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Genetic variability and character association studies in Indian mustard (*Brassica juncea* (L) Czern & Coss) genotypes for different quantitative traits

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Abstract

In the present experiment twenty-seven genotypes of Indian mustard are evaluated for thirteen quantitative and one biochemical trait for different measures of variability, inheritance and character association and path coefficient analysis. PCV and GCV analysis stated that traits such as SYP, TAW and NSB were high in both the parameters and the difference between the PCV and GCV value in all the traits were minute representing that involvement of environment in the expression of these traits were negligible. Traits namely DFF, DM, NSB, TAW, BYP, HI, SYP exhibited very high heritability as well as high genetic advance rendering these traits eligible for selection due to the existence of fixable component of genetic variance. Traits namely LMS, BYP, NSS and NSB were found to be significantly and positively associated with the trait SYP. In the path coefficient study, traits such as BYP, HI, NSMS, NPB, NSS, LMS, LSMS, OC, DFF and TAW revealed positive direct effect on the trait SYP which gives an insight of the magnitude of relationship with the trait of interest.

Keywords: Indian mustard, GCV, PCV, heritability, correlation coefficient, path analysis

Introduction

Indian mustard is scientifically identified as *Brassica juncea* (L.) Czern & Coss, a member of Cruciferae or Brassicaceae family, cultivated as a vital oilseed crop worldwide (Szöllösi., 2019) [1]. Among near about 100 species belonging to the genera Brassica, rapeseed-mustard group is the one to be exclusively exploited as oilseed crops all around the world (Singh *et al.*, 2018) [2]. It is believed that in the course of evolution, plants of *B. rapa* (AA) by *B. nigra* (BB) were being crossed to give rise to Indian mustard (AABB) (Nagaheru., 1935; Olson., 1960) [3, 4]. The assertion of mustard has been found in several ancient literature which evidences it be one of the primitive cultivated crops (Allchin, 1969) [5]. Mustard is not only acknowledged as an oilseed crop but also extensively used as condiment due to its unique flavour profile. Countries like India, Pakistan, Canada, Nepal, Great Britain, Hungary and the United States are the major stakeholder in the production of rapeseed-mustard. In Indian 86.72% area and 89.53% production is exclusively afforded by the states namely Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, West Bengal and Assam while Rajasthan solely contribute to 45.03% of the total production (DRMR, 2021) [6].

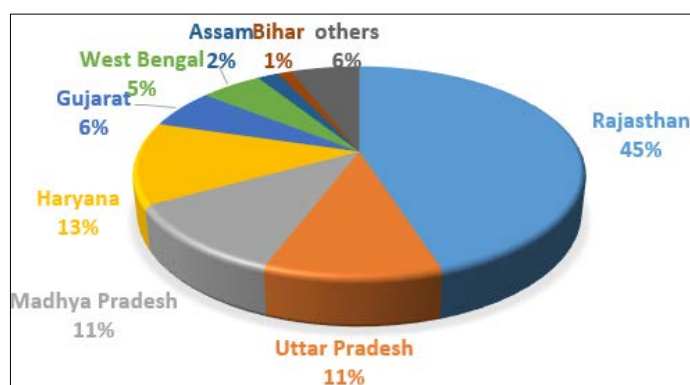


Fig 1: Production trend of rapeseed-mustard in India

Yearly India supplies nearly 10.6 million tonnes (MT) of edible oil which is way behind to fulfil its own need, causing India to import about 14-14.5 MT edible oil costing foreign exchange of USD 18.99 billion in the fiscal year ended March 31, 2022 (DFPD., 2021) [7]. Yield traits in mustard are governed by both additive and nonadditive nature of genes, making it challenging to improve (Manjunath *et al.*, 2017) [8]. Due to the prevalence of nonadditive gene action, yield is easily hampered by various environmental constrains every year. Thus, improvement of high yielding stable varieties is of primary prerequisite in making India self-reliant in its edible oil production. The primary groundwork of any improvement program starts with screening of already existing materials and further it takes one of the two ways, either selection of superior material to exploit the variability present in them or to create new variability using them. To predict the variation present in the materials, different measures of variability are used among which genetic parameters are most efficient. GCV, PCV measures the quantity of variation due to pure genetics devoid of environmental influence. Heritability measures the proportion of actual variation capable of transferring from one generation to other. Genetic advance along with heritability provides the tool to quantify the actual fixable amount of genetic variance. Character association study delineates the interrelationship between traits which

offers the scope for improvement of a trait with the help of judicious selection of other influential traits. Considering that, the present study estimated genetic variability, heritability, genetic advance, correlation coefficient and path analysis among different traits in twenty- seven genotypes in Indian mustard.

