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AMMI Analysis to Determine Relative Maturity Groups for the Classification of Soybean Genotypes

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Abstract: The classification of soybean cultivars into distinct maturity groups has great importance for their evaluation, selection and production in major soybean-growing regions of the world. The objective of this study was to identify stable soybean genotypes and classify them into Relative Maturity Groups (RMGs) by evaluating 20 commercial soybean cultivars using data from 17 environments across the main regions of Brazil for the following three traits: The number of days to flowering, the number of days to maturity and the length of the reproductive period. The evaluation was performed according to the additive main effects and multiplicative interaction (AMMI) method and efficiently distinguished stable genotypes for the generation of RMGs independently of the region analyzed. The established RMGs can be used separately for each region or adopted as a unique model for Brazil.

Key words: Soybean, adaptations, RMGs, Brazil, genotype, AMMI analysis, stability

INTRODUCTION

Companies in Brazil have been classifying soybean cultivars by their maturation cycle into simple groups labeled early, semiearly, intermediate, semilate and late (Alliprandini *et al*., 1994). Despite its considerable reliability, this classification is applicable only to local situations and certain specific conditions. In the United States, the cultivar relative maturity method is employed which classifies cultivars into groups varying from 00, the most Northern, to VIII, the most Southern (Zhang *et al*., 2007). The adaptation ranges for each North American maturity group extend between 200 and 300 km in the North-South direction in the United States (Bruns, 2009). This method has proved to be very useful because it classifies cultivars into distinct maturities and basically defines the adaptation region for each cultivar. These properties are important both for agricultural zoning and for harvest planning by individual farmers.

Alliprandini *et al*. (2009) used two years of soybean crop maturity data and published the first research on relative maturity groups (RMGs) in Brazil. According to these authors, their study results indicate that soybeans can be classified into five to nine RMGs, similar to what has been used in the United States. This pioneering study, conducted with conventional cultivars and developed in partnership with several companies, was a milestone in the creation of a network of tests for evaluating cultivars and in the understanding of RMGs. Currently, the use of conventional soybean cultivars is reduced with the increased usage of genetically modified cultivars which are grown on approximately 88.8% of the total area of Brazil where soybean is cultivated (Celeres, 2012).

To comprehend the behavior of a cultivar under different environmental conditions, the plant breeder must understand the genotype-environment interaction (G×E). This interaction can be described as the change in relative performance of the genotype due to environmental differences. The study of the G×E interaction is important to define not only the best-performing genotypes, e.g., those with the highest yield, but also those which are least influenced by the interaction which measures the adaptation of a cultivar. According to Meotti *et al*. (2012), this interaction is intrinsically correlated with the growth, reproduction and maturity periods of a cultivar because these are greatly influenced by the photoperiod.

Several methods to assess stability have been proposed. Additive main effects and multiplicative interaction (AMMI) analysis, in particular, combines statistical techniques, such as analysis of variance and Interaction Principal Component Analysis (IPCA) to

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model the main effects (genotypes and environment) and the G×E interaction effects, respectively (Mandel, 1971; Kempton, 1984; Zobel *et al*., 1988). AMMI analysis can help not only in the identification of high-yield and widely adapted genotypes but also in the implementation of the so-called agronomical zoning, aimed at making regionalized recommendations and selecting test locations (Gauch and Zobel, 1996). Zobel *et al*. (1988) list some of the advantages of this method: it allows a more detailed analysis of the G×E interaction; it guarantees genotype selection, capitalizing on its positive interactions with the environment; it provides more accurate estimates of genotypic responses; and it allows for easy graphical interpretation of results through so-called biplots, in which both genotype and environment are simultaneously represented. Several studies with other crops have been developed using this technique and seeking to establish environments and genotypes of greater stability (Guerra *et al*., 2009; Hassanpanah, 2010; Sadeghi *et al*., 2011).

Oliveira *et al*. (2006) studied the G×E interaction in the context of soybean yield and concluded that the AMMI1 model captured 36% of the sum of squares of the G×E interaction. Working with different populations of the F_2 generation, Maia *et al*. (2006) found a large proportion of stability in soybean lines using the AMMI methodology. Silva and Duarte (2006) used soybean culture to determine stability parameters through different methods and concluded that the methodologies of Eberhart and Russell and AMMI analysis had relatively weak association, suggesting that they should be applied together. Cucolotto *et al*. (2007) successfully explained the environment and the stability of the soybean cultivars that they studied using the AMMI model.

The goal of the present article was to establish, based on the AMMI analysis of genotype stability, a classification for the maturation of soybean into RMGs that may be used for any soybean genotype cultivated in Brazil. This classification will allow new cultivars to be categorized and duly allocated to RMGs by programs concerned with the genetic improvement of soybean.

MATERIALS AND METHODS

Twenty commercial soybean cultivars were evaluated, all of them genetically modified for resistance to glyphosate and provided by soybean genetic improvement companies in Brazil. These cultivars had different maturation attributes, such as the presence or absence of a long juvenile period and a determinate, semi-determinate or indeterminate growth type (Table 1). Trials were conducted in 17 different Brazilian locations (Table 2). For the analysis of the southern region of Brazil, seven locations in this region plus two in Mato Grosso do Sul (Midwest region of Brazil) were considered, providing a total of nine environments. The remaining eight locations were all in the central region. The study was conducted during the agricultural harvests of 2008/2009, 2009/2010 and 2010/2011 to assess the different flowering and maturation behaviors of the genotypes.

Table 1: Soybean genotypes by growth type, the presence of a long juvenile period (LJP) and relative maturity group (RMG), as tabulated according to data from Alliprandini *et al*. (2013)

Genotype	Growth type	LJP	RMGtab
Roos Camino RR	Indeterminate	No	5.6
BMX Titan RR	Indeterminate	No	5.6
CD 212 RR	Determinate	No	6.3
V-MAX RR	Indeterminate	No	6.4
CD 214 RR	Determinate	No	6.8
FTS Campo Mourão RR	Semideterminate	No	6.7
BRS 245 RR	Determinate	Yes	7.5
Fundacep 54 RR	Determinate	No	7.5
Fundacep 59 RR	Determinate	No	7.6
M7211 RR	Indeterminate	Yes	7.0
NK 7074 RR	Determinate	Yes	7.0
M7578 RR	Determinate	Yes	7.2
M7908 RR	Determinate	Yes	7.6
P98Y11	Determinate	Yes	7.6
CD 219 RR	Determinate	Yes	8.2
Valiosa RR	Determinate	Yes	8.1
TMG103 RR	Determinate	Yes	8.3
P98Y51	Determinate	Yes	8.6
P98Y70	Determinate	Yes	8.7
M9144 RR	Determinate	Yes	9.2

