



Pod yield stability analysis of runner peanut lines using AMMI

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ABSTRACT - The interaction between genotypes and environment (GxE) can influence the selection process and recommendation of peanut cultivars. The objective of this study was therefore to evaluate the influence of GxE interaction of peanut pod yield using AMMI. The yield of 18 peanut lines and the cultivars IAC Caiapo and Runner IAC 886 was assessed in 10 field trials in the state of São Paulo. Significant effects of genotypes, environments and GxE interactions were detected in the analysis. The first AMMI principal component (IPCA1) explained 42.3% of the sum of squares of the GxE interaction. Sixteen of the twenty lines/cultivars under evaluation presented medium to high stability. Genotypes L127, L118, L123 line and Runner IAC 886 accounted for the greatest part of GxE interaction. Lines L132, L149 and L1-50P presented the highest stability and pod yields, above the overall mean, reflecting outstanding potential for cultivar recommendation.

Key words: *Arachis hypogaea* L., adaptability, stability, AMMI, pod yield.

INTRODUCTION

In the 2004/2005 growing season, the world peanut production totaled around 33.14 million tons. Brazil produced 310,000 t in an area of 130,000 ha (USDA 2005). Over the past few years, the national production satisfied the domestic market and covered exports to the European Union, mainly. The state of São Paulo accounted for about 75% of the domestic yield, namely due to the technical development of the production system, which implies the use of high-yielding cultivars.

Opening opportunities on the international market and the need for more competitive peanut cultivars have led to the implantation of Virginia as substitute for Valencia type cultivars, owing to the higher yield potential in highly technical cropping systems (Sholar et al. 1995, Godoy et al. 1999). This group of cultivars has a runner or semi runner growth habit and a longer

vegetative cycle, which is associated with a higher yield potential. Besides targeting plant architecture and cycle, research has focused on breeding improved kernels for confectionery, known as runner market types.

The Instituto Agrônômico – IAC has developed runner cultivars in an attempt to meet the increasing market demand. In 1996, runner cultivar IAC Caiapo was released (Godoy et al. 1996). It presented higher pod yield in relation to local standards (Tatu cultivar) and partial and multiple resistance to the foliar diseases late leaf spot (*Cercosporidium personatum*), early leaf spot (*Cercospora arachidicola*), scab (*Sphaceloma arachidis*), web blotch (*Phoma arachidicola*), and rust (*Puccinia arachidis*) (Godoy et al. 1996, Godoy et al. 1999). Cultivar Runner IAC 886, released in 2001, has a high pod yield potential, particularly when a good foliar disease control were made, a 125 to 130-day cycle and a

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more uniform kernel size and shape, thus meeting the requirements of the foreign market (Godoy et al. 2002).

The expansion of the crop has raised the demand for breeding and development of novel cultivars. New cultivars should be chosen, after testing in a series of trials covering a range of environments. The yield performance of genotypes depends on the environment, resulting in different phenotypic responses. The inconsistent response of some genotypes compared with others is therefore due to changes in the genotype ranking or in the absolute differences between genotypes without rank change – an expression commonly known as genotype x environment interaction (GxE). Consequently, breeders should take the interactions of cultivars with environmental factors into consideration, since the effects caused by genotypes and environments expressed in the GxE interaction are statistically non-additive (Yue et al. 1997).

The selection of cultivars, based on the stability of different environments rather than on trait means in a specific environment, is a strategy to reduce the GxE interaction (Eberhart and Russel 1966). The recommendation of cultivars considers only the overall mean of the trials, which favors cultivars with excellent performance in the most favorable environments, but does not discriminate cultivars that are able to adapt to better or worse conditions. According to Murakami et al. (2004), knowledge on the performance and/or adaptability of genotypes to particular environments is highly important to estimate the agronomical value of cultivars and allows the recommendation for specific environments. In addition, performance stability allows the identification of stable genotypes, with a predictable performance in the different environments.