Materials and Methods

Site of the experiment

For the assessment of experimental materials, the trial was performed at the 31.25 °N and 75.707° E region of Agriculture Research Farm under the Faculty of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara (Punjab). Crop duration was around five months, which started from the mid of October lasting till the month of March.

Experimental Design and material

Twenty-seven genotypes of Indian mustard were used as experimental material. The resources were arranged in the Randomized Block Design manner with three replications including four rows per genotype with a measurement of 60 cm row and 15 cm plant spacing. All the recommended package of practices were maintained during the cropping period. List of genotypes (Table. 1)

Table 1: List of Genotypes

Code used	Genotypes
1.	Bhagirathi
2.	BR-23
3.	Durga
4.	Durga Mani
5.	Gujarat Mustard-1
6.	Gujarat Mustard-2
7.	JD-6
8.	KBS-3
9.	Kranti
10.	NRCHB-1
11.	Parbati Mustard
12.	PDZ-1
13.	Pusa Bold
14.	Pusa Jagannath
15.	Pusa Jai Kisan
16.	Pusa Karishma
17.	Pusa Mustard-24
18.	Pusa Mustard-27
19.	Pusa Mustard-28
20.	RH-119
21.	RH-30
22.	RH-701
23.	RNG-73
24.	Rohini
25.	SMR-9
26.	Urvashi
27.	Vaibhav

Observations recorded.

The observations were documented on randomly selected five competitive plants of each genotype from each replication. Observations for a total of 14 traits were noted. Traits such as Plant height (cm) (PH), Length of Main Shoot (cm)(LMS), No. of Primary Branches (NPB), No. of Secondary Branches (NSB), No. of Siliqua on main shoot (NSMS), Length of Siliqua on Main Shoot (LSMS), Number of seeds siliqua

¹(NSS), 1000-seed weight(TAW), Biological yield plant¹(BYP), Seed yield plant¹ (SYP), Harvest index (HI) were measured on individual plant basis. Oil content (OC) was worked out with the help of Soxhlet apparatus using N-Hexane as a solvent using the recommended method for mustard (Garcia-Vaquero *et al.*, 2022) [9].

Statistical analysis

The dataset was processed through analysis of variance to designate the sources of variation with the help of the Indostat software. From the data of ANOVA, other parameters such as phenotypic and genotypic coefficient of variance, heritability, genetic advance were worked out with the help of same software. The simple genotypic and phenotypic correlation between different traits was worked out. The software used for the data analysis are agricolae, R package version 1.3-5 (Mendiburu, 2021) [10]. Again, for path coefficient analysis the software Indostat was used.

Results and Discussion

Table 2: Analysis of variance

S.O.V.	Df	DFF	DM	PH	LMS	NPB	NSB	NSMS	LSMS	NSS	TAW	BYP	HI	OC	SYP
Replication	2	2.37	0.38	24.76	108.17	0.17	4.2	0.97	0.02	0.33	0	216.55	6.34	0.27	0.43
Treatment	26	83.64**	868.48**	1121.34**	125.50**	0.73*	13.47**	48.78*	0.10*	2.66*	2.26*	859.95**	33.52*	23.90*	43.81*
Error	52	1.037	2.95	20.57	40.41	0.3	2.53	7.82	0.03	0.12	0.05	72.36	5.25	0.11	0.2

Components of genetic variance

Different attributes of genetic parameters such as GCV, PCV, heritability, genetic advance and genetic advance at percent mean were measured. The phenotypic coefficient of variance was higher than genotypic coefficient of variance indicating that genotype along with environment played prevalent role in the expression of the trait. The genotypic coefficient of variance ranged from 3.885 to 21.906 where trait NSB exhibited lowest and trait LSMS exhibited highest GCV respectively. Deshmukh *et al.*, (1986) [11] proposed the consideration regarding GCV and PCV values where values below 10% were regarded as low, above 20% were regarded as high and in between 10-20% were regarded as moderate.

