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Some Direct and Indirect Selection Indices for Increased Yield of Peas (*Pisum sativum* L.)

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Abstract: The phenotypic expression of field pea (*Pisum sativum* L.) in terms of grain yield results as outcome of direct and indirect effects of various agronomic traits. An experiment was conducted at Vegetable Research Station, Bahawalpur, Pakistan during 2015-2016 to measure the effects of various yield attributes on the final yield. Ten genotypes of field pea viz; DP-1-14, DP-2-14, DP-3-14, DP-4-14, DP-5-14, DP-6-14, DP-7-14, DP-8-14, No. 267 and Pea-09 were grown in field under randomized complete block design replicated thrice. Data for various traits including plant height, branches per plant, number of clusters per plant, pods per plant, pod length, pod width, seeds per pod, 100-seed weight and grain yield per plant were recorded at maturity. Statistical analysis showed that plant height had the highest values of GCV% (57.77), heritability (0.95), genetic advance and percentage of genetic advance (116), while the highest value of phenotypic coefficient of variation was exhibited by number of cluster per plant. The highest significant and positive genotypic correlation was observed between seeds per pod and pod length (88%). 100-seed weight also showed significant and positive association with seeds per pod. Path analysis revealed that pod length had the highest direct effect on seed yield of peas (7.99) followed by number of cluster per pod (5.82) and branches per plant (5.19). The above mentioned traits may be considered while attempting for improvement in pea seed yield.

Keywords: Pea, variability, correlation, path analysis, yield attributes.

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1. Introduction

Pea (*Pisum sativum* L.) is originated from the Middle East and cultivated in diversified agroclimatic conditions of around 100 countries of the world (Gudadinni et al., 2017; Smykal et al., 2012). Pea is an important vegetable rich in protein (27%) and used as food and in animal feed (Koivunen et al., 2016; Singh et al., 2017). In recent years, demand of peas as seed as well as for fodder has been increased. Pea seeds and green pods have good balance of vitamins (Hussain et al., 2019; Santos et al., 2019).

Like other legumes, pea plant provides significant ecological advantage in low-input farming systems by fixing atmospheric nitrogen, and enriches the soil by supplying nutrient and improving (Ludidi et al., 2007; Tulbek et al., 2017). Therefore, peas have significant importance for the crop rotation (Li et al., 2018; Li et al., 2019; Ouda et al., 2018; Siddika, 2013; Teixeira et al., 2019). Peas have deep root system which penetrates into the soil up to the 1.0-1.5m and extract the minerals from deeper soil layers which are difficult to extract for other grain crops.

Field pea is excellent source of protein supplement in mulch animals and poultry ration along with minerals like copper, folic acid, manganese and thiamine (Hussain et al., 2019). It is good source of iron, magnesium, phosphorous and potassium (Singh et al., 2017). Peas have high level of two amino acids i.e. tryptophan and lysine which are lower in amount in cereals (Saharan and Khetarpaul, 1994). Field pea has high level of carbohydrates and lower fiber

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content with containing 86-87% total digestible nutrients, therefore this crop better for the animals feed (Saharan and Khetarpaul, 1994).

The genetic variability in peas, like any other crop, is important for breeding for their character improvements (Afreen et al., 2017). Correlation analysis is useful for measuring of degree of association of various yields related traits (Ahmad et al., 2014). Path analysis provides information about the direct and indirect impact of various attributes on the economic yield of the plant (Guleria et al., 2009; Jaiswal et al., 2015).

2. Materials and Methods

A Field experiment was conducted at Vegetable Research Station, Bahawalpur, Pakistan. Ten genotypes of field pea viz; DP-1-14, DP-2-14, DP-3-14, DP-4-14, DP-5-14, DP-6-14, DP-7-14, DP-8-14, No. 267 and Pea-09 were arranges in randomized complete block design (RCBD) with three replications. Data were recorded for various yield contributing traits including plant height, number of clusters, pod length, pod width, seed per pods, 100 seed weight, pods plant^{-1}, and branches plant^{-1}. Correlation and path analysis were used for the study the strength and direction of association among various traits and to measure the direct and indirect effects of various traits on seed yield. Broad sense heritability, Genetic advance (GA) and Genetic advance in percent of mean (GA%) were estimated using the formula suggested by Johnson et al. 1955 and Hanson et al. 1956.

Heritability, an index of character's transmission from parents to their offspring, was calculated by the formula;

$$H^2 b.s = \frac{V\boxed{?}}{V\boxed{?} + V\boxed{?}} = \frac{V\boxed{?}}{V\boxed{?}} \times 100$$

Correlation provides the direction and strength of association among various traits. Genotypic and phenotypic correlation coefficient were carried out using formula suggested by Miller et al. (1958), Johnson et al. (1955) and Hanson et al. (1956).

The genotypic and phenotypic correlation coefficients were calculated as under;

$$rgxy = \frac{\sigma^2 gxy}{\sqrt{(\sigma^2 gx)(\sigma^2 gy)}}$$

$$r_{pxy} = \frac{\sigma^2 pxy}{\sqrt{(\sigma^2 px)(\sigma^2 py)}}$$

The correlation coefficient were further partitioned into components of direct and indirect effects by path coefficient analysis developed by Wright (1934) and later described by Dewey and Lu (1959).

