generation with a reduced number of allelic combinations, and will be expected to show reduced variability in segregating generations (Beer *et al.*, 1995). COP analysis can be applied to an estimation of genetic diversity among cultivars

and parental germplasm, predicting breeding behavior of the progeny of crosses, summarizing regional crop diversity, identifying parents that have contributed to yield improvements, and searching trends in genetic diversity over time and space (Kim and Ward, 1997; Souza *et al.*, 1998).

Estimation of genetic variability by means of COP requires detailed pedigree data. Once pedigrees are known, the coefficient of parentage may be used as an estimate of genetic similarity (Cox *et al.*, 1985). In this way, COP can be used as an index of relationship. COP values range from zero, where cultivars are completely unrelated, to one, where two cultivars have all alleles in common (Martin *et al.*, 1991). The use of a COP data matrix can cluster genotypes and produce genealogically similar groups. These groups can be used to maximize heterozygosity in the progeny of crosses and to predict heterosis (Barbosa-Neto *et al.*, 1996; Souza *et al.*, 1998).

The objective of this work was to examine the genetic variability of wheat germplasm used in genetic improvement programs in the south of Brazil. We also wished to evaluate the degree of genetic relationship among genotypes, so as to predict the extent of the genetic base of wheat. Finally, we also identified the ancestral genotypes that contributed most to the genetic pool of Brazilian wheat. The aim of this approach was to place genotypes into groups of genetic similarity, to aid the amplification of genetic variation in artificial crosses.

Materials and Methods

Fifty-three wheat genotypes, classified by commercial release year, were included in this study (Table I). The sample included inbred lines and cultivars from different origins, chosen based on their importance, either commercial or as parents. Pedigrees were obtained from Zeven and Zeven-Hissink (1976), Zeven and Reiner (1991), Graingenes Database, and additional information was provided by wheat breeders. The pedigree of a genotype was traced back to its ancestors' parents or landraces. Coefficients of parentage (COP) were computed for all pairwise combinations of genotypes from pedigree information, according to Barbosa-Neto *et al.* (1996). In using this method, it was assumed that: 1) an inbred plant received half its genes from each parent; 2) parents used in crosses were homozygous and homogeneous; 3) ancestors for which no pedigree information was available were unrelated (COP = 0.00); 4) the COP value between a cultivar and a selection from that cultivar was 0.75. The genotypes were included in a relationship matrix and were grouped using the Un-

weighted Pair Group Method of clustering (NT-SYS software for PC). The groups were generated starting from the value 0.125 (grandparent / grandchild relationship). Mean COP values within and between clusters were computed, after deleting clusters with a single entry. The ancestors' parents were chosen based on literature and information obtained from wheat breeders, and the contribution to wheat germplasm was computed considering the frequency of genotypes with COP above 0.125 (ancestors x genotype).

Results and Discussion

The mean COP for all genotypes analyzed was 0.07, ranging from 0 to 0.82 (BR35 x IAC5), a value close to that obtained for wheat by Barbosa-Neto *et al.* (1996). Similar studies have shown a mean COP around 0.20 (Autrique *et al.*, 1996; Kim and Ward, 1997; Souza *et al.*, 1998). The violation of COP assumptions results in an underestimation of the true values. The assumption that genotypes without pedigree information were unrelated (COP = 0.00) contrib-

Table I - Group (Gr), year of release and origin of evaluated hexaploid wheat.

Genotype	Gr	Year	Origin	Genotype	Gr	year	Origin
Caldwell (CAL)	1	1981	U.S.A	BR18	8	1986	Brazil
Embrapa 15 (EMB15)	1	1992	Brazil	BR23	8	1987	Brazil
CEP 14	2	1985	Brazil	CEP24	9	1992	Brazil
CEP11	3	1984	Brazil	CNT10	9	1977	Brazil
BH1146	4	1955	Brazil	Cotiporã (COT)	9	1965	Brazil
BR32	4	1988	Brazil	Trintecinco (TRI)	9	1936	Brazil
BR35	4	1989	Brazil	BR43	10	1991	Brazil
E7414	4	1967	Brazil	Jacuí (JAC)	10	1973	Brazil
Frontana (FRO)	4	1943	Brazil	RS8	10	1991	Brazil
IAC5	4	1966	Brazil	Bezoataja (BEZ)	11	1967	Russia
IAS20	4	1963	Brazil	OC22	11	1992	Brazil
Nobre (NOB)	4	1969	Brazil	S8020	11	1984	Brazil
OC8148	4	1984	Brazil	OC935	12	*	Brazil
OC958	5	*	Brazil	OC94117	12	*	Brazil
PF79547	5	1981	Brazil	OC952	12	*	Brazil
BR15	6	1985	Brazil	CEP27	13	1995	Brazil
BR34	6	1989	Brazil	Embrapa 16 (EMB16)	14	1992	Brazil
IAS54	6	1970	Brazil	RS1	15	1984	Brazil
Anahuac 75 (ANA)	7	1981	Mexico	Bonaerense (BONA)	16	1987	Argentina
Cajeme 71 (CAJ)	7	1971	Mexico	BR38	17	1990	Brazil
Embrapa 24 (EMB24)	7	1993	Brazil	OC953	18	*	Brazil
Las Rosas Inta (LRI)	7	1983	Argentina	OC9941	18	*	Brazil
OC16	7	1989	Brazil	Peladinho (PEL)	19	1978	Brazil
OC18	7	1990	Brazil	Embrapa 40 (EMB40)	20	1995	Brazil
Sonora 64 (SON)	7	1975	Mexico	BR37	21	1990	Brazil
Alondra 4546 (ALO)	8	1980	Mexico	OC9511	22	*	Brazil
BR14	8	1985	Brazil				

