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RESEARCHARTICLE

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Unveiling Genetic Diversity in Pea: Characterization and Selection of Promising Genotypes for Pea Breeding

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Abstract

Peas (*Pisum sativum* L.) are the second most significant crop in pulses. It is model crop with rich genetic research history dating back to father of genetics, Gregor J. Mendel's work. It is consumed as green and dry peas in various regions around the globe. It is an excellent source of proteins, anti-oxidants, and fiber. Due to changes in climatic conditions yield of pea varieties has decreased in previous years. So, it is necessary to evaluate genetic diversity present in existing pea accessions and to search for various pea genotypes having the potential for changing climatic conditions. For this reason, twenty pea genotypes were field-tested using RCBD during 2022-23. After the vegetative stage, data was collected for traits like plant height, days to 50% flowering, length and width of the pods, pods per plant, 100-seed weight, seed diameter, number of seeds per pod and yield. Significant variation among the studied accessions for all the traits were shown by ANOVA. Most of the traits exhibited high heritability coupled with high genetic advance, indicating that these traits were governed by additive gene action. Hence hybridization and selection would be fruitful for these traits. Whereas, pod width showed low values of heritability and genetic advance. For all the studied traits magnitude of phenotypic coefficient of variance was greater than genotypic coefficient of variance, which revealed that these traits had additive environmental effect. According to correlation analysis, pod width showed no significant correlation with any other trait studied. Yield was largely attributed to plant height and seed diameter. PGRI-42 and PGRI-44 were observed to be most diverse genotypes in terms of studied morphological traits. Whereas, V20 and 19723 were almost genetically similar. This study would assist in selecting genotypes with a varied genetic background for use in future pea breeding programs.

KEYWORDS
Genetic diversity, Heritability, Correlation, Pea breeding, Morphological traits

1 | INTRODUCTION

Pea (*Pisum sativum* L.) is a cool-weather crop (2n=2x=14) with genome size approximately 4.45gb (Smykal et al. 2012). It is the second most important vegetable crop in legume family after common bean. It is model crop with rich genetic research history dating back to father of genetics, Gregor J. Mendel's work (Kumari et al. 2013). Pea is classified into two categories *P. fulvum* and *P. elatius* (wild peas) whereas *P. sativum* and *P. abyssinicum* (cultivated peas). Pea is the annual herbaceous plant with climbing or bushy type growing habit, which is grown worldwide for its edible pods or seeds. It is predominantly self-pollinated crop with high nutritive value. Pea crop is considered among the early crops cultivated by man. Area of Fertile Crescent is considered as the center of diversity of the crop. Pea is extensively used because it is enriched with essential amino acids particularly lysine and cheap source of proteins and other nutrients.

Pea belongs to the group of crops that are considered eco-friendly because of their nitrogen fixing ability, in this way it can reduce the use of nitrogen fertilizers and improves the soil health (Anglade et al.

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2015). Pea fits well in intensive agriculture due to its shorter growing season and ability to grow under water deficit conditions. Regardless of its high economic value productivity of pea remained low. In Pakistan during 2020-21 pea was cultivated over 6444 hectares with 5.47 million tons production (FAO, 2021). Due to prevailing climatic conditions, different biotic and abiotic stresses productivity of pea have declined during past years. Due to urbanization area under the cultivation is shrinking day by day as result of which annual yield is decreasing. Due to lesser genetic diversity in gene pool, breeding approaches are facing difficulties. By 2050 human population on the earth will increase up to 9.7 billion as predicted by the food and agriculture organization. Our crop production sector mainly depends on particular selected varieties under different environmental conditions resulting exposure to climate change impacts like disease and pest spreading (Govindaraj et al. 2015). The changing climatic conditions are putting even greater pressure on selection of natural plant population. Food security is considered to be dependent upon the genetic diversity, yet importance of genetic diversity for natural population attracts lesser attention. Even during the early history of plant breeding, natural genetic diversity and variations among the cultivated populations was used as a tool for improving cultivars. Distinctive traits regarding resilience to changing climatic conditions can be found through genetically diverse populations.

Total germplasm containing 98 thousand accessions of pea have been preserved worldwide. A lot of work has been done to study wild and cultivated pea genotypes using morphological traits, molecular approaches and biochemical assays. To explore genetic diversity molecular markers have been very useful in determining the relationship among various genotypes (Smykal et al. 2008).

To fulfil the growing needs of the protein, it is important to increase the yield of protein crops in the region. Although soybean is one of the basic plant-based protein sources but widespread adaptability of pea across different agro-climatic zones make it economically favorable crop to be grown as protein source. Protein contents in the pea ranges from 16% to 31% (Lam et al. 2018). Moreover, unlike soybean it is not allergen and it can be consumed directly without any heat treatment and processing. Intercropping of pea with other crops is being carried on in some regions to utilize minimum natural resources. Peas also improve the yield of successor crop as they improve the health of the soil by providing nitrogen to the soil through symbiotic associations in the root region. Wider adaptability of pea under different climatic conditions makes it favorable crop to be used as forage where good yield is not obtained. So, it can be used as a multipurpose, crop in various agriculture systems.

Pea breeder aims to develop varieties that are high yielding, different maturing types, high in protein content, rich in essential amino acids, resistant to bacterial and fungal diseases. Genetic variability plays an important role in the selection of plants with desired traits.

Distinctive parents can be selected for successful breeding program by using biometrical methods of genetic diversity. Assessment of genetic variability is crucial in finding the source of the desirable character within the range of available germplasm. Understanding of similarity and dissimilarity among the genotypes is helpful to study the variability.

There is further need of harnessing the genetic variability present in the pea germplasm using molecular markers. Because molecular markers are precise and efficient tool for identification and evaluation of variation in the germplasm. Parental lines can be selected using different molecular markers. Genetic marker map was constructed using single nucleotide polymorphism and 37 new markers were identified (Deulvot et al. 2010). A number of studies have reported variability, marker-trait association and phylogenetic relationship among different pea genotypes using Amplified Fragment Length Polymorphism (AFLP) markers (Dyachenko et al. 2014).

