



Genetic potential of black bean genotypes with predictable behaviors in multienvironment trials

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ABSTRACT. The aim of this study was to evaluate the phenotypic stability and specific and broad adaptability of common black bean genotypes for the Central and Center-South regions of Brazil by using the Annicchiarico and AMMI (weighted average of absolute scores: WAAS, and weighted average of absolute scores and productivity: WAASP) methodologies. We carried out 69 trials, with 43 and 26 trials in the Central and Center-South regions, respectively. Thirteen genotypes were evaluated in a randomized block design with three replications, during the rainy, dry, and winter seasons in 2 years. To obtain estimates of specific adaptation, we analyzed the parameters for each method obtained in the two geographic regions separately. To estimate broad adaptation, we used the average of the parameters obtained from each region. The lines identified with high specific adaptation in each region were not the same based on the Annicchiarico and AMMI (WAAS) methodologies. It was not possible to identify the same genotypes with

specific or broad stability by using these methods. By contrast, the Annicchiarico and AMMI (WAASP) methods presented very similar estimates of broad and specific adaptation. Based on these methods, the lines with more specific adaptation were CNFP 8000 and CNFP 7994, in the Central and Center-South regions, respectively, of which the CNFP 8000 line was more widely adapted.

Key words: AMMI; Annicchiarico; *Phaseolus vulgaris*; Genotype x environment interactions

INTRODUCTION

In recent years, Brazil has been ranked first in the production and consumption of common bean (*Phaseolus vulgaris* L.) (FAO, 2015). Black beans are the second most consumed type of bean in Brazil, representing 17% of the consumer market and corresponding to approximately 490,000 tons/year (Del Peloso and Melo, 2005). Together, the Central and Center-South regions of Brazil are responsible for 84% of Brazil's bean production (Pontes Junior et al., 2014).

The common bean is grown in the majority of the Brazilian states during more than one sowing period per year. This is done using different cultivation systems and under different environmental conditions, which leads to the occurrence of genotype x environment (GxE) interactions (Bertoldo et al., 2009; Pereira et al., 2009a, 2011; Domingues et al., 2013; Corrêa et al., 2016). Because of such interactions, the genotypes should be evaluated in a large number of environments so that the environmental effects can be measured and an improved certainty regarding the usage of new cultivars can be provided.

Adaptability and stability analyses can be used to minimize undesired effects of GxE interactions because they allow for the identification of cultivars that have predictable behaviors in response to variations in environmental conditions (Cruz and Regazzi, 2001). It is important to perform these analyses in different regions, to identify lineages that have both broad and specific adaptabilities and stabilities for each region. The obtained results can provide a level of certainty in decision-making processes. However, because of the low usage rate of common bean seeds by farmers (approximately 19%) (Peske, 2016) and, consequently, the small market potential for new cultivars, common bean cultivars in Brazil are currently only indicated based on the average productivity of the different regions and planting seasons. In addition, cultivars are rarely recommended for specific environments.

Several methods are commonly used to evaluate the stability and phenotypic adaptability of cultivars, and several studies have compared different approaches. Silva and Duarte (2006) and Pereira et al. (2009b) found a low association between the Annicchiarico (Annicchiarico, 1992) and AMMI (additive main effects and multiplicative interaction model; Gauch and Zobel, 1996) methodologies, thereby demonstrating that these methods can be used to complement one another.

The methodology proposed by Annicchiarico (1992) has been widely used because of its ease of interpretation and because it classifies the most adaptable and stable genotypes with the greatest average productivity (Silva Filho et al., 2008; Pereira et al., 2009b,c, 2012). The AMMI method is also commonly used. It combines analysis of variance for the main additive effects of genotypes and environments with principal component analysis for the multiplicative

effect of the GxE interaction (Gauch and Zobel, 1996). However, this methodology does not classify the most productive among the most stable genotypes (Melo et al., 2007; Silva Filho et al., 2008; Pereira et al., 2009b). This shortcoming becomes a problem when recommending new cultivars for the genetic improvement of plants, given that average productivity is one of the most relevant factors for the acceptance of new cultivars. With the goal of addressing this obstacle, it has been proposed that the AMMI methodology can make use of a supplementary genotype (Pacheco et al., 2005) that represents an additional reference genotype with which the evaluated genotypes can be compared. The reference genotype is defined based on the criteria of interest to the researcher. Another difficulty that generally occurs in the majority of studies that use the AMMI method is that the number of significant components defined by the decomposition of the GxE interaction is greater than the number of components used to study the stability (Melo et al., 2007; Rocha et al., 2007; Silva Filho et al., 2008; Pereira et al., 2009c; Gonçalves et al., 2010). To circumvent this problem, the use of a predictive evaluation via a cross-validation process has been proposed (Gauch, 1988). In this approach, the selected model is the one that displays the lowest average predictive difference among a large number of analyses (Oliveira et al., 2003). However, this method is difficult to use and, thus, impractical for implementation in routine plant breeding programs. In this regard, Pereira et al. (2009c) proposed calculation of the weighted average of the absolute scores (WAAS) of the first two principal components for each genotype, which are weighted by the percentage of variation explained by each component such that the genotypes with the lowest WAAS values are the most stable. Unfortunately, this method does not address all components identified as significant, nor does it include information about genotype productivity. Additionally, some of the aforementioned difficulties persist.

