

Research Article

Genetic association studies for yield and yield contributing traits in *Plantago ovata* Forsk.

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Abstract

Twenty four accessions of *Plantago ovata* were grown to study existing variability, correlation and cause and effect relationships between yield and its component traits with their possible view in future improvement programmes. Analysis of variances displayed highly significant differences among accessions for all the traits. High heritability (>75%) coupled with the high genetic advance (>30%) were observed for the traits viz., leaf width, number of spikes/plant, biological yield/plant and seed yield/plant suggesting predominance of additive gene action. Seed yield/plant exhibited highly significant and positive correlation with biological yield/plant followed by number of spikes/plant, effective tillers/plant, harvest index, seed weight/spike, spike weight and husk recovery both at genotypic and phenotypic level. Biological yield/plant, harvest index, spike weight, effective tillers/plant and husk recovery exhibited the highest positive and significant direct effect on seed yield/plant. Critical analysis of results obtained from character association and path analysis indicated that the traits viz., biological yield/plant, harvest index, spike weight, effective tillers/plant and husk recovery were of prime concern as they possessed high positive association and direct effects on seed yield/plant. These traits are more reliable for selection for yield improvement programmes in *Plantago ovata*.

Keywords

Plantago ovata, correlation, heritability, path coefficient analysis

Introduction

Plantago ovata (Forsk.) is one of the most important medicinal crop belongs to family *Plantaginaceae*. It has gained popularity both in traditional as well as modern medicine due to its pharmacological activities and has successfully placed itself in leading medicinal markets of the world especially in western countries. The husk, a rosy-white membranous covering of the seed (25%-30% by weight), known as Isabgol in Hindi and Blonde Psyllium in English, is most economic and therapeutic part of *P. ovata*. The mucilage present in the husk has the property of absorbing and retaining water that accounts for its utility as safe laxative, particularly beneficial in habitual constipation, chronic diarrhea and dysentery, (Sammantaray *et al.*, 2010). It is also having industrial importance especially for preparation of chocolate, ice cream and cosmetics, in printing and finishing industries (Kumar *et al.*, 2014). The by-products of dehusking are rich in starch and fatty acids usually used as cattle and pig feed in India (Fougat *et al.*, 2014).

P. ovata is indigenous to Mediterranean province and West Asia expanding upto Sulej and Sind in West Pakistan. In India, *P. ovata* is extensively cultivated in Western part of the country (Kour *et al.*, 2016). India continues to hold a monopoly in its production and trade (80% share) in world market. About 90% of the seeds and husks are exported, earning more than 200 crores rupees foreign exchange annually (Singh *et al.*, 2009; Kumar *et al.*, 2014). Despite its worth economic value to the country, productivity of *P. ovata* in India is far below the desired level to meet out global demand. Limited efforts has put forward in the genetic improvement of the crop, resulted in nearly stagnant yield of *P. ovata* (Singh and Lal, 2009) and this is further bounded by very narrow genetic base (Kaswan *et al.*, 2013) on account of small genome size (621Mb) based on 4 (2n=2x=8) heterochromatin rich chromosomes, low chiasmata frequency and recombination index (Kour *et al.*, 2016). Therefore, concerted efforts are required to develop improved high yielding varieties.

As an established fact, yield is a complex trait and is highly influenced by many genetic factors and environmental fluctuations. The Knowledge of variability, trait association between yield and yield components is essential for yield improvement through selection programme (Fraser and Eaton, 1983). Correlation analysis provides information that selection for one trait results in progress for other positively correlated traits. The importance of correlation studies in selection programmes is appreciable when highly heritable traits are associated with the important trait like yield. However, adding more and more traits may lead to complexity in understanding the true inherent association, thus emphasize the need of path analysis and hence permits the separation of relative contribution and identification of traits that are useful as selection criteria to improve crop yield (Khaliq *et al.*, 2004). Considering the above facts the present investigation was undertaken to establish suitable selection criteria for higher seed yield through study of genetic variability, inter-relationship and cause effect analysis between yield and its components in *P. ovata*.