The foremost goal of a plant breeder is to maximize the yield by improving production and allow widespread cultivation of pea in various agro-climatic zones. Yield is a complicated trait as it is based upon genotype, environment and their interaction, this trait is inherited quantitatively. A number of studies have confirmed that seed yield and yield associated characters are highly affected by genotype, environment and their interaction (Bocianowski et al. 2019). Genetic variability is prerequisite for improving yield or other characters as it provides a source of new combination of genes to adapt the plant in changing environmental conditions. Nature has dispersed all the genes that are beneficial for the survival of a specie on this ever-changing planet. Plant breeder just needs to find out the specific genes and utilize it for desired trait. Wild species are rich in diversity providing useful characters to be used in breeding program. In order to improve the yield of pea there is dire need to access the genetic diversity present in germplasm.

For improving yield and productivity of pea, association among different yield related traits must be understood. Because any negative association between yield and yield related traits may result in the genetic slippage. An understanding of associative characters can provide information to the breeder for effective selection of plants. Positively correlated and highly heritable traits are considered most affective for improving yield of peas (Georgieva et al. 2015).

The objectives of this study were to access the phenotypic diversity in available pea germplasm for

enriching the breeding collection of pea germplasm and character association between yield and other traits.

2 MATERIALS AND METHODS

Experimental Site

The current study was carried out in experimental fields of department of Plant Breeding and Genetics at University of Agriculture, Faisalabad during 2022-2023. Faisalabad is sited 186 m above sea level and positioned 73.13° on east longitude and 31.45° on north latitude. Faisalabad has high rate of evapotranspiration with arid climate and it also encompass flat plains of the Ravi and Chenab River in Punjab.

Experimental Material

Twenty pea (*Pisum sativum* L.) accessions were grown under the field conditions. These accessions were collected from National Agricultural Research Centre (NARC) Islamabad and Vegetable Research Institute (VRI) Faisalabad.

Experimental Layout

Seeds of genotypes were sown in randomized complete block design replicated twice, keeping the plant-to-plant distance 10 cm and row spacing 30 cm during December 2022. From crop sowing to crop harvesting, all recommended agronomic practices were implemented. Seeds were sown 3 cm deep in the soil on the sides of the beds. Width of beds were 1.5 meter each. Recommended dose of NPK fertilizers were applied in the ratio of 35:35:25 kilogram per acre. Field was irrigated regularly once a week and at the time of flower initiation and pod setting stage. Weeds were eradicated on weekly basis by hands. Four plants from each replication were taken for data collection. Data of the following parameters were collected.

Days to 50% Flowering

Data for days to 50% flowering were recorded by counting the days from the sowing to the date when half of the plants produced flowers in each replication for each genotype. Data were recorded as average of the genotype.

Plant Height (cm)

Plant height was measured at peak growth of plant, following that the color turned from green to brown. Plant height was measured from the base of a plant to the tip by using a meter rod. Plant height was measured from the five selected plants in each replication of each genotype. The arithmetic mean of five plants in each replication for each genotype was recorded as final plant height.

Number of Pods per Plant

The number of pods per plant were counted on selected plants at maximum growth in each replication for each genotype. The average number of pods per plant was recorded for each genotype. Data for the number of pods per plant was collected by counting the pods produced on a selected plant. Data were further computed by taking average values.

Pod Length (cm)

A measuring ruler was used to measure the length of the pod. For this purpose, three random pods were selected from each selected plant in each replication for each genotype and average value for each genotype was recorded in centimeter (cm).

Pod Width (cm)

Vernier caliper was used to measure the width of the pod. For this purpose, pod was placed between the jaws of Vernier caliper and reading was recorded. Three random pods from each plant of each genotype from each replication were selected and average value was recorded. Pod width was recorded in centimeter (cm).

Number of Seeds per Pod

Pods were opened and seeds were counted manually. Three pods were opened at random from each plant of each genotype from each replication and number of seeds were counted, then average value was recorded.

Seed Diameter (cm)

Data for the seed diameter were collected using Vernier caliper. Seeds were placed between the jaws of Vernier caliper and readings were recorded. For this purpose, three seeds from each plant of each genotype from each replication were selected at random and average value was recorded.

100 Seed Weight (g)

Seed weight was calculated after sun drying the seeds keeping the moisture contents at lower level. Electronic weighing balance was used to weigh 100 seeds weight in grams (g).

Yield (g)

Yield per plant were recorded after all the pickings of pods per plant from each replication of each genotype. Total weight of all the pickings per plant of each selected

plant was calculated. Average yield of five plants in each replication for each genotype was recorded.

Statistical Analysis

Analysis of Variance

The recorded data on different plant characters were subjected to analysis of variance for studying difference between genotypes.

Correlation

Correlation among different variables was studied using correlation analysis as suggested by Dewey and Lu (1959). For this purpose, STATISTIX 8.1 software was used.

$$r = \frac{n(\sum xy) - (\sum x)(\sum y)}{\sqrt{[n\sum x^2 - (\sum x)^2][n\sum y^2 - (\sum y)^2]}}$$

Principal Component Analysis

It is defined as the methodology of summarizing information of large dataset into small tables that can be visualized and analyzed more easily. Principal component analysis was used to study interrelationship among studied genotypes for yield related traits. PCA was executed using statistical procedure as suggested by Gabriel (1971). For this purpose, XLSTAT software was used.

Components of Genetic Variability

The phenotypic and genotypic coefficient of variability was calculated as per formula given by Burton and de Vane (1953). PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as: 0-10%=low, 10-20% = Moderate, > 20%= High.

$$PCV = \frac{\sqrt{Vp}}{X} \times 100$$

$$GCV = \frac{\sqrt{Vg}}{X} \times 100$$

$$ECV = \frac{\sqrt{Ve}}{X} \times 100$$

Estimation of Heritability (Broad Sense)

Heritability (h^2bs) was calculated as per formula given by Burton and de Vane (1953). The formula to estimate broad sense heritability is as follows:

$$h^2_{(B.S)} = {}^{Vg}/_{Vp} = {}^{Vg}/_{(Vg + Ve)}$$

V_g = genetic variance

V_p = phenotypic or total variance

V_e = environmental variance

Genetic Advance

The expected genetic advance resulted from selection of 5 percent superior individuals were worked out as suggested by Johnson et al. (1955). The genetic advance as percentage of mean was categorised into low, moderate and high as suggested by Johnson et al. (1955) < 20 = Low, 20 – 30 = Moderate, >30= High.

Genetic advance in the next generation can be computed by following formula:

Genetic advance (GA) = $K. \delta_p. h^2$

K = selection differential, being 2.06 at 5 and 1.75 at 10% selection intensity.

