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Genetic Variability and Heritability Estimation for Yield and Yield Related Traits in Garden Pea (*Pisum sativum* L.)

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ABSTRACT

A field trial was conducted during the Pea growing seasons of 2022 and 2023 to detect genetic variability and heritability of 22 pea genotypes comprising 17 accessions and 5 commercial varieties. The three replications randomized complete block design assessed 19 quantitative and six qualitative characters for maturity, yield, and yield component. Analysis of variance showed significant ($p<0.01$) differences among the genotypes for quantitative traits. P.G-3 is the pea genotype that had the shortest emergence time at 10.3 days, days to 50% flowering (111.4 days), pod length (11.3 cm), and seeds per pod (8.5). P.G-8 recorded the longest duration to first picking; it was 141.6 days. Also, P.G-7 registered a 5.56 average for picking number and 7.8 for branches. The highest stem recorded in P.G-2 with 198.2 cm, P.G-15 had the highest number of leaves (103.5) and pods (35.4), and P.G-16 had the largest pod diameter (1.15 cm). Tarnab Pea registered the highest weight for 100 fresh green seeds (47.0 g), while Bashir 2021 had the thickest stem (0.62 cm), and the highest yield (13.5 tons/ha). Due to their advance in early maturation and yield performance, P.G-7, P.G-8, and P.G-15 are recommended for multi-location trials and pea breeding programs.

INTRODUCTION

The garden pea, *Pisum sativum* L., is a cold season crop of the Fabaceae family. It is one of the major, reputable, and widely cultivated legume crops in the world. Its production comprises approximately 5.5 million hectares per annum, ranking it third among the most important grain legume crops after soybeans and common beans, according to Rana et al. (2017). Peas provide a substantial environmental advantage by helping to create low-input farming systems through their capacity to fix atmospheric nitrogen and through serving as a rotational crop, minimizing the use of outside inputs. Among flowering plants, legumes are the third-largest family, containing more than 650 genera and 18,000 species (Lewis *et al.* 2005). Legumes account for approximately 27% of the world's crop yield and are the second-most valuable plant family in agriculture after the Poaceae family (grasses) (Graham *et al.*, 2003). Peas were cultivated over 24854 hectares of land in Pakistan that yielded 170836 tons. The Khyber Pakhtunkhwa province, from 1959 hectares of land, contributed 15789 tons of pea (MINNFSR, 2019). Peas are grown due to their palatable, healthy green seeds and their capacity to improve soil. They are a wholesome, inexpensive, and readily accessible source of minerals, vitamins, and carbohydrates. 100-gram serving of this food contains 308 kcal of energy, 18.44 g of protein, 1.4 g of fat, 26 g of dietary fiber, 42.4 g of carbohydrates, 295 mg of phosphorus, 3.5 mg of iron and 116 mg of magnesium (FAO. 2016). Across the globe, legumes account for approximately a third of direct protein intake by individuals. They also account for quite a bit of culinary and industrial oils, fodder, and pasture for livestock. The major characteristic of legumes is the ability to entrap nitrogen through symbiotic relationships, highlighting their value as a source of nitrogen in agriculture and the natural world (Phillips, 1998). Legumes also accumulate natural compounds (secondary metabolites), like iso-flavonoids, which are thought to be good for human health because of their anti-cancer and other health-enhancing activities (Dixon *et al.* 2003).

Peas have been a core topic in plant biology since Gregor Mendel carried out studies on them (Ellis *et al.* 2011). In the first half of the 20th century, the significant findings of Mendel and Darwin constituted the science behind contemporary plant improvement. Similarly, advances in molecular research have transformed plant breeding, resulting in a shift towards molecular plant breeding and strengthening its interdisciplinary nature by virtue of recent developments in molecular biology, genetics, and biotechnology. The distance between fundamental research of plant biologists and plant breeders continues to be present despite the means being present for over a decade (Moose *et al.* 2008).

One of the earliest domesticated crops in the world is the pea (*Pisum sativum* L.) (Zohary *et al.* 2000). Peas were originally grown in the Mediterranean area, predominantly in the Middle East. Prior to the existence of agriculture, humans in the Middle East and Europe who engaged in the practice of hunting and gathering had peas as a common food source in their diet (Zohary *et al.* 2000). Subsequently, thousands of pea types were developed in numerous centuries of selection and improvement and these are currently conserved in various germplasm stocks globally (Smkal *et al.* 2011). The range of wild Pisum sativum species extends to Iran, Turkmenistan, southern Europe, northern Africa and anterior Asia (Maxted *et al*. 2010). Further, in the event of early accessions, it is mostly difficult to acquire accurate and complete information. The Pisum genus consists of a number of constituents, which are the wild *Pisum fulvum* found throughout Syria, Jordan, Lebanon and Israel, the domesticated *Pisum abyssinicum* that is present in Ethiopia and Yemen, probably cultivated separately from *Pisum sativum* and an extensive, varied assemblage that includes both domesticated and wild *P. sativum* subsp. elatius, all making up the *P. sativum* species. Whereas production of dry peas increased in the United States, Canada, and the Russian Federation, it fell in Europe (Upadhyaya *et al.* 2011).

Besides, correlation analysis determines the association between various qualities. In addition, it finds a strong measure of correlation between yield and its contributing factors, which helps plant breeders in the selection of species with advantageous and desirable traits (Naseer *et al.,* 2015). Since the presence of disadvantageous correlations between performance components occurs, selection for one of the contributing factors may at times fail to improve genotype performance. Thus, it is also important for plant breeders to know the phenotypic and genotypic correlations between yield and the factors that contribute to yield so that they can develop cultivars that are more likely to thrive. Testing of the available germplasm is done to identify the optimal genotypes. Thus, this experiment was conducted in an effort to choose the appropriate pea genotypes for future pea breeding program (Bacha *et al.* 2015).