Materials and Methods

The present investigation was carried out on *P. ovata* at Instructional Farm of the Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, Rajasthan (India) located at an elevation of 579.50 meters above mean sea level on latitude of 24°35' North and longitude of 70°42' East. The climate of Udaipur is sub-humid and the soils are sandy-loam in nature. Minimum and maximum night and day temperatures ranged from 8-11°C to 24-29°C, respectively during growth period and from 14-19°C to 30-38°C, respectively, during harvesting time. The experimental material comprised of twenty four accessions (desirable induced mutants, varieties and landraces) collected from western parts of India (Table 1). Mutants were developed through seeds of RI-89 irradiated through gamma rays at four doses (10, 20, 30 and 40 kR). Desirable mutants were sorted out from 30 and 40 kR doses. The experiment was laid out in a Randomized Block Design (RBD) with three replications during winter season of 2009-10. Each experimental plot size was 15 m × 4 m and seeds were sown in row by keeping spacing at 15 cm plant to plant and 30 cm apart from row. A basal dose of fertilizers was applied at the rate of 25 kg N, 20 kg P₂O₅ and 25 kg K₂O per hectare at the time of sowing and 25 kg N/ha was top-dressed one month after sowing. Recommended agronomic practices and plant protection measures were followed to raise a good crop.

Five competitive plants were randomly selected and tagged from each accession in each replication for morphological observation on thirteen traits *viz.* days to 50% flowering, plant height, leaf width, effective tillers/plant, number of spikes/plant, spike weight, seeds weight/spike, spike length, test weight, biological yield/plant, harvest index (%), days to maturity and seed yield/plant. In addition, two quality traits, husk recovery (%) and swelling factor were calculated according to Kalyansundaram *et al.* (1982) and Kokate (1994), respectively. The data was analysed using computer software Windostat (version 7.0) developed by Indostat Services Ltd., Hyderabad (India). Analysis of variance was carried out following Panse and Sukhatme (1967). The phenotypic and genotypic coefficients of variation (PCV, GCV) were computed as per method described by Burton (1954) and the correlation coefficients at genotypic and phenotypic levels were computed according to Johnson *et al.* (1955). Path coefficient analysis was done as suggested by Dewey and Lu (1959). In the present investigation, path analysis was carried out by taking seed yield/plant as resultant variable and its components as causal variables.

Results and Discussion

The analysis of variance indicated that mean square due to accessions were highly significant for all the traits studied, indicating the existence of substantial variability for different traits (Table 2). The phenotypic variance was partitioned into heritable (genotypic variance) and non-heritable (environmental variance) components. The low environmental effect observed for all the traits compared to genetic factors suggests that the traits may be under genetic control rather than the environment; hence improvement can be achieved through selection (Oyiga and Uguru, 2011). The magnitudinal difference between PCV and GCV was minimum for swelling factor, seed yield/plant followed by husk recovery, test weight, days to 50% flowering and harvest index; suggesting that these traits were least effected by environment.

Wide difference between the PCV and GCV was observed for spike weight coupled with moderate broad sense heritability (h^2_B) indicates that this character was much influenced by environmental fluctuation. High PVC and GCV were observed for leaf width followed by seed yield/plant, biological yield/plant and number of spikes/plant suggesting that selection of these traits may be effective as also reported by Godawat and Sharma (1994). With the help of PCV and GCV alone, it is not possible to determine the amount of variation, which is heritable. The measure of heritability reflects the strength of the

relationship between performance (phenotype) and breeding value (genotype) of the plants or magnitude of inheritance of quantitative traits and hence directs the breeders to decide which traits justify improvement through selection. Broad sense heritability estimates were high (>75%) for all the traits except plant height, spike weight and days to maturity. In the present study high heritability was observed for seed yield/plant, biological yield/plant, husk recovery, swelling factor, test weight, leaf width, harvest index, seed weight/spike, number of spikes/plant, days to 50% flowering, spike length and effective tillers/plant suggesting that they have high genetic potential with minimum role of environment in determining them. Since heritability is also influenced by the environmental factors, only information based upon heritability may not help in pinpointing the traits enforcing effective selection. Jhonson *et al.* (1955) suggested that heritability and genetic advance should be considered together for more reliable conclusion. A trait with high heritability and high genetic advance may possible due to additive gene action (Panse, 1957). High heritability and genetic advance as a per cent of mean was recorded for leaf width, seed yield/plant, biological yield/plant and number of spikes/plant suggesting predominance of additive gene action/effects hence, improvement on the basis of phenotypic value may be effective through direct selection as also suggested in earlier reports (Godawat and Sharma, 1994; Singh and Lal, 2009). Low heritability associated with low genetic advance was observed for the traits plant height, spike weight and days to maturity showed preponderance of non-additive genes for their inheritance.

