

# Genetic characterization of ninety elite soybean cultivars using coefficient of parentage

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**Abstract** – The objective of this work was to estimate the coefficient of parentage and to understand the genetic structure of 90 elite soybean cultivars, which are adapted to different Brazilian environments. A total of 4,005 coefficients of parentage ( $f$ ) were obtained and used to group the cultivars by UPGMA method. The constructed dendrogram showed several related cultivar groups which shared similar ancestors and clearly showed the genetic structure of the main Brazilian cultivars. Effective population sizes ( $N_e$ ) were also estimated for cultivars in different generations. The average  $f = 0.2124$  value, obtained from cultivars classified into four decades according to the release year, suggested effective soybean population sizes of 11 and 13 calculated using arithmetic and weighted means, respectively. The relatively small  $N_e$  and the high parentage coefficient support the conclusion that there is a high similarity degree among the main soybean cultivars in Brazil.

**Index terms:** *Glycine max*, effective population size, genetic similarity, parentage coefficient.

## Caracterização genética de noventa cultivares elites de soja por meio do coeficiente de parentesco

**Resumo** – O objetivo deste trabalho foi estimar o coeficiente de parentesco e conhecer a estrutura genética de 90 cultivares elites de soja adaptadas aos diferentes ambientes brasileiros. Foram obtidos 4.005 coeficientes de parentesco ( $f$ ), os quais foram utilizados para realizar o agrupamento das cultivares, pelo método UPGMA. O dendrograma formado permitiu observar vários grupos de cultivares que se aproximaram por possuírem ancestrais comuns, e mostra a estrutura genética das principais cultivares indicadas para o Brasil. Foi estimado também o tamanho efetivo populacional ( $N_e$ ) de cultivares em diferentes gerações. O valor de  $f$  calculado ( $f = 0,2124$ ) comparado com as médias ponderada e aritmética das cultivares organizadas segundo os períodos de lançamento durante quatro décadas revela que o  $N_e$  para a soja é de 11 e 13, para a média aritmética e ponderada, respectivamente. O  $N_e$  relativamente pequeno e o alto coeficiente de parentesco sustenta a conclusão de que existe alto grau de similaridade entre as principais cultivares de soja indicadas para o Brasil.

**Termos para indexação:** *Glycine max*, similaridade genética, tamanho efetivo populacional.

### Introduction

Soybean genetic breeding started recently in Brazil compared to other species of economic importance, but its contribution to the Brazilian agriculture has been very significant. The increase in yield in the traditional cropping regions, the expansion of the agricultural frontier, incorporating areas of the “Cerrados” as productive lands, and the increase of crop rotation are unquestionable results of the benefit obtained by creating new cultivars that are higher yielding and better adapted to these regions (Hiromoto, 1996).

The breeder has two choices when selecting parents for hybridization. The first is to maximize recombination, choosing genetically distant parents that have traits of interest, to obtain a recombinant population with wide genetic variability, increasing the chances to find genotypes that favorably combine these traits. The second choice is to minimize recombination using backcrossing for hybridization, selecting the donor parent among cultivars which are similar to the recurrent parent and carriers of the desirable trait for transfer.

There are different strategies to study genetic divergence among genotypes, one of them considers the

coefficient of parentage. Gizlice et al. (1993) studied soybean cultivars released between 1947 and 1988 and obtained mean parentage coefficients of 0.164 and 0.234 for cultivars from North and South of the United States, respectively. Similar results were obtained by Sneller et al. (1997), also with elite cultivars from North and South of United States. Cui et al. (2000) reported a mean coefficient of parentage of only 0.02 among Chinese soybean cultivars, which is considered a very low value and indicates high genetic diversity in this germplasm. In India, Bharadwaj et al. (2002) analyzed the coefficient of parentage of 66 cultivars released from 1968 through 2000 and concluded that 10 ancestral cultivars contributed with 72.6% of the gene pool. Cultivar Bragg was parent of 15 of the 66 investigated cultivars. Based on these results the authors concluded that the Indian soybean germplasm has a narrow genetic basis. Choi et al. (1999) showed that the average distances among improved soybean cultivars are usually smaller than that among wild soybean.

