Adaptive and agronomic performances of soybean genotypes derived from different genealogies through the use of several analytical strategies

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The objectives of the present study were: (i) to evaluate the genotypic performances of 45 soybean genotypes with the future finality of recommendation of varieties for the State of São Paulo, Brazil; (ii) to determine the stability and adaptability of the genotypes and compare the performance and accuracy of the Wricke’s ecovalence, additive main effects and multiplicative interaction analysis (AMMI), GGE-Biplot and harmonic mean of the relative performance of genotypic values (MHPRVG) methods; (iii) to evaluate the phenotypic, genotypic and environmental correlations among the traits of 45 genotypes in three environments. The exploration of genotype-by-environment interaction (GEI) allowed the identification of 21 genotypes with high mean grain yield, representing different relative maturity groups and stability levels to the environments. This group was subdivided by crop cycle, in which the genotypes 18, 36, 20, 34 and 33 were early cycles (108 to 125 days), while genotypes 11, 22, 44 (CD 219), 24, 23, 14, 32, 1, 12, 39, 30, 38, 7 and 26 were medium cycles (126 to 135 days) and genotypes 25 and 37 were late cycles (≥ 136 days). The interpretations obtained from the ecovalence, AMMI and GGE-biplot methods were more similar than those from the MHPRVG method. This was due to the method’s properties, which assigns more weight to grain yield and little weight to the adaptability and stability parameters. The genotypic and environmental correlations among traits enhanced the interpretations of the genotype x environmental interactions.

Key words: Glycine max, stability and adaptability, additive main effects and multiplicative interaction analysis (AMMI), GGE-biplot, harmonic mean of the relative performance of genotypic values (MHPRVG), restricted maximum likelihood/best linear unbiased procedure analysis (REML/BLUP).

INTRODUCTION

Soybean [Glycine max (L.) Merrill] is the most important crop in Brazil due to its large cultivation area in different regions of the country. During the 2012/2013 agricultural year, the soybean sown area was 27.7 million hectares while total soybean grain production was 81.5 million tons. In the State of São Paulo in 2012/2013 agricultural
The objectives of the present study were: (i) to evaluate the genotypic performances of 45 soybean genotypes with the future finality of recommendation of varieties for the State of São Paulo, Brazil; (ii) to determine the stability and adaptability of the genotypes and compare the performance and accuracy of the Wricke’s ecovariance, additive main effects and multiplicative interaction analysis (AMMI), GGE-Biplot and harmonic mean of the relative performance of genotypic values (MHPRVG) methods; (iii) to evaluate the phenotypic, genotypic and environmental correlations among the traits of 45 genotypes in three environments.

MATERIALS AND METHODS

The experiment investigated soybean genotypes previously developed in the genetic improvement program of the FCAV/UNESP – Jaboticabal, S. P., Brazil. The genotypes were originated from different types of crosses and then belonging to different relative maturity groups (Kaster and Farias, 2012). In turn, four varieties (CD219, CD216, MG/BR-46 and V-MAX) were used as checks (Table 1).

The trials were conducted in three environments in the State of São Paulo, Brazil, in Jaboticabal (2011/2012 and 2012/2013) and Piracicaba (2012/2013). In Jaboticabal, soybean was sown on November 21, 2011 (2011/2012) and on November 26, 2012 (2012/2013) while in Piracicaba, on November 6, 2012 (2012/2013).

Piracicaba (22°42’S latitude; 47°37’W longitude) is located in the soybean macroregion 2, Mid-South, in the edaphoclimatic region 203 while Jaboticabal (21°14’S latitude; 48°18’W longitude) is in macroregion 3, Southeast in the edaphoclimatic region 302 (Kaster and Farias, 2012).

The experimental design was a randomized block with three replications per experiment. The plots consisted of four 5-m long rows spaced 0.5 m. The plot useful area included only the plants in the two central rows. The standard agro-technical practices were applied following the recommendations for the soybean crop (Embrapa, 2011).

