

Genetic parameters and selection of intra and interspecific peanut lines grown under rainfed conditions¹

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ABSTRACT

The introgression of wild germplasm represents a valuable strategy for enhancing the variability of commercial crops. In this study, the genetic parameters and selection response of amphidiploid lines derived from three *Arachis* species were estimated. Field assays were conducted under rainfed conditions, using the early-maturing BR 1 cultivar as control. Agronomic traits were evaluated to estimate genetic and phenotypic parameters, as well as to calculate the selection index. Based on the yield data, the lines RC 53 P4, RC 51 P4 and RC 78 P1 showed a superior performance, with 5 % of gains in pod and seed yield, and a harvest index of 37 %, exceeding the control by 10 %. The genotypic determination coefficients for number of pods per plant, pod and seed yield, and harvest index were above 60 %, indicating sufficient genetic variability for breeding. Substantial genetic gains were also observed for the selection index, ranging from 0.71 % (harvest index) to 4.22 % (seed yield).

KEYWORDS: *Arachis hypogaea* L., gene introgression, drought tolerance.

RESUMO

Parâmetros genéticos e seleção de linhagens intra e interespecíficas de amendoim cultivadas em sequeiro

A introgressão de germoplasma selvagem representa uma estratégia valiosa para aumentar a variabilidade de culturas comerciais. Neste estudo, foram estimados os parâmetros genéticos e selecionadas linhagens anfidiplóides derivadas de três espécies de *Arachis*. Foram conduzidos ensaios de campo sob condições de sequeiro, utilizando-se a cultivar precoce BR 1 como testemunha. Características agrônômicas foram avaliadas para estimar parâmetros genéticos e fenotípicos e calcular o índice de seleção. Com base nos dados de produtividade, as linhagens RC 53 P4, RC 51 P4 e RC 78 P1 apresentaram desempenho superior, com ganhos de 5 % nas produtividades de vagens e sementes e índice de colheita de 37 %, superando a testemunha em 10 %. Os coeficientes de determinação genotípica para número de vagens por planta, produtividade de vagens e de sementes e índice de colheita ficaram acima de 60 %, indicando variabilidade genética suficiente para o melhoramento. Ganhos genéticos substanciais também foram observados para o índice de seleção, variando de 0,71 % (índice de colheita) a 4,22 % (produtividade de sementes).

PALAVRAS-CHAVE: *Arachis hypogaea* L., introgressão genética, tolerância à seca.

INTRODUCTION

Peanut (*Arachis hypogaea* L.) is an allotetraploid ($2n = 4x = 40$) that reproduces almost exclusively through autogamy. The *Arachis* genus comprises more than 80 species, including diploid ($2n = 2x = 20$) and tetraploid ($2n = 4x = 40$) germplasm, all with high genetic value for yield and tolerance to environmental stresses (Leal-Bertioli et al. 2017, Dutra et al. 2018). However, the use of

wild species in breeding programs has been limited, mainly due to ploidy differences and chromosomal barriers among species.

The cytogenetic base of peanut consists of the A and B genomes, derived from the hybridization of two diploid species, *A. duranensis* Krapov. and W. C. Gregory and *A. ipaensis* Krapov. and W. C. Gregory (Kochert et al. 1996). Given the narrowing genetic base of commercial cultivars after successive breeding cycles, the development of synthetic lines

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by combining these genomes could generate new tetraploids with strategic traits, thereby expanding opportunities for peanut improvement (Santos et al. 2013, Dutra et al. 2018).

Globally, peanut is cultivated to supply both grain and oil for food markets. Two subspecies dominate production, *fastigiata* and *hypogaea*, which differ in traits such as oil content, growth cycle, plant height, and seed size (Dutra et al. 2018, Morais et al. 2023). Brazil ranks among the largest producers, with 806,064 t harvested from 281,563 ha (IBGE 2024). Most production occurs in the São Paulo state, in the Southeast region, where large-scale farmers predominantly grow runner cultivars (subsp. *hypogaea*), characterized by late cycles and suitability for mechanized management. In contrast, in the South and Northeast regions, where agroecological systems are more common, upright cultivars (subsp. *fastigiata*) are preferred because of their shorter cycles and greater adaptation to environments with limited water availability (Vasconcelos et al. 2015).

