Exploring Genetic Variability, Trait Associations and Path Coefficient Analysis in Pea (*Pisum sativum* L.) to Advance Breeding Strategies

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ABSTRACT

The experiment was conducted at seed breeding farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, Madhya Pradesh, India during the *rabi* season (November, 2019–April, 2020) to estimate the parameters of genetic variability, assess the correlation among traits, and estimate direct and indirect effects. The ANOVA revealed that the mean sum of squares due to genotypes was highly significant for all the traits. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters. High values of phenotypic coefficient of variation and genotypic coefficient of variation were observed for most of the traits, while moderate values of phenotypic coefficient of variation and genotypic coefficient of variation were recorded for 100 seed weight, pod length, days to 50% flowering and days to first flower opening. High heritability with high genetic advance as a % of mean was recorded for most of the traits. Moderate heritability and high genetic advance were recorded for the number of primary branches plant^{-1}, secondary branches plant^{-1} and pod length, indicating the control of additive gene action. Meanwhile, high heritability with moderate genetic advance for days to maturity showed non-additive gene action. Correlation coefficients and path analysis for phenological and quantitative traits indicated that the most important traits are number of seeds plant^{-1}, number of effective pods plant^{-1}, biological yield plant^{-1} and harvest index. Hence, directional selection through these traits may effectively improve seed yield and its attributes.

KEYWORDS: Correlation coefficients, heritability, path analysis, pea, quantitative traits

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Pea (*Pisum sativum* L.) is a crop of profound historical significance grown worldwide (Kalapchieva et al., 2021). It belongs to the family *Fabaceae*, subfamily *Papillionaceae*, and *tribe Vicieae* and comprises two species, *Pisum fulvum* Sibth and *Pisum sativum* L. (Ali et al., 2021). The Genetic composition of Pea is ca. 4800 Mbp spread across 2n=2x=14 chromosomes (Bishnoi et al., 2021). Pea's journey from the Fertile Crescent to Russia, westward into Europe, and eastward into China and India is a testament to its remarkable resilience and adaptability, inspiring hope for future crop improvement programs (Warkentin et al., 2015). The four centers of origin based on genetic diversity were namely Central Asia, the Near East, Abyssinia (Ethiopia) and the Mediterranean (Smykal et al., 2014).

The nutritional value of dry pea seeds is impressive, with a rich protein content (22.5%) and all the essential amino acids. They also provide 56.5% carbohydrate, 1.1% fat, 2.2% minerals, 4.5% fibre, and essential vitamins like B_1 and B_5 (Anand et al., 2024b). In addition to its nutritional value, it enriches soils by fixing nitrogen from the atmosphere (Sanwal et al., 2024).

The lack of diverse genetic resources and the narrow genetic base in cultivated germplasm could hindered the effective utilization of conventional breeding and the development and utilization of genomic tools. Knowledge about the genetic makeup of a population is a fundamental need in breeding programs (Kahraman and Onder, 2009, Shilpashree et al., 2021). Yield and yield contributing traits result from the combination of environment and genetics, including regulatory and structural genes, and their variants reveal their genetic regulations. Thus, a change in phenotypic characteristics is a sign of genetic expression (Dean et al., 1999, Anand et al., 2024a). Breeding efforts have significantly improved yield potential and regional adaptation by conferring resistance or tolerance to biotic and abiotic stresses, plant type and grain characteristics (Reckling et al., 2018, Sanwal et al., 2024).

The nature and magnitude of genetic variability and how far to which the desirable traits are heritable are essential for exploiting the desirable traits (Mawblei et al., 2022). Heritability, indicating the proportion of phenotypic variance that are heritable (Bhardwaj et al., 2020, Singh et al. (2024). The genetic advance, indicate an improvement in the genetic value of the new population compared to the original one (Kumari et al., 2012, Katoch et al., 2016, Ofga and Petros, 2017, Shilpashree et al., 2021).

Yield is a complex character resulting from the actions and interactions of various component characters (Grafius, 1960, Uhlarik et al., 2022). It is also widely recognized that the genetic architecture of yield can be resolved better by studying its component characters, which enables the plant breeder to breed for high-yielding genotypes with desired combinations of traits (Ali et al., 2021, Kumar et al., 2022). The correlations are significant in plant breeding because they reflect the dependence between two or more traits (Falconer, 1981, Khan et al., 2022, Dhangrah et al., 2023). Path coefficient analysis calculates the direct and indirect contribution of various independent characters on a dependent character based on the assumption of mutual relationships among yield components. (Jeberson et al., 2016; Sharma et al., 2023). Determination of correlation and path coefficient between yield and yield attributes is essential for selecting favourable plant types for an effective pea breeding program (Katoch et al., 2016, Dhangrah et al., 2023).