The following agronomical traits were evaluated: grain yield (GY; in kg ha⁻¹), number of days to maturity (NDM; in days), number of days to flowering (NDF; in days), plant height at maturity (PHM; in cm), plant height at flowering (PHF; in cm), height of first pod insertion (HFPI; in cm), lodging (L; on a visual scale), varying from 1 (all plants of a plot were erect) to 5 (all plants of a plot were lodged) and agronomic value (AV; on a visual scale), ranging from 1 (plants with bad agronomic characteristics) to 5 (plants with excellent agronomic characteristics).

After data acquisition, we performed a combined analysis of variance to examine the main effects of the environment (E) and genotypes (G) and (GE) interaction effects. Where the F-statistics indicated significance, the means were separated using the Least Significant Difference (LSD) test at P = 0.05 in the Info-Gen software (Balzarini and Di Rienzo, 2013; Steel et al., 1997).

In the principal component analysis (PCA), standardized data of quantitative traits (NDF, NDM, PHF, PHM, HFPI and GY) were used. The eigenvalues associated with each eigenvector were represented as the variance of each principal component. Also, the PCA was performed to explore genotypic and environment correlations among quantitative traits of 45 genotypes in three environments (Johnson and Wichern, 2002; Balzarini, 2003).

Wricke’s (1965) ecovariance (W) measured stability on the basis of the contribution of a genotype to the GEI sums of squares. The more stable genotypes are associated with smaller W, values (Cruz and Carneiro, 2003). Grain yield data were subjected to Wricke’s
Table 1. Genealogy of the 45 soybean genotypes evaluated by the genetic improvement program of FCAV/UNESP, Jaboticabal.

| Genotype | Nomenclature | Genealogy |
|----------|--------------|-----------|
| Late Cycle (≥136 days) |
| 25 JAB 558 | CAC-1 × BR-17 | |
| 37 JAB 934 | Embrapa-48 × IAC-23 | |
| 5 JAB 616 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 43 MG/BR-46 | Commercial Variety | |
| Medium Cycle (126-135 days) |
| 6 JAB 617 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 38 JAB 933 | Embrapa-48 × IAC-22 | |
| 41 JAB 610 | Coodetec - 204 × Liderança | |
| 2 JAB 612 | (BRS-137×HARTWIG) × (IAC-8-2 × Embrapa-48) | |
| 12 JAB 623 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 13 JAB 625 | [[(BR-16 × Tainung-3) × (CAC-1 × BRS-137)] × [[Embrapa-59 × FT-2) × (MG/BR-46 × Coodetec-204)]] | |
| 23 JAB 472 | Embrapa-48 × MG/BR-46 | |
| 40 JAB 266 | Coodetec - 204 × Liderança | |
| 44 CD219 | Testemunha | |
| 30 JAB 777 | IAC-17 × BR-18 | |
| 32 JAB 798 | IAC-17 × BR-19 | |
| 4 JAB 615 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 29 JAB 716 | IAC-17 × BR-18 | |
| 39 JAB 265 | Coodetec - 204 × Liderança | |
| 24 JAB 501 | Embrapa-48 × MG/BR-46 | |
| 14 JAB 626 | [[(BR-16 × Tainung-3) × (CAC-1 × BRS-137)] × [[Embrapa-59 × FT-2) × (MG/BR-46 × Coodetec-204)]] | |
| 22 JAB 450 | Embrapa-48 × MG/BR-46 | |
| 7 JAB 618 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 19 JAB 338 | Embrapa-48 × MG/BR-46 | |
| 1 JAB 611 | (BR-16×TAINUNG-3) × (CAC-1× BRS-137) | |
| 15 JAB 627 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 10 JAB 621 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 26 JAB 587 | CAC-1 × BR-19 | |
| 8 JAB 619 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 17 JAB 630 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 11 JAB 261 | Coodetec - 204 × Liderança | |
| 16 JAB 629 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| Early Cycle (≤125 days) |
| 1 JAB 611 | (BR-16×TAINUNG-3) × (CAC-1× BRS-137) | |
| 15 JAB 627 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 10 JAB 621 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
| 26 JAB 587 | CAC-1 × BR-19 | |
| 8 JAB 619 | (Hartwig × BRS-134) × (Tainung-4 × Renascença) | |
| 17 JAB 630 | [[(Tainung-4 × Renascença) × (FT- Estrela × BRS-134)] × [[Embrapa-59 × Coodetec-204) × (CAC-1 × BRS-137)]] | |
Table 1. Contd.