MATERIALS AND METHODS

A germplasm collection of 15 accessions from National Agricultural Research Centre (NARC) Islamabad-Pakistan, 2 landraces from Peshawar and Bara, and 5 other varieties was evaluated. The experiment was conducted at horticulture research form Agriculture university Peshawar. The ridge system was used to provide plant-plants with 15 cm and row-to-row distance with 45 cm. The experimental plot was well plowed, leveled, and irrigated before seed sowing. The following quantitative and qualitative parameters were investigated during the experiment. Days to emergence, stem length, internode length, stem diameter, branches plant^{-1}, leaves plant^{-1}, first blossom node, days to fifty percent flowering, days to first picking, pods plant^{-1}, pod length, pod diameter, seeds pod^{-1}, fresh shelling percentage of pod, number of Pickings, 100-green pods weight, 100-fresh green seeds weight, yield (tons) ha^{-1} and root weight.

Statistical Analysis

The data was analyzed using the analysis of variance technique with the computer software MSTATC version 1.5. The mean ($\bar{X}$), standard deviation (SD) and coefficient of variation (CV) were calculated using the formulas provided by Steel and Torrie (1984).

RESULTS AND DISCUSSION

Days to Emergence

Days to emergence across the pea genotypes varied significantly, according to the analysis of variance. Table 1 provides the mean for the days till emergence. Amongst the different genotypes, average values for the traits ranged between 10.3 to 13.9 days. Maximum days taken to emergence (13.9) was noted for P.G-5, followed by Tarnab Pea (13.5), whereas minimum days were taken to emergence (10.3) were recorded for P.G-3. Vg, Vp and Ve were 12.619, 13.856 and 1.238 for days to emergence. GCV (10.185) and PCV (10.673) both were moderate. Broad sense heritability (h^2) (0.91) was high and G.A (4.746) was low.

Days to emergence showed significantly positive genotypic correlation with stem diameter (rg=0.990**), pod height (rg=0.635**), pod diameter (rg=0.441*), seeds pod^{-1} (rg=0.487*), 100-green pod weight (rg=0.519*), 100-green seed weight (rg=0.703**) and significantly negative association with number of leaves (rg=-0.471*), and fresh pod shelling percentage (rg=-0.657**). Days to emergence showed significantly positive phenotypic association with stem diameter (rp=0.550**), pod length (rp=0.377**), pod diameter (rp=0.245*), seeds pod^{-1} (rp=0.281*), 100-fresh pod weight (rp=0.277*), 100-seed weight (rp=0.264*) and yield tons (ha^{-1}) (rp=0.248*), while significantly negatively correlated with stem length (rp=-0.248*), number of flowers (rp=-0.322**) and fresh pod shelling percentage (rp=-0.400**).

Marked variation among various pea genotypes were observed for days to emergence Table 4.1a. Days to emergence had low genetic gain and high heritability for all the factors studied. The findings of this study agree with Jitendra *et al.* (2010), who also observed low heritability for number of days until emergence in garden peas. It was demonstrated by intermediate heritability and moderate genetic gain that additive and non-additive type gene activities control character. During correlation analysis, the duration of the emergence of plants had negative phenotypic and genotypic correlations with the duration to the first flowering, number of seeds per pod, and 100-green seed mass. However, it exhibited positive but statistically non-significant correlations with stem diameter, pods per vine, pod length, pod diameter, and 100-green pod mass. In 2008, Nawab *et al*. assessed the genetic diversity and relationship between the different physical traits of twelve different species of peas. They also presented that there existed a highly positive correlation between the days to the first picking and the days to emergence. Early developing traits had a positive impact on production and played a key role in genotypes fit to a cropping system and environment (Kosev 2013). Days to first pick and days to emergence had a significantly positive correlation. Additionally, there was a significant negative correlation between the pod length and the number of seeds pod^{-1}.

Number of branches plant^{-1}

The analysis of variance revealed significant variation among different pea genotypes for the trait number of branches per plant table1. The average data for this trait are presented in Table1. The mean data for the number of branches per plant ranged from 4.0 to 7.8. Specifically, genotype P.G-7 exhibited the highest number of branches per plant (7.8), followed by P.G-8 (7.2) while the lowest number of branches per plant (4.0) was recorded for P.G-4 followed by P.G-9 (4.7). Vg, Vp and Ve were 3.726, 3.862 and 0.136 respectively for number of branches plant^{-1}. GCV (7.939) and PCV (8.083) both were low. Broad sense heritability (h^2) (0.96) was high and G.A (2.654) was low.
Number of branches showed non-significant genotypic correlation, while phenotypic correlation showed positive association with seed diameter (rp= 0.37**).
The statistical analysis revealed notable variations among pea genotypes in terms of the number of branches per plant. The longer duration of flowering in certain genotypes, along with an increased number of branches, suggests a leaning towards higher vegetative growth. This might be due to genetic or environmental conditions. Some genotypes were observed to follow a determinate growth habit, which produced blooming and depletion of plants simultaneously. Consequently, these genotypes had a reduced number of branches per plant, as reported by Hussain and Badshah (2002). The variations seen in germplasm obtained from varying climatic conditions might have been due to differences in the rate of acclimatization (Hatam and Amanullah, 2001).
The principal branches plant-1 had the largest coefficients of variation, both phenotypically and genotypically, followed by number of pods plant-1, pod yield plant-1, nodes to first pod appearance and the first blossom node. The highest coefficients of variation, both phenotypically and genotypically were recorded for the first pod appearance. Subsequent parameters that were followed were the seeds per 250 g, pods per 250 g, and the total soluble solids as per Yadav et al., (2021). Singh et al. (2012), Dar et al. (2013), and Sharma and Sharma (2013) had similar results. There existed a moderate amount of Phenotypic Coefficient of Variation as well as Genotypic Coefficient of Variation for plant primary branches and per plant pod yield. This is consistent with the same reported by Srivastava et al. (2009) as well as Lal *et al*. (2011).
Number of primary branches per plant showed a significant positive phenotypic correlation with pod length but a negative phenotypic correlation with seed yield per plant. Additionally, genotypic negative correlation was found among the number of primary branches plant-1, plant height, fresh pod shelling percentage and seed yield per plant. Interestingly, no prominent association was found between the number of primary branches per plant and other characters at both genotypic and phenotypic levels. These findings are consistent with the study done by Singh and Singh (2006), which also noticed no significant association between the number of primary branches per plant and other characters.

