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ASSESSMENT OF THE GENETIC VARIABILITY FOR VARIOUS AGRONOMIC TRAITS OF PEA (*Pisum sativum* L.) GENOTYPES

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ABSTRACT

The present study was conducted to study genetic variability and association among agronomic characters of pea (*Pisum sativum* L.) genotypes. The field experiment was conducted using ten genotypes at College of Agricultural Sciences (CAS) of International University of Business Agriculture and Technology (IUBAT), Dhaka, Bangladesh during the Rabi season (November 2020 to March 2021). Treatments were using the randomized complete block design (RCBD) with three replications. Highly significant ($p \leq 0.01$) differences among the tested genotypes were observed. The results obtained revealed that the mean squares of the genotypes (G6) were best for 50% flowering (50.38), days to maturity (122.08) and fresh pod shelling percentage (65.29%). Genotype (G2) had highest plant height (142.08 cm), pods plant^{-1}(39.96) and seed yield plant^{-1} (52.04 gm). G9 had maximum 100-seed fresh (43.90 gm) and dry (21.29 gm) weight. Genotype (G5) had best primary branches plant^{-1} whereas G8 had maximum pod length (8.86 cm) and seeds pod^{-1} (6.26). The estimates of heritability and genetic advance were high for days to 50% flowering (0.99, 35.38%), plant height (0.95, 46.88%) and seed yield plant^{-1} (0.97, 62.47%). High heritability with moderate genetic advance were observed for days to maturity (0.97, 20.20%), pod length (0.95, 15.37%) fresh pod shelling percentage (0.82, 21.58%), 100-seed fresh (0.90, 29.52%) and dry weight (0.93, 22.68%). Significant and positive phenotypic coefficient of correlation was exhibited by seed yield plant^{-1} with plant height ($r_p = 0.64$), days to 50% flowering ($r_p= 0.63$), days to maturity ($r_p = 0.78$), pods plant^{-1} ($r_p = 0.72$), pod length ($r_p = 0.66$), fresh pod shelling percentage ($r_p = 0.64$), 100-seed fresh weight ($r_p = 0.65$) and 100-seed dry weight ($r_p = 0.62$). Significant and positive genotypic coefficient of correlation was exhibited by seed yield plant^{-1} with plant height ($r_g= 0.81$), days to maturity ($r_g= 0.70$) and pods plant^{-1} ($r_g= 0.84$). Among tested genotypes G6, G2, G9 and G5 performed better, therefore could be used in future breeding programs. These traits best contributing to yield variation that emphasis by breeders for future yield improvement of the crop. It can be conclude that pea yield can be successfully improved by studying genetic variability and its agronomic characters.

***Keywords*: Pea (*Pisum sativum L.*), Genotypes, Variability, Heritability, Genetic advance and Correlation coefficient**

Introduction

Pea (*Pisum sativum* L. 2n = 14, Fabaceae) is one of the most important cool season food legume crops in the world covering 6.59 million hectares (FAOSTAT, 2012) and is the third most widely grown grain legume worldwide (Tyagi *et al.,* 2012). Grains of pea are rich source of 27.8% protein, 42.65% carbohydrates, iron, sodium, phosphorus, potassium, vitamins and some other important elements, which are good for human and livestock consumption. The residues of peas provide nutritious food for cattle and dairy cows and thus provide an additional benefit to poor farming families. Dry pea grains are naturally dried ones that are consumed in soups, stews, dal, chatapati, fried dal and various other value-added cuisines (Parihar *et al.,* 2014; Amna *et al.,* 2020; Azam *et al.,* 2020). Genus *Pisum* comprises two species, *Pisum sativum* and *Pisum fulvum* of which *Pisum sativum* L. is cultivated pea and is becoming popular in human foods due to its hypo-cholesterolaemic properties. It is a safe food material with no problems of mycotoxin, pesticide or fungicide residues (Santalla *et al.*, 2001).

It may have originated in South Asia but it is one of the most important herbaceous vegetables in Bangladesh. The peas with an annual production of 13534166 tons and one of the most produced pulses crops in the world. Major pea producing countries include Canada, the Russian Federation, China, Ukraine, India, USA, France, Australia, Ethiopia and Germany (FAOSTAT, 2018). In Bangladesh, the annual production of pea is around 14550 mt from an area of 11753 ha with productivity level of 1240 kg/ha (Anonymous, 2020). Genetic variability has been considered as an important factor that is also essential prerequisite for crop improvement program for obtaining high yielding progenies (Tiwari and Lavanya, 2012). The evaluation of genetic variability is important to know the source of genes for a particular trait within the available germplasm (Chakraborty and Haque, 2000; Bhardwaj and Kohli, 1999). There was no common criterion for selection of genotypes based on specific objectives among the plant materials.