| No. | JAB   | Parental Pairs                                      |
|-----|-------|----------------------------------------------------|
| 34  | JAB 833 | Embrapa-48 × IAC-18                                 |
| 20  | JAB 449 | Embrapa-48 × MG/BR-46                               |
| 36  | JAB 930 | Embrapa-48 × IAC-21                                 |
| 35  | JAB 846 | Embrapa-48 × IAC-19                                 |
| 18  | JAB 304 | MG/BR-46 × IAC Foscarin-31                          |
| 9   | JAB 620 | (Hartwig × BRS-134) × (Coodetec-201 × BRS MS Bacuri) |
| 33  | JAB 829 | Embrapa-48 × IAC-17                                 |
| 28  | JAB 684 | IAC-17 × BR-16                                     |
| 27  | JAB 669 | IAC-17 × BR-16                                     |
| 21  | JAB 263 | MG/BR-46 × Coodetec – 204                          |
| 31  | JAB 264 | MG/BR-46 × Coodetec – 204                          |
| 3   | JAB 614 | (Hartwig × BRS-134) × (Coodetec-201 × BRS MS Bacuri) |
| 45  | V-MA×  | Commercial variety                                 |
| 42  | CD216  | Commercial variety                                 |

ecovalence analysis using GENES program (Cruz, 2006). The second method called AMMI was used to evaluate the stability and adaptability of grain yield trait (Shafii and Price, 1998; Zobel et al., 1988; Dias et al., 2013). The AMMI-1 analysis was carried out according to Vargas and Crossa (2000) using the SAS software (SAS INSTITUTE, 2003).

Subsequently, the GGE-biplot methodology was performed to explore the stability and adaptability of the grain yield trait of the 45 genotypes to all three environments. It removed the environmental main effect (E), focusing the response on the genotype (G) + genotype-by-environment interaction (GEI) (Yan and Hunt, 2002; Yan and Kang, 2002). This analysis was carried out using the Info-Gen software (Balzarini and Di Rienzo, 2013).

Finally, the MHPRVG method ranked genotypes based on the genotypic values, adaptability (PRVG, Relative Performance of Genotypes Value in relation to the median of each environment) and stability (MHVG, Harmonic Mean of the Genotypic Values through the environments), through REMBL/BLUP (restricted maximum likelihood/best linear unbiased procedure analysis). It was carried out with model 54 using the SELEGEN-REML/BLUP software (Resende, 2007b). The predicted genotypic values for genotype i in each environment j were expressed on the same scale of the evaluated trait.

RESULTS AND DISCUSSION

Combined analysis of variance identified significant differences (p<0.05) among genotypes and the genotype-by-environment interaction for all traits. Furthermore, significant differences (p<0.05) were evident for the following traits: NDF, NDM, PHF, PHM, HFPI, GY and AV among the different environments. For the lodging trait, the environment effect was not significant (p<0.05) by F-test. In the three environments, the 45 genotypes displayed the average values of 54 days, 127.5 days, 65 cm, 16 cm, 2920 kg ha⁻¹, 1.6 and 3.2 for the traits, NDF, NDM, PHF, PHM, HFPI, GY and AV, respectively. The relationship between the largest and the smallest mean square was 7.9 for the grain yield trait (Table 2).

In the principal components analysis, for the environment-genotype combinations, two eigenvalues were greater than one, explaining 69% of the variance contained in the six traits. The first principal component (PC1) kept 39% of the original variance. The NDF and NDM traits, especially, explained this retention of variance with principal component correlation values of 0.56 and 0.55, respectively (Table 3). The second principal component (PC2) retained 30% of the original variance. The PHM and GY traits explained this variance retention with principal component correlation values of 0.65 and 0.59, respectively (Table 3).

In the dispersion graph of the first two components, the traits NDF, NDM and HFPI had a greater inertia on the right, displaying positive correlations amongst them. In Piracicaba, located at higher latitude, the genotypes evinced greater average NDM and NDF while the cycles of these genotypes were smaller at lower latitude in Jaboticabal. On the other hand, the PHF and PHM traits were positively correlated. Majority of the genotypes exhibited determine growth habits which support the correlation amongst traits (Figure 1).