Days to 50 Percent Flowering

The analysis of variance indicated highly significant variation among pea genotypes for the trait days to 50 percent flowering (Table 1). The average data for days to 50 percent flowering are provided in Table 1. Amongst all the genotypes and varieties mean value for the days to 50 percent flowering varied from 51.5 to 111.4. Maximum days to 50 percent flowering was observed for Climax (111.4), followed by P.G-17 (110.9) and P.G-1 (108.9), while minimum days to 50 percent flowering was recorded for variety Leena Pak (51.4). Vg, Vp and Ve were 1172.096, 1179.971 and 7.875, respectively for days to 50 percent flowering. GCV (34.843) and PCV (34.960) both were high. Broad sense heritability (h^2) (0.99) and G.A (47.770) both were high.
Days to 50 percent flowering exhibited a significantly positive genotypic correlation with traits such as first blossom node (rg=0.572**), days to first picking (rg=0.854**), internode length (rg=0.540**) and 100-fresh green seed weight (rg=0.655**). Days to 50 percent flowering showed positive phenotypic association with first blossom node (rp=0.479**), days to first picking (rp=0.779**), internode length (rp=0.504**), pod length (rp=0.244*), yield tons (ha^{-1}) (rp=0.260*) and root weight (rp=0.334**).
Among pea genotypes, genotypic variance for the days to flower 50% was larger than environmental variance. The estimates for broad sense heritability and genetic advance (G.A) in days to 50 percent flowering indicated a larger degree of genetic influence over environmental influences. The findings in this study concur with the results given by Ahmad et al., (2014).
The genotypes also exhibited significantly high variations in time to 50 percent flowering. The phenomenon of early flowering in some genotypes reflects their fitness to certain environmental conditions. This implies that such genotypes can effectively use nutrients in stressful conditions and move early from the vegetative phase into the reproductive phase, in contrast to genotypes of longer duration to initiate flowering (Ishtiaq et al., 1996). Similar results have been documented by other research studies, such as Badshah and Hussain (2002), Singh et al. (2004), and Vocanson and Jeuffroy (2008). The nine field pea genotypes had considerable differences among

themselves for all the characteristics. The time to reach 50 percent flowering varied from 37 to 65 days with a mean of 50 days. Of particular mention is the Faridpur local genotype, which had the highest maturity duration (Azam et al. 2020). Days to 50% flowering exhibited significant and positive phenotypic correlations with days to maturity, fresh seeds weight at 100 (g), seeds per pod, seed yield per plant, and fresh pod shelling percentage.

It also had a phenotypic negative correlation with number of primary branches per plant. Furthermore, days to 50% flowering indicated significantly positive genotypic correlations with seed yield per plant and fresh pod shelling percentage, but negative genotypic correlations with days to maturity and number of primary branches per plant. Yet, it exhibited non-significant correlations with the rest of the other characters at phenotypic and genotypic levels. These results conform to those revealed by Singh and Singh (2006).

Days to First Picking

Analysis of variance showed greatly substantial variation amongst pea genotypes for the trait days to first picking (1). Mean for days to first picking are given in Table 1. Amongst all the genotypes and varieties mean value for the days to first picking varied from 65.0 to 141.6. Genotype P.G-8 displayed maximum days to first picking (141.6) followed by P.G-4 (137.5) while the minimum days to first picking was recorded for variety Leena Pak (65.0). Vg, Vp and Ve were 1723.236, 1754.639 and 31.402, respectively for days to first picking. GCV (37.383) and PCV (37.722) were high. Broad sense heritability (h^2) (0.98) and G.A (57.594) both were high.

Days to first picking exhibited a significantly positive genotypic correlation with first blossom node (rg=0.517*), days to 50 percent flowering (rg=0.854**), stem length (rg=0.557**) and internode length (rg=0.553*), while displaying a significantly negative association with pod diameter (rg=-0.507*). In addition, days to first picking showed a positive and significant phenotypic association with days to 50 percent flowering (rp=0.779**), stem length (rp=0.484**), internode length (rp= 0.49**), number of leaves (rp=0.318**), fresh pod shelling percentage (rp=0.269*), and root weight (rp=0.317**), while significantly negatively associated with number of picking (rp= -0.285*), pod diameter (rp= -0.424**) and seeds pod^{-1} (rp= -0.311*).

Profound variation among pea genotypes was observed for days to first harvest. Days to harvest is a critical characteristic, which assists in differentiating between early, mid, and late maturing genotypes. Nevertheless, early crop maturity is thought to be beneficial in peas since it confers protection to the plant against both biotic and abiotic stresses, eventually making a positive contribution towards total yield (Kumar and Abbo, 2001). In the present study, the genetic variation found in pea germplasm for days to first harvest matches the record by Ahmad et al. (2014). Twelve pea accessions were evaluated to analyze genetic diversity, which proved to show significant variation in days to first picking among the material under study. Rahman et al. (2019) also verified the genetic variation of days to first picking among eleven varieties of peas.

Days to first picking showed strong significant positive correlation with plant height and days to emergence. It showed strong significantly negative correlation with pod length. It seems that Rahman et al. (2019) carried out research on 11 advanced lines of garden pea and showed a significant and positive correlation between days to first picking and pod length, as well as plant height. The findings regarding the correlation between the days to first picking and pod length are contrary to those of existing research. This explanation could be due to differences in the pea germplasm and environmental conditions that were evaluated.