The current study was carried out to estimate genetic variability parameters, analyze patterns of trait associations, and measure the direct and indirect impact of yield-contributing traits on seed yield. These insights aim to facilitate future crop improvement programs.

2. MATERIALS AND METHODS

The present investigation was conducted at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, Madhya Pradesh, India during the *rabi* season November, 2019–April, 2020. Jabalpur is situated at 23.900 N latitude and 79.580 E longitudes at an altitude of 411.87 m above the mean sea level. This region has subtropical, semi-arid climate with hot and dry summer and cold winter with occasional showers. The experimental materials, comprising fifty-two pea genotypes, were sourced from the Field Pea Improvement Project at the Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, and the AICRP on MULLaRP, IIPR Kanpur (Table 1). The trials were meticulously planned in a Randomised Complete Block Design (RCBD) with three replications. Each genotype was sown in a two-row pattern, maintaining a 30×10 cm² distance. For each replication, five competitive plants were randomly selected from each plot to record various observations, except for days to first flower opening, days to 50% flowering, and days to maturity (DM), which were recorded on a plot basis.

The observations were recorded on 18 characters, providing a comprehensive view of the Pea genotypes. These characters include days to first flower opening (DFFO), days to 50% flowering (DFF), days to maturity (DM), number of primary branches plant⁻¹ (NPBPP), number of secondary branches plant⁻¹ (NSBPP), plant height (PH), number of nodes plant⁻¹ (NNPP), number of effective nodes plant⁻¹ (NENPP), pod bearing length (PBL), number of pods plant⁻¹ (NPPP), number of effective pods plant⁻¹ (NEPPP),

Table 1: List of genotypes used in the experiment

Sl. No.	Germplasm	Sl. No.	Germplasm
1.	DDR 52	27.	Rachna
2.	P 3	28.	FP 75-96
3.	FP 14-56	29.	Choti Safed (Anju)
4.	HFP 94-13	30.	FP 18-30
5.	FP 14-46	31.	FP 14-8
6.	KPMR 30	32.	Matar Rangpur
7.	FP 9-539	33.	FP 94-12
8.	PP 155	34.	JP 180
9.	DDR 54	35.	FP 14-33
10.	JP 885	36.	VRP 5
11.	HVP 2	37.	PSM 3
12.	IPF 99-25	38.	Safed Batara Gudda
13.	FP 1482	39.	FP 7562
14.	RP 3	40.	FP 1330
15.	KPMR 405	41.	Gol BataraTendua
16.	FP 14-27	42.	GS 10
17.	FP 14-21	43.	Aman
18.	KPMR 402	44.	FP 14 86
19.	DDR 55	45.	Arka Sampurna
20.	KPMR 327	46.	Arkel
21.	NDVP 4	47.	FP 1417
22.	KPMR 502	48.	JM 6
23.	VL 3	49.	DDR 27
24.	FP 14-13	50.	KPMR 585
25.	Jayanti	51.	FP 14-15
26.	B 22	52.	Pusa pragati

pod length (PL), number of seeds pod^{-1} (NSPP), number of seeds plant^{-1} (NSPPlt), 100 seed weight (100 SW), biological yield plant^{-1} (BYPP), harvest index (Hl) and seed yield plant^{-1} (SYPP).

The coefficient of variation at the genotypic and phenotypic levels was determined using the Burton's (1952) method. The phenotypic and genotypic variations were also calculated using the approach suggested by Burton and De Vane (1953), further ensuring the reliability of the results. Heritability was calculated in a broad sense using the formula suggested by Hanson et al. (1956). Expected genetic advance (GA) was calculated by the method suggested by Johnson et al., 1955. The correlation coefficients among the characters in all possible combinations were calculated using the procedure by Miller et al. (1958). Path coefficient

analysis was conducted to show the cause-and-effect relationship between yield and various yield components and partition the total correlation coefficient into direct and indirect effects. This procedure was developed by Wright (1921) and modified by Dewey and Lu (1959).