The GY trait was positively correlated with PHM but not with PHF. Also, GY trait was negatively
Table 2. Mean squares derived from ANOVA of measured traits$^1$ of 45 soybean genotypes in the three environments.

| Source of variation          | DF | NDF (days) | NDM (days) | PHF (cm) | PHM (cm) | HFPI (cm) | GY (kg ha$^{-1}$) | L (grades) | AV (grades) |
|-----------------------------|----|------------|------------|----------|----------|-----------|------------------|------------|-------------|
| Blocks / environments       | 6  | 12         | 22         | 288      | 289      | 25        | 1030311          | 1.2        | 0.7         |
| Genotypes                   | 44 | 125**      | 601**      | 545**    | 686**    | 89**      | 959015**         | 1.2**      | 1.0**       |
| Environments                | 2  | 1718.5**   | 10338**    | 2835*    | 3866**   | 1021**    | 173481534**      | 1.3NS      | 3.9*        |
| Genotypes x environments    | 88 | 14.5**     | 51**       | 154**    | 232**    | 26.6**    | 7756015**        | 1.1**      | 0.7**       |
| Error                       | 264| 4          | 14         | 59       | 52       | 9         | 512293           | 0.4        | 0.3         |
| Means                       |    | 54         | 127.5      | 65       | 83       | 16        | 2920             | 1.6        | 3.2         |
| CV(%)                       |    | 3.7        | 3          | 11.8     | 8.7      | 19.3      | 24.51            | 39.8       | 16.6        |
| Largest QMR / smallest QMR relation | 6.8 | 1.4 | 2.2       | 3.0      | 2.1      | 7.90      | 1.5              | 2.4        |

**: F-test significant at 0.01 probability level; *: F-test significant at 0.05 probability level; NS: F-test not significant at 0.05 probability level. CV (%): Coefficient of experimental variation. DF: Degrees of freedom; $^1$: NDF: number of days to flowering; NDM: number of days to maturity; PHF: plant height at flowering; PHM: plant height at maturity; HFPI: height of first pod insertion; GY: grain yield; L: lodging; AV: agronomic value.

Table 3. Eigenvalues and eigenvectors generated from the principal components analysis of the environment–genotype combinations.

| Eigenvalues | Eigenvectors |
|-------------|--------------|
| Lambda      | Valor        | Proportion | Cumulative proportion | Traits 1 | 2  | 3  |
| 1           | 2.36         | 0.39       | 0.39                   | NDF      | 0.56 | -0.12 | 0.14 |
| 2           | 1.8          | 0.3        | 0.69                   | NDM      | 0.55 | -0.17 | -0.29 |
| 3           | 0.97         | 0.16       | 0.86                   | PHF      | 0.39 | 0.44  | -0.4  |
| 4           | 0.39         | 0.06       | 0.92                   | PHM      | 0.22 | 0.65  | 0.06  |
| 5           | 0.25         | 0.04       | 0.96                   | HFPI     | 0.34 | -0.03 | 0.82  |
| 6           | 0.23         | 0.04       | 1                      | GY       | -0.24 | 0.59  | 0.23  |

correlated with the following traits NDF, NDM and HFPI. The genotypes evinced a higher average grain yield (4126 kg ha$^{-1}$) in 2011/2012 in Jaboticabal and 2012/2013 in Piracicaba, respectively. In the last two environments, the average crop cycles were longer (Figure 1).

Based on LSD($p<0.05$) test, a group of 21 genotypes displayed higher average mean grain yield, without statistical differences among them. This group was subdivided according to maturation cycle, genotypes 18, 36, 20, 34 and 33 were early cycles (108 to
Figure 1. Biplot showing the environment–genotype combinations (environment: mark’s colors; genotype: number). ●: commercial variety; progeny derived of ▲: single-way cross; ■: four-way cross; ♦: eight-way cross. Green marks: 2011/2012, in Jaboticabal, blue marks: 2012/2013, in Jaboticabal; orange marks: 2012/2013, in Piracicaba. NDF: number of days to flowering; NDM: number of days to maturity; PHF: plant height at flowering; PHM: plant height at maturity; HFPI: height of first pod insertion; GY: grain yield; L: lodging; AV: agronomic value. Based on LSD(p<0.05) test, the high yielding genotypes of early (red numbers), medium (blue numbers) and late (purple numbers) cycle.