Several methodologies have been suggested for studies of phenotypic adaptability and stability, which differ in the concepts and biometric procedures by which the GxE interaction is measured. Some are based on interaction variance (Wricke and Weber 1986, Magari and Kang 1997), on simple linear regression (Eberhart and Russel 1966) or multiple linear regression (Storck and Vencovsky 1994), as well as on non-linear models (Toler and Burrows 1998, Rosse and Vencovsky 2000), on multivariate methods such as the principal components analysis (Crossa 1990) and methods that integrate the variance analysis of the principal component analysis, also known as AMMI (*Additive main effects and multiplicative interaction*) analysis (Gauch and Zobel 1996).

Linear regression is the most commonly used procedure in the study of adaptability and stability, which are important strategies in the recommendation of cultivars. This methodology describes the average standard response of each genotype to environment improvement, although it does not contribute to identify the main relationships of the true causes of GxE interaction (Duarte and Vencovsky 1999). Over the last years, the use of multivariate methods or such that integrate uni and multivariate methods, such as AMMI analysis, have attracted interest. AMMI is a linear (additive effects) and bi-linear model (multiplicative effects) that integrates the variance analysis of the main effects, i.e. genotypes and environments, with the principal component analysis for the multiplicative effects of the GxE interaction (Gauch and Zobel 1996).

AMMI analysis can contribute to the identification of the most stable and productive genotypes, to the recommendation of region-specific cultivars, provide more precise estimates of genotypic responses, and an easy interpretation of the results in biplot graphs (Zobel et al. 1988).

The objective of this study was to evaluate the phenotypic adaptability and stability of eighteen lines and two peanut cultivars in relation to pod yield by AMMI analysis.

MATERIAL AND METHODS

To combine the favorable characteristics of two runner types - Runner IAC 886 and L65/3-1 - such as pod yield, disease resistance and improved grain size for export, the regionally adapted genotypes L65/3-1 x Runner IAC 886 and L65/3-1 x Regional Runner were crossed. Line L65/3-1 is a component of cultivar IAC Caiapo, with moderate to high foliar disease resistance. A regional runner accession was provided by a grower in the peanut region of the state of São Paulo. Advanced lines from these crosses with good yield potential, resistance to rust and late leaf spot, and good pod and kernel standards were selected.

The pod yields (in kg ha⁻¹) of the lines L113, L118, L121, L122, L123, L125, L127, L132, L137, L141, L144, L146, L147, L149, L1-38P, L1-48P, L1-4P, and L1-50P and of the IAC Caiapo and Runner IAC 886 cultivars were assessed. Ten field trials were carried out at the experimental stations Agência Paulista de Tecnologia

dos Agronegócios (APTA) - Departamento de Descentralização do Desenvolvimento (DDD), in Ribeirão Preto and Pindorama in the growing seasons of 2002/03, 2003/04 and 2004/05 (RP02, RP03, RP04, respectively), Adamantina 2003/04 (AD03), Campinas 2004/05 (CA04), and Votuporanga 2003/04 and 2004/05 (VT03 and VT04, respectively).

The field trials were carried out in a randomized block design with four replications. The design was not fully balanced due to the loss of some observations. Each plot consisted of five rows of five meter length, two of which were border lines.

The spacing between the lines was 0.9 m and the sowing density 10 plants per meter. The soil was calcareous and all experiments were fertilized with 250 kg ha⁻¹ of the compound fertilizer NPK in the proportion 4-14-8. Phytosanitary treatments were carried out according to crop recommendations and the plants harvested 125 to 140 days after sowing.

Analysis of variance was performed for each environment to detect differences between the lines/cultivars. Then the homogeneity between residual variances was verified. Analysis of joint variance, along with tests of effects of the genotype (G), environment (E) and magnitude of the GxE interaction were conducted. AMMI analysis was used to adjust the main or additive effects of genotype and environment through the analysis of variance, including the adjustment of the multiplicative effects for the GxE interaction through the principal component analysis.

The AMMI model equation is:

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^N \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij} + \varepsilon_{ij}$$

where Y_{ij} is the pod yield of the i^{th} genotype in the j^{th} environment; μ is the overall mean; g_i and e_j are fixed effects of the genotypes and environment deviations from the overall mean, respectively; λ_k is the singular value of the PCA axis k ($k=1,2, \dots, N, \dots, p=\text{rank of GxE matrix, obtained until } N < p$); γ_k and δ_{ik} are, respectively, the genotypic and environmental elements of singular vectors associated to λ_k and δ_k , respectively; N is the number of principal components retained in the model; ρ_{ij} is the residual GxE interaction, and ε_{ij} is the pooled error, assumed independent and $\varepsilon_{ij} \sim N(0, \sigma^2)$.

