

Yield adaptability and stability of semi-prostrate cowpea genotypes in the Northeast region of Brazil by REML/BLUP¹

Adaptabilidade e estabilidade produtiva de genótipos de feijão-caupi semiprostrados no Nordeste do Brasil via REML/BLUP

Maurisrael de Moura Rocha^{2*}, Kaesel Jackson Damasceno-Silva², José Ângelo Nogueira de Menezes-Júnior², Hélio Wilson Lemos de Carvalho³, Antônio Félix da Costa⁴, João Maria Pinheiro de Lima⁵, João Felinto dos Santos⁶, Cândida Hermínia Campos de Magalhães Bertini⁷, Adriana Rodrigues Passos⁸ and Otoniel Magalhães Moraes⁹

ABSTRACT - Cowpea is grown in different environmental conditions of the Northeast region of Brazil. Thus, selecting and developing cultivars with high yield, stability, and adaptability for this region is necessary due to the genotype × environment interaction. The objective of this work was to select cowpea lines of semi-prostrate plant simultaneously for high yield, adaptability, and genotypic stability in the Northeast region of Brazil by the REML/BLUP procedure. Twenty semi-prostrate genotypes—16 lines and four cultivars—were evaluated in 36 environments of the Northeast region from 2013-2015. The experiments were carried out under rainfed conditions in a completely randomized block design with four replications. The adaptability and genotypic stability were evaluated by the REML/BLUP procedure. The genotype × environment interaction was complex-type, with the grain yield ranging from 260 kg ha⁻¹ (Campo Grande do Piauí PI, 2015) to 2,764 kg ha⁻¹ (Arapipina PE, 2015), with overall mean of 1,304 kg ha⁻¹. According to the Harmonic Mean of Relative Performance of Genetic Values (HMRPGV) estimates, the cultivars BRS Marataoã and BRS Pajeú and the line MNC04-792F-129 had simultaneously high yield, adaptability, and genotypic stability, and can be recommended and grown with greater probability of success in all the environments of the Northeast region of Brazil.

Key words: *Vigna unguiculata*. Grain yield. Genotype × environment interaction. Mixed models.

RESUMO - O feijão-caupi é cultivado em diferentes condições ambientais na região Nordeste do Brasil. Devido à existência da interação entre genótipos e ambientes, torna-se necessário selecionar e desenvolver cultivares para essa região, com alta produtividade, adaptabilidade e estabilidade. Este trabalho teve como objetivo selecionar linhagens de feijão-caupi de porte semiprostrado simultaneamente para alta produtividade, adaptabilidade e estabilidade genotípica na região Nordeste do Brasil via procedimento REML/BLUP. Foram avaliados 20 genótipos de porte semiprostrado, sendo 16 linhagens e quatro cultivares, em 36 ambientes da Região Nordeste, no período de 2013 a 2015. Os experimentos foram conduzidos em condições de sequeiro em delineamento de blocos completos casualizados, com quatro repetições. A adaptabilidade e estabilidade genotípica foram avaliadas via procedimento REML/BLUP. A interação genótipos x ambientes foi do tipo complexa, com a produtividade de grãos variando de 260 kg ha⁻¹ (Campo Grande do Piauí-PI, 2015) a 2.764 kg ha⁻¹(Arapipina-PE, 2015) e média geral de 1.304 kg ha⁻¹. De acordo com as estimativas de média harmônica de desempenho relativo de valores genotípicos - MHPRVG, as cultivares BRS Marataoã e BRS Pajeú e a linhagem MNC04-792F-129 reúnem simultaneamente alta produtividade, adaptabilidade e estabilidade genotípica, podendo serem indicadas com maior probabilidade de sucesso no cultivo, para todos os ambientes da região Nordeste do Brasil.

Palavras-chave: *Vigna unguiculata*. Produtividade de grãos. Interação genótipos x ambientes. Modelos Mistos.

DOI: 10.5935/1806-6690.20170104

*Autor para correspondência

Recebido para publicação em 01/09/2016; aprovado em 12/04/2017

¹Pesquisa desenvolvida pela Embrapa (Empresa Brasileira de Pesquisa Agropecuária), Programa de Melhoramento de Feijão-caupi da Embrapa Meio-Norte, região Nordeste, Teresina-PI, Brasil

²Embrapa Meio-Norte, Teresina-PI, Brasil, maurisrael.rocha@embrapa.br, kaesel.damasceno@embrapa.br, jose-angelo.junior@embrapa.br

³Embrapa Tabuleiros Costeiros, Aracaju-SE, Brasil, helio.carvalho@embrapa.br

⁴Instituto Agrônomo de Pernambuco, Recife-PE, Brasil, felix.antonio@ipa.br

⁵Empresa de Pesquisa Agropecuária do Rio Grande do Norte, Natal-RN, Brasil, jmariaplina@gmail.com

⁶Empresa Estadual de Pesquisa Agropecuária da Paraíba, João Pessoa-PB, Brasil, joao_felinto_santos@hotmail.com

⁷Universidade Federal do Ceará, Fortaleza-CE, Brasil, candida@ufc.br

⁸Universidade Estadual de Feira de Santana, Feira de Santana-BA, Brasil, adrianarpassos@yahoo.com.br

⁹Universidade Estadual do Sudoeste da Bahia, Vitória da Conquista-BA, Brasil, moraisom@ig.com.br

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important crop species in the Northeast region of Brazil. It generates employment and income for the population of this region and is a source of energy and protein. Based on the estimates of CONAB (2017), the Northeast region presented in 2016 an area of 1,029,600 ha with a production of 196,100 Mg. This represents 82.56% and 54.00% of the area and production of this legume in Brazil, respectively. The largest national producers are the states of Mato Grosso (130.600 Mg), Ceará (56.700 Mg), and Maranhão (39.300 Mg).

