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Assessing Genetic Diversity and Agro-morphological Variation in Fieldpea Genotypes (*Pisum sativum* L.) using DUS Descriptors

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ABSTRACT

Background: DUS (Distinctness, Uniformity and Stability) characterization of crop varieties is essential for determining the novelty of a variety, ensuring phenotypic consistency across generations and verifying its stability in expression of traits over time. This process is integral to the protection of intellectual property rights and the regulation of seed certification.

Methods: One hundred fifty genotypes were evaluated using 20 agro-morphological DUS descriptors at three different locations in Haryana, India (Pulses Research Area, CCS HAU, Hisar, CCS HAU Rice Research Station, Kaul and KVK, Ambala) during the two years *i.e. Rabi* 2022-22 and 2023-24 (six environments) in Alfa-lattice design with three replications at each location.

Result: High magnitude of variability was observed among fieldpea genotypes for all the studied DUS traits except foliage waxy bloom, stipule rabbit eared stipules, type of stipule, days to 50% flowering and seed weight where single type of plant were observed. These descriptors remained stable across three locations (Hisar, Ambala and Kaul) and can be extremely useful for characterizing fieldpea genotypes. Stem anthocyanin coloration, stem colour, leaflets, flower colour, leaf axil colour, number of pod per axil, pod shape at distal end and seed surface displayed dimorphic variation while, foliage colour, seed shape and seed cotyledon colour exhibited tri-morphic variation and only pod curvature showed tetra-morphic variation. All the 150 genotypes were classified into five clusters, with the highest number of genotypes (63) in cluster III followed by cluster IV (44) and cluster V (22). Whereas, lowest number of genotypes were observed in cluster III (6) followed by cluster II (15).

Key words: Cluster, Distinctness, Fieldpea, Stability, Uniformity.

INTRODUCTION

Pulses are versatile and beneficial crops that support nutritional needs, economic stability, soil health, environmental sustainability, culinary diversity and economic stability. Their wide-ranging impact highlights their vital role in contemporary agriculture and global food systems, reinforcing their importance in ensuring food security and promoting sustainable farming practices. In particular, their ability to fix atmospheric nitrogen improves soil fertility, making them integral to eco-friendly and resource-conserving agricultural systems. Fieldpea, commonly referred to as Kapucijner pea, dun (grey-brown) pea, belongs to the *Fabaceae* family, *Faboideae* subfamily and *Fabeae* tribe. It is a diploid (2n=2x=14), predominantly a self-pollinated crop and thought to be the native of Ethiopia, the Mediterranean and Central Asia (Amit *et al.,* 2023a; Blixt, 1970). Fieldpea is an annual herbaceous plant with a robust tap root system, making it well-suited for dryland farming (Lenssen *et al.,* 2018). Its adaptability to marginal and stress-prone environments makes it a valuable legume in climate-resilient cropping systems (Sharma *et al.,* 2025).

Fieldpea, as being legume crop, is rich in protein (22.9%), carbohydrates (60.7%), ash (2.7%), fat (1.5%) and crude fiber (1.4%) with a caloric value of 343 kcal per 100 g (Duke, 1981). Like other crops, fieldpea is vulnerable to various abiotic and biotic stresses that significantly impact its sustainable production. As the population of world is increasing, so to meet out the demand of growing population there is need to increase the production and productivity of fieldpea. Their relatively low resource requirements also make them a sustainable option to ensure food security. Moreover, its inclusion in cereal-based systems improves nitrogen economy, reduces fertilizer inputs and enhances cropping system profitability (Parihar *et al.,* 2020; Sharma *et al.,* 2023). The effectiveness of a crop breeding program, for developing high-yielding varieties with specific traits, depends significantly on the accessibility of genetic resources and their effective utilization (Parihar *et al.,* 2022). Currently, the global repository of fieldpea germplasm, stored in the field/seed gene banks of different countries is about 98,000

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accessions which include various breeding lines, released varieties, mutants and wild species (Smýkal *et al.,* 2013 and Warkentin *et al.,* 2015).

Characterization and preliminary assessment constitute essential techniques that contribute to unraveling the scope and patterns of agro-morphological and molecular diversity within crop (Singh and Bhatt, 2012). The first step in categorizing crop germplasm involves morphological characterization (Amit *et al.,* 2025; Ghafoor *et al.,* 2003). Furthermore, a comprehensive understanding of genetic diversity is crucial for the effective management of gene banks and the strategic planning of experiments. To maintain, assess and utilize germplasm skillfully and effectively, a thorough examination of the extent of genetic diversity is imperative (Smith and Smith, 1989). DUS (Distinctness, Uniformity and Stability) descriptors encompass the morphological features of a plant, including traits such as size, shape, colour and other distinctive characteristics are employed as standardized criteria for this purpose (Rai *et al.,* 2024; Mondal *et al.,* 2014). More often than not the characters on which the breeders mull over to characterize the germplasm lines are not enough to distinguish them and are many a times influenced by environmental factors. Therefore, to differentiate different genotypes, stable and more reliable morphological descriptors, like DUS, are required. To support the aforementioned assertions, this research aimed to examine the DUS traits in both old cultivars as well as newly bred genotypes of fieldpea and to group them based on diversity.