The most important tasks for pea breeding the development of high yielding varieties with stable productivity with high output of seeds from the total biological yield (relatively high seed production the harvest index). Also sufficiently good resistance to diseases and unfavorable environmental conditions (drought, heat, high salt content in the soil) with different maturing types with high rate of organic matter accumulation during the initial phases of growth, sufficiently high intensity of photosynthesis, increases in protein content, essential amino acids and favorable rations (Gritton, 1986; Abdou *et al.,* 1999; Tiwari *et al.,* 2001). For all of these, genetic variability is very important to select suitable types among the segregating populations. It is necessary to partition the observed variability into its heritable and non-heritable components with the help of suitable genetic parameter such as genotypic coefficient of variation (GCV), heritability estimates and genetic advance etc. (Johnson *et al.,* 1955; Hanson *et al.,* 1956).

Genetic diversity has been considered as an important factor that essential prerequisite in the crop improvement program for obtaining high yielding progenies. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Moreover, genetic diversity among the segregating population helps select suitable types for commercial utilization (Pandey, 2009). Presence of high variability in the pea provides much more scope for its improvement. A great diversity is present in pea that may be used to develop new high yielding varieties (Georgieva *et al.,* 2016). A great proportion of variability has been observed in different agronomic characters of pea (Pallavi and Pandey, 2013). Local and exotic germplasm can be used in hybridization program for pea improvement (Javaid *et al.,* 2002).

For an effective breeding program of pea, it is necessary to know the importance and association of various components for genetic improvement to develop desired high yielding pea genotypes. Yield improvement cannot be solely achieved through direct selection because yield is a trait that depends on various yield-contributing characters (Kumar *et al.,* 2019). Correlation studies provide an opportunity to study the magnitude and direction of association of one character with another. The nature and magnitude of correlation coefficient helps breeders to determine the selection criteria for progress of various characters with yield. Pea yield could be enhanced by an understanding the interrelationship of yield and other traits at both phenotypic and genotypic levels for the initiation of effective breeding program (Ahmad *et al*., 2014). Unfavorable association between yield and its contributing components for the selection of desired attributes may result genetic slippage, and reduce the genetic advance and yield. The selection of highly heritable and positively correlated characters would be more effective. Pea productivity is too low to fulfill the required demand and this may be mainly due to the lack of high yielding varieties and resistance to biotic and abiotic stress (Kumar *et al.,* 2015). To meet the present demand, there is an essential germplasm evaluation for the genetic improvement of pea to develop desired high yielding genotypes. Thus, the present study was conducted to identify higher genotypes based on genetic variability and association between agronomic traits for further different breeding programs in the development of high yielding field pea varieties.

Materials and Methods

The field experiment was conducted at the experimental field of College of Agricultural Sciences (CAS) of International University of Business Agriculture and Technology (IUBAT), Dhaka 1230, Bangladesh during the Rabi season (November 2020 to March 2021). Ten genotypes of pea were studied to measure the variability, heritability, genetic advance and correlation coefficient among the genotypes Algera (G1), Bohatýr (G2), Zekon (G3), Alan (G4), Olivín (G5), Kamelot (G6), Primus (G7), Canis (G8), Tyrkys (G9) and Polaris (G10) in Table 1. Geographically, the experimental field is situated at the altitude of 12.9m above mean sea level (23° 52' 25" N - 90° 23' 47" E). The experiment was carried out in the Agro ecological region of “Madhupur Tract” (AEZ No. 28, Bangladesh). The land was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH range is 5.40– 5.67 and organic carbon content is 0.82%.

The seeds were sown in the field and seedlings were emerged five to twelve days after seed sowing. The experiment was conducted using the Randomized Complete Block Design (RCBD) with three replications. The unit plot size was 50 m × 4 m with a row-to-row distance of 60 cm and a plant-to-plant distance of 30 cm. The unit plots were fertilized with cow dung (10 t) and recommended dose of inorganic fertilizers (Urea 45 kg, TSP 62.5 kg and MP 50 kg ha^{-1}), respectively. The entire cow dung, TSP, MP and half of the urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two segments. First top dressing was done at 21 days after and second at 42 days after sowing.

