

Coefficient of Parentage in *Coffea arabica* L. Cultivars Grown in Brazil

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ABSTRACT

The coefficient of parentage among 121 cultivars of *Coffea arabica* L. in Brazil released from 1939 to 2009 was estimated and used to study the genetic diversity and the breeding pattern of the breeding programs. A low genetic diversity was observed within the *C. arabica* cultivars of Brazil. The genetic base of 121 cultivars released in Brazil between 1939 and 2009 was defined by 13 ancestors. Seven ancestors contribute with 97.55% of the genetic base of *C. arabica* cultivars. Bourbon Vermelho contributed with 52.76% for the genetic pool of the *C. arabica* cultivars of Brazil followed by Sumatra (19.05%) and Híbrido de Timor (11.59%). Mundo Novo and Icatu Vermelho contributed with 87.65% for the genetic base of the *C. arabica* cultivars. It was calculated that 97.55% of the genetic base of the Brazilian *C. arabica* cultivars is derived from seven ancestors, indicating a narrow genetic base. Among the first progenies, Mundo Novo contributed with 69.39% of the genetic base of *C. arabica* cultivars in Brazil. The increase in the genetic diversity among *C. arabica* cultivars observed in recent decades is due to the introduction of parental lines with diverse genetic base. High genetic diversity was observed among cultivars released by Empresa de Pesquisa Agropecuária de Minas Gerais/Universidade Federal de Viçosa, Fundação Procafé, and Instituto Agronômico do Paraná. The 121 Brazilian cultivars were clustered into four groups based on coefficient of parentage. The distributions of genotypes over the cluster groups showed the effect of parental line contribution.

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Abbreviations: AFLP, amplified fragment length polymorphism; COP, coefficient of parentage; EPAMIG, Empresa de Pesquisa Agropecuária de Minas Gerais; IAPAR, Instituto Agronômico do Paraná; IAC, Instituto Agronômico de Campinas; MDS, multidimensional scaling; UFV, Universidade Federal de Viçosa.

IN BRAZIL the first coffee seed was introduced in 1727 in the north of Brazil and rapidly distributed all over the country in the direction of north to south (Eccardi and Sandal, 2003). The first *Coffea arabica* cultivar introduced in Brazil was Nacional (also called Típica). Subsequent introduction was done in various times. Bourbon Vermelho was introduced in 1852 from the Reunion Island and coffee Sumatra from the Island of Sumatra in 1896 (Carvalho, 1957; Bettencourt, 1968, 1973).

Currently Brazil is the major producer and exporter of coffee for the international coffee market. The two principal species

Published in Crop Sci. 53:1237–1247 (2013).

doi: 10.2135/cropsci2012.09.0541

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of coffee cultivated in Brazil are *C. arabica* and *Coffea canephora* Pierre ex A. Froehner. *Coffea arabica* occupied the large portion of the area planted in São Paulo, Minas Gerais, and Parana. *Coffea arabica* is a true allotetraploid species with chromosome number of $2n = 4x = 44$ (Clarindo and Carvalho, 2008) and autogamous with variable rate of outcrossing reach up to 15% (Carvalho, 1988).

The first organized coffee breeding program was started in 1927 by the Instituto Agronômico de Campinas (IAC), São Paulo. Currently the coffee breeding research is performed in Minas Gerais, Paraná, Bahia, and Espírito Santos states. Several coffee cultivars were released from these research institutes for commercial production at different times. However, these cultivars shared the same parental lines. After the outbreak of the leaf rust during the 1970s, Icatu and Híbrido de Timor, two interspecific crosses between *C. arabica* and *C. canephora*, were introduced into the breeding programs as source of resistance against leaf rust. These introductions contributed to spread the genetic base of new cultivars with leaf rust resistance. A detailed description about the breeding program in Brazil and principal coffee varieties were discussed by Carvalho and Fazuoli (1993).

The genetic diversity available in the global germplasm collection is higher than the genetic diversity explored in applied plant breeding. The reduction in genetic diversity is the potential problem in plant improvement programs and it will result in genetic vulnerability (Zhou et al., 2002). This problem is also evident in *C. arabica*, which has low genetic diversity among cultivars. In any breeding program diversifying the genetic base and increasing the number of cultivars released for production with different genetic background is vital since it helps to reduce losses due to diseases, pest outbreak, and other abiotic stresses.

The success of any breeding program depends on the complete knowledge and understanding of the genetic diversity of the available germplasm. For this reason the breeders try to study the genetic diversity among cultivars using different techniques within the base population to select parents for the crossing programs and revise their breeding program.

In many crops, the genetic improvement for yield generally resulted in loss of genetic diversity among the cultivars (Walsh, 1981). So to avoid the loss of genetic diversity within the cultivars it is important to understand the coefficient of parentage among cultivars and the base population since it gives a direction to choose the parentals for the next crossing programs. Genetic diversity study among plant populations or species also helps in planning of crosses for hybrid or homozygous cultivar development (Cox et al., 1985b). One of the methods used to understand the relationship between genotypes or cultivars within the base population and to study the genetic diversity is the use of the coefficient of parentage (COP), which explains

the genetic and parental relationship between every cultivar within the base population.

Coefficient of parentage between two cultivars is defined as the probability that a random allele in one cultivar is identical by descent to a random allele at the same locus in other cultivar (Kempthorne, 1957; Falconer and Mackay, 1996). So the understanding this situation within the base population will help to select more divergent parental lines to develop cultivars with high genetic variability. Different studies were conducted to study the genetic diversity in different crop species using COP. The genetic diversity study on sugarcane (*Saccharum officinarum* L.) based on amplified fragment length polymorphism (AFLP) molecular markers and COP showed high genetic correlation between AFLP genetic similarity and COP (COP = 0.42, $P < 0.001$) (Lima et al., 2002). Coefficient of parentage was also used to study the genetic diversity and understand the breeding pattern of breeding programs in soybean [*Glycine max* (L.) Merr.] (Gizlice et al., 1993, 1994, 1996; Cox et al., 1985a; Zhou et al., 2002; Cui et al., 2000), wheat (*Triticum aestivum* L.) (Cox et al., 1985b), and barley (*Hordeum vulgare* L.) (Graner et al., 1994).

