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Adaptability and stability of cowpea genotypes to Brazilian Midwest

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This study aimed to evaluate cowpea genotypes for adaptability and stability of grain yield using different methods, in order to support the launch and/or cultivars recommendation for agribusiness in the Brazilian Midwest. Trials were conducted from 2010 to 2012 in four locations, totaling eight environments. We evaluated 20 cowpea genotypes arranged in a randomized block design with four replications. Studies of adaptability and stability of cowpea genotypes were estimated using different methods. The environments A1, A5, A6 and A8 are the most appropriate for selecting superior genotypes for adaptability and stability. The genotypes MNC03-737F-5-1 BRS-Tumucumaque, BRS-Guariba, MNC02-684F-5-6, MNC03-725F-3, MNC02-682F-2-6, BRS-Cauamé, BRS-Itaim and MNC03- 737F-5-11 showed adaptability and stability sufficient for recommendation for the region. Eberhart and Russell, Lin and Binns and AMMI methods can be used as a complementary way to better predict the genotype performance.

Key words: Genotype, environment interaction, selection *Vigna unguiculata.*

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) has a great socioeconomic importance, both as food and as a generator of employment and income. It is rich in protein, minerals and fiber (Frota et al., 2008) and constitutes a basic food component of rural and urban populations in North and Northeast of the Brazil. Currently the use of cowpea has expanded more intensively to the Midwest region of Brazil.

Small farmers, who still practice traditional farming, cultivate cowpea, in North and Northeast of the Brazil. Large scale cultivation of cowpea in the states of Mato Grosso and Mato Grosso do Sul, in the Brazilian Midwest began from 2006, and the production comes mainly from medium and large entrepreneurs, who adopt modern technologies for crop production with an average productivity of 960 kg ha^{-1} (Freire Filho et al., 2011).

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Table 1. Characteristics of each experimental environment.

Environments	Year	Municipality	Altitude (m)	Latitude	Longitude	Biome	Climate	Soil
A1	2010	Aquidauana	430	22°01’S	54°05’W	Pantanal	AW	Oxisol red
A2	2010	Chapadão do Sul	790	18°05’S	52°04’W	Cerrado	AW	Oxisol red
A3	2010	Dourados	147	20°03’S	55°05’W	Mata Atlântica	CW	Utisol red
A4	2011	Chapadão do Sul	790	18°05’S	52°04’W	Cerrado	AW	Oxisol red
A5	2011	Dourados	147	20°03’S	55°05’W	Mata Atlântica	CW	Utisol red
A6	2011	Chapadão do Sul	790	18°05’S	52°04’W	Cerrado	AW	Oxisol red
A7	2012	Aquidauana	430	22°01’S	54^o05’W	Pantanal	AW	Oxisol red
A8	2012	Dourados	147	20°03’S	55°05’W	Mata Atlântica	CW	Utisol red

An understanding of the genotype and environmental interactions in cow pea is important both for crop improvement and to ascertain the performance of genotypes to variations in the environmental factors. Despite of its importance most studies on cowpea have neglected the interactions between genotypes and environment, not providing detailed information on the performance of each genotype front to environmental variations. An analysis of adaptability and stability is essential to identify varieties with predictable performance and that are responsive to environmental variations in specific or wide conditions, making more reliable the recommendation of cultivars (Cruz et al., 2012).

Adaptability refers to the ability of genotypes to take advantage of the existing environmental conditions, whereas stability relates to the ability of a genotype response in a highly predictable manner to an environmental condition (Cruz et al., 2012). The choice of methods used for analysis depends on the experimental data, mainly related to the number of available environments, the precision required and the type of desired information. Several methods have been used to study the adaptability and stability of genotypes in cowpea (Ojo et al., 2006; Akande, 2007; Rocha et al., 2007; Barros et al., 2013).