Table 1

Days to Emergence, Number of Branches, Days to Flowering, Days to First Picking as Affected by Genetic Variability and Heritability of Garden Pea.

Genotypes	Days to emergence	Number of branches	Days to flowering	Days to first picking
PG-1	10.5	5.5	108.9	129.8
PG-2	12.1	6.5	101.2	138.7
PG-3	10.3	5.4	97.2	140.5
PG-4	10.5	4.0	104.0	137.5
PG-5	13.9	5.2	96.2	130.8
PG-6	12.2	6.8	100.2	134.6
PG-7	11.5	7.8	82.0	133.2
PG-8	12.7	7.2	99.7	141.6
PG-9	10.9	4.7	95.2	127.6
PG-10	11.5	5.8	97.3	136.7
PG-11	11.4	6.1	77.8	127.7
PG-12	11.6	6.0	99.0	149.6
PG-13	12.3	5.9	106.8	136.8
PG-14	13.3	5.6	79.7	122.5
PG-15	10.8	5.6	101.3	128.3
P.G-16	12.6	4.9	105.1	122.6
P.G-17	13.6	6.1	110.9	128.8
Lena Pak	11.8	5.0	51.4	57.7
Dassan	13.3	5.9	108.8	127.6
Climax	12.6	6.5	111.4	88.1
Bashir 2021	13.1	6.3	108.3	118.5
Tarnab Pea	13.5	6.8	94.0	128.2

Number of Pods per Plant

The analysis of variance indicated highly significant variation among pea genotypes for the trait number of pods per plant (Table 2). The average data for the number of pods per plant are provided in Table 4.5. The mean data for the number of pods per plant ranged from 35.4 to 23.0. The data showed that genotype P.G-15 had maximum number of pods plant^{-1} (35.4), followed by P.G-9 (34.9), while the minimum number of pods plant^{-1} (23.0) were recorded for Bashir 2021, followed by P.G-17 (23.6). Vg, Vp and Ve were 95.654, 100.441 and 4.787, respectively for number of pods plant^{-1}. GCV (18.279) and PCV (18.731) both were moderate. Broad sense heritability (h^2) (0.95) was high and G.A (13.362) was noted moderate.

Number of pods showed significantly positive genotypic association with pod shelling percentage (rg = 0.483*), while significantly negatively associated with pod length (rg = -0.465*) and 100-green pod weight (rg =-0.43*) and 100-fresh seed weight (rg = -0.795**). Number of flowers showed significantly positive phenotypic correlation with stem length (rp =0.310*), pod shelling percentage (rp = 0.378**), while significantly negatively associated with days to emergence (rp = -0.322**), number of pods (rp = -0.260*), pod length (rp = -0.367**), pod diameter (rp = -0.298*), seeds pod^{-1} (rp = -0.249*) and 100-green pod weight (g) (rp = -0.270*).

The flower is the main reproductive organ of the pea plant, which develops into a pod. The reproductive potential of the plant depends on how many flowers and pods it carries. The genotypes with more flowers thus produced a larger number of green pods. Having genetic variation in this character presents the opportunity to choose a desirable genotype to maximize the green pod production in peas. Shubha et al. (2018) also indicated variations in pea genotypes in terms of the number of pods per plant. Thirty garden pea genotypes were assessed for 10 quantitative yield-related characteristics and exhibited significant variations in the studied materials for these characteristics.

The parameter pods per plant had a significantly positive relationship with the days to first picking, days to flowering, first blossom node, number of leaves per plant, plant height, pods per plant, 100 green pod weight, 100 green seed weight, and the green pod yield. Devi et al. (2015) also obtained similar findings in their research, wherein they examined the genetic variation and correlation of significant yield traits in twenty-four pea genotypes. Their results showed that the flowering trait, more precisely the number of flowers per plant, is a crucial reproductive trait that has a direct impact on pod numbers and total yield.

Pod Length (cm)

The analysis of variance revealed highly significant variations among pea genotypes for the trait pod length (cm) (Table 2). The average values for pod length are provided in Table 2. The mean data for pod length (cm) ranged from 11.3cm to 6.6cm. The data showed that the variety Climax had highest pod length (cm) (11.3), followed by Bashir 2021 (11.1), while the lowest pod length (cm) (6.6) was recorded for P.G-8 and followed by P.G-5 (6.8). Vg, Vp and Ve were 7.986, 8.113 and 0.127, respectively for pod length. GCV (9.916) and PCV (9.994) both were low. Broad sense heritability (h^2) (0.98) was high and G.A (3.925) was noted low.

Pod length exhibited significantly positive genotypic associations with days to emergence (rg=0.635**), seed diameter (rg=0.590**), pod diameter (rg=0.716**), seeds per pod (rg=0.894**), 100-green pod weight (rg=0.955**), and 100-fresh seed weight (rg=0.967**). Conversely, it showed significant negative associations with seed length (rg= -0.498*), number of flowers (rg=-0.465*), and pod shelling percentage (rg= -0.913**). Furthermore, pod length demonstrated significantly positive phenotypic correlations with pod length (rp=0.377**), days to 50 percent flowering (rp=0.244*), number of pickings (rp=0.291*), seed diameter (rp=0.547**), pod diameter (rp=0.64**), seeds per pod (rp=0.796**), 100-green pod weight (rp=0.859**), 100-fresh seed weight (rp=0.295*), and yield (tons/ha) (rp=0.263*), while negatively associated with seed length (rp= -0.470**), number of flowers (-0.367**) and pod shelling percentage (rp= -0.367**).

