

Multivariate Analysis for Selection Indices of Farmers' Pea (*Pisum sativum* var. *arvense* L.) Varieties of Vindhyan Zone of Uttar Pradesh

Ruchi Bishnoi^{1*}, Shailesh Marker², Preeti Basser³, Rutvik J Joshi⁴, Jogender⁵, Maryam Razzaq⁶, Muhammad Awais^{7*}

¹Ph.D. Research Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Ummedganj-Kota, Agriculture University, Kota (Rajasthan)-324001

²Professor, Department of Genetics and Plant Breeding, Sri Karan Narendra Agriculture University, Jobner (Rajasthan)-303329 (Former Professor, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (U.P.)-211007)

³Ph.D. Research Scholar, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur (Rajasthan)-313004

⁴Ph.D. Research Scholar, Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand (Gujarat) - 388110

⁵Ph.D. Research Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Chaudhary Charan Singh Haryana Agricultural University, Hisar, (Haryana)-125004

⁶Seed Science and Technology, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad-38040, Pakistan

⁷Henan International Joint Laboratory of Laser Technology in Agricultural Sciences, Henan Agriculture University, Zhengzhou 450002, P. R. China

*Corresponding e-mail: dr.muhammad.awais@henau.edu.cn

Abstract

Genetic heterogeneity of farmers' varieties increases production system resilience in response to biotic and abiotic challenges, reducing the likelihood of crop failure as a whole. Variability is the prerequisite for selection of superior traits and parents. Multivariate analysis acts as an aid to the process of selection indices. Therefore, twenty-two farmers' varieties of pea (*Pisum sativum* var. *arvense* L.) of Vindhyan zone of Uttar Pradesh were studied at Field Experimentation Centre of Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj (Allahabad), U.P. in randomized block design (RBD) during *Rabi*, 2019-20 and *Rabi*, 2020-21. The observations so obtained for the two consecutive years were pooled for multivariate analyses. PC1, PC2, PC3 and PC4 contributed overall 78.68% of variance with eigen value greater than unity. DM, YP, WP, LP and NEN exhibited maximum variability for the characters which can be exploited to a greater extent. HI, DF50 and DM had positive correlation with YP whereas NSP, NPP and LP had negative association with YP. However, the confirmation can be provided by correlation and path coefficient analyses. In regards to farmers' varieties, PMKK-232 and PKKK-227 should be selected in PC1 for future breeding programme.

Keywords: Pea (*Pisum sativum* var. *arvense* L.), Principal component analysis (PCA), Farmers' varieties, Multivariate analysis

Introduction

Farmers' varieties are cultivars that have been historically developed by farmers in their fields over many years, or they may be wild relatives or land races of cultivars that farmers are familiar with (Chandrashekar and Vasudev, 2002). Farmers domesticated many wild relatives and/ or cultivated landraces, and they still do so today (Vodouhe *et al.*, 2011), hence they are substantially responsible for the remarkable genetic diversity that now occurs within species (intraspecific diversity) (Brush, 2004). Genetic heterogeneity of farmers' varieties increases production system resilience in response to biotic and abiotic challenges, reducing the likelihood of crop failure as a whole (Ceccarelli, 2012). Farmers' varieties occasionally outperform commercial varieties, particularly when grown in challenging conditions and in situations where farmers cannot afford the suggested inputs to increase the performance of formal sector improved materials (Burdon and Jeirsoz, 1990). Nevertheless, there is an alarming pace of loss of traditional knowledge and variability.

Additionally, in order to assist gene banks to expand and correctly protect these genetic resources, an examination of the genetic variability of farmer varieties is essential as it can offer the required fundamental data (Brondani *et al.*, 2006). Because these varieties exhibit good production stability despite having a low yield capacity, this genetic diversity is crucial for the viability of small farmers (Bishnoi *et al.*, 2021). Since there is a dearth of information on the farmers' varieties of pea (*Pisum sativum* var. *arvense* L.), multivariate analysis was conducted to learn more about the principal components, traits that contribute most to variations, and the parents to be used in subsequent breeding programmes.

Materials and methods

The twenty-two farmers' varieties of pea (*Pisum sativum* var. *arvense* L.) of Vindhyan zone of Uttar Pradesh were studied at Field Experimentation Centre of Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj (Allahabad), U.P. in randomized block design (RBD) during *Rabi*, 2019-20 and *Rabi*, 2020-21. The crop was raised in accordance with the good agricultural practices. Eleven quantitative traits were recorded during the study on five randomly selected plants in each entry of each replication for all the characters *viz.*, plant height (PH), number of pods per plant (NPP), length of pods (LP), width of pods (WP), number of effective nodes (NEN), number of seeds per pod (NSP), harvest index (HI), 100-seed weight (100SW) and seed yield per plant (YP), except days to flowering (DF50), days to maturity (DM) which were recorded on plot basis. The data so obtained for two years were pooled and then subjected to Rstudio 4.2.3 for data analysis (R Core Team, 2021). The multivariate analysis was done using 'factoextra' package (Kassambara, 2017).