The main purpose of a breeding program is launch superior cultivars to those existing. Thus, the lines are intensively evaluated for several agronomic characters. However, the relative ranking of the lines, in most cases, is not consistent, since variations may occur because of the interactions between genotype and environment. Therefore, this interaction takes leading role in the process of cultivar recommendation. In this way, cultivars with high yielding potential and good adaptability and stability, could be recommended with greater reliability for Brazilian regions.

Though several previous studies on cowpea have shown high genetic divergence (Santos et al., 2014a), as evidenced through correlations and path analysis (Santos et al., 2014b), there are few studies about the adaptability and stability of cowpea genotypes. Therefore, the aim of this study was to evaluate selected cowpea genotypes for the adaptability and stability of grains using different methods, in order to introduce and/or recommend cultivars for the crop agrobusiness in the Brazilian Midwest.

MATERIALS AND METHODS

Trials were conducted from February to July of 2010, 2011 and 2012 in the municipalities of Aquidauana, Chapadão do Sul and Dourados, located in the Midwest region of the Brazil. The trials in Chapadão do Sul were carried out only in 2010 and 2011, totaling eight environments (Table 1). It was used a randomized block design with four replications and 20 genotypes. Experimental plot consisted of four rows with five meters of length, spaced 0.50 m apart, considering as useful area the two central lines. The seeds of cowpea genotypes used in the trial were obtained from the Embrapa Meio-Norte, which included 16 pure lines and four commercial cultivars.

The trials were carried out in February, April and March, in Dourados, Aquidauana and Chapadão do Sul, respectively. Fertilization at the time of sowing consisted of 200 kg ha^{-1} of the commercial formulates 04-20-20 of NPK. One week after seedling emergence manual thinning was done, allowing eight plants per meter.

Data were subjected to joint analysis of variance and subsequently the adaptability and stability analysis through the methods of Eberhart and Russell (1966), Carneiro (1998) and AMMI model (Gauch and Zobel, 1988). Eberhart and Russell’s (1966) regression adopted was $Y_{ij} = m_i + b_i I_j + d_{ij} + e_{ij}$, wherein Y_{ij} is the mean observed of the genotype *i* in the environment *j*; d_{ij} is the regression deviation of the genotype *i* in the environment *j*; e_{ij} is the mean error associated with the average. The environmental index was estimated according to the equation $I_j = \overline{Y}_j - \overline{Y}_m$, with $\sum_{j=1}^{n} I_j = 0$, wherein $\overline{Y}_m$ is the overall mean; $\overline{Y}_j$ is the mean in the environmental *j*; *n* is the number of environments.

According to Eberhart and Russell (1966) method, genotype adaptability was measured by the parameter β_{1i}, while the behavior stability was evaluated by the variance of the regression deviations (σ^2_{di}) and by coefficient of determination (R^2) that, according to Cruz et al. (2012), is an auxiliary measure for assessing stability. When σ^2_{di} is significant and R^2 is higher than 80%, R^2 indicates acceptable predictability.

Carneiro (1998) adopts thr P_i measure as the mean square distance between the genotype *i* and the genotype with maximum response to the environment *j*, in the following way: $P_i = \sum_{j=1}^{n} \frac{(Y_{ij} - M_j)^2}{2n}$, wherein P_i is the superiority index of genotype *i*;

Table 2. Resume from the joint analysis of variance according to Eberhart and Russell method, regarding to yield grain (kg ha^{-1}), of 20 cowpea genotypes obtained in eight environments, from 2010 to 2012.

Sources of variation	Degrees of freedom	F-value	% variation
Environment (E)	7	258.88*	78.27
Genotype (G)	19	7.34*	6.02
G x E	133	2.73*	15.70
E/G	140	15.54*	-
Linear E	1	1812.14*	83.29
Linear G x E	19	3.95*	3.44
Combined deviation (E/G)	120	2.40*	13.25
Residue	477	-	-

*Significant ($P \leq 0.01$) by F-test.

