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FORAGE PEANUT VARIABILITY: GENETIC PARAMETERS FOR AGRONOMIC AND NUTRITIVE TRAITS IN TIME-SEPARATE TRIALS

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Abstract: Successful breeding programs depend on the information defined through the evaluation of parameters obtained according to the selection strategy, based on the correlated responses among the multiple traits evaluated and the environmental influence. As follows, the objective of this study was to estimate the genetic parameters for agronomic and nutritive traits of forage peanut to subsidize the selection of more adapted genotypes. We evaluated 67 genotypes in three separate trials with two common controls. Agronomic and nutritive data were analyzed using the mixed model methodology (REML/BLUP) for each trial. Genetic parameters were estimated for all the variables and genotypic values served as a basis for checking the genetic correlation among traits. There was genetic variability and environmental influence for the traits analyzed, except for nutritive ones. Individual heritabilities, in general, were low to moderate and the traits of forage production (vigor, height, ground cover, and total and leaves dry matter yields) correlated with each other in the three trials. There is a favorable condition for the selection of agronomic traits, with high accuracy and consistency among trials. There is the possibility of indirect selection with the use of agronomic traits related to forage yield.

Keywords: *Arachis pintoi* and *A. repens*, genetic correlation, heritability, repeatability, different trials.

Introduction

Pasture is the basis of Brazilian livestock production, and its productive potential can be intensified sustainably by intercropping with legume species (Pereira et al., 2015; Fioreli et al., 2018; Olivo et al., 2019). Forage legumes contribute to increasing the efficiency of extensive systems by supplying nutrients to the soil and increasing the volume and quality of forage. Among the species for this purpose forage peanut, particularly *Arachis pintoi* Krapov. & W. C. Greg. and *Arachis repens* Handro, stands out for its persistence, productivity, and high nutritional value (Andrade et al., 2012; Fioreli et al., 2018).

Despite the recent breeding program for forage peanut, its intercropping with grasses in pastures has shown a potential to contribute to the recovery of degrad-

ed areas and to animal production intensification. In a tropical climate, pastures intercropped with forage peanut show increases in the average daily animal gain of 0.75 kg day^{-1} in the rainy season, with about 20% more dry matter production of forage compared to pasture composed only by grass fertilized with N, allowing a stocking rate of up to 5.00 AU ha^{-1} (Pereira et al., 2015; 2019), which offers potential for reducing pasture maintenance and production costs.

The Forage Peanut Breeding Program (Assis and Valentim, 2013) seeks to develop new cultivars through multi-trait evaluation, selecting genotypes with high seed and dry matter yield throughout the year, faster ground cover, high nutrient content and resistance to pests and diseases (Assis et al., 2008; Menezes et al., 2012). In this sense, evaluation and harvest trials remain essential practices and aim to obtain information to define breeding program strategies, as well as to select more adapted and stable genotypes throughout the year (Menezes et al., 2012). In that manner, the genetic parameters estimation and the prediction of the genotypic values should be based on models in which the effects of environmental interactions and the phenotypic correlations among repeated measures are considered to increase their accuracy and, consequently, the estimates of selection gains (Viana and Resende, 2014).

The objective of this study was to estimate the genetic parameters for agronomic and nutritive traits of forage peanut in tropical conditions of the Brazilian Western Amazon via mixed models, in order to support the process of selecting more adapted and productive genotypes.

Material and Methods

Sixty-six forage peanut genotypes from the Active Germplasm Bank located at Embrapa Acre (Table 1) in Rio Branco, AC, Brazil were evaluated under the coordinates 10°01'34"S, 67°42'13"W (Datum WGS 84) and 160 m altitude.

Table 1. Identification of genotypes in the three time-separated trials of forage peanut.

---------- Trial I ----------											
Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]
1	14931	00064739-6	Ap	8	30333	00190125-5	Ap	15	32379	00065439-2	Ar
2	33260	00065493-9	Ar	9	39187	00065996-1	Ap	16	32409	00065445-9	Ap
3	39799	00066013-4	Ap	10	15083	00064741-2	Ap	17	34142	00065550-6	Ap
4	35068	00065601-7	ApxAr	11	14991	00064729-7	Ap	18[2]	37036	00065847-6	Ap
5	35041	00065599-3	ApxAp	12	35114	00065606-6	Ap	19	52*	-	Ap
6	35033	00065598-5	ApxAp	13	32352	00065437-6	Ar	68[3]	31828	00065390-7	Ap
7	40894	00190125-5	Ar	14	34436	00065561-3	Ar	69[4]	40550	00066060-5	Ap
---------- Trial II ----------											
Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]
20	39985	00066014-2	Ap	26	39772	00066011-8	Ap	32	38857	00065922-7	ApxAr
21	29220	00064736-2	Ar	27	40045	00066021-7	Ap	33	30384	00064818-8	Ap
22	12122	00064738-8	Ap	28	12106	00064724-8	Ar	34	13251	00190520-7	Ap
23	14982	00064728-9	Ap	29	29190	00064733-9	Ar	68	31828	00065390-7	Ap
24	30325	00064752-9	Ap	30	29203	00064734-7	Ar	69	40550	00066060-5	Ap
25	30601	00064829-5	Ap	31	35076	00065602-5	ApxAr	70[5]	40550	00066060-5	Ap
---------- Trial III ----------											
Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]
16	32409	00065445-9	Ap	47	31984	00065404-6	Ap	59	40185	00066034-0	Ar
35	30082	00065492-1	Ar	48	12114	00064725-5	Ar	60	36544	00065716-3	Ap
36	35122	00065607-4	Ap	49	40193	00066035-7	Ap	61	34363	00065559-7	Ar
37	32387	00065440-0	Ar	50	15121	00190518-1	Ap	62	34355	00065548-0	Ap
38	32280	00065417-8	Ar	51	16683	00064744-6	Ap	63	32433	00065449-1	Ap