In Brazil, Vello et al. (1988) calculated the parentage coefficient for each paired combination including 69 soybean cultivars indicated for Brazil conditions and reported a mean value of 0.16. Bonato (2000) developed a similar study including 100 soybean cultivars released since 1984 and obtained a mean value of 0.21. Miranda (2005), working with 457 Brazilian cultivars, reported a mean coefficient of parentage of 0.178. Those values were considered high and the authors suggested the use of genotypes with low parentage coefficient to increase genetic diversity.

The objective of this work was to evaluate the available genetic variability among parents for crossing, using estimatives of the coefficient of parentage, and to understand the genetic structure of 90 cultivars adapted to different Brazilian environments.

## Material and Methods

Ninety cultivars indicated by different companies and adapted to the several Brazilian environments were used (Table 1). They were selected according to their commercial success, adaptation and yield potential. The genealogies were obtained from diverse sources including technical documents, folders on released cultivars, and publications on the subject, as well as common knowledge. Their genetic similarity was obtained by the coefficient of parentage ( $f$ ) of each pair of cultivars calculated by the PROC INBREED of the SAS.

The coefficient of parentage was assumed zero ( $f = 0$ ) in the absence of any degree of kinship and one ( $f = 1$ ) when there is maximum degree of kinship. In this work the coefficients of parentage between two cultivars was considered one ( $f = 1$ ) if three or more backcrosses were used to derive one parent from the other. The mean and standard error of the coefficient of parentage for each cultivar and the general mean of all cultivars were calculated (Table 2).

The 90 cultivars were grouped in the NTSYS (Rolf, 1998) by using the UPGMA method (Unweighted Pair-Group Method Arithmetical Means) based on their coefficient of parentage.

The St. Martin expression, quoted by Vello et al. (1988), which related the effective population size ( $N_e$ ) to the coefficient of parentage for each  $t$  recombination cycle  $\{F_t = 1/N + [(N - 1)/N]F_{t-1}\}$  was used to estimate  $N_e$ . The expected  $F$  values were calculated for the different population sizes considering four generations of ten years each, starting in 1965. In sequence, the weighted and arithmetical means of three and four cultivar cycles were calculated to compare with the  $F$  value obtained in this study. The weighted mean was calculated assuming that 13.3% of the total of cultivars belonged to the 1<sup>st</sup> cycle ( $F_1$ ), 18.9% to the 2<sup>nd</sup> cycle ( $F_2$ ), 28.9% to the 3<sup>rd</sup> cycle ( $F_3$ ) and 38.9% to the 4<sup>th</sup> cycle ( $F_4$ ).

## Results and Discussion

The 4,005 coefficients of parentage ( $f$ ) estimated among the 90 cultivars ranged from 0 to 1. A total of 14 pairs of cultivars showed  $f = 0$ , which indicated maximum divergence, including: Campos Gerais and Bossier; Campos Gerais and BRS Celeste; Campos Gerais and Embrapa 20 (Doko RC) and, IAC 4 and FT Cometa. Cultivar Campos Gerais presented the largest number of cultivar pairs which comprised  $f = 0$  (seven pairs). Out the 4,005 coefficients of parentage estimated, 124 presented  $f = 1$ , which indicated that two cultivars had the same genetic origin, including Embrapa 4 and BR 4; Embrapa 33 and BR 27 (Cariri); BRSMA Seridó RCH and BR 28 (Seridó); Dourados and Santa Rosa; Paraná and Paranagoiana and, UFV 1 and Viçoja. Results of the last three cultivar pairs were also reported by Vello et al. (1988) in a similar study carried out with 69 cultivars.