Considering the area (1,247,100 ha) and total production (362,500 Mg) of cowpea in Brazil in 2016, and assuming that one hectare with this crop generates 0.8 jobs, the average annual consumption per capita is 18.21 kg (FEIJÃO..., 2009), the minimum price for a 60-kg bag is R\$ 80.00 (HETZEL, 2009), and the crop generated 997,680 jobs in 2016, produced a food supply for 19,906,645 people, and its production generated an income of R\$ 483,333,333.

Considering that cowpea is cultivated in a wide range of environments in Brazil, but the occurrence of genotype \times environment interaction (G \times E) may hinder the selection of superior genotypes and the recommendation of cultivars (CARVALHO *et al.*, 2016). Thus, in the final stages of a breeding program, elite lines are tested in various environments; this allows an investigation of the magnitude of the G \times E, adaptability, and production stability, which subsidize the recommendation of cultivars.

In the last 60 years, several methodologies to study the adaptability and stability of genotypes in multiple environments were developed to help the breeder to select the most stable and suitable genotypes for crops in different environments (CARVALHO *et al.*, 2016). The most commonly methodologies used in cowpea are the AMMI (BARROS *et al.*, 2013; DDAMULIRA *et al.*, 2015; SANTOS *et al.*, 2015), GGE Biplot (OKORONKWO; NWOFIA, 2016; OLAYIWOLA; SOREMI; OKELEYE, 2015; SANTOS *et al.*, 2016), and the Bayesian approach (BARROSO *et al.*, 2016; TEODORO *et al.*, 2015).

The REML/BLUP procedure has been one of the most used techniques in studies on adaptability and genotypic stability in Brazil; it is based on mixed models. This procedure estimates the components of variance by the Restricted Maximum Likelihood (REML) and the prediction of genetic values by the Best Linear Unbiased Prediction (BLUP) (CARIAS *et al.*, 2014). It was originally recommended for studies on quantitative genetics and selection of perennial plants (RESENDE, 2007a,b);

however, it has also been used in annual species such as rice (BORGES *et al.*, 2010), common bean (CHIORATO *et al.*, 2008; PEREIRA *et al.*, 2016), soybean (TESSELE *et al.*, 2016), and wheat (SILVA *et al.*, 2011).

The number of adaptability and stability studies in cowpea using the REML/BLUP procedure have increased (SANTOS *et al.*, 2016; TORRES *et al.*, 2015; TORRES *et al.*, 2016). This is because it allows simultaneous selection for yield, adaptability, and stability in the context of mixed models through the use of the Harmonic Mean of Relative Performance of Genetic Values (HMRPGV) method, proposed by Resende (2004).

The objective of this work was to select semi-prostrate cowpea lines simultaneously for high yield, adaptability, and genotypic stability in the Northeast region of Brazil by the REML/BLUP procedure.

MATERIAL AND METHODS

Twenty cowpea genotypes of semi-prostrate plant—16 lines and four cultivars—from the Embrapa Meio-Norte Cowpea Breeding Program (Table 1) were evaluated. These lines are part of the value-of-cultivation and use (VCU) trials, which are required for registering new cultivars by the National Register of Cultivars (RNC) of the Ministry of Agriculture, Livestock, and Food Supply (MAPA). These genotypes were selected in intermediate trials, which precede the VCU trials.

The genotypes were evaluated for grain yield (kg ha⁻¹) in 21 locations in the Northeast region of Brazil (Table 2) under rainfed conditions from 2013 to 2015. Some VCU trials were conducted in 1, 2, or 3 crop seasons, totaling 36 environments. Each environment was represented by the location initial letters and year of the crop season: APOD13, ARAP13, BARR13, CARI13, FREI13, ITAP13, MATA13, REDE13, SRMA13, UMBA13, URUC13, ARAR14, CARI14, BARR14, FEIR14, FREI14, GOIA14, IPAN14, ITAP14, MATA14, SERT14, SUMBA14, ARAR15, CAMP15, FEIR15, FREI15, IPAN15, GOIA15, LAGS15, NSDO15, PACA15, SAOJ15, SERT15, SRMA15, UMBA15 and URUC15.

The planting season varied according to the rainy season in the states, which occurred in January to March, except in Alagoas and Sergipe, which occurred in June. All the trials were conducted in a complete randomized block design with 20 treatments and four replications. The treatments were represented by a plot 3.20 m x 5.0 m with four 5 m rows spaced 0.80 m apart, with 0.25 m between plants; the evaluation area consisted of the two central rows. Four seeds were sown per hole, and 20 days after sowing the plants were thinned, leaving two plants per

hole. Cultural practices were carried out for the crop as recommended.

Individual analysis of variance for environments and joint analysis of variance for all environments were performed. The joint analysis of variance considered the effect of genotypes as fixed, and the effect of environments as random. The statistical model used followed the equation:

$$Y_{ijk} = \mu + g_i + e_j + ge_{ij} + \beta_{h(j)} + \varepsilon_{ijk} \quad (1)$$

wherein Y_{ijk} is the observed value of the genotype i in the environment j and block k ; μ is the overall mean of the trait; g_i is the effect of the genotype i ; e_j is the effect of the environment j ; ge_{ij} is the effect of the interaction of the genotype i with the environment j ; $\beta_{h(j)}$ is the effect of the block k within the environment j ; and ε_{ijk} is the experimental error associated with the plot ijk .