Trial III											
Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]	Code	Old BRA	New BRA	Sp[1]
39	31909	00065398-0	Ap	52	32280	00065417-8	Ar	64	32492	00065448-3	Ar
40	40223	00066036-5	Ap	53	40088	00066024-1	Ar	65	30872	00064844-4	Ap
41	39195	00065997-9	Ap	54	16357	00064748-7	Ap	66	30899	00064845-1	Ap
42	30635	00064831-1	Ap	55	37443	V 14475	Ar	67	30929	00064846-9	Ap
43	31275	00065341-0	Ap	56	14788	00064727-1	Ar	68	31828	00065390-7	Ap
44	31461	00065362-6	Ap	57	32361	00065438-4	Ar	69	40550	00066060-5	Ap
45	31526	00065366-7	Ap	58	22683	00064749-5	Ap				

[1]Sp: species (Ap: *Arachis pintoi*; Ar: *Arachis repens*). [2]cv. Alqueire-1; [3]cv. Belomonte; [4]cv. BRS Mandobi; [5]cv. BRS Mandobi propagated by seeds. *Local identification (without BRA).

The climate of the region is hot and humid equatorial type, characterized by high temperatures, with a maximum of 31 °C and a minimum of 21 °C average temperatures; relative humidity around 80%; and high rainfall, about 1,900 mm per year (Acre, 2010). The rainy season extends from October to April, and the water deficit occurs from June to September (Figure 1) (Inmet, 2017).

Genotypes were evaluated in three temporally distinct trials, beginning in December 2005 and ending in April 2013. The experimental area fertilization was performed based on pasture fertilization and liming, according to soil analysis for each trial (Table 2). Trial I was installed in Dystrophic Ultisol and Trial II and III were installed in Dystrophic Oxisol (Embrapa, 2018).

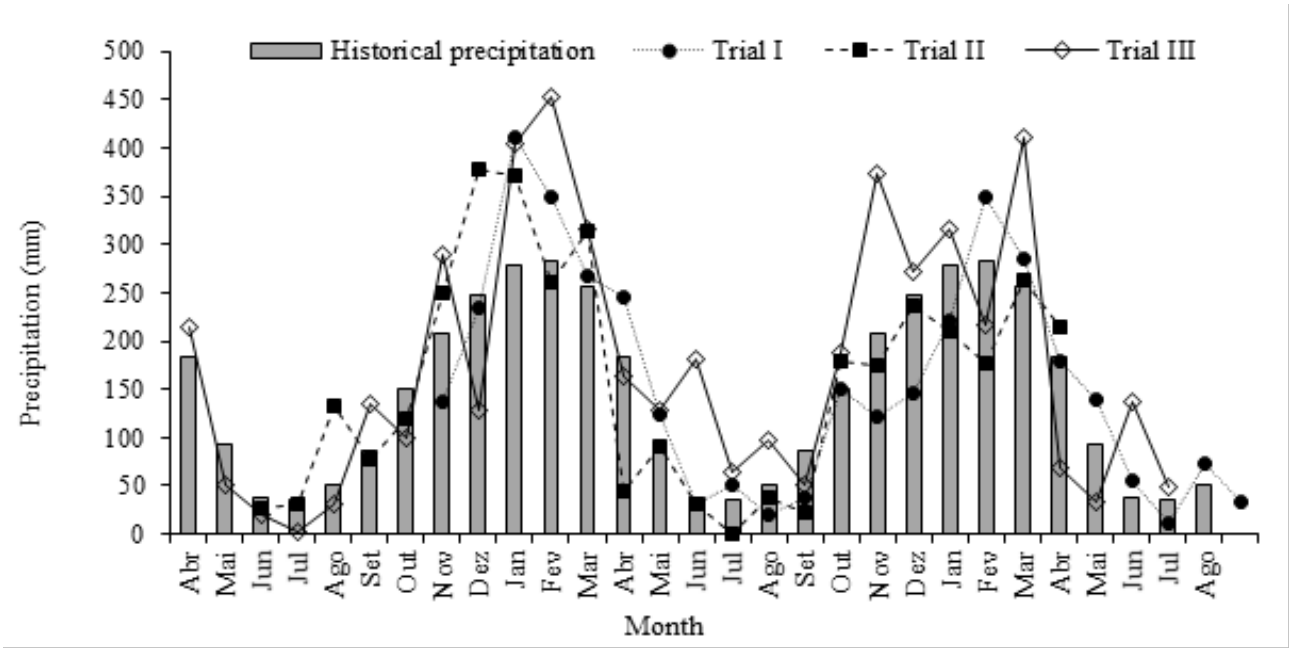

Figure 1. Precipitation over evaluation period of three time-separated forage peanut trials and historical average value (1969 to 2016) to Rio Branco, AC, Brazil (INMET, 2017).

Table 2. Chemical characteristics of experimental area soils of each forage peanut trial, collected at 0-20 cm of depth.

	K^+	Ca^{+2}	Mg^{+2}	Al^{+3}	H+Al	CEC[1]	P	BS[2]	OM[3]	pH[4]
Trial	---------- $cmol_c\ dm^{-3}$ ----------						$mg\ dm^{-3}$	%	$g\ kg^{-1}$	-
I	0.1	0.9	0.2	0.2	-	1.4	2.3	30.5	25.7	5.0
II	0.1	1.6	0.4	1.0	-	5.4	2.0	38.6	13.0	5.4
III	0.2	0.9	0.2	-	3.7	6.0	0.5	37.8	16.9	5.4

[1]Cationic exchange capacity; [2]Base-saturation percentage; [3]Organic matter; [4]Soil pH measured in water. Trial I: Dystrophic Ultisol; Trial II and III: Dystrophic Oxisol.

