GENETIC VARIABILITY AND PEDIGREE ANALYSIS OF BRAZILIAN COMMON BEAN ELITE GENOTYPES

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ABSTRACT: Genetic diversity is essential for any breeding program. However, breeders tend to concentrate on specific genotypes, which combine traits of interest and may be used as progenitors in several breeding programs. Common bean (*Phaseolus vulgaris* L.) breeding programs are not different in this sense. In this study, the genetic diversity of 21 common bean elite lines from the Bean Regional Trials conducted by the Embrapa Rice and Bean Research Center was evaluated using the Random Amplified Polymorphic DNA (RAPD) and pedigree analyses. Based on genetic dissimilarity, three groups were defined: group I - lines 1, 9 and 10, with low genetic distances among them (0.00 to 0.06), originated from 11 Mesoamerican parents; group II - 17 lines with genetic distances ranging from 0.03 to 0.33, originated from 50 parents (mostly Mesoamerican); and group III - line 21 (PR 93201472), which parents are the Andean cultivar 'Pompadour' and the cultivar 'Irai' (unknown origin). The genetic distances between line 21 and the lines of the other two groups varied from 0.68 to 0.93. Pedigree analyses demonstrated that cultivars 'Carioca', 'Cornell 49-242', 'Jamapa', 'Tlalnepantla 64', 'Tara' and 'Veranic 2', all of Mesoamerican origin, were the most widely used parents for developing lines present in group II.

Key words: *Phaseolus vulgaris*, Andean cultivars, Mesoamerican cultivars, RAPD molecular markers, genetic distances

VARIABILIDADE GENÉTICA E ANÁLISE DE PEDIGREE EM GENÓTIPOS ELITE BRASILEIROS DE FEIJOEIRO COMUM

RESUMO: Diversidade genética é um pré-requisito em qualquer tipo de programa de melhoramento. No entanto, os melhoristas tendem a se concentrar em alguns genótipos que reúnem características de interesse e estes são usados em diversos programas de melhoramento. Os programas de melhoramento do feijoeiro (*Phaseolus vulgaris* L.) não são diferentes quanto a esse aspecto. Visando o estudo da variabilidade genética, 21 cultivares-elite dos Ensaios Regionais de Feijão coordenados pela Embrapa Arroz e Feijão, foram caracterizados com marcadores moleculares Random Amplified Polymorphic DNA (RAPD). Também, os *pedigrees* dos 21 cultivares elite foram pesquisados com o objetivo de estudar os progenitores usados no seu desenvolvimento. Baseado nos dados de distância genética, um gráfico de dispersão foi construído e três grupos foram identificados: 1) grupo I, formado pelas linhas 1, 9 e 10, com baixa diversidade genética entre si (0,00 a 0,06), originadas de 11 progenitores de origem Mesoamericana; 2) grupo II, formado por 17 linhagens com distâncias genéticas variando de 0,03 a 0,33, originadas de 50 progenitores, a maioria de origem Mesoamericana; e, 3) grupo III, formado pelo cultivar PR 93201472 (linhagem 21), que tem os cultivares 'Pompadour' (origem Andina) e 'Irai' (origem desconhecida) como seus progenitores. As distâncias genéticas entre PR 93201472 e os outros 20 cultivares variaram entre 0,68 e 0,93. De acordo com seus *pedigrees*, os cultivares 'Carioca', 'Cornell 49-242', 'Jamapa', 'Tlalnepantla 64', 'Tara' e 'Veranic 2', todos de origem Mesoamericana, foram os progenitores mais empregados na geração das linhagens do grupo II.

Palavras-chave: *Phaseolus vulgaris* L., cultivares Andinos, cultivares Mesoamericanos, marcadores moleculares RAPD, distâncias genéticas

INTRODUCTION

Brazil, Mexico, Argentina and United States are the leading common bean (*Phaseolus vulgaris*) producers in the world. In Latin America and Africa, beans are major staple food and an important protein source. Brazil is the world leading producer of *Phaseolus* beans, but its production is destined to internal consumption. The U.S. is the leading exporter marketing 40% (0.4 million metric tons) of all their dry bean production overseas, while Argentina exports 99.5% of its production of 0.25 million metric tons (*Phaseolus* Crop Germplasm Committee Report, 1996; FAO, 1998).

