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Estimation of correlation and path analysis coefficient among yield and yield attribution trails of field pea (*Pisum sativum* L.)

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Abstract
Field pea (*Pisum sativum* L.) is one of the most important legume crops in India. In order to develop high yielding variety of field pea explosion of available genetic wealth of these crops is very essential. Therefore, this study was conceived to examine the variability and determine the relative importance of primary and secondary traits as selection criteria to improve productivity. The experiment material comprised of 14 genotypes for thirteen traits with three replications during the year 2016-17 at Bundelkhand University, Jhansi, U.P. Five competitive plants from each plot were randomly selected for recording observation for all the quantitative traits. The analysis of variance was found highly significant for all characters. High heritability and high genetic advance percent of mean plant height followed by harvest index, days to 50 % flowering and biological yield per plant. The genotype showed moderate high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). The magnitude of phenotypic coefficient of variance(PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance(GCV) which indicates very less environmental influence on the expression of the traits. Higher estimate of GCV was recorded for plant height followed by number of secondary branch per plant. Correlation analysis indicates that seed yield per plant exhibited highly significant and positive correlation with harvest index, 100 seed weight and Number of secondary branches per plant. Path analysis indicates that the highest positive and direct effect on seed yield per plant was exerted by biological yield per plant and harvest index. Highly positive indirect effect on seed yield per plant was exerted by number of pods per plant via days to maturity, biological yield per plant and harvest index. The characters identified above as important direct and indirect yield component can be used in formulation of selection strategies in field pea for selection of high yielding genotypes.

Keywords: GC, PCV, heritability, genetic advance, correlation and path analysis

Introduction
Field pea (*Pissium sativum* L.) is one of the self pollinated diploid (2n=14) annual pulse crop and is valued as high proteinious food. It is widely grown in the cooler temperate zone and in the highland of tropical region of the world. The pulse as a group in Ethiopia constitutes considerable number and diversity of crop species [1]. Field pea is amongst the most important legume crop of India belongs to family Leguminoseae, the area under pea production in India likely to be stagnating due to competition of irrigated wheat and other pulses crops with wider consumer use [2]. The plant breeder has to depends upon the variability present in the material for the improvement of qualitative and quantitative characters and their mutual association with seed yield [3, 4]

Heritability act as predictive tool in expressing the reliability of phenotypic traits and thus high heritability could assist in effective selection of particular characters and devise future breeding programme [5, 6]. Germplasm serve as most valuable natural reservoir for providing donor parent to improve the particular trait by genetic reconstruction of plant [7] therefore collection, conservation, of germplasm are essential for present as well as future crop improvement programmes. Correlation coefficient analysis revealed better understanding of yield component and assist in effective selection and hybridization programme as similar reported by [8, 9, 10].

Keeping this in background the present paper deals with the genetic variability for yield and quality traits in field pea.

Material and Method
The present investigation was carried out at Horticultural research farm, Bundelkhand University, Jhansi (U.P.) during Rabi season 2016-17. The experimental materials are collected from IIPR Kanpur (U.P.). Experiment was laid out in randomized block design with

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three replication. The seeds were sown at a spacing of 30 cm X 10 cm. Recommended agronomical practices were followed to maintain a good crop. The observation were recorded on five randomly selected competitive plants from each plot in every replication for the traits viz. Days to 50% flowering, Plant height (cm), Number of primary branches per plant, No. of secondary branch per plant, pod length, days to maturity of edible green pod, days to maturity, biological yield per plant, number of seed per pod, 100 dry seed weight, harvest index % and seed yield per plant.

The data were averaged and statistically analyzed for analysis of variance as per the method suggested by [11]. The genotypic correlation coefficients was described by [12] and as per formula given by [8]. The estimates of direct and indirect effect were calculated by the path coefficient analysis suggested by [13] and elaborated by [14] at both phenotypic and genotypic levels.

Result and Discussion
The analysis of variance present in table No.1 is highly significant for all the characters which indicate that high amount of genetic variability were present in the genetic material. High heritability with high genetic advance percent of mean represented in table no. 2 respectively viz. Plant height (94.80 % & 60.07 %) Harvest Index (92.20 % & 30.55%) and No. of pod per plants (73.70 and 26.07%). High heritability with moderate genetic advance respectively viz., 100 seed weight (77.60 & 15.02%) and Biological yield per plant (81.20 & 15.41%) and high heritability and low genetic advance percent of mean (73.40 & 3.61) and days to 50% flowering (82.60 & 7.11%). The presence of high heritability, high genetic advance & percent of mean is indicator of carrying the selection for future breeding programme. High heritability with moderate genetic advance percent mean and high heritability with low genetic advance percent of mean

which indicates that for it should not be used for future selection programme.