Although this type of study is available in different crops, to our knowledge there is no comprehensive study about the parentage and the genetic base of the *C. arabica* cultivars released in Brazil from different coffee breeding programs. The use of small numbers of parental lines in the early stage of *C. arabica* breeding in Brazil (Carvalho 1957) and the frequent use of Bourbon Vermelho as recurrent parent may have contributed for the narrow genetic base of the *C. arabica* cultivars released in Brazil. Cooper et al. (2001) suggested that these two phenomena could contribute for narrow genetic base during the breeding program of any crop species. These problems may put a danger on the future of coffee production combined with the climate change that cause disease and pest outbreak as happened in 1970s due to coffee leaf rust (Carvalho and Fazuoli, 1993). However, this consequence can be averted by broadening the genetic base of the breeding population and cultivars in the field (Cooper et al., 2001). Therefore, to formulate the future breeding program of *C. arabica* studying the COP among cultivars and the breeding population will provide important information. This objective can be achieved when information about the genetic diversity of *C. arabica* cultivars released all over the country is available for the breeding programs of the country. Therefore, to obtain such information the study of COP among cultivars of *C. arabica* released in Brazil by different research institutes is a crucial step. The information generated from this work will help the coffee breeding centers in Brazil to revise their breeding strategy and designing the future coffee improvement program of the country.

Therefore, this work was done with the following objectives: (i) analyze the coefficient of parentage among

C. arabica cultivars and the ancestral lines, (ii) study the genetic diversity among cultivars, (iii) estimate the genetic contribution of each ancestral line for each cultivar, and (iv) study the breeding pattern of the breeding programs.

MATERIALS AND METHODS

Cultivars of *Coffea arabica* Studied

For this study a total of 121 cultivars of *Coffea arabica* and 23 ancestral lines were included (Table 1). The cultivars included in this study were released from 1939 to 2009 by IAC, Empresa de Pesquisa Agropecuária de Minas Gerais/Universidade Federal de Viçosa (EPAMIG/UFV), Fundação Procafé, and Instituto Agronômico do Paraná (IAPAR).

Data Analysis

Analysis I – Estimation of Coefficient of Parentage: Estimation of the Coefficient of Parentage between Brazilian Cultivars

The pedigree information of each cultivar was obtained from the research center that developed the cultivar, journal articles, and the Ministry of Agriculture. Parentage information was used to estimate the coefficient of parentage between cultivars. The COP between cultivars was estimated for all possible combinations among cultivars and ancestral lines included in this study. Coefficient of parentage between two individuals is defined as the probability that a random allele at a random locus in one individual is identical by descent to a random allele at the same locus in another individual (Malécot, 1969; Kempthorne,

Table 1. List of 23 ancestral lines and 121 cultivars of *Coffea arabica* L. released from 1939-2009 with pedigree and year of release.

No.	Research center†	Name of the variety	First parent	Second parent	Year of release
1	Ancestral	<i>Coffea canephora</i> tetraploid	–	–	
2	Ancestral	<i>Coffea mauritiana</i> Lam.	–	–	
3	Ancestral	Híbrido de Timor (CIFC 4106)	–	–	
4	Ancestral	Nacional	–	–	
5	Ancestral	Maragogipe	–	–	
6	Ancestral	Amarelo de botucatu	–	–	
7	Ancestral	Sumatra	–	–	
8	Ancestral	Villa Sarchi	–	–	
9	Ancestral	Mokka	–	–	
10	Ancestral	CIFC 832/1	–	–	
11	Ancestral	CIFC 832/2	–	–	
12	Ancestral	CIFC 2570	–	–	
13	Ancestral	UFV 445-46	–	–	
14	Ancestral	UFV 438-52	–	–	
15	Ancestral	UFV 442-34	–	–	
16	Ancestral	UFV 446-08	–	–	
17	Ancestral	CIFC 440-10	–	–	
18	Ancestral	Catimor UFV 353	–	–	
19	Ancestral	Catimor UFV 386	–	–	
20	Ancestral	Blue Mountain	–	–	
21	Ancestral	<i>Coffea racemosa</i> Lour.	–	–	
22	Ancestral	Sarchimor IAC 1668	–	–	
23	Ancestral	Catindu (UFV 374 '643')	–	–	
1	IAC	Bourbon Vermelho	Típica	–	1939
2	IAC	Bourbon Vermelho IAC 662	Bourbon Vermelho	–	1939
3	IAC	Bourbon Amarelo	Bourbon Vermelho	Amarelo de Botucatu	1952
4	IAC	Bourbon Amarelo IAC J10	Bourbon Vermelho	Amarelo de Botucatu	1952
5	IAC	Bourbon Amarelo IAC J19	Bourbon Vermelho	Amarelo de Botucatu	1952
6	IAC	Bourbon Amarelo IAC J2	Bourbon Vermelho	Amarelo de Botucatu	1952
7	IAC	Bourbon Amarelo IAC J20	Bourbon Vermelho	Amarelo de Botucatu	1952
8	IAC	Bourbon Amarelo IAC J22	Bourbon Vermelho	Amarelo de Botucatu	1952
9	IAC	Bourbon Amarelo IAC J24	Bourbon Vermelho	Amarelo de Botucatu	1952
10	IAC	Bourbon Amarelo IAC J9	Bourbon Vermelho	Amarelo de Botucatu	1952
11	IAC	Ibairi IAC 4061	Bourbon Vermelho	Mokka	1999
12	IAC	Mundo Novo	Sumatra	Bourbon Vermelho	1977
13	IAC	Mundo Novo 515-20	Sumatra	Bourbon Vermelho	1977
14	IAC	Mundo Novo 374-19	Sumatra	Bourbon Vermelho	1977
15	IAC	Mundo Novo IAC 376-4	Sumatra	Bourbon Vermelho	1977
16	IAC	Mundo Novo IAC 379-19	Sumatra	Bourbon Vermelho	1977

(cont'd)

Table 1. Continued.