Y_{ij} is the yield of the genotype *i* in the environment *j*; M_j is the yield of the genotype with maximum response among all genotypes in in the environment *j*; *n* is the number of environments. This expression can be unfolded into:

$$P_i = \frac{[n(Y_i - M_g)^2 + \sum_{j=1}^{n}(Y_{ij} - Y_g - M_j + M_g)^2]}{2n},$$

wherein Y_g is the mean of the genotype *i* and M_g is the mean of the genotypes with maximum response. Considering that M_j represents a hypothetical genotype, the first term of the equation is the sum of squares for the genetic effect and the second is the sum of squares of the genotype x environment interaction.

In AMMI-biplot analysis, we considered the genotype and environments effects as fixes and the model according to the equation:

$$Y_{ij} = \mu + g_i + a_j + \sum_{k=1}^{n}\lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \bar{\varepsilon}_{ij}$$ wherein: Y_{ij}: is the average response of the i-th genotype (i = 1,2, ... ,G genotypes) in the j-th environment (j = 1,2, ... , A environments); μ: the overall mean of the trials; g_i: i-th genotype effect; a_j: j-ésimo environment effect; λ_k: k-th singular value (scalar) of the original interaction matrix (named by G x E); γ_{ik}: element corresponding to i-th genotype in k-th matrix column singular vector GE; α_{jk}: element corresponding to j-th environment in k-th matrix line singular vector GE; ρ_{ij}: noise associate to term $(ga)_{ij}$ of the classic genotype *i* with environment *j* interaction; $\ddot{e}_{ij}$: average experimental error. For defining the number of axes to be retained in order to explain the pattern related to interaction, we adopted the criteria proposed by Gauch and Zobel (1988), taking into consideration the proportion of the sum of squares from the interaction ($SS_{G \times E}$) accumulated until the n-th axis. Thus, the stopping point that determines the model selection for each family member of AMMI models (AMMI0, AMMI1,..., AMMIn) was obtained based on the significance of the F tests from Gollob (1968).

The interpretation of adaptability and stability of genotypes and environments, that is, its coordinates in the main axes of interaction (IPCA) was based on biplot graphical analysis (Gabriel, 1971), graph that contains two categories of points or markers; in case, one referring to genotypes and other to environment. First, we proceeded the graphic interpretation in biplot based on the variation of the main additive effects of genotype and environment and multiplicative effect of G x E interaction, and subsequently the interpretation based only on the multiplier effect of G x E interaction. All analysis were performed with Genes software (Cruz, 2013).

RESULTS AND DISCUSSION

In the joint analysis (Table 2), all effects were significant ($P \leq 0.01$), which indicates contrasts between the environments and the occurrence of differential response of genotypes across to environmental effects. This can be confirmed by looking up soil and climatic characteristics of each environment (Table 1), showing differences in altitude, latitude, longitude, climate and soil type, besides climatic effects such as precipitation and temperature. The existence of significant genotype x environment for grain yield that the analyzes of stability and adaptability are appropriate, the fact that the edaphoclimatic are the factors that most influence the adaptability and stability of genotypes.

We observed that the magnitude of environmental effect (78.27%) was more important than the effect of the G x E interaction (15.70%), and which was greater than the effect of genotypes (6.02%). These results indicate the existence of variability among the evaluated environments, and consequently, the performance of genotypes, justifying a more detailed study on the individual performance of cultivar in order to identify the magnitude of their interactions with the environment. These results are similar to those reported by Akande (2007), Sarvamangala et al. (2010) and Nunes et al. (2014).

Combined deviations were highly significant ($P \leq 0.01$), indicating the stability of the linear and nonlinear components involved in the phenotypic performance of the genotypes in the environments under study. It is perceived that only a small part of the G x E interaction can be explained by the linear relationship among

Table 3. Overall means (β_{0i}), estimates of coefficients of regression ($\hat{\beta}_{1i}$), regression deviations ($\hat{\sigma}^2_{di}$) and coefficients of determination (R^2), according to Eberhart and Russell method, regarding to yield grain (kg ha^{-1}), of 20 cowpea genotypes obtained in eight environments, from 2010 to 2013.