Correlation analysis helps the breeders to know mutual relationships between various variables along with its magnitude and direction and hence, display the major component traits on which simultaneous selection can be based for genetic improvement. Correlation between different traits is generally due to the presence of linkage disequilibrium, pleiotropic gene actions and epistatic effects of different genes (Abinasa *et al.*, 2011). Environment also plays an important role in the correlation. Genetic and environmental causes of correlation are combined together to give phenotypic correlation. Therefore, estimation of degree of genotypic and phenotypic correlation of seed yield with yield components is very important to utilize the available genetic variability through selection (Singh *et al.*, 1998). At genetic level, a negative correlation arises from repulsion linkages of gene(s) and positive correlation due to coupling phase of linkages (Sharma, 1998). A

positive genetic correlation between two desirable traits makes selection easy for improving both traits simultaneously while the reverse is the case for negative correlation. The *inter se* correlation coefficients at phenotypic and genotypic levels between different traits are given in Table 3. In majority of the cases, the genotypic correlation coefficients were higher than their corresponding phenotypic ones, which indicated little role of environment in expression of traits, suggesting inherent association between these traits at genotypic level. The seed yield/plant showed significant and positive correlation with biological yield/plant, number of spikes/plant, number of effective tillers/plant, harvest index, seed weight/spike, spike weight and husk recovery at genotypic and phenotypic levels. This indicates that selection for these traits would simultaneously lead to an improvement in seed yield/plant. Comparing the inter-relationship of other economic traits, it was further observed that with increase in plant height, there was corresponding increase in number of spike/plant, spike length and biological yield per plant. Selection for early flowering genotypes has to compromise with low test weight and harvest index due to early maturity. Plants with broader leaf width will help to accommodate high spike weight and seed, harvest index and husk recovery as these were found positively correlated. Days to 50% flowering and days to maturity had negative correlation with most of the traits.

As simple correlation does not provide the true contribution of the characters towards the yield (Dewey and Lu, 1959), a more detailed study of the relationships was carried out by partitioning these genotypic correlations into direct and indirect effects through path coefficient analysis that allows determination of the relative magnitude of each effect (Wright, 1921). The path analysis of seed yield per plant with fourteen characters is presented in Table 4. Among all the characters, biological yield/plant exerted the highest significant positive direct effect on seed yield/plant followed by harvest index, spike weight, effective tillers/plant and husk recovery. Aher and Aher (2013) also reported high direct effects of harvest index and husk recovery on seed yield. Accordingly these traits displayed a positive correlation with seed yield. The direct effects of number of spikes/plant and seed weight/spike with seed yield/plant were recorded negative, however, both these traits showed positive correlation coefficient with seed yield/plant due to the high positive indirect contribution of biological yield/plant and harvest index, hence indirect selection of these

traits would be effective for improving seed yield/plant. The lower residual effect (0.001) indicated that most of the variability in seed yield/plant for the genotypes could be explained by the independent variables included in the analysis (Singh and Chaudhary, 2004).

In view of the high estimates of genotypic coefficient of variation, heritability and genetic advance, the traits *viz.*, leaf width, effective tillers/plant, number of spikes/plant, seed weight/spike, biological yield/plant, harvest index, husk recovery and swelling factor were found prominent in the present study suggests that worthwhile improvement in these traits can be achieved through selection. Critical analysis of results obtained from trait association and path analysis indicated that the traits *viz.*, biological yield/plant, effective tillers/plant, harvest index, spike weight and husk recovery were of prime concern as they possessed high positive association and direct effects on seed yield/plant. These traits are more reliable for selection for seed yield improvement programmes of *P. ovata*.