In the present study, a new approach to the AMMI methodology is proposed in which information on adaptability is included. Thus, this proposed method can be used in genetic improvement programs by including information from all significant components identified in the GxE interactions. The aim was to evaluate the phenotypic stability and specific and broad adaptability of common black bean genotypes in the Central and Center-South regions of Brazil by using the Annicchiarico and AMMI methods.

MATERIAL AND METHODS

Trials used to recommend black bean cultivars were conducted during the rainy (October/November sowing), dry (January/February sowing), and winter (May/June sowing) seasons in 43 environments of the Central region of Brazil (in the States of Goiás, the Federal District, Mato Grosso, Mato Grosso do Sul, and Tocantins) and 26 environments in the Center-South region (in the States of Paraná, Santa Catarina, São Paulo, and Rio Grande do Sul), totaling 69 environments in 2 years. The experimental design was a completely randomized block design with three repetitions and plots with four 4.0-m long rows. The data on bean productivity were collected from the two center rows. Each trial consisted of 13 genotypes of the common black bean as follows: eight elite lineages (TB 9409, TB 9713, CNFP 10138, CNFP 7966, CNFP 7972, CNFP 7994, CNFP 8000, and CNFP 9328) and five cultivars (BRS Valente, FT Nobre, Diamante Negro, IPR Uirapuru, and FT Soberano).

The data on bean yield (kg/ha) were subjected to an individual analysis of variance in which the effect of the genotypes was fixed and the other effects were random. Selective accuracy (SA) was estimated using the equation,

$$SA = \left[1 - \left(\frac{1}{F} \right) \right]^{-0.5} \quad (\text{Equation 1})$$

where F is the value of the F-test for the source of variation of the lineages (Resende and Duarte, 2007). Subsequently, a joint analysis was performed on the stability and adaptability of the trials according to the region. For the trials in which the residual variances were not homogenous, the degrees of freedom of the mean error and of the GxE interaction were adjusted according to the Cochran method. The phenotypic means obtained in the joint analysis were subjected to a Scott and Knott means test at 10% probability. The Annicchiarico and AMMI methodologies were used to estimate the adaptability and stability parameters associated with the bean yield of eight elite lineages.

In the Annicchiarico methodology, stability is measured by the superiority of the genotype relative to the mean for each environment. This method is based on the estimation of a recommendation index for a particular genotype that shows a relatively superior behavior. In this method, the data are transformed beforehand into percentages using the mean of the genotypes of each location as a reference. For example, if a cultivar obtains an index equal to 103.0%, this cultivar will perform 3% better than the environmental average with a 75% probability.

The genotypic recommendation index ($w_{i(g)}$) was estimated as follows:

$$w_{i(g)} = \mu_{i(g)} - z_{(1-\alpha)} \delta_{zi(g)} \quad (\text{Equation 2})$$

where all environments are considered and $\mu_{i(g)}$ is the average percent of genotype i relative to the overall average, $z_{(1-\alpha)}$ is the percentile of the standard normal distribution, and $\delta_{zi(g)}$ is the standard deviation of the z_{ij} values associated with genotype i :

$$z_{ij} = \frac{100Y_{ij}}{\bar{Y}_{.j}} \quad (\text{Equation 3})$$

where Y_{ij} is the average of genotype i in environment j , $\bar{Y}_{.j}$ is the average of environment j . The index was also calculated using only the favorable environments (with a mean greater than the overall mean) or only the unfavorable ones (with a mean below the general mean). The adopted significance level was 75% or $\alpha = 0.25$, which is commonly used in these analyses (Cruz and Carneiro, 2006). In this method, the performance of the genotype and its stability are simultaneously considered such that the greatest recommendation index values (w_i) are obtained for those with the greatest average percentage (z_i) and the least amount of deviation (δ_{z_i}). Thus, w_i is considered to express the genotypic stability and adaptability (Cruz and Carneiro, 2006). The AMMI analysis includes additive components to enable the study of the principal effects (genotypes and environments) and the interaction of multiplicative components. In the principal component analysis, the variation contained in the significant components is called the pattern, whereas that contained in the non-significant components is called noise. To use the AMMI methodology, the following model was employed:

$$Y_{ij} = \mu + g_i + a_j + \sum_{k=1}^n \lambda_k y_{ik} a_{jk} + \rho_{ij} + \bar{e}_{ij} \quad (\text{Equation 4})$$

where Y_{ij} is the average response of genotype i in environment j , μ is the general average of the trials, g_i is the fixed effect of genotype i , a_j is the fixed effect of environment j , λ_k is the singular value (scalar) k of the matrix of original interactions (denoted GE), y_{ik} is the element corresponding to the i -th genotype in the singular vector of column k in the GE matrix, a_{jk} is the element corresponding to the j -th environment in the k -th singular vector of a line in the GE matrix, ρ_{ij} is the noise associated with the term $(ge)_{ij}$ of the classic interaction of genotype i with environment j , and \bar{e}_{ij} is the average experimental error. The Gollob F-test was used to select the model.