After eliminating the border plants, observations were recorded on ten randomly chosen plants for 11 quantitative traits. Days to 50% flowering (DTFF), Plant height (PH), Primary branches per plant (PBPP), Days to maturity (DTM), Pods per plant (PPP), Pod length (PL), Fresh pod shelling percentage (FPS%), 100-seed fresh weight (HSFW), 100-seed dry weight (HSDW), Seeds per pod (SPP), and Seed yield per plant (SYPP). The mean, range and standard deviation (σ_x) for each character have been calculated and analysis of variance for each of the character was performed. The mean square (MS) at error and phenotypic variances were estimated as per Johnson *et al.* (1955). Genotypic and phenotypic co-efficient of variation was calculated by the formula suggested by Burton (1952). Broad sense heritability was estimated (defined by Lush, 1949) by the following formula, suggested by Hanson *et al.* (1956) and Johnson *et* *al.* (1955). The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were measured with the formula suggested by Johnson *et al.* (1955) and later on adopted Hanson *et al.* (1956). Correlation coefficient was further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959), Singh and Choudhary (2006).

Result and Discussion

The mean values of various genotypes have also shown a wide range of variability for various characters, which were studied in the present investigation (Table 2). The range record for Day to 50% flowering (50.38 to 92.17), Plant height (63.33 to 136.13), Primary branches per plant (2.63 to 4.00), Days to maturity (122.00 to 180.25), Pods per plant (21.13 to 40.00), Pod length (6.85 to 8.84), Fresh pod shelling percentage (42.39% to 65.23%), 100-seed fresh weight (24.23 to 44.81), 100-seed dry weight (13.63 to 21.30), Seeds per pod (4.13 to 6.13), and Seed yield per plant (15.07 to 48.22). Similar results were also observed by Georgieva *et al.* (2016), Gudadinni *et al.* (2017), and Kumar *et al.* (2019).

Analysis of variance

An analysis of variance for randomized complete block design accommodating ten genotypes in three replications carried out for each of the eleven characters. The mean sum squares due to replications, genotypes, and errors for all the characters are presented in Table 3. Analysis of variance indicated that genotypic mean squares were highly significant ($p<0.01$) differences for all majorities of the traits. The variation due to replication was non-significant for all the characters under study, while seeds per pod had significant ($p<0.05$) difference among genotypes. These results indicate that the presence of variability among the genotypes that used for effective selection or crop improvement. The results reported by Fikreselassie (2012) and Singh *et al.* (2017) were also recorded similar observations in their study. The variation due to genotypes was highly significant for all majorities of the traits. This indicated the presence of sufficient genetic variability for the traits in order to select various genotypes for effective breeding programs.

Mean performance of genotypes

The average performance of the pea genotypes in the ten peas revealed significant differences for all traits. The Days to 50% flowering ranged from 50.38 (G6) to 92.17 days (G3) with an overall mean of 66.93 days (Table 2) and (Figure 1). Early flowering in pea results in early maturity therefore early flowering is desirable while breeding for early maturity. Possible factors of early flowering and maturation in certain species indicate their adaptability to a particular environment, better and more efficient use of nutrients in relatively hostile environments may lead to early completion of plant stages and relatively early reproductive stage (Ishtiaq, 1996). Comparison of genotypes the Plant height 63.33cm (G4) to 136.13cm (G2) with the mean value of 81.87cm (Table 2). Our results showed the existence of significant variation for plant height among the tested genotypes. As the height of plants varies between different species, it can be said that height is a genetic trait. Similar results have been published in previous work by Hussain *et al.* (2005), and Bozoglu *et al.* (2007). Primary branches per plant 2.63 (G1) to 4.00 (G8) with an overall mean of 3.44 branches. Days to maturity mean values among pea genotypes 122.00 days (G6) to 180.25 days (G8) with a mean value of 143.06 days (Table 2). On overall basis data for Pods per plant 21.13 (G1) to 40.00 (G2) with an overall mean of 29.86, Pod length among genotypes varied between 6.85 cm to 8.84 cm with the overall mean of 7.38 cm, Fresh pod shelling percentage ranged from 42.39% (G10) to 65.23% (G3) with the mean value of 54.39% (Table 2). The current results indicated the significant differences in genotypes for 100-seed fresh weight 24.23g to 44.81g with the mean value of 32.51g and lowest observed in G1 and highest G9 genotypes. Also, found the highest and lowest 100-seed dry weight 21.30g (G9) and 13.63g (G7) with the overall mean of 16.23g. In the existing investigation mean values for seeds pod^{-1} ranged from 4.13 (G8) to 6.13 (G6) with the mean value of 5.06 observed in genotypes. Mean values for seed yield plant^{-1} ranged from 15.07g (G6) to 48.22g (G2) with the grand mean of 30.14 g (Table 2). Our results showed the existence of significant variation among the tested genotypes. Similar results were previously published in peas by Ahmad *et al.* (2014), Jaiswal *et al.* (2015), and Gudadinni *et al.* (2017).

