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COMPARISON OF THREE METHODS USED FOR THE STUDY OF ADAPTATION AND PHENOTYPIC STABILITY IN THE COMMON BEAN (*Phaseolus vulgaris* L.)

João Batista Duarte[1] and Maria José de Oliveira Zimmermann[2]

ABSTRACT

The objective of the present work was to compare the acuity of three different methods of studying phenotypic stability for determining the variability in average yield data of the common bean. Data from twelve preliminary yield trials of 76 common bean genotypes grown in eight Brazilian locations were used. Two classical procedures based on linear regression analysis and the recent proposition of bisegmented linear regression were studied. Based on the proportion of estimates of coefficients of determination that were statistically significant or non significant for the genotypes studied, as well as on the magnitude of such estimates, it was concluded that the segmented linear regression procedure was slightly superior to the methods based on linear regression analysis. The two methods of linear regression showed similar results. The advantage of the bisegmented linear regression method was more evident when the behaviour of the genotypes in response to the environmental variation did not follow linearity.

INTRODUCTION

Since Allard and Bradshaw (1964) demonstrated the implications of genotype to environment interaction and their significance when making cultivar recommendations, various methods have been proposed for the identification of cultivars that show little interaction with the environment wherein they are grown (phenotypically stable

1 Departamento de Agricultura, Escola de Agronomia, Universidade Federal de Goiás, Caixa Postal 131, 74001 Goiânia, GO, Brasil. Send correspondence to J.B.D.

2 Centro Nacional de Pesquisa de Arroz e Feijão, EMBRAPA, Caixa Postal 179, 74001 Goiânia, GO, Brasil.

cultivars). Genotypes, with such stability, guarantee a good yield with decreased risk of losing production and allow reseachers to make general recommendations for a range of environments.

Among the many different procedures used for the identification of stable genotypes (Roemer, 1917; Plaisted and Peterson, 1959; Plaisted, 1960; Finlay and Wilkinson, 1963; Wricke, 1965; Eberhart and Russell, 1966; St-Pierre *et al.*, 1967; Perkins and Jinks, 1968; Verma *et al.*, 1978; Langer *et al.*, 1979; Silva and Barreto, 1985), those that evaluate yield stability through regression analysis have been preferred. These procedures allow the individual behaviour of the genotypes under a variety of environmental conditions to be known. The methods proposed by Finlay and Wilkinson (1963) and by Eberhart and Russell (1966) are considered the classical procedures. Both use a linear regression analysis of the average yield of each cultivar in each environment on an environmental index, which is determined from the average yields of all cultivars in each environment or by the average effect of the environments over the means of the cultivars, respectively.

According to Verma *et al.* (1978), such methods fail when the response of the genotype to environmental variations significantly deviates from linearity. They point out that relatively high yielding genotypes, that show low responses in poor environments but are capable of good responses under improved environmental conditions (theoretically ideal genotypes), can be eliminated because they show large deviations from linearity. Based on this observation, they proposed a procedure using segmented linear regression, which allows determination through two linear regression coefficients, which represent the responses of each cultivar to the poor and the favorable environments separately. Silva and Barreto (1985) modified the statistical methodology for the estimation of such coefficients, increasing the representativity of the estimated interaction response "curve".

The present research compares the methods of Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Silva and Barreto (1985) for their ability to explain the variation of average grain yields of some experimental lines and cultivars of common bean (*Phaseolus vulgaris* L.). The need for such a study was based on the fact that most of the research done on the phenotypic stability of the common bean has been performed using the two classical procedures, which are, at least theoretically, less informative than the segmented linear regression procedure (Verma *et al.*, 1978).

MATERIALS AND METHODS

Grain yield data (kg/ha) were taken from the preliminary yield trials of "mulatinho" bean type (EPRM's). The trials were coordinated and organized by the Nacional

Research Center for Rice and Beans (CNPAF), EMBRAPA. Experiments were selected from the agricultural years 1984/85 and 1985/86, from eight Brazilian locations, in a total of twelve different environments (Table I).

Table I - Locations where the selected trials were grown, institutions and number of experiments performed per year.