In this study, 3,867  $f$  values were greater than zero and lower than one, which allows the breeder to choose genotypes with different levels of divergence to take part in his breeding program. Mean and standard deviation of the estimated  $f$  for each cultivar were also

calculated (Table 2). These statistics positioned the cultivar kinship average and spread in relation to all others. The lowest values ( $0.0246 \pm 0.0275$ ) were observed for the FT Cometa cultivar and the highest ( $0.2741 \pm 0.1871$ ) were observed for the UFV 1 cultivar.

The overall mean and standard deviation of *f* was  $0.2124 \pm 0.1276$ . This value is higher than the 0.16 obtained by Vello et al. (1988) and the 0.178 reported by Miranda (2005). These two authors used practically all available soybean cultivars indicated by different companies without considering their commercial impact. This work

evaluated only successful cultivars selected into the same group studied by Miranda (2005). So, the mean *f* values increased from 0.178 to 0.212, showing that this group of elite cultivars presents a more restricted genetic basis.

A lower *f* value would be expected among the recent cultivars because diverse sources of resistance genes were used intensively against important diseases, such as stem canker (for example, the cultivars BRS 232 and BRS 184) and soybean cyst nematode ('BRS Jiripoca' and 'BRSMT Pintado') in Brazilian soybean breeding programs. On the other hand, the higher *f* could have