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References

- Abinasa, M., Ayana, A. and Bultosa, G. 2011. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. *durum*) genotypes. *African Journal of Agricultural Research*, **6(17)**: 3972-3979.
- Aher, A. R. and Aher, B. M. 2013. Genetic evaluation of isabgol (*Plantago ovata* F). *Bioinfolet*, **10 (3A)**: 822-827.
- Burton, 1954. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress, **1**: 277-283.
- Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518.
- Fogat, R.S., Joshi, C., Kulkarni, K., Kumar, S., Patel, A., Sakure, A. and Mistry, J. 2014. Rapid development of Microsatellite Markers for *Plantago ovata* Forsk.: Using Next Generation Sequencing and their cross-species transferability. *Agriculture*, **4**: 199-216.
- Fraser, J. and Eaton, G.W. 1983. Application of yield component analysis to crop research. *Field Crop Abst.*, **36**: 787-797.
- Godawat, S.L. and Sharma, A.K. 1994. Variability pattern in *Psyllium*. *Indian Journal of Plant Genetic Resources*, **7(1)**: 55-57.
- Johnson, A.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.
- Kalyansundaram, N.K., Patel, P.B. and Dalal, K.C. 1982. Nitrogen need of *Plantago ovata* Forsk. in relation to available nitrogen in soil. *Indian Journal of Agriculture Science*, **52(9)**: 240-242.
- Kaswan, V., Joshi, A. and Maloo, S.R. 2013. Genetic studies on divergence and quantitative characterization of plant isabgol (*Plantago ovata* Forsk.). *Research on Crops*, **14(2)**: 585-591.
- Khaliq, I., Parveen, N. and Chowdhry, M.A. 2004. Correlation and path coefficient analysis in bread wheat. *International Journal of Agriculture and Biology*, **4**: 633-635.
- Kokate, C.K. 1994. Determination of swelling factor. In: *Practical Pharmacognosy*, Vallabh Prakashan, p. 127.
- Kour, B., Kotwal, S., Dhar, M.K. and Kaul, S. 2016. Genetic Diversity Analysis in *Plantago ovata* and some of its wild allies using RAPD markers. *Russian Agricultural Sciences*, **42 (1)**: 37- 41.
- Kumar, M., Fogat, R.S., Sharma, A.K., Kulkarni, K., Ramesh, M.J.G., Sakure, A. and Kumar, S. 2014. Phenotypic and molecular characterization of selected species of *Plantago* with emphasis on *Plantago ovata*. *Australian Journal of Crop Science*, **8(12)**: 1639-1647.
- Oyiga, B.C. and Uguru, M.I. 2011. Genetic variation and contributions of some floral traits to pod yield in Bambara Groundnut (*Vigna subterranea* L. Verdc) under two cropping seasons in the derived savanna of the South-East Nigeria. *International Journal of Plant Breeding*, **5(1)**: 58-63.
- Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics*, **17**: 318-328.
- Panse, V.G. and Sukhatme, P.V. 1967. Statistical methods for agricultural workers, 2nd ed. Indian Council of Agricultural Research, New Delhi.



- Samantaray, S., Dhagat, U.M. and Maiti, S. 2010. Evaluation of genetic relationships in *Plantago* species using Random Amplified Polymorphic DNA (RAPD) markers. *Plant Biotechnology*, **27**: 297-303.
- Sharma, J.R. 1998. Statistical and Biometrical techniques in Plant Breeding. Publisher New Age International Pvt. Limited, New Delhi, p. 33-39.
- Singh, A.K., Singh, S.B. and Yasave, S.H. 1998. Correlation and path analysis in early generation. *Indian Journal of Genetics*, **58(3)**: 260-264.
- Singh, N. and Lal, R.K. 2009, Genetics of quantitative and qualitative traits of isabgol (*Plantago ovata*). *Genetics and Molecular Research*, **8 (3)**: 939-950.
- Singh, N., Lal, R.K. and Shasany, A.K. 2009. Phenotypic and RAPD diversity among 80 germplasm accessions of the medicinal plant isabgol (*Plantago ovata*, Plantaginaceae). *Genetics and Molecular Research*, **8(3)**: 1273-1284.
- Singh, R.K. and Chaudhary, B.D. 2004. Biometrical Methods in Quantitative Genetic Analysis, Kalyani Publishers, New Delhi, India, p. 318.
- Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*, **20**: 557-585.