The definition of the number of principal axes retained in the analysis was based on the F test of

Cornelius et al. (1992). A program developed by Duarte and Vencovsky (1999) of SAS (SAS Institute Inc 1997) software was used for all analyses.

The contribution of each genotype and environment to the GxE interaction is presented in a biplot graph where the scores of the principal component analysis were plotted.

RESULTS AND DISCUSSION

The analysis of joint variance presented a significant effect ($P < 0.01$) of the environment and GxE interaction, as well as of genotypes ($P < 0.05$), thus confirming the differential performance of lines/cultivars and the high environmental effect (Table 1). Considering the sum of squares for treatment, about 58.8, 6.7 and 34.5% of the sum of the squares was explained by the environment, genotypes and GxE interaction effects, respectively. Most of the existing variation (93.3%) is explained by environmental and interaction effects, which makes the breeder's work with selection more difficult.

According to AMMI analysis, the GxE interaction was divided into nine components, in which the model was only adjusted to the first component (IPCA1), due to its significance. Although the residue of AMMI1 analysis was significant at 5% probability, indicating the possibility of an adjustment to AMMI2, this model was not chosen. The reason is that the level of 5% increases the probability of error type I, i.e., the risk of accepting an AMMI model with more parameters, which does not occur at 1% probability.

AMMI analysis is used for partitioning the sum of squares interaction into two portions, known as pattern and noise. The noise portion suggests unpredictable and non-interpretable responses, while the pattern portion is obtained after discarding the noise, additional to the experimental errors, which allows a more in-depth study of the GxE interaction and the prediction ability of phenotypic responses of the genotypes under study, once they responded to certain environments in a systematic, significant and interpretable way. According to Oliveira et al. (2003a), one of the premises of AMMI analysis is that most of the pattern portion is concentrated on the first axis, increasing the number of axes and the risk of the noise portion.

Table 1. Joint variance analysis for peanut pod yield (in kg ha⁻¹) of 10 peanut trials, including the participation of GxE interaction according to AMMI analysis

Sources of variation	df	SS	MS	F	P>F
Total	742	268318593	361615		
Treatments	199	168528089	846875	2.49	0.0025
Environment (E)	9	99187526	11020836	32.46	0.0001
Genotypes (G)	19	11274224	593380	1.75	0.0328
GxE	171	58066338	339569	1.85	0.0001
IPCA1	27	24567756	909917	4.95	0.0000
Residual AMMI1	144	33498582	232629	1.27	0.0327
IPCA2	25	9553982	382159	2.08	0.0018
Residual AMMI2	119	23944599	201215	1.09	0.2516
Error	543	99790504	183776		

IPCA1 explained 42.3% of the sum of squares of the interaction and IPCA2 16.4%. Smaller values of around 23% (Sneller and Dombeck 1995), 36% (Oliveira et al. 2003a), and 26% (Rocha et al. 2004) were stated for soybean. Ariyo (1998) however found 86% of the sum of squares in the interaction explained by IPCA1 in soybean. For corn, a similar 29.8% value was observed by Oliveira et al. (2003b). A greater pattern portion was concentrated on the first AMMI axes; as the number of axes increased, the pattern portion decreased and the noise portion increased. Thus, even if only one axis (IPCA1) is selected to explain a small portion of the original sum of squares (GxE), the expectation is to capture the greatest part of the pattern portion, since the rest of SQ_{GxE} contains little relevant information (noise portion).

Figure 1 shows an AMMI biplot graphic, in which the values related to the means of the lines/cultivars and the environments (abscissa) are plotted, representing the additive effects as a function of the IPCA1 scores. These scores represent the multiplicative effects of the GxE interaction on the ordinate axis. Genotypes represented by scores close to zero show the pod yield stability as a function of the tested environments, whereas the combinations of genotypes and environments with IPCA scores of the same signal present positive specific interaction and combinations with opposite signals have negative interactions (Oliveira et al. 2003a, Rocha et al. 2004).