Studies on variation patterns of the seed protein phaseolin, alloenzymes and morphological evidences, revealed the existence of a Middle American and an Andean gene pools in *Phaseolus vulgaris* (Gepts et al., 1986; Singh et al., 1991a; Singh et al., 1991b). Phaseolin S is common among the three *Phaseolus* races in the Middle American gene pool, while Sb, Sd and B phaseolins are less common. On the other hand, phaseolin T, C and H are present in genotypes from the Andean gene pool. Not only the phaseolin patterns but also the size of the seeds differentiates Middle American from Andean gene pools. Mesoamerican landraces have usually smaller seeds than their Andean counterparts (Gepts, et al., 1986; Singh et al., 1990).

Biochemical studies have shown that the cultivated bean germplasm presents a low level of genetic diversity as compared to their wild ancestors (Gepts et al., 1986; Koenig et al., 1990; Sonnante et al., 1994; Johnson & Gepts, 1998). Progress in bean breeding around the world has been slow, probably because of a limited genetic variability of the parents which have been selected from the same gene pool.

Isozymes and DNA-based markers have been used to evaluate germplasm genetic diversity in *Phaseolus* species, within both cultivated and wild genetic materials; to analyze crop evolution; and the effect of domestication on genetic diversity (Gepts, 1988; Singh et al., 1990; Koening et al., 1990; Chase et al., 1991; Singh et al., 1991a, b, c; Arraes et al., 1992; Thome et al., 1996; Nienhuis et al., 1996; Alvarez et al., 1998, Vasconcelos, 1995; Beebe et al., 2000). Métais et al. (2000) evaluated the effectiveness of Restriction Fragment Length Polymorphism (RFLP), Direct Amplified Minisatellite DNA-PCR (DAMD-PCR), Inter Simple Sequence Repeat (ISSR) and Random Amplified Polymorphic DNA (RAPD) markers in the assessment of polymorphism and relationships between commercial lines of *P. vulgaris.* RAPD and RFLP analyses led to the same clustering of the bean lines. All analyzed genotypes could be distinguished by only seven RAPD markers.

The objectives of the present study were: to evaluate the genetic variability within 21 elite cultivars from the Bean Regional Trials coordinated by Embrapa Rice and Bean Research Center using RAPD markers; and to identify the parents involved in the development of these cultivars through pedigree analyses.

MATERIAL AND METHODS

The pedigree of each of the 21 elite lines from Regional Trails used in this study is shown in Table 1. Primary leaves from each individual line were collected, identified and stored at –80°C. DNA extraction was made according to Doyle & Doyle (1990). Amplification reactions of 25 μL each, contained 25 ng of DNA, 0.1 mmol L^{-1} of each dNTP (dATP, dCTP, dGTP, dTTP), 2.0 mmol L^{-1} of $MgCl_2$, 10 mmol L^{-1} Tris-HCl, pH 8.3, 50 mmol L^{-1} KCl, 0.4 μmol L^{-1} of one primer decamer (Operon Technologies, Alameda, CA, USA), and one unit of *Taq* DNA polymerase (Williams et al., 1990).

Each amplification cycle consisted of one denaturation step at 94°C for 15 s, one annealing step at 35°C for 30 s, and one extension step at 72°C for 1 min. After 40 cycles, an extra extension step was performed for 7 min at 72°C. Amplification products were analyzed on 1.2% agarose gels immersed on TBE buffer (90 μmol L^{-1} Tris-borate; 2 μmol L^{-1} EDTA, pH 8.0) containing 10 μg of ethidium bromide per mL (Williams et al., 1990). DNA bands were visualized under UV light and photographed with the Eagle Eye II photosystem (Stratagene, La Jolla, CA, USA).

Fourteen primers were tested and only two did not show polymorphic bands. The primers OPB15, OPB18, OPAT05, OPY10, OPAA18, OPBA18, OPBB20, OPAW19, OPAX03, OPAZ18, OPAX02 and OPAX18 revealed polymorphism. Only the strong and reproducible bands were used for analyses.

The clustering analysis was based on the genetic distance calculated by the Nei & Li method for binary data, using the GENES computer program (Cruz, 1997). Based on the genetic distances a dispersion graphic on two-dimensional space was obtained (Cruz & Soriano, 1994).