The mixed models approach through Restricted Maximum Likelihood (REML) and Best Linear Unbiased Prediction (BLUP) multivariate, i.e., REML/BLUP procedure, (RESENDE, 2007b) was used for the analysis of adaptability and stability. This procedure is a method

for ordering the genotype simultaneously regarding their genetic values (yield) and stability; it represents the BLUP procedure under the harmonic mean of the data. The lower the standard deviation of the genotypic behavior in the environments, the greater the harmonic mean of genotypic values (HMGV) in the environments. Thus, selection by the highest HMGV implies both selection for yield and stability (RESENDE, 2007b).

In the context of the mixed models, a simple and efficient measure is the relative performance of genotypic values (RPGV) in the environments, i.e., the adaptability of genetic values. The quantity $RPGV \cdot OM$ refers to the relative performance genotypic value multiplied by the overall mean of all environments, providing the average genotypic value, capitalizing the adaptability (RESENDE, 2007b).

Simultaneous selection for yield, adaptability, and stability in the context of mixed models can be performed by the Harmonic Mean of Relative Performance of Genetic Values (HMRPGV), proposed by Resende (2004). The quantity $HMRPGV \cdot OM$ refers

Table 1 - Semi-prostrate cowpea genotypes evaluated in the Northeast region of Brazil, from 2013 to 2015, their genealogy and commercial subclass

GC	Genotype	Genealogy	CS
G1	MNC04-768F-21	TE97-321G-2 × CE-315	ML
G2	MNC04-768F-16	TE97-321G-2 × CE-315	ML
G3	MNC04-768F-25	TE97-321G-2 × CE-315	ML
G4	MNC04-769F-26	CE-315 × TE97-304G-12	SV
G5	MNC04-769F-27	CE-315 × TE97-304G-12	ML
G6	MNC04-769F-31	CE-315 × TE97-304G-12	ML
G7	MNC04-769F-45	CE-315 × TE97-304G-12	SV
G8	MNC04-769F-46	CE-315 × TE97-304G-12	ML
G9	MNC04-769F-55	CE-315 × TE97-304G-12	ML
G10	MNC04-774F-78	TE97-309G-18 × TE97-304G-4	ML
G11	MNC04-774F-90	TE97-309G-18 × TE97-304G-4	SV
G12	MNC04-795F-154	(TE97-309G-24 × TE96-406-2E-28-2) × TE97-309G-24	SV
G13	MNC04-782F-108	MNC00-553D-8-1-2-3 × TV×5058-09C	ML
G14	MNC04-792F-123	MNC00-553D-8-1-2-3 × TV×5058-09C	SV
G15	MNC04-792F-129	CE-315 × TE97-304G-12	ML
G16	MNC04-795F-158	MNC99-518G-2 × IT92KD-279-3	SV
G17	BRS Marataoã	Seridó × TV×1836-013J	SV
G18	BRS Pajeú	CNC×405-17F × TE94-268-3D	ML
G19	BRS Pujante	TE90-180-26F × Epace 10	ML
G20	BRS Xiquexique	TE87-108-6G × TE87-98-8G	BL

GC = Genotype code; ML = Mulato; SV = Sempre-verde and BL = Branco Liso

to the HMRPGV multiplied by the overall mean of all environments, which provides the mean genotypic value penalized by instability and capitalized by adaptability.

The following statistical model was used for the randomized block designs with one observation per plot and several environments:

$$Y = Xb + Zg + Wga + e \quad (2)$$

wherein: y , b , g , ga , and e are the data vectors of fixed effects (mean of blocks through environments), of genotypic effects of the genotype (random), of effects of the genotype \times environment interaction (G \times E) (random), and of random errors, respectively; X , Z and W are the incidence matrices for b , g , and ga , respectively.

The Harmonic Mean of Genotypic Values (HMGV) was used for the evaluation of stability; the RPGV was used for the simultaneous evaluation of yield and adaptability; and the HMRPGV was used for the simultaneous evaluation of yield, adaptability, and

stability. These evaluation were carried out using the following expressions:

$$MHVG_i = a / \sum_{j=1}^a 1/Vg_j \quad (3)$$

$$PRVG_i = 1/a[\sum Vg_j / M_j] \quad (4)$$

$$MHPRVG_i = n / [\sum_{j=1}^n 1/Vg_{ij}] \quad (5)$$

wherein: n is the number of evaluation environments of the genotype i ; Vg_{ij} is the genotypic value of the genotype i in the environment j , expressed as a proportion of the average of this environment.