The identified significant variation in pod length among pea genotypes aligns with findings reported by Khan *et al.* (2013), who also observed comparable variation in pod length among 13 pea genotypes. Similar results were reported by Singh *et al.* (2019) and Bashir *et al.* (2019). Singh *et al.* (2019) examined 55 pea genotypes and noted significant genetic diversity concerning yield and yield-related traits. In a study conducted by Bashir *et al.* (2019), nine pea landraces obtained from mountainous regions were examined, with the cultivar Meteor serving as the control. The study revealed significant variability among the landraces, particularly in terms of pod length. This aligns with what Gudadinni *et al.* (2017) found, where they also identified notable differences in pod length among 26 pea genotypes. The present outcomes are reinforced by the previous observations of Singh and Singh (2006), who noted substantial variations in pod length among 37 advanced pea lines.

Pod length displayed a notably positive connection in terms of observable traits such as the number of pods per plant, pod diameter, 100-green pod weight, and 100-green seed weight. Additionally, it showed a significantly positive genotypic correlation with the number of axillary stems per plant, pod diameter, the number of pods per plant, 100-green seed weight, and 100-green pod weight. These results are consistent with Sharma *et al.* (2003), who also reported a significant relationship between length of pod and number of seeds pod^{-1}.

Pod Diameter (cm)

The statistical analysis revealed significant variation amongst pea genotypes for the trait pod diameter (cm) (Table 2). Mean for pod diameter are given in table 2. The mean data for pod diameter (cm) ranged from 0.69 to 1.15. The data showed that P.G-16 showed maximum pod diameter (cm) (1.15), followed by Leena Pak (1.14), while the minimum pod diameter (cm) (0.69) was recorded for P.G-15, followed by P.G-14 (0.76). Vg, Vp and Ve were 0.077, 0.081 and 0.004, respectively for pod diameter. GCV (0.642) and PCV (0.657) were low. Broad sense heritability (h^2) (0.95) was high and G.A (0.381) was noted low.

Pod diameter exhibited a significantly positive genotypic association with traits such as days to emergence (rg=0.441*), pod length (rg=0.716**), seeds per pod (rg=0.816**), 100-green pod weight (rg=0.621**), and 100-fresh seed weight (rg=0.772**), while negatively associated with pod shelling percentage (rg= -0.795**). Pod diameter showed significantly positive phenotypic association with days to emergence (rp=0.245*), stem diameter (rp=0.282*), pod length (rp=0.644**), seeds pod^{-1} (rp=0.672**) and 100-green pod weight (rp=0.470**), while negatively associated with first blossom node (rp= -0.261*), days to first picking (rp= -0.4245**), stem length (rp= -0.482**), internode length (rp= -0.294*), number of flowers (rp= -0.298*), pod shelling percentage (rp= -0.570**) and root weight (rp= -0.315**).

Pea seed size is determined by pod diameter and is thus a quality characteristic of the crop. Thicker pods with bigger seeds are more desirable than thinner pods with smaller seeds. This research demonstrated high diversity in pod diameter among pea genotypes. The findings of this research are in agreement with the results of Akansha et al. (2011). During the evaluation of twenty pea genotypes to identify the nature and degree of genetic variation, considerable variation in pod diameter among different pea varieties was observed. Bashir (2014) and Umar et al.

(2014) also observed variation in pod diameter among pea genotypes. Bashir (2014) directly examined genetic variation among 12 pea genotypes and found considerable variation in pod diameter among the tested materials. Umar et al. (2014) further reported the presence of genetic diversity among 128 exotic pea accessions with different origins regarding pod diameter.

Pod diameter showed a significant positive relationship with seeds per pod, weight of 100-green seeds, pod length, and weight of 100-green pods but a significant negative relationship with days to first picking. Ali et al. (2007), Nisar et al. (2008), Ghobary (2010), and Bashir (2014) found the same results and indicated a strong positive correlation between pod diameter and characteristics like seeds per pod, pod length, and seed yield per plant in garden pea.

Seeds Pod^{-1}

The analysis of variance revealed highly significant variation among pea genotypes for the trait seeds per pod (Table 2). Mean for pod diameter are given in Table 2. Seeds pod^{-1} amongst various pea genotype ranged from 5.9 to 8.5. Highest number of seed pod^{-1} (8.5) was noted for Climax, which was at par with P.G-17 (8.3), followed by Tarnab Pea (7.7), while the minimum number of seed pod^{-1} (5.9) was recorded for genotype P.G-5, followed by P.G-7 (6.0). Vg, Vp and Ve were 4.519, 4.635 and 0.116 respectively, for seeds pod^{-1}. GCV (8.089) and PCV (8.192) both were low. Broad sense heritability (h^2) (0.97) was noted high and G.A (2.938) was noted low.

The trait seeds per pod exhibited a significantly positive genotypic correlation with days to emergence (rg=0.487*), stem diameter (rg=0.469*), pod length (rg=0.89**), pod diameter (0.816**), 100-green pod weight (rg=0.749**), 100- fresh seed weight (rg=1.043**), while significantly negatively associated with stem length (rg= -0.608**) and pod shelling percentage (rg= -0.883). Seeds per pod demonstrated a significantly positive phenotypic association with days to emergence (rp= 0.281*) and seed diameter (rp=0.413**), pod length (rp=0.796**), pod diameter (rp=0.672**), 100-green pod weight (rp=0.470**), while significantly negatively associated with days to first picking (rp= -0.311*), stem length (rp= -0.486**), internode length (rp= -0.319**), number of flowers (rp= -0.249*), pod shelling percentage (rp= -0.570**) and root weight (rp= -0.315**).

Seed yield had significantly positive relationships with many traits like number of plants per branch, number of plants per node, pod length, length of internode, 100-green weight of seed, number of seeds per pod, number of seeds per plant, number of pods per plant, and maturity of the plant. The most positive correlation with seed yield was noted with seeds per plant, followed by pods per plant, hundred seed weight and internode length. These observations support the likelihood that an increase in one trait will cause an increase in the other associated trait. The importance of the number of pods per plant to seed yield in pea was also highlighted by Singh and Singh (2006) as well as Singh et al. (2011). The present findings agree with the findings reported by Gudadinni et al. (2017), where large differences in seeds pod-1 existed among pea genotypes.