* - inbred lines obtained in 1995.

uted to the low value of the mean COP, since there were several genotypes with no pedigree information. A specific example was reported by Souza *et al.* (1998), showing that spring wheat cultivars with the least documented pedigrees had low similarity to other clusters. The contribution of deviation from these assumptions may vary between crosses, but should be more significant, as individuals become more related (Burkhamer *et al.*, 1998). According to van Beuningen and Busch (1997a), variability may be underestimated, because the cultivars were assumed to be homogeneous and homozygous, and the ancestors were not pure lines.

Cluster analysis revealed 22 groups of related genotypes (Table I), constituting half of only one genotype and half of at least two genotypes. The groups with more than one genotype were used to estimate the mean COP within and between groups (Table II). As expected, the results showed the COP to be high within the same groups (mean =

0.26) and low among the groups (mean = 0.05). Group 10 (BR43, Jacuí and RS8) had the highest mean COP (0.43), revealing a strong relationship among these varieties. Groups 9 and 10 were the most closely related ones (COP = 0.15).

The ancestors' contribution analysis (Table III) revealed that the one that contributed most to the wheat gene pool (34%) was the ancestor Ciano 67, followed by Mentana (32%). These two cultivars may have had significant general combining ability, and may have expressed genes that contributed to wheat stability and adaptability. On the other hand, ancestors Turkey, Mediterranean, Norin 10 and Siete Cerros were only included in the gene pool since 1970. Before 1970, genotypes Red Egyptian and Alfredo Chaves 6 had greater importance. According to Martin *et al.* (1991), regional gene pools are often based on a limited number of original ancestors, these original ancestors remaining the core of the present germplasm base. Moreover, breeders have favored either backcrossing or

Table II - Mean coefficient of parentage (COP) within (on diagonal) and between (below diagonal) genotype groups.

	Groups											
	1	4	5	6	7	8	9	10	11	12	18	
1	0.24											
4	0.02	0.23										
5	0.02	0.12	0.19									
6	0.02	0.10	0.10	0.31								
7	0.02	0.08	0.08	0.08	0.24							
8	0.02	0.08	0.08	0.08	0.12	0.29						
9	0.02	0.06	0.06	0.06	0.06	0.06	0.25					
10	0.02	0.06	0.06	0.06	0.06	0.06	0.15	0.43				
11	0.02	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.29			
12	0.02	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.27		
18	0.02	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.13	

Table III - Ancestral parents of wheat germplasm: mean coefficient of parentage (COP) and percentage of contribution from two periods.

Ancestral	Origin	Mean COP	Total contribution (%)	Contribution 1930-1970 (%)	Contribution 1971-1999 (%)
Turkey	Ukraine	0.05	6	0	6
Mediterranean	U.S.A	0.03	4	0	4
Steinwedel	S.Africa	0.009	0	0	0
Red Egyptian	Africa	0.02	4	4	0
Alfredo Chaves 6	Brazil	0.03	6	4	0
Polyssu	Brazil	0.06	11	7	4
Kenya 58	Kenya	0.04	11	7	4
Norin 10	Japan	0.04	8	0	8
Mentana	Italy	0.09	32	13	19
Siete Cerros	Mexico	0.06	9	0	9
Ciano 67	Mexico	0.12	34	6	28
Colonias	Brazil	0.05	14	7	7
Combate	Brazil	0.05	13	11	2

repeated cycles of mating to adapted germplasm for the introduction of new germplasm into wheat gene pool (Mercado *et al.*, 1996).

Analyzing the pedigrees and COP of each group, it can be seen that groups can be determined for some ancestors (Table IV). The fact that only a few representative an-

Table IV - Pedigrees and groups of hexaploid wheat genotypes evaluated.