Genotypic Variations

The genetic variability present in the genotypes provides the raw material of any plant breeding program based on which selection works to develop superior genotypes. Thus, the greater amount of variation for character in breeding materials, the greater the chance of its improvement through selection.

The genotypic variance (V_g), environmental variance (V_e), heritability ($h^{2(bs)}$), and genetic advance (%) for all the characters of genotypes studied in the present investigation (Table 3), was greater than the genotypic variance (V_g), of the variant, indicating variability presented in the genetic material, which was not only due to genotypic effects but also due to environmental influences. Iqbal *et al.* (2015), Gudadini *et al.* (2017), Pandey *et al.* (2015), Barcchiya *et al.* (2018), Katoch *et al.* (2016), Bashir *et al.* (2014), and Meena *et al.* (2017), was observed that relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. In the present study, highest V_g and V_e were observed for days to plant height and days to maturity. It indicates the existence of broad genetic base, which would be amenable for further selection. Similar searches have been previously reported by Pandey *et al.* (2015), Saxesena *et al.* (2014), Gudadini *et al.* (2017), Kumar *et al.* (2015), and Katoch *et al.* (2016). Medium V_g and V_e days to 50% flowering and seed yield per plant were observed. This implied the equal importance of additive and non-additive gene action in these characters.

These results are consistent with previous reports from Barcchiya *et al.* (2018), Gudadini *et al.* (2017) and Thakur *et al.* (2016). Low V_g and V_e were observed for a days to mature. Similar results were obtained by Georgieva *et al.* (2016), Katoch *et al.* (2016), Thakur *et al.* (2016), and Barcchiya *et al.* (2018). High genetic advance only occurs due to additive gene action Panse and Sukhatme (1967). Thus, the heritability combined with genetic advance will be more effective than the heritability alone. Very high estimates of heritability with high values of genetic advance by over percent mean were observed for all traits except maturity days that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection. These results are in accordance with the findings of Pandey *et al.* (2015), Gudadini *et al.* (2017), Georgieva *et al.* (2016), and Thakur *et al.* (2016). Seed yield per plant, plant height and days to maturity exhibited high degree of additive components like high estimates of heritability coupled with high genetic advance and presence of high (V_g) and (V_e), it indicates in peas genetic improvement can be achieve through selection by using the existing genotypes for above characters.

Correlation coefficients

Estimates of Pearson's correlation coefficient among the ten characters of the pea genotypes are presented in Table 4 and Figure 1(D). Significantly positive genotypic relationship was observed for seed yield plant^{-1} with days to 50% flowering (r_g= 0.587), plant height (r_g= 0.807), days to maturity (r= 0.696) pods plant^{-1} (r_g= 0.842), pod length (r_g= 0.413), fresh pod shelling percentage (r_g= 0.523) and 100-seed dry weight (r_p= 0.517). Negative genotypic relationship was exhibited by seed yield plant^{-1} and primary branches plant^{-1} (r_g= -0.097). Rest of the traits showed non-significant genotypic association with seed yield plant^{-1} (Table 4). Positive association between yield and pods per plant was also reported earlier by Tyagi and Shrivastava (2002), Sharma *et al.* (2003), and Patel *et al.* (2006).

Days to 50% flowering significant and positive phenotypic correlation with days to maturity (r_p= 0.630**), fresh pod shelling percentage (r_p= 0.707**), 100 seeds fresh weight, seeds pod^{-1} and seed yield plant^{-1} (r_p= 0.630*); Day to 50% flowering showed phenotypic negative association with primary branches plant^{-1} (r_p= -0.125). Days to 50% flowering showed significant positive genotypic association with fresh pod shelling percentage (r_g= 0.768**) and seed yield plant^{-1} (r_g= 0.587*) while negative genotypic association with primary branches plant^{-1} (r_g= -0.152) and days to maturity (r_g= -0.202). Days to 50% flowering showed non-significant correlation with all other traits both at genotypic and phenotypic levels (Table 4). These results are in accordance with the findings of Singh and Singh (2006).