Location/State	Institution	Number of experiments	
		1984/85	1985/86
Goiânia/GO	CNPAF	2	1
Vilhena/RO	UEPAE	-	1
Rio Branco/AC	UEPAE	1	1
Lavras/MG	ESAL	1	-
Irecê/BA	EPABA	2	-
Nova Soure/BA	EPABA	1	-
Ipirá/BA	EPABA	1	-
Aracaju/SE	CNPCO	1	-

Experiments from Goiânia (GO) and Irecê (BA) in the agricultural year 1984/85 were done at two soil fertility levels. Treatments were the 76 common bean genotypes (experimental lines and cultivars) from the "mulatinho" commercial grain type. The cultivar Carioca was also included as a standard for yield stability. The selection of experiments to be included in the present study was based on the heterogeneity of the residual variances which were obtained from the analyses of variances that were performed for each location and year, separately. Only experiments differing less than four times between the largest and the smallest residual mean squares were included (Steel and Torrie, 1980).

Average grain yields of each individual treatment in each environment were submitted to joint variance analysis, considering years and locations as different environments (macroenvironments). The study of the significant interaction of genotypes with environments made possible the discrimination of phenotypically stable or unstable genotypes. The evaluation was made using the methods of Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Silva and Barreto (1985).

Finlay and Wilkinson (1963) Method

Average yield data (Y_{ij}, where i = 1, 2, ..., n treatments and j = 1, 2, ..., m environments) were transformed according to a logarithmic scale as was required by the procedure, such as $Y'_{ij} = \log Y_{ij}$.

A linear regression equation was calculated for each genotype, taking as the independent variable the environmental index (X'_j) given by $X'_j = Y'_{ij}/n$ and as the dependent variable the log transformed average yield of each genotype in each environment (Y'_{ij}).

The ability of the procedure to explain data variation for each genotype was evaluated by the coefficient of determination r'^2_i: ($r'^2_i = SQ_{Regression\ i}/SQ_{Total\ i}$). The hypothesis H_o: $r'^2_i = 0$ was tested by $t = r'_i/sr'_i$, with $sr'_i = \sqrt{(1 - r'^2_i) / (m - 2)}$ and with (m - 2) degrees of freedom (Steel and Torrie, 1980).

Eberhart and Russell (1966) Method

Raw data were submitted to linear regression analysis, taking as an independent variable the environmental index (I_j) given by $I_j = (\sum_i Y_{ij}/n) - (\sum\sum_{i\ j} Y_{ij}/mn)$ and as dependent variable the average yield of each genotype in each environment (Y_{ij}).

As before, the coefficient of determination (r^2_i) was estimated and statistically tested for each genotype.

Silva and Barreto (1985) Method

Data were analysed based on the following model of multiple regression:

$Y_{ij} = \beta 0_i + \beta 1_i X1_j + \beta 2_i X2_j$, where

Y_{ij} : is the average yield of the i^{th} genotype in the environment j;

$\beta 0_i$: is the average yield of the i^{th} genotype in the average environment;

$\beta 1_i$: is the linear regression coefficient which measures the response of the i^{th} genotype to the unfavorable environments;

$X1_j$: is the first independent variable which is defined as the environmental index j as proposed by Eberhart and Russell (1966);

$\beta 2_i$: is the linear regression coefficient which gives the response differential for genotype i in the favorable environments in relation to that presented in the unfavorable environments; and

$X2_j$: is the second independent variable that is given by $X2_j = X1_j$ if $X1_j \geq 0$ and $X2_j = 0$ if $X1_j \leq 0$.

Parameter estimation was made using matrices (Neter and Wasserman, 1974) through the system of normal equations $\hat{\beta} = (X'X)^{-1} X'Y$, where

$\hat{\beta}$: is a column vector of order 3 with parameter estimates equal to $\hat{\beta}_0$, $\hat{\beta}_1$ and $\hat{\beta}_2$;
X : is the m x 3 matrix and
Y : is the observations vector.

The coefficient of determination (R_i^2), which indicated the efficiency of the method for explaining the variation of the data for each genotype, was estimated by

$$R_i^2 = (\hat{\beta}'X'Y - FC)_i / (Y'Y - FC)_i, \text{ were:}$$

$(\hat{\beta}'X'Y - FC)_i$: is the segmented linear regression sum of squares for the i^{th} genotype with $FC = (\sum_i Y_{ij})^2/m$; and
$(Y'Y - FC)_i$: is the total sum of squares for the i^{th} genotype.

For the statistical testing of the estimate R_i^2 against zero (null hypothesis), the F test was used as follows:

$F = QR/QD$, with $QR = (\hat{\beta}'X'Y - FC)_i/2$ and
$QD = (Y'Y - \hat{\beta}'Y'Y)_i/(m - 3)$ (Steel and Torrie, 1980).