The method produces scores for the interaction principal component analysis (IPCA) for each genotype, which reflect their contribution to the GxE interaction. To identify the most stable genotypes, the means of the absolute scores were obtained following the method of Pereira et al. (2009b), obtained for each genotype for the principal components that were significant at 1% probability by the F-test weighted by the explanatory power of each component. Thus, the genotype with the lowest WAAS is the most stable. The expression used was

$$WAAS_i = \frac{\sum_{i=1}^n (PE_i * IPCA_i)}{\sum_{i=1}^n PE_i} \quad (\text{Equation 5})$$

where $WAAS_i$ is the weighted average of the absolute scores for genotype i , PE_i is the percentage of explanation of the i -th significant principal component, and $IPCA_i$ is the estimate of the i -th significant principal component.

With the goal of adding a new parameter to the AMMI methodology, by associating the stability with the adaptability, the use of the weighted mean of absolute scores and productivity (WAASP) was proposed. This value is the weighted mean of the average productivity of the genotypes, with a weight equal to 3, and that of the WAAS, with a weight equal to 2, that allows for the simultaneous evaluation of adaptability and stability. To obtain the WAASP, the productivity and WAAS data were transformed to the same scale to be directly comparable. The greatest productivity value was considered to be 100%, and all other values were compared relative to this value. In the case of WAAS, all values were subtracted from 100 to invert the scale, and subsequently, the percentage relative to the greatest value for each genotype was obtained.

The expression used was

$$WAASP_i = \frac{\left\{ 3 * \left[\left(\frac{TF_i}{TF_{greatest}} \right) * 100 \right] \right\} + \left\{ 2 * \left[\left(\frac{100 - WAAS_i}{WAAS_{least}} \right) * 100 \right] \right\}}{5} \quad (\text{Equation 6})$$

where $WAASP_i$ is the weighted average of the absolute scores and the productivity for genotype i , TF_i is the average productivity of genotype i , $TF_{greatest}$ is the genotype with the greatest mean productivity, $WAAS_i$ is the weighted mean of the absolute scores of genotype i , and $WAAS_{least}$ is the genotype with the lowest WAAS value.

To obtain the estimates of the stability and adaptability specific to the regions, the parameters obtained with each method were analyzed separately for the two geographic regions. To estimate the broad stability and adaptability, the mean of the parameters obtained in each region was used, and a broad adaptation of the genotypes was considered for those with the highest estimates for this mean. Furthermore, estimates were obtained separately for the

Spearman's correlation between the AMMI (WAAS) x Annicchiarico and AMMI (WAASP) x Annicchiarico methodologies for the two regions to determine the agreement of the genotype classifications. The estimation of the parameters and the significance tests were performed using Gene (Cruz, 2007) and SAS version 9.1 (SAS Institute, 2008).

RESULTS AND DISCUSSION

Significant genotype effects were found in 74% of the trials, and the values for the coefficient of variation were all less than 25%, indicating good experimental precision (Tables 1 and 2). The magnitude of the SA estimates were high ($70 \leq SA < 90$) or very high ($SA \geq 90$) in 65% of the cases and moderate ($50 \leq SA < 70$) in 16% of the cases, thus confirming the good experimental precision (Tables 1 and 2). The use of the accuracy as a measure of experimental precision, as suggested by Resende and Duarte (2007), has the advantage of being independent of the magnitude of the mean. Thus, it better reflects what is desired in the experiment, i.e., an evaluation of the lineages or the uncertainty in using the phenotypic expression as an indicator of genotypic variation.

Table 1. Locations for the assessment trials in the Center-South region and a summary of the individual analyses of variance.