MATERIALS AND METHODS

One hundred fifty genotypes were evaluated using 20 agro-morphological DUS descriptors at three different locations (Pulses Research Area, CCS HAU, Hisar, CCS HAU Rice Research Station, Kaul and KVK, Ambala) during the two years *i.e. Rabi* 2022-23 and 2023-24 (six environments) in Alfa-lattice design with three replications at each location. All the studied genotypes were arranged in 15 blocks, with each block containing 10 genotypes and each line representing a single genotype with spacing of 45 cm × 10 cm. DUS (distinctness, uniformity and stability) testing guidelines, established by PPV and FRA (2001), Government of India, were employed to evaluate all these genotypes based on morphological traits. All these descriptors were observed at various stages of plant growth by visual observation of a group of plants or plant parts at a specific stage of the crop at all six environments.

The ordinal scale data of morphological characters was transformed into binary characters as per method of Sneath and Sokal (1973) that were reflecting the variations present in each trait. Hierarchical cluster analysis (HCA) based on the Average Linkage Between Groups Method, often called UPGMA (Unweighted Pair-Group Method using Arithmetic Averages) along with Euclidean distances, was employed for estimating the genetic divergence among the studied fieldpea genotypes.

RESULTS AND DISCUSSION

DUS traits based variability analysis

In the present study, an ample amount of variability was observed across almost all the examined traits, including stem anthocyanin coloration, stem colour, presence or absence of leaflets, flower colour, leaf axil colour, pod number per axil, pod shape at the distal end and seed surface, all of which displayed dimorphic variation. Foliage colour, plant height, seed shape and seed cotyledon colour exhibited tri-morphic variation, while only pod curvature showed tetra-morphic variation (Fig 1). Foliage waxy bloom, stipule rabbit eared stipules, type of stipule, days to 50% flowering and seed weight in all genotypes, indicated no variation, which makes these less useful descriptors for grouping of genotypes. Similar results were obtained by Tun *et al.* (2020); Srilatha *et al.* (2022); Bishnoi *et al.* (2023) and Anand *et al.* (2024). They observed variation for various traits *viz.,* stem anthocyanin coloration, seed surface, seed cotyledon colour, number of pod per axil, foliage colour and seed cotyledon colour in fieldpea. These descriptors remained stable across three locations (Hisar, Ambala and Kaul) and can be extremely useful for characterizing fieldpea genotypes. Similarly, variation in stem anthocyanin coloration, leaflets, flower colour, leaf axil colour, pod number per axil, pod shape at the distal end, seed surface, foliage colour, seed shape and seed cotyledon colour were also observed by Yadav and Ravika (2014) and Anand *et al.* (2024). Table 1 displays the scoring of the twelve DUS descriptors that exhibited variation.

Stem anthocyanincolouration

At the initiation of the first flower, a visual assessment was performed to ascertain stem colourand the presence or absence of anthocyanin pigment in the stem. Among the 150 genotypes studied, 128 (85.33%) genotypes showed no anthocyanin colouration in the stem (green stem colour), while the remaining 22 (14.67%) demonstrated anthocyanin colouration (purple stem colour).

Foliage colour

On the basis of foliage colour, fieldpea genotypes were categorized into three groups *viz.,* light green, green and dark green. Scrutiny during the initiation of first flower by observing of a group of plants, it was found that out of total 150 genotypes, 28 (18.67%) genotypes were having light green foliage colour, 86 (57.33%) green and 36 (24.00%) dark green.

Leaf descriptors

Since photosynthesis and transpiration primarily take place in the leaf, so, it is crucial to consider leaf characteristics when assessing a crop plant's production potential. Leaf descriptors include leaf, leaflets and leaf axil colour. The visual evaluation of leaflets and leaf axil colour was observed during initiation of first flower and it was observed that in 20 genotypes (13.33%) leaflets were absent and in 130 leaflets (86.67%) were present. Whereas, it was found

that out of 150 genotypes, 131 (87.33%) showed no anthocyanin colouration in the leaf axil, while the remaining 19 (12.67%) displayed anthocyanin colouration in the leaf axil.