The HMRPGV method (RESENDE, 2007a) has the advantages of providing adaptability and genotypic—rather than phenotypic—stability; allowing the managing of heterogeneity of variances. Moreover, this method can be applied to any number of environments, eliminate noises of the genotype \times environment interaction (G \times E),

Table 2 - Altitude, geographic coordinate, biome, ecosystem, and climate of the locations where the value-of-cultivation and use trials of semi-prostrate cowpea were conducted in the Northeast region of Brazil, from 2013 to 2015

Location	Altitude	Latitude	Longitude	Biome	Ecosystem	Climate
Arapiraca-AL	264 m	09°45'07" S	36°39'39" W	Caatinga	Agreste	TSu
Feira de Santana-BA	234 m	12°16'01" S	38°58'01" W	Caatinga	Sertão	BSh
Barreira-CE	123 m	04°17'13" S	38°38'34" W	Caatinga	Sertão	BSh
Itapipoca-CE	109 m	03°29'38" S	39°34'44" W	Caatinga	Sertão	TAs
Redenção-CE	88 m	04°13'30" S	38°43'46" W	Caatinga	Sertão	TQSu
Pacajus-CE	60 m	04°10'22" S	38°27'39" W	Caatinga	Sertão	BSh
Mata Roma-MA	73 m	03°37'30" S	43°06'39" W	Cerrado	Meio-Norte	TAw
São R. das Mangabeiras-MA	225 m	07°01'19" S	45°26'51" W	Cerrado	Meio-Norte	TAw
Lagoa Seca-PB	634 m	07°10'15" S	35°51'14" W	Caatinga	Agreste	TAs
Araripina-PE	622 m	07°34'33" S	40°29'52" W	Caatinga	Sertão	BSh
Serra Talhada-PE	444 m	07°59'09" S	38°17'45" W	Caatinga	Sertão	BSh
Goiana-PE	444 m	07°33'39" S	35°00'10" W	Caatinga	Zona da Mata	TAs
São João do Piauí-PI	222 m	08°21'28" S	42°14'49" W	Caatinga	Sertão	BSh
Campo Grande do Piauí-PI	443 m	07°07'55" S	41°02'09" W	Caatinga	Sertão	BSh
Uruçuí-PI	167 m	07°13'44" S	44°33'41" W	Cerrado	Meio-Norte	TAw
Apodi-RN	67 m	05°39'50" S	37°47'56" W	Caatinga	Sertão	BSh
Ipanguaçu-RN	16 m	05°29'52" S	36°51'18" W	Caatinga	Sertão	BSh
Carira-SE	351 m	10°21'29" S	37°42'03" W	Caatinga	Sertão	BSh
Frei Paulo-SE	272 m	10°32'56" S	37°32'02" W	Caatinga	Sertão	BSh
Umbaúba-SE	130 m	11°22'58" S	37°39'28" W	Caatinga	Sertão	TAs
Nossa S. das Dores-SE	204 m	10°29'30" S	37°11'36" W	Caatinga	Sertão	TAs

TSu = Tropical sub-humid; TQSu = Tropical hot sub-humid; BSh = Semi-arid mild; TAs = Tropical with dry summer season; Taw = Tropical with dry winter season; Ts = Tropical dry

while considering the heritability of these effects; and allows the computation of genetic gain with selection by the three attributes simultaneously.

The analysis of variance was performed using the SAS software (SAS INSTITUTE, 2002). The analyses of adaptability and genotypic stability were performed by the model 54 of the Selegen-Reml/Blup software (RESENDE, 2007b).

RESULTS AND DISCUSSION

The joint analysis of variance for grain yield is presented in Table 3. Although all genotypes have shown a high inbreeding level and some relation (Table 1) and underwent several selection cycles, they differed significantly ($p < 0.01$), denoting the existence of selectable variability. Barros *et al.* (2013) and Santos *et al.* (2015), evaluated the grain yield of 20 cowpea genotypes for adaptability and productive stability in the Mid-North region and in Mato Grosso do Sul, Brazil, respectively, and also found differences between genotypes with a high inbreeding level.

The environments also differed for grain yield ($p < 0.01$), denoting that the characteristics of the testing environments (Table 2), combined with climatic variations affected this trait. Barroso *et al.* (2016) evaluate the grain yield of 20 cowpea genotypes in six environments of Mato Grosso do Sul and also found differences between the testing environments, and affirmed that the edaphoclimatic factors had the greatest effect on the adaptability and stability of the genotypes.

Contrasts between environments for grain yield were also observed by Ddamulira *et al.* (2015) who evaluated the adaptability and stability of 25 cowpea genotypes in three environments in Uganda, and Carvalho *et al.* (2015) who evaluated 20 cowpea genotypes in several environments of the Agreste and Tabuleiros Costeiros

regions in the states of Alagoas and Sergipe, Brazil.

The Araripina-PE environment in 2015 (ARAR15) was the most favorable for grain yield (2,764 kg ha⁻¹), while Campo Grande Piauí-PI, 2015 (CAMP15) was the least favorable (260 kg ha⁻¹) (Table 1).

The G×E interaction for grain yield was significant ($p < 0.01$) (Table 3); it showed the different behavior of the genotypes depending on the testing environments. This lead to difficulties in the selection of superior genotypes and recommending cultivars (CARVALHO *et al.*, 2016; ROCHA *et al.*, 2012), since the cultivars adapted to a particular condition may not perform well in other environmental conditions (TEODORO *et al.*, 2015). Olayiwola, Soremi and Okeleye (2015) evaluated the adaptability and stability of the grain yield of seven cowpea genotypes in four environments in Nigeria, and Santos *et al.* (2015) evaluated the grain yield of 25 cowpea genotypes in three environments in Uganda; both studies found different behavior of genotypes depending on the growing environments.