Table 2: Test environments by southern and central regions for the soybean harvests of 2008-2011

Location	Elevation (m)	Latitude
Southern environments		
Cruz Alta	452	28°60'S
Passo Fundo	660	28°45'S
Passo Fundo2	687	28°30'S
Cascavel	750	25°10'S
Cascavel2	781	25°05'S
Palotina	333	24°30'S
Rolândia	645	23°20'S
Dourados	450	22°20'S
Maracaju	384	21°60'S
Central environments		
S. Gabriel Oeste	650	19°40'S
Goiatuba	750	18°05'S
Morrinhos	850	17°95'S
Rio Verde	715	17°80'S
Cristalina	1189	16°80'S
Sorriso	355	12°20'S
Porto Nacional	240	10°70'S
Balsas	245	07°05'S

The preparation of the experimental areas began with the desiccation of weeds and the fertilization of planting furrows. Sowing was performed using an experimental plot seeder for direct planting, preferably in the first half of November to diminish photoperiod-related effects. All the plots underwent phytosanitary control. Each plot comprised four 5.0 m rows with 0.5 m spacing between the

rows. The two external rows served as borders; thus, there was 5.0 m^2 of useful area per plot.

The experimental design was based on randomized blocks, with two repetitions in each experimental year. The following assessments were made on each plot: the number of days to reach full flowering (NDF) which occurs during the R_2 stage and the number of days to maturity (NDM), counted from sowing to maturation at stage R_8, when at least 95% of the pods reach maturity (Fehr and Caviness, 1977). The number of days in the reproductive period (NDRP) was determined from the number of days between full flowering and maturity. After collection, the data were first split into two groups by region (southern and central regions of Brazil) and then considered as a whole to perform a joint analysis of variance.

The AMMI analysis combines analysis of variance and PCA in a single model that is additive regarding the main effects of genotypes and environments and multiplicative regarding the interaction effects (Gauch and Zobel, 1996). The following equation describes the model:

$$Y_{ij} = \mu_i + g_i + e_j + \sum_{k=1}^{p} \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + e_{ij}$$

where, Y_{ij} is the mean response of the replicates of the i^{th} genotype in the j^{th} environment; μ_i is the overall mean; g_i is the main effect of genotype "i" (i = 1, 2, 3, …, g); e_j is the main effect of environment "j" (j = 1, 2, 3,…, e) and:

$$\sum_{k=1}^{p} \lambda_k \gamma_{ik} \alpha_{jk}$$

is the standard in which γ_{ik} is the singular value of the kth axis of the interaction, γ_{jk} is the singular value of the ith genotype on the kth axis, α_{jk} is the singular value of the jth environment on the kth axis, p is the number of axes retained in the model and k is the non-null characteristic root (k = 1, 2,.., min (g-1, e-1)). The residual of the interaction (noise) is ρ_{ij} and finally, e_{ij} is the mean experimental error.

The multiplicative part is analyzed through its principal components by decomposing the G×E sums of squares into different axes or components called IPCAs or AMMIs (Duarte and Vencovsky, 1999). Once in possession of the IPCA1 and IPCA2 scores, the AMMI stability value (ASV) is given by the equation from Purchase *et al.* (2000), as described below:

$$ASV_i = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1)\right]^2 + (IPCA2)^2}$$

where, SS IPCA1 and SS IPCA2 are the sums of squares of the AMMI analysis for the first and second axes, respectively and IPCA1 an IPCA2 are the respective PCA scores. Lower values indicate genotypes of greater stability.

The scores were calculated for the data from the southern and central regions separately and then together to represent Brazil. Using each of the three sets of scores, the most stable genotypes for the southern and central regions as well as Brazil were chosen. Regression analysis was then performed on the stable genotypes previously selected. With the fitted equation which involves the maturation date and control samples with defined RMGs (Alliprandini *et al.*, 2009), the RMGs of the remaining genotypes were calculated and compared with those recently established and published by Alliprandini *et al.* (2013). In these analyses, the computational program GENES (Cruz, 2001) and software of the Statistical Analysis System (SAS Institute, Inc., Cary, NC, USA) were used.

RESULTS AND DISCUSSION

The trials took place in a diversified group of environments (Table 1), representative of the main regions of Brazil where soybean is cultivated. The genotypes tested are represented in Table 2. The analysis of the southern region resulted in low variation coefficients: 1.7% for the NDF, 0.8% for the NDM and 1.8% for the NDRP (Table 3). For the central region, the values were as follows: 4.2% for the NDF, 1.4% for the NDM and 3.7% for the NDRP (Table 4). According to Carvalho *et al.* (2002), these low coefficients are evidence of a well-conducted experimental arrangement. The variation coefficients for the central region were higher because of the greater variety of the environments, especially regarding latitude in the southern part of this region. The analysis of data

Table 3: Summary of the joint analysis of variance for soybean traits measured in the southern region and consisting of the number of days to flowering (NDF), to maturity (NDM) and in the reproductive period (NDRP)

		SS		
SV	DF	NDF	NDM	NDRP
(B/L)/Y	27	43.4	73.0	131.3
Genotypes (G)	19	60692.1**	98163.2**	9763.7**
Years (Y)	2	13429.3**	10174.8^{ns}	489.1^{ns}
Locations (L)	8	129687.8**	121116.4**	14052.5$_{ns}$
G×Y	38	1750.7**	2630.4**	1845.9**
G×L	152	3752.2**	5546.4**	7132.2**
Y×L	16	16560.0**	21796.3**	29933.3**
G×Y×L	304	2920.2**	7510.0**	8130.5**
Residual	513	462.0	595.9	949.6
Mean (days)		55.6	129.7	74.1
Heritability (%)		98.0	98.4	86.6
CV (%)		1.7	0.8	1.8

^{ns}Not significant, **significant at the 1% probability level (p = 0.01), SV: Source of variation, DF: Degrees of freedom; SS: Sum of squares and CV: Coefficient of variation

Table 4: Summary of the joint analysis of variance for soybean traits measured in the central region and consisting of the number of days to flowering (NDF), to maturity (NDM) and in the reproductive period (NDRP)