Analysis of Variance

To allocate the variation present, analysis of variance was carried out. The result revealed block difference to be non-significant for all the traits whereas treatments were regarded as significant source of variance for all the traits in the study. Among these traits such as DFF, DM, PH, LMS, NSB, BYP were showing highly significant values (Table. 2.). The outcome indicated occurrence of negligible variation between the replication while substantial amount of variability among the genotypes. Based on this data other genetic parameters were estimated further in the study.

According to the scale, traits such as SYP, TAW and NSB depicted high GCV coupled with high PCV while traits like DFF, DM, PH HI, BYP and NSMS exposed moderated GCV along with moderate PVC. Traits namely LSMS, OC, NSS, LMS and NPB exhibited low GCV coupled with low PCV (Table. 3.) (Figure.1). The results have indicated even though all of the traits displayed PCV value higher than the corresponding GCV values, the differences were rather small suggesting minor impact of environment on the expression of the traits. The traits explaining higher GCV unveil existence of variability in the experimental material which is the prerequisite for effective selection.

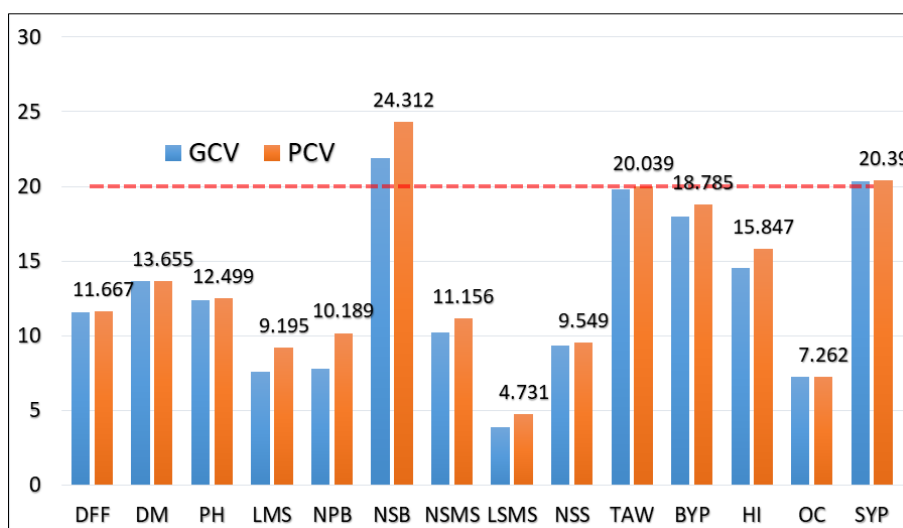


Fig 2: Genotypic coefficient of variance and phenotypic coefficient of variance of different traits, red dashed line indicating threshold for high PCV and GCV value

Heritability and Genetic advance

To predict the proportion of genotypic variance in entire or phenotypic variance, the measure of broad sense heritability was estimated. In addition to heritability, genetic advance as percent of mean provides a more precise assessment of the genetic components of the total variance. Likewise, these parameters predict the response of the experimental material to selection for certain traits. Heritability for the trait DM (99.7%) was found to be the highest followed by the traits

such as SYP, OC, DFF, PH, TAW, NSS, NSMS, HI, NSB, LMS, LSMS and NPB. NPB ranked lowest with 59% of heritability. As the values go higher than 80% it is considered as very high, if values range from 60-79%, it is considered to be moderately high, when it ranges from 40-59, considered as medium, while values less than 40% are considered low (Singh., 2001; Teklu *et al.*, 2014) [12, 13]. The traits namely DM, SYP, OC, DFF, PH, TAW, NSS, NSMS, HI and NSB has fallen under very high range of heritability representing

the variance present in these traits are mostly of genotypic kind, thus selection may be rewarding. Again, traits such as LMS, LSMS moderately high level of heritability and NPB exposed medium level of heritability indicating higher level of environmental influence rendering them less suitable for selection. The genetic advance is a great measure for valuable selection as it indicates the progress in the selected population which indirectly specifies inheritance of certain trait. Genetic advance coinciding with heritability is a more consistent than heritability alone in forecasting subsequent result during selection of the individual genotype. In the study, highest genetic advance as percent of mean observed in the trait SYP was 41.807% and the lowest was observed in the trait LSMS (6.57%). The genetic advance as percent of mean (GAM) values are classified into low (less than 10%), medium (10-20%) and high (above 20%) (Johnson *et al.* 1955) [14]. On the basis of this distribution, the traits namely SYP, HI, BYP, TAW, NSB, PH, DM and DFF has exhibited high genetic advance as percent of mean values while traits namely OC, NSS, NSMS, NBP, LMS were observed to exhibit moderate