The overall mean grain yield was 1,304 kg ha⁻¹. This mean is well above the national (369 kg ha⁻¹) and world (461.30 kg ha⁻¹) mean for cowpea grain yield (FREIRE FILHO, 2011) and is also above the means obtained in other studies on cowpea genotypes in Brazil (BARROS *et al.*, 2013; SANTOS *et al.*, 2015; TORRES *et al.*, 2015, 2016). This shows the great potential of this line group in regard to grain yield and the possibility of selecting lines with higher means than the commercial cultivars.

According to estimates of components of variance (REML), the environmental variance was contributed most to the phenotypic variance (Table 4), representing 83% this variance, followed by the G×E (14%) and genotypic (3%) variances.

Evaluations of genotypes in multi-environments conducted by Chiorato *et al.* (2008) and Pereira *et al.* (2016) in common bean, and by Torres *et al.* (2015) and Oliveira, Fontes and Rocha (2015) in cowpea also

Table 3 - Joint analysis of variance for grain yield of 20 semi-prostrate cowpea genotypes evaluated in 36 environments of the Northeast region of Brazil, from 2013 to 2015

Blocks/Environments	DF	Mean square	p>F
Genotypes (G)	108	400743.00	<.0001
Environments (E)	35	1123875.00	<.0001
G×E	19	32661824.80	<.0001
Residue	665	309937.00	<.0001
CV (%)	2052	183926.00	
Overall mean (kg ha ⁻¹)	32,88		
Blocks/Environments	1.304		

found higher proportion of environmental variance than genotypic and environmental variances for grain yield.

The low genotype variance found in the group of genotypes evaluated (Table 4) was expected considering that some lines showed relation to each other (Table 1) and all are highly inbred, i.e., they have already undergone several selection cycles for high grain yield. Torres *et al.* (2015, 2016) evaluated the grain yield of 20 cowpea genotypes in multi-environments of Mato Grosso do Sul and also found lower estimates for the genotypic variance than environmental and G×E variances.

The trait yield is controlled by several genes and, therefore, is heavily affected by the environment

(Figure 1). In spite of the great effect of the environmental factors, denoted by the relative coefficient of variation (0.18), the heritability at an average genotypic level among the various environments was high (0.73) since the environmental effects were minimized. This allowed a high accuracy (0.85) in the selection of lines based on the average of the environments (Table 4). The heritability obtained in the present study was higher than those estimated by Torres *et al.* (2015, 2016), who evaluated the grain yield of 20 cowpea genotypes in multi-environment of Mato Grosso do Sul and found estimates of 0.68 and 0.54.

According to Chiorato *et al.* (2008), heritability at average level is determined based on the number of replicates and evaluated plants. In the case of the present

Figure 1 - Behavior of the grain yield of 36 testing environments obtained from the evaluation 20 semi-prostrate cowpea genotypes in the Northeast region of Brazil from 2013 to 2015

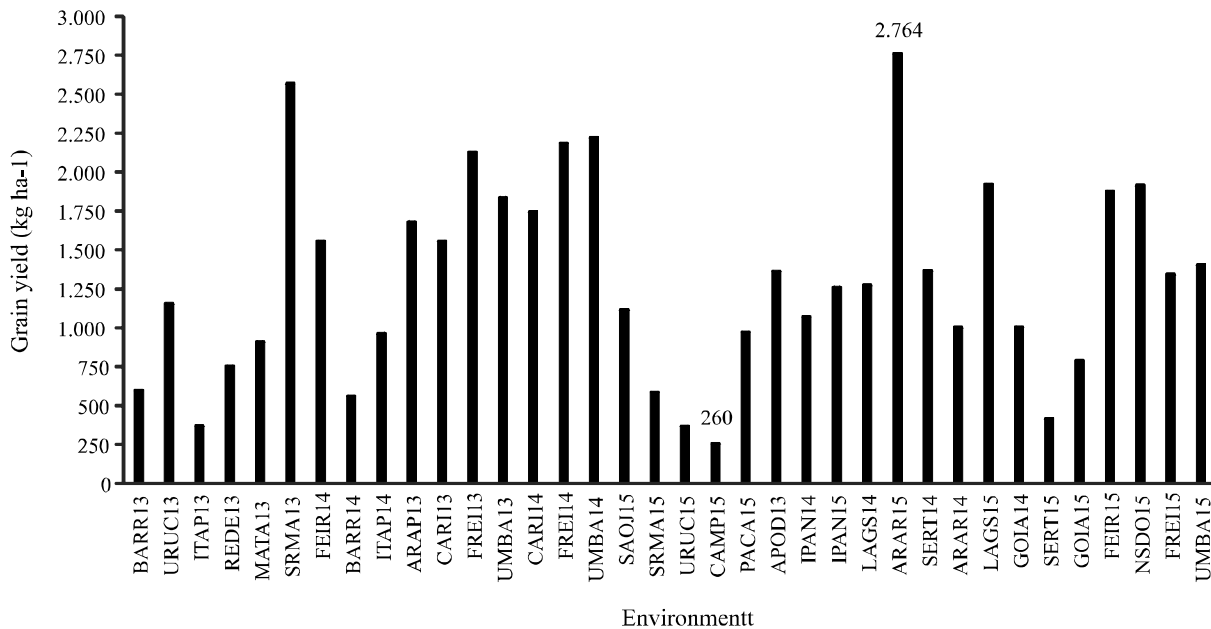


Table 4 - Estimates of components of variance (individual REML) and genetic parameters of 20 semi-prostrate cowpea genotypes evaluated in 36 environments in the Northeast region of Brazil, from 2013 to 2015

Parameter	Estimate
Genotypic variance (σ^2_g)	5703.91
Residual variance (σ^2_a)	182382.39
Genotype × environment interaction variance (σ^2_{ga})	31759.69
Phenotypic variance (σ^2_p)	219845.99
Heritability genotype mean (h^2_a)	0.73
Genotype selection Accuracy (Acgen)	0.85
Genotypic correlation between environments (rgloc)	0.15
Relative coefficient of variation (Cvg%/Cve%)	0.18

study, the size of the evaluation area in the experimental unit may have contributed positively to minimize the environmental effects, since the genotypes were represented by 80 plants in the evaluation area of the plot.