Identification	Genotypes	β_{0i}	$\hat{\beta}_{1i}$ (1)	$\hat{\sigma}^2_{di}$ (2)	R² (%)
G1	MNC02-675F-4-9	802 ^{b}	1.00^{ns}	3934.40^{ns}	91.85
G2	MNC02-675F-4-2	785 ^{b}	0.92^{ns}	11221.45^{ns}	87.50
G3	MNC02-675F-9-2	698 ^{b}	0.94^{ns}	-12555.85^{ns}	98.27
G4	MNC02-675F-9-3	782 ^{b}	1.06^{ns}	11184.20^{ns}	90.33
G5	MNC02-676F-3	886 ^{a}	0.88^{ns}	21179.47*	82.31
G6	MNC02-682F-2-6	916 ^{a}	0.65^{ns}	36334.69**	64.51
G7	MNC02-683F-1	744 ^{b}	0.76^{ns}	27218.04*	75.34
G8	MNC02-684F-5-6	895 ^{a}	0.85^{ns}	-1238.08^{ns}	91.74
G9	MNC03-725F-3	874 ^{a}	1.09^{ns}	17291.85^{ns}	88.94
G10	MNC03-736F-7	668 ^{b}	0.69^{ns}	18750.77*	75.67
G11	MNC03-737F-5-1	910 ^{a}	1.44**	-1636.31^{ns}	96.99
G12	MNC03-737F-5-4	859 ^{a}	1.28^{ns}	-9581.43^{ns}	98.26
G13	MNC03-737F-5-9	873 ^{a}	1.27^{ns}	6974.84^{ns}	94.05
G14	MNC03-737F-5-10	696 ^{b}	1.16^{ns}	20888.70*	89.23
G15	MNC03-737F-5-11	897 ^{a}	1.23^{ns}	62718.19**	81.14
G16	MNC03-737F-11	815 ^{b}	0.79^{ns}	32107.30**	74.62
G17	BRS-Tumucumaque	1.173 ^{a}	0.92^{ns}	21851.01*	83.61
G18	BRS-Cauamé	896 ^{a}	0.87^{ns}	41770.17**	74.74
G19	BRS-Itaim	883 ^{a}	1.02^{ns}	54517.18**	76.77
G20	BRS-Guariba	1.031 ^{a}	1.08^{ns}	28622.44*	85.59
-	Mean	854,53			

^{ns}, ** and *: not significant, significant a 1 and 5% of probability respectively; $^{(1), (2)}$: significant by t-test; significant by F-test, respectively; Means followed by the same letter in the same column do not differ by the Skott and Knott test.

genotypes and environments, indicating that the G x E interaction is not adequately explained by the regression.

The average grain yield (β_0) ranged from 668 to 1,173 kg ha^{-1} for genotypes MNC03-736F-7 and BRS-Tumucumaque, respectively, with overall mean of 854.53 kg ha^{-1}, standing out with better adaptation those genotypes with average yield grain above this mean such as BRS-Guariba, MNC02-682F-2-6, MNC03-737F-5-1 and MNC02-676F-3 (Table 3).

Considering the twelve genotypes that showed better adaptation (β_0 > overall mean), similar to the unit, indicating that the genotypes had wide adaptability to the evaluated environments. The genotype MNC03-737F-5-1 proved to be very effective in increasing average yields under unfavorable conditions ($\hat{\beta}_{1i} > 1$), suggesting that it has a great ability to adapt to stressful environment. However, the use of this should be careful, since, to unsuitable environmental conditions, i.e., in regions involving low technological level and/or subject to soil and climatic variations, it yield can be reduced. The genotypes MNC02-676F-3, MNC02-682F-2-6, MNC02-684F-5-6, MNC03-725F-3, MNC03-737F-5-4, MNC03-737F-5-9, MNC03-737F-5-11, BRS-Tumucumaque, BRS-Cauamé, BRS-Itaim and BRS-Guariba have shown to be wide adaptation, suggesting that these genotypes tolerate different environmental conditions keeping their average yield around the overall mean.

