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Consistency of two stability analysis methods in potatoes

Consistência de dois métodos de análise de estabilidade em batata

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ABSTRACT

The objective of this research was to compare the consistency of the bi-segmented and AMMI (additive main effects and multiplicative interaction analysis) methods for estimating yield stability in potatoes. Data of ten genotypes evaluated in 34 environments (local, growing season and year combinations) of the Rio Grande do Sul state, Brazil, in 1994 and 1995 were used. Three data sets were analyzed: 34-environment data set and two 17-environment data subsets, which were chosen by randomly dividing the total data set. For the 34-environment data set, the models gave similar results in relation to the stable genotypes, but they differed with regard to the unstable genotypes. For the 17-environment data sets, the bi-segmented model showed more consistent results, either between subsets or between these and the total data set. For the AMMI model, only the Santo Amor genotype showed consistency between one of the subsets and the total data set. In this work, the bi-segmented method was shown to be more consistent than the AMMI model.

Key words: ***Solanum tuberosum,*** *G x E interaction, AMMI model, bi-segmented method.*

RESUMO

O objetivo deste trabalho foi comparar a consistência dos métodos bi-segmentado e AMMI (additive main effects and multiplicative interaction analysis) em análise de estabilidade de ensaios de rendimento de batata. Foram utilizados dados de dez genótipos avaliados em 34 ambientes (combinações de local, período de cultivo e ano) do Rio Grande do Sul, Brasil, em 1994 e 1995. Três conjuntos de dados foram analisados: o conjunto de dados dos 34 ambientes e dois sub-conjuntos de dados de 17 ambientes, que foram escolhidos pela divisão aleatória do conjunto total de dados. Para o conjunto de dados dos 34 ambientes, os modelos deram resultados semelhantes quanto aos genótipos estáveis, mas divergiram quanto aos instáveis. Para os subconjuntos de dados de 17 ambientes, o modelo bi-segmentado revelou resultados mais consistentes, tanto entre os subconjuntos quanto entre estes e o conjunto total. Para o modelo AMMI, apenas o genótipo Santo Amor mostrou consistência entre um dos subconjuntos e o conjunto total. Neste trabalho, o método bi-segmentado mostrou-se mais consistente do que o modelo AMMI.

Palavras-chave: ***Solanum tuberosum***, *interação G x E, modelo AMMI, método bi-segmentado.*

INTRODUCTION

The genotype x environment interaction (G x E) is very important for plant breeding, mainly concerning the development of improved and superior genotypes (ALLARD & BRADSHAW, 1964; EBERHART & RUSSEL, 1966). The differential response of genotypes to environments makes it difficult to select high yielding and stable genotypes (COOPER & DELACY, 1994), restricting the recommendation of cultivars to specific regions and locals, where they express their superior genetic potential (KANG & MAGARI, 1996). In order to minimize these problems, the breeder conducts his trials in as many locations as possible, aiming to evaluate and measure the interaction effect (FARIAS et al., 1996).

To study the G x E interaction and to associate it to genotype stability, several models have been proposed. Among the models recently presented, two stand out. The bi-segmented model, proposed by

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SILVA & BARRETO (1985) and modified by CRUZ et al. (1989), and the AMMI model (additive main effects and multiplicative interaction analysis), proposed by ZOBEL et al. (1988) and modified by GAUCH (1993). For the bi-segmented method, the stability is represented by the variance component due to the deviations of regression (σ^2_{di}). The slope of straight lines B_{1i} and B_{1i} + B_{2i} represents the adaptability of genotypes to the more or less favorable environments, respectively. As a bi-segmented regression, the model represents better the performance of genotypes in several environments (CRUZ et al., 1989).

The AMMI model has been used for modeling and better understanding G x E interaction (GAUCH, 1988; ZOBEL et al., 1988; GAUCH & ZOBEL, 1996). For GAUCH & FURNAS (1991). The best estimator to represent the genotype stability is the first main component (PCA 1). In a previous study, using the same data, PEREIRA & COSTA (1998) compared the AMMI analysis to the regression analysis, concluding that the AMMI model is more efficient in describing the G x E interaction, on the basis of sum of squares of the interaction.