**Table 1.** Soybean cultivars and their genealogies used to estimate the coefficients of parentage.

N <sup>o</sup>	Cultivars	Genealogies	N <sup>o</sup>	Cultivars	Genealogies
1	Bossier	Lee selection (S 100 × CNS)	46	CD 216	OC91-671 x Dx 7
2	BR 4	Hill × Hood	47	Davis	[Roanoke × (Ogden × CNS)] × Ralsoy × Ogden)
3	BR 6 (Nova Bragg)	Bragg(3) × Santa Rosa	48	DM Vitória	IAC 8 × UFV 9
4	BR 10 (Teresina)	UFV 1 × IAC73-2736-10	49	Doko	Viçoja × (Hill × PI 240664)
5	BR 15 (Mato Grosso)	Santa Rosa × LoD76-761	50	Dourados	Andrews selection
6	BR 16	D 69-B 10-M 58 × Davis	51	Embrapa 1	IAS 5(6) × Paranaíba
7	BR 27 (Cariri)	BR78-22043 × (Bragg × IAC73-2736)	52	Embrapa 4	BR 4(6) × Paranaíba
8	BR 28 (Seridó)	Santa Rosa × BR78 11202	53	Embrapa 20 (Doko RC)	Doko(4) × IAC 7
9	BR 30	União (2) × Lo76-1763	54	Embrapa 33	BR 27 (Cariri) (6) × FT Cristalina
10	BR 36	IAS 4 (2) × BR78-22043	55	Embrapa 48	(Davis × Paraná) × (IAS 4 × BR5)
11	BR 37	União (2) × Lo76-1763	56	Embrapa 58	Paraná × BR83-147
12	BR 38	FT 2 × União	57	Embrapa 59	FT Abyara × BR83-147
13	Bragg	Jackson × D49-2491	58	Emgopa 301	IAC 4 × Júpiter
14	BR/Emgopa 314(Garça-Branca)	Emgopa 301 × Embrapa 20 (Doko RC)	59	Emgopa 308 (Serra Dourada)	Emgopa 301 selection
15	BRS 66	FT Abyara × BR83-147	60	Emgopa 313	IAC 7 × (Santa Rosa x Go79-3068)
16	BRS 132	BR80-20703 × Nissei	61	FT 2	IAS 5 selection
17	BRS 133	FT Abyara × BR83-147	62	FT Abyara	União × Sant'Ana
18	BRS 134	BR83-147 × BR84-8309	63	FT Cometa	FT-420 × Williams
19	BRS 136	FT Manacá × BR83-147	64	FT Cristalina	UFV 1 selection
20	BRS 137	Dourados 1(5) × Ocepar 9-SS 1	65	FT Estrela	M-2 × FT 1
21	BRS 153	Embrapa 1 (IAS 5RC) × Braxton	66	FT Guaira	Lancer × União
22	BRS 154	Embrapa 1 (IAS 5RC) × Braxton	67	FT Jatobá	FT-9510 × Sant'Ana
23	BRS 156	FT 5 × [Dourados-1(5) × Ocepar 9-SS 1] × Tracy M	68	IAC 4	IAC 2 × Hardee
24	BRS 183	Embrapa 1(3) × IAC 12	69	IAC 7	Davis × (Hill × PI 240664)
25	BRS 184	FT Guaira × IAC 13	70	IAC 8	Bragg × (Hill × PI 240664)=E70-51
26	BRS 185	FT Abyara × IAC 13	71	IAS 4	seleção em R60-390 (Hood × Jackson)
27	BRS 213	BR94-23354 × BR94-23321	72	IAS 5	Hill × D52-810
28	BRS 214	Sharkey × (Hartwig × BR92-31814)	73	MG/BR 22 (Garimpo)	Bossier × Paraná
29	BRS 232	BR85-18565(3) × [Embrapa 4(3) × Tracy M]	74	MG/BR 46 (Conquista)	Lo75-4484 × Numbaira
30	BRS Barreiras	FT Abyara × [IAC 12 × (Lancer × BR80-6989)]	75	MT/BR 45 (Paiguás)	Doko × IAC 7
31	BRS Celeste	Bossier × BR 1	76	MT/BR 51 (Xingu)	BR83-9520-1(2) × FT Estrela
32	BRS Gralha	BR83-9520 × Doko	77	Ocepar 3 (Primavera)	(Halesoy × Volstate) × (Hood × Rhosa)
33	BRS Jiripoca	Sharkey × [Hartwig × (BR87-567(3) × FT Estrela)]	78	Ocepar 4 (Iguaçu)	R70-733 × Davis
34	BRS Milena	FT Abyara × BR83-147	79	Ocepar 9-SS 1	Paraná natural mutation
35	BRS Raimunda	Braxton × BR92-31857	80	Ocepar 14	Davis × União
36	BRS Sambaíba	FT 5 × [Dourados 1(4) × Ocepar 9-SS 1]	81	Paraná	Hill × D52-810
37	BRS GO Jatai	Emgopa 313 (Anhanguera)(6) × BR92-31910	82	Paranagoiana	Paraná natural mutation
38	BRSMA Seridó RCH	BR 28 (Seridó)(6) × Embrapa 20 (Doko RC)	83	Sant'Ana	D51-5427 × D49-2491
39	BRS MG 68	Braxton × {FT 5 × [Dourados 1(5) × Ocepar 9-SS 1]}	84	Santa Rosa	D49772 × La41-1219
40	BRSMT Pintado	Sharkey × [Hartwig × (BR87-567(3) × FT Estrela)]	85	São Luiz	Hardee × Semmes
41	BRSMT Uirapuru	BR83-9520-1(2) × FT Estrela	86	Spring	Williams × Essex
42	Campos Gerais	Arksoy × Ogden	87	Tropical	Hampton × E70-51
43	CD 201	Ocepar 4 (Iguaçu)(5) × Williams 20	88	UFV 1	Seleção em Viçoja (D49-2491(2) × Improved Pelican)
44	CD 202	CEPS77-16 × Invicta	89	União	D65-2874 × Hood
45	CD 206	OC87-5085 × FT Abyara	90	Viçoja	D4902491(2) × Improved Pelican

stemmed from the introgression of the resistance genes often performed on elite cultivars by backcrossing. It could also have stemmed from the restricted number of cultivars included in this study, which sampled germplasm derived by backcrossing and germplasm closely related to other successful cultivars.