genetic advance as percent of mean values and LSMS alone exhibited low genetic advance as percent of mean values. The traits manifesting high genetic advance as percent of mean values indicated that the genetic variability present will be inherited in the progeny thus assisting in selection. Important traits namely DFF, DM, NSB, TAW, BYP, HI, SYP revealed very high heritability coinciding with high genetic advance as percent mean depict the preponderance of additive component of gene action for these traits thus selection will be sufficiently worthwhile. The traits namely LMS, NPB, NSMS, NSS and OC have exhibited high heritability with moderate genetic advance as percent mean indicated preponderance of both additive and non-additive components of genetic variance, offering opportunity of improvement through mindful selection. Trait namely LSMS contributing high heritability coupled with low genetic advance as percent mean indicating incidence of genetic variability nevertheless the components are mostly non-additive in nature which makes it difficult to fix these traits through selection.

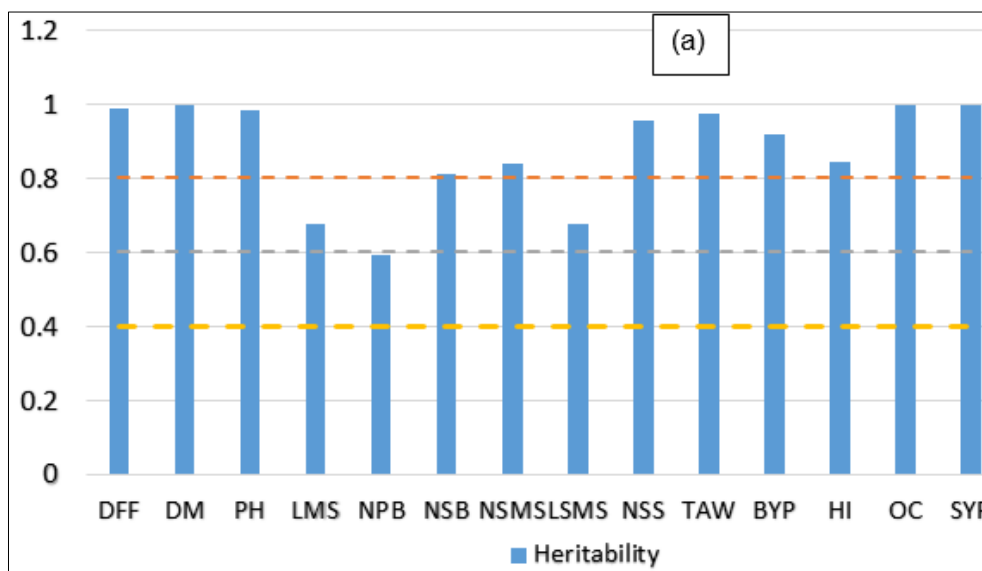


Fig 3 a): Heritability of different traits, Red dashed line indicating the minimum level of very high heritability, grey dashed line indicating threshold level of moderately high heritability and yellow dashed line indicating the threshold level of moderate heritability

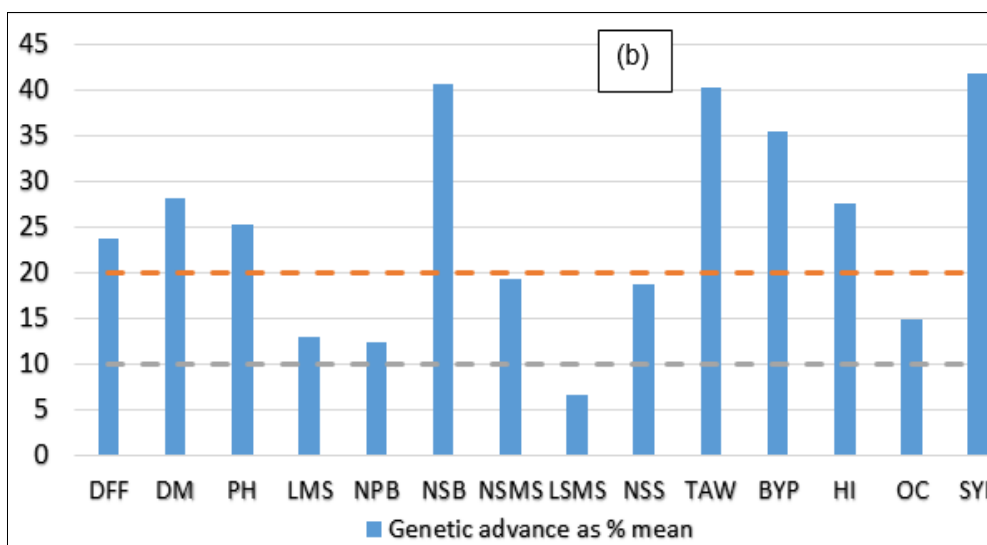


Fig 3b): Genetic Advance as percent mean of different traits, red dashed line indicating the threshold level of high genetic advance and grey line indicating moderate heritability