Most commercial peanut cultivars in Brazil have been developed through crosses involving closely related parents, thereby restricting the genetic base of the progenies (Dutra et al. 2018, Ramos et al. 2022). Introgressing alleles from wild germplasm represents a valuable strategy to enhance breeding programs and broaden genetic variability. Leal-Bertioli et al. (2017) conducted interspecific crosses using *Arachis* wild germplasm (*A. batizocoi* K9484 and *A. duranensis* SeSn 2848) to introgress favorable genes into peanut cultivars. They obtained several promising progenies with improved earliness, foliar disease resistance, and drought tolerance. Some of these progenies used BR 1 (*A. hypogaea* subsp. *fastigiata*) as the maternal parent, generating the population {BR 1 × [BR 1 × (*A. batizocoi* K9484 × *A. duranensis* SeSn 2848)^{4x}]}, which was extensively studied by Ramos et al. (2020) and Dutra et al. (2018).

From these studies, several progenies were evaluated, leading to the selection of eight F7 lines with desirable traits such as earliness, drought tolerance, and pod yield. In this scenario, the present study aimed to estimate genetic parameters and selection indices for these lines, based on agronomic data collected across two locations in one year under rainfed conditions.

MATERIAL AND METHODS

The plant material consisted of eight F7 peanut lines derived from a cross between the BR 1 cultivar (*A. hypogaea* subsp. *fastigiata*) and a synthetic amphidiploid (*A. batizocoi* K9484 × *A. duranensis* SeSn 2848)^{4x}, followed by a backcross with BR 1, generating the population BR 1 × [BR 1 × (*A. batizocoi* × *A. duranensis*)^{4x}]. The initial crosses and backcrosses were conducted by Leal-Bertioli et al. (2017). Subsequent generations (F2 to F7) were advanced using the single-seed descent method under water-restricted conditions, with selection focused on pod production, earliness, and drought tolerance, as described by Dutra et al. (2018) and Ramos et al. (2020).

The recurrent parent, BR 1, is an early-maturing upright cultivar adapted to the Brazilian semiarid region (Vasconcelos et al. 2015, Pereira et al. 2016).

Field trials were conducted under rainfed conditions in Alagoinha (6°57'00.0"S; 35°32'42.0"W) and Campina Grande (7°13'50"S; 35°52'52"W), both located in the semiarid region of the Paraíba state, Brazil. Sowing was performed on April 26, 2023, in Alagoinha, and on June 20, 2023, in Campina Grande. Seeds of the eight amphidiploid lines and BR 1 were sown in sandy loam soil, previously fertilized with dolomitic limestone (3,000 kg ha⁻¹), monoammonium phosphate (241 kg ha⁻¹), ammonium sulfate (125 kg ha⁻¹), and potassium chloride (100 kg ha⁻¹). The experimental design was a randomized block, with nine treatments (eight amphidiploid lines and BR 1 as a control) and four replicates. Spacing was 0.7 × 0.2 m (rows × plants), followed by thinning to two plants per hole at 15 days after emergence (DAE). Each plot consisted of a row (3.5 m²) with 50 plants.

Crop management followed the recommendations of Santos et al. (2006). No disease occurrence was recorded. Pest control, when required, was performed with neem oil, and manual weeding was carried out at 20 and 40 DAE. Harvesting began when 70 % of the plants in each plot reached full pod maturation, between 85 and 90 DAE (Santos et al. 2013). Seed processing consisted of natural field drying for one week. The following traits were evaluated: main stem height, number of mature pods per plant, 100-seed weight, harvest index, pod yield, seed yield, and seed return. The harvest index was calculated as (pod yield/total plant weight) × 100 (Morais et al. 2023).

Data were analyzed using the Genes software, version 1990.2022.27 (Cruz 2013). Normality was tested with the Lilliefors goodness-of-fit test. Analysis of variance and mean grouping were performed using the F-test and the Scott-Knott test.