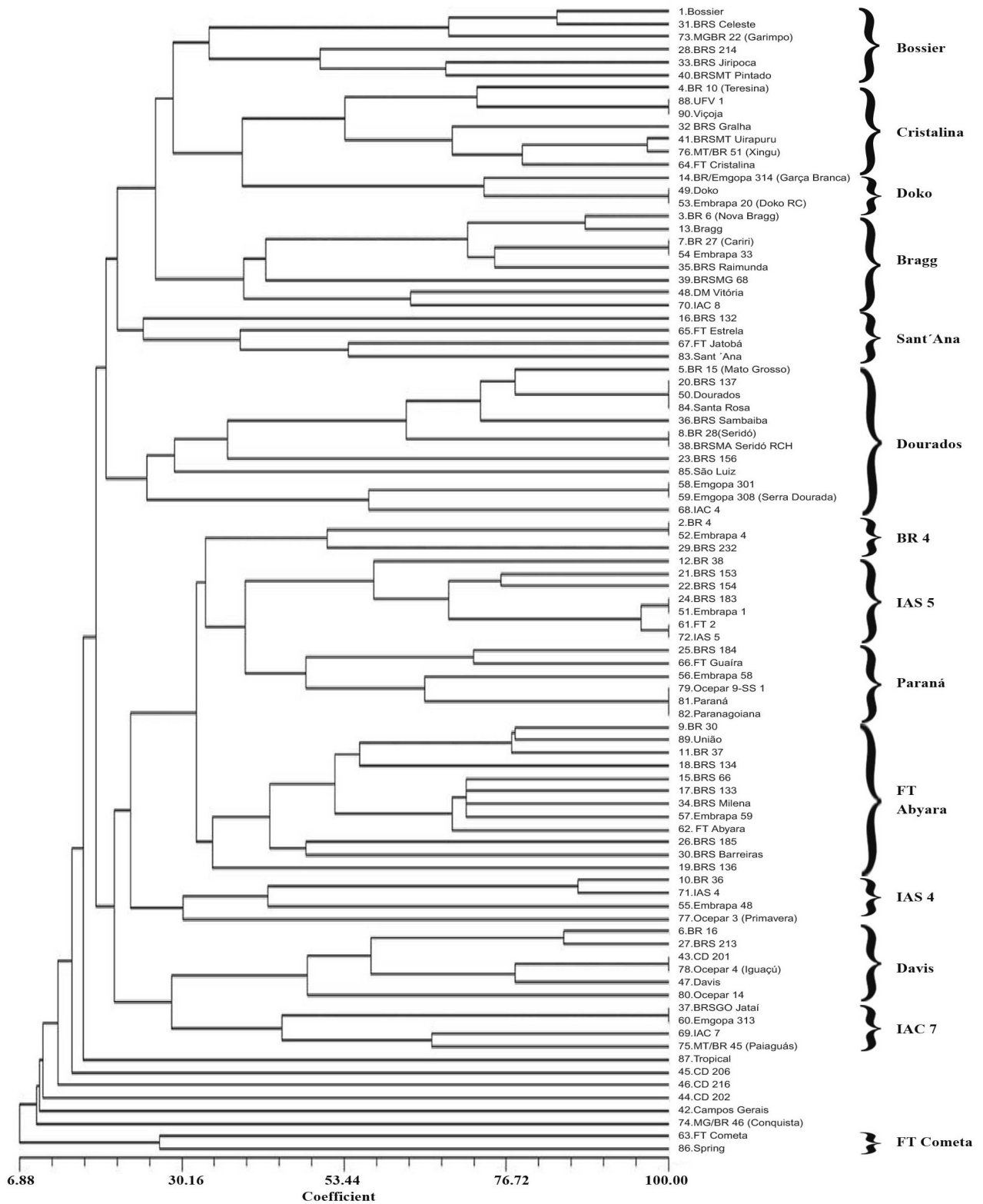
During crossing programs, plant genetic improvement endeavors to generate variability to enable the combination of desirable traits from different parents. In this study, the coefficients of parentage of the 90 cultivars were grouped by the UPGMA method to better visualize the genetic structure of the main Brazilian cultivars, which is shown in the form of a dendrogram (Figure 1). The several formed groups depicted some cultivars that are close because they share a common ancestor, such as the case of Bossier that grouped with six cultivars.

