

An investigation of genotype-environment interaction and stability for pea (*Pisum sativum* L.) seed yield

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Summary: Eighteen pea breeding lines and three check cultivars were tested in two years with and without irrigation. The linear regression can explain only a small part of GEI so the use of regression technique was not possible for interpreting the data. In this case the *ecovalence*, *stability variance* and *superiority measure* stability parameters cannot describe properly the genotype's response. With the AMMI method it is possible to group properly the genotypes according to their response.

Abbreviations: GEI = genotype-environment interaction, AMMI = additive main effects and multiplicative interaction

Introduction

Evaluation of genotypes for performance consistency in different environments is important both in plant breeding programs and in variety testing.

In one of the first reports investigating GEI in peas, *Snoad & Arthur* (1974) found significant GEI for every one of the characters investigated and a significant part of this interaction was accounted for the differences between the linear regression coefficients. In most cases the residual deviations were also significant. Later in another study (*Snoad & Arthur* 1976) using the same data, accurate predictability of genotype behaviour based on linear regression was not possible.

Singh et al. (1984) reported non-significant linear components of GEI for seed yield and yield components. The deviations from linearity were highly significant except 100 seed weight. *Gupta* (1986) in 12 parents and 66 their F_1 hybrids found both linear and non-linear components of GEI for flowering time, plant height and number of reproductive nodes, the linear component being the higher. In the case of pod yield only the non-linear component was important. The early genotypes seemed to be more stable but they were poor yielders.

In a 10 parent diallel cross of vining peas the general combining abilities of the investigated traits (flowering time, number of flowering nodes on the main stem, pods per plant, seeds per pod, pod length, 100 seed weight and seed yield) interact significantly with years and plant densities (*Csizmadia* 1987).

Abd-El Moneim et al. (1990) found that for herbage and seed yield a large proportion of GEI was accounted for the linear regression. Although the non-linear component was also significant, its magnitude was smaller compared to the linear component. They concluded that except but one all the stable genotypes were suitable for poor environments.

Biarnès-Dumoulin et al. (1996) found that number of the first flower and mean number of reproductive nodes of the main stem as genotypic covariates, and the water balance during flowering as environmental covariate explained 64% of the total GEI. These suggest that differential response of the genotypes as to their earliness and duration of the seed set period is responsible for an important part of GEI when grown in environments with drought stress during flowering.

In Hungary there is a great fluctuation in pea yields over years and locations compared to cereals, indicating extreme sensitivity of current pea genotypes to the environmental effects. From the results of numerous line and variety trials high GEIs was estimated, the ratio of the variability accounted for this interaction and genotypes varied between 0.54 and 4.3 (*unpublished data*).

The aims of the present study are to: (a) evaluate yield potentials of new promising pea breeding lines under different environmental conditions and (b) measure GEI and study their adaptation.

Materials and methods

Twenty-one pea genotypes (18 breeding lines and 3 check cultivars) were sown at Ujmajor in 1998 and 1999 in irrigated

and non-irrigated pea nurseries. Random block design was applied with four replications. The trials were sown with an Oyord plot drill on 9 x 1.5 m plots, with 11 cm row-distance and with 100 plant/m² plant densities. In the irrigated nursery a line-sprinkler was used: from blooming till full seed-filling stage three irrigations were applied each with 30 mm water. Plots were harvested with a plot combine at 15–20% water content, and yields corrected for 14% water content.

Statistical procedures

Presence of GEI was detected by standard analysis of variances and joint regression analysis applied to divide interaction mean square into two parts: (a) heterogeneity of linear regression coefficients and (b) pooled deviations from individual regressions (Eberhart & Russel 1966; Prabhakaran & Jain 1994).

Ecovalence (W_i), stability variance (σ_i^2) and superiority measure (P_i) stability parameters were calculated on means of genotypes (Becker & Leon 1988; Lin et al. 1986; Kang, 1990).

The AMMI (additive main effects and multiplicative interaction) model makes use of standard ANOVA procedures to separate additive variance from the genotype-environment interaction variance and then uses principal components analysis to extract the pattern from the GEI portion of ANOVA (Gauch 1990 and 1992; Zobel 1990).

Results and discussion

The pooled analysis of variance for seed yield (Table 1) shows that differences both among genotypes and between environments is highly significant. A high proportion of the

Table 1 Mean squares from joint regression analysis of seed yield of 21 entries of peas evaluated with and without irrigation for two years

Source of variation	df	MS
Genotypes	20	159 363.93***
Environments	3	2 573 569.49***
G x E	60	126 730.35***
Joint regression	3	2 573 569.49***
Heterogeneity between regression	20	129 358.73***
Remainder	40	125 416.16***
Pooled error	240	42 183.49

*** = significant at 0.1% level

sum of squares is partitioned to GEI (41.1%) compared to that of the genotypes (17.2%). Both linear and non-linear components of GEI are significant. The linear regression can explain only 34.1% of GEI so the usefulness of the regression approach for interpretation of the data seems to be doubtful.

As an alternative approach three stability parameters were estimated (Table 2). The *ecovalence* (W_i) is the squared and summed GEI effects across all environments for a genotype. *Stability variance* (σ_i^2) is the unbiased variance of a genotype across environments. These two stability parameters ranks the genotypes in a similar manner: the most stable genotypes are A, N and D.