The trial I, 500 kg ha^{-1} of dolomitic limestone was applied before planting in the conventional tillage, and immediately after planting fertilization with 50 kg ha^{-1} of P_2O_5 (triple superphosphate), 30 kg ha^{-1} of K_2O (potassium chloride) and 40 kg ha^{-1} of FTE BR12 (micronutrients). The trial was installed in December 2005, with a uniformization cut in October 2006. Nineteen genotypes were evaluated in eight evaluations, one in the dry season and seven in the rainy season, from December 2006 to November 2008. Biomass harvests were performed in all evaluations except in the dry season because of low leaf production.

In Trial II, 50 kg ha^{-1} of P_2O_5, 40 kg ha^{-1} of K_2O and 40 kg ha^{-1} of FTE BR12 were applied immediately after planting. This trial was installed in December 2008, with a uniformization cut performed in April 2009. In February 2010 side-dressing fertilization was performed with 40 kg ha^{-1} of P_2O_5, 50 kg ha^{-1} of K_2O and 40 kg ha^{-1} of FTE BR12 and repeated in February 2011. Sixteen genotypes were evaluated in eight harvests from July 2009 to April 2011, in which six harvests were performed in the rainy season and two in the dry season.

In Trial III, 110 kg ha^{-1} of dolomitic limestone was applied before planting in conventional tillage and performed fertilization after planting with 80 kg ha^{-1} of P_2O_5 and 40 kg ha^{-1} of K_2O. This Trial was installed in December 2010 with a uniformization cut in April 2011. The side-dressing fertilization was performed with 15 kg ha^{-1} of P_2O_5, 15 kg ha^{-1} of K_2O and 10 kg ha^{-1} of FTE BR12 in March 2012. Thirty-three genotypes were evaluated in 12 evaluations with 11 harvests, from May 2011 to July 2013. Eight evaluations with harvests were made in the rainy season and four evaluations with three harvests were made in the dry season. In this trial, there were also two applications of 0.3 mL L^{-1} azoxystrobin and cyproconazole systemic fungicide in all plots in April and May 2012 for Rhizoctonia control.

Harvests were made after the establishment period, which for Trial I was 10 months after planting and for Trials II and III was 4 months. The nutritive (bromatological) analyses were performed with 70-day mean of regrowth in dry and rainy seasons.

The three trials were vegetatively implanted, with two stolons per pit and 0.5 m between pits and between rows. To standardize, each stolon was about 25 cm long with five internodes, of which three were covered with soil. In Trial II, cv. BRS Mandobi was also implanted by seed with 0.5 m between pits and rows with two seeds per pit. All the trials had as control the cultivars BRS Mandobi and Belmonte (currently called cv. Belomonte [Mapa, 2017]) vegetatively propagated and were conducted in a randomized complete block design, with four replications for Trial I and III and five replications for Trial II. The trials had a 1 m^2 plot of usable area.

Agronomic and aerial biomass chemical evaluations were performed. The occurrence of pests and diseases, plant vigor, and flowering were obtained visually by grading scale, according to increasing intensity observed for each trait, adapted from Menezes et al. (2012):

- pests and diseases: 0 (no damage) to 10 (death of all plants in the plot), according to severity scale and incidence area;
- plant vigor: 0: without plant material; 1: - - - -; 2: - - -; 3: - -; 4: -; 5: 0; 6: +; 7: ++; 8: +++; 9: ++++; with grades ranging from very bad to excellent;
- flowering: 0 – no flowers; 1: 1% to 10% of flowering; 2: 11% to 20%; 3: 21% to 30%; 4: 31% to 40%; 5: 41% to 50%; 6: 51% to 60%; 7: 61% to 70%; 8: 71% to 80%; 9: 81% to 90% and 10: 91% to 100%.

The ground cover (GC) was estimated visually (%) with a subdivided square of 1 m × 1 m, and the stand height (cm) by the mean of three measurements performed in the plot, as made by Menezes et al. (2102). Total (TDMY) and leaf (LDMY) dry matter yield, were quantified after each evaluation (with aerial biomass harvest at 2 cm above ground) by forced-air drying at 55 ºC for 72 hours and estimated in kg ha^{-1}. The nutritive value traits, evaluated after weighing and total dry matter sampling, were neutral detergent

fiber (NDF) and acid detergent fiber (ADF), according to Goering and Van Soest (1970), and crude protein content (CP), by the modified Kjeldahl method (Silva and Queiroz, 2001), in kg ha^{-1} of dry matter.

Data were analyzed jointly for each trial by the Restricted Maximum Likelihood (REML) method (Patterson and Thompson, 1971) to estimate the variance components and by the Best Linear Unbiased Prediction (BLUP) (Henderson, 1975) to predict genotypic values. The models used were based on those proposed by Resende (2002) for the analysis of unrelated perennial plants and one observation per plot.

For each trait within each trial, the repeatability model was used: **y** = **Xu** + **Zg** + **Wp** + **Tm** + **e**; where **y** is the data vector, **u** is the vector of the effect of evaluation-repetition combinations (considered fixed) plus the general mean, **g** is the vector of genotypic effects (considered random), **p** is the vector of permanent environment effect (plots, considered random), **m** is the vector of the genotype x evaluations interaction effects and **e** is the vector of errors or residuals (random). Capital letters represent the incidence matrices for these effects.