δ_p = standard deviation of the phenotypic variance of the population under selection.

h^2 = heritability estimates in fraction of the trait under study.

3 RESULTS AND DISCUSSION

Days to 50% Flowering

Highly significant differences were showed by the genotypes for days to 50% flowering at 0.01% probability level (Table 1). The genotype Verve showed maximum number of days to 50% flowering (82.0) followed by genotypes 276 and PGRI-42 showing 80.5 and 79.5 days. The mean performance of genotypes Motipak and 19566 showed minimum number of days to 50% flowering (68.5) and (69.5) as displayed (Fig. 1). The range for the number of days to 50% flowering varied from 68.5 to 82.0. These findings showed similarity with the results of Azmat et al. (2011).

The magnitude of genetic components of variation for days to 50% flowering is presented Table 2. The PCV was found to be greater than GCV which means that the trait days to 50% flowering was influenced by environment to some extent as reported by Gupta et al. (2018). The genotypic variance was smaller than phenotypic variance but greater than environmental variance indicating higher degree of genetic variability for this trait. Results from this study exhibited that GCV and PCV assessed for days to 50 % flowering were low (i.e. less than 10%) which were also observed by Iqbal et al. (2015). The heritability observed for this character was high (85%) which exhibits great extent of genetic effects in determination of this character. High genetic advance as percent of mean was observed for days to 50 % flowering (9.24). High values of heritability, as well as genetic advance as a percentage of mean concluded that selection would be effective for improvement of this trait as previously reported by Khan et al. (2017).

Plant Height (cm)

It was displayed by analysis of variance that highly significant difference is present among genotypes at 0.01 % probability level (Table 1). Wide range of variability was shown by plant height from (53.39 cm) to (183.89 cm). Maximum plant height was shown by genotype PGRI-41 that showed highest mean value

Table 1: Analysis of variance for morphological traits in twenty genotypes of *Pisum sativum.*

Trait	Source	DF	SS	MSS	F
Days to 50% Flowering	Replication	1	3.03	3.02	1.32
	Genotype	19	539.48	28.39	12.4**
	Error	19	43.48	2.28	10.28
Plant Height (cm)	Replication	1	87.3	87.26	0.84
	Genotype	19	54924.2	2890.75	27.78**
	Error	19	1976.9	104.05	30.77
Number of Pods	Replication	1	0.4	0.35	0.02
	Genotype	19	9262.5	487.5	30.32**
	Error	19	305.4	16.08	4.74
Pod Length (cm)	Replication	1	0.21	0.21	1.83
	Genotype	19	18.18	0.95	8.4**
	Error	19	2.16	0.11	6
Pod Width (cm)	Replication	1	0.02	0.02	1.8
	Genotype	19	0.73	0.03	3.24**
	Error	19	0.22	0.01	4.98
Number of Seeds per Pod	Replication	1	0.05	0.05	0.46
	Genotype	19	15.67	0.82	7.46**
	Error	19	2.09	0.11	6.24
Seed Diameter (cm)	Replication	1	0.001	0.0007	0.51
	Genotype	19	0.22	0.01	7.71**
	Error	19	0.03	0.001	3.04
100-seed Weight (g)	Replication	1	26.41	26.4	3.95
	Genotype	19	1016.47	53.49	8.01**
	Error	19	126.81	6.67	4.02
Yield (g)	Replication	1	3	3.02	0.09
	Genotype	19	4185.1	220.26	6.77**
	Error	19	617.8	32.51	9.25

Table 2: Basic statistics and genetic components of variation for morphological traits in twenty genotypes of *Pisum sativum.*

Genetic Components	Days to 50 % Flowering	Plant Height	Number of Pods per Plant	Pod Length	Pod Width	Seeds per Pod	Seed Diameter	Seed Weight	Yield
Maximum	82.00	183.89	77.62	7.00	1.36	5.04	0.92	37.62	45.50
Minimum	68.50	53.39	5.12	4.32	0.68	3.20	0.59	17.75	3.62
Grand mean	74.27	115.25	20.98	5.92	1.03	4.15	0.71	24.85	20.51
Standard error of mean (SEm)	1.06	2.84	2.83	0.23	0.07	0.23	0.02	1.82	4.03
Critical difference (CD) 5%	3.16	8.41	8.39	0.70	0.22	0.69	0.08	5.40	11.93
Critical difference (CD) 1%	4.32	11.48	11.47	0.96	0.31	0.95	0.11	7.39	16.31
Environmental variance	2.28	16.13	16.07	0.11	0.01	0.11	0.001	6.67	32.51
Genotypic variance	13.05	215.97	235.71	0.42	0.01	0.35	0.005	23.41	93.87
Phenotypic variance	15.34	232.1	251.78	0.53	0.02	0.46	0.006	30.08	126.39
Environmental coefficient of variance	2.03	8.85	19.10	5.69	10.50	7.99	5.39	10.39	27.78
Genotypic coefficient of variance	4.86	32.39	73.17	10.96	11.12	14.38	9.85	19.46	47.22
Phenotypic coefficient of variance	5.27	33.57	75.62	12.35	15.31	16.45	11.23	22.06	54.79
Heritability (Broad Sense)	0.85	0.93	0.93	0.78	0.52	0.76	0.76	0.77	0.74
Genetic advance	6.86	29.20	30.60	1.18	0.17	1.07	0.12	8.79	17.20
Genetic advance as percentage of mean	9.24	64.36	145.84	20.04	16.64	25.89	17.81	35.37	83.83

(183.89), followed by PGRI-43 and PGRI-44 having mean values (149.60 cm) and (149.55 cm). On the other hand, lowest mean performance (53.39 cm) was showed by genotype Mission in mean comparison graph (Fig. 2). Genotypic differences for plant height in pea germplasm have also been reported by Iqbal et al. (2015).

The magnitude of genetic components of variation for plant height is presented in table 2. The PCV is found to be more than GCV which means that plant height has some interaction with environment. Results from this study showed that GCV and PCV assessed for plant height were high which were also observed by Sonali et al. (2009). High heritability was observed for plant height which shows good extent of genetic effects in determination of this character. The genotypic variance was smaller than phenotypic variance but greater than environmental variance indicating higher degree of genetic variability for this trait as previously observed by Georgieva et al. (2016). Genetic advance as percent of mean was high (29.20) which revealed that plant height was governed by additive genes and selection would be beneficial for improvement of this trait. Jeberson et al. (2016) reported high genetic advance as percent of mean for plant height.