No.	Research center [†]	Name of the variety	First parent	Second parent	Year of release
17	IAC	Mundo Novo IAC 382-14	Sumatra	Bourbon Vermelho	1977
18	IAC	Mundo Novo IAC 388-17	Sumatra	Bourbon Vermelho	1977
19	IAC	Mundo Novo IAC 388-17-1	Sumatra	Bourbon Vermelho	1977
20	IAC	Mundo Novo IAC 388-6	Sumatra	Bourbon Vermelho	1977
21	IAC	Mundo Novo IAC 464-12	Sumatra	Bourbon Vermelho	1977
22	IAC	Mundo Novo IAC 467-11	Sumatra	Bourbon Vermelho	1977
23	IAC	Mundo Novo IAC 480-6	Sumatra	Bourbon Vermelho	1977
24	IAC	Mundo Novo IAC 501-5	Sumatra	Bourbon Vermelho	1977
25	IAC	Mundo Novo IAC 502-1	Sumatra	Bourbon Vermelho	1977
26	IAC	Mundo Novo IAC 515-11	Sumatra	Bourbon Vermelho	1977
27	IAC	Icatu Vermelho	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
28	IAC	Icatu Vermelho IAC 2941	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
29	IAC	Icatu Vermelho IAC 2942	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
30	IAC	Icatu Vermelho IAC 2945	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
31	IAC	Icatu Vermelho IAC 4040	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
32	IAC	Icatu Vermelho IAC 4041	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
33	IAC	Icatu Vermelho IAC 4043	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
34	IAC	Icatu Vermelho IAC 4045	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
35	IAC	Icatu Vermelho IAC 4046	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
36	IAC	Icatu Vermelho IAC 4228	<i>C. canephora</i> tetraploid	Bourbon Vermelho	1992
37	IAC	Caturra Vermelho (IAC 477)	Bourbon Vermelho	–	1951
38	IAC	Obatã: IAC 1669-20-F2	Villa Sarchi	Híbrido de Timor CIFC 832/2	1996
39	IAC	Tupi: IAC 1669-33	Villa Sarchi	Híbrido de Timor CIFC 832/2	1996
40	IAC	Laurina IAC 870	<i>C. arabica</i>	<i>C. mauritiana</i>	1999
41	IAC	Acaiá IAC 474	Mundo Novo	–	1977
42	IAC	Acaiá IAC 474-1	Mundo Novo	–	1977
43	IAC	Acaiá IAC 474-19	Mundo Novo	–	1977
44	IAC	Acaiá IAC 474-20	Mundo Novo	–	1977
45	IAC	Acaiá IAC 474-4	Mundo Novo	–	1977
46	IAC	Acaiá IAC 474-6	Mundo Novo	–	1977
47	IAC	Acaiá IAC 474-7	Mundo Novo	–	1977
48	IAC	Mundo Novo Amarelo IAC 4266	Bourbon Amarelo	Mundo Novo	1951
49	IAC	Caturra Amarelo IAC 476	Caturra Vermelho	–	1951
50	IAC	Caturra Amarelo IAC 476-11	Caturra Vermelho	–	1951
51	IAC	Catuai Vermelho	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
52	IAC	Catuai Vermelho IAC 144	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
53	IAC	Catuai Vermelho IAC 15	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
54	IAC	Catuai Vermelho IAC 24	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
55	IAC	Catuai Vermelho IAC 44	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
56	IAC	Catuai Vermelho IAC 51	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
57	IAC	Catuai Vermelho IAC 72	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
58	IAC	Catuai Vermelho IAC 81	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
59	IAC	Catuai Vermelho IAC 99	Caturra Amarelo, IAC 476-11	Mundo Novo IAC 374-19	1972
60	IAC	Catuai Amarelo	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
61	IAC	Catuai Amarelo IAC 100	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
62	IAC	Catuai Amarelo IAC 17	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
63	IAC	Catuai Amarelo IAC 32	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
64	IAC	Catuai Amarelo IAC 39	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
65	IAC	Catuai Amarelo IAC 47	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
66	IAC	Catuai Amarelo IAC 62	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
67	IAC	Catuai Amarelo IAC 74	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
68	IAC	Catuai Amarelo IAC 86	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
69	IAC	Catuai Amarelo IAC 30	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972
70	IAC	Catuai Amarelo IAC 70	Caturra Amarelo IAC 476-11	Mundo Novo IAC 374-19	1972

(cont'd)

Table 1. Continued.