Location	Altitude (m)	Season	Mean squared		Productivity (kg/ha)	CV _c (%)	SA
			Treatments	Error			
Ponta Grossa-PR	969	Dry/2003	389,129 ^{ns}	187,132	1949	22.2	0.72
Ponta Grossa-PR	969	Wet/2003	439,048*	175,261	3569	11.7	0.78
Taquarituba-SP	618	Wet/2004	751,390**	117,376	2390	14.3	0.92
Itaberá-SP	651	Wet/2004	299,100*	112,587	2920	11.5	0.79
Parapanema-SP	610	Wet/2004	467,368**	96,048	2611	11.9	0.00
Abelardo Luz-SC	760	Wet/2003	387,347 ^{ns}	262,498	3916	13.1	0.57
C. Novos-SC	934	Wet/2003	64,346 ^{ns}	37,031	1056	18.2	0.65
Abelardo Luz-SC	760	Dry/2003	147,838*	62,043	2191	11.4	0.76
Major Vieira-SC	786	Wet/2003	293,351**	68,292	1831	14.3	0.88
Concórdia-SC	569	Wet/2003	354,428**	113,912	2255	14.9	0.82
Roncador-PR	762	Dry/2003	183,289**	50,485	1383	16.3	0.85
Taquarituba-SP	618	Wet/2003	369,722**	56,549	2217	10.7	0.92
Capão Bonito-SP	705	Wet/2003	366,642 ^{ns}	284,165	4110	12.9	0.47
Londrina-PR	585	Wet/2003	640,498*	219,548	1938	24.2	0.81
Prudentópolis-PR	840	Dry/2004	220,195*	93,244	2554	11.9	0.76
Ponta Grossa-PR	969	Dry/2004	511,985**	83,494	3163	9.1	0.00
Major Vieira-SC	786	Dry/2004	178,248**	30,298	1663	10.5	0.91
Roncador-PR	762	Wet/2004	101,612**	23,747	871	17.7	0.00
Prudentópolis-PR	840	Wet/2004	470,860**	40,774	2246	8.9	0.96
Laranjeiras-PR	840	Wet/2004	129,640*	43,358	2538	8.2	0.82
C. Novos-SC	934	Wet/2004	80,000*	33,801	1367	13.5	0.76
Abelardo Luz-SC	760	Wet/2004	465,473*	158,017	3958	10.0	0.81
Ponta Grossa-PR	969	Wet/2004	630,750*	213,519	3320	13.9	0.81
Passo Fundo-RS	687	Wet/2003	250,151**	48,213	1858	11.8	0.90
Passo Fundo-RS	687	Wet/2002	148,605*	52,866	3065	7.5	0.00
Abelardo Luz-SC	760	Dry/2004	115,335 ^{ns}	106,091	2184	14.9	0.28
Mean	-	-	-	-	2428	13.3	0.65

*and **Significant at 5 and 1% probability, respectively, according to the F-test. CV_c: experimental coefficient of variation; SA: selective accuracy.

The average productivities of the Center-South region (Table 1) varied between 871 and 4110 kg/ha, demonstrating that the environmental conditions experienced by the genotypes were different.

Table 2. Locations for the assessment trials in the Central region and a summary of the individual analyses of variance.

Location	Altitude (m)	Season	Mean squared		Productivity (kg/ha)	CV _e (%)	SA
			Treatment	Error			
Dueré-TO	235	Winter/2004	103,964 ^{ns}	114,872	1817	18.7	0.00
S. A. Goiás-GO	770	Dry/2003	169,991*	62,414	1277	19.6	0.80
Goiatuba-GO	807	Winter/2003	153,593 ^{ns}	113,986	1877	17.9	0.51
S. A. Goiás-GO	770	Winter/2003	387,691*	142,640	2019	18.7	0.00
Rio Verde-GO	715	Winter/2003	246,537 ^{ns}	167,317	2400	17.0	0.57
Urutai-GO	807	Winter/2003	385,795 ^{ns}	269,732	2677	19.4	0.55
Cristalina-GO	1189	Winter/2003	1416,966**	252,109	2525	19.9	0.91
Rio Verde-GO	807	Wet/2003	890,179**	82,075	2288	12.5	0.95
Ipameri-GO	764	Wet/2003	330,685**	79,490	3044	9.3	0.87
Anápolis-GO	1017	Wet/2003	208,086 ^{ns}	123,104	1870	18.8	0.64
Formosa-GO	916	Wet/2003	518,038**	92,866	2299	13.3	0.91
Panamá-GO	733	Dry/2004	148,973*	58,817	1245	19.5	0.78
Anápolis-GO	1017	Dry/2004	236,833*	94,942	1560	19.8	0.77
S. A. Goiás-GO	770	Wet/2004	433,116**	60,694	1969	12.5	0.93
Dueré-TO	235	Winter/2003	313,776**	74,503	1755	15.6	0.87
Planaltina-DF	944	Winter/2003	389,305*	146,094	2482	15.4	0.79
Sinop-MT	345	Wet/2003	243,799**	61,795	1321	18.8	0.86
Anápolis-GO	1017	Winter/2004	598,836 ^{ns}	301,948	3082	17.8	0.70
S. A. Goiás-GO	770	Winter/2004	103,861 ^{ns}	71,688	2487	10.8	0.56
Rio Verde-GO	807	Winter/2004	218,253 ^{ns}	115,424	2995	11.3	0.69
Itumbiara-GO	448	Winter/2004	256,492*	107,752	1961	16.7	0.76
Planaltina-DF	944	Wet/2003	152,205 ^{ns}	190,776	2481	17.6	0.00
Urutai-GO	807	Winter/2004	77,882**	19,450	1672	8.3	0.87
Morrinhos-GO	771	Winter/2004	210,337**	60,844	1944	12.7	0.00
Sinop-MT	345	Dry/2004	91,467*	35,689	1153	16.4	0.78
Cáceres-MT	118	Winter/2004	280,151 ^{ns}	151,610	2295	16.9	0.68
Dianópolis-TO	693	Winter/2003	309,476 ^{ns}	210,484	3331	13.8	0.57
Palmas-TO	230	Winter/2003	166,305*	57,386	2177	11.0	0.00
Cáceres-MT	118	Winter/2003	53,470 ^{ns}	255,509	2840	17.8	0.00
Morrinhos-GO	771	Wet/2004	244,289**	53,762	2018	11.5	0.88
Urutai-GO	807	Wet/2004	484,146**	81,348	2040	13.9	0.91
Cristalina-GO	1189	Winter/2004	480,477**	86,650	2951	9.9	0.00
C. Alegre-GO	877	Wet/2003	103,934 ^{ns}	68,173	1195	21.9	0.59
S. A. Goiás-GO	770	Wet/2004	173,477**	19,065	1519	9.1	0.94
Anápolis-GO	1017	Wet/2004	256,431**	38,172	2578	7.6	0.92
Rio Verde-GO	807	Wet/2004	684,442**	191,497	2564	17.1	0.85
Cristalina-GO	1189	Wet/2004	428,605**	96,722	1644	18.9	0.88
G. Dourados-MS	400	Dry/2003	140,838*	64,131	1695	14.9	0.74
Dourados-MS	430	Dry/2003	197,857**	28,164	1808	9.3	0.93
Aquidauana-MS	147	Dry/2003	374,454**	13,062	1719	6.6	0.98
Aquidauana-MS	147	Dry/2004	181,766**	12,810	1719	6.6	0.96
Planaltina-DF	944	Winter/2004	370,446*	151,787	3422	11.4	0.77
Planaltina-DF	944	Wet/2004	544,875**	130,046	3379	10.7	0.87
Mean	-	-	-	-	2165	14.6	0.66