Regarding to predictability, nine genotypes showed no significant regression deviation ($\hat{\sigma}^2_{di} = 0$), indicating stability, it means that these genotypes not varied their average yield over the years and places, being weakly influenced by environmental conditions. We also observe that only six genotypes showed R² lower than 80%. The coefficient of determination higher than the above represents low dispersion of data, indicating high reliability in the type of environmental response determined aby regression. Thus, this value should be used as reference so that the regression satisfactorily explain the performance of a genotype depending on an environment (Cruz et al., 2012).

P_i values, according to the method proposed by Lin and Binns (1988), for all environments and their deployment to favorable and unfavorable environments according to the methodology suggested by Carneiro (1998) are shown in Table 4. We observed that among the twenty genotypes were identified five that stood out showing the lower P_i overall values: BRS-Tumucumaque, BRS-Guariba, MNC03-737F-5-1, MNC02-682F-2-6 and

Table 4. Estimates of the parameters overall, favorable and unfavorable P_i, regarding to yield grain (kg ha^{-1}), of 20 cowpea genotypes obtained in eight environments, from 2010 to 2012.

Identification	Genotypes	Overall mean	Overall P_i /1000	P_i (Favorable)	P_i (Unfavorable)
G1	MNC02-675F-4-9	802 ^{b}	145.50	167.27	139.04
G2	MNC02-675F-4-2	785 ^{b}	166.70	184.95	151.26
G3	MNC02-675F-9-2	698 ^{b}	198.12	205.43	153.66
G4	MNC02-675F-9-3	782 ^{b}	163.21	179.92	141.46
G5	MNC02-676F-3	886 ^{a}	112.25	109.7	91.04
G6	MNC02-682F-2-6	916 ^{a}	83.40	151.97	117.17
G7	MNC02-683F-1	744 ^{b}	203.86	310.27	157.77
G8	MNC02-684F-5-6	895 ^{a}	97.84	77.89	60.02
G9	MNC03-725F-3	874 ^{a}	113.43	123.87	96.64
G10	MNC03-736F-7	668 ^{b}	246.59	365.05	237.87
G11	MNC03-737F-5-1	910 ^{a}	83.45	65.75	51.31
G12	MNC03-737F-5-4	859 ^{a}	114.58	124.65	97.45
G13	MNC03-737F-5-9	873 ^{a}	121.17	128.42	107.3
G14	MNC03-737F-5-10	696 ^{b}	202.57	238.48	155.1
G15	MNC03-737F-5-11	897 ^{a}	130.28	161.68	128.12
G16	MNC03-737F-11	815 ^{b}	176.91	198.73	153.48
G17	BRS-Tumucumaque	1,173 ^{a}	21.75	36.91	6.59
G18	BRS-Cauamé	896 ^{a}	129.16	156.64	118.47
G19	BRS-Itaim	883 ^{a}	131.97	164.48	132.13
G20	BRS-Guariba	1,031 ^{a}	58.53	53.24	45.37
-	Mean	854.53			

Means followed by different letters in the same column do not differ by Skott-Knott test ($P \leq 0.05$).

MNC02-684F-5-6. According to Cruz et al. (2012), a great advantage of the Lin and Binns method is the immediate identification of the most stable genotypes due to the uniqueness of the P_i parameter, but this method only shows a general parameter estimation for recommending cultivars. However, modifying the method proposed by Carneiro (1998) provides an estimate of P_i for favorable and unfavorable environments that provide greater robustness to the method.