3. Results and Discussion

The genetic variation is a baseline for the breeding program of any crop lead to the crop improvement. So, various traits contributing to the final economic yield were evaluated. In field pea, plant height had the highest GCV and PCV percentage (57.77% and 59.28%, respectively) which indicated the high level of variation (Table 1). High heritability (0.95) along with high percentage of genetic advance (116) for plant height could play an important role in grain yield improvement. Number of cluster, 100 seed weight, pods plant^{-1}, and branches plant^{-1}had high values of GCV% and PCV% along with larger values of heritability. The results were in accordance with Nawab et al. (2008) and Georgieva et al. (2016). The heritability for all the included traits had high values i.e. plant height (0.94) had highest heritability that was followed by the pod length (0.89).Whereas, genetic advance was high for the plant height and 100 seed weight. The similar results were also reported by Kumar and Goh (2002) and Gowher et al. (2013).

Table 1. Genetic variability of various yield related traits of peas

Traits	GCV (%)	PCV (%)	Heritability	GA	GA%
PH	57.77	59.28	0.95	77.17	116
NC.P	50.93	69.42	0.54	2.74	76.98
P.P	20.69	28.60	0.52	5.71	30.85
PL	12.73	13.45	0.89	1.52	24.81
PW	9.47	12.38	0.58	0.12	14.94
S.P	5.27	14.10	0.14	0.16	4.06
B.P	20.56	26.45	0.60	0.88	32.93
SW100	22.68	26.62	0.73	5.47	39.83
Y.P	20.2	28.13	0.51	2.29	29.87

PH=Plant height, NC.P=Number of clusters per plant, P.P= Pods per plant, PL= Pod length, PW=Pod width, S.P=Seeds per pod, B.P=Branches per plant, SW100=100 seed weight, Y.P=Grain yield per plant.

Table 2. Genotypic (lower triangular) and phenotypic (upper triangular) correlation matrix among various traits of peas

	PH	**NC.P**	**P.P**	**PL**	**PW**	**S.P**	**B.P**	**SW100**	**YP**
PH	1	-0.06	0.01	-0.03	0.3	-0.18	-0.12	0.10	0.17
NC.P	-0.15	1	0.42	-0.48	-0.31	-0.16	-0.13	-0.38	-0.04
P.P	-0.04	0.45	1	-0.52	-0.06	-0.08	0.46	-0.30	0.25
PL	-0.04	-0.65	-0.59	1	0.48	0.43	-0.14	0.41	0.09
PW	0.41	-0.70	-0.17	0.74	1	-0.02	0.15	0.45	0.28
S.P	-0.59	-0.49	-0.87	0.88	0.53	1	0.16	0.32	-0.06
BP	-0.20	-0.55	0.32	-0.09	0.20	0.05	1	0.28	0.03
100SW	0.09	-0.67	-0.45	0.55	0.71	0.84	0.48	1	0.42
YP	0.24	-0.15	0.01	0.26	0.45	-0.03	-0.15	0.67	1

PH=Plant height, NC.P=Number of clusters per plant, P.P= Pods per plant, PL= Pod length, PW=Pod width, S.P=Seeds per pod, B.P=Branches per plant, SW100=100 seed weight, Y.P=Grain yield per plant.

The GCV (57.77%), PCV (59.28%), heritability (0.94%) and genetic advance (77.17) for plant height had higher values than number of pods per plant and seeds per pod. These results were agreed with Habtamu and Million (2013).

3.1. Genotypic correlation

The value of genotypic correlation between pod length and seeds per pod was highest i.e. 0.88, followed by seeds per pod and 100 seed weight (0.84) and then 100 seed weight and grain yield (0.67) of pea plant. The interpretation of this result was that pod length had more association and effect over seeds per pod ultimately over the yield indirectly. The correlation value of 100 seed weight had more direct effect on the peas yield (0.67) that was followed by pod width, pod length and plant height with correlation values 0.45>0.26>0.24 respectively (Table 2).

The results were in accordance with the Yirga et al. (2015) for the plant height which had positive correlation with the grain yield (0.24) and had negative correlation with pods per plant (-0.04). Togay et al. (2008) also reported that there was positive correlation of seeds per plant with branches per plant (0.05) and negative correlation (-0.59) with plant height.

3.2. Phenotypic Correlation

Phenotype is outcome of both the genotype and the environment in which genotype is growing (Kumar et al., 2017). There was negative correlation of number of cluster per plant with pod length (-0.48), while positive correlation with the pods plant^{-1} (0.42) (Table 2). Pods plant^{-1} had high negative correlation with pod length (-0.52) however, positive correlation with branches plant^{-1}, and yield of pea plant (0.25). Pod length had high positive correlation with pod width (0.48) followed by the seeds per pod (0.43) and 100 seed weight (0.41). Pod width had high correlation with the 100 seed weight. Yield of plant had positive phenotypic correlation with 100-seed weight, seeds per plant and pods per plant with values 0.42, 0.28 and 0.25 respectively. Similar results had been reported by Kumar et al. (2017).