The aim of this study was to compare the consistency of the bi-segmented and AMMI (additive main effects and multiplicative interaction analysis) methods for estimating yield stability in potatoes, using data of ten potato genotypes tested in 34 environment of the Rio Grande do Sul state.

$T(X_j)$

MATERIAL AND METHODS

Total tuber yield data of ten potato (***Solanum tuberosum***) genotypes tested in 34 environments (local, growing season and year combinations) of production areas of Rio Grande do Sul state, in 1994 and 1995 was evaluated. The following genotypes were tested: Atlantic, Baronesa, Cristal, Macaca, Monte Bonito, Santo Amor, Trapeira, 2AC-917-7-80, C-1226-35-80 and CR-1290-5-82. Atlantic was introduced in Brazil from the United States of America and the other genotypes were developed by the breeding program of Embrapa Clima Temperado. The experimental design was a randomized complete block with four replications and plots consisting of two 25-plant rows, spaced in 0.30m between plants and 0.80m between rows. The cultural practices were the ones used in each region.

The data was submitted to variance analysis (ANOVA). The G x E interaction effects were estimated using the two models: the bi-segmented regression and the additive main effects and multiplicative interaction analysis (AMMI). The first one is a bi-segmented regression in such a way that each genotype is characterized by two regression lines, one representing unfavorable environments (B_{1i}) and the other favorable environments (B_{1i} + B_{2i}) (CRUZ et al., 1989). In the AMMI model (ZOBEL et al., 1988), the additive part of the model is estimated by ANOVA and the multiplicative part is estimated by the principal component analysis.

The bi-segmented model is described by CRUZ et al. (1989), as:

$Y_{ij} = B_{0i} + B_{1i} X_j + B_{2i} T(X_j) + \delta_{ij} + e_{ij}$ where: σ^2_{di} is the observed mean yield of the i-th genotype in the j-th environment; B_{0i} is the intercept of the regression equation; B_{1i} is the linear regression coefficient associated with the variable X_j; B_{2i} is the linear regression coefficient associated with the variable ;δ_{ij} is the deviation of regression; e_{ij} is the error associated with Y_{ij}; X_j is the environment index defined as

$$X_j = \frac{Y._j}{m} - \frac{Y..}{mn}, \text{ where } \sum X_j = 0 \text{ ; } T(X_j) = 0$$

if $X_j \leq 0$; $T(X_j) = X_j - X_p$ if $X_j > 0$, where X_P is the favorable environment mean.

The AMMI model is described by GAUCH (1993) as:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum {}_n \lambda_n \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

where: Y_{ger} is the yield of genotype *g* in the environment *e* for *r* replications; μ is the overall mean; α_g is the deviation of the mean of the genotype *g*; β_e is the deviation of the mean of the environment *e*; λ_n is the eigenvalue of the principal component axis, *n*; Y_{gn} is the eigenvalue of the genotype *g* for the axis of principal components *n*; δ_{en} is the eigenvalue of the environment *e* for the axis of the principal components *n*; is the residue of the interaction; is the error associated to Y_{ger}.

The ANOVA was used to verify the significance of the interaction G x E, whereas the models were applied to estimate the interaction. The effects of genotypes were considered fix and the effects of environment random.

For the bi-segmented analysis, GENES 2001.0 software (CRUZ, 2001) was applied, and for the AMMI analysis, the MATMODEL, version 2.0 (GAUCH, 1993) was used.

The analysis of the G x E interaction was performed on the 34-environment data set to estimate the stability of genotypes by the two models. The data of the two 17-environment data subsets were taken by randomly dividing the 34-environment data set. The three data sets (total and two subsets) were analyzed to compare the consistency of the two models.

RESULTS

The analysis of variance (ANOVA) of the 34-environment data set showed significance ($P \leq 0,05$) for genotypes, environments and G x E interaction (Table 1). Also, the ANOVA of the two 17-environment data subsets revealed significance for all factors of variation, including the G x E interaction (Table 2).

For both models, bi-segmented (σ^2_{di}) and AMMI (PCA 1), Santo Amor and Trapeira showed to be the most stable genotypes for the 34-environment data set (Table 3). Monte Bonito and CR-1290-5-82 were the most unstable genotypes for the bi-segmented model, whereas Macaca and Cristal were the most unstable ones for the AMMI model, as previously reported (PEREIRA & COSTA, 1998).