No.	Research center [†]	Name of the variety	First parent	Second parent	Year of release
71	IAC	Ouro Verde IAC H5010-5	Catuai Amarelo IAC 70	Mundo Novo IAC 515-20	2000
72	IAC	Ouro Bronze IAC 4925	Catuai Amarelo IAC 70	Mundo Novo IAC 515-20	2000
73	IAC	Ouro Verde Amarelo IAC 4397	Catuai Amarelo IAC 70	Mundo Novo IAC 515-20	2000
74	IAC	Icatu Amarelo	Bourbon amarelo	Icatu Vermelho	1992
75	IAC	Icatu Amarelo IAC 2907	Bourbon amarelo	Icatu Vermelho	1992
76	IAC	Icatu Amarelo IAC 2944	Bourbon amarelo	Icatu Vermelho	1992
77	IAC	Icatu Amarelo IAC 3686	Bourbon amarelo	Icatu Vermelho	1992
78	IAC	Icatu Precoce: IAC 3282	Bourbon amarelo	Icatu Vermelho	1992
79	IAC	Catuai Amarelo *F6	Icatu	Catuai	2000
80	IAC	Catuai Amarelo 2SL	Icatu	Catuai	2000
81	IAC	Catuai Amarelo 3SM	Icatu	Catuai	2000
82	IAC	Catuai Amarelo Multilínea F5	Icatu	Catuai	2000
83	IAC	Catuai Vermelho	Icatu	Catuai	2000
84	IAC	Catuai Vermelho 19/8	Icatu	Catuai	2000
85	IAC	Catuai Vermelho 20/15	Icatu	Catuai	2000
86	IAC	Catuai Vermelho 24/137	Icatu	Catuai	2000
87	IAC	Catuai Vermelho 36/6	Icatu	Catuai	2000
88	IAC	Catuai Vermelho MultilíneaF5	Icatu	Catuai	2000
89	IAC	Obatã amarelo IAC 4739	Obatã IAC 1669-20	Catuai Amarelo	1996
90	IAC	Tupi amarelo IAC 5167	Tupi IAC 1669-33,	Catuai Amarelo	1996
91	EPAMIG/UFV	Tupi RN IAC 1669-13	Villa Sarchi	Híbrido de Timor	1996
92	EPAMIG/UFV	Oeiras MG 6850	Caturra Vermelho (CIFC 19/1)	Híbrido de Timor CIFC 832/1	1999
93	EPAMIG/UFV	Pau Brasil MG1	Catuai Vermelho IAC 141	Híbrido de Timor UFV 442-34	2004
94	EPAMIG/UFV	Sacramento MG1	Catuai Vermelho IAC 81	Híbrido de Timor UFV 438-52	2004
95	EPAMIG/UFV	Paraíso MG 1	Catuai Amarelo IAC 30	Híbrido de Timor UFV 445-46	2002
96	EPAMIG/UFV	Araponga MG1	Catuai Amarelo IAC 86	Híbrido de Timor UFV 446-08	2004
97	EPAMIG/UFV	Catiguá MG1	Catuai Amarelo IAC 86	Híbrido de Timor UFV 440-10	2004
98	EPAMIG/UFV	Catiguá MG2	Catuai Amarelo IAC 86	Híbrido de Timor UFV 440-10	2004
99	EPAMIG/UFV	Catiguá MGS3	Catuai Amarelo IAC 86	Híbrido de Timor UFV 440-10	2007
100	EPAMIG/UFV	Acaia Cerrado MG 1474	Mundo Novo	–	1989
101	EPAMIG/UFV	Rubi MG 1192	Catuai	Mundo Novo	1985
102	EPAMIG/UFV	Topázio MG 1190	Catuai Amarelo	Mundo Novo,	1988
103	IAPAR	IAPAR 59	Villa Sarchi CIFC 971/10	Híbrido de Timor CIFC 832/2	1992
104	IAPAR	IPR 97	Villa Sarchi CIFC 971/10	Híbrido de Timor CIFC 832/2	2001
105	IAPAR	IPR 98	Villa Sarchi CIFC 971/10	Híbrido de Timor CIFC 832/2	2001
106	IAPAR	IPR 99	Villa Sarchi CIFC 971/10	Híbrido de Timor CIFC 832/2	2001
107	IAPAR	IPR 104	Villa Sarchi CIFC 971/10	Híbrido de Timor CIFC 832/2	2001
108	IAPAR	IPR 102	Catuai	Icatu	2001
109	IAPAR	IPR 103	Catuai	Icatu	2001
110	IAPAR	IPR 105	Mundo Novo 374-19	Caturra Amarelo IAC 476-11	2001
111	IAPAR	IPR 106	Catuai	Icatu	2001
112	IAPAR	IPR 107	IAPAR 59	Mundo Novo IAC 376-4	2001
113	IAPAR	IPR 108	IAPAR 59	Catuai	2001
114	Procafé	IBC-Palma 1	Catuai Vermelho IAC 81	Catimor UFV 353	2000
115	Procafé	IBC-Palma 2	Catuai Vermelho IAC 81	Catimor UFV 353	2000
116	Procafé	Sabiá	Catimor UFV 386	Acaia	2000
117	Procafé	Canário	Catuai amarelo	Híbrido de Timor	2000
118	Procafé	Siriema	<i>C. racemosa</i>	<i>C. arabica</i> Blue Mountain	2000
119	Procafé	Saira	Catuai Amarelo IAC	Catindu (UFV 374, '643'),	2004
120	Procafé	Acauã	Mundo Novo IAC 388-17	Sarchimor IAC 1668	2000
121	Procafé	Travessia	Catuai Amarelo	Mundo Novo	2009

[†]IAC, Instituto de Agrônomo Campinas; EPAMIG, Empresa de Pesquisa Agropecuária de Minas Gerais; UFV, Universidade Federal de Viçosa; IAPAR, Instituto Agrônomo do Paraná; Procafé, Fundação Procafé.

1957). Coefficient of parentage values were computed by the formula $COP_{XY} = 1/2(pCOP_{XA} + qCOP_{XB})$, in which Y is a genotype, A and B are the parents of Y , X is a second genotype that is not a descendent of genotype Y , and p and q were the percentage contribution of A and B to Y (Kempthorne, 1957; Zhou et al., 2002).

During the estimation of the coefficient of parentage the following assumptions were considered in case when it is necessary.

- The assumption adapted from Cox et al. (1985a) was considered here during estimation of the COP. When the cultivars are developed from an introduced selection, the value of COP between the cultivar and the ancestor and direct selection from that ancestor or introduction is 0.75. The value COP between two selections from the same ancestors or introductions is $(0.75)^2 = 0.56$
- If the genotype P and Q are derived from different crosses, the coefficient of parentage between P and Q is unaffected by inbreeding.
- If the progenitors of the genotype Z are unknown, then set F_Z to 1 for self-fertilizing crops and to 0 for outcrossing crops.
- If the number of self-generation is unknown for a breeding line, set F_Z to 0.9375 equivalent to F_4 generation.
- If P and Q are sister lines, their coefficient of parentage is affected by selfing up to their most recent common ancestor Z and $COP_{PQ} = (1 + F_Z)/2$.

After estimating the coefficient of parentage between cultivars and parental lines, the following analysis was done to explain the general trend of COP.

Estimation of Coefficient of Parentage among Year of Release

To analyze the consequence of the breeding program on the diversity of cultivars released along the years, the cultivars were grouped according to their year of release: 1939 to 1959, 1960 to 1979, 1980 to 1999, and 2000 to 2009. The mean coefficient of parentage among year of release was estimated based on the method elaborated by Gizlice et al. (1996).

Estimation of Coefficient of Parentage among Research Institute

The cultivars were grouped based on the research institute released for production. So the cultivars grouped in four groups as cultivars from IAC, cultivars from EPAMIG/UFV, cultivars from Fundação Procafé, and cultivars from IAPAR. The COP mean was estimated in the same way as indicated above.

Analysis II – Multidimensional Scaling Analysis and Cluster Analysis

The approach used here is similar to that described by Gizlice et al. (1996). The first step in the analysis was to generate a set of Euclidean coordinates for each cultivar by multidimensional scaling (MDS) (SAS Institute, 2007). Based on the stress value, which measures the extent of which the geometrical representation falls short of a perfect match with the original COP matrix (Johnson and Wichern, 1992; Kruskal, 1964), the number of

dimensions was determined. The R^2 was calculated from the comparison of input COP data with predicted values derived from the MDS coordinates. The options used in MDS analysis (SIMILAR = 1, COEF = IDENTITY, and LEVEL = ABSOLUTE) are the same as those described by (Gizlice et al., 1996).