Also, our results are given further support by the work of Avci and Ceyhan (2006), who also reported outstanding differences in seeds per pod between different pea genotypes. Fikreselassie (2012) reported outstanding differences in seeds per pod in 25 renowned pea genotypes. In the current research, there was a strong phenotypic positive correlation between seed yield per plant and seeds per pod. Moreover, a strong genotypic positive association with pods per plant, fresh pod shelling percentage, days to maturity, 100-fresh seeds weight and pod length existed. The rest of the traits had non-significant genotypic relationships with seeds per pod, Sureja and Sharma (2004), Chaudhary and Sharma (2003), Choudhary et al., (2004), Singh and Singh (2005), Sonali et al. (2009) and Nawab et al. (2008) obtained the same findings.

Number of Pickings

The statistical analysis showed greatly substantial distinction amongst pea genotypes for the trait number of pickings (Table 2). Mean for number of pickings are given in table 2. Amongst all the genotypes and varieties mean value for this trait fluctuated in between 3.46 to 5.56. The data showed that genotype P.G-7 gave maximum number of pickings (5.56), followed by Bashir 2021 (5.26). Minimum number of pickings (3.46) were recorded for P.G-4, followed by P.G-8 (3.79). Vg, Vp and Ve were 2.443, 2.574 and 0.131 respectively for number of pickings. GCV (7.312) and PCV (7.506) both were low. Broad sense heritability (h^2) (0.94) was noted high and G.A (2.132) was low.

Number of pickings showed significantly positive genotypic correlation with100-green pod weight (rg=0.426*) and negatively associated with fresh pod shelling (rg=-0.453*). Number of pickings showed significantly positive phenotypic association with stem diameter (rp=0.253*), pod length (rp=0.291*), 100-green pod weight (rp=0.316**), while negatively associated with first picking days (rp= -0.285*), number of leaves (rp= -0.33**), number of flowers (rp= -0.260*) and pod shelling percentage (rp= -0.317**).

Analysis of variance showed highly significant differences among pea genotypes as was witnessed for number of picking (ANOVA Table 4.8a). The variation in number of pickings among the different lines and varieties may be due to inherited traits of individual genotypes (Damor et al., 2017). Kalloo et al., (2005) also witnessed similar varietal differences. Pod diameter and number of pickings revealed low heritability with low genetic advance indicating the importance of non-additive genes for these traits suggesting thus that their improvement may be achieved through heterotic breeding. Plant pods per plant, average plant pod weight, duration of picking, plant pods yield per plant, height of the plant and number of seeds per pod can be improved by pointing out that these characters had low variability in both genotypic and phenotypic terms with low heritability and genetic advance (G.A) (Sharma, et al 2010).

100-Fresh Green Seed Weight (g)

Analysis of variance displayed significant variances amongst pea genotypes for the trait 100-fresh green seeds weight (Table 2). Mean for 100-fresh green seeds weight are given in table 2. The mean 100-fresh green seed weight (g) among different genotypes ranged between 21.3 to 47.0 g. Maximum 100-fresh green seed weight (47.0 g) was noted for variety Tarnab Pea, followed by genotype P.G-1 (43.7 g) and P.G-13 (40.3 g). Minimum data for 100-fresh green seed weight (21.3 g) was recorded for P.G-3, followed by P.G-8. Vg, Vp and Ve were 178.55, 184.57 and 6.02, respectively for 100-fresh green seeds weight. GCV (24.59) and PCV (25.01) both were high. Broad sense heritability (h^2) (0.96) was high and G.A (18.40) was noted moderate.

The trait 100-fresh green seeds weight exhibited significantly positive genotypic associations with traits such as days to emergence (rg=0.703**), days to 50 percent flowering (rg=0.655**), stem diameter (rg=0.848**), pod length (rg=0.967**), pod diameter (rg=0.772**), seeds per pod (rg=1.043**), and yield tons (ha^{-1}) (rg=0.530*), while significantly negative association with leaves number (rg= -0.426*), flowers number (rg= -0.795**) and pod shelling (%) (rg= -0.857**). 100-fresh seeds weight showed significantly positive phenotypic association with traits days to emergence (rp=0.264*), stem diameter (rp=0.301*), pod length (rp=0.295*), seeds pod^{-1} (rp=0.312*) and 100-fresh green pods weight (rp=0.246*), while negatively associated with pod shelling (%) (rp= -0.396**).

Singh *et al*. (2011) and Achakzai (2012) have also stated similar findings were observed, where 100-seeds weight exhibited a significant and positive association with seed yield per plant. In order to enhance pea yield, it is crucial to prioritize correlated traits based on the strength of their correlation. The phenotypic correlation coefficients exhibited higher values compared to their corresponding genotypic correlation coefficients, representing a more significant contribution of phenotypic factors in determining the association. The genotypic variance exceeded the environmental variance for the 100-seed fresh weight. High heritability in the broad sense was estimated, but there was a low genetic advance for the 100-seed fresh weight. Siddika *et al*. (2013) reported similar findings, observed high heritability with low genetic advance in their study on 26 lines of pea, specifically in relation to 100-seed fresh-green weight. Our findings align with previous research by Singh and Singh (2006), who reported in a study involving 37 lines of pea, high heritability and low genetic advance for 100-seed weight.

The correlation between the 100-seed fresh weight and various traits was observed. A positive correlation found with seeds per pod, 100-seed dry weight, and seed yield per plant. On the other hand, there was a negative genotypic association between 100-seed fresh weight and plant height, while no significant associations were observed for the remaining traits at both phenotypic and genotypic levels. The current study aligns with the results of Aman *et al.*, (2021).