Plant height exhibited significant positive phenotypic association with pods plant^{-1} (r_p= 0.536*) and seed yield plant^{-1} (r_p= 0.630**) and significant positive genotypic correlation with seed yield plant^{-1} (r_g= 0.807**) while it showed genotypic negative association with primary branches plant^{-1} (r_g= -0.202), pod length (r_g= -0.030) and 100-seeds fresh weight (r_g= -0.038). Plant height showed non-significant coefficient of correlation both at genotypic and phenotypic levels with other traits (Table 4). Current findings are similar with the results of Gul *et al.* (2005), Fikreselassie (2012), Habtamu and Million (2013), and Siddika *et al.* (2013).

Primary branches plant^{-1} revealed significant positive phenotypic correlation with pod length (r_p= 0.422*) and negative phenotypic correlation with seed yield plant^{-1} (r_p= -0.010) while it showed genotypic negative correlation with fresh pod shelling percentage (r_g= -0.308) and plant height (r_g= -0.202) and seed yield plant^{-1} (r_g= -0.097). Primary branches plant^{-1} had non-significant association both at genotypic and phenotypic levels with rest of the traits (Table 4). Singh and Singh (2006) found non-significant association between primary branches plant^{-1} and these results are not in conformity with the findings of Singh (1984).

Days to maturity exhibited significant positive phenotypic relationship with pods plant^{-1} (r_p= 0.629), pod length (r_p= 0.819), fresh pod shelling percentage (r_p= 0.678), 100-seeds fresh weight (r_p= 0.636) 100-seeds dry weight (r_p= 0.424), seeds pod^{-1}(r_p= 0.498*) and seed yield plant^{-1} (r_p= 0.777) and pods plant (r_p= 0.629). Days to maturity had negative genotypic association with days to 50% flowering (r_g= -0.202) while rest of the traits showed non-significant associations both at phenotypic and genotypic levels with days to maturity (Table 4). The current findings of Habtamu and Million (2013), Singh (1984), Fikreselassie (2012) and Singh and Singh (2006).

Pods plant^{-1} exhibited significant positive phenotypic correlation with pod length (r_p= 0.659), 100-seed fresh weight (r_p= 0.435) and seed yield plant^{-1} (r_p= 0.716). Significant positive genotypic association were observed for pods plan^{-1} with pod length (r_g= 0.580), 100-seed dry weight (r_g= 0.421), seeds pod^{-1} (r= 0.534) and seed yield plant^{-1} (r_g= 0.842). Rest of the traits had non-significant association both at phenotypic and genotypic levels with pods plant^{-1} (Table 4). The results of Fikreselassie (2012) and Singh (1984) also observed significant association of pods plant^{-1} with seed yield plant^{-1} both at phenotypic and genotypic levels.

In the present study pod length exhibited significant positive phenotypic association with fresh pod shelling percentage (r_p= 0.402), 100-seed fresh weight (r_p= 0.756), 100-seed dry weight (r_p= 0.559), seeds pod^{-1} (r_p= 0.568) and seed yield plant (r_p= 0.656). Pod length showed significant genotypic positive association with 100-seed fresh weight (r_g= 0.770), 100-seeds dry weight (rg= 0.608), seeds pod^{-1} (r_g= 0.797) and seed yield plant^{-1} (r_g= 0.413). The remaining traits showed non-significant association both at phenotypic and genotypic levels with pod length (Table 4). The current findings are in accordance with the results of Habtamu and Million (2013) and Siddika *et al.* (2013) showed non-significant correlation both at phenotypic and genotypic levels.

The fresh pod shelling percentage was phenotypically significant positive with 100-seed fresh weight (r_p= 0.658), 100-seed dry weight (r_p= 0.529 and seed yield plant^{-1} (r_p= 0.644). Fresh pod shelling percentage exhibited significant positive genotypic association with 100-seed fresh weight (r_g= 0.547), 100-seed dry weight (r_g= 0.457), seeds pod^{-1} (r_g= 0.485) and seed yield plant^{-1} (r_p= 0.523) negative genotypic association with primary branches plant^{-1} (r_g= -0.308). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with fresh pod shelling percentage (Table 4). Our results are further in support to the findings of Aman *et al.* (2021) revealed significant differences for fresh pod shelling percentage.

The association of 100-seed fresh weight was positive significant with 100-seed dry weight (r_p= 0.899), seeds pod^{-1}(r_p= 0.484) and seed yield plant^{-1} (r_P= 0.654) while significant positive genotypic association with 100-seed dry weight (r_g= 0.873) and seeds pod^{-1} (r_g= 0.709). 100-seed fresh weight had negative genotypic association with plant height (r_g= -0.038). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with 100-seed fresh weight (Table 4). The current study agreed with the results (Aman *et al.,* 2021).