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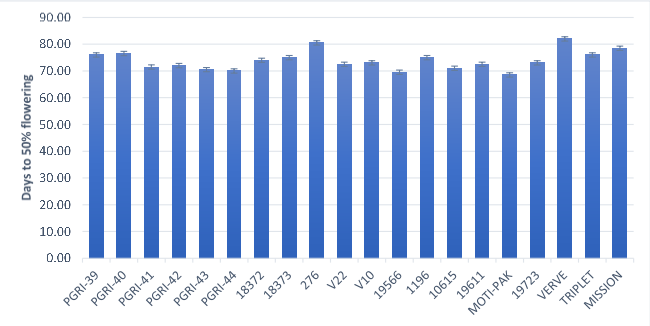

Fig. 1: Mean values of twenty genotypes of *Pisum sativum* for days to 50% Flowering.

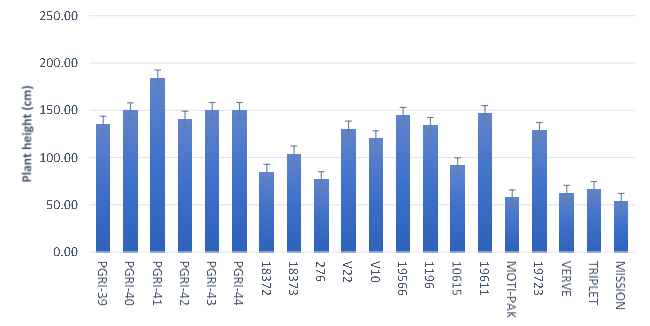

Fig. 2: Mean values of twenty genotypes of *Pisum sativum* for Plant Height.

Number of Pods per Plant

Differences were highly significant for pods per plant among the studied pea accessions revealed by analysis of variance at 0.01% probability level (Table 1). Accession 1196 showed maximum number of pods per plant. Whereas the lowest pods per plant were observed for genotypes Mission and 18372 respectively (Fig. 3). The range for pods per plant varied from 5.12 to 77.62. Kumar et al. (2019) reported variation in vegetable pea genotypes for the number of pods per plant. Formation of more pods per plants in legumes impersonates as feasible option in order to increase yield (Dhama et al. 2010).

The values of genetic components of variation for flowers per plant are presented (Table 2). The character number of pods per plant showed higher phenotypic coefficient of variance than genotypic coefficient of variance unveiling the influence of environment to some extent and some scope for improvement through selection. Similar conclusions were obtained by Kumar et al. (2019). High genetic advance as percent of mean and high heritability was shown by pods per plant. High heritability coupled with high genetic advance as percent of mean explained that the selection for this trait could be helpful in increasing number of pods per plant as explained earlier by Bhuvaneswari et al. (2017).

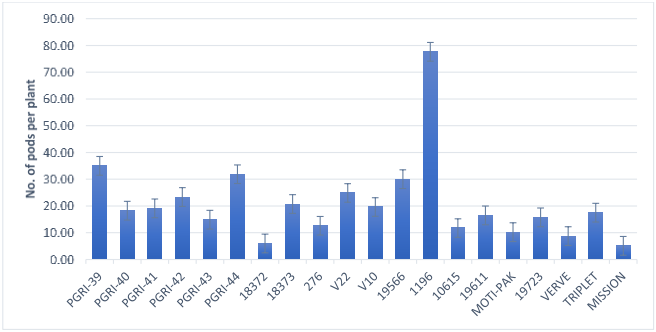

Fig. 3: Mean values of twenty genotypes of *Pisum sativum* for Number of Pods per Plant.

Pod Length

Significant differences were presented by all the genotypes for pod length at 0.01% probability level (Table 1). Genotype PGRI-42 highest mean value. Meanwhile genotype 18372 showed lowest mean performance for pod length (Fig. 4). The range for pod length was observed form 4.32 cm to 7.0 cm. During pod development and formation stage nutrients availability may results in vigorousness and maximum translocation of plant reserves towards pod development and formation. Genotypic differences for the pod length in pea germplasm have also been provided by Khan et al. (2017).

The magnitude of genetic components of variation for pod length is presented in Table 2. Genotypic coefficient of variance was less than phenotypic coefficient of variance showing some extent of variation with environment as reported by Gupta et al. (2018). High heritability (78%) and genetic advance as percent of mean indicated improvement through selection would be fruitful as stated by Kumar et al. (2019). High genetic advance was observed suggesting additive gene action.

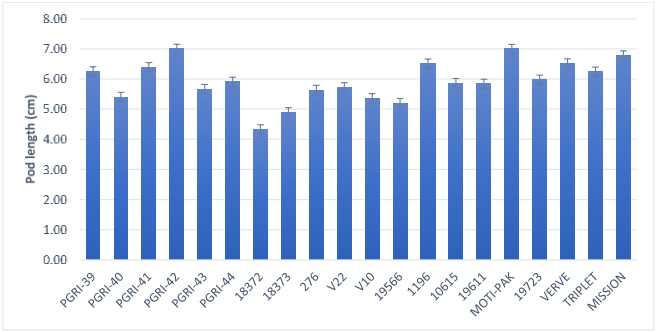

Fig. 4: Mean values of twenty genotypes of *Pisum sativum* for Pod Length.

Pod Width

For pod width high significant variability was observed within the genotypes at 0.01% probability level (Table

1). Fig. 5 shows that accession Motipak showed maximum pod width followed by 18372. While accession Verve showed minimum pod width (Fig. 5). The range for pod width varied from 0.68 cm to 1.36 cm. The results showed similarity with the findings of Umar et al. (2014).

The values of genetic components of variation for pod width are presented (Table 2). Genotypic variance was lower than phenotypic variance for pod width. Least environmental influence is suggested by higher PCV as compared to GCV as found earlier by Iqbal et al. (2015). Moderate values of phenotypic and genotypic variance showing small variability for the pod width were the reason for moderate genetic advance value (0.17) as previously observed by Sonali et al. (2009). Moderate heritability coupled with moderate genetic advance was found for pod width exhibited non-additive gene action selection will be ineffective as previously reported by Singh et al. (2017).