Character Association study

Seed yield is a complex trait and mostly get influenced by other traits which are codependent. Inter-relationship assessment of seed yield with different traits can help in improving the dependent trait indirectly when direct improvement is restricted. Seed yield is a complex trait and mostly get influenced by other traits which are co-dependent. Inter-relationship assessment of seed yield with different traits can help in improving the dependent trait indirectly when direct improvement is restricted. Thus, character association study plays a crucial role in predicting the overall performance of an entry. In the present experiment, phenotypic and genotypic correlation have been worked out between all the traits in all possible combination. The phenotypic and genotypic correlation of 14 traits is depicted in the figure. 3. and figure.4 respectively. Genotypic correlation coefficient values for most of the traits were higher than the phenotypic correlation coefficient which designates that the association is not merely due to environment.

comparable findings have been obtained in the research works of Akabarie *et al.*, 2015, Devi *et al.*, 2018 and Yadav *et al.*, 2020 [15-17].

The phenotypic correlation study revealed that seed yield per plant (SYP) was positively and significantly associated with the traits namely LMS (0.4609), NSB (0.4677), BYP (0.6364) and HI (0.568) where BYP showed significance at 0.01 level of significance and HI showed significance at 0.001 level of significance and traits such as LMS and NSB showed significance at 0.05 level of significance (Figure.4).

The genotypic correlation study revealed significant positive correlation matrix with the traits namely LMS (0.43), BYP (0.64), NSS (0.45) and NSB (0.53). Traits such as NSS and LMS exhibited significance at 0.05% level while the trait NSB showed significance at 0.01% level and the trait BYP was found to be significant even at 0.001% level (Figure.3.).

Further these traits are correlated with an array of traits which can provide a different measure of enhancement in those traits.

In the phenotypic correlation study of the trait BYP displayed positive and significant relationship with traits SYP, LMS, NSB and NSS while genotypic correlation study revealed similar relationship with those same traits including another trait HI.

The trait NSB exposed significant positive correlation with the traits namely SYP, NPB and BYP at both phenotypic and genotypic level.

The trait NSS revealed positive and significant phenotypic association with the traits namely PH, LMS and BYP whereas genotypic correlation study explained significant association with the trait SYP except for the traits mentioned above.

Both phenotypic and genotypic correlation study of LMS exhibited positive significant association with the same set of traits namely SYP, DFF, PH, NSMS, NSS and BYP.

In the present study, the traits positively correlated with SYP namely LMS, BYP, NSS, NSB are supposed to enhance the performance of the correlated trait progressively. Likewise, plants with higher length of main shoot (LMS) are more likely to give better seed yield than the plant having short length of main shoot. Similarly, if the biological yield per plant (BYP) is higher the plant automatically will produce higher SYP. More number of secondary branches (NSB) will rise the SYP value. Again, the plants carrying a greater number of seed per siliquae (NSS) are supposed to provide more seed yield. The traits namely HI (-0.27) and DFF (0.02) exhibiting negative non-significant correlation and almost no correlation respectively. Except for these traits mentioned above all other traits exposed positive non-significant association with the trait of interest.

Similarly, Devi *et al.*, (2018) [16] Kasturi *et al.*, (2022) [18] and Ray *et al.*, (2019) [19] found positive correlation between SYP and these traits.