3. RESULTS AND DISCUSSION

3.1. Estimation of parameters of genetic variability

The analysis of variance revealed that the mean sum of squares due to genotypes was significant for all the traits studied, indicating sufficient variability among the genotypes (Table 2).

The estimation of genotypic and phenotypic components of variation is a fundamental step in comprehending the relative extent of heritable and non-heritable components of variation. The higher magnitude of phenotypic coefficients of variation compared to the genotypic coefficient of variation for yield and yield attributes studied, indicates the significant influence of the environment on the expression of these traits. Similar findings are reported by Katoch et al. (2016) and Thakur et al. (2022), Kumar et al. (2023) (Table 3).

The highest PCV and GCV, was recorded for the number of pods plant^{-1} followed by the number of effective nodes plant^{-1}, number of effective pods plant^{-1}, number of seeds plant^{-1} and other trait studied. Similar findings were reported by Tolessa et al. (2017) and Singh et al. (2019). The trait 100 seed weight, pod length, days to first flowering, and days to 50% flowering were found to have moderate phenotypic and genotypic coefficient of variation. Jeberson et al. (2016) found similar results. The days to maturity had low coefficients of variation, which was also reported by Tolessa et al. (2017).

3.2. Heritability

An attempt was made to estimate the broad sense heritability in the present investigation, which involves all types of gene expressions. If the heritability of a character is very high (70% or more), Selection for such traits should be simple because the genotype and phenotype coincide closely due to the environment's minimal impact on the phenotype; however, because the environment's propensity to mask genotypic effects makes selecting traits with low heritability extremely difficult or practically unsuitable (Bhardwaj et al., 2020). Since the estimate of heritability in a broad sense includes the contribution of both additive and non-additive effects, these are of limited value unless the level of additive gene action is known.

In the present investigation, most characters expressed high heritability estimates except for the number of secondary branches plant^{-1}, pod length, and primary branches plant^{-1}, which show moderate heritability (Table 3). Similarly high

Table 2: Analysis of variance yield and its components

SV	d.f	DFFO	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL
Replications	2	4.75	3.30	4.10	1.72	2.19	37.47	31.08	11.69	13.17
Treatments	51	168.00**	165.16**	127.26**	0.79**	2.13**	2825.16**	651.94**	82.84**	160.13**
Error	102	0.56	0.85	0.65	0.18	0.27	13.71	4.87	1.42	2.82
SEd±		0.61	0.75	0.65	0.35	0.42	3.02	1.80	0.97	1.37
CD (*p*<0.05)		1.21	1.49	0.13	.069	0.84	5.99	3.57	1.93	2.72
CD (*p*<0.01)		1.60	1.98	0.17	.92	1.11	7.93	4.73	2.56	3.60

Table 2: Continue...

SV	d.f	NPPP	NEPPP	PL	NSPP	NS/P	100 SW	BYPP	HI	SYPP
Replications	2	14.07	9.80	0.23	0.08	295.27	0.05	29.41	8.01	8.48
Treatments	51	189.61**	130.51**	1.68**	2.02**	156.64**	30.32**	275.25**	161.84**	414.73**
Error	102	2.18	1.72	0.27	0.13	40.91	0.05	5.02	5.28	1.19
SEd±		1.20	1.07	0.42	0.30	5.22	0.19	1.82	1.87	0.89
CD (*p*<0.05)		2.39	2.12	0.84	0.60	10.35	0.39	3.62	3.72	1.77
CD (*p*<0.01)		3.16	2.81	1.12	0.80	13.70	0.52	4.80	4.92	2.34