Flower colour

Flower colour is used as a consistent morphological marker to distinguish fieldpea genotypes. The colour of standard petal of flower is categorized as either white, blue, pink, red or purple as per DUS descriptors. The purple colour of the pea is due to the accumulation of anthocyanins, while the white pea flowers lack these pigments. In our investigation, on visual assessment at initiation of first flower, most of the genotypes (144 *i.e.* 96.0%) exhibited white coloured standard petal and only 6 (4.0%) genotypes exhibited purple coloured standard petal.

Pod descriptors

Pod descriptors are crucial for the morphological characterization of genotypes, as they help in identification and are key indicators of yield potential and other agronomic traits. In the current study only single (31

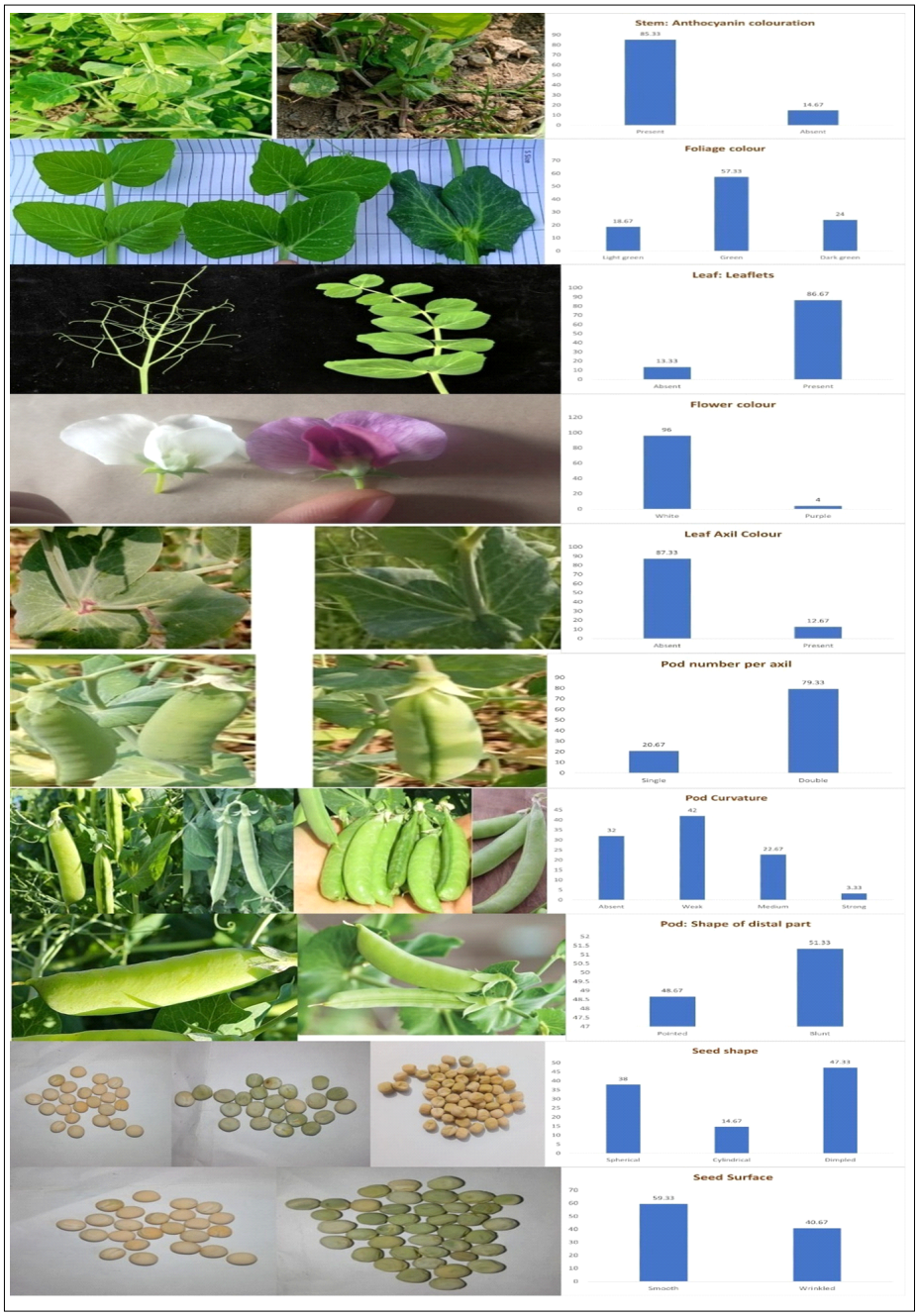


Fig 1: Depiction of variation and their frequency found in DUS descriptors of fieldpea.