In the present findings 100-seed dry weight exhibited significant positive phenotypic correlation with seeds pod^{-1} (r_P= 0.484) and seed yield plant^{-1} (r_P= 0.624) and genotypic positive correlation with days to maturity (rg= 0.435), pods plant^{-1} (r_g= 0.421), pod length (r_g= 0.608), fresh pod shelling percentage (r_g= 0.457) and 100-seed fresh weight (r_g= 0.873). Rest of the traits showed non-significant association both at phenotypic and genotypic levels with 100-seed dry weight (Table 4). Similar results of Singh and Singh (2006) and Siddika *et al.* (2013).

In the present conclusions seeds pod^{-1} exhibited significant phenotypic positive association with seed yield plant^{-1} (r_P= 0.452) and significant genotypic positive correlation with days to maturity, (r_g= 0.677), pods plant^{-1} (r_g= 0.534), pod length (r_g= 0.797), fresh pod shelling percentage (rg= 0.485), 100-seed fresh weight (r= 0.709) and 100-seed dry weight (r_g= 0.606). Rest of the traits showed non-significant genotypic association with seeds pod^{-1} (Table 4). Chaudhary and Sharma (2003), Sureja and Sharma (2004), Choudhary *et al.,* (2004), Singh and Singh (2005), Nawab *et al.* (2008) and Sonali *et al.* (2009) got the same result.

Conclusions

Significant differences were observed among the pea genotypes for all the studied traits. The genotypes contributing maximum heritability coupled with high genetic advance indicating more genetic influence and lesser environmental influence with considering the analysis of variance of yield contributing characters for find the desirable traits which have active relative contribution to the heritability, genotypic and phenotypic correlation coefficient to aim at developing improved varieties.

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Author's contribution

Conceptualization of research work and designing of experiments (S Kumar); Execution of field/ lab experiments and data collection (S Kumar, R Islam, M M Rahman and M Chakma); Analysis of data and interpretation (S Kumar, B Ali and W Ahmed); Preparation of manuscript (S Kumar), and revised the whole manuscript (M S Miah). All authors read and approved the final manuscript.

Table 1 : Source of diverse genotypes used in the current study

Genotypes	Year	Origin	Seed	Leaf	Pedigree	Breeding company
G1 (Algera*)	1989	CS	brown	N	(Weibuls Parvus × Violetta) × Kobald	SELGEN, CZ
G2 (Bohatýr)	1980	CS	yellow	N	(Kralicky Unicum × Pyram) × Dick Trom	SELGEN, CZ
G3 (Zekon)	1999	CZ	green	LS	(Sum x LU0040) × Emerald	SELGEN, CZ
G4 (Alan)	1993	CS	yellow	N	NDR × (R27 × Danielle)	ELITA, CZ
G5 (Olivín)	1990	CS	green	N	Luzany15 × Dippes Gelbe Victoria	Breeding St.Hor. Streda SK
G6 (Kamelot)	2001	CZ	yellow	LS	(Sum × LU0040) × Emerald	SELGEN, CZ
G7 (Primus)	1995	CZ	yellow	N	(Multipod×Finale)×141)×(Dick Trom × HP)×Ludik)	ELITA, CZ
G8 (Canis)	2000	SW	yellow	LS	Bohatyr × U 51041	Svalof Weibull, AB
G9 (Tyrkys)	1984	CS	green	N	Luzansky Krl-2 × Dick Trom	SELGEN, CZ
G10 (Polaris*)	1984	CS	green	N	Rondo CB × Kocovsky 11	SELGEN CZ

**Pisum sativum* subsp. *arvense*; CS = Czechoslovakia; CZ = Czech Republic; DN = Denmark; LS = leafless type; N = normal leaf type; SK = Slovakia; SW = Sweden

Table 2 : Performance of pea genotypes for yield and yield contributing characters.

