

Original Research Article

Stability analysis in field pea (*Pisum Sativum* L.) genotypes under various environmental conditions

ABSTRACT

Present study was undertaken to estimate the G x E interactions and identify stable genotypes for yield traits in field pea. A total of 43 field pea genotypes were evaluated in Randomized Complete Block Design (RCBD) in three replications along with three different dates of sowing at Breeder Seed Production Unit (soybean), Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur during Rabi Season 2022 - 2023. The analysis of variance was applied on 16 different quantitative traits both individually and pooled under various environment conditions. The stability analysis for seed yield per plant was assessed using Eberhart and Russell's model, revealing significant variations among different genotypes and environmental conditions. The mean squares attributed to both environment and genotype-environment interactions (E + G x E) indicated significant interactions between genotypes and environments. Further, partitioning of genotype-environment (linear) interactions was found to be highly significant for seed yield per plant. Genotypes SHIKHA, KPMR 485 and HFP 94-12 were found to be ideal and stable genotypes for seed yield per plant as that possessed mean value higher than general mean, regression coefficient near to unity ($B_i=1$) with minimum deviation from regression ($S^2_{di}=0$). Thus, identified stable genotypes can be utilized for different seasons and regions for obtaining the stable yield performance.

Keywords: Stability Analysis; stable genotypes; field pea

1. INTRODUCTION

The genus *Pisum* of the family Fabaceae includes the two species of pea, *Pisum fulvum* and *Pisum sativum*, as well as various wild subspecies (*abyssinicum*) of *Pisum sativum*. Garden peas (*Pisum sativum* var. *hortense*) and field peas (*Pisum sativum* var. *arvense*) are the two species of cultivated peas. One species of the genus *Pisum*, *Pisum sativum* ssp. *Abyssinicum*, is thought to be a progenitor and closely resembles the cultivated pea. (Jing *et al.* 2010) [2]. This is self-pollinating rabi pulse crop with the chromosome number $2n=14$ is the field pea. Pea is in the Mediterranean region and grown at higher altitudes in tropical regions where the temperature ranges from 7 to 30 degrees Celsius.

Garden peas are used for food; thus, they are harvested when the pods are still green and boiled grains are used for later uses as vegetables and others dietary purposes. For a variety of cuisine recipes, field peas are utilized as dried, whole or split dals or as flour (besan). The nutritional value of pea seeds is the primary measure used to assess it. It has a high nutritional value and is a significant source of protein (between 21 and 25 percent) with high quantities of lysine and tryptophan amino acids (Bhat *et al.*, 2013 [3], Gregory *et al.*, 2016) [4], although it contains relatively low cysteine and methionine amino acids (Cheyhan and Avci, 2005) [5]. This is regarded as the most affordable source of protein in the diet. Since it is herbaceous plant, it is frequently cultivated for food and fodder. Including the essential vitamins B1 and B5, dry pea seeds have 56.5% carbohydrates, 1.1% fat, 2.2% minerals, and 4.5% fiber. Animal feed is made from the stalks, broken cotyledons, and seed coat.

Yield is the major breeding trait which is influenced by the environment. Search for the stable genes to identify the donors and breeding methodology is an important procedure to collect the genes in a single locus. For this type of work, first of all screening of the genotypes in different growing three environments and record the influence of genes governing yield traits is of important activity to select genotypes. Identification of stable lines with the good performance of the genotypes in maximum environment will be of the best option to select the promising genotypes. Stability analysis provided by Eberhart and Ruseel, 1966 [1] will be of best option to calculate effects as per the statistical parameters.

Eberhart and Ruseel introduced a conceptual framework in 1966 that involved the utilization of two distinct parameters. The first parameter, known as the regression coefficient (b_i), served the purpose of assessing the relative reactivity of a specific cultivar concerning the mean of all cultivars, which was referred to as the environmental index. The second parameter, named the deviation from the regression mean square (S^2_{di}), was designed to gauge the extent of correspondence between the projected response and the actual observed response. In their initial proposition, Eberhart and Ruseel employed cultivar averages as the response variable and experiment averages as the environmental index in their analytical approach.