Table 1: Scoring of twelve diverse DUS descriptors in 150 field pea genotypes.

Genotypes	Stem: Anthocyanin colouration	Stem colour	Foliage colour	Leaf leaflets	Flower colour	Leaf: Axil colour	Pod number per axil	Pod curvature	Pod: Shape of distal part	Plant height	Seed: Shape	Seed cotyledon colour	Seed surface
Aman	1	1	5	1	1	1	1	3	9	7	3	7	1
DMR-7	1	1	7	9	1	2	2	3	9	7	3	3	2
HFP 1024	1	1	5	9	1	2	2	5	9	7	1	7	1
HFP 1104	1	1	5	9	1	1	1	5	1	7	2	3	1
HFP 1107	1	1	3	9	1	1	1	1	1	7	3	5	2
HFP 1120	1	1	5	9	1	1	1	5	1	7	3	5	2
HFP 1129	1	1	5	9	1	2	2	3	1	7	1	3	1
HFP 1130	1	1	7	9	1	2	1	5	9	7	3	5	2
HFP 1132	1	1	5	9	2	1	2	3	1	7	1	3	1
HFP 1137	1	1	7	1	1	1	1	7	1	5	1	3	1
HFP 1140	1	1	7	9	1	1	2	3	1	7	1	7	1
HFP 1201	1	1	5	9	1	2	1	3	9	3	3	5	2
HFP 1302	9	9	3	1	1	1	2	3	9	5	3	3	2
HFP 1306	1	1	5	1	1	1	2	3	9	5	2	7	1
HFP 1314	1	1	5	9	1	1	2	3	9	7	3	5	2
HFP 1315	1	1	5	9	1	1	2	3	9	7	3	5	1
HFP 1405	1	1	7	9	1	1	1	3	1	7	3	5	2
HFP 1425	1	1	7	1	1	1	2	3	9	5	3	3	2
HFP 1426	1	1	7	1	1	1	2	7	1	5	2	5	2
HFP 1428	1	1	7	9	1	1	2	5	1	3	3	7	2
HFP 1463	1	1	7	9	1	1	2	5	1	5	3	5	2
HFP 1545	1	1	5	9	1	1	2	3	9	5	3	5	2
HFP 1574	9	9	3	9	1	1	2	3	9	5	1	3	1
HFP 1602	1	1	5	9	1	2	2	5	9	7	1	3	1
HFP 1607	1	1	7	1	1	1	2	1	1	5	3	5	2
HFP 1702	1	1	3	9	1	1	2	5	9	7	3	3	1
HFP 1709	1	1	5	1	1	1	2	1	9	3	1	7	1
HFP 1711	1	1	5	9	1	1	2	5	9	5	3	3	2
HFP 1809	1	1	5	9	1	1	1	1	9	7	2	7	1
HFP 1811	1	1	5	9	1	1	2	3	1	7	2	3	1
HFP 1817	9	9	5	9	1	1	2	5	1	7	2	5	2
HFP 9907B	1	1	5	9	1	1	1	1	1	7	3	5	2
HFP 0110	1	1	5	9	1	1	2	5	1	7	3	3	2
HFP 0130	1	1	7	9	1	1	1	5	9	7	3	3	2
HFP 0145	1	1	5	9	1	2	2	5	1	7	1	3	1
HFP 0149	1	1	5	9	2	1	2	1	9	7	1	3	1
HFP 2008	1	1	5	9	1	1	2	1	9	7	1	5	1

Table 1: Continue....

Table 1: Continue....