		SS		
SV	DF	NDF	NDM	NDRP
(B/L)/Y	24	125.2	117.1	318.3
Genotypes (G)	19	35646.4**	84453.6**	14088.3**
Years (Y)	2	1877.3^{ns}	3178.3^{ns}	419.9^{ns}
Locations (L)	7	25023.8**	67516.6**	24471.5**
G×Y	38	749.6^{ns}	788.4^{ns}	1001.1^{ns}
G×L	133	5021.3**	6533.0**	6941.4**
Y×L	14	12219.6**	19678.8**	6956.6**
G×Y×L	266	4709.6**	4564.7**	7163.5**
Residual	456	1545.2	1219.9	2895.1
Mean (days)		43.7	110.4	66.6
Heritability (%)		97.8	98.8	93.0
CV (%)		4.2	1.4	3.7

^{ns}Not significant, **significant at the 1% probability level (p = 0.01), SV: Source of variation, DF: Degrees of freedom; SS: Sum of squares and CV: Coefficient of variation

Table 5: Summary of the joint analysis of variance for soybean traits measured at all locations in the study (Brazil) and consisting of the number of days to flowering (NDF), to maturity (NDM) and in the reproductive period (NDRP)

		SS		
SV	DF	NDF	NDM	NDRP
(B/L)/Y	51	168.7	190.1	449.6
Genotypes (G)	19	92940.4**	180174.1**	21855.5**
Years (Y)	2	7062.1^{ns}	4879.9^{ns}	869.6^{ns}
Locations (L)	16	226527.5**	377455.5**	66215.0**
G×Y	38	1640.1**	2097.8**	1935.4**
G×L	304	12171.7**	14522.1**	16069.9**
Y×L	32	37024.2**	49948.4**	36929.4**
G×Y×L	608	8490.2**	13395.7**	16205.7**
Residual	969	2007.3	1815.8	3844.8
Mean (days)		50.0	120.6	70.5
Heritability (%)		98.5	99.1	93.2
CV (%)		2.8	1.1	2.8

^{ns}Not significant, **significant at the 1% probability level (p = 0.01), SV: Source of variation, DF: Degrees of freedom; SS: Sum of squares and CV: Coefficient of variation

from the southern region showed that all the effects were significant for the NDF, therefore highly influential, from the trial years assessed to the genotypes and their interactions. The year factor was not significant for the NDM trait and for the NDRP trait, no significant effect was observed for the year factor or the genotype-year interaction. The joint analysis of the data from the central region (Table 4) shows that the effect of the year factor and the genotype-year interaction were not significant for any trait; therefore, the growth year did not affect the analysis in this region or produce significant differences in the duration of the maturation or the reproductive period of the tested genotypes. These results suggested that the number of test years in the central region may be reduced, as long as multiple locations are sampled. In addition, pluviometric data from the state of Paraná indicate that there was less rain in 2008 in the western and southwestern regions which may have been relevant for the analysis (SIMEPAR, 2011).

The largest variances were due to location for all the traits (Table 3, 4 and 5). Mean heritability data were obtained using the analysis of variance, as in Cruz (2001) and remained above 85% which indicates a strong genetic component to the analyzed traits that varied according to the genotype. Interaction effects could be observed in all the situations in both regions studied, most notably in the year-location interaction. This interaction highlights the large differences between test years and locations and the necessity of considering both factors together for a correct evaluation.

The effects of the different genotypes tested were also significant for the characteristics under analysis and the highest percentage value which also had the highest variation, was found for the NDM trait. Alliprandini *et al.* (2009) demonstrate that this amplitude of variation allows the classification of genotypes into five to nine different relative maturity groups. The effects of the genotype-location interaction were also significant for all three traits but displayed low variability values when compared with the main effects. This pattern indicates that interaction exists but is of lesser importance because of the regional adaptation through latitude and longitude (Tables 3, 4 and 5). Nevertheless, all these effects must be taken into account to correctly evaluate the genotypes regarding the assessed characteristics. In practice, the genotype-year interaction displayed the lowest value in all situations, as occurred in an earlier study. Alliprandini *et al.* (2009) also reported that this interaction was low for all environments which suggested that genotypes can be efficiently classified into RMGs when the environments representative of the regions in which the cultivar will be grown and commercialized are considered. This conclusion gains further strength when we assess the triple interaction among genotype, year and location which has a p value below 0.01 in all cases. An analysis of the G×E interaction compared with the other interactions (Table 6) shows that the values for the genotype-location interaction were greater than those for the genotype-year interaction (Table 6) which is indicative of the importance of conducting evaluations in different environments. According to Cruz (2001), these interactions force the plant breeder to conduct a detailed study of the cultivar performance and the environment, namely, through the analysis of genotype stability and adaptability. The triple interaction was also significant for all the traits. It is important to know which genotypes are more stable and more predictable because they will be used as references for defining the maturity groups.

The data regarding flowering (NDF) and maturity (NDM) showed the expected mean values when the

Table 6: Percentages of genotype×environment interactions for the three analyses of traits in transgenic soybean within southern, central and Brazil regions between 2008 and 2011

	Southern			Central			Brazil		
Parameter	NDF	NDM	NDRP	NDF	NDM	NDRP	NDF	NDM	NDRP
G×Y	20.7	16.7	10.7	7.1	6.6	6.6	7.3	6.9	5.6
G×L	44.6	35.3	41.6	47.9	54.9	45.9	54.5	48.3	46.9
G×Y×L	34.6	47.8	47.5	44.9	38.4	47.4	38.1	44.6	47.3

G: genotypes, Y: Years, L: Locations, NDF: No. of days to flowering; NDM: No. of days to maturity and NDRP, No. of days in the reproductive period

Table 7: Phenotype correlation matrix with Pearson correlation coefficients for traits of transgenic soybean in the analyses of the southern and central regions considered separately and combined (Brazil)

	Southern			Central			Brazil		
Parameter	NDF	NDM	NDRP	NDF	NDM	NDRP	NDF	NDM	NDRP
NDF	1	0.836**	0.083**	1	0.864**	0.169**	1	0.872**	0.194**
NDM		1	0.616**		1	0.642**		1	0.650**
NDRP			1			1			1

Significant at the 1% probability level, NDF: No. of days to flowering, NDM: No. of days to maturity and NDRP, No. of days in the reproductive period

cultivars were grown within their regions of adaptation. However, the cultivars obtained from breeding programs in the central region did tend to increase the duration of their flowering period when cultivated in the South of Brazil because of their long juvenile period. Analogously, the cultivars developed in the South and lacking characteristics of juvenility tend to speed up their flowering and maturation cycle when cultivated at lower latitudes (Bruns, 2009). Aside from the photoperiodic effects on the cultivars, there was also a temperature influence which strengthened toward the north. The effect of temperature on the genotypes at different latitudes is, however, unclear because in the cultivars of the Midwest, the long juvenile period favors an increased initial growth period prior to flowering which causes the cultivars to prolong the cycle when sown in the South (Destro *et al*., 2001).