RESULTS AND DISCUSSION

General information on cultivars/lines involved in the breeding program to obtain the elite lines of the Bean Regional Trials is presented in Table 2. The DNA amplification results presented 32 polymorphic and 46 monomorphic bands, among the 21 bean cultivars. Based on the genetic distances a two-dimensional dispersion graph was obtained. In the dispersion graph, it was possible to distinguish three different groups (Table 3, Figure 1).

The first group was formed by three black seed lines with identical genealogies, LR 9115398 (1), AN 9021334 (9) and AN 9021336 (10), derived from 11 Mesoamerican parents. These lines presented low genetic distances between them (0.00 to 0.06) (Figure 1). Lines (9) and (10) showed a genetic distance of zero, while line (1) presented a genetic distance of 0.06 in relation to lines (9) and (10) (Table 3). These lines carries anthracnose and rust resistance genes, derived from the cultivar Honduras 35 known in Brazil as Ouro Negro (Faleiro et al., 2000; Alzate-Marin et al., 2001).

Table 1 - Seed color and pedigrees of the 21 elite common bean lines of the Bean Regional Trials coordinated by Embrapa Rice and Bean.

BRT line[a]	Color	Size[d]	Pedigree
1. LR 9115398	Black[b]	Small (20.5)	(((G 2698 x (BRASIL 343 x BRASIL 1096)) x (CAUCA 41))x (ICA TUI x S 166 AN)x (G 2084 x51051) x (SB 12))x (XAN 87)))/HONDURAS 35
2. LR 9115453	Brown	Small (20.4)	(DRO 4784) / ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA) x PORRILLO SINTETICO x PI 310878) x NEP BAYO 22))// (AROANA x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA)))/ (OJO DE LIEBRE x ((PORRILLO SINTETICO x CACAHUATE 73) x (JAMAPA x CACAHUATE 72)))
3. A 774	Brown	Small (20.4)	((51051xICA BUNSI)x (51052 x CORNELL 49242))/// (CARIOCA x MEX. 168)/ CARIOCA 80 // (CARIOCA x MEX. 168) / ((ICA TUI x TLALNEPANTLA 64) x (PORRILLO SINTETICO x JULES))
4. PR 9115957	Brown	Small (22.0)	(TLALNEPANTLA 64 x AROANA) / GOIANO PRECOCE
5. FEB 163	Purple	Small (16.8)	(CARIOCA x MEX. 168) / ((AETE 1/38 x (VERANIC 2 x TLALNEPANTLA 64)) x (JAMAPA x TARA))// (CARIOCA x MEX. 168)//(((PORRILLO No. 1 x GENTRY 21439) x (51052 x CORNELL 49-242)) x (GENTRY No. 12307 x GARRAPATO))/// CARIOCA x MEX. 168/ ((ICA TUI x TLALNEPANTLA 64) x (PORRILLO SINTETICO x JULES))// ((22-G-4 x GENTRY 21439) x (51052 x CORNELL 49-242))/ ((PORRILLO No. 1 x GENTRY 21439) x (51052 x CORNELL 49242) x (GENTRY No. 12307 x GARRAPATO))
6. RAO 33	Red	Small (24.4)	(((POMPADOUR CHECA x (G 03645 x G 02045)) x (G 03974 x G 04485))/(51052 x COPAN) = ((POMPADOUR CHECA x (JAMAPA x GENTRY 21439)) x (JIN 10 x TURRIALBA 1))/(51052 x COPAN)
7. LM 93204217	Black[c]	Small (21.2)	((PORRILLO SINTÉTICO x TURRIALBA 1) x (ICA PIJAO x NEGRO JAMAPA))// (((VERANIC 2 x TLALNEPANTLA 64)F1 x ((JAMAPA x TARA)F1x AETE 1/37)))/ (((IPA 7419 x (HONDURAS 46 x VENEZUELA 54))///((AROANA x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA))) // (G 4326/((S 166 AN x ECUADOR 299) x ((VERANIC 2 x TLALNEPANTLA 64) X (JAMAPA X TARA))))