Table 1. Description of the *Plantago ovata* accessions used in the study

No.	Accession	Source	No.	Accession	Source
1	Gumary	Anand (Gujarat)	13	RI-142 (Mutant)	Jodhpur (Rajasthan)
2	GI-2	Anand (Gujarat)	14	RI-145 (Mutant)	Jodhpur (Rajasthan)
3	GI-4	Dantiwada (Gujarat)	15	RI-147 (Mutant)	Jodhpur (Rajasthan)
4	Palampur-2	Dantiwada (Gujarat)	16	RI-148 (Mutant)	Jodhpur (Rajasthan)
5	PB-62	Hisar (Haryana)	17	RI-150 (Mutant)	Jodhpur (Rajasthan)
6	PB-7	Hisar (Haryana)	18	RI-153 (Mutant)	Jodhpur (Rajasthan)
7	MIB-125	Mandsaur(Madhya Pradesh)	19	RI-154 (Mutant)	Jodhpur (Rajasthan)
8	RI-89	Jodhpur (Rajasthan)	20	RI-155 (Mutant)	Jodhpur (Rajasthan)
9	RI-136 (Mutant)	Jodhpur (Rajasthan)	21	RI-165 (Mutant)	Jodhpur (Rajasthan)
10	RI-137 (Mutant)	Jodhpur (Rajasthan)	22	RI-166 (Mutant)	Jodhpur (Rajasthan)
11	RI-138 (Mutant)	Jodhpur (Rajasthan)	23	RI-167	Jaislmer (Rajasthan)
12	RI-139 (Mutant)	Jodhpur (Rajasthan)	24	RI-168 (selection from RI-167)	Jaislmer (Rajasthan)



Table 2. Estimates of genetic parameters in *Plantago ovata* for various yield contributing traits

Trait	Mean \pm SE	MS	Vp	Vg	Ve	PCV	GCV	ECV	h ² B (%)	GA (% of mean)
Days to 50 % flowering	60.32 \pm 0.57	15.09**	5.67	4.71	0.96	3.95	3.60	1.63	83.02	6.75
Plant height (cm)	28.46 \pm 0.52	4.64**	2.08	1.28	0.80	5.07	3.98	3.14	61.57	6.43
Leaf width (cm)	0.52 \pm 0.04	0.11**	0.04	0.03	0.004	37.83	35.82	12.16	89.66	69.85
Effective tillers/ plant	3.60 \pm 0.17	0.87**	0.34	0.26	0.08	16.27	14.20	7.95	76.10	25.50
Number of spikes/plant	13.89 \pm 0.73	26.74**	9.99	8.38	1.61	22.75	20.84	9.14	83.86	39.31
Spike weight (g)	0.19 \pm 0.01	0.001**	0.001	0.0003	0.0002	12.07	9.51	7.44	62.00	14.16
Seeds weight/spike (g)	0.12 \pm 0.00	0.001**	0.0002	0.0002	0.00003	11.62	10.84	4.17	87.14	19.68
Spike length (cm)	2.64 \pm 0.06	0.18**	0.07	0.06	0.01	9.93	9.02	4.15	82.53	16.90
Test weight (g)	1.65 \pm 0.02	0.05**	0.02	0.02	0.001	7.90	7.66	1.92	94.11	15.47
Biological yield/plant (g)	5.14 \pm 0.08	3.70**	1.25	1.23	0.02	21.73	21.54	2.89	98.24	44.00
Harvest index (%)	32.71 \pm 0.62	28.19**	10.16	9.01	1.14	9.74	9.18	3.27	88.76	17.80
Days to maturity	120.29 \pm 1.13	17.08**	8.24	4.42	3.82	2.39	1.75	1.63	53.61	2.64
Husk recovery (%)	24.48 \pm 0.23	19.26**	6.52	6.37	0.15	10.43	10.31	1.60	97.64	20.99
Swelling factor (cc/g)	7.97 \pm 0.07	1.98**	0.67	0.66	0.02	10.28	10.16	1.59	97.62	20.67
Seed yield/plant (g)	1.69 \pm 0.02	0.54**	0.18	0.18	0.001	25.05	24.98	1.87	99.44	51.44