The nonhierarchical cluster analysis among the cultivars investigated in this study was done using FASTCLUS procedure of SAS statistical package using the MDS Euclidean coordinates as source data (SAS Institute, 2007). The PROC MEAN procedure was used to calculate mean COP within and among clusters for each analysis. The principal coordinate analysis using 1 – COP as distance was done using GENALEX 6.2 (Peakall and Smouse, 2006) to understand the graphic dispersion of the cultivars released by different research center and the ancestral lines.

Analysis III – Estimation of the Genetic Contribution

The relative contribution of each ancestor and the first progenies to the cultivars of *C. arabica* were estimated according to the method elaborated by Gizlice et al. (1994).

Estimation of the Genetic Contribution for Ancestor Lines

The method described by Gizlice et al. (1994) was used to estimate the genetic contribution of the ancestor lines. According to the method to estimate the genetic contribution of the ancestors, the COP among the ancestors was considered zero so that the COP could be used directly to estimate the contribution of the gene base.

Estimation of the Genetic Contribution for First Progenies

To estimate the genetic contribution of the first progeny, the COP between the ancestors and the first progenies was considered zero so that the COP was used to estimate directly the genetic contribution of each first progeny. The first progeny was defined as cultivars and breeding lines for which there were no available intermediates between them and at least one of the ancestors.

RESULTS

Genetic Diversity Study

The coefficient of parentage estimated ranged from 0 to 0.97. The mean COP estimated was 0.607, which is very high. This estimated COP was the base for all analysis and results presented in this work.

Genetic Diversity among Cultivars Released in Different Time of Period

A total of 121 cultivars of *C. arabica* was released from 1939 to 2009. Among these cultivars, 53.71% were released after 1980 (Table 2). The genetic diversity among cultivars of *C. arabica* increased for those cultivars released after 1980 (Table 2). The mean COP increased from 0.839 (before 1959) to 0.902 (in 1960–1970). After this period the mean COP reduced substantially for the last four decades with minimum value of 0.463, which indicated

Table 2. Coefficient of parentage means of the Brazilian *Coffea arabica* L. cultivars within and between year of released.

Year of release	Up to 1959	1960–1979	1980–1999	2000–2009
Ate 1959	0.839			
1960–1979	0.825	0.902		
1980–1999	0.536	0.55	0.507	
2000–2009	0.560	0.601	0.450	0.463
Number of cultivars released	17	42	27	38

Table 3. The mean coefficient of parentage of the Brazilian *Coffea arabica* L. cultivars within and among research institutes.

Research center†	IAC	EPAMIG/UFV	Fundação Procafé	IAPAR
IAC	0.719			
EPAMIG/UFV	0.519	0.468		
Fundação Procafé	0.573	0.419	0.514	
IAPAR	0.513	0.436	0.437	0.435
Number of cultivars	90	12	8	11

†IAC, Instituto de Agrônomo Campinas; EPAMIG, Empresa de Pesquisa Agropecuária de Minas Gerais; UFV, Universidade Federal de Viçosa; IAPAR, Instituto Agrônomo do Paraná.

the introduction of new parental lines in the breeding programs such as Híbrido de Timor and Icatu.

Genetic Diversity among Cultivars Released by Different Research Centers

Among the 121 *C. arabica* cultivars released from 1939 to 2009 in Brazil, 74.38% (90) were released by the IAC (Table 1). The mean COP among research centers indicated high mean COP within cultivars released by IAC. The mean COP among cultivars from other research institutes showed low mean value in relation to IAC. The lowest mean COP was recorded among *C. arabica* cultivars released by IAPAR, which is 0.435, followed by EPAMIG/UFV (Table 3).

Multivariate and Cluster Analysis

The analysis PROC MDS of SAS (SAS Institute, 2007) with 20 dimensions produced an excellent Euclidian representation of the COP matrix with $R^2 = 0.99$ and stress = 0.02 (Kruskal, 1964). The 20 dimensional coordinates from the MDS analysis was used to produce the best cluster groups using the FASTCLUS analysis. The cluster group ranging from 4 to 12 was used to select the best cluster group, and the acceptable cluster group was selected based on the criteria

Table 4. The mean coefficient of parentage between clusters formed based on coefficient of parentage among 121 varieties of *Coffea arabica* cultivars.

Cluster	I	II	III	IV	V
I	0.822				
II	0.565	0.703			
III	0.376	0.257	0.437		
IV	0.442	0.314	0.375	0.436	
V	0.182	0.123	0.094	0.187	0.00
No.	74	27	7	10	3

set by Gizlice et al. (1996), Cui et al. (2000), and Zhou et al. (2002). Based on the cluster analysis using MDS coordinates, four acceptable clusters were formed out of seven clusters obtained. Three clusters were considered unacceptable because they have just one member in each cluster. The first and the second cluster had the highest mean COP 0.822 and 0.703, respectively, which indicated that the groups had the same genetic base (Tables 4 and 5). For the cluster I the two ancestors Bourbon Vermelho and Sumatra contributed with more than 90% of the genetic base (Table 5). To see the distribution of the cultivars in two dimensional plots, the principal coordinate analysis was performed based on 1 – COP. The two-dimensional graph was constructed from 1 – COP using GENALEX 6.2 software (Peakall and Smouse, 2006) (Fig. 1). The graphic presentation of the clusters was done based on the mean COP data among clusters (Table 4) using STATISTICA software (StatSoft, Inc., 2004) (Fig. 2).