Phenotypic and genetic parameters were estimated based on the genotypic quadratic component (ϕg), quadratic component of genotype \times environment interaction ($\phi g \times e$), coefficient of genotypic determination, coefficient of genetic variation (cvg), coefficient of environmental variation (Cve), and relative coefficient of variation (CVg/CVe) (Vencovsky & Barriga 1992, Cruz 2012). The selection index was estimated using the Mulamba & Mock model, with a selection intensity of 33.33 %.

RESULTS AND DISCUSSION

A significant statistical effect ($p \leq 0.05$) was observed among genotypes for most traits (Table 1), indicating sufficient variability to be exploited in peanut breeding. Environmental effects were significant for all traits, except 100-seed weight. Genotype \times environment ($G \times E$) interactions were significant for number of pods, pod yield and seed yield, showing that genotypes were influenced by environmental variation - particularly in Campina Grande, where reduced rainfall volume and irregular distribution during the onset of pod and seed development (Figure 1) affected

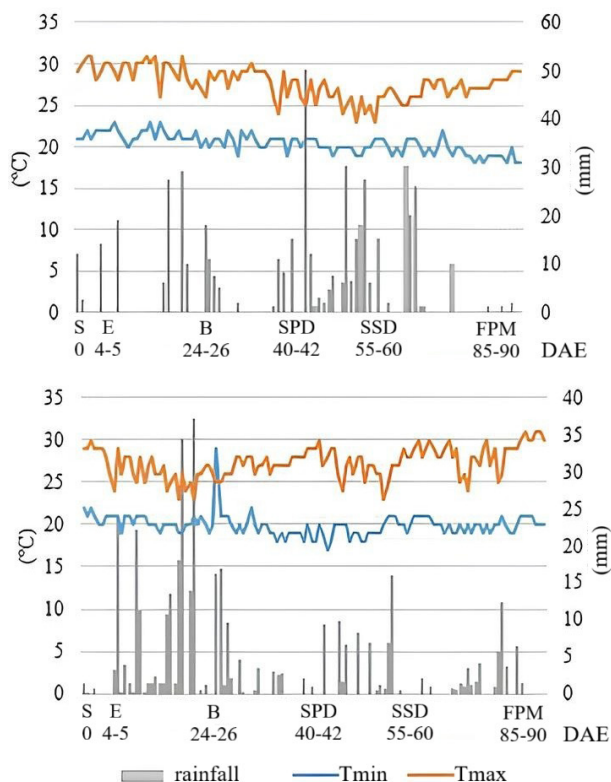


Figure 1. Climate data recorded in Alagoinha (A) and Campina Grande (B) (Paraíba state, Brazil) and phenological stages of early-maturing *fastigiata* peanut. S: sowing; E: emergence; B: blooming; SPD: start of pod development; SSD: start of seed development; FPM: full pod maturation; DAE: days after emergence. Rainfall during the cycle: Alagoinha: 588 mm; Campina Grande: 382 mm.

Table 1. Combined analysis of variance and estimates of genetic and phenotypic parameters in amphidiploid peanut lines grown under rainfed conditions in Alagoinha and Campina Grande (Paraíba state, Brazil).

Source of variation	DF	Mean square						
		HMA	NP	PY	SY	W100S	SR	HI
B/E	6	13.08	2.19	506,292.33	187,223	21.23	10.51	23.57
G	8	15.83	4.63*	124,870.53*	64,139.62*	4.71	16.77	20.79**
E	1	7,523**	1,101**	20,371,025**	14,738,341**	117.68	1,761.21**	310.54*
G \times E	8	25.09	6.04**	134,142.55*	60,457.55*	5.44	8.48	11.46
Error	48	12.54	1.845	50,732.76	25,128.94	8.07	8.59	6.37
Mean		55.39	14.83	2,135.21	1,430.08	43.50	65.71	36.37
CVe (%)		6.39	9.16	10.55	11.08	6.53	4.46	6.94
Source of variation		Estimation of genetic and phenotypic parameters						
		HMA	NP	PY	SY	W100S	SR	HI
Φg		0.411	0.34	9,267.22	4,876.33	0.00	1.02	1.80
Φga		3.14	1.05	20,852.45	8,832.15	0.00	0.00	1.27
GDC (%)		20.80	60.16	60.00	60.82	0.00	48.75	69.35
CVg (%)		1.16	3.98	4.51	4.88	0.00	1.54	3.69
CVg/Cve		0.18	0.43	0.43	0.44	0.00	0.35	0.53