For cases with only one evaluation (Trial I nutritive value traits) the following model was used: **y** = **Xr** + **Zg** + **e**; where **y** is the data vector, **r** is the vector of repetition effects (considered fixed) plus the general mean, **g** is the vector of genotypic effects (considered random), and **e** is the vector of errors or residuals (random). Capital letters represent the incidence matrices for these effects.

Because of the effect of serial correlation, intrinsic to repeated measurement data, several residual structures for the repeatability model were tested and selected by the likelihood ratio test (LRT) and the Akaike (AIC) and Bayesian Information (BIC) criteria, observed for each matrix in the models where convergence can be found (Littlel et al., 2000). The variance components matrix, unstructured matrix (first-order), and analytical factor matrix (first-order) were selected.

The variance components obtained by the REML method for each analysis were used to estimate the respective genetic parameters (heritabilities, repeatabilities, coefficients of determination, coefficients of variation, and correlations), according to Holland et al. (2003) and Resende (2002). The genotypic, permanent plot, and genotype × evaluations interaction variabilities, according to each model, were tested by the deviance analysis, also based on the LRT test, according to Resende (2007). This test subtracts the functions $-2\text{Log}_e L$, where L is the likelihood equation of the complete model and of the model without the tested effect, and compares this difference to the tabulated χ^2 value. If the value is significant, the tested effect has variability. The same procedure is applied for selecting the residual structure matrices.

The genotypic correlation through the evaluations was estimated as follows (Eq. 1):

$$r_m = \frac{\sigma_g^2}{\sigma_g^2+\sigma_m^2} \quad \text{(Eq. 1)}$$

where σ^2_g is the genotypic variance, and σ^2_m is the genotype x evaluations interaction variance. The individual repeatability, in turn, was given by (Eq. 2):

$$r = \frac{\sigma_g^2+\sigma_p^2}{\sigma_g^2+\sigma_p^2+\sigma_m^2+\sigma_e^2} \quad \text{(Eq. 2)}$$

and classified according to the criterion proposed by Resende (2002), considering low repeatability (< 0.30), moderate ($0.30 \leq r \leq 0.60$), and high (> 0.60).

The coefficient of determination of genotype x evaluation interaction (c^2_m) and permanent plot (c^2_p) effects were given by Eq. 3 and Eq. 4, respectively:

$$c_m^2 = \frac{\sigma_m^2}{\sigma_g^2+\sigma_p^2+\sigma_m^2+\sigma_e^2} \quad \text{(Eq. 3)}$$

$$c_p^2 = \frac{\sigma_p^2}{\sigma_g^2+\sigma_p^2+\sigma_m^2+\sigma_e^2} \quad \text{(Eq. 4)}$$

The mean heritability of the plot was given by (Eq. 5):

$$h_m^2 = \frac{mh_g^2}{1+(m-1)r} \quad \text{(Eq. 5)}$$

where m is the number of evaluations and h^2_g is the individual heritability in the broad sense, estimated by Eq. 6 for the repeatabil-

ity model and Eq. 7 for the model with just one evaluation:

$$h_g^2 = \frac{\sigma_g^2}{\sigma_g^2+\sigma_p^2+\sigma_m^2+\sigma_e^2} \quad \text{(Eq. 6)}$$

$$h_g^2 = \frac{\sigma_g^2}{\sigma_g^2+\sigma_e^2} \quad \text{(Eq. 7)}$$

The classification of individual (h^2_g) and mean heritabilities (h^2_m) followed the criterion proposed by Resende (2002), considering magnitudes: low (< 0.15), moderate ($0.15 \leq h^2 \leq 0.50$) and high (> 0.50).

The ratio of the coefficients of genetic and residual variation was calculated by Eq. 8 (see Eq. 9 and Eq. 10) where $\bar{x}$ is the mean value of the variable, following the interpretation by Vencovsky (1987):

$$Ratio = \frac{CV_g}{CV_e} \quad \text{(Eq. 8)}$$

$$CV_g = \frac{\sqrt{\sigma_g^2}}{\bar{x}}100 \quad \text{(Eq. 9)}$$

$$CV_e = \frac{\sqrt{\sigma_e^2}}{\bar{x}}100 \quad \text{(Eq. 10)}$$

The accuracy (Ac) was given by (Eq. 11):

$$Ac = \sqrt{h_m^2} \quad \text{(Eq. 11)}$$

The Pearson correlation was estimated based on genotypic values as follows (Eq. 12):

$$\rho = \frac{Cov(X,Y)}{\sqrt{Var(X)Var(Y)}} \quad \text{(Eq. 12)}$$

were ρ is the coefficient of correlation, Var and Cov were variances and covariances between the traits X and Y, respectively, tested at 5% e 1% of probability by Student's t-test. The correlation classifications follow criteria proposed by Resende (2015), considering low (< |0.33|), moderate ($|0.33| \leq \rho \leq |0.66|$), and high (> |0.66|).

All statistical procedure was performed in SAS® software, by the command PROC MIXED for the mixed models and PROC CORR for correlations (SAS, 2010).

Results and discussion

There was genotypic variability in the joint analysis of all evaluations over the years for most traits in the three trials, except for fiber in acid detergent (ADF) and neutral detergent (NDF) for Trial I and NDF for Trial II (Table 3), which confirms the high agronomic variability already observed for forage peanut genotypes (Carvalho and Quesenberry, 2012; Menezes et al., 2012; Fernandes et al., 2017b; Simeão et al., 2017).