The G×E variance was the second most important (14%) (Table 4), which resulted from the low genotypic correlation between environments (0.15). These results showed the existence of G×E of complex-type, and that the best lines in one environment will not necessarily be the best in others (RESENDE, 2007a). This represents a certain difficulty in the selection of genotypes with broader adaptation, which justifies the use of the genotypes' stability and adaptability in the selection of lines.

Barros *et al.* (2013) evaluated the grain yield of 20 cowpea genotypes in the Mid-North region of Brazil and also found the G×E as the second factor affecting the phenotypic variance. On the other hand, Torres *et al.* (2016) found similar percentages for the G×E and environmental

variances evaluating the grain yield of cowpea genotypes in environments of Mato Grosso do Sul. Moreover, Barroso *et al.* (2016) found the genotypic variance as the second component influencing the phenotypic variance in Mato Grosso do Sul. The magnitudes of the components of variance may be different from one study to another, since they depend on the genetic variability of the genotypes, on the characteristics of the environments, and on the magnitude of the G×E interaction.

According to the mean component estimates (BLUP) and the confidence intervals associated with genotypic values ($u+g$), the genotypes G17 (BRS Marataoã), G15 (MNC04-792F-129) and G18 (BRS Pajeú) were superior than most of the genotypes evaluated and presented the highest genetic gains compared to the overall mean, with 137.82 kg or 10.56%; 111.09 kg or 8.52% and 101.27 kg or 7.76%, respectively (Table 5). These gains were lower than those observed by Torres *et al.* (2016), who evaluated

Table 5 - Estimates of mean components (individual BLUP) of the effects (g) and predicted genotypic values ($u+g$) free from interaction with environments, confidence interval lower limit (CILL), confidence interval higher limit (CIHL) and genetic gain (Gg) of 20 semi-prostrate cowpea genotypes evaluated in 36 environments of the Northeast region of Brazil, from 2013 to 2015

Order	G	$u + g$	(LIIC – LSIC) ¹	Gg
G17	137.82	1,442.28	1,359.87 – 1,524.69	137.82
G15	84.36	1,388.83	1,306.42 – 1,471.24	111.09
G18	81.64	1,386.11	1,303.70 – 1,468.52	101.27
G01	60.24	1,364.70	1,282.29 – 1,447.11	91.01
G13	43.25	1,347.72	1,265.30 – 1,430.13	81.46
G19	38.67	1,343.13	1,260.72 – 1,425.54	74.33
G04	28.94	1,333.40	1,250.99 – 1,415.82	67.84
G02	21.82	1,326.28	1,243.87 – 1,408.69	62.09
G08	8.95	1,313.42	1,231.01 – 1,395.83	56.19
G16	2.78	1,307.24	1,224.83 – 1,389.65	50.85
G09	-11.73	1,292.74	1,210.33 – 1,375.15	45.16
G05	-17.77	1,286.70	1,204.28 – 1,369.11	39.91
G03	-22.50	1,281.97	1,199.56 – 1,364.38	35.11
G20	-31.55	1,272.91	1,190.50 – 1,355.32	30.35
G12	-39.38	1,265.08	1,182.67 – 1,347.49	25.70
G14	-46.12	1,258.34	1,175.93 – 1,340.75	21.21
G07	-55.22	1,249.24	1,166.83 – 1,331.65	16.71
G10	-69.52	1,234.94	1,152.53 – 1,317.36	11.93
G11	-85.09	1,219.37	1,136.96 – 1,301.78	6.82
G06	-129.58	1,174.89	1,092.47 – 1,257.30	0
Overall mean (u)		1,304.46		

¹Confidence interval associated to the genotypic value estimates, at 95% probability

the grain yield of 20 cowpea genotypes in four environments of Mato Grosso do Sul and found gain estimates for the two best genotypes of 18.79% and 18.04%.

The genetic gain depends on the differential of the selection and heritability of the trait. Although the heritability of grain yield was high, a factors that may have led to lower gains than those observed by Torres *et al.* (2015, 2016) was the differences between the overall mean and the means of the superior genotypes, which in the present study were small compared to the differences found by those authors.

The results of stability (HMGV), adaptability (RPGV), and simultaneous stability and adaptability (HMRPGV) of the genotypes evaluated are presented in Table 6. The five best genotypes, based on the criteria HMGV, RPGV, and HMRPGV were the best based on the criterion of the mean genotypic value (Table 5). The coincidence was 100%, with inversion of order among the coincident ones between the genotypic value and the other parameters. According to Resende (2007a), the use of these attributes or selection criteria can provide further refinement in selection. Torres *et al.* (2016) state that this is an indication that these genotypes have high adaptive synergism in the 36 environments tested and exhibit good predictability, i.e., maintenance of grains yield in the different environments.