8. TB 94-01	Black	Small (18.4)	(((IPA 7419 x (HONDURAS 46 x VENEZUELA 54))///(((AROANA x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA))) //G 4326/((S 166 AN x ECUADOR 299) x ((VERANIC 2 x TLALNEPANTLA 64) x(JAMAPA x TARA))))/ ((NEP 2 x ICA PIJAO) x F4(RIO TIBAGI^{*3} x CORNELL 49242))
9. AN 9021334	Black	Small (18.8)	SAME AS LR 9115398
10. AN 9021336	Black	Small (17.8)	SAME AS LR 9115398
11. LM 93204303	Cream-beige	Small (13.9)	(CARIOCA/RIO TIBAGI) / (((CARIOCA x ((PI 307824 x PI 310797) x (TURRIALBA 4 x CORNELL 49-242))/// (CARIOCA x MEX. 168)//((AETÉ 1/38 x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA)))/ ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA) x AETÉ 1/37)))
12. LM 93204319	Cream-beige	Small (17.0)	(CARIOCA/RIO TIBAGI) / ((51052 x CACAHUATE 72) x CARIOCA$^{*2)}$
13. LM 93204328	Cream-beige	Small (17.8)	SAME AS LM 93204319
14. LM 93204453	Cream-beige	Small (19.4)	(JALO EEP 558, CANARIO 101, BONITAS?)/ (((VERANIC 2 x CORNELL 49-242) x (PI 309796 x CACAHUATE 72)) x (PI 310814 x TURRIALBA 1)) x (CROSSES AMONG MULTIPLES PROGENITORS) x (JAMAPA x PI 310878)) x (AETÉ 1/38 x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA)))//(((CARIOCA x ((PI 307824 x PI 310797) x (TURRIALBA 4 x CORNELL 49-242)) /// (CARIOCA x MEX. 168)//(AETÉ 1/38 x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPAxTARA))) /((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA) x AETÉ 1/37)/((51052 x CACAHUATE 72) x CARIOCA^{*2})
15. AN 9021470	Brown	Small (18.8)	(IPA-7419 x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA)) x (MEX 168))/((IPA 7419 x (HONDURAS 46 x VENEZUELA 54))///(AROANA x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA))//G 4326 / ((S 166 AN x ECUADOR 299) x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA))))
16. LM 9220225	Brown	Small (18.9)	DRO 4784 / ((((VERANIC 2 x CORNELL 49-242) x (PI 309796 x CACAHUATE 72)) x (PI 310814 x TURRIALBA 1)) x (CROSSES AMONG MULTIPLES PROGENITORS) x (JAMAPA x PI 310878))) x (AETÉ 1/38 x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA)))
17. L 96029	Brown	Small (13.1)	(((VERANIC 2 x TLALNEPANTLA 64)F1 x (JAMAPA x TARA)F1) x AETE 1/37) / (LINEA 32 x TURRIALBA 1)
18. LM 93203246	Pink	Small (16.3)	ADVANCED MATERIAL RECEIBED FROM CIAT 1981/ ROSINHA G2 RMC
19. LM 93203304	Pink	Small (23.6)	HI822510?/ (((ICA 10310 x ((VERANIC 2 x TLALNEPANTLA 64) x (TURRIALBA 4 x CORNELL 49-242)) x ((S 166 AN x 51054) x ((VERANIC 2 x TLALNEPANTLA 64) x (JAMAPA x TARA))) // (ADVANCED MATERIAL RECEIBED FROM CIAT 1981/ ROSINHA G2 RM)
20. LR 93201684	Purple	Small (21.5)	CF (BEAN HARVEST) / ((POMPADOUR CHECA x ((JAMAPA x GENTRY 21439) x (JIN 10 x TURRIALBA 1))) x (51052 x COPAN))
21. PR 93201472	Manteigão	Medium (40.0)	POMPADOUR/IRAI

[a]BRT =Bean Regional Trial; [b]Lines 1 to 6 correspond to trial BRT 1995-96; [c]Lines 7 to 21 correspond to trial BRT 1997-98; [d]Size according to Singh et al., (1991a), weight of 100 seeds in grams.

Table 2 - General information on cultivars/lines involved in the breeding program to obtain the elite lines of the Bean Regional Trials coordinated by Embrapa Rice and Beans.