Estimate of GCV is more than high PCV respectively viz. Plan height (29.95 & 30.77) Number of secondary branches per plant (16.40 & 23.94) and harvest index % (15.43 & 16.08) is indicator of breeding further selection. Similar result were also reported by [15, 9, 16]

Estimate of genotypic correlation among the twelve characters of field pea genotypes are present in Table 3 at genotypic level, Seed yield per plant exhibited highly significant and positive correlation with Harvest Index % (0.952**), 100 Seed weight (0.622), No. of Secondary branches /Plant (0.284), and No. of Primary Branches/Plant (0.245), similar result were found by [17]. The significant but negative correlation with Seed yield /plant was recorded with Pod length (-0.910). Path coefficient analysis were estimated on genotypic as well as phenotypic levels to resolve the direct and indirect effects for different traits on seed yield as present in Table 4. At genotypic level the highest positive direct effect on biological yield per plant (1.91) followed by Harvest Index (0.926), No. of seed per pod (0.560), 100 Dry seed weight (0.405) and No. of secondary branches/plant (0.556) this indicates that direct contribution of these traits was too low to be considered by any consequences.

Highly Positive indirect effects, days to maturity, edible green pod (0.995) via No. of Pod/Plant followed by Biological yield per plant (0.865) via Plant height and days to maturity, edible green pod (0.570) with plant. The genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficient in the experiment as found by [18, 19] also. However in general genotypic correlation coefficients were higher in magnitude from the corresponding phenotypic correlation values. Similar result have been reported by [20, 21, 22, 23, 24]

Table 1: Analysis of variance for thirteen characters of Field pea genotypes

Characters	Mean Sum of Square		
	Replication (d.f.=2)	Treatment (d.f=11)	Error (d.f.=22
Days to 50% flowering.	1.789	19.378**	1.273
Plant Height (cm).	40.094	1902.953**	34.287
Number of primary branches per plant.	4.565	9.721**	0.160
Number of secondary branches per plant.	0.115	1.297**	3.550
Number of pod per plant.	2.071	19.999**	2.128
Pod length (cm).	0.274	0.384**	0.072
Days to maturity of edible green pods.	11.813	12.279**	1.322
Days to maturity.	1.594	7.211**	3.288
Biological yield per plant (g).	2.666	26.769**	1.923
Number of seed per pod.	0.074	0.617**	0.787
100 dry seed weight (g).	1.429	6.067**	0.533
Harvest index (%).	7.190	42.912**	1.185
Seed yield per plant (g)	0.667	2.753**	0.777

** = Significant at 5% level   * = Significant at 1% level respectively

Table 2: Genetic parameter of 13 characters of field pea (*Pisum sativum* L.)

Sr. No.	Genotypes	Range		Grand Mean	Heritability (h²)	GCV	PCV	GA	GA % of mean
		Min.	Max.						
1.	Days to 50% flowering	60.00	67.33	64.7143	82.60	3.80	4.18	4.60	7.11%
2.	Plant Height (cm)	40.93	115.20	83.320	94.80	29.95	30.77	50.05	60.07%
3.	No. of Primary Branch/plant	3.07	4.87	3.6381	46.60	11.96	17.52	0.61	16.80%
4.	No. of Secondary Branch/plant	2.67	5.13	3.4167	46.90	16.40	23.94	0.79	23.17%
5.	Number of Pod/ Plant	12.53	20.33	16.5786	73.70	14.72	17.15	4.32	26.07%
6.	Pod Length (cm)	3.72	4.83	4.1167	59.00	7.83	10.19	0.51	12.41%
7.	Days to Maturity of Edible green pod.	90.33	96.33	93.2381	73.40	2.05	2.39	3.37	3.61%
8.	Days to maturity	109.00	114.00	110.8810	28.50	1.03	1.93	1.26	1.14%
9.	Biological yield/plant (gm)	19.67	41.00	34.6667	81.20	8.30	9.22	5.34	15.41%

10.	Number of seed / pod	3.20	4.60	3.8857	45.00	9.83	14.67	0.53	13.63%
11.	100 Seed weight (gm)	14.47	18.77	16.3810	77.60	8.29	09.41	2.46	15.02%
12.	Harvest index (%)	16.79	29.54	24.1643	92.20	15.43	16.08	7.38	30.55%
13.	Seed yield / plant (gm)	6.14	9.60	8.1912	45.90	9.91	14.63	1.13	13.80%

H^2: heritability, GCV: Genotypic coefficient of variance, PCV: Phenotypic coefficient of variance, GA: genetics advance, GA%: Genetic advance percentage of mean