B: block; G: genotype; E: environment; Cve: environmental coefficient of variation; DF: degree of freedom; HMA: height of main axis; NP: number of pods per plant; PY: pod yield; SY: seed yield; W100S: weight of 100 seeds; SR: seed return; HI: harvest index; ** and *: significant at $p \leq 0.01$ and $p \leq 0.05$, respectively; Φg : genotypic quadratic component; Φga : quadratic component of $G \times E$ interaction; GDC: genotypic determination coefficient; CVg: coefficient of genetic variation; CVg/Cve: ratio between genetic and environmental coefficient of variation.

performance. Water shortage or delay during these stages often limits grain production and seed return, even in early-maturing cultivars (Pereira et al. 2016).

Estimates of genetic and phenotypic parameters are presented in Table 1. Genotypic determination coefficient values, which represent heritability when genotypes are considered random effects (Cruz 2012), were high for number of pods per plant (60.15 %), pod yield (60.00 %), seed yield (60.82 %), and harvest index (69.35 %), indicating adequate potential for genetic gains through selection in subsequent generations.

The CVg/CVe ratio was < 1 for all traits, reflecting an unfavorable condition for selection due to the predominance of environmental variance (Bordin et al. 2022). In such cases, greater caution is required in selection strategies. Ramos et al. (2020), who evaluated genotypic prediction and selection gains in early generations of these same progenies, reported that CVg ranged from low to moderate, suggesting potential for genetic progress in later cycles, owing to the predominance of additive effects. Heritability values were high for most traits (> 70.6 %), supporting the potential for family selection, except for number of pods per plant, which showed heritability below 20 %.

The agronomic traits of the genotypes are presented in Table 2. Significant differences were detected for number of pods per plant, pod yield, seed yield, and harvest index. The first three traits directly contribute to peanut production, whereas harvest index is a key parameter, as it estimates the plant's efficiency in partitioning photosynthates to ensure fruit development. In peanut, the harvest index of drought-tolerant cultivars grown in the

dry season is typically around 35 %, since irregular rainfall leads the root system to adjust water uptake to sustain canopy growth (Duarte et al. 2013, Morais et al. 2023). Prolonged drought, however, markedly reduces this value. Figure 2 illustrates the growth of peanut lines during flowering (30-35 DAE) and seed development (60-65 DAE), in Alagoinha and Campina Grande. The limited rainfall in Campina Grande visibly restricted plant growth, reducing canopy development. Average harvest index values were 36 % in Alagoinha and 32 % in Campina Grande.

In general, the amphidiploid lines RC 53 P4, RC 51 P4, and RC 78 P1 performed best in both trials for pod and seed yield, exceeding the mean of BR 1 by 5 and 6 %, respectively. These gains are noteworthy, considering that only one backcross cycle was performed at the F1 stage to introgress drought-tolerance genes, while still maintaining the seed yield of BR 1. This cultivar is widely adopted in the semiarid region due to its stable yield of 2,700 kg ha⁻¹ of pods and 1,250 kg ha⁻¹ of seeds under dry-season conditions (Vasconcelos et al. 2015, Dutra et al. 2018, Ramos et al. 2020). A 5 % yield gain translates into an additional 85 kg ha⁻¹ of pods and 60 kg ha⁻¹ of seeds. Moreover, in previous studies, these lines were tested under 15-day water stress in field assays and selected as drought-tolerant among 281 progenies (Dutra et al. 2018).

For harvest index, most amphidiploid lines ranged from 36 to 38 %, indicating that the selection cycles conducted from F2 segregating progenies effectively contributed to the composition of an elite core, closely aligned with the BR 1 standard. The lines RC 53 P4, RC 51 P4, and RC 78 P1 had harvest index of 37 %, surpassing the BR 1 by 10 %.