2. MATERIAL AND METHODS

Experimental material consisted of 43 field pea genotypes were obtained from Field Pea Improvement Project, Department of Plant Breeding & Genetics, College of Agriculture, JNKVV, Jabalpur. The experiment was laid out in Randomized Complete Block Design (RCBD) in three replications along with three different dates of sowing (5th November 2022 – (normal), 5th December 2022 – (late) and 5th January 2023 – (extra late). All the genotypes were sown in four rows pattern keeping 30.0 cm row to row and 10.0 cm plant to plant distance. A total of 16 yield attributing trait based observations were made. Further, Observations for days to fifty percent flowering (days), days to maturity (days), number of primary branches per plant, number of secondary branches per plant, plant height (cm), number of nodes per plant, number of effective nodes per plant, pod bearing length (cm), number of pods per plant, number of effective pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g) were recorded each of the three environments individually. The observations based on mean of the five individual plants was statistically analysed to find out stability present in the experimental material for each traits. The stability analysis was done as per Eberhart and Russell (1966) model.

3. RESULTS AND DISCUSSION

The analysis of variance for various yield characters has been presented in table 1. The analysis of variance revealed that the differences among the genotypes were highly significant for all the traits except numbers of nodes per plant. The variation due to environment (linear) was found significant for all the traits. The G X E linear was found to be highly significant for all traits such as biological yield per plant, number of pods per plant, seed yield per plant, number of seeds per pod and pod length. While, numbers of nodes per plant is non-significant. This suggested that the genotype x environment interaction was of predictable nature based on linearity. Traits reporting high significant genotypes X environment interactions under study suggested that these characters are highly influenced by the change in the environmental conditions. However, it was significant for days to maturity, harvest index, days to fifty percent flowering and number of effective nodes per plant. This result is in agreement with Ceyhan *et al.* (2012) [6].

The stability parameters for seed yield per plant and its contributing traits under 43 genotypes is presented in table 2. The genotypes SHIKHA, KPMR 485 and HFP 94-12 were found to be ideal and stable genotypes for seed yield per plant as that possessed mean value higher than general mean, regression coefficient near to unity ($B_i=1$) with minimum deviation from regression ($S^2_{di}=0$). The genotypes HFP 94-13 and KPMR 502 were could be regard as stable genotype for seed yield per plant as that possessed mean value lower than general mean, regression coefficient near to unity ($B_i=1$) with minimum deviation from regression ($S^2_{di}=0$). The genotypes DDR 52, RP 3, AMAN, MATAR RANGPUR and KASHI SAMRIDDHI exhibited regression coefficient lower than unity ($B_i<1$) coupled with least deviation from regression ($S^2_{di}=0$) hence these genotypes can be regarded as above average stability suitable for poor environment. Rest all the genotypes exhibited deviating S^2_{di} values (deviating from zero) with varying B_i values are considered unstable for seed yield per plant. Similar results were found by Ceyhan *et al.* (2012) [6], Rezene *et al.* (2014) [7], Fikere *et al.* (2014) [8] and Parihar *et al.* (2022) [9].

Table 1. Analysis of variance for phenotypic stability for yield & yield attributing traits of pea genotypes in pooled over environments (Eberhart and Russell model 1966)

Source of variation	D.F.	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL	NPPP	NEPPP	PL	NSPP	100 SW	BYPP	HI	SYPP
Rep. within Env.	6	0.79	2.180*	0.09**	0.14**	0.17**	0.64**	0.14**	0.10**	0.007**	0.034**	0.054**	0.08**	0.16**	0.21**	5.31**	0.32**
Varieties	42	106.59**	75.49**	0.33**	0.49**	1169.93**	12.52	1.57**	131.86**	20.43**	19.42**	0.93**	0.71**	14.54**	16.61**	92.32**	7.96**
Env. + (Var.*Env.)	86	7.63**	27.36**	0.074**	0.22**	119.13**	5.44	0.80**	30.86**	10.25**	8.89**	0.32**	0.29**	0.031**	12.32**	35.49**	5.45**
Environments (Lin.)	1	307.96**	1859.78**	1.33**	10.62**	6554.31**	325.87**	45.76**	1776.89**	509.03**	434.40**	10.52**	10.09**	2.54**	542.59**	1209.17**	278.61**
Var.*Env. (Lin.)	42	7.25**	11.02**	0.12**	0.19**	87.87**	3.37	0.55**	20.87**	8.87**	7.87**	0.39**	0.36**	0.004**	12.26**	42.36**	4.51**
Pooled Deviation	43	5.92**	8.55**	0.04**	0.15**	74.08**	68.52**	2.41**	60.33**	4.72**	4.97**	0.04**	0.08**	0.73**	5.16**	6.45**	1.36**
Pooled Error	252	0.26	0.24	0.014	0.013	0.35	0.18	0.032	0.072	0.061	0.068	0.023	0.024	0.005	0.066	3.07	0.13
Total	128	40.10	43.15	0.16	0.31	463.92	7.76	1.05	64.00	13.59	12.35	0.51	0.432	4.79	13.73	54.14	6.27