*and **Significant at 5 and 1% probability, respectively, according to the F-test. CV_e: experimental coefficient of variation; SA: selective accuracy.

The same effect was observed in the Central Region (Table 2), in which the average productivities varied from 1153 to 3422 kg/ha. In the joint analysis of the two regions, all effects were significant. This indicates variability for the selection of genotypes, variation among the evaluated environments, and the occurrence of a differentiated response of the genotypes to the environments, which determines the need for an analysis of stability and adaptability (Table 3).

Table 3. Summary of the joint analysis of variance with the use of the original GxE interaction via the AMMI model for 13 black common bean genotypes evaluated in the Central and Center-South regions of Brazil.

Source of variation	Central				Center-South			
	% [†]	d.f.	SS	MS	% [†]	d.f.	SS	MS
Genotype (G)	-	12	23,734,170	1,977,848**	-	12	10,568,653	880,721*
Environment (E)	-	42	620,921,839	14,783,853**	-	25	749,435,646	29,977,426**
GxE	-	353 [‡]	141,402,904	400,575**	-	205 [‡]	90,913,404	443,480**
IPCA 1	24	53	33,930,159	640,192**	23	36	21,066,863	585,191**
Residual 1	-	300	107,472,745	358,242**	-	169	69,846,542	413,293**
IPCA 2	18	51	25,874,470	507,343**	18	34	16,557,859	486,996**
Residual 2	-	249	81,598,275	327,704**	-	135	53,288,683	394,731**
IPCA 3	15	49	21,257,749	433,832**	15	32	13,701,942	428,186**
Residual 3	-	200	60,340,526	301,703**	-	103	39,586,741	384,337**
IPCA 4	9	47	12,514,278	266,261**	10	30	8,929,265	297,642**
Residual 4	-	153	47,826,249	312,590**	-	73	30,657,476	419,965**
IPCA 5	8	45	10,713,039	238,068 ^{ns}	9	28	7,854,755	280,527**
Residual 5	-	108	37,113,210	343,641**	-	45	22,802,721	506,727**
IPCA 6	-	-	-	-	8	26	6,994,674	269,026 ^{ns}
Residual 6	-	-	-	-	-	19	15,808,047	832,002**
Error	-	717 [†]	-	154,356	-	422 [†]	-	157,555

[†]Proportion of explanation of the principal components. [‡]Values adjusted by the Cochran method (1954) based on the heterogeneity of the residual MS values. * and **Significant at 5 and 1% probability, respectively, according to the F-test.

The Annicchiarico method led to the identification of CNFP 8000, IPR Uirapuru, and FT Nobre as superior genotypes for the Central region of Brazil; these genotypes exceeded the mean of the environments by 5.3, 4.6, and 3.1%, respectively. Considering the unfavorable environments, the genotypes that exceeded the mean were FT Nobre, CNFP 8000, IPR Uirapuru, and CNFP 7966, with respective values of 6.0, 5.9, 3.7, and 1.2%. For the favorable environments, the best genotypes were CNFP 8000, CNFP 7994, and CNFP 10138, which showed 4.4, 3.0, and 0.9% superiority relative to the mean, respectively (Table 4). Based on these results, the best genotype for all three environments in the Central region was CNFP 8000, which ranked first in the general analysis and in the favorable environments and second in the unfavorable environments. Genotypes CNFP 7966 and CNFP 7994 displayed adaptability specific to the unfavorable and favorable environments, respectively. All genotypes identified as being most stable and best adapted in this region were classified by the test of means into a group of the most productive genotypes (Table 4).