According to the heritability classification criterion proposed by Resende (2002), individual heritabilities (h^2_g) were low (< 15%) to moderate ($15\% < h^2_g < 50\%$) magnitudes. Only CP from Trial I showed high-magnitude heritability. This highlights the importance of evaluating genotypes by genotypic value, as pointed out by Assis et al. (2008), and not just by phenotypic averages. The inheritance estimated in the broad sense considers the additive and dominance genetic variances, which are especially important in the breeding of vegetative propagation plants, as in this stage of the improvement program of forage peanut, since the genotype is fully inherited. In addition, the magnitude of heritability determines the difficulty level in improving the trait, indicating the most efficient selection strategy (Resende, 2002). In this case, the selection based on the traits focused on forage production and quality, such as vigor, ground cover (GC), height, total (TDMY), and leaves dry matter yield (LDMY) and crude protein (CP), in the trial I and II tends to be more efficient due to the variability among genotypes and greater individual heritabilities observed in each trial.

The coefficients of determination of genotype x evaluation interaction effects (c^2_m) were significant for most of the traits, except for the occurrence of pests in Trial I and ADF and NDF in Trial III. This interaction can be problematic for the breeder, as it indicates oscillation of the best genotypes among harvests (Resende et al., 2008). In cases where the magnitude of c^2_m was greater than h^2_g, as for disease occurrence in the three trials, pest occurrence and flowering in Trial II and III, vigor, GC and NDF in Trial II and CP in Trial III (Table 3), this interaction suggests a greater environment influence, mainly over the seasons, which can be observed consistently in the seasonality of pests and diseases occurrence and flowering (Carvalho et al., 2009; Menezes et al., 2012).

Table 3. Individual heritabilities in broad sense (h^2_g), coefficient of determination of genotype x evaluation interaction (c^2_m) and permanent plot (c^2_p) effects, genotypic correlation through the evaluations (r_m), mean heritabilities of plot (h^2_m), accuracy of selection (Ac), genetic (CV_g) and residual (CV_e) coefficients of variation and individual repeatability (r) in the joint analysis of seasons for the three trials of forage peanut.

Traits	Trial I								
	h^2_g	c^2_m	c^2_p	r_m	h^2_m	Ac	CV_g	CV_e	r
Pest	0.04±0.02**	0.04	0.01	0.50	0.55	0.74	2.20	10.36	0.04
Disease	0.06±0.03**	0.12**	0.01	0.31	0.58	0.76	4.19	16.10	0.06
Vigor	0.40±0.07**	0.13**	0.10**	0.76	0.89	0.94	14.09	13.61	0.50
Flower	0.33±0.06**	0.21**	0.01*	0.61	0.88	0.94	35.02	41.32	0.33
GC	0.43±0.07**	0.30**	0.08**	0.59	0.87	0.93	22.93	15.06	0.51
Height	0.33±0.06**	0.19**	0.21**	0.63	0.79	0.89	33.26	30.54	0.53
CP[1]	0.55±0.23*	-	-	-	0.83	0.91	9.27	8.42	-
ADF[1]	0.19±0.13	-	-	-	0.48	0.69	3.61	7.49	-
NDF[1]	0.17±0.13	-	-	-	0.45	0.67	3.57	7.90	-
TDMY	0.30±0.06**	0.24**	0.15**	0.55	0.78	0.88	32.35	33.29	0.44
LDMY	0.30±0.06**	0.13**	0.12**	0.70	0.83	0.91	31.96	38.82	0.42
Traits	**Trial II**								
	h^2_g	c^2_m	c^2_p	r_m	h^2_m	Ac	CV_g	CV_e	r
Pest	0.11±0.04**	0.21**	0.01	0.34	0.71	0.84	16.89	41.32	0.12
Disease	0.14±0.04**	0.34**	0.02	0.29	0.70	0.84	19.87	37.79	0.15
Vigor	0.21±0.05**	0.22**	0.04**	0.49	0.81	0.90	5.36	8.46	0.25
Flower	0.28±0.06**	0.39**	0.02*	0.42	0.82	0.91	46.07	48.26	0.30
GC	0.18±0.04**	0.21**	0.03**	0.45	0.79	0.89	4.91	8.86	0.20
Height	0.38±0.06**	0.22**	0.09**	0.63	0.88	0.94	19.08	17.43	0.47
CP[1]	0.34±0.10**	0.14**	0.07	0.71	0.79	0.89	4.82	5.58	0.41
ADF[1]	0.24±0.08**	0.13**	0.04	0.66	0.73	0.85	3.54	5.54	0.28
NDF[1]	0.06±0.04	0.11*	0.01	0.35	0.40	0.63	1.51	5.61	0.06
TDMY	0.40±0.07**	0.20**	0.15**	0.67	0.87	0.93	21.44	16.93	0.55
LDMY	0.40±0.07**	0.17**	0.15**	0.70	0.87	0.93	21.00	17.73	0.55
Traits	**Trial III**								
	h^2_g	c^2_m	c^2_p	r_m	h^2_m	Ac	CV_g	CV_e	r
Pest	0.10±0.02**	0.11**	0.01	0.48	0.79	0.89	10.47	29.83	0.10
Disease	0.10±0.02**	0.18**	0.09**	0.35	0.66	0.81	17.87	46.36	0.18
Vigor	0.18±0.03**	0.13**	0.03**	0.58	0.85	0.92	5.59	10.77	0.21
Flower	0.36±0.04**	0.40**	0.01**	0.48	0.90	0.95	70.59	56.00	0.38
GC	0.10±0.02**	0.07**	0.03**	0.59	0.76	0.87	3.05	8.88	0.13
Height	0.41±0.04**	0.23**	0.10**	0.64	0.89	0.94	23.72	18.85	0.41
CP[1]	0.08±0.03**	0.15**	0.04	0.34	0.55	0.74	2.02	6.11	0.12
ADF[1]	0.06±0.02**	0.04	0.03	0.57	0.52	0.72	1.91	7.52	0.09
NDF[1]	0.11±0.03**	0.02	0.01	0.88	0.73	0.86	2.00	5.49	0.12
TDMY	0.43±0.05**	0.19**	0.15**	0.70	0.88	0.94	18.48	13.37	0.58
LDMY	0.25±0.05**	0.19**	0.14**	0.57	0.75	0.87	18.24	23.34	0.39