HFP 920	1	1	7	9	1	1	2	3	9	5	1	5	1
HFP 9426	9	9	3	9	1	1	2	3	9	7	3	5	2
HFP 9907A	1	1	5	1	1	1	1	1	1	7	3	5	2
HUDP 1301	1	1	5	9	1	1	2	1	9	5	3	3	2
HUDP 1302	1	1	5	9	1	1	2	1	9	5	3	3	2
HUDP 1711	1	1	5	9	1	1	1	3	9	7	3	5	2
HUDP 1715	1	1	7	9	1	1	2	3	9	7	1	7	1
HUDP 1802	1	1	5	9	1	1	2	3	9	7	1	3	1
HUPT 1701	1	1	3	9	1	1	2	3	9	7	2	3	1
HUPT 1709	1	1	3	1	1	1	2	5	1	7	3	3	2
HUTP 1705	1	1	7	1	1	1	1	3	9	7	1	3	1
IPF 11-13	1	1	3	9	1	1	2	5	9	7	1	5	1
IPF 11-15	9	9	5	9	1	1	2	3	9	7	2	7	2
IPF 17-18	1	1	5	9	1	2	2	7	9	7	1	5	1
IPF 17-19	1	1	5	9	1	1	2	3	9	7	1	5	1
IPF 19-11	1	1	3	9	1	1	2	1	1	7	1	7	1
IPF 19-18	9	9	5	9	1	1	1	3	9	7	1	7	1
IPF 20-11	1	1	5	9	1	1	2	1	9	7	1	7	1
IPF 20-21	1	1	5	9	1	1	2	5	1	7	2	3	1
IPF 21-13	9	9	5	9	1	2	2	5	1	7	1	7	1
IPF 21-16	1	1	3	9	1	1	2	1	1	7	3	3	1
IPF 21-21	9	9	3	9	1	1	2	1	1	7	2	3	1
IPF 5-19	1	1	7	9	1	1	1	3	9	7	1	3	1
IPFD 13-2	1	1	5	9	1	1	2	1	9	7	3	3	1
IPFD 17-2	1	1	5	9	1	1	1	1	1	5	3	3	2
IPFD 17-6	1	1	7	9	2	1	2	1	1	5	1	7	1
IPFD 18-3	9	9	5	1	1	1	1	5	1	5	3	3	2
IPFD 19-1	1	1	5	9	1	1	2	1	1	7	1	7	1
IPFD 19-15	1	1	7	9	1	1	2	3	1	7	3	3	2
IPFD 19-3	1	1	5	1	1	1	2	5	9	3	1	3	1
IPFD 19-9	1	1	3	1	1	1	2	1	9	7	1	5	1
IPFD 20-3	1	1	3	9	1	1	2	3	1	7	3	3	1
IPFD 20-9	1	1	5	9	2	1	2	3	9	5	3	5	1
IPFD 21-4	1	1	3	9	1	1	2	3	1	3	1	7	1
IPFD 21-5	1	1	7	9	1	1	2	1	9	7	1	3	1
IPFD 21-7	1	1	3	9	1	2	2	3	9	7	3	3	2
KPF 1024	1	1	5	9	1	1	2	5	9	7	3	7	2
KPF 115	1	1	5	9	1	1	2	1	1	7	3	3	1
KPF 14-29	1	1	5	9	1	1	2	3	9	7	3	3	2
KPF 14-35	1	1	5	9	1	1	1	1	9	3	1	7	1

Table 1: Continue....

Table 1: Continue....

KPF 14-36	9	9	5	9	1	1	2	1	1	7	1	3	1
KPF 14-64	1	1	7	9	1	1	2	1	1	7	3	3	2
KPF 432	1	1	5	9	1	1	2	1	9	7	1	3	1
KPMR 745	9	9	3	9	1	1	2	1	1	7	3	5	2
KPMR 851	1	1	7	9	1	1	2	1	1	7	3	5	2
KPMR 890	1	1	7	9	1	2	2	3	1	7	2	3	1
KPMR 910	1	1	5	9	1	1	2	1	1	7	1	7	1
KPMR 937	1	1	5	9	1	1	2	3	9	7	3	3	2
KPMR 942	1	1	3	9	1	1	2	3	9	7	2	7	1
KPMR 954	1	1	3	9	1	2	2	1	1	5	2	7	1
KPMR 957	1	1	7	9	1	1	2	3	1	7	2	3	1
NDP 11-101	1	1	7	9	1	2	1	3	1	5	1	7	1
NDP 11-102	1	1	5	9	1	1	2	5	1	7	1	7	1
NDP 2018-3	9	9	3	9	1	1	2	1	1	7	1	3	1
NDPD 2017-06	1	1	5	9	1	1	1	1	9	5	3	3	2
Pant P 250	1	1	5	1	1	1	2	5	1	7	3	3	2
Pant P 402	1	1	5	1	1	1	1	3	1	7	3	3	1
Pant P 42	1	1	3	9	1	1	2	3	1	7	1	3	1
Pant P 479	1	1	7	9	1	1	2	3	9	7	2	3	1
Pant P 484	1	1	7	1	1	1	2	3	1	5	2	3	1
Pant P 508	1	1	5	9	1	1	2	5	1	7	1	3	1
Pant P 509	1	1	7	9	1	1	2	1	1	7	3	3	2
Pant P 514	1	1	5	9	1	1	2	1	9	7	1	3	1
Pant P 516	1	1	5	9	1	1	2	1	9	7	3	5	2
Pant P 517	1	1	5	9	1	1	2	3	1	7	3	3	1
Pant P 523	1	1	3	9	1	1	1	1	1	7	1	3	1
Pant P 74	1	1	5	9	1	1	2	1	1	5	1	3	1
Pant P-125	9	9	5	9	1	1	2	5	1	7	3	7	2
Pant P-180	1	1	3	1	1	1	2	1	9	7	1	3	1
Pant P-184	1	1	5	9	1	1	2	3	9	7	2	7	1
Pant P-186	9	9	7	9	1	1	2	3	9	7	2	7	1
Pant P-207	1	1	5	9	1	1	2	3	9	7	3	7	1
Pant P-215	1	1	5	9	1	1	2	3	9	5	3	5	2
Pant P-347	1	1	5	9	1	1	2	3	1	7	3	5	2
Pant P-365	1	1	5	9	1	1	2	3	9	5	1	7	1
Pant P-367	9	9	7	9	1	1	2	3	1	7	3	7	1
Pant P-375	1	1	3	9	2	2	2	3	9	7	3	5	2
Pant P-38	1	1	5	1	1	1	2	3	9	5	3	3	2
Pant P-397	1	1	7	9	1	1	2	3	9	7	3	7	2
Pant P-399	1	1	5	9	1	1	2	3	9	7	3	7	2