Table 3: Parameters of genetic variability for yield traits in pea

Sl. No.	Character	Mean	Range		PCV (%)	GCV (%)	h2b (%)	GA as % of mean
			Min.	Max.				5%
1.	Days to first flower opening	56.07	36.33	69.33	13.38	13.32	99.01	27.30
2.	Days to 50% flowering	62.34	43.33	77.00	11.96	11.87	98.46	24.26
3.	Days to maturity	93.83	77.66	108.00	6.97	6.92	98.48	14.15
4.	No. of PB plant^{-1}	1.98	1.01	3.56	31.42	22.73	52.33	33.87
5.	No. of SB plant^{-1}	3.73	2.23	6.05	25.27	21.10	69.70	36.29
6.	Plant height	87.16	39.39	149.56	35.37	35.12	98.56	71.82
7.	No. of node plant^{-1}	48.93	23.70	86.09	30.35	30.01	97.79	61.14
8.	No. of EN plant^{-1}	11.82	6.28	36.15	45.18	44.04	95.00	88.43
9.	Pod bearing length	50.05	17.35	108.97	39.38	39.23	99.27	80.53
10.	No. of pods plant^{-1}	17.57	7.22	38.12	45.75	44.97	96.62	91.06
11.	No. of EP plant^{-1}	15.32	6.24	30.88	43.60	42.75	96.15	86.36
12.	Pod length	5.55	4.11	7.22	15.54	12.34	63.14	20.21
13.	No. of seed pod^{-1}	4.07	2.71	6.24	21.53	19.48	81.88	36.32
14.	No. of seed plant^{-1}	60.54	23.96	152.21	43.05	41.74	93.98	83.35
15.	100 seed weight	17.97	12.37	26.32	17.72	17.67	99.41	36.30
16.	Biological yield plant^{-1}	28.95	16.51	61.82	33.68	32.78	94.72	65.72
17.	Harvest index	36.64	17.86	46.62	20.68	19.71	90.81	38.69
18.	Seed yield plant^{-1}	10.49	5.15	20.12	36.52	35.01	91.98	69.12

*Classes of heritability (%): High >70%, Moderate 50–70%, Low <50%; *Classes of GA as % of mean at 5%: high >20%, Moderate 10-20%, Low <10%; *Classes of PCV (%), GCV (%): high >20, Moderate 10–20, Low <10

heritability was reported by Pratap et al. (2024) for plant height, effective pods plant^{-1}, harvest index and seed yield plant^{-1}, while Singh et al. (2024) and Kumar et al. (2023) for plant height, days to 50% flowering, 100-grain weight and days to maturity.

3.3. Genetic advance

As the genetic advance estimates depend upon the unit of the characters under measurement, the values of genetic advance were expressed as a % of the mean to compare expected genetic gain for different characters from one generation of selection in a hypothetical selection programme. Estimates of genetic advances help predict the level of improvement that may be accomplished by enhancing certain traits. The highest genetic advance as % of mean (at 5% selection intensity) was recorded for number of pods plant^{-1} (91.06) followed by number of effective nodes plant^{-1} (88.43), number of effective pods plant^{-1} (86.36), number of seeds plant^{-1} (83.35) and other traits studied. Moderate genetic advance as a % of the mean was recorded for days to maturity (14.15) (Table 3). Results supported with the findings of Jeberson et al. (2016) for number of seeds pod^{-1} and 100 seed weight, Jagadeesh et al. (2023) for plant height and seeds plant^{-1}.

High heritability coupled with high genetic advance as a % of the mean would offer a better scope of selection for pod-bearing length, number of effective pods plant^{-1}, number of seeds plant^{-1}, number of pods plant^{-1}, and number of effective nodes plant^{-1} because these traits were govern by additive gene effects. Singh et al. (2017) observed high heritability coupled with high genetic advance for number of seeds plant^{-1}. Similarly Pratap et al. (2024) and Sharma et al. (2023) reported for the traits viz., plant height, effective pods plant^{-1}, harvest index and seed yield plant^{-1}.

3.4. Association analysis

In the present investigation, correlations were calculated at phenotypic and genotypic levels in all possible character combinations of pea genotypes. In general, phenotypic correlation coefficients were higher in magnitude than genotypic correlation coefficients, which indicated that the environment affects character expression (Table 4, 5).

The phenotypic correlation coefficient was studied considering eighteen component traits, out of which traits viz. number of seeds plant^{-1} (0.8957), number of effective pods plant^{-1} (0.8145), biological yield plant^{-1} (0.8119), number of pods plant^{-1} (0.7201), number of effective nodes plant^{-1} (0.5143), number of nodes plant^{-1} (0.5123), plant height (0.4672), harvest index (0.4303) and pod bearing length (0.3820) had a significant positive correlation with seed yield plant^{-1} which indicated that effective improvement in field pea yield through these components could be achieved (Table 4). Ofga et al. (2017), observed positive association of days to maturity, seeds pod^{-1} and harvest index with seed yield plant^{-1}. Singh et al. (2017), found number of seeds plant^{-1}, number of pods plant^{-1}, weight of 100 seeds, number of seeds pod^{-1} positively correlated with each other and other yield attributes. Singh et al. (2018) observed a significant positive correlation between the seed yield plant^{-1} and the harvest index, biological yield plant^{-1}, plant height, number of seeds pod^{-1}, number of primary branches plant^{-1}, number of pods plant^{-1}, and 100-seed weight. Ali et al. (2021) found positive correlation with seed yield plant^{-1} with plant height, days to 50% flowering, days to maturity, pods plant^{-1}, pod length, 100-seed dry weight.