The group formed by cultivar Bossier included 'BRS Celeste' with 83% similarity, which decreased to 71% when the cultivar MG/BR 22 (Garimpo) was included. It also involved cultivars BRS Jiripoca and BRSMT Pintado with 70% similarity. The group similarity decreased to 49% when 'BRS 214' was included. Cultivar BRS 214 is not resistant to soybean cyst nematode but has resistant sources as 'Sharkey' and 'Hartwig' in its genealogy (Table 1), which justify the presence in this group.

Another group was formed by cultivar Cristalina involving the pair 'UFV 1' and 'Viçoja' with 100% similarity. Group similarity decreased to 73% when cultivar BR 10 (Teresina) was included. Next in this group were cultivars BRSMT Uirapuru and MT/BR 51 (Xingu) with 97% similarity, which decreased to 80 and 71%, respectively, when cultivars FT Cristalina and

**Table 2.** Mean and standard deviations of the coefficients of parentage of the 90 soybean cultivars adapted to different Brazilian environments.

Nº	Cultivars	Means	S. deviations	Nº	Cultivars	Means	S. deviations
1	Bossier	0,2512	0,1382	46	CD 216	0,1192	0,0457
2	BR 4	0,2565	0,1283	47	Davis	0,2130	0,1506
3	BR 6 (Nova Bragg)	0,2334	0,1539	48	DM Vitória	0,2293	0,1203
4	BR 10 (Teresina)	0,2325	0,1314	49	Doko	0,2213	0,1481
5	BR 15 (Mato Grosso)	0,1980	0,1512	50	Dourados	0,2040	0,1893
6	BR 16	0,2491	0,1081	51	Embrapa 1	0,2549	0,1991
7	BR 27 (Cariri)	0,2291	0,1498	52	Embrapa 4	0,2565	0,1283
8	BR 28 (Seridó)	0,2265	0,1597	53	Embrapa 20 (Doko RC)	0,2242	0,1577
9	BR 30	0,2198	0,1409	54	Embrapa 33	0,2291	0,1498
10	BR 36	0,2006	0,1159	55	Embrapa 48	0,2295	0,0979
11	BR 37	0,2198	0,1409	56	Embrapa 58	0,2473	0,1470
12	BR 38	0,2633	0,1580	57	Embrapa 59	0,2577	0,1474
13	Bragg	0,2288	0,1578	58	Emgopa 301	0,1532	0,1278
14	BR/Emgopa 314(Garça-Branca)	0,1944	0,1329	59	Emgopa 308 (Serra Dourada)	0,1532	0,1278
15	BRS 66	0,2577	0,1474	60	Emgopa 313	0,1611	0,1167
16	BRS 132	0,1290	0,0558	61	FT 2	0,2484	0,1824
17	BRS 133	0,2577	0,1474	62	FT Abyara	0,2717	0,1435
18	BRS 134	0,2520	0,1518	63	FT Cometa	0,0246	0,0275
19	BRS 136	0,1753	0,1007	64	FT Cristalina	0,2578	0,1456
20	BRS 137	0,2040	0,1893	65	FT Estrela	0,1228	0,0768
21	BRS 153	0,2451	0,1424	66	FT Guaira	0,2476	0,1317
22	BRS 154	0,2451	0,1424	67	FT Jatobá	0,2240	0,1094
23	BRS 156	0,1765	0,0745	68	IAC 4	0,1247	0,1170
24	BRS 183	0,2483	0,1889	69	IAC 7	0,1961	0,1105
25	BRS 184	0,2240	0,1305	70	IAC 8	0,1928	0,1042
26	BRS 185	0,2364	0,1171	71	IAS 4	0,1845	0,1107
27	BRS 213	0,2431	0,1166	72	IAS 5	0,2484	0,1824
28	BRS 214	0,2046	0,0942	73	MG/BR 22 (Garimpo)	0,2566	0,1258
29	BRS 232	0,2201	0,0982	74	MG/BR 46 (Conquista)	0,0914	0,0423
30	BRS Barreiras	0,2466	0,1110	75	MT/BR 45 (Paiaguás)	0,2126	0,1116
31	BRS Celeste	0,2126	0,1080	76	MT/BR 51 (Xingu)	0,2328	0,1477
32	BRS Gralha	0,2477	0,1426	77	Ocepar 3 (Primavera)	0,1474	0,0605
33	BRS Jiripoca	0,2084	0,0996	78	Ocepar 4 (Iguaçu)	0,2256	0,1442
34	BRS Milena	0,2577	0,1474	79	Ocepar 9-SS 1	0,2501	0,1723
35	BRS Raimunda	0,2268	0,1435	80	Ocepar 14	0,2463	0,1238
36	BRS Sambaíba	0,2167	0,1483	81	Paraná	0,2501	0,1723
37	BRSO Jataí	0,1611	0,1167	82	Paranagoiana	0,2507	0,1729
38	BRSMA Seridó RCH	0,2265	0,1597	83	Sant' Ana	0,2305	0,1093
39	BRSMG 68	0,2220	0,1008	84	Santa Rosa	0,2040	0,1893
40	BRSMT Pintado	0,2084	0,0996	85	São Luiz	0,1998	0,0696
41	BRSMT Uirapuru	0,2328	0,1477	86	Spring	0,1162	0,0449
42	Campos Gerais	0,0939	0,0629	87	Tropical	0,1537	0,0647
43	CD 201	0,2256	0,1442	88	UFV 1	0,2741	0,1871
44	CD 202	0,1012	0,0397	89	União	0,2704	0,1733
45	CD 206	0,1387	0,0806	90	Viçoja	0,2575	0,1582