Similar results were obtained by Torres *et al.* (2015) who evaluated the grain yield of 20 cowpea genotypes in the State of Mato Grosso do Sul and found a percentage of coincidence in the ordering of the five best genotypes by the genotypic value, HMGV, RPGV and HMRPGV

of 100%, but without inversion of order between the coincident ones. Different results were reported by Torres *et al.* (2016), with a percentage of coincidence in the ordering of the five best genotypes by the genotypic value, with HMGV and HMRPGV of 80%, and with PRGV of 40%, evaluating grain yield of 20 cowpea genotypes in environments of Mato Grosso do Sul.

The three best genotypes (G17 - BRS Marataoã, G15 - MNC04-792F-129 and G18 - BRS Pajeú) by the criterion MHPRVG*MG had grain yield of 1,458, 1,423 and 1,409 kg ha⁻¹ (Table 6), i.e., an average superiority of 12.9 and 8%, respectively, over the overall mean of the 36 environments. According to Resende (2007a), these values are obtained through a process that already penalizes the lines for the instability in the environments and capitalizes the capacity of response (adaptability) to the improvement of the environment. These properties are intrinsic to the HMRPGV method.

The values of RPGV and HMRPGV (Table 6) indicate exactly the average superiority of the genotype in relation to the average of a given environment. Thus, the cultivar BRS Marataoã (G17) and the line MNC04-792F-129 (G15) respond on average with 1.12 and 1.09 times, respectively, the mean of any environment in which they are grown.

In general, the cultivars BRS Marataoã and BRS Pajeú, and the line MNC04-792F-129 were superior, simultaneously, for grain yield, adaptability and stability, and can be recommended for the environments of the Northeast region of Brazil with a lower risk of losses in grain yield due mainly to unpredictable environmental factors. According to Torres *et al.* (2016), genotypes that

Table 6 - Genetic value stability (HMGV), genetic values adaptability (RPGV), simultaneous genetic value adaptability and stability (HMRPGV), genotypic value capitalizing the adaptability (RPGV*OM) and genotypic value penalized by instability and capitalized by adaptability (HMRPGV*OM) of 20 semi-prostrate cowpea genotypes evaluated in 36 environments of Northeast region of Brazil, from 2013 to 2015

Order	MHVG	Order	PRVG	PRVG*MG	Order	MHPRVG	MHPRVG*MG
G17	1,077	G17	1.14	1,479	G17	1.12	1,458
G18	1,066	G18	1.10	1,441	G18	1.09	1,423
G15	1,031	G15	1.09	1,423	G15	1.08	1,409
G01	1,009	G01	1.07	1,397	G01	1.06	1,383
G13	992	G13	1.04	1,363	G13	1.04	1,358
G16	972	G19	1.03	1,350	G19	1.02	1,337
G02	969	G02	1.03	1,340	G02	1.02	1,334
G19	965	G04	1.02	1,333	G04	1.01	1,325
G04	952	G16	1.01	1,324	G16	1.01	1,316
G08	943	G08	1.01	1,322	G08	1.00	1,306

Continued Table 6

G03	916	G03	0.98	1,282	G5	0.98	1,275
G20	911	G05	0.98	1,282	G03	0.98	1,275
G05	911	G09	0.98	1,280	G09	0.97	1,272
G09	897	G20	0.96	1,272	G20	0.97	1,266
G14	877	G12	0.95	1,241	G14	0.95	1,236
G10	859	G14	0.95	1,239	G12	0.95	1,234
G12	857	G07	0.93	1,219	G10	0.93	1,208
G07	832	G10	0.93	1,215	G07	0.93	1,208
G11	794	G11	0.90	1,173	G11	0.89	1,158
G06	738	G06	0.85	1,113	G06	0.84	1,096
Overall mean							1,304

simultaneously have these three attributes can be used as selection criteria in breeding programs.

CONCLUSION

The cultivars BRS Marataoã and BRS Pajeú and the line MNC04-792F-129 combine simultaneously high yield, adaptability, and genotypic stability, and can be recommended and grown with greater probability of success in all evaluated environments of the Northeast region of Brazil.

ACKNOWLEDGEMENTS

The authors thank the partners of the cowpea genetic breeding network in the Northeast Region for the structural support and personnel in conducting the tests; and Dr. Marcos Deon Vilela de Resende, for the assistance in the statistical analysis of adaptability and stability via REML/BLUP procedure.

REFERENCES

- BARROS, M. A. *et al.* Adaptabilidade e estabilidade produtiva de feijão-caupi de porte semiprostrado. **Pesquisa Agropecuária Brasileira**, v. 48, n. 4, p. 403-410, 2013.
- BARROSO, L. M. A. *et al.* Bayesian approach increases accuracy when selecting cowpea genotypes with high adaptability and phenotypic stability. **Genetics and Molecular Research**, v. 15, n. 1, p. 1-11, 2016.
- BORGES, V. *et al.* Desempenho genotípico de linhagens de arroz de terras altas utilizando metodologia de modelos mistos. **Bragantia**, v. 69, n. 4, p. 833-842, 2010.

CARIAS, C. M. O. M. *et al.* Produtividade de grãos de cafeeiro conilon de diferentes grupos de maturação pelo procedimento REML/BLUP. **Semina: Ciências Agrárias**, v. 35, n. 2, p. 707-718, 2014.

CARVALHO, H. W. L. *et al.* **Adaptabilidade e estabilidade de cultivares de feijão-caupi de porte ereto na Zona Agreste do Nordeste brasileiro**. Aracaju: Embrapa Tabuleiros Costeiros, 2015. 26 p. (Embrapa Tabuleiros Costeiros. Boletim de Pesquisa, 83).