Given the above, we verified that the genotypes BRS-Tumucumaque, BRS-Guariba, MNC03-737F-5-1 and MNC02-684F-5-6 showed the lowest P_i values both in favorable and in unfavorable environments, especially the BRS-Tumucumaque, which was the most yield, considering the overall mean, with the lowest P_i overall value and P_i in favorable and in unfavorable environments and also one of the smaller contribution to the interaction, thus can be considered of general adaptation and high predictability. In studies with cowpea, Adewale et al. (2010); Shiringani and Shimelis (2011) found results related to the P_i parameter, thus confirming that the most adapted and stable genotypes are associated with high incomes.

Another important fact was that the genotype MNC03-737F-5-1, demonstrated wide adaptability and stability by presenting lower P_i values in favorable and unfavorable environments, however, by Eberhart and Russel (1966) method this genotype has proved to be very demanding in unfavorable conditions ($\hat{\beta}_{1i}$ > 1) suggesting that it has great ability to exploit advantageously improving the environment. Thus it can be inferred that the combined use of these two methods brings more detailed information about the adaptability and stability of evaluated genotypes. This results corroborate those obtained by Almeida et al. (2012), where, working with different group of genotypes and environments, the authors concluded that it is recommended the use of Lin and Binns methodology in conjunction with Eberhart and Russel (1966) method.

The genotypes MNC02-675F-4-2, MNC02-675F-9-2, MNC02-676F-3, MNC02-683F-1, MNC02-684F-5-6, MNC03-737F-11, BRS-Tumucumaque and BRS-Cauamé showed lower P_i values in the unfavorable environments when compared to favorable environments or overall P_i, indicating that these genotypes have a specific adaptation to unfavorable conditions. It should also be emphasized that smaller P_i values reduce the deviation around the maximum yield for each environment. Thus, greater stability is associated with higher yield. However, the estimation of the P_i parameter is highly correlated to yield, so genotypes with lower grain yield will have a high P_i value, without necessarily being highly unstable.

Thus, although the genotypes MNC02-675F-4-9, MNC02-675F-4-2, MNC02-675F-9-2 and MNC02-675F-

Table 5. Analysis of additive main effects and multiplicative interaction regarding to yield grain (kg ha^{-1}), of 15 cowpea genotypes obtained in eight environments, from 2010 to 2012.

S.V	Degrees of freedom	F-value	%SS$_{G\ x\ E}$/PCA $^{(1)}$	%SS$_{G\ x\ E\ Acummulate}$
Genotypes (G)	19	7.34*	-	-
Environments (E)	7	258.88*	-	-
G x E	133	2.73*	-	-
PCA 1	25	6.57*	52.52	52.52
Residue$_{AMMI1}$	108	1.55*	-	
PCA 2	23	1.82*	22.15	74.67
Residue$_{AMMI2}$	85	1.21^{ns}	-	
Mean error	477	-	-	-

* and ^{ns}: not significant and significant a 1% of probability respectively; $^{(1)}$: Percentage of the sum of squares of the genotype x environment interaction captured by IPCA.

9-3 present high overall P_i values, it were considered by the (Eberhart and Russel, 1966) methodology as high stability (regression deviations no significant). However growing of these genotypes should be thoroughly evaluated, because it yielded below the overall average.

In AMMI analysis, the SS$_{G\ x\ E}$ was decomposed in four IPCAs; however, only the first two axes (IPCA1 and IPCA3) were significant by the F_R test and explained 52.52 and 22.15%, respectively, covering a total of 74.67% of the SQ$_{G\ x\ E}$. For the interpretation are shown only the first two IPCAs, since the residue of IPCA2 was not significant by the F_R test. This indicates that the most predictive model is AMMI2. So this was selected for the study of stability and adaptability of genotypes and environments (Table 5). Similar results to those reported by Freire Filho et al. (2005), where the authors observed that the first two components explained 72% of the standard variance. Already Asio et al. (2005) reported that the first principal component explained 87.9% of the entire variation.

The graphical interpretation in *biplot* was based on the variation due to the main additive effects of genotype and environment and multiplicative effect of G x E interaction (AMMI 2), as well as only based on multiplicative effect of G x E interaction (AMMI 1). In this last case, the effect of G x E interaction is analyzed, aiming to confirm the observed stability in *biplot* AMMI 2.