Yield (tons ha^{-1})

The statistical analysis showed substantial variations amongst different pea genotypes with respect to the yield trait (tons ha^{-1}) (Table 2). Mean for yield (tons ha^{-1}) are given in table 2. The mean yield (tons ha^{-1}) among different genotypes ranged from 4.5 to 13.5. Highest yield (tons ha^{-1}) was recorded for Bashir 2021 (13.5), followed by P.G-10 (10.9), while the minimum yield (tons ha^{-1}) was recorded for P.G-12 (4.5), followed by P.G-3 (6.5). Vg, Vp and Ve were 11.804, 12.138 and 0.334, respectively for yield (tons ha^{-1}). GCV (11.719) and PCV (11.884) both were moderate. Broad sense heritability (h^2) (0.97) was noted high and G.A (4.743) was noted as low.

Yield tons (ha^{-1}) displayed significantly positive genotypic association with 100-fresh seeds weight (rg= 0.530*), while there was a significantly positive phenotypic correlation with days to emergence (rp=0.248*) and days to 50 percent flowering pod length (rp=0.263*) and 100-green pod weight (rp=0.306*).

There were considerable variations in pod yield between the genotypes. Hatam and Amanullah (2001) also found grain yield, plant height, stem girth, and pods per plant significantly correlated with each other under field and rain conditions. For understanding the interrelationship between the characters under study, and their relationship with yield and with one another, the genotypic and phenotypic correlations were calculated. Overall, the genotypic correlations exceeded the respective phenotypic correlations, proving the intrinsic relationships among various traits. The correlation coefficients among various traits, both phenotypic and genotypic, showing a positive association between yield and number of pods per plant, pod length (cm), number of seeds per pod, and shelling percentage (%). However, total phenol content (g/100g) showed a considerable negative correlation, as cited by Kumar *et al*., (2015).

Table 2

Number of Pods, Pod Length (cm), Pod Diameter (cm), Seeds Pod-1 Number of Picking, 100-Green Seeds Weight (g), Yield Tons (ha-1) as Affected by Genetic Variability and Heritability of Garden Pea.

Genotypes	Number of pods	Pod length (cm)	Pod diameter (cm)	Seeds pod^{-1}	Number of pickings	100-green seeds weight (g)	Yield tons (ha^{-1})
PG-1	31.6	6.9	0.74	6.3	4.92	43.7	9.9
PG-2	34.6	7.2	0.88	6.6	3.96	28.7	8.6
PG-3	25.6	6.8	0.82	6.4	5.02	21.3 J	6.5 I
PG-4	27.4	7.0	0.79	6.1	3.46	25.3	7.6
PG-5	31.7	6.8	0.79	5.9	4.94	25.7	8.3
PG-6	29.8	7.0	0.77	6.6	4.07	33.0	9.8
PG-7	31.4	7.2	0.80	6.9	5.56	22.3	6.4
PG-8	26.2	6.6	0.83	6.4	3.79	21.7	10.2
PG-9	34.9	7.3	0.86	7.2	3.90	22.7	7.1
PG-10	28.7	7.2	0.80	6.0	5.18	26.3	10.9
PG-11	30.1	6.8	0.97	6.7	4.22	21.7	6.6
PG-12	26.0	7.8	0.98	6.8	4.90	33.3	4.5
PG-13	24.0	7.7	0.83	6.5	4.98	40.3	8.9
PG-14	29.8	7.0	0.76	6.6	4.49	22.7	6.8
PG-15	35.4	6.9	0.69	6.4	3.85	27.7	10.2
P.G-16	31.0	11.0	1.15	7.4	4.78	28.0	8.2
P.G-17	23.6	10.8	1.10	8.3	5.03	38.0	10.2
Lena Pak	28.3	8.4	1.14	7.6	5.24	25.7	9.2
Dassan	26.3	7.7	0.94	6.8	3.84	35.0	10.1
Climax	26.1	11.3	1.06	8.5	4.10	37.3	6.8
Bashir 2021	23.0	11.1	0.89	7.5	5.26	36.0	13.5
Tarnab Pea	27.5	10.9	0.92	7.7	5.38 A	47.0	9.9

Table 3

Genotypic Variance, Phenotypic Variance, Phenotypic coefficient of variability (%), Genotypic Coefficient of Variability (%), Broad sense heritability (h2), Genetic Advance (G.A) as Affected by Genetic Variability and Heritability of Garden Pea.

Parameters	Genotypic Variance	Phenotypic Variance	Environmental Variance	Phenotypic coefficient of variability (%)	Genotypic coefficient of variability (%)	Broad sense heritability (h^2)	Genetic advance (G.A)
Days to emergence	12.62	13.856	1.238	10.673	10.185	0.91	4.746
Stem length (cm)	3936.376	4053.276	116.90	49.764	49.041	0.97	86.561
Internode length (cm)	11.500	11.695	0.194	11.464	11.368	0.98	4.708
Stem diameter (cm)	0.025	0.026	0.001	2.347	2.285	0.94	0.214
Number of branches	3.726	3.862	0.136	8.083	7.939	0.96	2.654
Number of leaves	618.065	655.964	37.898	28.625	27.786	0.94	33.785
First blossom node	41.900	44.064	2.164	15.629	15.240	0.95	8.837
Days to 50% flowering	1172.096	1179.971	7.875	34.960	34.843	0.99	47.770
Days to first picking	1723.236	1754.639	31.402	37.722	37.383	0.98	57.594
Number of pods plant^{-1}	95.654	100.441	4.787	18.731	18.279	0.95	13.362
Pod length	7.986	8.113	0.127	9.994	9.916	0.98	3.925
Pod diameter	0.077	0.081	0.004	0.657	0.642	0.95	0.381
Seeds pod^{-1}	4.519	4.635	0.116	8.192	8.089	0.97	2.938
Pod shelling percentage	372.678	393.311	20.633	25.936	25.246	0.94	26.308
Number of pickings	2.443	2.574	0.131	7.506	7.312	0.94	2.132
100-green pods weight (g)	19744.10	20308.94	564.841	84.916	83.723	0.97	193.964
100-green seeds weight (g)	178.55	184.57	6.02	25.01	24.59	0.96	18.40
Yield tons (ha-1)	11.804	12.138	0.334	11.884	11.719	0.97	4.743
Root weight (g)	0.238	0.247	0.008	5.322	5.232	0.96	0.672