Table 2 Mean seed yield, ecovalence (W_i), stability variance (σ_i^2) and superiority measure (P_i) for the investigated pea genotypes.

Genotypes	Seed yield (kg/ha)	W_i	σ_i^2	P_i
A F ₇ -845-BC1/1/4	4675	13906	2101	1319188
B F ₈ -846/14	4736	271056	93193	1128948
C F ₈ -842/44	4458	318974	110847	2118982
D F ₈ -761/54	4576	71197	19560	1658220
E F ₇ -845-BC1/1/5	4846	252311	86287	822763
F F ₈ -844/15	4621	312448	108442	1500283
G UM 6729	4737	385217	135252	1125668
H UM 6881	4905	1474266	536481	678358
I UM 1414	4599	814954	293576	1575470
J UM 9300302	5135	754144	271173	247046
K UM 1139	4726	338638	118091	1156651
L UM 1142	4716	151323	49081	1187602
M UM 1141	4860	158248	51632	787156
N F ₁₀ -556/16	4905	68133	18432	677336
O F ₇ -742-BC/15/53	4200	280104	96526	3310172
P F ₇ -742-BC/12/76	4572	604982	216218	1672797
Q F ₁₁ -556/12	4492	318978	110848	1981194
R F ₁₁ -531/8	4816	471665	167101	899970
S Chk Erbi	4628	225528	76419	1474876
T Chk Luzsányi	4592	157419	51326	1601249
U Chk Delta	4906	160345	52404	674598

The *superiority measure* (P_i) estimates simultaneously yield potential and stability and is defined as the distance mean square between a genotype's response and the maximum response averaged over all environments. P_i values represents superiority in the sense of general adaptability so a narrowly adapted genotype (poor in general adaptability but good in specific adaptability) may be easily discarded. In our case the rank of genotypes according to P_i is identical to the rank of yields. It would mean that simply selecting for yield could result improvement in stability which is inconsistent with the empirical observations.

The conclusions could have been drawn based on these three stability parameters seem rather doubtful.

Multivariate techniques do not require *a priori* assumptions (such as linearity) about the form of genetic response. A genotype is described in multidimensional space with each dimension representing an environment. The *additive main effects and multiplicative interaction* (AMMI) seems to be an extremely powerful analytical tool to interpret genotype x environment data because of the use of biplot and data validation procedures. The AMMI analysis table for seed yield in Table 3. shows that GEI is significant and accounts for 27.7% of the total variation. The contribution of genotypes to the total sum of squares is only 10.3%. The first

Table 3 AMMI analysis of variance for pea seed yield

Source of variation	df	MS
Treatments	83	892 200.13***
Genotypes	20	637 747.19***
Environments	3	10 295 979.00***
Interactions	60	506 828.81***
IPCA 1	22	723 017.44***
IPCA 2	20	554 228.38***
IPCA 3	18	208 101.01 n.s.
Residuals	252	189 932.11 n.s.
Error		193 131.69

*** = 0.1% level,

n. s. = non significant

interaction axis (IPCA 1) from the AMMI analysis separates out 52.3% of the sum of squares from the GEI, the first two together 88.8% and a final non-significant residual. The biplot between interaction PCA 1 eigenvalues and the seed yield means of genotypes and environments (*Figure 1*) visualises the response of genotypes to irrigation. The check

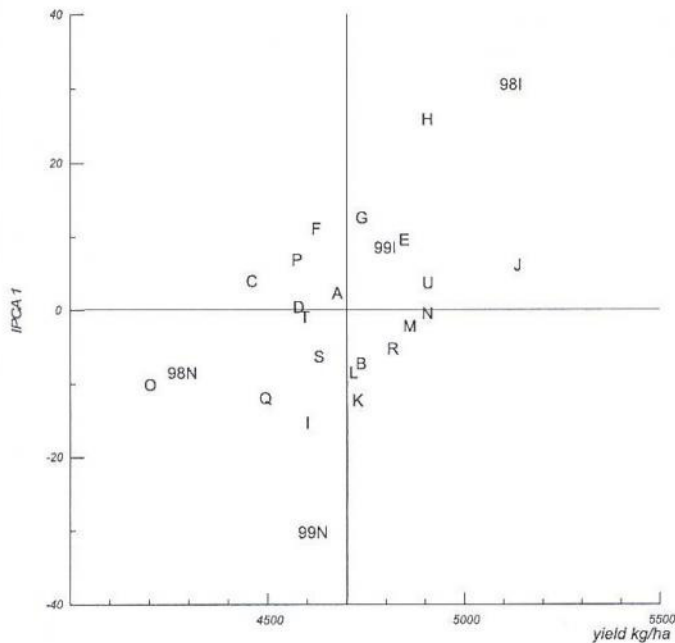


Figure 1 Biplot of the yields (kg/ha) and IPCA1 values of 21 pea genotypes grown with (I) and without (N) irrigation for two years (98 and 99). Horizontal line is IPCA1=0, vertical line represents the grand mean

cultivars have fairly good general adaptations and the breeding lines show much wider responses. From the genotypes with above average yields N, M and U show good general adaptation. Genotypes E, G and especially H have more specific adaptation to better (in our case irrigated) environments. The adaptation of the highest yielder genotype (J) is between the two. Genotypes O, Q and I are better adapted to poorer (without irrigation) environments and they have below-average yielding potential.

In our case the use of AMMI method proved to be efficient in grouping pea genotypes according to their response to irrigation.

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