3.5. Path coefficient analysis

Path coefficient analysis was carried out using all possible genotypic correlation coefficients among various characters under study. It measures various independent characters' direct and indirect contribution to a dependent character. These coefficients are free from units and directional and may be more or less than unity, enabling too easy interpretation. Correlation coefficients indicate a simple association between variables. In a biological system, however, the relationships may be very complex. Therefore,

Table 4: Genotypic correlation for physiological and yield traits in pea genotypes

	DFFO	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL
DFFO	1.0000	0.9872	0.4976	-0.3422	-0.2671	0.1431	0.1842	0.0778	0.2714
DFF		1.0000	0.516	-0.3142	-0.2307	0.1720	0.1922	0.0923	0.2694
DM			1.0000	-0.0898	-0.0904	0.0602	0.0903	0.1164	0.0151
NPBPP				1.0000	0.6562	0.4609	0.4840	0.1712	0.3140
NSBPP					1.0000	0.3554	0.2856	-0.0064	0.2170
PH						1.0000	0.6860	0.4042	0.8718
NNPP							1.0000	0.6852	0.5897
NENPP								1.0000	0.3136
PBL									1.0000

Table 4: Continue...

	NPPP	NEPPP	PL	NS/Pod	NS/Pt	100 SW	BY/P	HI	SY/P
DFFO	0.1900	0.2871	0.0869	-0.2522	0.1752	-0.2625	0.1396	0.0277	0.1528
DFF	0.1739	0.2484	0.1068	-0.2043	0.1610	-0.2386	0.1301	0.0098	0.1443
DM	-0.0070	-0.0174	0.0168	-0.0992	-0.0443	-0.1926	-0.0228	-0.1989	-0.1194
NPBPP	0.1958	0.2329	-0.0241	-0.0609	0.1981	-0.1770	0.2328	-0.2842	0.0958
NSBPP	-0.0200	-0.0342	-0.0489	0.0698	0.0948	-0.0065	0.2223	-0.3890	0.0311
PH	0.5303	0.5145	-0.2176	-0.2559	0.4353	-0.0749	0.6462	-0.2569	0.4797
NNPP	0.7132	0.6789	-0.0071	-0.4348	0.5229	-0.2669	0.6238	-0.0995	0.5250
NENPP	0.8561	0.7059	-0.0427	-0.2918	0.6226	-0.4406	0.5121	0.0596	0.5236
PBL	0.4428	0.4622	-0.2133	-0.3809	0.3443	0.0132	0.5727	-0.2454	0.4111
NPPP	1.0000	0.9370	-0.0593	-0.3642	0.8306	-0.4837	0.6105	0.2712	0.7408
NEPPP		1.0000	-0.0743	-0.3906	0.8790	-0.4251	0.6730	0.3455	0.8350
PL			1.0000	0.2866	0.0517	-0.1253	-0.0332	0.1444	0.0390
NS/Pod				1.0000	0.0364	-0.0821	-0.1000	0.0929	-0.0380
NS/Pt					1.0000	-0.4910	0.6869	0.3947	0.8905
100 SW						1.0000	0.0043	-0.1455	-0.1035
BY/Pt							1.0000	-0.1723	0.8180
HI								1.0000	0.4086
SY/Pt									1.0000

Significance levels (p=0.05); (p=0.01); If correlation r=0.1729, 0.2260

it is essential to study the relationships among the variables comprehensively. Path coefficient analysis, however, provides a realistic basis for allocating appropriate weightage to various attributes while designing a pragmatic programme for improving crop yields (Sharma et al., 2023).

Path coefficient analysis of different characters contributing towards seed yield showed that Biological yield plant[-1] (0.6936) had the highest positive direct effect followed by days to 50% flowering (0.4854), harvest index (0.4383), number of effective pods plant[-1] (0.2588), number of seeds plant[-1] (0.1137) and 100 seed weight (0.0958) indicates

authentic relationships with seed yield plant[-1], and direct selection for these traits would result in higher breeding efficiency for improving yield (Table 6). Similarly Pratap et al. (2024) reported that biological yield plant[-1] had the highest direct effect on seed yield, followed by the harvest index, number of seeds pod[-1], number of effective nodes plant[-1], and days to 50% flowering. Sharma et al. (2023) found Positive direct effect of days to 50% flowering, number of seeds pod[-1] and number of pods plant[-1] on pod yield plant[-1]. Ofga et al. (2017) found positive direct effect of 100-seed weight on seed yield plant[-1].