	CULTIVAR/ LINE	ELITE LINES - TABLE 1 (^{n}=total usage frequency of these cultivars/lines)	CULTIVAR/LINE ORIGIN	NOTE
1	51051	1^1, 3^1, 9^1, 10^1	Costa Rica	Rust differential[a]
2	51052	3^1,5^3, 6^1, 12^1, 14^1, 20^1	Costa Rica	Turrialba 4N[bd]
3	51054	19^1	Costa Rica	[b]
4	AETÉ 1/37	11^1, 14^1	Brazil	Parana - Brazil[b]
5	AETE 1/38	11^1, 14^2, 16^1	Brazil	[b]
6	AROANA	2^1, 4^1, 7^1, 8^1, 15^1	Brazil	Chumbinho 79 x Actopan (Mexico) (brown and small seed)[d]
7	BAT 477	3^1	Colombia (CIAT)	(51051 x ICA Bunsi) x (51052 x Cornell 49-242)
8	BRASIL 1096	1^1, 9^1, 10^1	Brazil	
9	BRASIL 343	1^1, 9^1, 10^1	Brazil	Brown seeds
10	CACAHUATE 72	2^1, 12^1, 13^1, 14^2, 16^1	Mexico (list of CIAT)	Seed yield high. Moderate resistance to bean rust and angular leaf spot. Resistant to bean common mosaic virus (single dominant I-gene). Inbred backcross (BC253) line from ICA Pijao/Puebla 152[c]
11	CACAHUATE 73	2^1	Mexico	Seed yield high. Moderate resistance to bean rust and angular leaf spot. Resistant to bean common mosaic virus (single dominant I-gene). Inbred backcross (BC253) line from ICA Pijao/Puebla 152[c]
12	CARIOCA	3^2, 5^3, 11^3, 12^2, 13^2, 14^3	Brazil (list of CIAT) (Central America?)[d]	Resistant to *Macrophomina phaseolina* (Mp) (Mayek-Perez et al., 1999)/ Race Middle American[c]
13	CARIOCA 80	3^1	Brazil (list of CIAT)	
14	CAUCA 41	1^1, 9^1, 10^1	Colombia	Negrito Chiquito - G 2515[bc]
15	COPAN	6^1, 20^1	Honduras	Mexico 80 x BAT 724[d]
16	CORNELL 49-242	3^1, 5^3, 8^1, 11^1, 14^2, 16^1, 19^1	Venezuela (Central America?)[d]	*I* and *bc-u* genes. Middle American (Vasconcelos, 1995). Anthracnose differential.
17	DRO 4784	2^1, 16^1	Colombia (CIAT)	
18	ECUADOR 299	7^1, 8^1, 15^1	Ecuador	Rust differential. Gene *Ur*-3. Resistant to Andean isolates[a]
19	G 4326	7^1, 8^1, 15^1	Mexico	Zacatecas (list of CIAT)
20	G 2084	1^1, 9^1, 10^1	Nicaragua	Gentry 21555 (list of CIAT)
21	G 2698	1^1, 9^1, 10^1	Venezuela	S-234 (Venezuela 23) (list of CIAT)
22	GARRAPATO	5^2	Mexico (list of CIAT)	BGMV resistance source (Urrea et al., 1996)
23	GENTRY 21439	6^1, 20^1	Guatemala	(list of CIAT)
24	GENTRY 12307	5^2	Mexico	PI203937. G 879[b]
25	GOIANO PRECOCE	4^1	Brazil	
26	HONDURAS 35	1^1, 9^1, 10^1	Honduras[d]	Middle American (Vasconcelos, 1995). Cultivar Ouro Negro.
27	HONDURAS 46	7^1, 8^1, 15^1	Honduras	Small dark and brilliant seeds[d]

Continue..

Table 2 - Continuation.