Genotype	Pedigree	Gr.	Ancestors
CAL	FZ//H/HU	1	Med
EMB15	CNT10/BR35//PF75172/SEL.TON 75-59	1	Med
BH1146	PG1//FT/MT	4	Mt; Pol; Cas; K
BR32	IAS60/IN//IAS62/3/ALONDRA SIB/4/IAS59	4	Mt; Pol; Cas; K
BR35	IAC5*2/3/CNT7*3/LD//IAC5/HADDEN	4	Mt; Pol; Cas; K
E7414	IAS20//IAS20/INIA66	4	Mt; Pol; Cas; K
FRO	FT/MT	4	Mt; Pol; Cas; K
IAC5	FN/K58//PG1	4	Mt; Pol; Cas; K
IAS20	CAS//FN/K58	4	Mt; Pol; Cas; K
NOB	CO 824-51/YT 54//CO 296-52	4	Mt; Pol; Cas; K
OC8148	IAC5/ALD SIB	4	Mt; Pol; Cas; K
OC958	LD/6/KVZ/LD*6/AGE/3/LD*6/KUZ//LD*6/WTP/4/IAS63/ALD/5/	5	Mt; Cia
PF79547	(IAS58-IAS55/ALD "s"/IAC5) ALD "s"	5	Mt; Cia
BR15	IAS54*2/TK80//PF 69193	6	Mt; Cia
BR34	ALZ110/2*IAS54/6/TP/4/TZPP /SON64/ / NAPO /3/ CIA/5/PF6968	6	Mt; Cia
IAS54	IAS16/4/N10 B17/Y53//Y50/3/KT 54B	6	Mt; Cia
ANA	II 12300//LR 64/8156/3/NT67	7	Cia; Tky; N10; Mt; SC
CAJ	CIA67/3/SON64/KR//SIETE CIERROS	7	Cia; Tky; N10; Mt; SC
EMB24	SEL.TON/PF79763/3/NBOZU/LD*3//B7902	7	Cia; Tky; N10; Mt; SC
LRI	KLAT//INIA/BB/4/NP876/PJ/CAL/3/BB	7	Cia; Tky; N10; Mt; SC
OC16	SISKIN SIB/VEERY SIB	7	Cia; Tky; N10; Mt; SC
OC18	KAVRAZ/BUHO SIB//KN/BB	7	Cia; Tky; N10; Mt; SC
SON	YT94/N 10b//2*Y54	7	Cia; Tky; N10; Mt; SC
ALO	D6301/NAI60//WEIQUE/RED MACE/3/CIA*2/CHR	8	Cia; Cas; Tky; N10
BR14	IAS63/ALONDRA SIB//GTO/LV	8	Cia; Cas; Tky; N10
BR18	ALONDRA SIB	8	Cia; Cas; Tky; N10
BR23	CC/ALONDRA SIB/3/IAS54/COP//CNT8	8	Cia; Cas; Tky; N10
CEP24	BR3/CEP7887//CEP7775/CEP11	9	Cas; Cte
CNT10	IAS46/IAS49//IAS46/TK66	9	Cas; Cte
COT	VP*2/E NA101	9	Cas; Cte
TRI	AC3/AC4	9	Cas; Cte
BR43	PF833007/JACUI	10	Mt
JAC	S8/TP	10	Mt
RS8	CNT10/BURGAS//JACUI	10	Mt
BEZ	LUT17/SKOROSPELKA2	11	Tky; Cia; Cas
OC22	KNS/BB//CJ SIB/3/ALONDRA SIB/4/RS3	11	Tky; Cia; Cas
S8020	COXILHA/KAVRAZ	11	Tky; Cia; Cas
OC935	BTU/PG868	12	Mt; Cia; SC
OC94117	URES80/PG868	12	Mt; Cia; SC
OC952	SERI/PG868	12	Mt; Cia; SC
OC953	PG864/GEN	18	*
OC9941	GEN/2*PF83144	18	*

* - There were no representative ancestors of this group.

Cas – Colonias; Cia – Ciano; Cte – Combate; K – Kenya58; Med – Mediterranean; Mt – Mentana; N10 – Norin10; Pol – Polysu; SC – Siete Cerros; Tky – Turkey.

cestors of the groups were observed suggests again that this set of wheat germplasm reflects a narrow genetic base.

Comparing wheats from USA, Canada and Mexico, based on average COP, those from Mexico were more diverse than those from breeding programs in the USA and Canada (van Beuningen and Busch, 1997a). Despite the relatively low genetic similarity estimates based on COP in our work, we concluded that Brazilian germplasm was developed from a narrow genetic background, as revealed by the small number of ancestors investigated.

Conclusions

Genetic variability was detected among the genotypes evaluated. Based on the examined samples, Ciano 67 and Mentana were the most important genotypes in the constitution of the current wheat germplasm. Moreover, the genetic base of wheat germplasm is constituted by a restricted number of ancestor genotypes. Coefficient of Parentage (COP) analysis was effective in evaluating the variability and genetic base of wheat.

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