Genetic Contribution of Ancestor Lines and the First Progeny

Genetic Contribution of Ancestor Lines for the Brazilian *Coffea arabica* Cultivars

The genetic base of 121 cultivars released in Brazil between 1939 and 2009 was defined by 13 ancestors. The contribution of the ancestors for the genetic base of *C. arabica* in Brazil ranged from 0.408 to 52.76% (Table 6). The seven ancestors, Bourbon Vermelho, Sumatra, Híbrido de Timor, Amarelo de botucatu, Villa Sarchi, *C. canephora* tetraploid, and Catimor, contribute 97.55% to the genetic base of *C. arabica* cultivars in Brazil. This indicates the low genetic diversity among the released *C. arabica* cultivars. The analysis of genetic contribution of the principal ancestors to the cultivars of *C. arabica* showed that Bourbon Vermelho contributed 52.76% for the genetic pool followed by Sumatra (19.05%) and Híbrido de Timor (11.58%).

Table 5. The three most important ancestors and their relative genetic contribution (GC) to four nonhierarchical clusters of Brazilian *Coffea arabica* cultivars.

Cluster	Ancestor name	% GC	Ancestor name	% GC	Ancestor name	% GC
I	Bourbon Vermelho	63.18	Sumatra	31.30	Amarelo Botucatu	6.45
II	Bourbon Vermelho	71.05	<i>Coffea canephora</i> tetraploid	21.45	Sumatra	7.49
III	Híbrido de Timor	42.85	Villa Sarchi	57.14		
IV	Bourbon Vermelho	47.88	Híbrido de Timor	52.12		

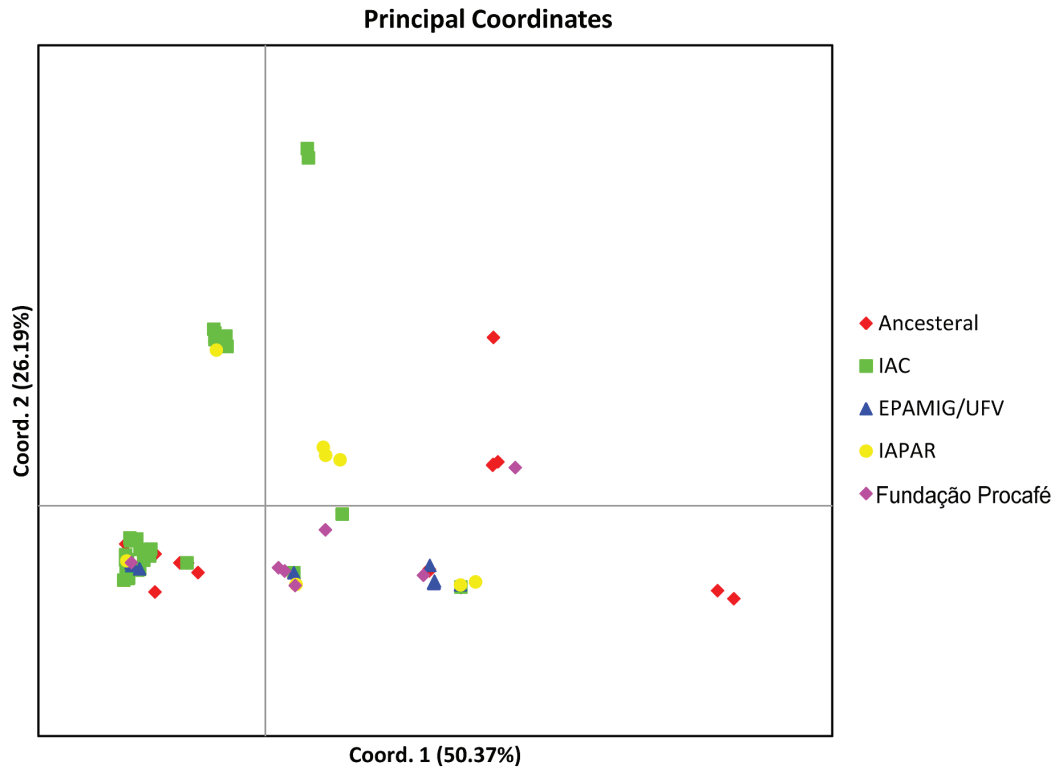


Figure 1. Plot of 121 cultivars of *C. arabica* released from 1939 to 2009 by different research centers in Brazil [Instituto Agronômico de Campinas (IAC), Empresa de Pesquisa Agropecuária de Minas Gerais/Universidade Federal de Viçosa (EPAMIG/UFV), Fundação Procafé, and Instituto Agronômico do Paraná (IAPAR)] and ancestral lines using principal coordinate analysis using the 1 – coefficient of parentage among varieties using the software GENALEX 6.2 (Peakall and Smouse, 2006). Coord., coordinate.