Genotypes	DTFF	PH	PBPP	DTM	PPP	PL	FPS%	HSFW	HSDW	SPP	SYPP
G1	52.46	68.59	2.63	143.50	21.13	6.85	47.96	24.23	14.48	4.63	25.45
G2	80.67	136.13	3.00	150.00	40.00	7.11	58.60	28.97	16.32	5.00	48.22
G3	92.17	85.56	3.25	142.00	24.25	6.74	65.23	32.58	14.89	5.25	28.66
G4	63.92	63.25	3.13	138.25	26.38	6.87	63.39	30.98	15.50	5.25	23.64
G5	71.21	64.38	3.75	149.63	31.50	7.57	53.36	33.04	16.81	5.00	24.59
G6	50.38	67.38	3.50	122.00	24.75	7.08	44.31	30.51	14.97	4.38	15.07
G7	61.92	77.13	3.88	135.00	30.88	7.68	45.52	28.71	13.79	5.63	24.94
G8	71.67	81.88	4.00	180.25	37.00	8.84	63.16	41.25	17.82	4.13	46.23
G9	73.11	86.88	3.63	147.50	33.50	7.96	59.96	44.81	21.30	6.13	38.71
G10	51.83	87.50	3.63	122.50	29.25	7.16	42.39	30.05	16.40	5.25	25.91
Mean	66.93	81.87	3.44	143.06	29.86	7.38	54.39	32.51	16.23	5.06	30.14
$LSD_{(0.05)}$	2.26	9.05	0.86	5.25	9.01	0.26	6.09	3.26	0.99	0.94	3.30

DTFF= Days to 50% flowering, PH= Plant height (cm), PBPP= Primary branches plant^{-1}, DTM= Days to maturity, PPP= Pods plant^{-1}, PL= Pod length (cm), FPS%= Fresh pod shelling percentage, HSFW= 100-seed fresh weight (gm), HSDW= 100-seed dry weight (gm), SPP= Seeds pod^{-1} and SYPP= Seed yield plant^{-1} (gm)

Table 3 : Analysis of variance (mean sum of squares) and Genetic variability components of eleven important characters in respect of ten pea genotypes.

Parameters	Replication	Genotypes	Error	CV	Genotypic variance (V_g)	Environmental variance (V_e)	Heritability $h^{2\ (bs)}$	Genetic advance (%)
	DF=2	DF=9	DF=29					
DTFF	1.24	550.06**	1.75	1.98	182.77	1.75	0.99	35.38
PH	1.19	1539.89**	27.87	6.44	504.01	27.87	0.95	46.88
PBPP	0.20	1.36**	0.25	14.38	0.37	0.25	0.59	23.35
DTM	0.69	848.09**	9.39	2.14	279.57	9.39	0.97	20.20
PPP	16.48	107.03**	27.59	18.11	26.48	27.59	0.49	21.85
PL	0.02	1.35**	0.02	2.08	0.44	0.02	0.95	15.37
FPS%	10.00	180.72**	12.64	6.45	56.03	12.64	0.82	21.58
HSFW	0.44	103.34**	3.62	5.83	33.24	3.62	0.90	29.52
HSDW	0.04	14.36**	0.33	3.57	4.67	0.33	0.93	22.68
SPP	1.28	0.85*	0.31	10.11	0.18	0.31	0.37	8.36
SYPP	12.16	361.12**	3.72	6.37	119.13	3.72	0.97	62.47

DTFF= Days to 50% flowering, PH= Plant height (cm), PBPP= Primary branches plant^{-1}, DTM= Days to maturity, PPP= Pods plant^{-1}, PL= Pod length (cm), FPS%= Fresh pod shelling percentage, HSFW= 100-seed fresh weight (gm), HSDW= 100-seed dry weight (gm), SPP= Seeds pod^{-1} and SYPP= Seed yield plant^{-1} (gm)

Table 4 : Phenotypic (above diagonal) and genotypic (below diagonal) Pearson's correlation coefficients between different traits in pea genotypes.

	DTFF	PH	PBPP	DTM	PPP	PL	FPS%	HSFW	HSDW	SPP	SYPP
DTFF	-	0.297	-0.125	0.630**	0.355	0.333	0.707**	0.438*	0.355	0.395*	0.630**
PH	0.449*	-	-0.187	0.169	0.536**	0.066	0.146	0.090	0.187	0.151	0.637**
PBPP	-0.152	-0.202	-	0.029	0.275	0.422*	-0.220	0.204	0.188	0.061	-0.010
DTM	-0.202	0.210	0.074	-	0.629**	0.819**	0.678**	0.636**	0.424*	0.498*	0.777**
PPP	0.434*	0.717**	0.332	0.590*	-	0.659**	0.371	0.435*	0.350	0.344	0.716**
PL	0.123	-0.030	0.611**	0.703**	0.580**	-	0.402*	0.756**	0.559*	0.568*	0.656**
FPS%	0.768**	0.180	-0.308	0.604**	0.291	0.209	-	0.658**	0.529*	0.364	0.644*
HSFW	0.343	-0.038	0.397	0.526*	0.369	0.770**	0.547**	-	0.899**	0.484*	0.654**
HSDW	0.266	0.147	0.341	0.435*	0.421*	0.608**	0.457*	0.873**	-	0.411*	0.624*
SPP	0.382	0.072	0.217	0.677**	0.534*	0.797**	0.485*	0.709**	0.606**	-	0.452*
SYPP	0.587*	0.807**	-0.097	0.696**	0.842**	0.413*	0.523*	0.381	0.517*	0.551*	-