Table 1: Continue....

Table 1: Continue....

Pant P-42	1	1	5	9	1	1	1	1	9	5	2	3	1
Pant P-449	1	1	7	1	1	1	1	1	9	7	3	3	2
Pant P-455	9	9	7	9	1	1	2	7	1	7	1	3	1
Pant P-462	1	1	7	9	1	1	1	5	1	7	1	3	1
Pant P-473	1	1	5	9	1	1	2	5	1	7	3	3	2
Pant P-474	1	1	5	9	1	1	1	3	9	7	3	5	2
Pant P-479	1	1	5	9	1	1	2	5	1	7	3	5	2
Pant P-484	1	1	7	9	1	1	2	1	1	7	3	3	2
Pant P-498	1	1	5	9	1	2	1	5	1	7	2	3	2
Pant P-501	1	1	7	9	1	1	2	3	9	7	1	3	1
PMR 935	9	9	5	9	1	1	2	3	1	7	1	7	1
RFFG 170	9	9	5	9	1	1	2	1	1	5	3	7	2
RFP 11-09	1	1	3	9	1	1	2	1	1	5	3	5	2
RFP 2009-02	9	9	5	9	1	1	2	1	9	7	2	3	2
RFP 2010-11	1	1	5	9	1	1	2	3	9	7	1	7	1
RFP 2010-21	1	1	5	9	1	1	2	5	1	7	3	7	1
RFP 2011-1	1	1	5	9	1	1	1	3	9	7	1	3	1
RFP 2011-1	1	1	7	9	1	2	2	1	9	5	3	7	2
RFP 2012-122-1	1	1	5	9	1	1	2	1	9	7	3	5	2
RFP-72	1	1	5	9	1	1	2	3	1	7	2	7	1
RFPG 112	1	1	3	9	1	1	2	1	9	7	1	3	1
RFPG 114	1	1	3	9	1	2	2	3	9	5	3	5	2
RFPG 180	1	1	5	9	2	1	1	3	9	7	3	5	2
RNCP 14-13	9	9	5	9	1	1	2	1	9	7	1	7	1
RPFG 144	9	9	3	9	1	1	2	5	1	7	3	5	2
SKAU-P-17	1	1	5	9	1	1	2	1	1	7	1	7	1
SKVAP-8	1	1	3	9	1	1	2	5	1	7	1	7	1
SPC 101	1	1	5	9	1	1	2	3	9	7	3	5	1
VL-55	1	1	5	9	1	1	2	3	1	5	3	5	1
VL-56	1	1	5	9	1	2	2	5	1	5	1	3	1
VL-66	1	1	5	9	1	2	2	5	1	7	1	3	1
VL-67	9	9	5	9	1	1	2	5	9	7	1	3	1
WBFP-14-5-9	1	1	7	9	1	1	1	7	1	7	1	3	1
State and note			LG=3					A=1		So=3	Sp=1	Cr =3	
	A=1	G=1	G=5	A=1	W=1	G=1	S=1	We=3	Po=1	Md=5	Cy=2	G=5	Sm=1
	P=9	Pr =9	DG=7	P=9	P=2	Pr = 2	D=2	M=5	Bt=9	Lo=7	Dim =3	Y=7	Wr=7
								St=7					

A = Absent, P = Present, G = Green, Pr = Purple, LG = Light green, DG = Dark green, W =White, S = Single, D = Double, We= Weak, M = Medium, St = Strong, Po = Pointed, Bt = Blunt, So = Short, Md = Medium, Lo = Long, Sp = Spherical, Cy = Cylindrical, Dim = Dimpled, Cr = Creamy, Y = Yellow, Sm = Smooth, Wr = Wrinkled.