Note- * & ** indicate level of significant at 5% and 1 %, respectively.

DFF- days to fifty percent flowering, DM- days to maturity, NPBPP- number of primary branches per plant, NSBPP- number of secondary branches per plant, PH- plant height, NNPP- number of nodes per plant, NENPP- number of effective nodes per plant, PBL- pod bearing length, NPPP- number of pods per plant, NEPPP- number of effective pods per plant, PL- pod length, NSPP- number of seeds per pod, 100 SW- hundred seed weight, BYPP- biological yield per plant, HI- harvest index, SYPP- seed yield per plant.

Table 2. Stability parameters (ER 1966) for seed yield per plant of pea genotypes:

Genotypes	Seed yield per plant		
	Mean	β_i	σ^2_{di}
SHIKHA	9.623	1.084	-0.178
RACHNA	10.973	0.577	3.918**
JAYANTI	10.021	0.752	0.160**
DOUBLE BRANCHING	7.428	1.270	0.824**
VL 1	7.386	1.171	5.065**
DDR 39	7.316	0.925	0.107**
VL 3	7.667	1.343	1.216**
PP 14	10.092	1.015	1.610**
DDR 52	6.727	0.044**	0.058*
RP 3	9.533	0.790*	0.007
IPFD 12-2	8.932	1.138	0.209**
TRIPLE BRANCHING	6.696	0.588	2.188**
AMAN	7.553	0.033**	-0.004
DDR 54	6.341	1.139	0.178**
JP 885(Purple)	3.697	0.955	0.347**
HUP 2	8.358	0.728	0.758**
KPMR 302	7.396	1.032	0.545**
KPMR 423	8.284	1.270	0.987**
KPMR 486	8.016	1.586*	0.118**
KPMR 327	8.288	1.295	0.597**
KPF 151	7.073	0.864	1.419**
KPMR 485	10.281	1.061	0.073
PP 86	9.316	0.647	1.307**
KPMR 503	6.779	1.935	1.658**
HFP 94-12	11.521	0.970	-0.352
KALAMATAR	6.140	2.058	5.310**

IPFD 11-5	8.009	2.179	1.607**
DDR 94-14	5.387	1.825	1.186**
KPMR 502	6.494	0.892	0.068
HUVP 12	6.409	0.394	2.538**
HFP 94-13	7.114	1.039	-0.773
KPMR 402	6.780	0.714	0.217**
Safed Batri Gudda	7.197	0.621	0.149**
Batanamoolchand	5.680	0.967	0.416**
Matar Rangpur	4.866	0.690*	0.025
Kashi Samriddhi	8.982	0.588*	0.041
Kali batri	7.337	0.725	1.799**
Gol Batra Tenduna	10.049	0.870	0.568**
IPF 99-25	8.619	0.544	0.951**
TALL WHITE(HYBRID	6.736	0.923	0.116**
TALL GREEN(HYBRID)	8.181	0.375	1.365**
JP 885	7.740	0.854	1.797**
KALASONA	8.760	0.394	0.936**
POPULATION MEAN	7.809		

Note- * & ** significant at 5% and 1% levels, respectively

4. CONCLUSION

Stability analysis confirmed that out of 43 field pea genotypes SHIKHA, KPMR 485 and HFP 94-12 were the Ideal & stable genotypes for seed yield per pant while the genotypes RACHNA, SHIKHA, JP885, KPMR 402, TRIPLE BRANCHING, TALL GREEN (HYBRID), and KPMR 485 showed stability for more than two traits. Thus, stable genotypes can be utilized for different seasons and regions for obtaining the stable yield performance. These identified genotypes will also be utilized in hybridization programme for the development of genotypes stable for yield in multivariate environment.

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