[1]Only one evaluation. * and ** significant at 5 e 1% by deviance analysis based on LRT test, respectively. (-) Values not available for this analysis. Occurrences of Pest and Disease: visual scale of 0 to 10; Vigor: visual scale of 0 to 9; Flower: flowering in scale of 0 to 10; GC: ground cover, %; Height: plant height, cm; CP: crude protein content of aerial biomass, kg ha^{-1}; ADF and NDF: acid and neutral detergent fiber content, kg ha^{-1}; TDMY: total dry matter yield per harvest, kg ha^{-1}; LDMY: leaf dry matter yield per harvest, kg ha^{-1}.

The genotypic correlation through evaluations (r_m), associated with c^2_m, allows to estimate the predictability of the genotypes' behavior in relation to environmental changes (Rosado et al., 2012), indicating the coincidence among the best genotypes in all evaluations (Resende et al., 2008). For most traits, more than 50% of the genotypes revealed constant performance throughout the evaluations in Trial I (except the occurrence

of disease, with 31%) and in Trial III (except the occurrence of pest and disease, flowering and CP, with values from 34 to 48%). In Trial II, height, CP, ADF, TDMY, and LDMY had values up to 63% and the other traits ranged from 29 to 49% (Table 3). Overall, these results reinforce the evidence observed by Simeão et al. (2017) that genotypes tend to maintain productive performance throughout evaluations. On the other hand, the other traits reflect the greater influence of the genotypes' interaction in different seasons of the evaluations, indicating that studies by specific seasons can bring relevant information for species improvement.

The coefficients of determination of permanent plot effects (c^2_p) were significant for most of the traits. For the occurrence of pest and disease in Trial I and II, pest in Trial III, and for nutritive value traits in Trial II and III, c^2_p was not significant, indicating there were no specific conditions of environmental favoring for these traits, contributing to the crudest estimate of the punctual effects of the environment (Braz et al., 2013). According to Viana and Resende (2014), the permanent effects start acting after planting and remain during the evaluations, for example, because of the soil structure and fertility in the plot. In this case, there is a greater influence on the traits related to forage production, such as vigor, GC, height, TDMY, and LDMY (Table 3).

On the other hand, nutritive value traits and occurrence of pests and diseases, with less variability, tend to be more influenced by environmental seasonality, as observed by Menezes et al. (2012) in the rainy and dry seasons, with less permanent effects influence. Although significance was observed for most of the traits evaluated, the magnitudes of c^2_p were consistently lower than the magnitudes of h^2_g.

The mean heritabilities of the plot (h^2_m), important when there is a more considerable environmental influence or less genetic control (Braz et al., 2013), were moderate to high (Table 3). Occurrences of pest and disease in the three trials, ADF and NDF in Trial III and NDF in Trial II showed low individual heritability. Therefore, the use of mean heritabilities tends to improve the selection efficiency, since the mean values of the plot are considered, consequently improving the precision level because of the weighting of the variances by the proportional number of repetitions and evaluations (Resende, 2002; Rosado et al., 2012).

Accuracy of selection (Ac), directly related to h^2_m, was up to 70% in three trials, except for ADF and NDF of Trial I and NDF of Trial II. This accuracy level is considered appropriate in the early stages of the breeding program (Viana and Resende, 2014).

Genetic coefficients of variation (CV_g) were below 10% only for nutritive value traits in all trials, for vigor and GC of Trial II and III, and for occurrence of disease in Trial I. This variability, associated with their respective residual coefficient of variation values (CV_e), provided a ratio CV_g/CV_e above to unit just for vigor, GC, height, CP, and ADF of Trial I, height, TDMY and LDMY of Trial II and flowering, height and TDMY of Trial III (Table 3), which indicates these traits can be more easily improved in the breeding program, allowing more prospects for gains with the selection.

Individual repeatabilities (r), which indicate the maximum value that heritability can reach this location, were low ($r < 0,3$) magnitude for the incidence of pests and disease in the three trials (Table 3). In Trial II and III, vigor, GC, and the nutritive value traits, except CP in Trial II, also showed low repeatability, according to the classification criteria proposed by Resende (2002), indicating a high number of evaluations will be necessary to predict the real value of individuals. The proportion of variance attributed to genetic causes is mixed with the effects of a permanent plot on the genotypes development (Braz et al., 2013), indicating that the trait has a superior influence of the interaction with the environment since the variance of this effect also comprise the denominator for calculating repeatability. The other traits had moderate repeatability ($0,3 < r < 0,6$), which reduces the number of necessary evaluations and can optimize the time and resources employed in conducting the trials (Fernandes et al., 2017a).

The genotype means, for each trait according to the trials and seasons are shown in Table 4. For the occurrence of pests and diseases, the means were low, which is in agreement with what was observed by Menezes et al. (2012) under the same study conditions. The low values observed are the result of the natural occurrence of pests and diseases in the crop since there was no introduction of insects or inoculation of pathogens. Consequently, there is a need for further studies, since there are few reports of damage caused by the occurrence of pests and diseases to the forage peanut crop, which should be monitored and considered in future actions in the breeding program.