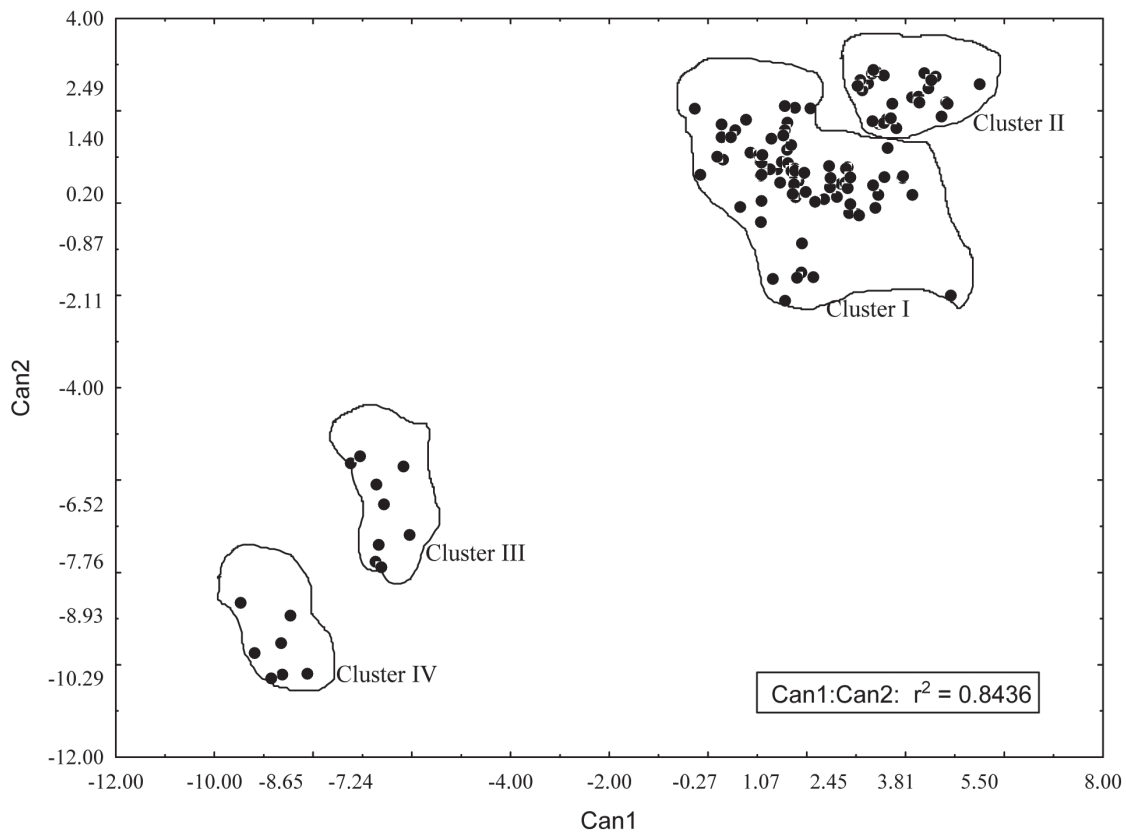


Figure 2. Plot of four cluster representing 121 cultivars of *C. arabica* released in Brazil from 1939 to 2009. The score was obtained by averaging multidimensional scaling. The complement of the linear distance (1 – distance) between any two cultivars estimates the coefficient of parentage between them. Distance ≥ 1 indicate no relationship.

Table 6. Relative genetic contribution of the ancestor lines for the 121 cultivars of *Coffea arabica* released in Brazil from 1939 until 2009 and their first progenies.

No.	Name of ancestor	%	Accumulative	Contribution
				The first progeny
1	Bourbon Vermelho	52.76	52.76	Bourbon Amarelo, Ibairi 4061, Mundo Novo, Caturra Vermelho, and Icatu Vermelho
2	Sumatra	19.05	71.81	Mundo Novo
3	Híbrido de Timor	11.59	83.40	Obatã, Tupi, Tupi-RN, IAPA 59, Pau Brasil, Sacramento, Paraíso, Araponga, Catiguá MG1, Catiguá MG2, Catiguá MG3, Canário, IPR 98, IPR 99, and IPR 104
4	Amarelo de botucatu	4.49	87.89	Bourbon Amarelo
5	Villa Sarchi	4.09	91.98	Obatã, Tupi, Tupi-RN, IAPAR 59, IPR 98, IPR 99, and IPR 104
6	<i>Coffea canephora</i> tetraploid	3.52	95.50	Icatu Vermelho
7	Catimor	2.04	97.55	IBC-Palma I, IBC-Palma II, and Sabia Tardio
8	<i>Coffea mauritiana</i>	0.41	97.96	Laurina IAC 870
9	Mokka	0.41	98.36	Ibairi IAC 4061
10	Blue Mountain	0.41	98.77	Siriema
11	<i>Coffea racemosa</i>	0.41	99.18	Siriema
12	Sarchimor IAC 1668	0.41	99.59	Saíra
13	Catindu	0.41	100	Saíra

Table 7. Relative genetic contribution of the first progenies for the cultivars of *Coffea arabica* L. released from 1939 until 2009.

No.	Cultivar name	Contribution in %	
		Individual	Accumulated
1	Mundo Novo	69.38	69.38
2	Icatu Vermelho	18.27	87.65
3	Bourbon Amarelo	5.92	93.58
4	IAPAR 59	1.97	95.55
5	IPR 104	1.48	97.04
6	Caturra Vermelho IAC 477	0.99	98.02
7	Obatã IAC 1669-20	0.99	99.01
8	Tupi IAC 1669-33	0.99	100
Total		100	

Genetic Contribution of the First Progenies for the Brazilian *Coffea arabica* Cultivars

The relative contribution of the first progenies for the coffee cultivars released in Brazil showed that Mundo Novo and Icatu Vermelho contributed with 69.38 and 18.27% for the genetic base of the cultivars in Brazil, respectively (Table 7). Mundo Novo is the first progeny of Bourbon Vermelho, which contributed 69.38% for the genetic pool of cultivars. Mundo Novo and Icatu Vermelho contributed 87.65% for the genetic base of the *C. arabica* cultivars released in Brazil (Table 7). The genetic contribution of first progenies to the gene pool of *C. arabica* ranged from 0.99 up to 69.38%.

DISCUSSION

Genetic Diversity Study

Genetic Diversity among Cultivars Released in Different Time of Period

The genetic diversity among Brazilian *C. arabica* cultivars increased in recent decades (Table 2). The increase in genetic diversity among cultivars was accompanied with the introduction of new parental lines in the breeding

programs for the cultivars developed after 1980. The high mean COP among cultivars released before 1959 (0.839) and 1960 to 1979 (0.902) (Table 2) is due to small number of parental lines involved in the development of cultivars during these period and the cultivars shared the same parental lines, which was explained by the high mean COP (Table 2). The low mean COP (0.463) (Table 2) for the cultivars released after 2000 showed the involvement of different parental lines in the development of cultivars, which diversify the genetic base of the *C. arabica* cultivars released during this period. This fact consequently increased the genetic diversity among *C. arabica* cultivars. Even if a lot of work is done to diversify the genetic base of *C. arabica* cultivars in Brazil still the mean COP value among cultivars is very high when compared with other crops such as soybean (Cox et al., 1985a; Gizlice et al., 1993; Cui et al., 2000; Zhou et al., 2002), barley (Graner et al., 1994), and bread wheat (Cox et al., 1985b).