Table 3. Path analysis for yield related traits of peas

	PH	**NC.P**	**PP**	**PL**	**PW**	**S.P**	**B.P**	**100SW**
PH	**4.38**	-0.91	-0.01	-0.29	-2.05	0.11	-1.06	0.11
NC.P	-0.67	**5.82**	0.04	-5.23	3.53	0.09	-2.87	-0.86
P.P	-0.16	2.65	**0.09**	-4.74	0.88	0.16	1.67	-0.54
PL	-0.16	-3.82	-0.06	**7.99**	-3.75	-0.16	-0.50	0.71
PW	1.76	-4.08	-0.02	5.95	**-5.03**	-0.1	1.05	0.91
S.P	-2.59	-2.87	-0.08	7.04	-2.68	**-0.18**	0.25	1.09
BP	-0.88	-3.22	0.03	-0.77	-1.02	-0.01	**5.19**	0.54
100-SW	0.38	-3.88	-0.04	4.43	-3.57	-0.16	2.17	**1.29**

PH=Plant height, NC.P=Number of clusters per plant, P.P= Pods per plant, PL= Pod length, PW=Pod width, S.P=Seeds per pod, B.P=Branches per plant, SW100=100 seed weight, Y.P=Grain yield per plant.

The phenotypic correlation value of 100 seed weight was positive with number of branches per plant (0.28) and had negative correlation with pods per plant (-0.30). The same results were reported by Siddika et al. (2013). Yirga et al. (2015) had also reported similar result for the plant height which had high phenotypic correlation with yield. Habtamu and Million, (2013) reported that the pods per plant had highly significant negative correlation with pod length (-0.52) and the plant height had negative correlation with seeds per pod (-0.18).

3.3. Path analysis

Path analysis is used in the estimation of direct and indirect effects of various traits on the seed yield. The direct effect of pod length, number of cluster per plant, branches plant^{-1}, plant height and 100 seed weight on seed yield of pea genotypes was positive and very high with values 7.99>5.82>5.19>4.38>1.29 respectively (Table 3). Pods plant^{-1} had negligible direct effect and seeds per pod had moderate negative direct effect. Pod width had very high negative effect on the seed yield. Siddika et al. (2013) worked out that 100-seed weight had direct positive effect on the grain yield. Yirga et al. (2015) had also reported that plant height and pods plant^{-1} had direct positive effective on the grain yield.

Plant height had negative indirect effect on seed yield through cluster plant^{-1}, pod plant^{-1}, pod length, pod width, branches plant^{-1}. Through seeds per pod and 100 seed weight, plant height showed low positive indirect effect on the seed yield. Number of clusters plant^{-1} had very high positive indirect effect through pod width (3.53) and had high negative indirect effect through pod length (-5.23) on the seed yield. Pods per plant had very high positive indirect effect through cluster of pods (2.65) followed by the branches plant^{-1} (1.67) and very high negative indirect effect through pod length (-4.74) on the seed yield.

Pod length had high positive indirect effect through 100 seed weight (0.71) and very high negative indirect effect through number of cluster of pods (-3.82) followed by the pod width (-3.75) on the seed yield. Pod width had very high positive indirect effect via pod length (5.95), plant height (1.76) and branches plant^{-1} (1.05) upon the seed yield at both genotypic and phenotypic levels. Seeds per pod had very high positive effect upon the seed yield via pod length (7.04) followed by 100 seed weight (1.09). Branches plant^{-1} had high positive indirect effect on seed yield via 100 seed weight (0.54) and very high negative effect through number of clusters (-3.22).

The negative indirect correlation was reported by the Yirga et al. (2015) between plant height and pods plant^{-1}. The plant height had positive indirect effect over grain yield through 100 seed weight (0.38) and negative effect through pods per plant (-0.16). The pods plant^{-1} had negative indirect effect on the yield of dry through pod length (-4.74) and 100 seed weight (-0.54). These results were also reported by the Siddika et al. (2013). Togay et al. (2008) also showed the negative indirect effect of plant height through number of pods plant^{-1} and positive effect through number of branches plant^{-1} (0.25). Rasaei et al. (2011) reported that there was high direct positive direct effect of pod length (7.99) on the grain yield improvement.

Residual effect is the measure of deviation of observed value from the theoretical values. This effect is basically due to environment which is not under human control. So, phenotype is outcome of both of environment and genotypes. The observed data had residual value 0.03 and its value can be minimized through improving the management practices for better and accurate results.

5. Conclusion

All yield related traits had significant effect on the yield of field pea. Plant height is an important trait in breeding point of view because of high values of genetic coefficient of variance along with higher value of heritability, genetic advance and genetic advance percentage. Pod width and pod length had highest degree of association with the grain yield. Pod length had very high positive direct effect over the grain yield followed by the number of clusters and plant height respectively. Whereas, other traits had indirect effect on the grain yield like number of seed per pod, number of pods plant^{-1} and plant height.

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Author's Contribution: Author Imtiz Ali contributed in experiment upto 50%, Muhammad Tariq Mehmood contributed 10% and all other remaining authors contributed 8% respectively.

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