Figure 2. Average grain yield (GY) of 45 soybean genotypes across three environments.

125 days), while genotypes 11, 22, 44 (CD219), 24, 23, 14, 32, 1, 12, 39, 30, 38, 7, and 26 were medium cycles (126 to 135 days) and genotypes 25 and 37 were late cycles (≥136 days). In this high average grain yield group, the highest value 3535 kg ha⁻¹ was obtained for genotype 11 while the smallest value was evinced by genotype 37 (3029 kg ha⁻¹) (Figure 2). The classification of genotypes by relative maturity group has been used by other authors (Alliprandini et al., 2009; Cavassim et al., 2013).

Ecovalence analysis shows that the five high yielding genotypes of early cycle were 18, 36, 20, 34 and 33. The
environment sensitive genotype 18 (3299 kg ha\(^{-1}\); NDM = 122 days; \(W_i(\%) = 4.7\)) derived from the MG/BR-46 x IAC Foscarin-31 cross. The other early cycle genotypes, 36 (3170 kg ha\(^{-1}\); NDM = 123 days; \(W_i(\%) = 1.7\)), 20 (3147 kg ha\(^{-1}\); NDM = 123 days; \(W_i(\%) = 1.4\)), 34 (3082 kg ha\(^{-1}\); NDM = 125 days; \(W_i(\%) = 0.1\)) and 33 (3030 kg ha\(^{-1}\); NDM = 118 days; \(W_i(\%) = 2.6\)) were stable (Figure 3).

Genotypes 36 (Embrapa-48 x IAC-21), 20 (Embrapa-48 x MG/BR46), 34 (Embrapa-48 x IAC-18) and 33 (Embrapa-48 x IAC-17) were half-sib progenies with a common parent, Embrapa-48 (Table 1).

Genotype 20 exhibited the greatest mean value for plant height at maturity (Figure 6) and also had good performances in unfavorable environments (E1 and E3) by AMMI-1 analysis (Figure 4). This genotype resulted from the crossing of Embrapa-48, a drought tolerant variety (Pitol and Broch, 2010) and MG/BR-46, with a long juvenile period. While by the AMMI-1 method, Genotypes 34 and 36 were stable and Genotypes 18 and 33 were sensitive to the environment. They showed adaptive performances to the favorable environment (E2) (Figure 4).

Ecovalence analysis of sixteen high yielding genotypes of medium cycles showed that five were sensitive to environment: 11 (3324 kg ha\(^{-1}\); NDM = 131 days; \(W_i(\%) = 1.8\)), 23 (3329 kg ha\(^{-1}\); NDM = 133 days; \(W_i(\%) = 1.4\)), 12 (3094 kg ha\(^{-1}\); NDM = 134 days; \(W_i(\%) = 0.3\)), 7 (3034 kg ha\(^{-1}\); NDM = 131 days; \(W_i(\%) = 2.0\)), 38 (3052 kg ha\(^{-1}\); NDM = 135 days; \(W_i(\%) = 0.2\)), 32 (3122 kg ha\(^{-1}\); NDM = 132 days; \(W_i(\%) = 0.4\)), 30 (3082 kg ha\(^{-1}\); NDM = 132 days; \(W_i(\%) = 0.9\)), 26 (3030 kg ha\(^{-1}\); NDM = 129 days; \(W_i(\%) = 1.0\)) and 39 (3093 kg ha\(^{-1}\); NDM = 132 days; \(W_i(\%) = 1.4\)) (Figure 3). The AMMI-1 analysis showed that Genotypes 30, 7, and 39 were stable and adapted to unfavorable environments (E1 and E3) while Genotypes 14, 23, 32, 12, 38 and 26 were stable and adapted to the favorable environment (E2) (Figure 4).