Comparison of Methods

The comparison drawn between the methods of Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Silva and Barreto (1985) was based on the statistical significance of the estimates of the coefficients of determination $r_i'^2$, r_i^2 and R_i^2 presented by the *n* genotypes in the respective methodologies. Estimates obtained from each method were divided into three groups: those that were significant at the 1% probability level (1), those that were significant only at the 5% probability level (2) and the non significant (3). For each methodology, the percentage of genotypes which fell into group 1 (performance very well explained by the model), into group 2 (performance explained by the model) and into group 3 (performance not explained by the model) were calculated. Using this approach, the method with the highest proportion of significant estimates (at 1% and 5%), was indicated as the one that best explained the observed variation of the grain yield data for common bean genotypes (Duarte, 1988).

Comparisons among the absolute values of $r_i'^2$, r_i^2 and R_i^2, of the same genotype were used as additional criteria for the definition of a more efficient model to describe the observed variation in the data.

RESULTS AND DISCUSSION

Although the quality or means of comparison among the methods used to study phenotypic stability has frequently been questioned because of the many ways in which this phenomenon has been studied (Becker, 1981; Lin *et al.*, 1986; Becker and Leon, 1988), verification of the fit of specific models to observed data using the regression techniques employed in the present work, should not suffer any restriction because the regressions were done using the same group of genotypes and environments.

Table II shows the percentage of the tested genotypes that showed significant estimates for the coefficient of determination ($r_i'^2$, r_i^2 and R_i^2) at the 1% and 5% probability levels, as well as the percentage of genotypes which gave non significant estimates. The results show that the three techniques can explain, at the 5% probability level, the observed variation of more than 70% of the tested genotypes. It was also found that the proportion of genotypes with coefficient of determination estimates that were significant at the 1% probability level (from 45 to 51%) was twice that of genotypes with estimates that were significant only at the 5% probability level (from 25 to 29%). Therefore, in about 50% of the genotypes studied the procedures which were compared explained well the observed variation and in more than 25% of the remaining genotypes these techniques satisfactorily explained the variation in the data.

Table II - Proportion of genotypes with significant and non significant coefficient of determination estimates ($r_i'^2$, r_i^2 and R_i^2) obtained using the regression procedures of Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Silva and Barreto (1985).

Methods	% of genotypes		
	**	*	n.s.
Finlay and Wilkinson ($r_i'^2$)	48	26	26
Eberhart and Russell (r_i^2)	45	25	30
Silva e Barreto (R_i^2)	51	29	20

** : significant at the 1% probability level;

* : significant only at the 5% probability level; and

n.s.: non significant at the 5% probability level.

There was considerable similarity between the results that were obtained using the two linear regression procedures (Finlay and Wilkinson, 1963 and Eberhart and Russell, 1966). Twenty-six percent of the genotypes studied did not have their behaviour

satisfactorily explained by the Finlay and Wilkinson (1963) procedure. This also occurred in 30% of the genotypes when the Eberhart and Russell (1966) procedure was used. Since their basic principles are the same, the slight advantage observed with the first method was undoubtedly due to the log transformation of the data, which assures a greater linearity to the estimated responses.

Taking into account the estimates that were individually obtained for the 76 genotypes using the same two procedures (Table III), it was found that an almost perfect correspondence existed among them for their absolute values as well as for their statistical significance when compared to 0. Only seven genotypes (the ones numbered 11, 25, 45, 52, 53, 66 and 67), which had non significant estimates at the 5% probability level through the Eberhart and Russell (1966) method, showed significant estimates with the Finlay and Wilkinson (1963) procedure at the same probability level. Consequently, such genotypes had their performance better explained by the second procedure than by the first. Four other genotypes (numbers 8, 26, 38 and 63) showed the opposite behaviour with significant estimates obtained by Eberhart and Russell (1966) (number 26 at 1% level) and non significant estimates by Finlay and Wilkinson (1963).

Table III - Coefficient of determination estimates obtained for common bean genotypes by the regression methods of Finlay and Wilkinson (1963) ($r_i'^2$); Eberhart and Russell (1966) (r_i^2) and Silva and Barreto (1985) (R_i^2).