According to the AMMI1 biplot graphic (Figure 1), apart from L123, L118, L127 and Runner IAC 886, the

peanut lines/cultivars performed similarly in the test environments. This confirms the instability of these genotypes in the test environments, demonstrated in the GxE interaction analysis for each combination of genotype and environment (Table 2).

The most stable genotypes with the lowest IPCA1 scores were L144, L1-38P, L149, L147, L146, L1-48P, L132, and L1-50P (Table 2). Among these, lines L144 and L146 presented the lowest pod yield (around 4900 kg ha⁻¹). In spite of the low yield, L144 line presented an important differential for the export market, i.e., a weight of 71 grams for 100 grains; it can be recommended as a line with high yield stability and larger grain size. The pod yield stability in the lines L122, L113, L121, L1-4P, L125, L137, L141 and the IAC Caiapo cultivar was average owing to the magnitude of the GxE interaction (Table 2). Pod yield stability ranged from medium to high in sixteen of twenty lines/cultivars. This high proportion is probably due to the fact that the parents of these crosses have a high concentration of genes responsible for pod yield and disease resistance, which can influence the genotype stability in relation to environmental adversities.

Since there are also other criteria in the appraisal of the cultivars, stability must be associated to genotypes with good pod yield. Therefore, other lines with good pod yield and stability would be L132 and L149, with pod yields above the overall mean (5500 kg ha⁻¹), as well as L1-50P with approximately 5670 kg ha⁻¹, with a great potential. Lines L137 and L1-4P attained top yields (of over 5700 kg ha⁻¹) and average stability.