genotype) and double (119 genotype) pods per axil were found, with frequencies of 20.67% and 79.33%, respectively. Whereas, pod curvature, at fully developed green pod, exhibited significant diversity, dividing the 150 fieldpea into four clear categories *viz.,* absent, weak, medium and strong, with frequency of 48 (32%), 63 (42%), 34 (22.67%) and 5 (3.33%), respectively. Further, the shape of distal part of the pods was observed as pointed or blunt. In this study, among the 150 fieldpea genotypes, 73 genotypes (48.67%) had pointed distal end shape of pods, while the remaining 77 genotypes (51.33%) had blunt.

Plant height

It's an important descriptor which classifies fieldpea in dwarf, medium and tall types. It has played a key role in overall improvement in productivity of fieldpea which was mainly achieved through conventional breeding for tailoring short plant height type which were lodging resistant (Parihar *et al.,* 2022). In our study out of 150 genotypes, six genotypes (4.0%) were observed with short, 38 (25.33%) with medium and 112 (74.67%) with tall height.

Seed descriptors

The acceptance of premium fieldpea genotypes by consumers and the determination of their prices are influenced by various seed descriptors. Seed coat color, seed shape and seed dimpling are the major components of visual seed quality. Usually creamish, spherical shaped smooth seeds without dimples are preferred. On the basis of seed shape, out of 150 genotypes, 57 (38.00%) genotypes exhibited spherical seed shape, while 22 (14.67%) genotypes showed cylindrical and remaining 71 (47.33%) were categorised as dimpled seed shape. As far as seed cotyledon colour is considered, 72(48.00%) genotypes had creamy, while 38(25.33%) had green and 40 (26.67%) had yellow seed cotyledon colour. Furthermore, surface of seed either smooth or wrinkled was visualized by observing a number of mature seed. Out of total 150 genotypes 89 (59.33%) genotypes were classified as smooth, while 61(40.67%) had wrinkled seed surface. A similar study on seed descriptor was reported by Bishnoi *et al.* (2023) and Anand *et al.* (2024) in fieldpea.

Diversity analysis using DUS descriptors

Genetic divergence analysis is a crucial technique in plant breeding that assesses the variation among different genetic lines or varieties within a species. This analysis helps to identify the extent of genetic differences, which can be vital for selecting diverse parental lines for hybridization. In the present study, Hierarchical Cluster Analysis (HCA) based on the Average Linkage Between Groups Method, often called UPGMA (Unweighted pair-group method using arithmetic averages) along with Euclidean distances, was employed for estimating the genetic divergence among the studied fieldpea genotypes. The 150 fieldpea genotypes were grouped into five clusters based on their genetic divergence which are presented in Table 2 and Fig 2. The maximum number of genotypes were grouped into Cluster I (63 genotypes) followed by cluster IV (44) and cluster V (22). Whereas, lowest number of genotypes were observed in cluster III (6) followed by cluster II (15).

This suggests that genotypes from these clusters may be used as parents for hybridization programs to develop desirable types, as crosses between genetically divergent lines will generate heterotic segregants (Amit *et al.,* 2023b).

Table 2: Cluster wise grouping of fieldpea genotypes based on DUS descriptors.

