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Stability Analysis in Field Pea (*Pisum sativum* L.) Genotypes under Various Environmental Conditions

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Present study was undertaken to estimate the G x E interactions and identify the 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 BSP Soybean Unit, Department of Genetics and Plant Breeding, 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 environmental conditions. The stability analysis for seed yield per plant was assessed using Eberhart and Russell's model,

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revealing significant variations among different genotypes and environmental conditions. The mean squares attributed to both environments 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 ideal and stable genotypes for seed yield per plant as that possessed mean value higher than general mean, regression coefficient near to unity (Bi=1) with minimum deviation from regression (S^2di~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 [1]. 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 Slade 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 [2,3], although it contains relatively low cysteine and methionine amino acids [4]. 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, [5] 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 (bi), 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^2di), 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. Stable performance is always beneficial to overcome the yield penalty from changing environmental conditions. This mode predicts the suitable genotypes performing constant traits in the next changing environment. Regarding these three environments, they always provided the most promising ones for direct selection and utilization in crop improvement programs.

2. MATERIALS 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 (5^{th} November 2022 – (normal), 5^{th} December 2022 – (late) and 5^{th} 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 and pooled environments. The observations based on mean of the five individual plants was statistically analyzed to find out stability present in the experimental material for each traits especially for yield. 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 the trait numbers of nodes per plant was non-significant. This finding 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 changing of 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 the finding of Ceyhan et al*.* [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 (Bi=1) with minimum deviation from regression (S^2di~0). The genotypes HFP 94-13 and KPMR 502 were regard as stable genotype for seed yield per plant as that possessed mean value lower than general mean, regression coefficient near to unity (Bi=1) with minimum deviation from regression (S^2di~0). The genotypes DDR 52, RP 3, Aman, Matar Rangpur and Kashi Samriddhi exhibited regression coefficient lower than unity (Bi<1) coupled with least deviation from regression (S^2di~0) hence, these genotypes can be regarded as above

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 levels 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

Genotypes	Seed yield per plant		
	Mean	βi	σ²di
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**
Batana moolchand	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*

average stability suitable for poor environment. Rest all the genotypes exhibited deviating S^2di values (deviating from zero) with varying Bi values are considered unstable for seed yield per plant. Similar results were found by Ceyhan et al. [6], Rezene et al. [7], Fikere et al. [8] and Parihar et al. [9].

4. CONCLUSION

On the basis of finding obtained from this investigation it is concluded that genotypes Shikha, KPMR 485 and HFP 94-12 were the Ideal & stable for seed yield per plant while the genotypes Rachna, Shikha, JP 885, KPMR 402, Triple Branching, Tall Green (Hybrid), and KPMR

485 were found stable for more than two yield attributing traits. These identified stable genotypes might be utilized in cultivation programme for different seasons and regions for obtaining the stable yield performance. These identified genotypes will also be utilized in hybridization programme as a donor for the development of new improved field pea lines contributing stable yield performance under changing environmental conditions.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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