Results and discussion

Multivariate analysis helps to predict the principal components that contribute maximum to the yield of the crop. Table 1 and graph 1, indicates the eigen values, percentage of variance and cumulative percentage of variance. In the current investigation, 4 out of 11 principal components reported eigen values greater than unity, which all together gave 78.68% of variance. In which, 35.27% of total variance was explained by PC 1, followed by PC2

(22.18%), PC3 (12.12%) and PC4 (9.10%). Principal component having eigen value more than unity exhibits more variability among the field pea genotypes for selection of distantly related parents (Kumar *et al.*, 2023). Similar approach of PCA was carried out by Parihar *et al.*, 2014, Bhuvanewari *et al.*, 2017, Arif *et al.*, 2020 and Pratap *et al.*, 2021. Further the individual characters were evaluated for the variance present in each dimensions or principal components, as depicted in table 2. It was noticed that the maximum contribution for variations in PC1 was reflected by DM (22.15 %), followed by LP (19.16 %) and NSP (10.82 %) whereas minimum contributions were of WP (0.47 %). Similarly, WP (25.06 %) contributed maximum towards the variance in PC2, followed by NEN (23.21 %) and NPP (13.68 %). YP (24.66 %) followed by WP (22.31 %) and NEN (15.32 %) reported maximum contribution in case of PC3. HI (28.70 %) had greater influence in PC 4 followed by NSP (18.34 %) and DF50 (17.57 %). Therefore, the respective characters should be emphasized during the selection of parents for hybridization purpose.

The visualization of the graph so prepared with Dim1 and Dim2 at x-axis and y-axis respectively (as shown in graph 2) illustrate the diversity among the traits. The traits, DF50 and HI had highest contribution towards the variations whereas DM and LP had the least influence in principle components. In regards to the variations exhibited by the individual characters, HI and DF50 showed least variations and DM, YP, WP, LP and NEN showed greater amount of variations. As, mentioned by Bishnoi *et al.*, 2023, the variations offer the scope for genetic improvement. These variations are therefore, helpful in improving the farmer's varieties of pea. As illustrated in the graph, YP makes acute angle with HI, DF50 and DM, indicating positive association. The characters, *viz.*, NSP, NPP and LP made approximate 180° angle with YP, which means negative correlation with YP in farmer's pea varieties. Similar trends can be seen in the correlation matrix of the study conducted by Bishnoi *et al.*, 2021. The characters *viz.* NEN, WP and PH made right angle with YP, indicating no relation with yield. However, correlation matrix and path coefficient present significant relationships among the traits of the crop. Bishnoi *et al.*, 2021 gave confirmation to this result through correlation coefficient analysis.

Multivariate analysis can also help in selection of parents for future breeding programme. In the current investigation, as shown in table 3, farmers' variety PMKK-232 (37.68%) showed maximum contribution in PC1, followed by PKKK-227 (30.92%) whereas PRRA-370 A and PKKKK-228 had no contribution. This makes two different groups. Similarly, FSAB-428 (27.41 %), followed by PKKKK-228 (15.78 %) had maximum influence in PC2. PMRA-502 (26.12 %) followed by PRRA-370 (15.49 %) showed greater influence than other genotypes. PATK-278 (33.06 %) had highest contribution in PC4. Therefore, these parents should be selected for exploiting variability. Since PC1 exhibited maximum variation, so the selection of farmers' varieties from PC1 may report to be more favourable.

Conclusion

Variability is the prerequisite for selection of superior traits and parents. Multivariate analysis acts as an aid to the process of selection indices. PC1, PC2, PC3 and PC4 contributed overall 78.68% of variance. DM, YP, WP, LP and NEN had maximum variability for the characters

which can be exploited to a greater extent. HI, DF50 and DM had positive correlation with YP whereas NSP, NPP and LP had negative association with YP. However, correlation and path coefficient analyses will give an accurate result. In regards to farmers' varieties, PMKK-232 and PKKK-227 should be selected in PC1 for further breeding programme. Similarly, FSAB-428 and PKKKK-228 in PC2; PMRA-502 and PRRA-370 in PC3 and PATK-278 in PC4 should be selected.

Table 1. Eigen value, percentage of variance and cumulative percentage of variance among principal components for farmers' varieties of pea.