CARVALHO, L. C. B. *et al.* Evolution of methodology for the study of adaptability and stability in cultivated species. **African Journal of Agricultural Research**, v. 11, n. 12, p. 990-1000, 2016.

CHIORATO, A. F. *et al.* Prediction of genotypic values and estimate of genetic parameters in common bean. **Brazilian Archives of Biology and Technology**, v. 51, n. 3, p. 465-472, 2008.

COMPANHIA NACIONAL DE ABASTECIMENTO. **Acompanhamento da safra brasileira de grãos**. v. 4, safra 2016/17, n. 10. Brasília: CONAB, 2017. p. 95. Disponível em: <http://www.conab.gov.br/OlalaCMS/uploads/arquivos/17_07_12_11_17_01_boletim_graos_julho_2017.pdf>. 2017. Acesso em: 14 jul. 2017.

DDAMULIRA, G. *et al.* Grain yield and protein content of Brazilian cowpea genotypes under diverse Ugandan environments. **American Journal of Plant Science**, v. 6, p. 2074-2084, 2015.

FEIJÃO, oferta e demanda brasileiras. In: **AGRIANUAL 2009: anuário da agricultura brasileira**. São Paulo: Instituto FNP, 2009. p. 317.

FREIRE FILHO, F. R. (Ed.) **Feijão-caupi no Brasil: produção, melhoramento genético, avanços e desafios**. Teresina: Embrapa Meio-Norte, 2011. 84 p.

HETZEL, S. Com preço alto, área de feijão deve crescer. In: **AGRIANUAL 2009: anuário da agricultura brasileira**. São Paulo: Instituto FNP, 2009. p. 312-313.

- OKORONKWO, C. M.; NWOPIA, G. E. Yield stability and inter relationships between seed yield and associated traits of 25 cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. **African Journal of Agricultural Science and Technology**, v. 4, n. 5, p. 728-734, 2016.
- OLAYIWOLA, M. O.; SOREMI, P. A. S.; OKELEYE, K. A. Evaluation of some cowpea [*Vigna unguiculata* (L.) Walp.] genotypes for stability of performance over 4 years. **Current Research in Agricultural Sciences**, v. 2, n. 1, p. 22- 30, 2015.
- OLIVEIRA, I. J.; FONTES, J. R. A.; ROCHA, M. M. Seleção de genótipos de feijão-caupi para adaptabilidade e estabilidade produtiva no Estado do Amazonas. **Revista de Ciências Agrárias**, v. 58, n. 3, p. 292-300, 2015.
- PEREIRA, T. C. V. *et al.* Reflexos da interação genótipo x ambiente sobre o melhoramento genético de feijão. **Ciência Rural**, v. 46, n. 3, p. 411-417, 2016.
- RESENDE, M. D. V. **Matemática e estatística na análise de experimentos e no melhoramento genético**. Colombo: Embrapa Florestas, 2007a. 362 p.
- RESENDE, M. D. V. **Métodos estatísticos ótimos na análise de experimentos de campo**. Colombo: Embrapa Florestas, 2004. 65 p. (Embrapa Florestas. Documentos, 100).
- RESENDE, M. D. V. **Selegen-Reml/Blup**: sistema estatístico e seleção genética computadorizada via modelos lineares mistos. Colombo: Embrapa Florestas, 2007b. 359 p.
- ROCHA, M. M. *et al.* Adaptabilidade e estabilidade de genótipos de feijão-caupi quanto à produção de grãos frescos, em Teresina-PI. **Revista Científica Rural**, v. 14, n. 1, p. 40-55, 2012.
- SANTOS, A. *et al.* Adaptabilidade e estabilidade de genótipos de feijão-caupi ereto via REML/BLUP e GGE Biplot. **Bragantia**, v. 75, n. 3, p. 55-62, 2016.
- SANTOS, A. *et al.* Adaptability and stability of cowpea genotypes to Brazil Midwest. **African Journal of Agricultural Research**, v. 10, n. 41, p. 3901-3908, 2015.
- SAS INSTITUTE INC. **SAS/STAT user's guide**. Version 8.1. Cary, 2002. v. 1, 890 p.
- SILVA, R. R. *et al.* Adaptabilidade e estabilidade de cultivares de trigo em diferentes épocas de semeadura, no Paraná. **Pesquisa Agropecuária Brasileira**, v. 46, n. 11, p. 1439-1447, 2011.
- TEODORO, P. E. *et al.* Perspectiva bayesiana na seleção de genótipos de feijão-caupi em ensaios de valor de cultivo e uso. **Pesquisa Agropecuária Brasileira**, v. 50, n. 10, p. 878-885, 2015.
- TESSELE, A. *et al.* Adaptability and stability of soybean cultivars under different times of sowing in Southern Brazil. **Journal of Plant Sciences**, v. 4, n. 2, p. 17-22, 2016.
- TORRES, F. E. *et al.* Interação genótipos x ambientes em genótipos de feijão-caupi semiprostrados via modelos mistos. **Bragantia**, v. 74, n. 3, p. 15-20, 2015.
- TORRES, F. E. *et al.* Simultaneous selection for cowpea (*Vigna unguiculata* L.) genotypes with adaptability and yield stability using mixed models. **Genetics and Molecular Research**, v. 15, n. 2, 1-11, 2016.