There were significant differences in the length of the reproductive periods, with the observed mean NDRPs slightly greater in the South, given the local conditions relative to the central region, where the cultivars developed earlier. George *et al*. (1990) studying soybean cultivars from different maturity groups, showed that soybean maturity is delayed as temperature decreases in high-elevation environments and that the duration of the vegetative phase increases along with the time until maturity, with these same patterns also observed in the experiments conducted in the South. According to Kantolic and Slafer (2007), the sensitivity to photoperiod remains high even during the reproductive period, regardless of the duration of the photoperiodic exposure.

After conducting the joint analyses, the NDF and NDM values were found to be highly correlated (Table 7), with correlation coefficients of approximately 0.85 which indicates that these parameters are directly correlated and that excellent predictive power can be obtained using only one of the two traits. Coefficients above 0.90 were found by Peluzio *et al*. (2005) and Nogueira *et al*. (2012). By contrast, a low correlation between the durations of the flowering and the reproductive periods was observed in all the analyses, with correlation coefficients between 0.08 and 0.19. Therefore, the only parameter selected for verification with the AMMI methodology was the maturity (NDM).

According to the AMMI analysis of the data from the southern region, the first and second genotypic components for the NDM represented 29.7 and 21.7% of the sum of squares of the interaction, respectively (Table 8 and Fig. 1). Therefore, it is possible to explain 51.4% of the G×E interaction for the maturity parameter using only two components.

For the data from the central region, the NDM values for the first principal component were different and more significant. From the AMMI2 biplot which shows the interaction effects between IPCA1 and IPCA2, the percentages for these two parameters were 47.9 and 13.6%, respectively and 61.5% for the two components combined (Fig. 2). In this type of graphical representation, the genotypes and environments considered to be more stable are those found closer to the origin, i.e., those that do not contribute much to the G×E interaction. Duarte and Vencovsky (1999) state that genotypes should be assessed in their respective adaptation ranges, being stable and adapted to the test environments.

In the analysis that accounted for all the environments together (Brazil), the values for the first two principal components were 30.8 and 17%, respectively (Fig. 3). The first principal component which explains more of the variation, was associated with the data from the central region, perhaps because the environments studied in this region can be considered more homogeneous than those in the South. The conclusions drawn by Oliveira *et al*. (2006) cite elevation, maximum temperature, rainfall and end-of-cycle diseases as important components of the G×E interaction aside, from the maturation genotypic factor. The analysis of the

Table 8: Eigenvalues and cumulative percentages for the number of days to maturity (NDM) trait by AMMI analysis; IPCA1 and IPCA2 axes and ASV** for the maturity of genotypes studied in nine envirouments of the southern (s) region, eight environments of the central (c) region and all envirouments of Brazil (br) from 2008 to 2011

	Southern NDM			Central NDM			Brazil NDM		
Parameter	Eigen value	Axis prop.	Cum (%)	Eigenvalue	Axis prop.	Cum (%)	Eigenvalue	Axis prop.	Cum (%)
1	2327.27	0.30	29.67	2851.61	0.48	47.98	4625.97	0.31	30.82
2	1702.81	0.22	51.38	809.98	0.14	61.61	2553.95	0.17	47.84
3	992.33	0.13	64.03	483.86	0.08	69.75	1620.49	0.11	58.64
4	677.42	0.09	72.67	450.87	0.08	77.34	1481.14	0.10	68.51
5	410.25	0.05	77.90	354.23	0.06	83.30	980.21	0.07	75.04
6	354.84	0.05	82.42	323.59	0.05	88.74	749.14	0.05	80.03
7	295.82	0.04	86.20	215.71	0.04	92.37	538.24	0.04	83.62
8	283.77	0.04	89.81	100.79	0.02	94.07	420.20	0.03	86.42
9	209.07	0.03	92.48	79.00	0.01	95.40	375.79	0.03	88.92
10	170.64	0.02	94.65	68.70	0.01	96.55	324.48	0.02	91.08
Genotype	**IPCA1**	**IPCA2**	**ASVs**	**IPCA1**	**IPCA2**	**ASVc**	**IPCA1**	**IPCA2**	**ASVbr**
1	-1.22	2.89	3.34	-2.34	-0.58	8.27	2.92	2.84	6.01
2	-1.18	2.87	3.29	-2.87	-0.64	10.12	3.13	2.65	6.25
3	-2.44	0.75	3.42	-1.46	-0.67	5.19	2.25	-0.71	4.14
4	-1.05	1.37	1.98	-2.09	-0.60	7.39	2.27	0.85	4.20
5	-1.26	-0.91	1.94	-1.29	-0.29	4.54	1.26	-2.06	3.08
6	-0.04	0.33	0.34	-1.78	0.12	6.25	1.43	-0.14	2.59
7	2.44	-2.42	4.12	0.09	0.14	0.34	-1.19	0.34	2.18
8	-0.47	-0.70	0.95	0.79	3.75	4.68	-0.49	-2.10	2.28
9	-0.80	-0.60	1.24	-0.20	-1.19	1.38	0.42	0.17	0.79
10	-1.03	-0.53	1.51	-0.59	1.26	2.43	0.90	-1.69	2.35
11	-1.26	-1.24	2.13	-0.82	0.98	3.07	0.92	-2.05	2.64
12	-1.01	-0.77	1.59	-0.69	1.30	2.75	0.76	-1.93	2.37
13	-0.61	-1.38	1.61	0.57	-0.39	2.03	-0.43	-0.76	1.09
14	0.19	-0.91	0.95	0.92	0.83	3.33	-1.02	-0.94	2.07
15	-0.57	-1.79	1.95	2.19	-1.64	7.89	-1.59	0.10	2.88
16	0.94	0.37	1.33	1.76	0.30	6.20	-1.75	0.01	3.17
17	1.86	0.20	2.54	2.58	-0.40	9.09	-2.86	0.34	5.20
18	1.29	-0.66	1.88	2.43	-0.60	8.59	-2.63	0.32	4.78
19	3.05	2.17	4.70	0.82	-1.71	3.37	-1.63	3.30	4.42
20	3.19	0.96	4.47	1.98	0.03	6.97	-2.67	1.44	5.05

**Region designation

component scores can show how genotypes and environment interact: Scores with the same sign interact positively, displaying adaptive synergism, whereas scores of opposite signs suggest negative interaction (Duarte and Vencovsky, 1999).