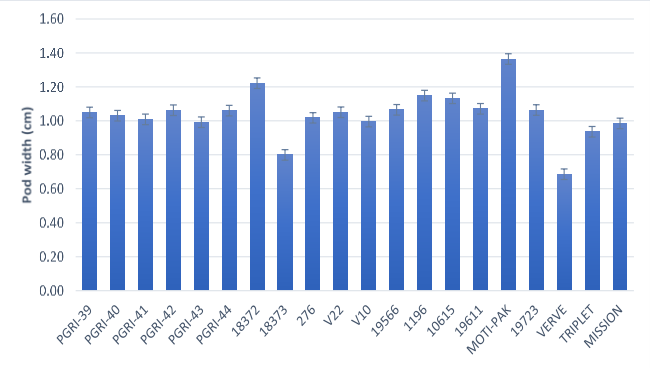

Fig. 5: Mean values of twenty genotypes of *Pisum sativum* for Pod Width.

Number of Seeds per Pod

The variation between the pea accessions for seeds per pod was highly significant at 0.01% probability level (Table 1). Maximum value for number of seeds per pod was observed in genotype PGRI-40 as shown in Fig. 6. On the other hand, accessions PGRI-44 showed the lowest number of seeds per pod. Seeds per pod displayed range from 3.20 to 5.04. Environmental variation at the time of fertilization might be reason for a smaller number of seeds. Genotypic differences for seeds per pod were also reported by Khan et al. (2017).

The magnitude of genetic components of variation for seeds per pod is presented (Table 2). The GCV was smaller than PCV which showed that environmental influenced on seeds per pod was very little. High genetic advance as percent of mean along with high heritability and genetic advance exhibited by seeds per pod showing involvement of additive genes as suggested by Iqbal et al. (2015).

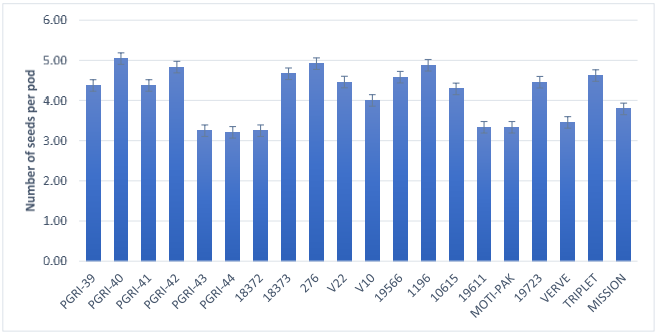

Fig. 6: Mean values of twenty genotypes of *Pisum sativum* for Number of Seeds per Pod.

Seeds Diameter

The variation between the pea accessions for seed diameter was highly significant at 0.01% probability level (Table 1). Maximum seed diameter was found in genotype PGRI-44 as shown in Fig. 7. On the other hand, accessions 276 and 18373. Seed diameter showed range from 0.59 to 0.92 cm. Fluctuations in the environment at the time of fertilization might be the reason for less diameter of seeds. Genotypic differences for seed size were also been validated by Khan et al. (2017).

The values of genetic components of variation for seed diameter are presented table 2. The GCV was smaller than PCV indicating that there was very little influence of environment on seed diameter. Moderate genetic advance as percent of mean along with high heritability and genetic advance exhibited by seed diameter revealing the involvement of additive genes. Low values of phenotypic and genotypic variance showing small variability for seeds per pod were the reason for low genetic advance value.

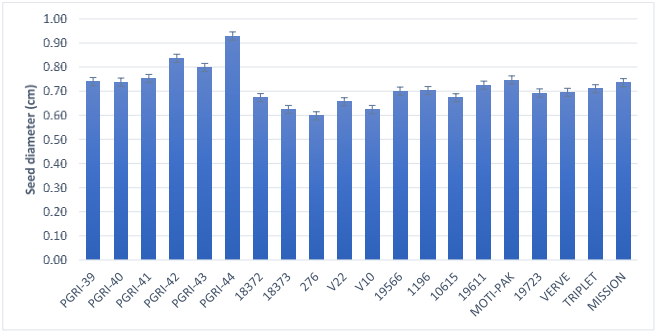

Fig. 7: Mean values of twenty genotypes of *Pisum sativum* for Seed Diameter.

Hundred Seeds Weight

Highly significant differences were revealed by studying genotypes for hundred seed weight at 0.01% probability level (Table 1). Highest hundred seed weight was

shown by accession PGRI-41. While the lowest hundred seed weight was shown by genotypes V10 as depicted in Fig. 8. Similar results for genotypic differences for hundred seeds weight in pea germplasm were also reported by Khan et al. (2017).

The magnitude of genetic components of variation for hundred seeds weight is presented (Table 2). The genotypic variance was smaller than phenotypic variance but greater than environmental variance indicating higher degree of genetic variability for this trait as previously found out by Georgieva et al. (2016). High heritability (77%) and genetic advance as percent of mean (35.37) was showed for hundred seeds weight showing that the trait was governed by additive gene action as observed by Kumar et al. (2019). High genetic advance for hundred seeds weight was due to moderate values of genotypic and phenotypic variances exhibiting moderate variability for the traits as previously reported by Sonali et al. (2009).

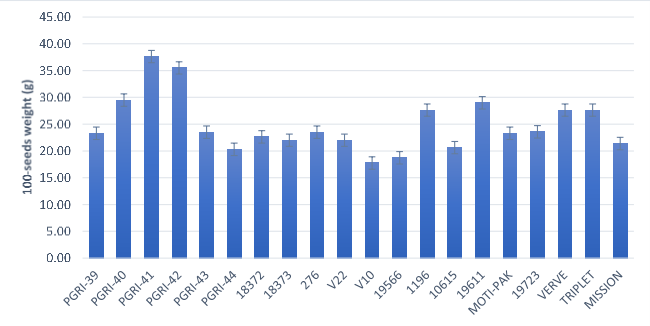

Fig. 8: Mean values of twenty genotypes of *Pisum sativum* for Hundred Seed Weight.

Yield (g)

It was revealed in the analysis of variance that studied pea genotypes were highly significantly different for yield per plant at 0.01% probability level (Table 1). Highest yield per plant was showed by accession PGRI-42 succeeded by PGRI-43 and PGRI-44 and lowest yield was showed by genotype Mission (4.62 g) as shown in Fig. 9. Yield ranged from minimum value of 3.62 g to maximum value of 45.50 g. Genotypic differences for yield in pea germplasm were also reported by Nisar et al. (2008) and Khan et al. (2017).