Principal Components	Eigen value	Percentage of variance	Cumulative percentage of variance
PC1	3.88	35.27	35.27
PC2	2.44	22.18	57.46
PC3	1.33	12.12	69.58
PC4	1.00	9.10	78.68
PC5	0.87	7.87	86.55

Table 2. Variance present in each dimensions or principal components for individual characters of farmers' pea varieties.

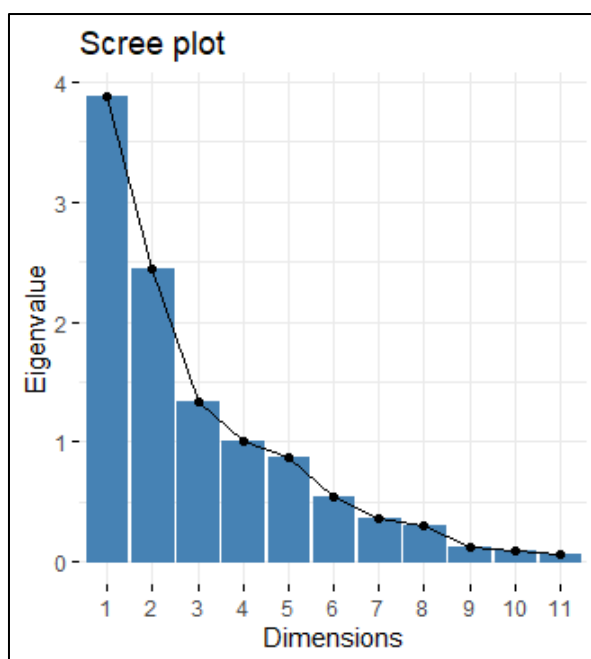
Characters	Dim.1	Dim.2	Dim.3	Dim.4
DF50	3.75	0.48	4.33	17.57
DM	22.16	0.02	1.39	0.02
PH	7.29	9.25	8.86	4.97
NPP	6.50	13.68	17.11	12.46
LP	19.16	0.71	0.10	3.92
WP	0.48	25.06	22.31	0.33
NEN	2.16	23.21	15.33	4.04
NSP	10.82	7.26	2.61	18.34
HI	3.14	12.66	3.30	28.71
100SW	10.22	6.66	0.00	7.35
YP	14.32	1.01	24.66	2.31

Table 3. Variance present in each dimensions or principal components for individual farmers' varieties of pea.

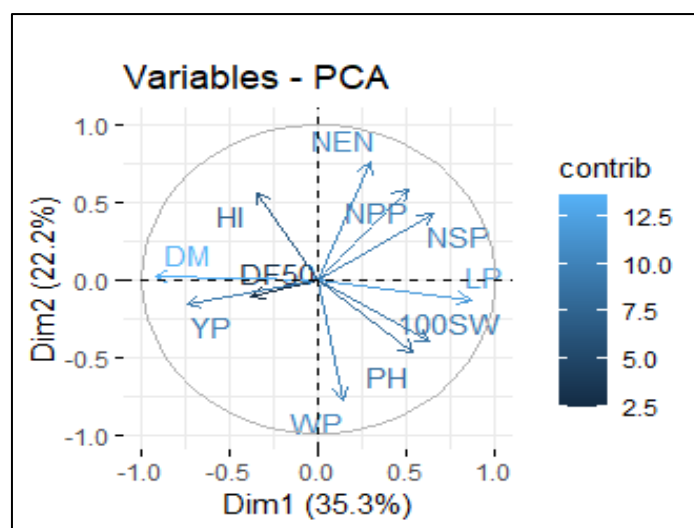
Farmers' pea varieties	Dim.1	Dim.2	Dim.3	Dim.4
PLCM-225	1.43	11.57	3.00	1.07
PSAB-309	5.33	0.50	3.26	1.66
PRRA-370	0.46	0.50	15.49	0.00
PRRA-370 A	0.00	4.52	11.30	0.79
PBCM-250	0.22	7.17	0.63	2.60
PSLM-226	0.10	0.43	2.89	0.17

FSAB-428	1.01	27.41	0.05	5.46
FAIV 425	0.11	0.01	0.47	0.79
PARB-223	3.17	0.85	0.71	10.44
PATK-278	6.56	4.99	9.00	33.06
PARA-308 (2)	3.07	1.20	0.20	8.47
PRBJ-229	0.49	0.28	2.53	6.56
PKKKK-228	0.00	15.78	0.00	2.75
PRAV-230	0.27	0.09	6.60	0.62
PAKA-230	0.36	11.65	0.39	4.59
PSAK-307	0.30	0.18	8.09	1.35
PSRA-358	0.48	1.12	0.09	3.75
PKKK-227	30.92	0.01	5.80	0.20
PMKK-232	37.68	0.31	3.36	1.00
PARB-223 A (3)	2.35	1.56	0.01	6.61
PARA-501	0.04	6.32	0.02	0.01
PMRA-502	5.63	3.55	26.12	8.06

Graph 1. Scree plot graph for principal components in farmers' pea varieties.