Genotype number	$r_i'^2$	r_i^2	R_i^2	Genotype identification
1	0.62**	0.64**	0.64**	L 12155
2	0.06	0.05	0.05	Aroana
3	0.68**	0.59**	0.72**	L 12118
4	0.37*	0.46*	0.46*	L 11152
5	0.68**	0.64**	0.68**	LM 21303-0
6	0.04	0.24	0.39*	82 PVBZ 1901
7	0.70**	0.71**	0.77**	82 PVBZ 1718
8	0.21	0.46*	0.63**	82 PVBZ 1777
9	0.54**	0.53**	0.56**	L 11130
10	0.32	0.28	0.32	LM 21525-0
11	0.41*	0.32	0.32	LM 10034-0
12	0.65**	0.60**	0.61**	Mulatinho Vagem Roxa
13	0.57**	0.35*	0.65**	L 10238

Continued

Table III - Continued.

Genotype number	$r_i'^2$	r_i^2	R_i^2	Genotype identification
14	0.04	0.04	0.04	L 11090
15	0.57**	0.59**	0.61**	A 331
16	0.57**	0.63**	0.64**	ESAL 501
17	0.70**	0.73**	0.73**	LM 21525-0
18	0.64**	0.67**	0.80**	LM 10402-0
19	0.21	0.22	0.25	82 PVBZ 1783
20	0.26	0.28	0.28	L 11132
21	0.85**	0.85**	0.85**	L 10099
22	0.72**	0.77**	0.79**	LM 21306-0
23	0.58**	0.60**	0.60**	A 300
24	0.73**	0.69**	0.70**	LM 30877-0
25	0.40*	0.19	0.39*	A 275
26	0.31	0.50**	0.61**	LM 21322-0
27	0.44*	0.34*	0.38*	A 329
28	0.73**	0.66**	0.66**	EMGOPA 201
29	0.29	0.25	0.25	A 317
30	0.43*	0.45*	0.45*	L 11080
31	0.80**	0.68**	0.71**	L 11077
32	0.78**	0.80**	0.80**	82 PVBZ 1758
33	0.45*	0.37*	0.45*	L 10146
34	0.35*	0.36*	0.37*	LM 10033-0
35	0.42*	0.43*	0.43*	L 11093
36	0.20	0.20	0.27	Paraná-1
37	0.75**	0.77**	0.85**	Cornell 49242
38	0.29	0.33*	0.34	82 PVBZ 1529
39	0.77**	0.68**	0.70**	A 156
40	0.55**	0.48*	0.50*	L 10111
41	0.84**	0.87**	0.92**	82 PVMX 1638
42	0.42*	0.46*	0.49*	82 PVBZ 1767
43	0.63**	0.48*	0.68*	LM 21387-0
44	0.20	0.18	0.18	LM 30864-0
45	0.39*	0.25	0.50*	L 11150

Continued

Table III - Continued

Genotype number	$r_i^{2'}$	r_i^2	R_i^2	Genotype identification
46	0.51**	0.50*	0.50*	ESAL 508
47	0.33	0.21	0.36*	A 274
48	0.23	0.15	0.24	L 11088
49	0.72**	0.54**	0.55**	82 PVBZ 1879
50	0.67**	0.77**	0.82**	82 PVMX 1637
51	0.40*	0.39*	0.46*	L 11133
52	0.34*	0.15	0.34*	82 PVBZ 1843
53	0.38*	0.29	0.39*	L 11076
54	0.46*	0.58**	0.61**	A 154
55	0.50*	0.56**	0.67**	A 266
56	0.74**	0.76**	0.77**	ESAL 506
57	0.51**	0.55**	0.57**	BAT 841
58	0.81**	0.70**	0.74**	L 10110
59	0.65**	0.54**	0.55**	LM 10367-0
60	0.69**	0.76**	0.82**	A 344
61	0.57**	0.50*	0.52**	Carioca
62	0.55**	0.53**	0.58**	L 13497
63	0.30	0.44*	0.67**	ESAL 505
64	0.47*	0.47*	0.47*	LM 30068-0
65	0.20	0.17	0.19	L 11086
66	0.40*	0.20	0.40*	CP 1035
67	0.37*	0.33	0.36*	A 254
68	0.56**	0.45*	0.45*	ESAL 509
69	0.54**	0.58**	0.64**	A 251
70	0.13	0.17	0.17	82 PVBZ 1723
71	0.44*	0.52**	0.60**	ESAL 504
72	0.12	0.10	0.18	LM 30995-0
73	0.37*	0.44*	0.45*	LM 10027-1
74	0.26	0.32	0.42*	A 323
75	0.11	0.13	0.15	IPA 74-19
76	0.59**	0.52**	0.52**	L 10323

* and ** - Values which were significant at the 5 and 1% probability levels respectively.