In the graphical representation of the AMMI2 analysis, genotypes and stable environments are those whose points are situated near to the origin, i.e., the score values are almost zero in the two axes of the interaction (IPCA1 and IPCA2). The genotypes that contribute less to the G x E interaction were MNC02-675F-9-2 (3), MNC02-675F-9-3 (4), MNC02-675F-4-2 (2), MNC02-675F-4-9 (1) and MNC02-684F-5-6 (8) and the environments A2, A4 and A8 were the most stable, whose point is located near the origin, that is, the scores are lower value for the two axes of interaction (Figure 1A and B).

The genotypes MNC02-675F-4-9 (1), MNC03-725F-3 (9) and MNC03-737F-5-11 (15) interact positively with the A2 and A5 environments because besides having the same sign scores, the points relating to these genotypes suggest a common direction and the vectors starting from the origin with a small angle between them. The genotypes MNC03-737F-11 (16), MNC03-736F-7 (10), MNC02-683F-1 (7), MNC02-684F-5-6 (8), MNC02-675F-4-2 (2) and BRS-Cauamé (18) also demonstrated positive specific interaction with the environment A3, A8 and A4 by similar interpretation. There has been a clear lack adaptation of genotypes MNC03-737F-5-11 (15) and MNC03-725F-3 (9) with the environments A7 and A6 in the two graphs (markers pointing in opposite directions).

In *biplot* AMMI1 the abscissa axis represents the main effects (mean of genotypes and environment) and the axis of ordinates represents the scores for the genotype by environment interaction of said axis. Genotypes and stable environments are those whose points are located near to zero. It are identify which genotypes that have grain yield lower or higher than the average overall production through vertical reference line.

The genotypes MNC02-675F-4-9 (1), MNC02-675F-4-2 (2), MNC02-675F-9-2 (3), MNC02-675F-9-3 (4), MNC02-683F-1 (7), MNC03-736F-7 (10), MNC03-737F-5-10 (14) and MNC03-737F-11 (16) have yield less than the overall average, which is 854.53 kg ha^{-1}, while the other genotypes have yield equal to or higher than the average. The environments with low yield are A2, A3, A4 and A7, and the environments that have the highest yield are A1, A5, A6 and A8. The points located around zero from the horizontal axis IPCA1 correspond to genotypes MNC02-675F-9-3 (4), BRS-Itaim (19), MNC03-736F-7 (10) and MNC02-684F-5-6 (8) and the environments A2, A3, A8 and A6 more stable, being the first two associated to low yield and the last two associated to high yield (Figure 1A).

The environmental stability has great importance because it informs about the reliability of ordering of genotypes in a given test environment, compared to the average rating for the tested environments. The most