	CULTIVAR/ LINE	ELITE LINES - TABLE 1 (^{n}=total usage frequency of these cultivars/lines)	CULTIVAR/LINE ORIGIN	NOTE
28	ICA BUNSI	3^1	Colombia	Magdalena 8 x Japon 3[d]/ *I* and *bc-u* genes
29	ICA PIJAO	7^1, 8^1	Colombia	Porrillo Sintético x Mexico 11
30	ICA TUI	1^1, 3^1, 5^1 , 9^1, 10^1	Colombia[d]	Selection in Venezuela 44[d]/ *I* and *bc-u* genes[a]
31	IRAI	21^1	Brazil	
32	IPA 7419	7^1, 8^1, 15^2	Brazil	L 3-0-50 x Costa Rica
33	JAMAPA	2^3, 5^3, 6^1, 7^3, 8^2, 11^2, 14^4, 15^3, 16^2, 17^1, 19^1, 20^1	Mexico[d]	Mixture of 15 lines from Veracruz 87 collection/*I* and *bc-u* genes / Middle American (Singh et al., 1991a). Resistant to *Macrophomina phaseolina* (Mayek-Perez et al., 1999)/ Mesoamerica race (Singh et al., 1991a)
34	JIN 10	6^1, 20^1	Nicaragua	(list of CIAT)
35	JULES	3^1, 5^1	United States of America	GN Nebraska #1 sel. 27/GN 1140 (= to Tara)[b]
36	LINEA 32	17^1	Colombia (List of CIAT)	(PI 203958 x Red Mexican UI-35) x a curly top-resistant early short bush Dark Red Kidney type breeding line, DRK 801 x Sutter Pink. Mexican bean with effective level field resistant to fusarium root rot[c]
37	MEX. 168	3^2, 5^3, 11^1, 14^1, 15^1	Mexico	Rio Tibagi x Guanajuato 31 (Mesoamerica x Durango races)[c], Anthracnose resistance source[e]
38	NEGRO JAMAPA	7^1	Mexico	Gentry 21157 (list of CIAT)
39	NEP 2	8^1	Costa Rica	Rust differential resistant to Andean isolates[a]. Small white seed from cultivar San Fernando (S 182 N), selection from Turrialba through mutagenesis[d] / *I* and *bc-u* genes (Middle American)
40	NEP BAYO 22	2^1	Costa Rica	[d]
41	OJO DE LIEBRE	2^1	Mexico	[c](Gentry 22129, Gentry 22538)
42	PI 307824	11^1, 14^1	El Salvador	Porrillo 1c
43	PI 309796	14^1, 16^1	Mexico	Jalisco (Mex). Gentry 21149[bc]
44	PI 310797	11^1, 14^1	Guatemala	Huehuetenango (G)[bc]
45	PI 310814	14^1, 16^1	Nicaragua	Gentry 21556. Granada (N)[c]
46	PI 310878	2^1, 14^1, 16^1	Nicaragua	Rojo Claro[c]
47	POMPADOUR (CHECA)	6^1, 20^1	Dominican Republic	Andean, rust resistant (Bassett, 1996). Red and pink mottled median size seeds Selected from cultivar Pompadour[d]
48	POMPADOUR	21^1	Dominican Republic	[d]
49	PORRILLO No. 1	5^2	El Salvador	Selected from cultivar Santa Clara (Venezuela)[d]/ Middle American
50	PORRILLO SINTETICO	2^2, 3^1, 5^1	El Salvador	Selected from Porrillo 1[d]/*I* e *bc-u* genes/ Mesoamerica race[c]
51	RIO TIBAGI	8^1, 11^1, 12^1, 13^1	Costa Rica	Selected from cultivar S 89 N[d]/Mesoamerica race[c]
52	ROSINHA G2RMC	18^1, 19^1	Brazil	
53	S 166 AN	1^1, 7^1, 8^1, 9^1, 10^1, 15^1, 19^1	Costa Rica	[d]
54	SB 12	1^1, 9^1, 10^1	Zambia	Gandajika A 65. *Arachis hypogaea*[c]
55	TARA	2^2, 5^1, 7^2, 8^1, 11^2, 14^3, 15^3, 16^1, 17^1, 19^1	United States of America	GN Nebraska #1 Sel. 27/GN 1140 (= to Jules)[b]. Resistant to some pathotypes of *U. appendiculatus*. Tolerant to the bean common bacterial blight. Developed in Nebraska[c].
56	TLALNEPANTLA 64	2^2, 3^1 ,4^1 5^2, 7^3, 8^2, 11^2, 14^3, 15^3, 16^1, 17^1, 19^2	Mexico	Collected in 1943.PI 207.262, Mexico 56, G 1320[bc]
57	TURRIALBA 1	6^1, 7^1, 14^1, 16^1, 17^1, 19^1	Costa Rica	S 19 N - Centro American bulk selection[d]/*I* and *bc-u* genes
58	TURRIALBA 4	11^1, 14^1, 19^1	Costa Rica	Individual selection from Guatemala[d]/*I* and *bc-u* genes.
59	VENEZUELA 54	7^1, 8^1, 15^1	Venezuela	[c]
60	VERANIC 2	2^2, 5^1, 7^3, 8^2, 11^2, 14^4, 15^3, 16^2, 17^1, 19^2	Nicaragua	Selected from Jamapa (Mexico)[d]
61	XAN 87	1^1, 9^1, 10^1	Colombia (CIAT)	(BAT 450 x SEL 29)[d]

[a]Sandlin et al., 1999; [b]CIAT. http://webpc.ciat.cgiar.org:8080/urg/bean_search.jsp (04-07-02); [c]USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network - (GRIN). [Online Database] National Germplasm Resources Laboratory, Beltsville, Maryland. Available: www.ars-grin.gov/cgi-bin/npgs/html/acc_search.pl (02-07-02); [d]Voysest, 1983; [e] Balardin & Pastor Corrales, 1990.