Table 3: Estimates of genotypic correlation coefficient among yield and its contributing characters in field pea

S. No.	Characters	Plant Height (cm)	No. of Primary Branch/plant	No. of Secondary Branch/plant	No. of Pod/ Plant	Pod Length (cm)	Days to Maturity of Edible green pod	Days to maturity	Biological yield per plant	No. of seed / pod	100 Seed yield (gm)	Harvest index (%)	Seed Yield / plant
1.	Days to 50% flowering	-0.179	-0.075	-0.436	-0.261*	0.370**	0.533**	0.517**	0.077	0.159	-0.012	-0.219	-0.356
2.	Plant Height (cm)		-0.134	-0.047	0.497**	-0.024	-0.381	-0.548	0.727**	0.209	-0.338	-0.442	-0.163
3.	No. of Primary Branch/plant			0.240*	-0.070	0.496**	0.603**	0.660**	0.265*	-0.052	0.969**	-0.042	0.245*
4.	No. of Secondary Branch/plant				0.094	-0.349	0.030	0.231*	0.024	-0.542	-0.282	0.047	0.284*
5.	Number. of Pod/ Plant					-0.580	-0.666	-0.976	-0.145	0.647**	-0.285	0.010	0.101
6.	Pod Length (cm)						0.866**	1.126	0.551**	-0.234	0.142	-0.823	-0.910
7.	Days to Maturity of Edible green pods							1.104	0.180	-0.296	0.471**	-0.394	-0.543
8.	Days to maturity								0.302	-0.301	0.658**	-0.398	-0.194
9.	Biological yield / plant (gm)									-0.360	0.128	-0.654	-0.224
10.	No. of seed / pod										-0.340	0.143	-0.053
11.	100 Seed yield (gm)											0.359**	0.622**
12.	Harvest index (%)												0.952**

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

Table 4: Genotypic path coefficients showing direct and indirect effects of different characters on seed yield per plant (g)

S. No.	Characters	Days to 50% flowering	Plant Height (cm)	No. of Primary Branch/ plant	No. of Secondary Branch/ plant	No. of Pod/ Plant	Pod Length (cm)	Days to Maturity Edible green pod	Days to maturity	Biological yield	No. of seed / pod	100 dry Seed weight (g)	Harvest index%
1.	Days to 50% flowering	0.240	0.163	0.009	-0.242	-0.003	0.110	-0.797	0.191	0.092	0.089	-0.005	-0.203
2.	Plant Height (cm)	-0.043	-0.912	0.016	-0.026	0.005	-0.007	0.570	-0.202	0.865	0.117	-0.137	-0.409
3.	No. of Primary Branch/ plant	-0.018	0.122	-0.122	0.133	-0.001	0.148	-0.901	0.244	0.315	-0.029	0.392	-0.038
4.	No. of Secondary Branch/plant	-0.105	0.043	-0.029	0.556	0.001	-0.104	-0.046	0.085	0.028	-0.304	0.104	0.043
5.	Number of Pod/ Plant	-0.063	-0.454	0.009	0.052	0.010	-.0173	0.995	-0.360	-0.172	0.362	-0.115	0.009
6.	Pod Length (cm)	0.089	0.022	-0.061	-0.194	-0.006	0.298	-1.294	0.416	0.656	-0.131	0.057	0.762
7.	Days to Maturity Edible green pod	0.128	0.348	-0.074	0.017	-0.007	0.258	-1.495	0.407	0.215	-0.166	0.191	-0.365
8.	Days to maturity	0.124	0.500	-0.081	0.128	-0.010	0.336	-1.649	0.369	0.360	-0.168	0.266	-0.368
9.	Biological yield / (gm)	0.019	-0.662	-0.032	0.013	-0.002	0.164	-0.270	0.111	1.191	-0.202	0.052	-0.606
10.	No. of seed /	0.038	-0.191	0.006	-0.301	0.007	-0.070	0.442	-0.111	-0.429	0.560	-0.138	0.133

	pod											
11.	100 dry Seed weight (gm)	-0.003	0.309	-0.118	0.157	-0.003	0.042	-0.703	0.243	0.152	0.190	0.405	0.332
12.	Harvest index %	-0.053	0.403	0.005	0.026	0.000	-0.245	0.589	-0.147	-0.779	0.080	0.145	0.926
13.	"r" value Seed Yield / plant	-0.356	-0.163	0.245	0.284	0.101	-0.910	-0.543	-0.194	-0.224	-0.053	0.622	0.952

Residual effect – 0.4974

Application of Research
Study of genetic variability for different quantitative traits in field Pea (*Pisum sativum* L.) genotypes

Research Category
Genetics and Plant Breeding

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