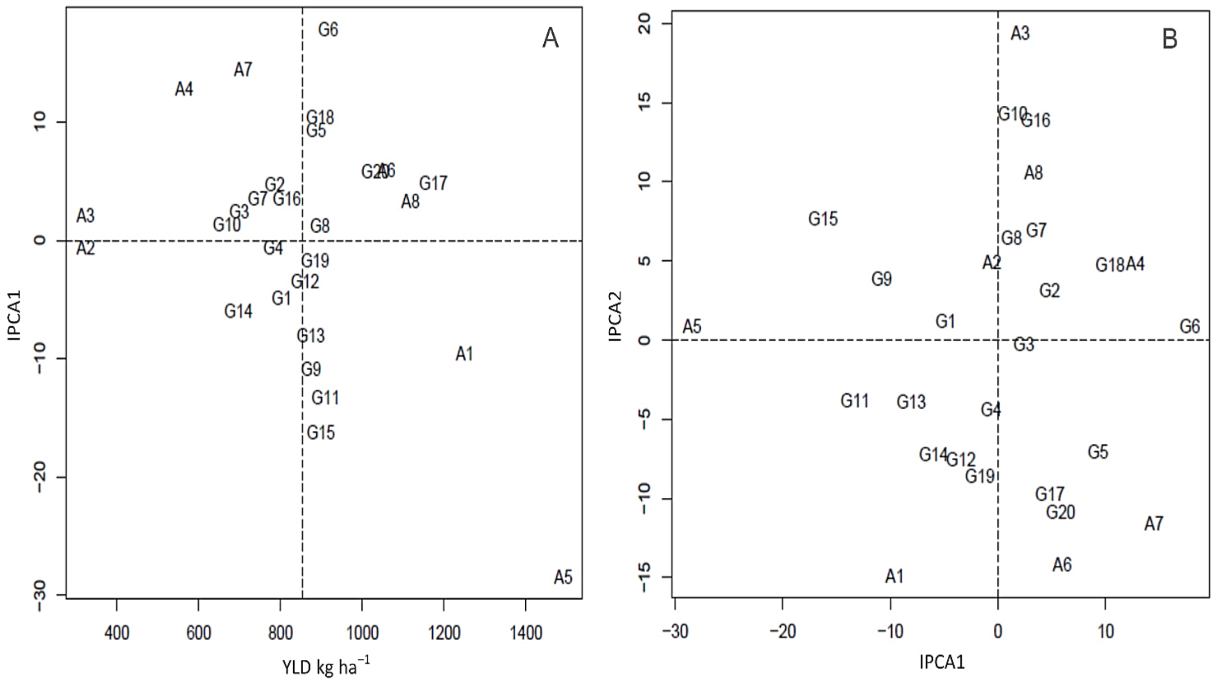

Figure 1. *Biplot* AMMI1 (A) and MMI2 (B) analysis for yield grain (kg ha^{-1}), of 20 cowpea genotypes obtained in eight environments, from 2010 to 2012. A1: Aquidauana, 2010; A2: Chapadão do Sul, 2010; A3: Dourados, 2010; A4; Aquidauana, 2011; A5: Chapadão do Sul, 2011; A6: Dourados, 2011; A7: Aquidauana, 2012 and A8: Dourados, 2012.

unstable environments were A1, A5 and A7, and the environments A5 and A5 environments showed instability associated with high grain yield, which corroborates the fact that the location Aquidauana have presented positive interaction with the agricultural year 2010 and Chapadão do Sul with 2011.

We observed that there is a disagreement among the Eberhart and Russel (1966) and AMMI methods, because the environments classified as unfavorable by environmental indices obtained by the Eberhart and Russell (1966) methodology are considered as stable in the AMMI analysis, such as CS10 and DS10. This probably is because the Eberhart and Russel (1966) methodology considers an environmental index, which refers to the average of an environment subtracted from the overall average, therefore, not take into account the present G x E interaction. The genotypes BRS-Tumucumaque (17) and BRS-Guariba (20) were the most productives, however, these genotypes presented one of the greatest deviations and contributed more to G x E interaction. In the AMMI method, the selection of genotypes with high stability usually results in low grain yields and, consequently, the selection for higher grain yield can lead to less stability (Pacheco et al., 2005). The genotypes MNC03-737F-5-1 (8) and BRS-Itaim (19) obtained grain yield above the overall average and at the same time were predictable, showing that these gather overall adaptability (Eberhart and Russel, 1966), can be grown in all studied environments.

Conclusions

The genotypes MNC03-737F-5-1, BRS-Tumucumaque, BRS-Guariba, MNC02-684F-5-6, MNC03-725F-3, MNC02-682F-2-6, BRS-Cauamé, BRS-Itaim and MNC03-737F-5-11 gather yield adaptability and stability sufficient for recommendation for Brazilian Midwest. Eberhart and Russell, Lin and Binns and AMMI methods can be used in a complementary way for the better predict the genotypes performance. The environments A1, A5, A6 and A8 are the most suitable for selecting superior genotypes for adaptability and stability.

Conflict of Interest

The authors have not declared any conflict of interest.

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