Table 5: Phenotypic correlation for physiological and yield traits in advanced genotypes of pea

	DFFO	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL
DFFO	1.0000	0.9828***	0.4955***	-0.2406**	-0.2160**	0.1411	0.1806*	0.0786	0.2688***
DFF		1.0000	0.5143***	-0.2201**	-0.1816*	0.1684*	0.1868*	0.0916	0.2653***
DM			1.0000	-0.0576	-0.0732	0.0588	0.0868	0.1133	0.0142
NPBPP				1.0000	0.6970***	0.3433***	0.3716***	0.1585*	0.2134*
NSBPP					1.0000	0.3071***	0.2571**	0.0284	0.1672*
PH						1.0000	0.6869***	0.4095***	0.8570***
NNPP							1.0000	0.6849***	0.5743***
NENPP								1.0000	0.2911***
PBL									1.0000

Table 5: Continue...

	NPPP	NEPPP	PL	NS/Pod	NS/Pt	100 SW	BYPP	HI	SYPP
DFFO	0.1882*	0.2831***	0.0610	-0.2373**	0.1672*	-0.2601**	0.1332	0.0255	0.1436
DFF	0.1709*	0.2439**	0.0706	-0.1960*	0.1513	-0.2357**	0.1203	0.0113	0.1328
DM	-0.0069	-0.0173	0.0016	-0.0962	-0.0457	-0.1904*	-0.0252	-0.1929*	-0.1173
NPBPP	0.1681*	0.1271	-0.0620	-0.0726	0.1490	-0.1270	0.1789*	-0.2083**	0.0777
NSBPP	0.0064	0.0009	-0.0650	0.0336	0.0790	-0.0023	0.1874*	-0.3094***	0.0312
PH	0.5337***	0.5166***	-0.1816*	-0.2412**	0.4288***	-0.0749	0.6398***	-0.2484**	0.4672
NNPP	0.7141***	0.6798***	-0.0294	-0.4068***	0.5134***	-0.2635***	0.6185***	-0.0919	0.5123
NENPP	0.8568***	0.7109***	-0.0562	-0.2888***	0.6099***	-0.4284***	0.5105***	0.0577	0.5143
PBL	0.4226***	0.4399***	-0.1666*	-0.3388***	0.3243***	0.0129	0.5467***	-0.2377**	0.3820
NPPP	1.0000	0.9362***	-0.0722	-0.3516***	0.8101***	-0.4745***	0.6075***	0.2536**	0.7201
NEPPP		1.0000	-0.0792	-0.3705***	0.8593***	-0.4156***	0.6674***	0.3318***	0.8145
PL			1.0000	0.4055***	0.1178	-0.1048	0.0113	0.2074**	0.1173
NS/Pod				1.0000	0.0879	-0.0790	-0.0634	0.1537	0.0294
NS/Pt					1.0000	-0.4764***	0.6889***	0.4113***	0.8957
100SW						1.0000	0.0032	-0.1379	-0.0993
BYPP							1.0000	-0.1548	0.8119
HI								1.0000	0.4303
SYPP									1.0000

Table 6: Genotypic path table indicating direct and indirect effect of independent traits on seed yield plant^{-1}