**Figure 1.** Dendrogram plotted by UPGMA based on coefficients of parentage between 90 cultivars adapted to different Brazilian enviroment.



BRTS Gralha were added. The next group was formed by cultivars Doko and Embrapa 20 (Doko RC) with 100% similarity, which decreased to 73% when 'BR/Emgopa 314' (Garça-Branca) was grouped together. This group joined the Cristalina group with 40% similarity and the Bossier group with 30% similarity.

The following group stemming from cultivar Bragg included 'BR 6' (New Bragg) with 88% similarity. In the same group, 'BR 27' (Cariri) and 'Embrapa 33' showed 100% similarity. Cultivars BRS Raimunda, BRSMG 68, DM Vitória and IAC 8, which were also part of this group, had similarities ranging from 64 to 40%. The group of cultivar Sant'Ana was identified next, and included cultivars BRS 132, FT Estrela, FT Jatobá and Sant'Ana, whose similarity ranged from 54 to 24%.

A large group formed around the cultivar Dourados showed three cultivars: BRS 137, Dourados and Santa Rosa, with 100% similarity. In the group, 'BR 28' (Seridó) clustered with 'BRSMA Sambaíba' and 'Emgopa 301' with 'Emgopa 308' (Serra Dourada). The other cultivars in the group, such as BR 15 (Mato Grosso), BRS Sambaíba, BRS 156, São Luiz and IAC 4, had similarities ranging from 78 to 57%. In the next group, the cultivars clustered around 'BR 4' that showed 100% similarity with 'Embrapa 4'. The group similarity decreased to 50% when cultivar BRS 232 was included.

The next group identified as IAS 5 was formed by seven cultivars, including two 100% similarity pairs, 'BR 183' and 'Embrapa 1', and 'FT2' and 'IAS 5'. These two pairs regrouped with 95% similarity, and when cultivars BR 38, BRS 153 and BRS 154 were included, the group similarity decreased to 58%. Cultivar Paraná grouped with five others and showed 100% similarity with 'Ocepar 9-SS 1' and 'Paranagoiana'. When cultivars BRS 184, FT Guaira and Embrapa 58 were added to the group, the similarity ranged from 73 to 48%.