** - Significant at 1% level of significance, SE= standard error, MS= mean squares, Vp= phenotypic variance, Vg= genotypic variance, Ve= environmental variance, PCV= phenotypic coefficient of variation, GCV= genotypic coefficient of variation, ECV= environmental coefficient of variation, h²B= broad sense heritability (%), GA= genetic advance



Table 3. Genotypic and phenotypic correlations among various yield contributing traits in *Plantago ovata*

Traits		DF (days)	PH (cm)	LW (cm)	ET/P	NS/P	SW (g)	Se W/S (g)	SL (cm)	TW (g)	BY/P (g)	HI (%)	DM (days)	HR (%)	SF (cc/g)	SY/P (g)
DF (days)	G	1.000	0.179	-0.279*	-0.020	0.119	-0.221	-0.133	0.026	-0.522**	0.211	-0.387**	0.989**	-0.185	-0.232	0.049
	P	1.000	0.102	-0.213	-0.008	0.180	0.026	-0.112	-0.022	-0.383**	0.183	-0.212	0.960**	-0.103	-0.135	0.075
PH (cm)	G		1.000	-0.062	0.232	0.245*	0.030	0.015	0.489**	-0.046	0.307*	-0.247*	0.193	0.023	-0.311*	0.175
	P		1.000	-0.079	0.166	0.142	-0.092	0.003	0.276*	-0.053	0.311*	-0.311*	0.067	0.007	-0.276*	0.144
LW (cm)	G			1.000	0.008	0.018	0.419**	0.425**	0.150	0.114	0.088	0.315*	-0.249*	0.456**	-0.168	0.174
	P			1.000	0.015	0.058	0.395**	0.382**	0.113	0.126	0.082	0.281*	-0.121	0.453**	-0.138	0.169
ET/P	G				1.000	0.632**	0.114	0.260*	0.292*	-0.046	0.505**	0.544**	-0.112	0.486**	0.086	0.640**
	P				1.000	0.569**	0.147	0.163	0.208	-0.034	0.458**	0.436**	-0.060	0.439**	0.078	0.577**
NS/P	G					1.000	0.016	0.089	0.110	-0.128	0.944**	0.297*	0.031	0.451**	0.097	0.918**
	P					1.000	0.173	0.078	0.067	-0.081	0.885**	0.291*	0.147	0.453**	0.130	0.870**
SW (g)	G						1.000	0.997**	0.685**	0.457**	0.364**	0.540**	-0.294*	0.159	-0.050	0.503**
	P						1.000	0.749**	0.405**	0.427**	0.258*	0.471**	0.131	0.185	0.072	0.411**
Se W/S (g)	G							1.000	0.483**	0.472**	0.292*	0.719**	-0.118	0.258*	-0.011	0.515**
	P							1.000	0.368**	0.415**	0.258*	0.534**	-0.083	0.229	0.009	0.446**
SL (cm)	G								1.000	0.168	0.223	0.150	0.004	0.260*	0.043	0.228
	P								1.000	0.130	0.193	0.142	-0.069	0.216	0.005	0.202
TW (g)	G									1.000	-0.054	0.440**	-0.563**	-0.090	0.129	0.099
	P									1.000	-0.057	0.415**	-0.266*	-0.056	0.154	0.111
BY/P (g)	G										1.000	0.201	0.194	0.329**	0.088	0.937**
	P										1.000	0.142	0.127	0.319*	0.093	0.913**
HI (%)	G											1.000	-0.493**	0.488**	0.133	0.525**
	P											1.000	-0.160	0.446**	0.157	0.526**
DM (days)	G												1.000	-0.293*	-0.319*	-0.003
	P												1.000	-0.108	-0.111	0.049
HR (%)	G													1.000	0.401**	0.458**
	P													1.000	0.402**	0.454**
SF (cc/g)	G														1.000	0.093
	P														1.000	0.034
SY/P (g)	G															1.000
	P															1.000

*,** -Significant at 5% and 1% level of significance, respectively PH: Plant height (cm), DF: Days to 50% flowering: LW: Leaf width (cm), ET/P: Effective tillers/plant, NS/P: Number of spikes/plant, SW: spike weight (g), SeW/S: Seeds weight/spike (g), SL: Spike length (cm), TW: Test weight (g), SY/P: Seed yield/plant (g), BY/P: Biological yield/plant (g), HI: Harvest index (%), DM: Days to maturity, HR: Husk recovery (%), SF: Swelling factor (cc/g).