Cascavel in 2008/2009, 2009/2010 and 2010/2011; Rolândia in 2009/2010 and Cruz Alta in 2008/2009 were chosen as the most stable environments in the South. If there is repeatability in the stability of an environment over the years, then that environment can be highly reliable for tests (Duarte and Vencovsky, 1999). The location of Cascavel stands out in the South because of its highly repeatable stability, with high stability in the three years of testing. For the central region, the following environments were selected as the most stable: Rio Verde in 2008/2009, 2009/2010 and 2010/2011; Cristalina in 2008/09 and Sorriso in 2009/2010. The central region contains one environment with a consistently high stability at the Rio Verde location, as confirmed by Pacheco *et al.* (2009), who identified Rio Verde and Placas as key locations for the development of soybean breeding programs.

AMMI analysis uses the decomposition of the interaction sum of squares to find the best fit for the model. This makes it possible to identify genotypes and environments in a biplot, where the best locations, specific adaptations and genotype stabilities can be easily observed.

The stable genotypes were found to lie in an intermediate maturation range. At least two additional cultivars that were classified as unstable but displayed lower ASVs in the latest and earliest maturation groups were also chosen. This addition was performed because the late cultivars grown in the southern region suffered greater insect infestation which made the assessment of their maturity more difficult. The following cultivars comprise the final definition of stable cultivars for the southern region using the AMMI methodology and the corresponding ASVs (Table 8) for maturation (NDM) as a reference: FTS Campo Mourão RR, Fundacep 54RR, Fundacep 59RR, P98Y11 and Valiosa RR; additionally, the BMX Titan RR and M9144RR cultivars were included because of their low ASVs at the maturity extremes. For this region, five cultivars were selected as stable, four of which display determinate growth and one shows semideterminate growth.

The data for the central region also demonstrated that stable genotypes occur in an intermediate maturation

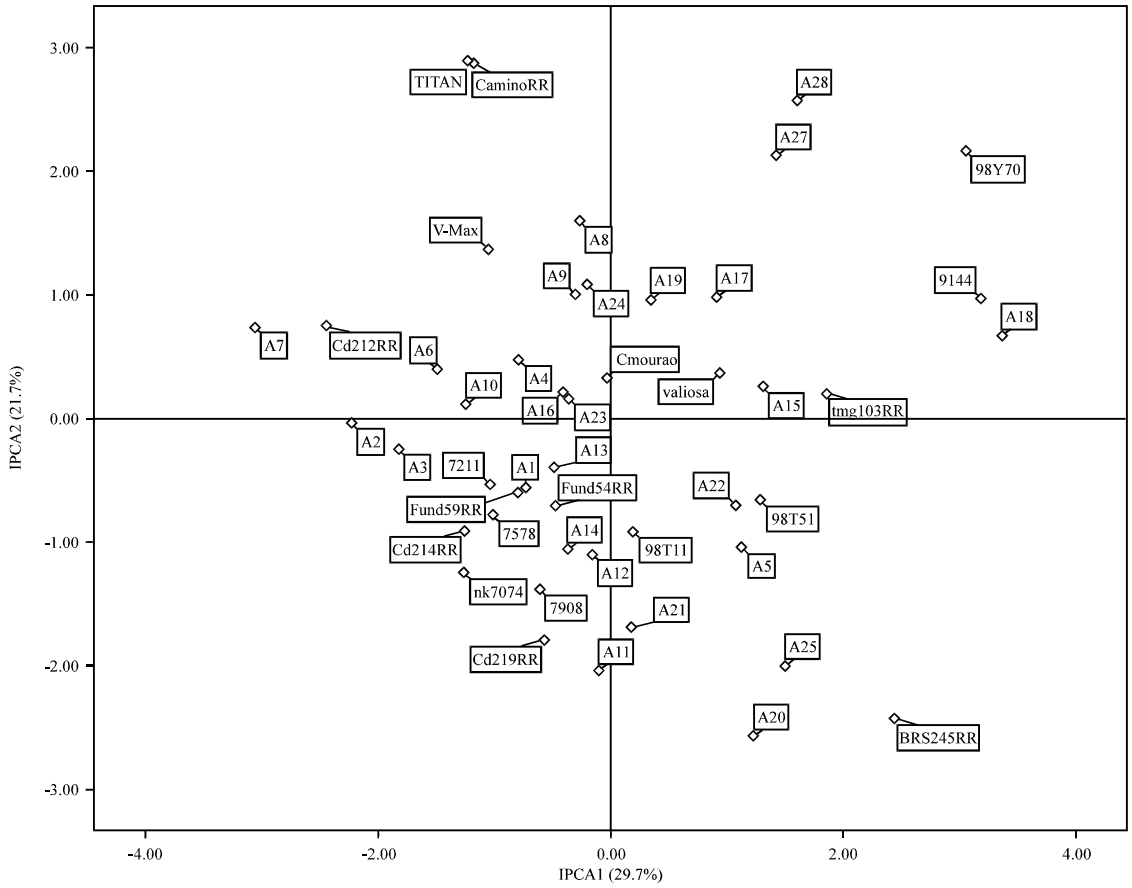

Fig. 1: AMMI2 maturity biplot using data from the southern region showing IPCA1×IPCA2, 20 genotype and 27 environment

range. Similarly, two new cultivars were defined with extreme maturities because in this region, the early genotypes originating from the South speed up their cycles and develop extremely early because they lack a long juvenile period which also makes their accurate evaluation more difficult. Thus, in addition to the genotypes assigned by AMMI, ROOS Camino RR and P98Y70 were also assigned to the RMG of this region. Using the lowest ASVs for maturation, the following stable cultivars were defined for the central region: BRS245RR, Fundacep 59RR, M7211RR, M7578RR and M7908RR. Five genotypes were selected as stable, only one of which having an indeterminate growth type.

When considering the joint analysis of all locations and genotypes, the most stable cultivars were also found in a narrow maturity range. The following extreme genotypes were defined by the aforementioned criterion: ROOS Camino RR and P98Y70. In addition, the following were defined as stable according to the AMMI analysis: BRS245RR, Fundacep 54RR, Fundacep 59RR, M7908RR and P98Y11. All five stable genotypes were selected and demonstrated determinate growth. Only one genotype was classified as stable in all of the three location-specific analyses conducted, namely, Fundacep 59RR. The following genotypes were stable in two of the three analyses: BRS245RR, Fundacep 54RR, M7908RR and P98Y11. Figure 4 shows the regression plots for the three analyses conducted by region in this study according to the genotypes considered as stable. The remaining RMGs were determined using the regression equation and the maturation obtained in the analysis. In general, with small deviations from the expected results, the methodology was efficient in calculating the RMGs on a broad scale. The same result was obtained in the study by Alliprandini *et al.* (2009) in which the RMGs could also be established on a broad scale.