	DFFO	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL	NPPP
DFFO	-0.4622	-0.4563	-0.2300	0.1582	0.1234	-0.0661	-0.0851	-0.0360	-0.1255	-0.0878
DFF	0.4792	0.4854	02509	-0.1525	-0.1120	0.0835	0.933	0.0448	0.1308	0.0844
DM	0.0048	0.0050	0.0096	-0.009	-0.0009	0.0006	0.0009	0.0011	0.0001	-0.0001
NPBPP	-0.0152	-0.0140	-0.0040	0.0444	0.0291	0.0205	0.0215	0.0076	0.0139	0.0087
NSBPP	-0.0082	-0.0070	-0.0028	0.0200	0.0305	0.0180	0.0087	-0.0002	0.0066	-0.0006
PH	-0.0067	-0.0081	-0.0028	-0.0216	-0.0166	-0.0468	-0.0321	-0.0189	-0.0408	-0.0248
NNPP	-0.0140	-0.0147	-0.0069	-0.0369	-0.0218	-0.0523	-0.0762	-0.0522	-0.0450	-0.0544
NENPP	0.0006	0.0007	0.0009	0.0014	-0.0001	0.0033	0.0055	0.0081	0.0025	0.0069
PBL	0.0133	0.0132	0.0007	0.0154	0.0106	0.0427	0.0289	0.0153	0.0489	0.0217
NPPP	-0.0057	-0.0052	0.0002	-0.0058	0.0006	-0.0158	-0.0213	-0.0256	-0.0132	-0.0299
NEPPP	0.0743	0.0643	-0.0045	0.0344	-0.0088	0.1332	0.1757	0.1827	0.1196	0.2425
PL	0.0000	0.0001	0.0000	0.0000	0.0000	-0.0001	0.0000	0.0000	-0.0001	0.0000
NSPP	-0.0112	-0.0091	-0.0044	-0.0027	0.0031	-0.0114	0.0194	-0.0130	-0.0170	-0.0162
NSPPlt	0.0199	0.0183	-0.0050	0.0225	0.0108	0.0495	0.0594	0.0708	0.0391	0.0944
100 SW	-0.0251	-0.0229	-0.0184	-0.0169	-0.0006	-0.0072	-0.0256	-0.0422	0.0013	-0.0463
BYPP	0.0968	0.0903	-0.0158	0.1614	0.1542	0.4482	0.4327	0.3552	0.3972	0.4235
HI	0.0121	0.0043	-0.0872	-0.1246	-0.1705	-0.1126	-0.0419	0.0261	-0.1076	0.1189

Table 6: Continue...

	NEPPP	PL	NSPP	NSPPlt	100 SW	BYPP	HI	SYPP
DFFO	-0.1327	-0.0401	0.1166	-0.0810	0.1213	-0.0645	-0.0128	0.1528
DFF	0.1206	0.0518	-0.0992	0.0782	-0.1158	0.0632	0.0048	0.1443
DM	-0.0002	0.0002	-0.0010	-0.0004	-0.0019	-0.0002	-0.0019	-0.1194
NPBPP	0.0059	-0.0011	-0.0027	0.0088	-0.0079	0.0103	-0.0126	0.0958
NSBPP	-0.0010	-0.0015	0.0021	0.0029	-0.0002	0.0068	-0.0119	0.0311
PH	-0.0241	0.0102	0.0120	-0.0204	0.0035	-0.0303	0.0120	0.4797
NNPP	-0.0518	0.0005	0.0331	-0.0399	0.0204	-0.0476	0.0073	0.5250
NENPP	0.0057	-0.0003	-0.0024	0.0050	-0.0036	0.0041	0.0005	0.5236
PBL	0.0226	-0.0104	-0.0186	0.0168	0.0006	0.0280	-0.0120	0.4111
NPPP	-0.0280	0.0018	0.0109	-0.0248	0.0144	-0.0182	-0.0081	0.7408
NEPPP	0.2588	-0.0192	-0.1011	0.2275	-0.1100	0.1742	0.0894	0.8358
PL	0.0000	0.0005	0.0001	0.0000	-0.0001	0.0000	0.0001	0.0390
NSPP	-0.0174	0.0126	0.0445	0.0016	-0.0037	-0.0045	0.0041	-0.0380
NSPPlt	0.0999	0.0059	0.0041	0.1137	-0.0558	0.0781	0.0449	0.8905
100 SW	-0.0407	-0.0120	-0.0079	-0.0470	0.0958	0.0004	-0.0139	-0.1035
BYPP	0.4668	-0.0230	-0.0694	0.4765	0.0030	0.6936	-0.1195	0.8180
HI	0.1514	0.0633	0.0407	0.1730	-0.0638	-0.0755	0.4383	0.4086

R square=0.9956; Residual effect=0.0663

4. CONCLUSION

A considerable amount of genetic variability was found for most traits among 52 genotypes. High heritability coupled with high or moderate genetic advance was observed for most traits, indicating the preponderance of additive gene action in the inheritance of these traits. Based on the results obtained from correlation and path coefficient analyses, indirect selection through the traits demonstrates a positive association and direct effect on seed yield, significantly enhancing seed yield.

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