The results of the stability analysis of the two 17-environment data subsets showed differences between the two models (Table 3). For the bi-segmented model, the two data subsets had similar results. Santo Amor and Trapeira were the most stable genotypes, except that they were inversely classified in the subsets. CR-1290-5-82, Monte Bonito and Macaca were the most unstable genotypes in both data subsets.

Correlation coefficients of stability values for the 34-environment data set, estimated by the AMMI model, with stability values for the 17-environment data subsets 1 and 2, calculated by the bi-segmented model, were high (r = 0.77 and 0.73, respectively) (Table 4). Within the AMMI model estimates, correlations between the estimates for 34-environment data set and for the two 17-environment data subsets, and between estimates for the two data subsets were very low and not significant. The correlation coefficient between the two models for the 34-environment data set was high and significant (r = 0.79). The bi-segmented model estimates for the 34-environment data set was very highly correlated with the estimates for the data subsets 1 and 2 (r = 0.99 and 0.97, respectively).

DISCUSSION

High and stable yield is one of the main objectives of potato breeding programs, besides good quality and resistance to the main diseases. Differential responses of genotypes to variation in environments make selection difficult (PEREIRA & COSTA, 1998). Many studies have been reported on methods to estimate the stability of genotypes and environments (FINLAY & WILKINSON, 1963; EBERHART & RUSSEL, 1966; TAI, 1971; GAUCH & ZOBEL, 1989; GAUCH & FURNAS, 1991; SILVA, 1995a/b), but the interest continues into looking for models that reliably and precisely estimate stability parameters.

In this work, the analysis of bi-segmented and AMMI models resulted in different stability estimates (Table 3). The parameters estimated for the 34-environment data set by the bi-segmented and the AMMI models were high and positively correlated (Table 4.). Santo Amor and Trapeira, were the most stable genotypes, regardless of the models used. Since the correlation was not perfect, the ranking of genotypes differed, explaining the difference in relation to the most stable genotypes.

Considering the results of the analysis of the two 17-environment subsets, the bi-segmented model showed more consistency than the AMMI model in classifying the genotypes for stability. In the bi-segmented model, correlation coefficients between the stability estimates of the total data set and the two data subsets were close to 1, showing consistency of the results.

Regression deviations were low for the total data set as well as for the two data subsets. High regression deviations can be considered as an indication of inadequacy of the linear model postulated to represent the relation between yield and the environment index (SILVA, 1995b). Therefore, regression can be used, but with caution for evaluation

Table 1 – Mean squares for the analysis of variance of total tuber yield data (t ha^{-1}) of ten potato genotypes in 34-environments (local, growing season and year combinations) of the Rio Grande do Sul state.

Sources of variation	Degree of freedom	Sum of squares	Mean square	F	P ≤ F
Blocks/environment	102	3,719.243	36.463		
Genotypes (G)	9	10,018.095	1,113.122	103.220	< 0.001
Environments (E)	33	129,020.891	3,909.724	107.224	< 0.001
G x E	297	22,688.833	76.393	7.084	< 0.001
Error	918	9,899.718	10.784		
Total	1.359	175,346.779			
General mean	22.35				
CV(%)	14.69				

Table 2 – Mean squares for the analysis of variance of total tuber yield (t ha^{-1}) of ten potato genotypes for two subsets of 17-environments randomly chosen from the set of 34-environments (local, growing season and year combinations) of the Rio Grande do Sul state.

Sources of variation	Degree of freedom	Subset 1		Subset 2	
		Mean square	P ≤ F	Mean square	P ≤ F
Blocks/environment	51	18.630		54.296	
Genotypes (G)	9	799.607	< 0.001	390.126	< 0.001
Environments (E)	16	5,193.506	< 0.001	2,287.384	< 0.001
G x E	144	83.054	< 0.001	69.720	< 0.001
Error	459	9.918		11.650	
General mean		24.97		19.73	
CV(%)		12.61		17.30	

of the phenotypic stability, since the bi-segmented linear regression analysis can fail as any statistical modeling technique, but it constitutes an additional tool that breeders can use for selection (SILVA, 1995b).