The following group formed by 'FT Abyara' included the cluster formed by the sister cultivars BRS 66, BRS 133, BRS Milena and Embrapa 59 with 72% similarity. When cultivar FT Abyara was added, the

group similarity fell to 70%. In sequence, cultivars BR 30 and União grouped with 78% similarity, which decreased to 77% when 'BR 37' was included. The similarity of other cultivars such as BRS 134, BRS 185, BRS Barreiras as well as BRS 136 ranged from 56 to 35%. These cultivars joined the Paraná, IAS 5 and BR 4 groups to form a larger cluster with similarity of approximately 32%. The next group formed by cultivar IAS 4 included BR 36 and IAS 4 with 87% similarity, which decreased to 42% when Embrapa 48 was grouped together.

In the group formed by cultivars with Davis genealogy, the pair BR 16 and BRS 213 showed 85% similarity. The pair 'CD 201' and 'Ocepar 4' (Iguaçu) showed 100% similarity, which decreased to 78%, when 'Davis' was included in the group, and to 48%, when the 'Ocepar 14' was included. The group formed by cultivar IAC 7 was the next, comprising the pair 'BRSGO Jataí' and 'Emgopa 313' as well as the pair 'IAC 7' and 'MT/BR 45' (Paiaguás), showing 100 and 78% similarity, respectively. When these two pairs were joined, the group similarity decreased to 44%. Some cultivars did not belong to any group, such as Tropical and MG/BR 46 (Conquista). The last group was formed by only two cultivars, FT Cometa and Spring, that showed 26% similarity.

Selecting parents with lower similarity allows expression of larger genetic variability in the derived populations and improves the chances of selecting desirable traits, both qualitative and quantitative. Thus, crosses involving genotypes belonging to more distant groups must produce populations with greater genetic variability (Figure 1).

However, in backcrossing programs, high agronomic similarity is sought among parents for selection of specific qualitative traits to correct some shortcoming, for example, susceptibility to a certain disease. Therefore, the breeder can choose genetically closer genotypes according to the available information in Figure 1.

The values estimated for  $f$  considering different effective sizes ( $N_e$  11 to 13) for cultivars in different generations are presented in Table 3. When the

**Table 3.** Effective population size ( $N_e$ ), weighted means (W) and arithmetical means (A) in the  $t^{\text{th}}$  generation.

$N_e$	F in the $t^{\text{th}}$ generation				Mean	
	$F_1$	$F_2$	$F_3$	$F_4$	W	A
11	0,0909	0,1736	0,2487	0,3170	0,2405	0,2075
12	0,0833	0,1597	0,2297	0,2939	0,2224	0,1917
13	0,0769	0,1479	0,2135	0,2740	0,2069	0,1781
No. cultivars	12	17	26	35		

calculated  $f$  value ( $f = 0.2124$ ) was compared with the weighted and arithmetical means obtained from the four cycles or generations of cultivars, effective population size for soybean is between 11 and 13. Considering that most of the cultivars were recommended in the last decade, the greater value of  $N_e = 13$  should better represent reality. When these values are compared with those reported by Vello et al. (1988) and Miranda (2005) of 11 to 15 and 13 to 16, respectively, in similar studies, it could be verified that the effective population size, considering the main soybean cultivars released in Brazil, has decreased a little.

Considering that only cultivars of greater economic importance were included, the reduction in the effective size was not as significant as expected. The introgressions of genotypes with resistance to stem canker and soybean cyst nematode may have contributed to maintenance of the effective population size for soybean in Brazil.

### Conclusions

1. The group of 90 elite cultivars studied has a restricted genetic variability in relation to the whole set of cultivars indicated in Brazil.
2. The effective population size among the 90 elite Brazilian soybean cultivars is small.
3. The dendrogram shows the genetic structure of the 90 Brazilian soybean cultivars, and can help breeders choose parents for soybean breeding programs.

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