Genotypes 32 (IAC-17 x BR-19) and 30 (IAC-17 x BR-18) were half-sib progenies. Genotypes 26 (CAC-1 x BR-19) and 25 (CAC-1 x BR-17) were also half-sib progenies. Other half-sib progenies were the following genotypes: 38 (Embrapa-48 x IAC-22) and 37 (Embrapa-48 x IAC-23); and 32 (IAC-17 x BR-19) and 26 (CAC-1 x BR-19). Moreover, Genotypes 39 and 23 derived from crosses of (Coodetec - 204 x Liderança) and (Embrapa-48 x MG/BR46), respectively. Genotypes 14, 12 and 7 derived from complex crosses (Table 1).
Based on the ecovalence analysis, two high yielding genotypes of late cycle, 25 (3100 kg ha\(^{-1}\), NDM = 138 days; \(W_l(\%) = 1.3\)) and 37 (3029 kg ha\(^{-1}\), NDM = 138 days; \(W_l(\%) = 2.8\)) were stable to the environments (Figure 3). These genotypes 25 (CAC-1 x BR-17) and 37 (Embrapa-48 x IAC-23) were derived from biparental crosses (Table 1). The AMMI-1 analysis shows that Genotypes 37 and 25 were stable and adapted to unfavorable environments (E1 and E3) (Figure 4).

In the AMMI-1 biplot, the E3 environment (2012/2013, Piracicaba) was the most stable while E2 environment (2012/2013, Jaboticabal) was unstable (Figure 4). The climate conditions in the E2 environment were more favorable than those observed in E3 and E1 (2011/2012, Jaboticabal) environments. The E3 and E1 environments had lower discrimination powers of genotypes than the E2 environment (Figure 4).

The polygon view of the GGE-biplot showing the three environments, explains 94% of genotype and genotype x environment (G and GE) variation. The vertex genotypes were 3, 16, 27, 9, 18, 11, 24 and 40. In the sector which contained E2 environment, Genotypes, 11, 24 and 18 were vertexes of the polygon. In the sector which contained environment E1, genotype 40 was the vertex of the polygon. Finally, the sector which contained E3 environment, genotype 26 was the one which exhibited high grain yield. Here, GE interaction component was greater than the G component, all environments being in different sectors (Figure 5). The genotypic correlations among traits of 45 genotypes in the three environments were studied by principal component analysis. The PC1 (65.1%) separated four genotypes (18, 34, 33 and 36) with early cycles of 17 genotypes (11, 22, 44, 24, 32, 1, 39, 30, 38, 12, 26, 37, 23, 14, 25 and 7) with medium and late cycles. The early cycle Genotype 20 remained on the right side of the graph possibly due to the highest plant height at maturity. The traits HFPI, NDF and GY were separated from traits NDM, PHF and PHM by PC2 (13.9%). GY and NDF traits showed positive genotypic correlation. While NDM trait showed positive genotypic correlation with PHF and PHM traits. Among the medium and late cycle genotypes, nine genotypes (11, 22, 44, 24, 32, 1, 39, 30, 38) displayed higher mean values for NDF, HFPI and GY than the other eight genotypes (12, 26, 37, 23, 14, 25 and 7). These last genotypes showed higher average values for NDM, PHF and PHM than the first genotypes (Figure 6).

The environmental correlations among traits of the 45 genotypes in the three environments were also studied by principal component analysis. PC1 (78.9%) separated the E2 environment under good water availability from the E1 and E3 environments under drought stress. Also, PC1 separated GY, PHM and PHF traits from NDF, NDM and HFPI traits. PC2 (21.1%) separated NDF, HFPI, PHM and GY traits from NDM and PHF traits. The E2 environment, with greater water availability had positive environmental correlation with GY and PHM traits, while E3 environment, at higher latitude, had positive environmental correlation with NDM trait and to a smaller degree with the PHF trait. Finally, E1 environment with
Figure 5. Polygon view of the GGE-Biplot based on grain yield of 45 soybean genotypes tested in three environments. ●: commercial variety; progeny derived of ▲: single way cross ■: four-way cross, ♦: eight-way cross; E1: 2011/2012 in Jaboticabal, E2: 2012/2013 in Jaboticabal; E3: 2012/2013 in Piracicaba; Based on LSD($p<0.05$) test, the high yielding genotypes of early (red numbers), medium (blue numbers) and late (purple numbers) cycle.