In the Center-South region, genotypes CNFP 7994, CNFP 8000, and TB 9713 were identified with a recommendation index (w_i) greater than 100%, and these genotypes exceeded the mean of the environments by 5.8, 2.0, and 1.2%, respectively. In the unfavorable environments, in addition to the genotypes identified in the general analysis, the FT Nobre genotype was also identified as being superior by producing an index value 1.3% greater than the average. Considering the favorable environments, the notable genotypes were CNFP 7994, CNFP 10138, CNFP 8000, and IPR Uirapuru with w_i values of 1.8, 1.7, 1.4, and 1.3%, respectively (Table 4). In this region, it is worth highlighting the CNFP 7994 genotype, which ranked first in the three rounds of analysis (i.e., general, unfavorable, and favorable), which indicates that this genotype is the most adapted to the Center-South region of Brazil. This same genotype was the most productive along with CNFP 8000 according to the test of means (Table 4). When considering the two regions simultaneously, the best genotype was CNFP 8000, which was superior to the mean for the environments in all rounds of analysis (w_i , w_{id} , and $w_{if} > 100$), with an average superiority relative to the two regions and the two types of

environments of 3.6%. This genotype was also recommended by Torga et al. (2013a,b), when they decomposed the GxE interaction in the genotypes x sowing season and genotypes x location/years, for these two regions, separately.

Table 4. Estimates of the parameters of adaptability and phenotypic stability of 13 genotypes of the black common bean, which were evaluated in the Central and Center-South regions of Brazil during 2003 and 2004 by the Annicchiarico (1992) method.

Genotype	Central							Center-South						
	Mean	w_i	C	w_{id}	C	w_{if}	C	Mean	w_i	C	w_{id}	C	w_{if}	C
CNFP 8000	2352 ^a	105.2	1	105.9	2	104.3	1	2592 ^a	102.0	2	102.9	3	101.3	4
FT Nobre	2286 ^a	103.1	3	106.0	1	100.2	4	2441 ^c	97.8	5	101.3	4	93.2	12
IPR Uirapuru	2278 ^a	104.6	2	103.7	3	99.3	6	2444 ^c	96.0	6	94.0	6	100.7	2
CNFP 7994	2261 ^a	100.1	4	97.6	7	103.0	2	2627 ^a	105.8	1	109.0	1	101.8	1
BRS Valente	2232 ^a	99.6	5	99.3	5	99.8	5	2354 ^d	92.7	10	89.9	12	96.8	9
CNFP 10138	2227 ^a	98.4	7	96.2	8	100.9	3	2425 ^c	94.4	8	90.1	11	101.4	3
CNFP 7966	2226 ^a	99.3	6	101.2	4	97.1	7	2389 ^c	95.7	7	93.9	7	98.4	8
CNFP 9328	2112 ^b	94.2	8	98.3	6	89.6	12	2495 ^b	99.3	4	99.0	5	99.6	6
D. Negro	2109 ^b	92.9	9	90.1	10	96.4	8	2324 ^d	92.3	11	91.5	10	93.4	11
TB 9713	2082 ^b	91.9	10	90.7	9	93.3	9	2526 ^b	101.2	3	105.3	2	96.2	7
FT Soberano	2047 ^b	91.3	11	90.0	11	92.8	10	2288 ^d	91.1	12	93.7	8	87.9	13
CNFP 7972	1983 ^c	88.0	12	88.8	12	87.0	13	2319 ^d	90.2	13	84.3	13	99.6	5
TB 9409	1959 ^c	84.8	13	80.4	13	90.3	11	2338 ^d	93.4	9	92.9	9	94.4	10

Means (kg/ha) followed by the same superscript letters do not differ significantly according to the Scott-Knott test at 10% probability. C = classification of the genotypes with regard to the stability and adaptability; w_i = recommendation index, classified into favorable environments (w_{if}) and unfavorable environments (w_{id}).

As previously mentioned, the most stable and adapted genotypes were also the most productive. This is expected given that the model used in the Annicchiarico method to measure genotype superiority uses the mean for each environment as a reference. Therefore, the risk of adopting a particular cultivar is estimated, and this estimate is obtained relative to the mean (Silva Filho et al., 2008; Pereira et al., 2009c, 2012).