Graph 2. Graph between Dim1 and Dim2 for the traits of farmers' pea varieties under study.



Acknowledgment:

Authors are grateful to Chairman, Registrar and General at Registrar of Protection of Plant Varieties and Farmers' Rights Authority, Ministry of Agriculture and Farmers' Welfare, Government of India, for providing financial assistant to this project.

References

- Arif, U., Ahmed, M.J., Rabbani, M.A. and Arif, A.A. (2020) Assessment of genetic diversity in pea (*Pisum sativum* L.) landraces based on physico-chemical and nutritive quality using cluster and principal component analysis. *Pakistan Journal of Botany*, 52:1–6.
- Bhuvaneswari, S., Sharma, S.K., Punitha, P., Shashidhar, K.S., Naveenkumar, K.L. and Prakash, N. (2017) Evaluation of morphological diversity of field pea [*Pisum sativum* subsp. *arvense* (L.)] germplasm under sub-tropical climate of Manipur. *Legume Research*, 40 (2): 215-223.
- Bishnoi, R., Marker, S., Kumar, K.V.Y. and Taranum, S.A. (2021) Genetic Variability Parameters for Quantitative Traits in Farmers' Pea (*Pisum sativum* var. *arvense* L.) Varieties. *Biological Forum – An International Journal*, 13(4): 320-325.
- Bishnoi, R., Marker, S., Nayak, A.K., Basser, P., Mayank and Sharma, K.K. (2023) Morphological Characterization and Morphological Traits based Genetic Diversity Analysis of Farmer's Pea (*Pisum sativum* L.) Varieties of Uttar Pradesh using DUS Descriptors, as per PPV and FRA, 2001. *Legume Research*. 46(7): 830-836.
- Brondani, C., Borba, T.C.O., Rangel, P.H.N. and Brondani, R.P.V. (2006) Determination of genetic variability of traditional varieties of Brazilian rice using microsatellite markers. *Genetics and Molecular Biology*, 29(4): 501-504.
- Brush, S. (2004) *Farmers' Bounty: Locating Crop Diversity in the Contemporary World*. Yale University Press, New Haven and London.

Burdon, J.J., and Jarosz, A.M. (1990) “Disease in Mixed Cultivars, Composites, and Natural Plant Populations: Some Epidemiological and Evolutionary Consequences,” in H.D. Brown, M.T. Clegg, A.L. Kahler and B.S. Weir (eds.), *Plant Population Genetics, Breeding and Genetic Resources*. Sinauer Associates, Sunderland, MA, pp. 215–28.

Ceccarelli, S. (2012) “Landraces: Importance and Use in Breeding and Environmentally Friendly Agronomic Systems,” in N. Maxted et al. (eds.), *Agrobiodiversity Conservation: Securing the Diversity of Crop Wild Relatives and Landraces*, CAB International, Wallingford, UK, pp. 103–17.

Chandrashekar, S. and Vasudev, S. (2002) The Indian Plant Variety Protection Act Beneficiaries: The Indian Farmer or the Corporate Seed Company? *Journal of Intellectual Property Rights*, 07(6):506-515.

Kassambara, A., Mundt, F. (2017). Package “factoextra” for R: Extract and Visualize the Results of Multivariate Data Analyses. *R Package.Version*. 1-77.

Kumar, S., Soni, S., Kumar, H., Maurya, B.K., Singh, A.K., Singh, R.K. and Dwivedi, S.V. (2023) Assessment of genetic variability for agro-morphological traits of vegetable pea (*Pisum sativum* var. *hortense* L.) under Bundelkhand region. *Research Square*, doi: <https://doi.org/10.21203/rs.3.rs-2722419/v1>.

Parihar, A.K., Dixit, G.P., Pathak, V. and Singh, D. (2014). Assessment of the genetic components and trait associations in diverse set of Field pea (*Pisum sativum* L.) genotypes. *Bangladesh Journal of Botany*. 43(3): 323-330.

Pratap, V., Sharma, V., Kumar, H., Kamaluddin, Shukla, G., and Kumar, M. (2021) Multivariate Analysis of Quantitative Traits in Field Pea (*Pisum sativum* var. *arvense*). *Legume Research*. Doi:10.18805/LR-4604

R Core Team. (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

Vodouhe, R., A. Dansi, H.T. Avohou, B. Kpèki and F. Azihou (2011) Plant Domestication and its Contributions to In Situ Conservation of Genetic Resources in Benin. *International Journal of Biodiversity and Conservation*, 3(2): 40–50.