Table 9 shows the RMG values calculated through linear regression from the most stable cultivars for each region using the mean maturation values obtained in the trials and the previously published RMGs for comparison (Alliprandini *et al.*, 2013). This table shows the RMGs calculated using the data from the southern region, all of

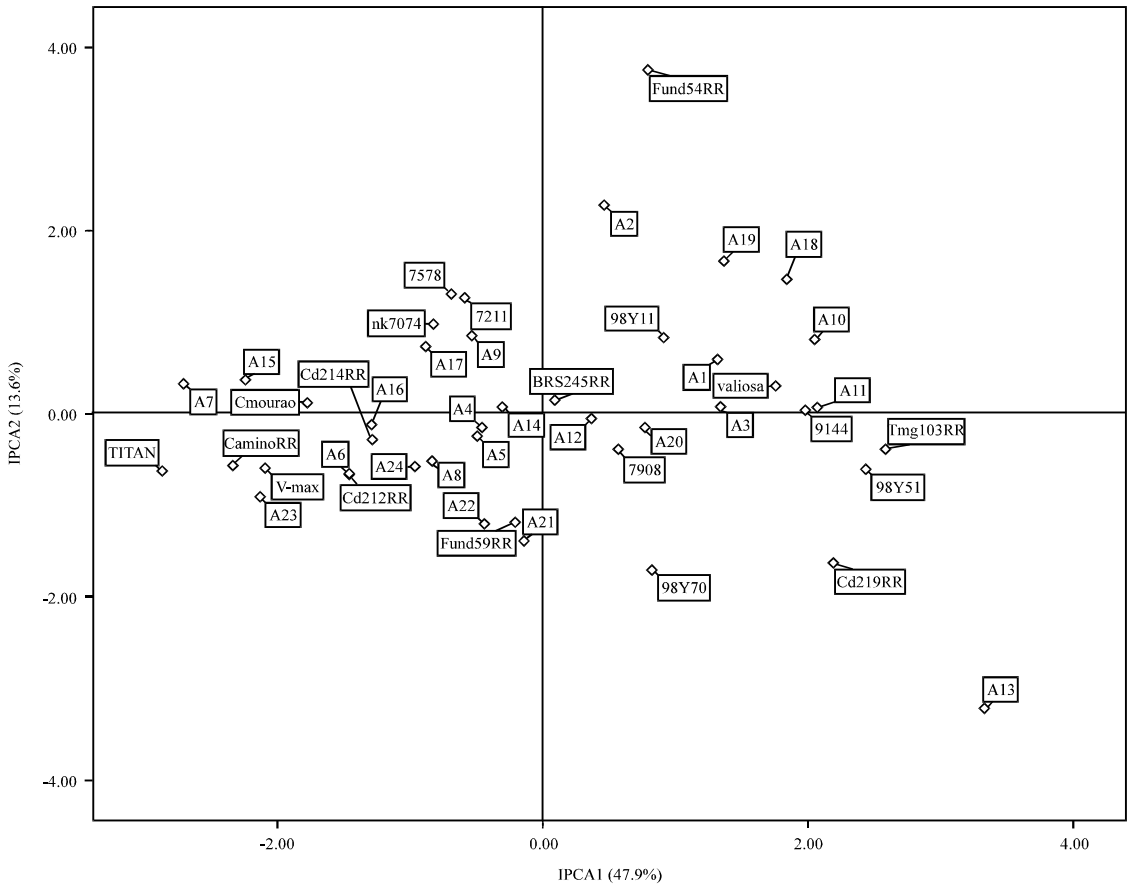

Fig. 2: AMMI2 maturity biplot using data from the central region and showing IPCA1×IPCA2, 20 genotypes and 24 environments

Table 9: Relative maturity groups (RMGs) defined by regression for the southern, central and Brazil regions using stable cultivars as determined through AMMI analysis (1988), the number of days to maturity (NDM) in the central (C) and southern (S) regions and the respective tabulated RMG values

		Calculated RMG			
	NDM				Tabulated
Genotype	C/S	Southern	Central	Brazil	RMG
ROOS CaminoRR	96/112	5.6	6.0	5.8	5.6
BMX TITAN RR	98/114	5.7	6.1	6.0	5.6
CD212RR	98/118	6.2	6.1	6.2	6.3
V-MaxRR	101/121	6.4	6.4	6.5	6.4
CD214RR	101/124	6.8	6.4	6.7	6.8
FTS CMOURÃO RR	104/125	6.9	6.7	6.9	6.7
BRS245RR	105/126	7.0	7.3	7.2	7.5
FUND54RR	109/127	7.4	7.3	7.5	7.5
FUND59RR	106/127	7.3	7.5	7.5	7.6
M7211RR	107/129	7.0	6.8	7.0	7.0
NK7074	109/131	7.0	6.9	7.1	7.0
M7578RR	112/129	7.2	7.1	7.2	7.2
M7908RR	112/131	7.4	7.6	7.6	7.6
P98Y11	112/131	7.4	7.5	7.6	7.6
CD219RR	118/134	7.7	8.2	8.1	8.2
VALIOSA RR	119/140	8.3	8.3	8.4	8.1
TMG103RR	121/141	8.4	8.5	8.6	8.3
P98Y51	123/141	8.5	8.7	8.7	8.6
P98Y70	126/144	8.7	8.9	8.9	8.7
M9144RR	129/149	9.2	9.3	9.4	9.2

Southern $y = 0.0994x-5.5832$ $R^2 = 0.967$, Central $y = 0.1034x-4.0343$ $R^2 = 0.937$ and Brazil $y = 0.1024x-4.9086$, $R^2 = 0.961$