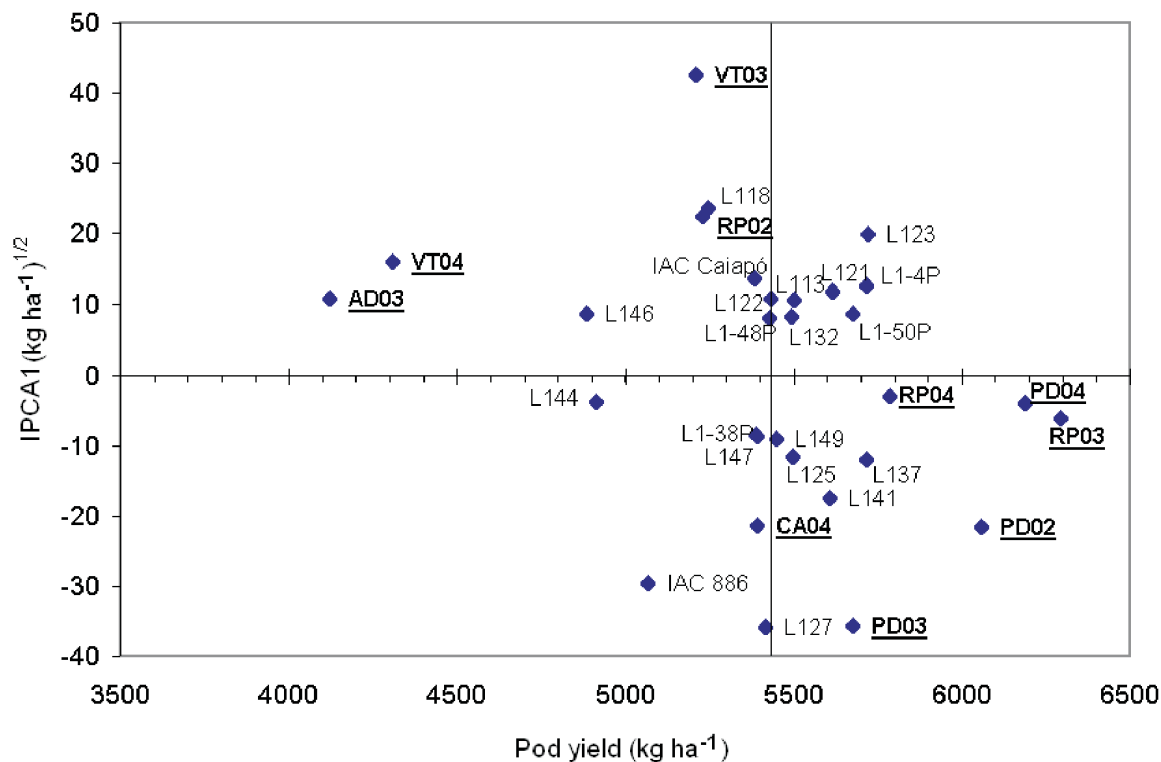


Figure 1. AMMI1 biplot graphic for pod yield data in kg ha^{-1} of 18 lines and two peanut cultivars (IAC Caiapo and Runner IAC 886) assessed in 10 experiments in the state of São Paulo (VT03 and VT04=Votuporanga 2003/04 and 2004/05, respectively; AD03=Adamantina 2003/04; RP02, RP03 and RP04=Ribeirão Preto 2002/03, 2003/04 and 2004/05, respectively; CA04=Campinas 2004/05; PD02, PD03 and PD04=Pindorama 2002/03, 2003/04 and 2004/05, respectively). The vertical line in the center represents the overall trial mean (5426 kg ha^{-1})

Of the control cultivars, the stability of IAC Caiapo was average and the pod yield slightly below the general mean, whereas the stability and pod yield of Runner IAC 886 were both low. This can be explained by the better performance of IAC Caiapo cultivar in unfavorable environments, mainly due to disease infestation (Godoy et al. 1999). Runner IAC 886 cultivar has a high pod yield potential, but is very susceptible to foliar diseases, which requires a better phytosanitary control and consequently boosts production costs.

IAC Caiapo and Runner IAC 886 were initially used as parents in the crosses to develop the lines. Since most yield components are controlled by a large number of genes, it is possible to affirm that there was a combination of desirable traits in both parents to form superior genotypes in the crosses since high-yielding lines (exceeding their parents) were found with moderate disease resistance (data not shown) and good pod yield stability.

The environmental effects were more variable than the line performances, indicating strong GxE interaction (Figure 1). In addition, the difference of the environments regarding the contribution to the GxE interaction was high. The environments PD03 and VT03 had the highest IPCA1 values and most unstable pod yields. On the other hand, IPCA1 values in PD04, RP03 and RP04 were lower than at the other locations, indicating a greater stability, as expressed by the lower variation in the GxE scores. These environments were also more favorable to genotype yield performance (Figure 1). Thus, the latter environments would be suitable selection sites for breeding tests when targeting a wide range of environments.

Although the environments in Votuporanga (VT03 and VT04) produced the same result for IPCA1 they were very different in relation to pod yield. The environments in Pindorama (PD02, PD03 and PD04) also presented the same sign of IPCA1, although with better

Table 2. Matrix of the GxE interaction for each genotype and environment combination based on AMMI analysis

Genotypes	Environments									
	RP02	RP03	RP04	PD02	PD03	PD04	AD03	VT03	VT04	CA04
L113	403.1	699.3	-810.3	33.4	570.7	-306.7	3.7	-577.0	-84.2	68.0
L118	765.2	-326.1	-814.1	-220.4	883.0	49.7	-771.9	-191.6	-76.0	702.2
L121	253.9	466.8	-715.2	-93.5	715.6	-117.6	201.4	-263.7	-938.3	490.6
L122	1048.4	-853.2	1.8	218.4	-154.9	177.4	-805.4	294.2	6.1	67.1
L123	66.0	-437.0	-880.6	279.2	949.8	-599.5	38.5	-210.7	222.5	571.8
L125	-31.4	51.1	406.6	34.9	-632.3	-161.3	723.7	-278.7	-10.9	-101.8
L127	-865.2	1098.7	1154.5	-643.7	-1693.9	586.6	281.1	31.62	95.8	-245.6
L132	1001.4	-522.9	46.1	40.7	416.7	5.5	33.2	-120.7	-290.7	-609.4
L137	-38.8	18.8	118.9	-486.1	-842.6	-32.8	704.2	58.8	324.0	175.6
L141	334.5	172.8	150.7	245.2	-1548.8	-150.7	723.8	792.5	-372.1	-347.8
L144	390.6	334.4	184.6	157.1	-188.3	-549.8	69.03	3.2	104.6	-535.5
L146	-230.3	-392.0	-647.0	248.5	-54.6	366.9	-864.2	711.0	564.4	297.1
L147	-564.0	217.8	-188.8	1.7	-299.3	155.3	1054.0	-354.8	-118.9	97.1
L149	-312.5	372.2	647.0	397.5	-319.4	-9.4	-821.0	823.1	-58.9	-718.7
L1-38P	-476.8	-783.5	1023.4	-275.2	-387.5	-116.0	325.0	241.9	-401.3	849.9
L1-48P	-379.0	-243.6	-442.2	201.9	278.2	-293.8	-485.6	405.4	650.1	308.5
L1-4P	-517.3	-630.4	-541.9	-197.6	1243.6	438.5	281.8	-180.3	167.2	-63.5
L1-50P	-276.8	-1007.5	890.5	668.7	795.1	145.1	-769.0	-71.2	-464.8	89.9
IAC Caiapo	597.1	632.4	-910.3	89.0	542.5	53.8	-478.0	-595.7	132.0	-62.7
IAC 886	-1168.1	1131.7	1326.1	-699.7	-273.6	358.7	555.5	-547.2	349.3	-1032.8