According to the AMMI model, the original GxE interaction may be decomposed into 12 components (i.e., ranks within the GE matrix) for the Central and Center-South regions. In this type of analysis, the appropriate model associates significance with the axes and non-significance with the residuals. However, in this study, the analysis was problematic in that non-significance was found for the component (axis), and the residuals continued to be significant (Table 3). Thus, the selected model was the last one to display significance for the component. Oliveira et al. (2003) suggested that with regard to the level of significance, the use of 1% instead of 5% reduces the likelihood of a type I error; however, this approach increases the likelihood of the occurrence of a type II error. According to Gauch and Zobel (1996), the first AMMI components capture a greater percentage of the real performance “pattern”, and with the subsequent accumulation of components, there is a decrease in the percentage of the “pattern” and an increase in imprecise information (i.e., “noise”), thus reducing the predictive power of the AMMI analysis. Therefore, the significance level adopted in the present study to classify the principal components as significant was 1%, thereby selecting the AMMI 4 and AMMI 5 models for the Central and Center-South regions, respectively (Table 3).

For the common bean, methodologies that identify materials with broad adaptations are advantageous. This is mainly because of the seed production market, given that the rate of seed usage by farmers is low (close to 15%), which makes it difficult to have a specific indication for each crop region. The identification of the most stable lineages using the AMMI method

was performed using information from the significant principal components to obtain the mean of the absolute scores for each genotype weighted by the percent of explanation of each component (WAAS) (Tables 3 and 5) (Pereira et al., 2009c). A lower value of the weighted average indicates a more stable genotype, which is attributed to the lower contribution of the GxE interaction.

Table 5. Values of the significant principal components (IPCA) for each genotype of the Central and Center-South regions of Brazil that were used to calculate the WAAS and for classification of the genotypes with regard to the stability using the AMMI (WAAS) and AMMI (WAASP) methods.

Genotypes	Central									
	Mean	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	WAAS	C	WAASP	C
CNFP 8000	2352 ^a	-6.25	24.06	-6.65	-0.57	-	10.5	6	98.7	1
FT Nobre	2286 ^a	11.88	-12.47	8.52	3.67	-	10.2	4	97.2	2
IPR Uirapuru	2269 ^a	-4.20	-3.17	32.92	3.11	-	10.3	5	96.7	3
CNFP 7994	2261 ^a	-12.78	24.90	-0.95	15.50	-	13.8	10	95.0	6
BRS Valente	2232 ^a	1.62	-9.14	8.67	28.97	-	9.0	3	96.4	4
CNFP 10138	2227 ^a	-12.83	16.20	5.86	-22.86	-	13.5	9	94.3	7
CNFP 7966	2226 ^a	20.03	12.96	1.59	-0.65	-	11.3	7	95.2	5
CNFP 9328	2112 ^b	36.66	-0.85	-15.80	-3.10	-	17.5	13	89.6	11
D. Negro	2109 ^b	-0.36	-18.48	17.45	-18.00	-	11.6	8	92.1	8
TB 9713	2083 ^b	-14.43	-23.72	-19.94	-3.04	-	16.7	12	89.2	12
FT Soberano	2047 ^b	-3.67	-9.79	-15.77	4.37	-	8.2	2	92.0	9
CNFP 7972	1983 ^c	11.45	5.14	-4.65	-7.39	-	7.6	1	90.6	10
TB 9409	1959 ^c	-27.15	-5.65	-11.26	-0.02	-	14.0	11	87.2	13
	Center-South									
CNFP 7994	2627 ^a	-9.38	-11.82	18.66	-0.04	-12.41	11.0	8	97.5	1
CNFP 8000	2592 ^a	-17.09	-17.34	12.12	-11.85	-10.22	14.7	11	95.1	4
TB 9713	2516 ^b	16.27	7.09	-21.60	-14.55	-12.68	14.5	10	93.4	6
CNFP 9328	2496 ^b	2.01	15.10	-11.78	-3.23	-14.43	8.7	5	95.4	2
IPR Uirapuru	2444 ^c	9.80	2.04	5.07	8.80	7.10	6.5	2	95.2	3
FT Nobre	2441 ^c	-12.11	33.34	12.95	-1.31	3.87	15.1	12	91.5	10
CNFP 10138	2425 ^c	-19.07	1.14	-8.66	4.77	1.67	8.7	4	93.8	5
CNFP 7966	2389 ^c	-7.17	-13.83	-11.89	10.85	1.89	9.6	6	92.6	9
BRS Valente	2364 ^d	5.99	5.43	6.82	4.04	20.59	7.5	3	92.9	8
TB 9409	2338 ^d	0.77	3.27	8.81	-13.41	3.05	4.9	1	94.3	7
D. Negro	2324 ^d	9.24	-15.50	-7.49	-18.55	19.67	12.8	9	89.8	12
CNFP 7972	2319 ^d	-12.05	-3.44	-16.37	19.32	1.67	10.6	7	90.6	11
FT Soberano	2288 ^d	32.80	-5.48	13.36	15.16	-9.77	17.3	13	87.0	13

Means followed by the same superscript letters do not differ significantly according to a Scott-Knott test at 10% probability. WAAS = weighted mean of the absolute scores. C = classification of the genotypes with regard to the stability. WAASP = weighted mean of absolute scores and productivity.