Table 3 - Genetic distances among pairs of common bean elite cultivars from the Regional Trials coordinated by Embrapa Rice and Beans.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1. LR 9115398	0																				
2. LR 9115453	0.19	0.00																			
3. A 774	0.27	0.14	0.00																		
4. PR 9115957	0.27	0.16	0.24	0.00																	
5. FEB 163	0.31	0.20	0.14	0.29	0.00																
6. RAO 33	0.21	0.15	0.22	0.31	0.28	0.00															
7. RAO 34	0.23	0.10	0.11	0.13	0.17	0.17	0.00														
8. TB 94-01	0.15	0.10	0.10	0.19	0.16	0.15	0.07	0.00													
9. AN 9021334	0.06	0.20	0.29	0.29	0.27	0.23	0.24	0.16	0.00												
10. AN 9021336	0.06	0.20	0.29	0.29	0.27	0.23	0.24	0.16	0.00	0.00											
11. LM 93204303	0.19	0.15	0.12	0.11	0.15	0.24	0.12	0.08	0.15	0.15	0.00										
12. LM 93204319	0.19	0.07	0.07	0.16	0.13	0.12	0.03	0.03	0.20	0.20	0.08	0.00									
13. LM 93204328	0.15	0.10	0.10	0.13	0.16	0.15	0.07	0.06	0.16	0.16	0.04	0.03	0.00								
14. LM 93204453	0.19	0.13	0.14	0.16	0.20	0.12	0.10	0.10	0.20	0.20	0.08	0.07	0.03	0.00							
15. AN 9021470	0.21	0.10	0.17	0.13	0.16	0.23	0.13	0.13	0.16	0.16	0.07	0.10	0.06	0.10	0.00						
16. LM 9220225	0.16	0.10	0.19	0.20	0.17	0.20	0.14	0.13	0.10	0.10	0.08	0.10	0.07	0.10	0.07	0.00					
17. L 96029	0.23	0.10	0.11	0.20	0.10	0.17	0.07	0.07	0.17	0.17	0.08	0.03	0.07	0.10	0.07	0.07	0.00				
18. LM 93203246	0.20	0.21	0.29	0.24	0.15	0.31	0.25	0.24	0.21	0.21	0.17	0.21	0.18	0.21	0.18	0.13	0.19	0.00			
19. LM 93203304	0.19	0.07	0.14	0.23	0.13	0.15	0.10	0.10	0.20	0.20	0.15	0.07	0.10	0.13	0.16	0.10	0.10	0.15	0.00		
20. LR 93201684	0.24	0.19	0.28	0.14	0.33	0.22	0.15	0.21	0.26	0.26	0.13	0.19	0.14	0.19	0.21	0.15	0.23	0.27	0.19	0.00	
21. PR 93201472	0.88	0.87	0.93	0.68	0.87	0.92	0.86	0.87	0.87	0.87	0.79	0.87	0.81	0.80	0.74	0.86	0.86	0.76	0.87	0.85	0.00

The second group was formed by 17 lines, with different seed colors, originated from 50 parents, with a genetic distance between 0.03 and 0.33 between them (Figure 1). The smallest distance was observed between the cream beige seed lines LM 93204319 (12) and LM 93204328 (13), which have identical genealogies. The highest distance was observed between lines FEB 163 (5) and LR 93201684 (20). Despite the fact that lines LR 93201684 (20) and RAO 33 (6) have Andean cultivar 'Pompadour' as progenitor in their pedigrees, they do not form a separate group. Probably those lines have low percentage of Andean genes in concordance with the small size of their seeds. Almost all lines of groups I and II were originated in Central America and Caribbean (Mexico, Costa Rica, Dominican Republic and Nicaragua), and all have small seeds, characteristic of the Mesoamerican gene pool (Tables 1, 2 and 3).