Considering the results and disregarding those cases in which one procedure was superior to the other, the regressions of Finlay and Wilkinson (1963) and Eberhart and Russell (1966) were found to be equally efficient in describing genotypic responses to the environmental variations. However, straightforward biological interpretation, made possible by the Eberhart and Russell (1966) methodology represents an obvious advantage of this procedure over the other, which uses log transformed data.

The Silva and Barreto (1985) technique, when compared with the other two, was found to be slightly superior. While segmented linear regression explained satisfactorily the variation that was observed in 80% of the genotypes (51% of them reaching significance for R_i^2 at the 1% probability level also), the regression procedures of Finlay and Wilkinson (1963) and Eberhart and Russell (1966) only explained 74 and 70% of the data, respectively (Table II). These results agree with those that were obtained by Riede and Barreto (1985) in wheat and by Peixoto *et al.* (1985) in sugar cane.

When comparing coefficient of determination estimates that were obtained for each individual genotype with the three procedures (Table III), there was a correspondence in value and in statistical significance among all three. Results comparing Silva and Barreto (1985) with Finlay and Wilkinson (1963) showed that, for 62% of the genotypes, estimates R_i^2 were superior to $r_i'^2$. Six of these genotypes (6, 8, 26, 47, 63 and 74) showed $r_i'^2$ estimates that were not different from zero at the 5% probability level, but had R_i^2 estimates that were significant at the 5 or 1% probability level. These genotypes show a tendency to have a non linear response to environmental variations. The Silva and Barreto (1985) procedure provides a better identification of such cases. Of the genotypes in which R_i^2 estimates were not different from zero, only genotype number 11 showed significant estimate at the 5% level for $r_i'^2$, but had a low absolute value ($r_i'^2 = 0.41$).

Segmented linear regression analysis gave larger coefficient of determination estimates for 74% of the tested genotypes when compared to the Eberhart and Russell (1966) method. Nine of these genotypes (6, 25, 45, 47, 52, 53, 66, 67, and 74), for which r_i^2 estimates were statistically non significant, showed significant R_i^2 estimates at the 5% level (none of them were significant at the 1% probability level). As was previously observed with the Eberhart and Russell (1966) procedure, such genotypes showed non linear responses to environmental variation. Of the genotypes that had R_i^2 estimates that were not statistically different from zero, only genotype number 38 showed significance for r_i^2 at the 5% probability level, although the absolute value of the estimate r_i^2 was lower than the value of the estimate R_i^2 (Table III).

From the results it is clear that there exists an advantage in using the Silva and Barreto (1985) procedure over the linear regression methods of Finlay and Wilkinson (1963) and Eberhart and Russell (1966) when looking at the degree to which each is able to explain the variation in the data. Even for the genotypes that showed a linear response,

a slight superiority appeared in a large proportion of them. For those that did not show a linear response, the segmented regression analysis was the alternative that could explain the behaviour of a number, but not all of the genotypes. Considering that the Silva and Barreto (1985) procedure allows one to discriminate between the behaviour of genotypes in both favoured and unfavoured environmental conditions, it is technically more efficient than the other two for describing the adaptability and yield stability of the genotypes studied. Cruz *et al.* (1989) recently proposed other modifications for that methodology, which ease and improve the precision of parameter estimations.

The behaviour of a fair proportion of the studied genotypes (19.7%) was not satisfactorily explained by the three procedures. Therefore, it is suggested that research for the development of alternative methods for the study of adaptation and phenotypic stability continue, in order to achieve better models that are also biologically acceptable.

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RESUMO

O trabalho teve como objetivo comparar três métodos de estudo de estabilidade fenotípica quanto à sua capacidade de explicar a variação nos dados de produtividade média, em 76 genótipos de feijoeiro comum. Para isso, foram utilizados dados de doze ensaios preliminares de rendimento, conduzidos em oito localidades brasileiras. Os métodos escolhidos para comparação foram dois métodos clássicos de regressão linear simples e a recente proposta da regressão linear bi-segmentada.

Com base nas proporções das estimativas de coeficiente de determinação significativas e não significativas estatisticamente, para os genótipos estudados, bem como na magnitude destas estimativas, pôde-se concluir que o método da regressão segmentada mostrou-se ligeiramente superior aos métodos de regressão linear simples. Esta superioridade manifestou-se especialmente quando o comportamento do genótipo às variações ambientais não obedeceu a linearidade. Os métodos de regressão linear simples apresentaram resultados semelhantes entre si.

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