In the Central region, the first four components explained 66% of the variation (Table 3). The most stable genotypes in this region were CNFP 7972, FT Soberano, and BRS Valente with WAAS values of 7.6, 8.2, and 9.0, respectively (Table 5). The genotypes with the least amount of stability were CNFP 9328, TB 9713, and TB 9409 with values of 17.5, 16.7, and 14.0, respectively. In the Center-South region, five principal components were significant and explained 75% of the total variation (Table 3). The genotypes that showed the least contribution to the GxE interaction were TB 9409, IPR Uirapuru, and BRS Valente, which displayed the lowest WAAS values of 4.9, 6.5, and 7.5, respectively. The most stable genotypes were FT Soberano, FT Nobre, and CNFP 8000 that displayed WAAS values of 17.3, 15.1, and 14.7, respectively (Table 5).

It can be observed that the genotypes classified as being among the most stable for the two regions, with the exception of BRS Valente in the Central region, were not the most productive (Table 5). For the Center-South region, the TB 9409 and BRS Valente genotypes, which ranked first and third in stability, respectively, were the least productive when classified

according to the test of means (Table 5). The same result occurred for the Central region with the CNFP 7972 and FT Soberano genotypes, which were classified as the most stable genotypes but not the most productive. This may be considered a negative aspect of this methodology, given that to make recommendations for cultivars the factor of greatest relevance is the average productivity. This cannot be ignored in the final decision of selecting favorable lineages in a cultivar development program.

To circumvent the problem that the most stable genotypes were not among the most productive according to the AMMI methodology, the WAASP method was proposed to add information regarding the average productivity and stability. WAASP allowed for the identification of the CNFP 8000, FT Nobre, and IPR Uirapuru genotypes as the most adapted and stable for the Central region with values of 98.7, 97.2, and 96.7, respectively. In addition, the TB 9404, TB 9713, and CNFP 9328 genotypes were identified as being the least adapted and stable (Table 5). In the Center-South region, the WAASP method identified the CNFP 7994 (97.5), CNFP 9328 (95.4), and IPR Uirapuru (95.2) genotypes as the most stable, whereas the FT Soberano, Diamante Negro, and CNFP 7972 genotypes were among the least stable and adapted (Table 5). Based on the average WAASP values of the two regions, the genotypes with the broadest adaptation were CNFP 8000, CNFP 7994, and IPR Uirapuru. These genotypes may be recommended for the two regions without causing losses for the producers. CNFP 8000 was commercially launched as a cultivar with the name of BRS Esplendor in 13 Brazilian states (Costa et al., 2011).

In the Central region, the Spearman's correlation estimates for AMMI (WAAS) x Annicchiarico and AMMI (WAASP) x Annicchiarico were 0.13 and 0.92, respectively. In the Center-South region, the corresponding estimates were 0.35 and 0.80, respectively. It can be observed that with the use of the WAASP methodology, a greater similarity was obtained with the Annicchiarico results, indicating that it is possible to add information about average productivity of the beans to the AMMI methodology. Integration of bean productivity information into the AMMI method allows for identification of stable lineages with the best agronomic performance. This is a positive result because one of the cited advantages of the Annicchiarico method is the identification of the most stable genotypes among the most productive ones, which was also achieved by the WAASP methodology.

Because the stability and adaptability parameters of each methodology are different, the genotypes identified as being the most stable differed in some cases. Therefore, in the selection of the methods to be used, factors such as ease of analysis and interpretation of the results should be considered. In a study comparing the different methods for the analysis of stability and adaptability, Pereira et al. (2009b, 2012) recommended the use of the Annicchiarico methodology due its ease of use and because it identifies the most stable and adapted genotypes from among the most productive ones. Oliveira et al. (2003) suggested that, for the purposes of recommending cultivars, the most stable genotypes should also display a desirable performance, which is evaluated by the means. By taking these criteria into consideration when evaluating the stability of the suite of final tests with the goal of indicating which cultivars to use, the Annicchiarico and AMMI (WAASP) methodologies would be recommended for programs that develop cultivars. This is because these methods classify the most stable and adapted genotypes from among the most productive ones, whereas this is not the case with the AMMI (WAAS) analysis.

In conclusion, the lineage with the greatest specific adaptation for the Central region was CNFP 8000, whereas CNFP 7994 was identified for the Center-South region. In addition,

the genotype with the broadest adaptation was CNFP 8000. The Annicchiarico and AMMI (WAAS) methodologies did not identify the same genotypes from among the most stable and adapted ones. The Annicchiarico and AMMI (WAASP) methodologies identified similar genotypes as being the most stable and adapted ones. The lineages with the greatest specific adaptation for the Central and Center-South regions of Brazil did not coincide when using the Annicchiarico and AMMI methodologies. The AMMI-WAASP methodology is efficient and easy to implement in plant-breeding programs.

Conflicts of interest

The authors declare no conflict of interest.

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