Table 4. Path analysis (at genotypic level) showing direct (bold and underline values) and indirect effects of various traits on seed yield/plant in *Plantago ovata*

Trait	DF (days)	PH (cm)	LW (cm)	ET/ P	NS/P	SW (g)	Se W/S (g)	SL (cm)	TW (g)	BY/P(g)	HI (%)	DM	HR (%)	SF (cc/g)	r _g
DF (days)	<u>0.043</u>	0.005	0.007	-0.001	-0.016	-0.013	0.003	-0.002	0.005	0.201	-0.129	-0.043	-0.006	-0.004	0.049
PH (cm)	0.008	<u>0.028</u>	0.001	0.014	-0.032	0.002	0.001	-0.043	0.000	0.292	-0.082	-0.008	0.001	-0.005	0.175
LW (cm)	-0.012	-0.002	<u>-0.024</u>	0.001	-0.002	0.025	-0.009	-0.013	-0.001	0.084	0.105	0.011	0.014	-0.003	0.174
ET/ P	-0.001	0.006	0.000	<u>0.059</u>	-0.084	0.007	-0.005	-0.025	0.000	0.480	0.181	0.005	0.015	0.001	0.640**
NS/P	0.005	0.007	0.000	0.037	<u>-0.133</u>	0.001	-0.002	-0.010	0.001	0.897	0.099	-0.001	0.014	0.002	0.918**
SW (g)	-0.010	0.001	-0.010	0.007	-0.002	<u>0.061</u>	-0.022	-0.060	-0.005	0.346	0.180	0.013	0.005	-0.001	0.503**
Se W/S (g)	-0.006	0.000	-0.010	0.015	-0.012	0.065	<u>-0.020</u>	-0.042	-0.005	0.277	0.240	0.005	0.008	0.000	0.515**
SL (cm)	0.001	0.014	-0.004	0.017	-0.015	0.042	-0.010	<u>-0.087</u>	-0.002	0.212	0.050	0.000	0.008	0.001	0.228
TW (g)	-0.022	-0.001	-0.003	-0.003	0.017	0.028	-0.010	-0.015	<u>-0.011</u>	-0.052	0.147	0.024	-0.003	0.002	0.099
BY/P(g)	0.009	0.009	-0.002	0.030	-0.125	0.022	-0.006	-0.019	0.001	<u>0.950</u>	0.067	-0.008	0.010	0.001	0.937**
HI (%)	-0.017	-0.007	-0.008	0.032	-0.039	0.033	-0.015	-0.013	-0.005	0.191	<u>0.334</u>	0.021	0.015	0.002	0.525**
DM	0.044	0.005	0.006	-0.007	-0.004	-0.018	0.002	0.000	0.006	0.184	-0.165	<u>-0.043</u>	-0.009	-0.005	-0.003
HR (%)	-0.008	0.001	-0.011	0.029	-0.060	0.010	-0.005	-0.023	0.001	0.313	0.163	0.013	<u>0.030</u>	0.006	0.458**
SF (cc/g)	-0.010	-0.009	0.004	0.005	-0.013	-0.003	0.000	-0.004	-0.001	0.033	0.044	0.014	0.012	<u>0.016</u>	0.088

Residual effect= 0.001, **- Significant at 1% level of significance, PH: Plant height (cm), DF: Days to 50% flowering; LW: Leaf width (cm), ET/P: Effective tillers/plant, NS/P: Number of spikes/plant, SW: spike weight (g), SeW/S: Seeds weight/spike (g), SL: Spike length (cm), TW: Test weight (g), SY/P: Seed yield/plant (g), BY/P: Biological yield/plant (g), HI: Harvest index (%), DM: Days to maturity, HR: Husk recovery (%), SF: Swelling factor (cc/g), r_g- genotypic correlation of traits with seed yield/plant