Table 2. Agronomic traits of peanut lines grown under dry-season conditions in Alagoinha and Campina Grande (Paraíba state, Brazil).

Lines	HMA (cm)	NP	PY (kg ha ⁻¹)	SY (kg ha ⁻¹)	W100S (g)	SR (%)	HI (%)
RC 96 P9	54.09	14.29 b*	2,116.78 b	1,380.74 b	42.58	63.79	36.30 a
RC 79 P9	52.91	14.83 b	2,112.14 b	1,404.45 b	44.29	65.47	34.02 b
RC 53 P4	55.24	15.34 a	2,282.71 a	1,570.85 a	42.42	68.24	36.73 a
RC 51 P4	55.03	16.03 a	2,331.06 a	1,545.04 a	44.28	65.08	37.11 a
RC 82 P6	55.99	13.67 b	1,947.74 b	1,292.83 b	43.22	64.36	38.39 a
RC 78 P1	54.83	14.56 b	2,201.41 a	1,472.27 a	44.52	66.16	36.41 a
RC 51 P8	57.57	14.49 b	2,067.79 b	1,412.72 b	43.54	67.29	37.71 a
RC 79 P6	56.76	14.42 b	1,996.74 b	1,347.11 b	42.97	66.41	37.09 a
BR1	56.12	15.79 a	2,160.53 b	1,444.69 b	43.71	64.60	33.54 b

HMA: height of main axis; NP: number of pods per plant; PY: pod yield; SY: seed yield; W100S: weight of 100 seeds; SR: seed return; HI: harvest index. * Means followed by the same letter do not differ statistically according to the Scott-Knott test.



Figure 2. Growth of peanut lines during flowering (30-35 DAE) and seed development (60-65 DAE) in Alagoinha (A e C) and Campina Grande (B e D) (Paraíba state, Brazil).

Germplasm banks of commercial species hold numerous accessions with different ploidy levels that could be exploited in breeding programs aimed at introgressing genes of agronomic interest. One of the major challenges in using these resources is the presence of chromosomal barriers and the high penetrance of undesirable phenotypic traits, which necessitate backcrossing cycles to recover the phenotype of the commercial variety.

The first generation of amphidiploid peanut lines generated via interspecific crossing [BR 1 \times (*A. batizocoi* K9484 \times *A. duranensis* SeSn 2848)^{4x}] produced progenies with undesirable pod and seed traits, including small seed size, pod constriction, and beak formation, none of which were present in the maternal parent, BR 1. To eliminate these traits, a backcross cycle was performed, followed by successive selection pressure to restore the BR 1 pattern (Leal-Bertioli et al. 2017, Dutra et al. 2018). Although time-

consuming and meticulous, this strategy was highly effective, as it enabled the introgression of valuable genes and broadened the genetic base through the incorporation of diploid species. Figure 3 illustrates the phenotypic recovery achieved after backcrossing, showing that the F7 population now closely resembles the commercial cultivar BR 1, whose pod and seed traits are highly valued by farmers practicing agroecological management.

The agronomic data from amphidiploid lines grown in Alagoinha and Campina Grande were used to estimate the selection index following the methodology of Mulamba & Mock (Table 3). Significant genetic gains were observed, ranging from 0.71 % (harvest index) to 4.22 % (seed yield), supporting the selection of RC 53 P4, RC 51 P4, and RC 78 P1 for cultivar development. These findings are consistent with previous reports (Dutra et al. 2018, Ramos et al. 2020).

Table 3. Estimates for the mean of the original population (Xo), mean of the selected population (Xs), broad-sense heritability (h^2 %), and expected gain from selection (SG) for traits evaluated using the Mulamba & Mock selection index in Alagoinha and Campina Grande (Paraíba state, Brazil).