Table 4. Genotypic means for the trials I, II and III of forage peanut genotypes in the joint analysis of seasons.

Trial	Pt	Ds	Vg	Fw	GC	Hg	CP	ADF	NDF	TDMY	LDMY
I	2.72	3.03	6.56	2.49	80.58	6.63	206.25	337.03	427.43	2,326.05	1,363.21
II	2.09	2.06	7.03	1.78	93.31	5.50	212.26	336.38	591.05	2,327.36	1,373.78
III	2.35	2.14	7.36	1.17	94.07	5.29	233.12	302.61	535.42	1,695.02	844.17

Occurrences of Pest (Pt) and Disease (Ds): visual scale of 0 to 10; Vigor (Vg): visual scale of 0 to 9; Flower (Fw): flowering in scale of 0 to 10; GC: ground cover,%; Height: plant height, cm; CP: crude protein content of aerial biomass, kg ha^{-1}; ADF and NDF: acid and neutral detergent fiber content, kg ha^{-1}; TDMY: total dry matter yield per harvest, kg ha^{-1}; LDMY: leaf dry matter yield per harvest, kg ha^{-1}.

Genotypic vigor means were high, above 7 for Trait II and III, which was also observed through phenotypic means under the same study conditions by Valentim et al. (2003), indicating that the species normally has good visual performance.

Flowering was low in the three trials, but the high CV_g, above 40%, indicates a high residual variation for this trait, which is also common for the species in the Cerrado Biome (Carvalho et al., 2009). GC was high, allowing coverage above 80% in the three trials throughout the entire evaluation period, as observed by Valentim et al. (2003). Assis et al. (2008), evaluating the establishment of forage peanut genotypes in the same edaphoclimatic conditions, observed GC genotypic values above 90% after six months of planting, which reinforces the species' soil protection capacity over the course of the year.

The mean height was above 5 cm for all trials and the mean TDMY for Trial I and II for each harvest was above 2,300 kg ha^{-1}. For Trial III, the mean TDMY was 1,700 kg ha^{-1} for each harvest. The mean LDMY was 1,700 kg ha^{-1} in Trial I and II and 840 kg ha^{-1} in Trial III. The annual mean phenotypic production was 7,700 to 8,700 kg ha^{-1} for TDMY and about 4,700 to 5,500 kg ha^{-1} for LDMY considering the three trials. Simeão et al. (2017) obtained genotypic TDMY values of 1,657 kg ha^{-1} and LDMY of 940 kg ha^{-1}, with a mean regrowth time of 130 days, and Fernandes et al. (2017b) observed phenotypic annual means of TDMY up to 8,680 kg ha^{-1}, however in the Cerrado Biome, with a more intense dry season throughout the year, which reinforces the importance of selecting ecotypes adapted to different biomes.

The genotypic means of nutritive value traits of the aerial biomass, composed of leaves and stems, from Trial I and II were close to those observed by Simeão et al. (2017) only for forage peanut leaves. This demonstrates the species' nutritional value, with small differentiation between leaves and stems throughout the evaluations, which makes the species a nutritionally stable forage option throughout the year.

The coefficients of genotypic correlation were significant, positive and varied from moderate (0.34 to 0.66) to high magnitude (> 0.67), according to the classification proposed by Resende (2015), among the traits aimed at forage production (vigor, GC, height, TDMY, and LDMY) (Table 5). The correlations were of smaller magnitude only between height and GC and between dry matter yields and GC and vigor in Trial III.

Table 5. Genotypic correlations between agronomic and nutritive value traits of forage peanut in the Trial I, II and III, in the joint analysis of seasons.

Traits	Trial I[1]									
	Pest	Disease	Vigor	Flower	GC	Height	CP	ADF	NDF	TDMY
Pest	-	-	-	-	-	-	-	-	-	-
Disease	-0.01	-	-	-	-	-	-	-	-	-
Vigor	-0.04	-0.11	-	-	-	-	-	-	-	-
Flower	0.17	0.27	-0.37	-	-	-	-	-	-	-
GC	-0.11	0.04	0.91**	-0.31	-	-	-	-	-	-
Height	0.57**	-0.13	0.56**	0.02	0.35	-	-	-	-	-
CP	-0.25	-0.30	0.47*	-0.28	0.45*	-0.03	-	-	-	-
ADF	0.36	0.04	-0.13	-0.07	-0.29	0.21	-0.25	-	-	-
NDF	0.27	-0.11	-0.09	-0.43	-0.05	-0.03	-0.11	0.51*	-	-
TDMY	-0.08	-0.17	0.97**	-0.44*	0.89**	0.50*	0.39	-0.13	-0.10	-
LDMY	-0.09	-0.22	0.96**	-0.45*	0.87**	0.48*	0.47*	-0.17	-0.14	0.98**
Traits	Trial II[2]									
	Pest	Disease	Vigor	Flower	GC	Height	CP	ADF	NDF	TDMY
Pest	-	-	-	-	-	-	-	-	-	-
Disease	0.52*	-	-	-	-	-	-	-	-	-
Vigor	-0.63**	-0.90**	-	-	-	-	-	-	-	-
Flower	0.26	0.58*	-0.49*	-	-	-	-	-	-	-
GC	-0.45	-0.84**	0.87**	-0.46	-	-	-	-	-	-
Height	0.62**	-0.07	0.06	-0.06	0.28	-	-	-	-	-
CP	-0.12	-0.38	0.35	0.01	0.20	-0.13	-	-	-	-
ADF	0.41	0.07	0.04	-0.21	0.06	0.48	0.32	-	-	-
NDF	-0.07	-0.60**	0.61**	-0.55*	0.52*	0.28	0.53*	0.59*	-	-
TDMY	-0.21	-0.65**	0.78**	-0.43	0.83**	0.48*	0.08	0.26	0.46	-
LDMY	-0.09	-0.66**	0.74**	-0.48*	0.78**	0.57*	0.14	0.31	0.53*	0.97**
Traits	Trial III[3]									
	Pest	Disease	Vigor	Flower	GC	Height	CP	ADF	NDF	TDMY
Pest	-	-	-	-	-	-	-	-	-	-
Disease	0.38*	-	-	-	-	-	-	-	-	-
Vigor	-0.68**	-0.83**	-	-	-	-	-	-	-	-
Flower	0.20	0.07	-0.19	-	-	-	-	-	-	-
GC	-0.24	-0.56**	0.56**	-0.20	-	-	-	-	-	-
Height	0.52**	0.13	-0.29	0.28	-0.32	-	-	-	-	-
CP	-0.2	-0.36*	0.39*	-0.14	0.29	-0.22	-	-	-	-
ADF	0.21	-0.11	-0.05	0.33	-0.19	-0.09	0.02	-	-	-
NDF	-0.31	-0.20	0.28	-0.35*	0.07	-0.60**	0.47**	0.39*	-	-
TDMY	0.32	-0.34*	0.16	0.28	0.31	0.66**	-0.02	0.10	-0.43*	-
LDMY	0.42*	-0.18	0.04	0.23	0.23	0.76**	-0.06	0.00	-0.45**	0.95**