In the AMMI analysis, there was some inconsistency of stability of the genotypes in the two data subsets. In the data subset 1, Atlantic and 2AC-917-7-80 were the most stable genotypes and Santo Amor and CR-1290-5-82 were the most unstable. On the other hand, in the data subset 2, 2AC-917-7-80 and Santo Amor showed to be the most stable genotypes, and Trapeira and Baronesa the most unstable. Compared to the 34-environment data set, the most stable and the unstable genotypes for the data subset 1 did not match. In fact, there was a change in the classification of Santo Amor from stable to unstable. In the data subset 2, only Santo Amor was stable, coinciding with the estimation of the total environment data set.

Correlation coefficients between estimations of the models and data set combinations indicate consistency of two stability methods (Tables 4). Therefore, the AMMI model gave less consistent estimates than the bi-segmented analysis. It may be a result of the low representation of the sum of squares of the principal components, which should be grouped, in a higher number of components to truly represent the stability of the genotypes. The percentage of sum of square for treatments must be explained by 80-95% of the sum of squares of the first principal component – genotype, environment and interaction (GAUCH &

Table 3 - Stability parameters for total yield of ten potato genotypes estimated by the bi-segmented model (σ^2_{di}), and by the AMMI model (PCA 1), for the 34-environment (local, growing season and year combinations) data set and for two randomly chosen 17-environment data subsets.

Genotype	σ^2_{di}			PCA 1		
	Set	Subset 1	Subset 2	Set	Subset 1	Subset 2
Santo Amor	0.594	0.288	1.490	5.328	-220.137	12.692
Trapeira	1.359	1.549	0.964	-13.682	70.900	-147.792
Baronesa	2.299*	3.100*	2.069*	-34.592	75.375	119.521
2^AC-917-7-80	2.813*	3.623*	2.442*	32.340	-2.048	8.017
Cristal	3.437*	3.698*	2.028*	-119.710	55.362	70.204
C-1226-35-80	4.701*	5.701*	3.705*	30.616	75.125	-24.368
Atlantic	7.269*	7.351*	8.795*	63.661	1.673	-17.983
Macaca	9.163*	7.828*	9.572*	-120.392	-71.898	-94.866
Monte Bonito	10.377*	9.692*	9.089*	104.638	82.247	18.325
CR-1290-5-82	11.627*	10.118*	13.612*	51.738	83.651	56.250
Percentage of the sum of squares of the G x E interaction				44.60	60.0	43.58

*Values different from zero by the t test at 5% significance.

Table 4 - Simple correlation coefficients between stability values estimated by the bi-segmented model (σ^2_{di}), and by the AMMI model (PCA 1), for the 34-environment (local, growing season and year combinations) data set and for two randomly chosen 17-environment data subsets of total tuber yield of ten potato genotypes, in the Rio Grande do Sul state.

Model – Data	AMMI Set	Bi-seg. Subset 1	Bi-seg. Subset 2	AMMI Subset 1	AMMI Subset 2
Bi-Seg. – Set	0.79^{*}	0.99^{**}	0.97^{**}	-0.29^{ns}	-0.20^{ns}
AMMI - Set		0.77^{*}	0.73^{*}	-0.15^{ns}	0.03^{ns}
Bi-Seg. - Subset 1			0.93^{**}	-0.37^{ns}	-0.23^{ns}
Bi-seg. – Subset 2				-0.17^{ns}	-0.24^{ns}
AMMI – Subset 1					-0.04^{ns}
AMMI - Subset 2					

* and ** significant at 0.05 and 0.01 probability levels by test t, respectively.

^{ns} Not significant (P>0.05).

FURNAS, 1991), since 90% of the treatment sum of squares captures almost all real information of the data. According to these authors, the AMMI model is highly informative when both, the principal effects and the interaction, are significant, which is commonly observed in field experiments.

In the previous study (PEREIRA & COSTA, 1998), although the AMMI analysis had been more efficient in describing the G x E interaction than the linear regression technique, the percentage of sum of squares explained by the first principal component was only 44,6%. Therefore, it might explain the lower consistency of the AMMI model than the bi-segmented method in estimating stability parameters.

Although both methods have identified Santo Amor and Trapeira, as the most stable genotypes, the bi-segmented method was shown to be more consistent than the AMMI model in estimating yield stability of potatoes.

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