Cluster	No. of genotypes	Name of genotypes
1	63	Aman, HFP 1104, HFP 1107, HFP 1120, HFP 1137, HFP 1306, HFP 1314, HFP 1405, HFP 1425, HFP 1426, HFP 1428, HFP 1463, HFP 1545, HFP 1607, HFP 1709, HFP 1711, HFP 1809, HFP 9907B, HFP0110, HFP0130, HFP9907A, HUDP 1301, HUDP 1302, HUDP 1711, HUPT 1709, HUTP 1705, IPF 5_19, IPFD 17_2, IPFD 19_15, IPFD 19_3, IPFD 19_9, IPFD 21_4, KPF 1024, KPF 14_29, KPF 14_35, KPF 14_64, KPMR 851, KPMR 937, KPMR 954, NDP 11_101, NDPD 2017_06, Pant P 250 , Pant P 402, Pant P 484, Pant P 509, Pant P 516, Pant P 523, Pant P_180, Pant P_215, Pant P_347, Pant P_38, Pant P_397, Pant P_399, Pant P_42, Pant P_449, Pant P_462, Pant P_473, Pant P_474, Pant P_479, Pant P_484, RFP 2011_11, RFP 2012_122_1, WBFP_14_5_9
2	15	DMR_7, HFP 1024, HFP 1129, HFP 1130, HFP 1201, HFP 1602, HFP0145, IPF 17_18, IPFD 21_7, KPMR 890, Pant P_498, RFP 2011_1, RFPG 114, VL_56, VL_66
3	6	HFP 1132, HFP0149, IPFD 17_6, IPFD 20_9, Pant P_375, RFPG 180
4	44	HFP 1140, HFP 1315, HFP 1702, HFP 1811, HFP2008, HFP920, HUDP 1715, HUDP 1802, HUPT 1701, IPF 11_13, IPF 17_19, IPF 19_11, IPF 20_11, IPF 20_21, IPF 21_16, IPFD 13_2, IPFD 19_1, IPFD 20_3, IPFD 21_5, KPF 115, KPF 432, KPMR 910, KPMR 942, KPMR 957, NDP 11_102, Pant P 42, Pant P 479, Pant P 508, Pant P 514, Pant P 517, Pant P 74, Pant P_184, Pant P_207, Pant P_365, Pant P_501, RFP 11_09, RFP 2010_11, RFP 2010_21, RFP_72, RFPG 112, SKAU_P_17, SKVAP_8, SPC 101, VL_55
5	22	HFP 1302, HFP 1574, HFP 1817, HFP9426, IPF 11_15, IPF 19_18, IPF 21_13, IPF 21_21, IPFD 18_3, KPF 14_36, KPMR 745, NDP 2018_3, Pant P_125, Pant P_186, Pant P_367, Pant P_455, PMR 935, RFFG 170, RFP 2009_02, RNCP 14_13, RPFG 144, VL_67

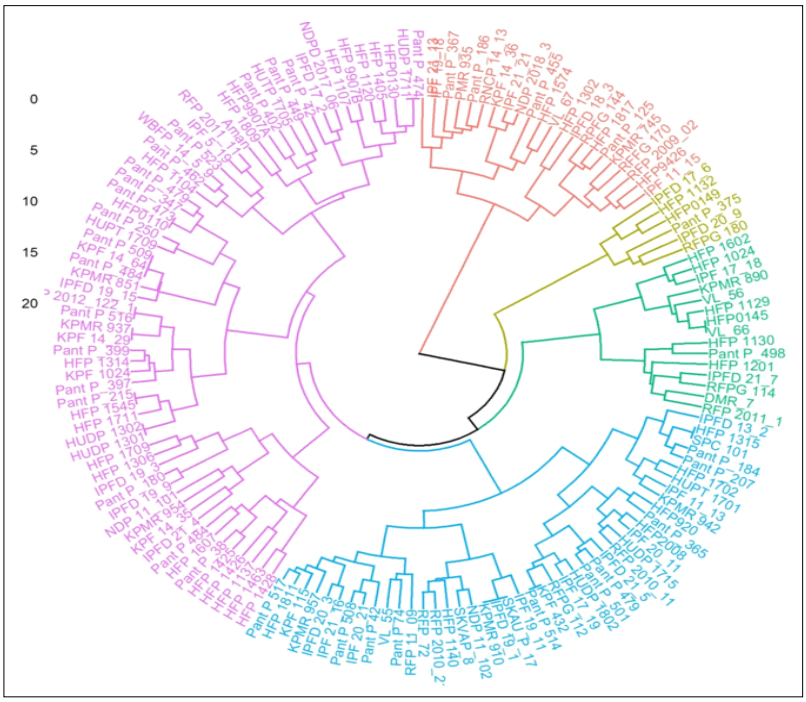


Fig 2: Dendrogram depicting distribution of 150 fieldpea genotypes into five distinct clusters.

Previous studies of Shrestha *et al.* (2023) and Bishnoi *et al.* (2023) have also reported the grouping of pea genotypes into four and five clusters respectively.

CONCLUSION

Morphological characterization is crucial for obtaining essential information about a genotype and for determining its genetic purity. The Protection of Plant Varieties and Farmers' Rights Authority (PPV and FR) requires the characterization and registration of both existing and new plant varieties, including those developed by farmers, as a part of national and botanical resources conservation. In the present study, an ample amount of variability was observed across almost all the traits examined, including stem anthocyanin coloration, stem colour, leaflets, flower colour, leaf axil colour, number of pod per axil, pod shape at the distal end and seed surface, which displayed dimorphic variation. Foliage colour, seed shape and seed cotyledon colour exhibited tri-morphic variation while, only pod curvature showed tetra-morphic variation. Overall, current DUS characterization of fieldpea genotypes can serve as a valuable reference for future breeding programs, aiding in the identification and classification of distinct genotypes based on specific traits.

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Data availability statement

All data relevant to the manuscript are provided within the text.

Conflict of interest

The authors declare no conflicts of interest.

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