[1]Trial I: performed between the years of 2006 and 2008; [2]Trial II: performed between the years of 2009 and 2011; [3]Trial III: performed between the years of 2011 and 2013. * and ** significant by Student t test at 5% e 1%, respectively. (-) Missing values or data. Flower: flowering; GC: ground cover, %; CP: crude protein content of aerial biomass; ADF and NDF: acid and neutral detergent fiber content; TDMY: total dry matter yield per harvest; LDMY: leaf dry matter yield per harvest.

Height showed a significant positive correlation of moderate magnitude with PMST and PMSF in the three trials. Height represents a non-destructive variable and is easily measured before harvest and has been recommended for use via indirect selection aimed at gains in dry matter, which is only obtained after harvesting (Menezes et al., 2014). Indirect selection facilitates the increment of a difficult target trait to obtain or has low heritability, especially if the correlated response is high (Resende, 2002). This answer is relevant in multicharacteristic selection, as it determines the trait to be used. However, its application considering height and TDMY in forage peanut needs further investigation, mainly be-

cause it varies in relation to the significance and magnitudes of correlation. On the other hand, GC and vigor, also non-destructive variables, demonstrated a very significant and, more generally, high magnitude correlation with TDMY in trials I and II. In addition to the possibility of indirect selection, high correlations are also important in genetic divergence studies, as they assist in reduce the number of traits used because of the redundancy of information (Menezes et al., 2012).

The occurrence of pests and disease correlated significantly with each other in moderate magnitude in trials II and III. The occurrence of pests demonstrated a highly significant median correlation with height, which may have occurred as a result of the higher canopy height favoring the accommodation of insects, which feed mainly on leaf tissues (Ivelina, 2018).

The occurrence of disease was negatively correlated, also with moderate magnitude, with TDMY in trials II and III. According to Viana et al. (2004), high productions are related to the lower occurrence of diseases, because of less leaf area loss, causing greater photosynthetic process and, consequently, superior vigor and production of plants. In fact, vigor also correlated negatively and with high significance with disease in trials II and III (Table 5).

Flowering had a negative correlation of medium magnitude with NDF in trials II and III. Flowering tends to be highly variable between genotypes and experimental sites, in addition to being directly influenced by management and water availability (Carvalho et al., 2009; Dávila et al., 2011; Menezes et al., 2012). On the other hand, NDF and ADF have less variability between genotypes, with little variation throughout the year (Fernandes et al., 2017b).

In this study, a lack of variability was observed for NDF in trials I and II (Table 3). There was also a significant negative correlation of moderate magnitude of flowering with TDMY and LDMY in trial I and with LDMY in Trial II. The relationship between flowering and nutritive value variables may be related to seasonal factors. The increase in forage yield associated with smaller flower production could explain the inverse relationship between flowering and NDF contents, which is related to vegetative growth and physiological maturation of forage species (Detmann et al., 2003).

In general, the correlations between variables related to forage production (vigor, height, TDMY, LDMY, and GC) were consistent throughout the trials, showing that this set of variables retains well-established and highly responsive relationships to aerial biomass production in forage peanut. The analysis and use of non-destructive variables, generally easier to obtain can optimize experimental conduction, promoting the reduction of evaluation time, and incurring in lower costs of resources and labor for the breeding program (Fernandes et al., 2017a).

The lack of correlation between some traits in some trials may have its origin in punctual correlations throughout the year, in specific dry and rainy seasons, for example. This would justify the analysis of data for each season, to score any correlations and performance of ecotypes for the region of study. This also tends to reinforce the effects of environmental and genotypic influences on the complex interactions between genotypes throughout the year and increase the potential for use and adaptation in each condition and location (Assis et al., 2008; Simeão et al., 2017).

Conclusion

There is genetic variability among the accessions of the Active Bank of Forage Peanut Germplasm for agronomic traits evaluated throughout the year, with high consistency among trials and favorable conditions for selection, with high accuracy.

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