Traits	Xo	Xs	h^2 %	SG	SG %	Selected lines
NP	14.83	15.32	60.16	0.30	2.01	RC 53 P4, RC 51 P4, and RC 78 P1
PY (kg ha ⁻¹)	2,135.21	2,271.73	59.37	81.05	3.80	
SY (kg ha ⁻¹)	1,430.08	1,529.39	60.82	60.40	4.22	
HI (%)	36.38	36.75	69.35	0.26	0.71	

NP: number of pods; PY: pod yield; SY: seed yield; HI: harvest index.

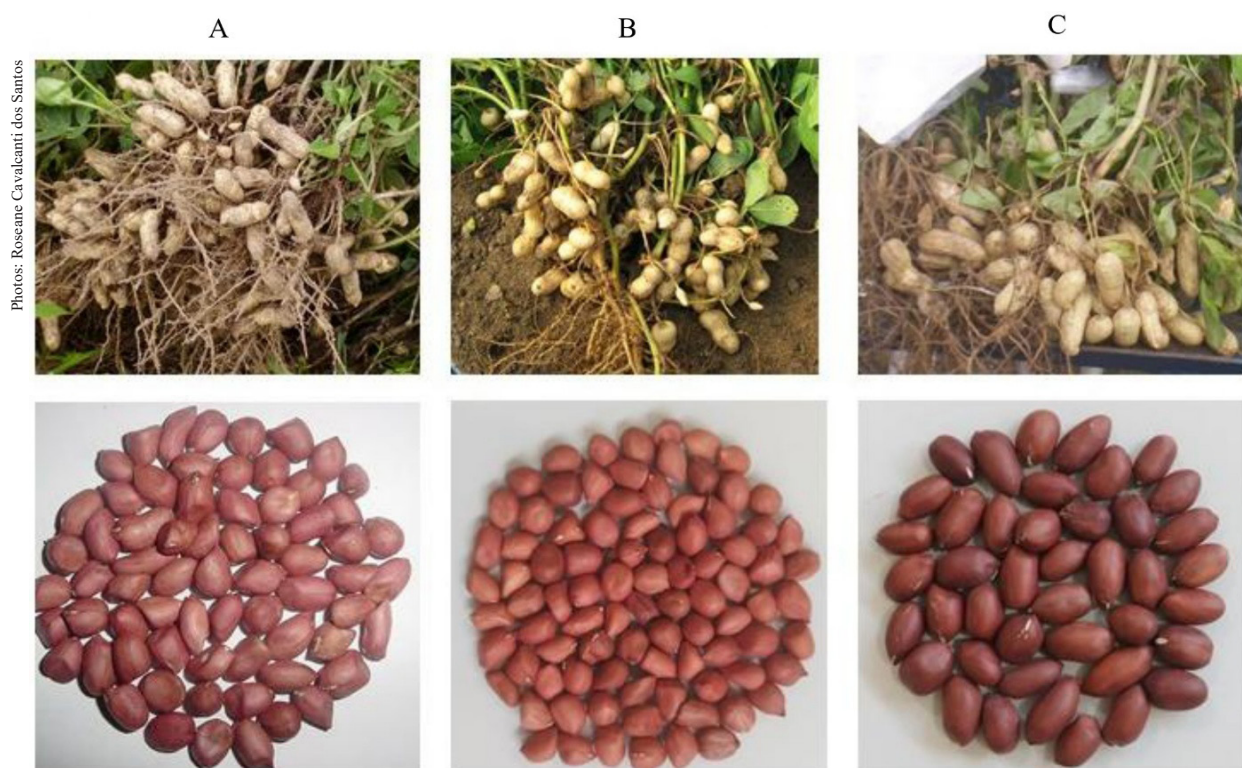


Figure 3. Pod and seed patterns of parental BR 1 (A), amphidiploid peanut lines generated via interspecific crossing [BR 1 \times (*A. batizocoi* K9484 \times *A. duranensis* SeSn 2848)^{4x}] (B), and backcrossed progenies {BR 1 \times [BR 1 \times (*A. batizocoi* \times *A. duranensis*)^{4x}]} (C).

CONCLUSION

The amphidiploid peanut lines RC 53 P4, RC 51 P4, and RC 78 P1 are highly promising for advancing breeding programs, based on earliness and production traits evaluated in two environments of the Paraíba state, Brazil.

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