Figure 6. Biplot showing the genotypic correlations among the traits of the 45 soybean genotypes in the three environments. ●: commercial variety; progeny derived of ▲: single way cross ■: four-way cross, ♦: eight-way cross; Based on LSD($p<0.05$) test, the high yielding genotypes of early (red numbers), medium (blue numbers) and late (purple numbers) cycle. NDF: number of days to flowering; NDM: number of days to maturity; PHF: plant height at flowering; PHM: plant height at maturity; HFPI: height of first pod insertion; GY: grain yield; L: lodging; AV: agronomic value.
Figure 7. The Biplot of environmental correlations among traits of the 45 soybean genotypes in three environments, E1: 2011/2012, in Jaboticabal, E2: 2012/2013, in Jaboticabal and E3: 2012/2013, in Piracicaba. Number of days to flowering (NDF), number of days to maturity (NDM), plant height at flowering (PHF), plant height at maturity (PHM), height of first pod insertion (HFPI) and mean grain yield (GY).

Drought stress had positive environmental correlation with NDF and HFPI traits (Figure 7).

Based on the REML/BLUP mixed model, the contribution of the variance components confirmed that 68.9% was attributed to the environment, 21.1% to the GxE interaction and 10% to the evaluated genotypes. The average genotypic value for the GY trait was \( \mu = 2920 \) while for E1, E2 and E3 environments the respective values were \( \mu_1 = 2758 \), \( \mu_2 = 4126 \) and \( \mu_3 = 1876 \), respectively. In turn, Neto et al. (2013) reported non-significant variation for rice genotypes.

The MHPRVG method classified the genotypic values of the 21 high average grain yield genotypes in the following descending order (show in parentheses), genotypes 11 (1), 22 (2), 44 (3), 24 (5), 23 (4), 14 (6), 18 (7), 36 (9), 20 (8), 32 (12), 1 (17), 25 (10), 12 (15), 39 (11), 34 (13), 30 (14), 38 (18), 7 (19), 26 (16), 33 (20) and 37 (24). The MHPRVG method classified the genotypes especially according to the genotypic values while stability and adaptability parameters had little weight. The genotypic values were positively correlated with stability (MHVG, Harmonic Mean of the Genotypic Values through the environments) and adaptability (PRVG, Relative Performance of Genotypes Value in relation to the median of each environment) values (Figure 8).

Among the twenty high mean grain yield genotypes, 16 resulted from single crosses; two others, from four-way crosses; and two others, from eight-way crosses. Still, a great number of genotypes remained related by two common parents, Embrapa-48 and MG/BR-46. The Embrapa-48 variety belongs to the 6.8 maturity group with the following genealogy (Davis x Paraná) x (IAS 4 x BR5). While MG/BR-46 variety belongs to the 8.1 maturity group and derived from the following genealogy Lo76-4484/Numbará.

The narrow genetic base of genotypes was supported by other studies which evaluated soybean genotypes of different improvement programs and releasing periods (Priotli et al., 2004; Priolli et al., 2010) as well as those studies based on the coefficient of percentage (Vello et al., 1988; Miranda et al., 2007).

Regarding the methodologies used, the interpretations obtained from the ecovalence, AMMI and GGE-biplot methods were more similar than those from the MHPRVG analysis. This was due to the method's properties, which assigns more weight to grain yield and little weight to adaptability and stability parameters. The results clearly show the need for further assessments of genotypes in more environments to decrease the coefficient of variation and increase the heritability of traits. More studies should also better define performances such as stability and adaptability of the genotypes, in addition to assess other important agronomic parameters, e.g., seed weight, seed oil and...
protein content.

**Conclusion**

The study of the G×E interaction allowed identifying 21 genotypes with high grain productivity, different relative maturity groups and stability levels to different environments. The interpretations obtained from the ecovalence, AMMI and GGE-biplot methods were more similar than the interpretations obtained from the MHPRVG analysis. This was due to the properties of the method which assigns more weight to grain yield and little weight to adaptability and stability parameters. The genotypic and environmental correlations among traits enhanced the interpretations of the genotype × environmental interactions.

**Conflict of Interests**

The authors have not declared any conflict of interests.

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