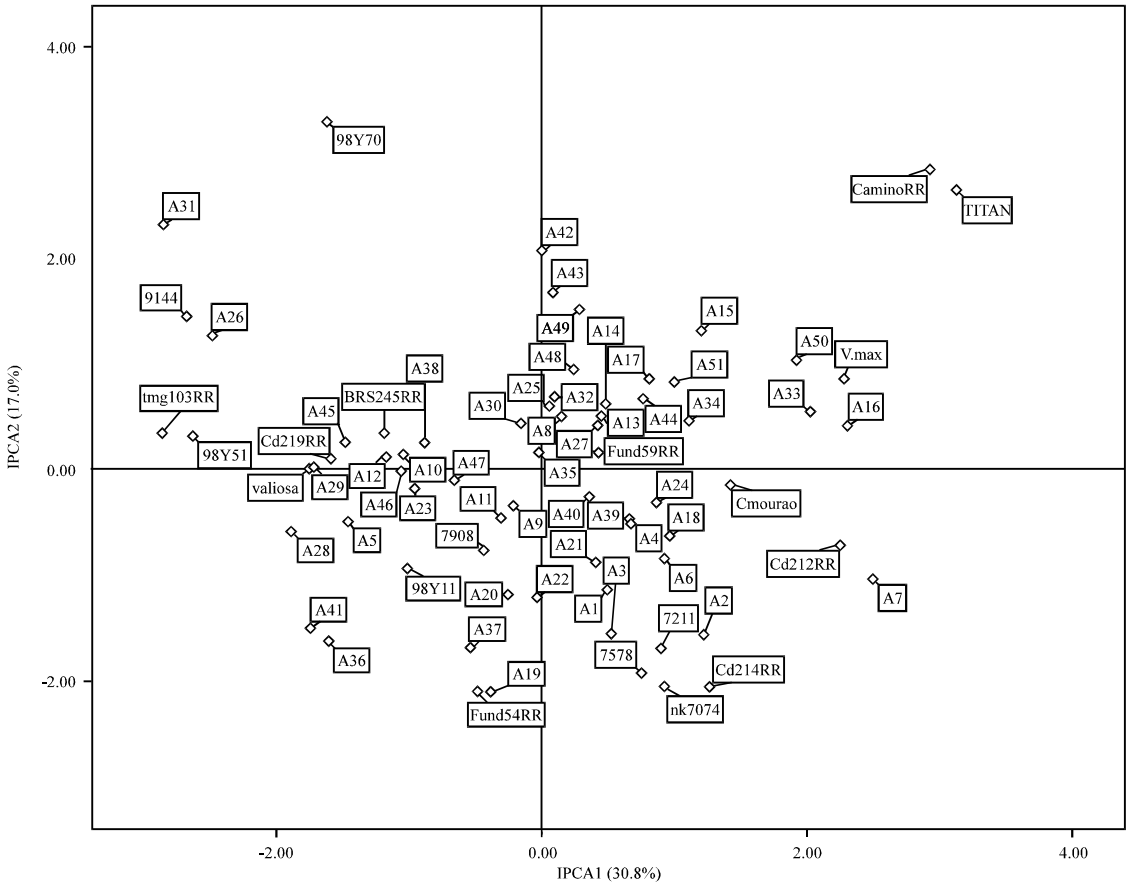

Fig. 3: AMMI2 maturity biplot using data from all regions (Brazil) and showing IPCA1×IPCA2, 20 genotypes and 51 environments

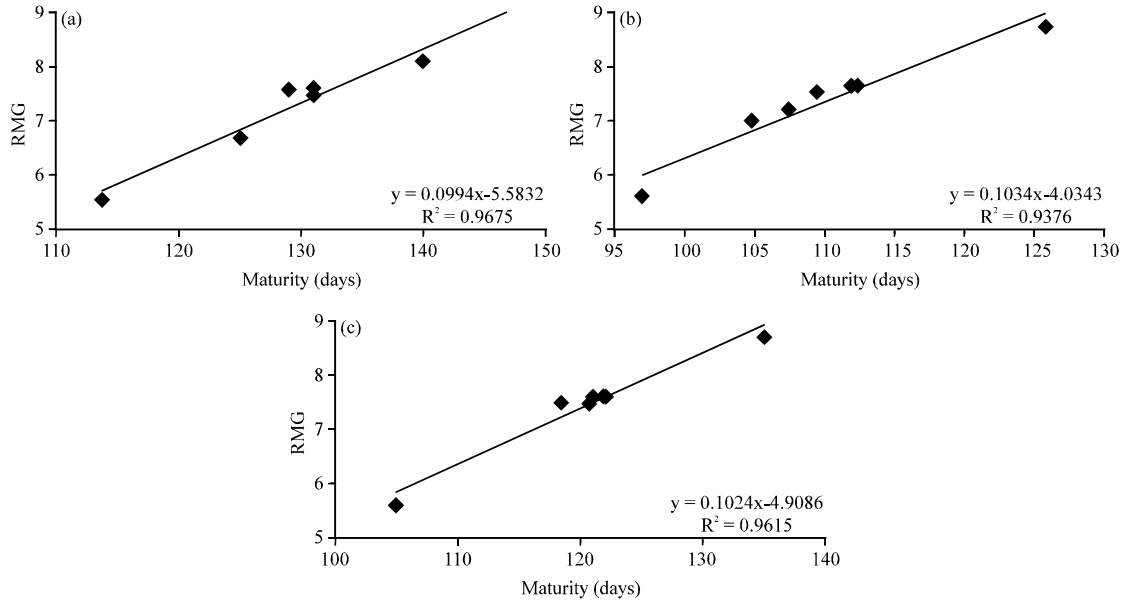

Fig. 4(a-c): Regression plots using data obtained from the stable genotypes in the (a) Southern, (b) Central regions and (c) All environments in Brazil

which were within expectations, with the small exception of late cultivars and those originating from the central region. In other words, analysis of the data from the southern region allows the classification of practically all the genotypes into one wide maturity spectrum; however, the inclusion of comparison genotypes with long juvenile periods and extremely late maturity must be avoided. Still, the data in Table 9 from the central region were mostly adequate to calculate the RMGs, with the exception of the earlier material and that originating from the southern region which did not fit the regression well.

In the general analysis with all the data from all the locations, the calculated RMGs were also in agreement with the expected results, with the exception of the earlier genotypes from the southern region and very late genotypes (Table 9). The analyses for the central region and for all locations and genotypes were similar to one another, but the analysis of the central region is more precise and should be used as a reference to classify the genotypes for Central region. The fact that stable genotypes were found in a better fitted spectrum suggests that new cultivars and new environments should be used, given the constant need to update RMG Table. The data from the southern region also showed a good fit and can be used for this region. Therefore, further studies on this subject are of great importance, including the examination of more genotypes and test locations so that the network may be expanded and the reliability of the RMGs may thereby be improved.

CONCLUSION

The genotypes considered to be stable should be used as references in future trials of this nature. The relative maturity groups (RMGs) determined here provided good estimates, as expected, proving to be valid for all of Brazil without undergoing significant changes depending on the test region or the germplasm being assessed. The RMGs are an important reference for the soybean production chain. The AMMI methodology can be used to calculate RMGs. The partition of regions may or may not be performed, depending on the specific objectives of each breeding program.