The values of genetic components of variation for yield are presented (Table 2). The genotypic variance was smaller than phenotypic variance but greater than environmental variance indicating higher degree of genetic variability for this trait as previously reported by Georgieva et al. (2016). High heritability and high genetic advance as percent of mean were shown for yield per plant showing that the trait was governed by additive gene action as observed by Nisar et al. (2008). Moderate genetic advance for yield per plant was due to high values of genotypic and phenotypic variances showing high variability for the traits as previously reported by Nisar et al. (2011) (Fig. 10).

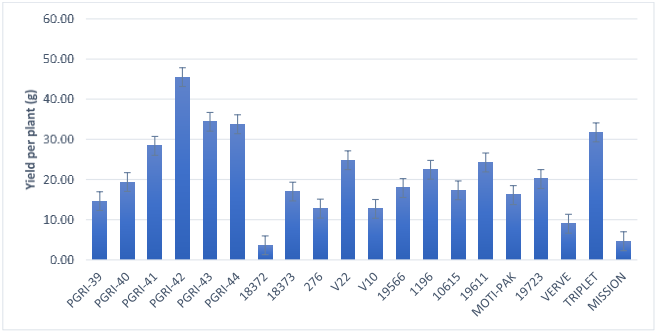

Fig. 9: Mean values of twenty genotypes of *Pisum sativum* for Yield per Plant.

Genotypic Correlation

Genotypic correlation is a measure of the degree to which the genetic factors underlying one trait are associated with the genetic factors underlying another trait. The Table 3 shows the correlation coefficients between nine different traits. For example, the correlation coefficient between days to 50% flowering and plant height was -0.3631, which indicated a weak negative correlation between these two traits. This meant that plants that produced flower earlier tended to be slightly taller, and vice versa. On the other hand, the correlation coefficient between plant height and yield was 0.59, which indicated a strong positive correlation between these two traits. Which meant that taller plants tended to have higher yields. Similarly, correlation coefficient between pod length and seed diameter was 0.49* which depicted a strong positive correlation between these two traits.

It was revealed in the analysis that days to 50% flowering were positively correlated with pod width which showed that plant that bore flowers late would have wider pods. Whereas number of pods per plant and seeds per pod had no significant genotypic correlation with any other trait studied. Pod length was positively correlated with seed diameter and seed weight, which revealed that plant that was taller would also have larger and heavier seeds. Pod width showed highly significant negative correlation with days to 50% flowering, showing that plant that produced flowers earlier had wider pods than those plants that produced flowers later. Seed diameter showed positive correlation with pod length and yield, larger the seed size was more would be yield and vice versa. Seed weight and yield had significant positive correlation, which meant that greater the seed weight more would be the yield. Yield was correlated positively with plant height, seed diameter and seed weight.

Table 3: Genotypic correlation coefficient of morphological traits in twenty genotypes of *Pisum sativum.*

	Days to 50% Flowering	Plant Height	Number of Pods	Pod Length	Pod Width	Seeds per Pod	Seed Diameter	Seed Weight	Yield
Days to 50% Flowering	1**								
Plant Height	-0.36 ns	1**							
Number of Pods	-0.09 ns	0.43 ns	1**						
Pod Length	0.23 ns	-0.15 ns	0.15 ns	1**					
Pod Width	-0.70**	0.07 ns	0.15 ns	0.11 ns	1**				
Seeds per Pod	0.38 ns	0.21 ns	0.42 ns	-0.003 ns	-0.12 ns	1**			
Seed Diameter	-0.23 ns	0.42 ns	0.16 ns	0.49 *	0.29 ns	-0.34 ns	1**		
Seed Weight	0.39 ns	0.34 ns	0.07 ns	0.47 *	-0.05 ns	0.25 ns	0.36 ns	1**	
Yield	-0.19 ns	0.59 **	0.26 ns	0.34 ns	-0.02 ns	0.20 ns	0.71 **	0.52 *	1**

** = highly significant, * = significant, **ns** = non-significant

Table 4: Phenotypic correlation coefficient of morphological traits in twenty genotypes of *Pisum sativum.*

	Days to 50% Flowering	Plant Height	Number of Pods	Pod Length	Pod Width	Seeds per Pod	Seed Diameter	Seed Weight	Yield
Days to 50% Flowering	1**								
Plant Height	-0.37 *	1**							
Number of Pods	-0.09 ns	0.43 **	1**						
Pod Length	0.20 ns	-0.11 ns	0.13 ns	1**					
Pod Width	-0.45 **	0.04 ns	0.13 ns	0.02 ns	1**				
Seeds per Pod	0.30 ns	0.15 ns	0.34 *	0.03 ns	-0.14 ns	1**			
Seed Diameter	-0.21 ns	0.36 *	0.10 ns	0.35 *	0.08 ns	-0.34 *	1**		
Seed Weight	0.28 ns	0.33 *	0.08 ns	0.42 **	-0.13ns	0.25 ns	0.24 ns	1**	
Yield	-0.19 ns	0.53 **	0.29 ns	0.29 ns	0.04 ns	0.12 ns	0.55 **	0.46 **	1**

** = highly significant, * = significant, **ns** = non-significant

Overall, the genotypic correlation coefficients in this table could be used by plant breeders to identify which traits were likely to be inherited together, and to select plants with desirable combinations of traits for further breeding programs.

Phenotypic Correlation

The strength of the relationship between two traits was measured by phenotypic correlation based on their observable or physical characteristics. The Table 4 shows the correlation coefficients between nine different traits. For example, the correlation coefficient between days to 50% flowering and plant height was -0.37*, indicating a significant negative correlation between the two traits. This meant that as the days to 50% flowering increased, the plant height decreased. On the other hand, the correlation coefficient between plant height and yield was 0.53**, indicating a highly significant and positive correlation between plant height and yield, indicating that as the height of plant increased, the yield also increased.

Correlation coefficient of plant height indicates strong positive correlation with number of pods 0.43**, seed diameter 0.36*, yield 0.53** and 100-seed weight 0.33*. Number of pods per plant had highly significantly positive correlation with plant height 0.43**, which showed taller the plant, more would be number of pods and vice versa. Pod length had a positive significant correlation coefficient for two traits i.e. seed diameter 0.35 * and 100-seed weight 0.42**. Pod width showed negatively significant correlation with days to 50% flowering, while no correlation was observed with all other traits studied. Seeds per pod were negatively correlated with seed diameter -0.34*, whereas significantly positive correlation with number of pods per plant 0.34* was observed. Seed diameter showed highly significant correlation with yield and significant correlation with plant height. This character showed negative correlation with seeds per pod, depicting that lesser the seeds in a pod more would be diameter of the seeds. 100-seed weight was positively correlated with plant height, pod length and yield. Overall yield had positive significant correlation with plant height, seed diameter and 100-seed weight. So, these three characters had positive relationship with yield, which showed that genotype might be selected with higher values of these traits.