responses in pod yield in VT03 and VT04. The signs for IPCA1 in the environments in Ribeirão Preto (RP02, RP03 and RP04) were different, as expected in view of the GxE interaction in these environments.

The environment of Adamantina 2003/04, where the pod yield was low (4120 kg ha⁻¹), seemed unfavorable for the study genotypes. Highest yield means were achieved in Ribeirão Preto 2003/04, 2004/05, Pindorama 2002/03, 2003/04 and 2004/05, of 6290, 5785, 6059, 5670 and 6188 kg ha⁻¹, respectively.

According to Oliveira et al. (2003a) the environmental stability expresses the reliability in the genotype classification in a particular environment in relation to the classification of the environment means. Therefore, according to the data presented, the genotypes of Pindorama are more recommendable for selection and recommendation purposes.

Several studies on peanut pod yield adaptability and stability have been conducted. Godoy et al. (1999)

assessed yield performance, pod yield stability and adaptability of three peanut cultivars in several typical crop environments as well as the severity of foliar diseases in the state of São Paulo. The pod yield of IAC Caiapo exceeded Tatu and the yield development was more stable (predictable) than in the cultivars Florunner and Tatu at the three disease control levels. Távora et al. (1988) observed a weaker performance of cultivar Tatu in terms of pod yield and pod yield stability, while cultivar 55437 was more stable and had a good pod yield potential. Great adaptability was observed for most test cultivars, including Tatu, and good pod yield stability of BR1 and IAC Tupã, according to Santos et al. (1999).

All these studies used methods based on linear regression analysis, which has a few drawbacks: i) lack of information in cases of non-linearity, ii) great dependency on the group of genotypes and environments tested and iii) tendency to overestimate

different response patterns since the variation of GxE interaction is explained by the regression coefficient only.

The AMMI analysis showed that it is possible to

obtain a less contaminated GxE interaction matrix by unpredictable factors (noise), which provides better estimates of genotypic responses as a function of the environments.

Análise da estabilidade produtiva de linhagens de amendoim rasteiro utilizando o método AMMI

RESUMO - A interação de genótipos com o ambiente (GxA) pode influenciar no processo de seleção e recomendação de cultivares de amendoim. Assim, o objetivo desse trabalho foi avaliar a influência da interação GxA na produtividade de vagens de amendoim, utilizando o método AMMI. Foi avaliado o comportamento de 18 linhagens e duas cultivares (IAC Caipó e Runner IAC 886), em 10 ensaios realizados no Estado de São Paulo. Foi detectado efeito significativo para genótipos, ambientes e interação GxA, na análise conjunta. O primeiro componente principal (IPCA1) explicou 42,3% da soma de quadrados da interação GxA. Dezesesseis linhagens/cultivares avaliadas apresentaram estabilidade média a alta. Os genótipos L127, L118, L123 e a cultivar Runner IAC 886 foram as que mais contribuíram para interação GxA. Além disso, as linhagens L132, L149 e a L1-50P possuem ampla estabilidade e produtividade acima da média geral, apresentando grande potencial para fins de recomendação.

Palavras-chave: *Arachis hypogaea* L., adaptabilidade, estabilidade, AMMI, produtividade.

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