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REFERENCES

Alliprandini, L.F., J.F.F. Toledo, N. Fonseca Jr., L.A. Almeida and R.A.S. Kiihl, 1994. Effects of genotype×environment interaction on soybean yield in Parana state, Brazil. Pesq. Agropec. Bras., 29: 1433-1444.

Alliprandini, L.F., C. Abatti, P.F. Bertagnolli, J.E. Cavassim and H.L. Gabe *et al*., 2009. Understanding soybean maturity groups in Brazil: Environment, cultivar classification and stability. Crop Sci., 49: 801-808.

Alliprandini, L.F., J.E. Cavassim, M.A.R. Oliveira, M.N. Matsumoto and L.C. Prado *et al*., 2013. Soybean cultivar classification into relative maturity groups in Brazil during the harvests from 2001/2002 to 2011/2012. Proceedings of the Conference for Plant Breeding, August 5-8, 2013, Uberlandia, MG., Brazil.

Bruns, H.A., 2009. A survey of factors involved in crop maturity. Agronomy J., 101: 60-66.

Carvalho, C.G.P., C.A.A. Arias, J.F.F. Toledo, L.A. Almeida, R.A.S. Kiihl and M.F. Oliveira, 2002. Genotype×environment interaction on soybean yielding performance in Parana State. Pesquisa Agropecuaria Brasileira, 37: 989-1000.

Celeres, 2012. Biotechnology report. Celeres Consultoria, Uberlandia.

Cruz, C.D., 2001. Genes program: Windows version: Computational application for genetics and statistics. Editora UFV, Vicosa.

Cucolotto, M., V.C. Pipolo, D.D. Garbuglio, N.S. Fonseca Jr., D. Destro and M.K. Kamikoga, 2007. Genotype×environment interaction in soybean: Evaluation through three methodologies. Crop Breed. Appl. Biotechnol., 7: 270-277.

Destro, D., V. Carpentieri-Pipolo, R.A.D.S. Kiihl and L.A. de Almeida, 2001. Photoperiodic and genetic control of the long juvenile period in soybean: A review. Crop Breed. Appl. Biotechnol., 1: 72-92.

Duarte, J.B. and R. Vencovsky, 1999. Genotype-environment interaction: An introduction to AMMI analysis. Monograph Series, Brazilian Society of Genetics.

Fehr, W.R. and C.E. Caviness, 1977. Stages of soybean development. Spec. Rep. 80. Iowa State University. Ames, IA.

Gauch, H.G. and R.W. Zobel, 1996. AMMI Analysis of Yield Trials. In: Genotype-by-Environment Interaction, Kang, M.S. and H.G. Gauch (Eds.). CRC Press, Boca Raton, FL., USA., pp: 85-122.

George, T., D.P. Bartholomew and P.W. Singleton, 1990. Effect of temperature and maturity group on phenology of field grown nodulating and nonnodulating soybean isolines. Biotronics, 19: 49-59.

Guerra, E.P., R.A. de Oliveira, E. Daros, J.L.C. Zambon, O.T. Ido and J.C. Bespalhok Filho, 2009. Stability and adaptability of early maturing sugarcane clones by AMMI analysis. Crop Breed. Appl. Biotechnol., 9: 260-267.

Hassanpanah, D., 2010. Analysis of GxE interaction by using the additive main effects and multiplicative interaction in potato cultivars. Int. J. Plant Breed. Genet., 4: 23-29.

Kantolic, A.G. and G.A. Slafer, 2007. Development and seed number in indeterminate soybean as affected by timing and duration of exposure to long photoperiods after flowering. Ann. Bot., 99: 925-933.

Kempton, R.A., 1984. The use of biplots in interpreting variety by environment interactions. J. Agric. Sci., 103: 123-135.

Maia, M.C.C., N.A. Vello, M.M. Rocha, J.B. Pinheiro and N.F. Silva Jr., 2006. Adaptability and stability of soybean experimental lines selected for agronomic traits and insect resistance by uni-multivariate method. Bragantia, 65: 215-226.

Mandel, J., 1971. A new analysis of variance model for non-additive data. Technometrics, 13: 1-18.

Meotti, G.V., G. Benin, R.R. Silva, E. Beche and L.B. Munaro, 2012. Sowing dates and agronomic performance of soybean cultivars. Pesq. Agropec. Bras., 47: 14-21.

Nogueira, A.P.O., T. Sediyama, L.B. Sousa, O.T. Hamawaki, C.D. Cruz, D.G. Pereira and E. Matsuo, 2012. Path analysis and correlation among traits in soybean grown using two sowing dates. Biosci. J., 28: 877-888.

Oliveira, A.B., J.B. Duarte, L.J. Chaves and M.A. Couto, 2006. Environmental and genotypic factors associated with genotype by environment interactions in soybean. Crop Breed. Appl. Biotechnol., 6: 79-86.

Pacheco, R.M., J.B. Duarte, P.I.M. Souza, S.A. Silva and J. Nunes Jr., 2009. Key locations for soybean genotype assessment in Central Brazil. Pesq. Agropec. Bras., 44: 478-486.

Peluzio, J.M., R.D. Almeida, R.R. Fidelis, D. Almeida Jr., E.L. Brito and E.R. Francisco, 2005. Correlations among traits of soybean in Gurupi, Tocantins. Rev. Ceres, 52: 779-786.

Purchase, J.L., H. Hatting and Cs. Vandenventer, 2000. Genotype×environment interaction of winter wheat in south Africa: II. Stability analysis of yield performance. South Afr. J. Plant Soil, 17: 101-107.

SIMEPAR, 2011. Climate prediction for Verao/2009. 20 December 2011.

Sadeghi, S.M., H. Samizadeh, E. Amiri and M. Ashouri, 2011. Additive main effects and multiplicative interactions (AMMI) analysis of dry leaf yield in tobacco hybrids across environments. Afr. J. Biotechnol., 10: 4358-4364.

Silva, W.C.J. and J.B. Duarte, 2006. Statistical methods to study phenotypic adaptability and stability in soybean. Pesq. Agropec. Bras., 41: 23-30.

Zhang, L.X., S. Kyei-Boahen, J. Zhang, M.H. Zhang, T.B. Freeland, C.E. Watson Jr. and X.M. Liu, 2007. Modifications of optimum adaptation zones for soybean maturity groups in the USA. Crop Manage., 10.1094/CM-2007-0927-01-RS

Zobel, R.W., M.J. Wright and H.G. Gauch, 1988. Statistical analysis of a yield trial. Agron. J., 80: 388-393.