It was important to note that phenotypic correlation did not necessarily imply causation. Correlation only indicated that two traits were associated with each other, but it did not necessarily mean that one trait caused the other. Therefore, further experiments and analyses are needed to establish causal relationships between the different traits.

Principal Component Analysis

Principal component analysis (PCA) is a type of multivariate statistical method used to analyze and simplify the inter-relationship between a large set of populations without losing important information relating

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to the original dataset. In this study, PCA was performed on mean data using XLSTAT software. From nine principal components (PCs), the first four PCs exhibited more than one eigenvalue. Among twenty pea genotypes studied for genetic diversity, the first three PCs contributed 69.98% in total variation, while the remaining 30.02% was shown by other principal components.

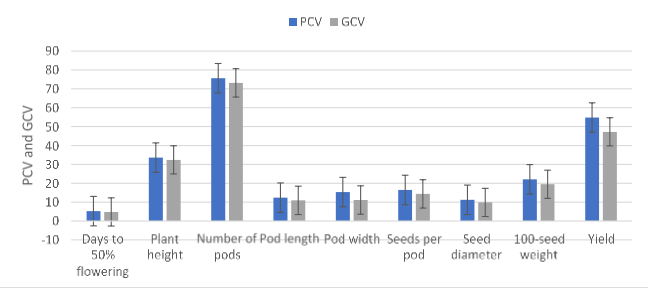

Fig. 10: Phenotypic Coefficient Variance versus Genotypic Coefficient of Variance for all studied traits in pea genotypes.

Scree Plot

Scree plot (Fig. 11) described percentage variance correlated with each principal component by presenting a relationship between principal component numbers and eigenvalues. PC-I exhibited 32.8% variation having eigenvalue 2.95 in pea germplasm. It was noticeable from the scree plot that variation was diminished from PC-VI to PC-IX and maximum variability was gained from PC-I to PC-V. By examining the graph, it was clear that PC-I acquired the highest variation. So, accession selection from this principal component would be resourceful (Fig. 11).

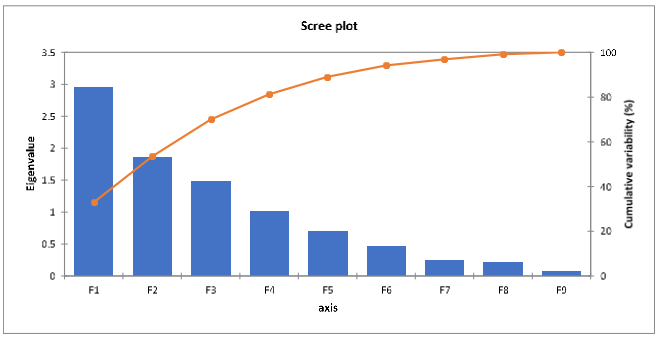

Fig. 11: Graph between principal components and eigenvalues.

Biplot

The variables were placed on plots as vectors as presented by principal component biplot (Fig. 11). Contribution of variables in the diversity of the germplasm was exhibited by the distance of every variable with reference to PC-I and PC-II. For specific variable, the principal component, biplot was constructed in relation to the input of the genotypes. Lengthiest vectors were of days to 50% flowering, plant height, 100-seed weight, seed diameter, pod width and in relation to both axis their values were determined. The vectors which were in opposite direction were correlated negatively as clearly shown (Fig. 12). For that specific trait, the accessions closer to protrusions were more representative. The above presented findings were validated by (Zhao et al. 2020; Umar et al. 2014).

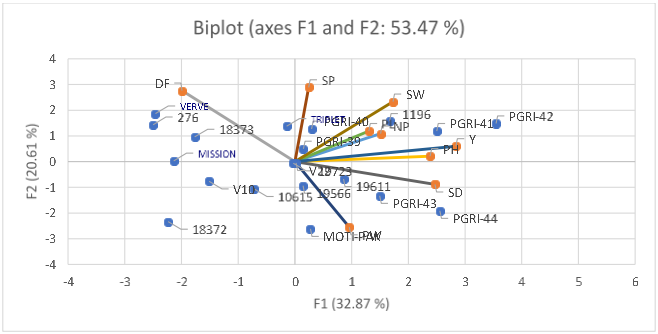

Fig. 12: Biplot graph between Principal Components and Variable Vectors.

Conclusion

This study has successfully identified significant genetic diversity among twenty pea genotypes. Traits like pods per plant and number of days to flowering having high heritability measures are mostly impacted by additive gene action, hence show potential of selection tools for developing superior pea cultivars. Correlation and principal component analyses revealed key traits for yield improvement, including plant height, seed diameter, number of pods per plant, and 100-seed weight, highlighting their significance in genetic variation and potential breeding targets. The diverse genotypes, particularly PGRI-42 and PGRI-44, present opportunities for targeted breeding strategies. Overall, these findings will guide genetic improvement efforts in pea crops, enhancing agricultural productivity and food security. Future research should utilize these findings to improve pea crops by employing advanced selective breeding methods and molecular marker-assisted selection techniques.

Authors' Contributions

MS and AS conceived the idea. MS designed the layout of the article and wrote the paper. AS supervised the study. MH and HI performed statistical analysis. AA contributed to the figures. ZA and AS revised and approved the final version of the manuscript. All authors contributed to the article and approved the submitted version.

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REFERENCES

Anglade, J., Billen, G., & Garnier, J. (2015). Relationships for estimating N_2 fixation in legumes: Incidence for N balance of legume-based cropping systems in Europe. Ecosphere, 6(3), 1–24.

Azmat, M.A., Nawab, N.N., Khan, A.A., Ashraf, M., Niaz, S., & Mahmood, K. (2011). Characterization of pea germplasm. International Journal of Vegetable Science, 17(3), 246–258.

Bhuvaneswari, S., Sharma, S.K., Punitha, P., Shashidhar, K.S., Naveenkumar, K.L., & 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.