Qualitative Traits

The qualitative parameters of 22 pea genotypes are presented in table 4. Concerning flower color, it was observed that 14 pea germplasms, including cultivated pea varieties, displayed flowers with a white color. Only eight germplasms P.G-2, P.G-3, P.G-6, P.G-7, P.G-8, P.G-11, P.G-12 and P.G-14 formed purple colored flowers. Regarding the pod shape of the distal end, 8 pea genotypes were noted to produce pods with a blunt distal end, it was observed that the distal end of the pods in eight genotypes was blunt, whereas all other cultivated varieties of peas exhibited pods with a pointed distal end. Regarding pod degree of curvature only 2 pea varieties namely Bashir 2021 and P.G-17 produced pod with strong degree of curvature while P.G-3, P.G-11, P.G-13, P.G-14, P.G-15, Leena Pak, Dassan, Climax and P.G-16 did not show any curvature in their pods, 7 genotypes namely P.G-1, P.G-4, P.G-6, P.G-7, P.G-9, P.G-12 and variety Tarnab Pea pods exhibited a moderate level of curvature, whereas the rest of the genotype displayed a less degree of curvature in their pods. For seeds shape traits P.G-1, P.G-4, P.G-5, P.G-7, P.G-9, P.G-10, P.G-12 and P.G-13 produced ellipsoid and wrinkled seeds while P.G-3, P.G-15, P.G-16, Dassan and Leena Pak produced irregular and wrinkled seeds. The genotypes namely P.G-2, P.G-6, P.G-8, P.G-11, P.G-14 and variety Climax showed cylindrical shaped seeds. Pea genotypes namely P.G-1, P.G-4, P.G-5, P.G-6, P.G-7, P.G-8, P.G-9, P.G-10, P.G-11, P.G-12, P.G-13 and P.G-15 developed smooth surface seeds while P.G-2, P.G-3, P.G-14, P.G-17 and varieties namely Bashir 2021, climax, Tarnab Pea, Leena Pak and Dassan developed wrinkled surface seeds. As seeds mature, their color shifts from green to a creamy in many genetic variations, although some genotypes retain a green appearance. However it altered to brown color for P.G-2 and P.G-3, P.G-6 while P.G-1, P.G-4, P.G-5, P.G-9, P.G-10, P.G-12, P.G-13, P.G-15 and variety Leena Pak showed whitish color while in case of P.G-14, P.G-16, P.G-17 and varieties namely Bashir 2021, Dassan and Climax seeds color showed greenish color P.G-7 and P.G-11 changed from green to grey color.

Table 4

Flower Color (FC), Pod Shape (PS), Pod Degree of Curvature (PDC), Seed Shape (SS), Seed Surface (Ss) and Seed Color (SC) as Affected by Genetic Variability and Heritability of Garden Pea.

Genotype	FC	PS	PDC	SS	Ss	SC
P.G-1	white	blunt	medium	ellipsoid	smooth	whitish
P.G-2	purple	blunt	weak	cylindrical	wrinkled	brownish
P.G-3	purple	blunt	absent	irregular	wrinkled	brownish
P.G-4	white	pointed	medium	ellipsoid	smooth	whitish
P.G-5	white	pointed	weak	ellipsoid	smooth	whitish
P.G-6	purple	pointed	medium	cylindrical	smooth	brownish
P.G-7	purple	pointed	medium	ellipsoid	smooth	grey
P.G-8	purple	pointed	weak	cylindrical	smooth	grey
P.G-9	white	blunt	medium	ellipsoid	smooth	whitish
P.G-10	white	blunt	weak	ellipsoid	smooth	whitish
P.G-11	purple	inflated	absent	cylindrical	smooth	grey
P.G-12	purple	constricted	medium	ellipsoid	smooth	whitish
P.G-13	white	pointed	absent	ellipsoid	smooth	whitish
P.G-14	purple	blunt	absent	cylindrical	wrinkled	green
P.G-15	white	pointed	absent	irregular	smooth	whitish
P.G-16	White	blunt	absent	Irregular	wrinkled	green
P.G-17	White	blunt	strong	irregular	wrinkled	green
Leena Pak	white	pointed	absent	irregular	wrinkled	whitish
Dassan	white	blunt	absent	irregular	wrinkled	green
Climax	white	pointed	absent	cylindrical	wrinkled	green
Bashir 2021	white	pointed	strong	rhomboid	wrinkled	green
Tarnab Pea	white	pointed	medium	rhomboid	wrinkled	whitish

CONCLUSION

According to the present research analysis, it was determined that there was substantial difference among the pea genotypes for yield and yield attribute traits. Pea genotype Climax gave the highest first blossom node, days to flowering, internode length, pod length and seed pod-1. Pea genotypes Bashir 2021 gave augmented stem diameter, 100-fresh green pod weight and yield t ha-1. PG-15 was promising with the greater number of leaves plant-1 and number of pods plant-1. PG-8, PG-10, PG-15, PG-16 and PG-17 genotypes also produced higher yield tons (ha-1).

Recommendations

On the basis of superior yield and yield related characters' performance, pea genotypes PG-8, PG-10, PG-13, PG-15, PG-16 and PG-17 are recommended for further research in multiple locations yield trails. Similarly, the genetic possibilities for the genotypes under investigation to the desirable traits could be utilized in future breeding of peas.

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