*, ** = significant at 5% and 1% probability level, respectively

DTFF= Days to 50% flowering, PH= Plant height (cm), PBPP= Primary branches plant^{-1}, DTM= Days to maturity, PPP= Pods plant^{-1}, PL= Pod length (cm), FPS%= Fresh pod shelling percentage, HSFW= 100-seed fresh weight (gm), HSDW= 100-seed dry weight (gm), SPP= Seeds pod^{-1} and SYPP= Seed yield plant^{-1} (gm)

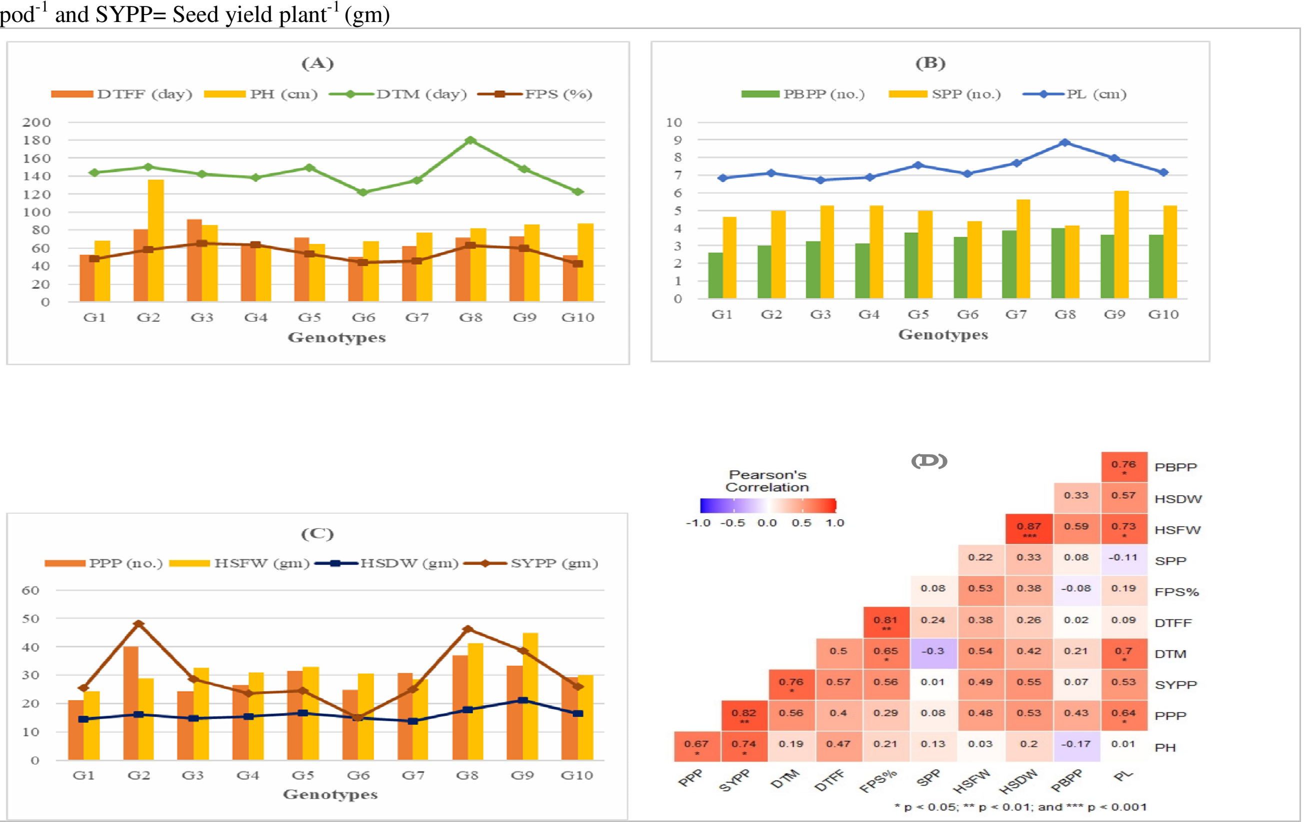

Fig. 1 : Means values of morphological and yield related traits of pea as influenced by different genotypes (A, B, C), and (D) Correlation coefficients.

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