Genetic Diversity among Cultivars Released by Different Research Centers

Among the research institutes involved in coffee breeding, IAC is the oldest one and it is a prominent research institute well known for its research work especially on *C. arabica*. Instituto Agrônomo de Campinas released 74.34% of the cultivars of *C. arabica* in Brazil. The highest mean COP was recorded from the cultivars released by IAC (0.719) (Table 3), which indicated the low genetic diversity among cultivars released by them. The basic reason for the high mean COP is because most of the cultivars of *C. arabica* released by IAC are sister lines as shown in Table 1 (cultivars Mundo Novo, Catuaí, and Bourbon Vermelho) that have the same genetic composition. Other research institutes (EPAMIG/UFV, Fundação Procafé, and IAPAR) released cultivars with different genetic background resulting in low mean COP (Table 3). Among the research institutes IAPAR recorded the lowest mean COP

(0.435) (Table 3), showing the higher genetic diversity among cultivars released by the center. The lower mean COP value presented by IAPAR, EPAMIG/UFV, and Fundação Procafé when compared by the IAC showed the possibility of increasing the genetic diversity among cultivars of *C. arabica*. The highest value of mean COP among research institutes (Table 3) indicated the existence of high germplasm exchange among them. This section also demonstrated the possibility of increasing the genetic diversity among cultivars released without losing the productivity and the quality since most of the *C. arabica* cultivars released in recent years showed high cup quality and productivity. The study of genetic diversity among the accessions of *C. arabica* from Ethiopia, Eritria, Yemen, and Brazil found in germplasm bank of IAC showed the availability of high genetic variability that can be exploited in the future breeding program of coffee in Brazil (Silvestrini et al., 2007). This research result showed the potential of the germplasm collection existed in Brazil for development of new cultivars with diverse genetic base.

Multivariate and Cluster Analysis

The cluster analysis performed based on the 20 dimensional scales produced by PROC MDS (SAS Institute, 2007) perfectly classified the 121 cultivars in each respective groups. These cultivars released by IAC grouped in cluster I and cluster II. These two clusters showed low genetic diversity, which was explained by high mean COP within clusters (0.822 and 0.703, respectively) (Table 4). The low genetic diversity observed in cluster I and cluster II can be explained by the analysis of the genetic contribution of ancestors for the cluster. The analysis of the genetic contribution of the parental lines (ancestors) showed that Bourbon Vermelho contributed with 63.18 and 71.05% for the genetic base of cluster I and cluster II, respectively (Table 5). High mean COP between this clusters showed genetic similarity of the cultivars between cluster I and cluster II. Most of the cultivars grouped in cluster I and cluster II were developed by IAC. The low mean COP in cluster III and cluster IV showed the existence of higher genetic diversity within cultivars. The high genetic diversity between cultivars in cluster III and cluster IV was the result of incorporation of new parental lines in the breeding programs. The cultivars developed by these research institutes were grouped in cluster III and cluster IV. The cluster analysis showed a clear breeding pattern of *C. arabica* in Brazil in relation to breeding programs.

In addition, the use of COP to study the genetic diversity among cultivars in *C. arabica* is a valuable tool for breeders to understand the current situation of their cultivars and plan a better breeding program to increase the genetic diversity of the cultivars that will be released in the future. Understanding the real breeding pattern of cultivars also helps to incorporate new parental lines to diversify the genetic base of future cultivars.

Genetic Contribution of Ancestors and First Progenies

Genetic Contribution of Ancestors for the Brazilian *Coffea arabica* Cultivars

A percentage of 97.55 of the genetic base of the Brazilian *C. arabica* cultivars is constituted by seven ancestors as indicated by the narrow genetic base of the cultivars (Table 6). Bourbon Vermelho, which contributed with 52.76% for the genetic base, was involved in most of the crossing programs since it was considered productive and with good cup quality (Carvalho, 1957; Carvalho and Fazuoli, 1993). This resulted in the low genetic diversity among *C. arabica* cultivars released in Brazil. To reverse this situation and increase the genetic base of the cultivars in coffee, introducing of new ancestor lines will be crucial. The introduction of Híbrido de Timor, which is an interspecific hybrid between *C. arabica* and *C. canephora* var. *robusta* L. Linden, played an important role to diversify the genetic base in *C. arabica* cultivars in Brazil. Híbrido de Timor was involved in several crossing programs to develop new cultivars of *C. arabica* after it was confirmed to have resistance genes to coffee leaf rust (*Hemileia vastatrix*). For this reason most of the *C. arabica* cultivars released in recent years contain Híbrido de Timor in their genetic background. So Híbrido de Timor has great contribution in diversifying the genetic base of the *C. arabica* cultivars in Brazil. In this study, the research institutes also showed that it was possible to developed cultivars with different genetic background, keeping high yield and good cup quality.

Genetic Contribution of the First Progenies for the Brazilian *Coffea arabica* Cultivars

Mundo Novo, a widely grown cultivar in Brazil, with high yield and good cup quality (Carvalho and Fazuoli, 1993; Carvalho, 1957), was used to developed several cultivars in Brazil. The biased selection practice toward Mundo Novo resulted in low genetic diversity among cultivars of *C. arabica* in Brazil. Mundo Novo is the first progeny of Bourbon Vermelho and Sumatra, which contributed with 69.38% for the genetic base of *C. arabica* cultivars (Table 7). The study of the genetic contribution of the ancestors and first progeny showed that the genetic diversity in *C. arabica* cultivars in Brazil is still very low and more needs to be done to change this situation. The breeding institutions can increase the genetic diversity among the cultivars of *C. arabica* by introducing new ancestors (parental lines) or selecting potential parental lines from the existing germplasm banks of coffee (Silvestrini et al., 2007).

The study showed high mean coefficient of parentage among *C. arabica* cultivars released in Brazil from 1939 to 2009. In addition, the result showed that the basic reason for the low genetic variability among the *C. arabica* cultivars is because most of the cultivars released are sister lines with similar genetic background. The genetic base of the

C. arabica cultivars released in Brazil is determined by 13 ancestral lines. The study also showed the importance of recent introduction of new parental lines (such as Híbrido de Timor) in the breeding programs to diversify the genetic background and increase the genetic diversity among cultivars of *C. arabica*. Even with the introduction of new parental lines in recent years, the COP among cultivars of *C. arabica* in Brazil is still very high when compared with other crops. Finally the result obtained from this work can be used by coffee breeders in the country as a starting point to design future breeding programs of *C. arabica*.

Acknowledgments

The authors would like to thank The Third World Academy of Science (The Academy of Science for the Developing World) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (National Council for Scientific and Technological Development) for providing the fellowship for the first author. This research was supported by Consórcio Brasileiro de Pesquisa e Desenvolvimento do Café (CBP&D/Café), Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and Financiadora de Estudos e Projetos (FINEP).

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