Bocianowski, J., Księżak, J., & Nowosad, K. (2019). Genotype by environment interaction for seed yield in pea (*Pisum sativum* L.) using additive main effects and multiplicative interaction model. *Euphytica, 215*(11), 191.

Burton, G.W., & Devane, D.E. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal, 45(1), 478–481.

Deulvot, C., Charrel, H., Marty, A., Jacquin, F., Donnadieu, C., Lejeune-Hénaut, I., Burstin, J., & Aubert, G. (2010). Highly-multiplexed SNP genotyping for genetic mapping and germplasm diversity studies in pea. BMC Genomics, 11(1), 1–10.

Dewey, D.R., & Lu, K. (1959). A correlation and path-coefficient analysis of component of crested wheatgrass seed production. Agronomy Journal, 51(9), 515–518.

Dhama, S.K., Tyagi, N.K., & Singh, P. (2010). Interrelationship and path analysis for seed yield and its component characters under eight environments in pea (Pisum sativum L.). Legume Research, 33(2), 87–94.

Dyachenko, E., Ryzhova, N., Vishnyakova, M., & Kochieva, E. (2014). Molecular genetic diversity of the pea (Pisum sativum L.) from the Vavilov Research Institute collection detected by the AFLP analysis. Russian Journal of Genetics, 50(1), 916–924.

Food and Agriculture Organization of the United Nations. (2022). Pea Pakistan data. Retrieved from https://www.fao.org/faostat/en/#data/QCL (Accessed on September 10, 2022).

Gabriel, K.R. (1971). The biplot graphic display of matrices with application to principal component analysis. Biometrika, 58(3), 453–467.

Georgieva, N., Nikolova, I., & Kosev, V. (2016). Evaluation of genetic divergence and heritability in pea (*Pisum sativum* L.). Journal of BioScience and Biotechnology, 5(1), 61–67.

Govindaraj, M., Vetriventhan, M., & Srinivasan, M. (2015). Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. Genetic Research International, 1(1), 23–36.

Gupta, A., Singh, M., & Dumi, T. (2018). Estimation of character association and direct and indirect effects in pea (*Pisum sativum* L.). International Journal of Current Science, 6(5), 1924–1927.

Iqbal, M., Bashir, I., Iqbal, M., Nadeem, K., Lateef, A., Chishti, S., & Niaz, S. (2015). Association pattern among yield and its related attributes in peas (*Pisum sativum* L.). Journal of Agricultural Research, 53(2), 173–177.

Jeberson, M.S., Shashidhar, K.S., & Iyanar, K. (2016). Estimation of genetic variability, expected genetic advance, correlation, and path analysis in field pea (*Pisum sativum* L.). Electronic Journal of Plant Breeding, 7(4), 1074–1078.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1995). Estimates of genetic and environmental variability in soybeans. Agronomy, 47(7): 314-318.

Khan, M.R.A., Mahmud, F., Reza, M.A., Mahbub, M.M., Shirazy, B.J., & Rahman, M.M. (2017). Genetic diversity, correlation, and path analysis for yield and yield components of pea (*Pisum sativum* L.). *Journal of Agricultural Science, 13*(1), 11–16.

Kumar, M., Jeberson, M.S., Singh, N.B., Sharma, R., AV, D. and Singh, V. (2019). Genetic diversity and trait association analysis in field pea (Pisum sativum L.) genotypes. Journal of Pharmacognosy and Phytotherapy. 8(2): 2186-2193.

Kumari, P., Basal, N., Singh, A.K., Rai, V.P., Srivastava, C.P., & Singh, P.K. (2013). Genetic diversity studies in pea (*Pisum sativum* L.) using simple sequence repeat markers. *Genetics and Molecular Research, 12*(3), 3540–3550.

Lam, A., Karaca, A.C., Tyler, R., & Nickerson, M. (2018). Pea protein isolates: Structure, extraction, and functionality. *Food Reviews International, 34*(2), 126–147.

Nisar, M., Ghafoor, A., & Khan, M.R. (2011). Phenotypic variation in the agronomic and morphological traits of *Pisum sativum* L. germplasm obtained from different parts of the world. *Russian Journal of Genetics, 47*(1), 19–25.

Nisar, M., Ghafoor, A., Ahmad, H., Khan, M.R., Qureshi, A.S., Ali, H., & Islam, M. (2008). Evaluation of genetic diversity of pea germplasm through phenotypic trait analysis. Pakistan Journal of Botany, 40(5), 2081–2086.

Shivasubramanian, S., & Menon, M. (1973). Heterosis and inbreeding depression in rice. Madras Agricultural Journal, 60(1), 1139–1144.

Singh, S.K., Mazeed, A., Singh, V.P., Srivastava, S., Dwivedi, A.K., Yadav, S.K., & Srivastava, R.K. (2017). Evaluation of seed yield and genetic divergence in the germplasms of Pisum sativum L. var. arvense. Journal of Pharmacognosy and Phytotherapy*, 6*(6), 1016–1021.

Smykal, P., Aubert, G., Burstin, J., Coyne, C.J., Ellis, N.T., Flavell, A.J., Ford, R., Hýbl, M., Macas, J., & Neumann, P. (2012). Pea (Pisum sativum L.) in the genomic era. Agronomy, 2(2), 74–115.

Smykal, P., Horáček, J., Dostálová, R., & Hýbl, M. (2008). Variety discrimination in pea (Pisum sativum L.) by molecular, biochemical and morphological markers. Journal of Applied Genetics, 49(2), 155–166.

Sonali, G., Nirmala, C., & Saroj, D. (2009). Genetic variability, correlation, and path analysis studies in pea (*Pisum sativum* L.). *Crop Research, 38*(3), 179–183.

Umar, H.M.I., Ur-Rehman, S., Bilal, M., Atif, S., Naqvi, H., Manzoor, S., Ghafoor, A., Khalid, M., Iqbal, M.,
Qayyoum, A. (2014). Evaluation of genetic diversity in pea (Pisum sativum) based on morpho-agronomic characteristics for yield and yield associated traits. Journal of Biodiversity and Environmental Sciences, 4(5), 323-328.
Zhao, T., Su, W., Qin, Y., Wang, L., & Kang, Y. (2020). Phenotypic diversity of pea (*Pisum sativum* L.) varieties and the polyphenols, flavonoids, and antioxidant activity of their seeds. Ciencia Rural, 50(5), 1678–4596.