A third group, was formed only by *manteigão* line PR 93201472 (21) derived from a cross between the Andean cultivar 'Pompadour' originated in the Dominican Republic (Voysest, 1983) and cultivar 'Irai', of unknown origin. These lines, with medium size seeds presented the highest genetic distances in relation to the other lines tested (0.68 and 0.93) (Tables 1, 2 and 3).

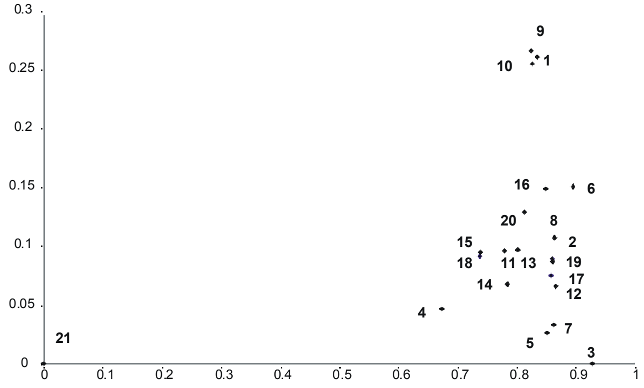

Figure 1- Graphic dispersion of the 21 common bean cultivars of the Bean Elite Regional Trials coordinated by Embrapa Rice and Beans.

The low genetic variability of the parents used in the original crosses and the frequent use of the same parents for the development of these cultivars may have been the cause of low genetic variability observed in this work.

For instance, the Mesoamerican cultivars/lines 'Jamapa', 'Carioca', 'Veranic 2' (selected from 'Jamapa'), 'Cornell 49-242', 'Tlalnepantla 64' (PI 207.262) and 'Tara' have been used for the development of most of the 17 lines in group II (Vasconcelos, 1995; Gepts et al., 1986; Koenig et al., 1990; Singh et al., 1991b; Voysest, 1983, 2000) (Tables 1 and 2). Voysest (2000) pointed out that Mesoamerican cultivars 'Jamapa' and 'Carioca', released in 1958 and 1966, respectively, are among the five cultivars most frequently grown in Latin America. Although these cultivars have been important because of their genetic stability and yield, their use as commercial cultivars and as parents in several breeding programs may have contributed for the reduction of the genetic variability of the new commercial cultivars in Brazil and other of Latin America countries. The cultivar/line 'Tara' and 'Tlalnepantla 64' (PI 207.262) are used as source of resistance to *Xanthomonas axonopodis* pv. *phaseoli*. The latter is also used as source of resistance for anthracnose. Cultivar 'Cornell 49-242' carries anthracnose and leaf spot resistance genes and is one of the 12 differential varieties used to classify pathotypes of the pathogens *Colletotrichum lindemuthianum* and *Phaeoisariopsis griseola* (Young & Kelly, 1996; Pastor-Corrales, 1992; Pastor-Corrales & Jara, 1995). Lines FEB 163, LM 93204303 and LM 93204453 have in common the same six gene donors described above. Lines TB 94-01, LM 9220225 and LM 93203304 have in their genealogies at least three of the above cultivars used as source of genes (Tables 1 and 2).

Although results show a low genetic variability among 17 bean lines (group II), derived from 50 cultivars (mostly Mesoamerican), there is no doubt that the Mesoamerican germplasm from different bean races (Mesoamerican, Durango and Jalisco) may contain important genetic variability to be incorporated into bean breeding programs. Indeed, Beebe et al. (2000) have demonstrated, by analyzing 269 Mesoamerican bean landraces, that this gene pool is an important source of genetic variability that remains to be explored.

Using 12 RAPD primers, the 21 lines could be classified into 3 groups, variation were detect in 17 lines of group II, duplicate lines were identified in groups I and II. This type of information is essential for germplasm conservation and improvement. Knowledge of the pedigree of a cultivar may be useful for the identification of sources of genes of interest and understand its role in genetic variability. However, the pedigree information is not always available for the breeder. In these cases, molecular markers can be used as an accurate tool to detect similarity/divergence and identificate duplicated bean lines or accessions among bean cultivars. Molecular analyses, in conjunction with morphological and agronomic evaluations of cultivars are recommended, because they provide complementary information and increase the resolving power of genetic diversity analysis (Singh, et al., 1991c).

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