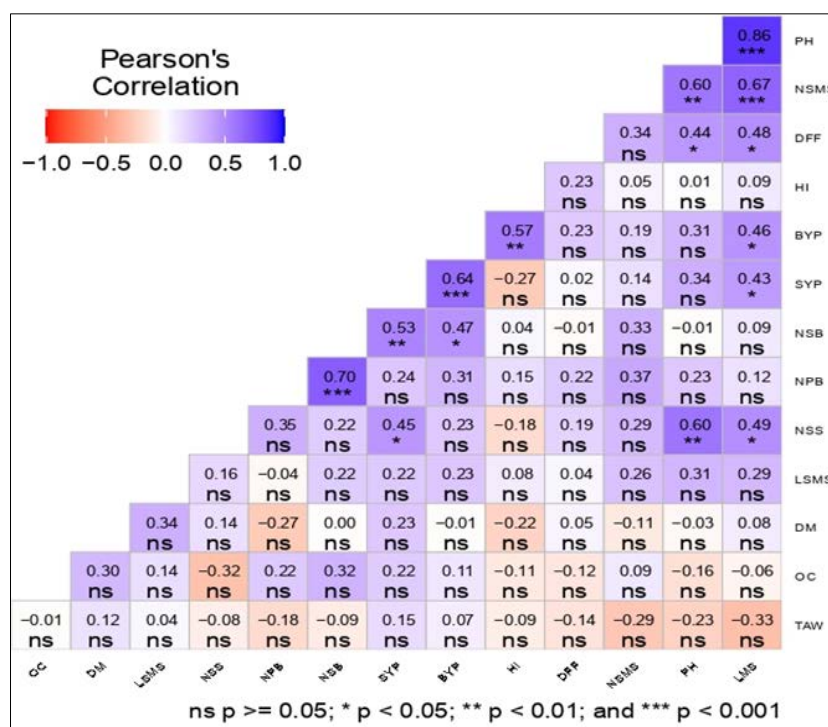


Fig 3: Genotypic Correlation matrix of 27 genotypes for 14 traits

	DFP	DM	PH	LMS	NPB	NSB	NSMS	LSMS	NSS	TAW	BYP	HI	OC
DM	0.0497												
PH	0.4435	-0.0339											
LMS	0.4823	0.08	0.8585										
NPB	0.223	-0.2658	0.2309	0.1245									
NSB	-0.014	-0.002	-0.009	0.0945	0.699								
NSMS	0.3444	-0.108	0.5961	0.6694	0.372	0.328							
LSMS	0.0401	0.3444	0.3129	0.2933	-0.037	0.215	0.2648						
NSS	0.1901	0.1363	0.5964	0.4868	0.345	0.218	0.2907	0.1647					
TAW	-0.135	0.116	-0.2283	-0.3303	-0.184	-0.093	-0.2882	0.0357	-0.084				
BYP	0.0223	0.2287	0.3378	0.4322	0.2378	0.531	0.1356	0.2205	0.447	0.1527			
HI	0.2339	-0.2226	0.0103	0.095	0.1462	0.037	0.0501	0.0819	-0.183	-0.089	-0.2662		
OC	-0.123	0.2962	-0.1552	-0.0578	0.2215	0.320	0.0946	0.1365	-0.315	-0.008	0.2182	-0.113	
SYP	0.228	-0.0059	0.309	0.4609	0.3126	0.4677	0.187	0.2334	0.231	0.0696	0.6364	0.568	0.105

Ns $p \geq 0.05$; * $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

Fig 4: Phenotypic Correlation matrix of 27 genotypes for 14 traits

Path coefficient study

The direction and magnitude of correlation was explained through path coefficient analysis. This way, the total correlation is dissociated into direct and indirect effects. This gives an insight about the true association of a trait in respect with the dependable trait. In the current study (Figure. 5.), (table. 4.), the trait BYP had highest positive direct effect (0.8883) on SYP followed by the traits namely HI (0.75), NSMS (0.1157), NPB (0.056), NSS (0.04), LMS (0.039), LSMS (0.035), OC (0.025), DFF (0.011) and TAW (0.0092). highest negative direct effect was exhibited by the traits namely PH (-0.1841) followed by NSB (-0.1697) and DM (-0.0424). This indicates that minute alteration in these traits can exactly contribute to improvement of the trait of our interest

which is seed yield.

Furthermore, the traits which are indirectly influencing these traits can be utilized for finetuning of the directly impacting traits which further can bring about changes in the trait of interest. In the study, the trait PH showed high level of indirect effect via the traits namely NSB, NSS, LMS, PH, DM, OC. This way the comprehensive performance of a trait can be influenced with the help of these interrelated web of traits.

Similar trend of result has been obtained by Patel *et al.*, (2019) [20] and Kasturi *et al.*, (2022) [18] where trait namely BYP, NSS, DFF, HI showed positive direct effect while NSB, PH, DM showed negative direct effect.

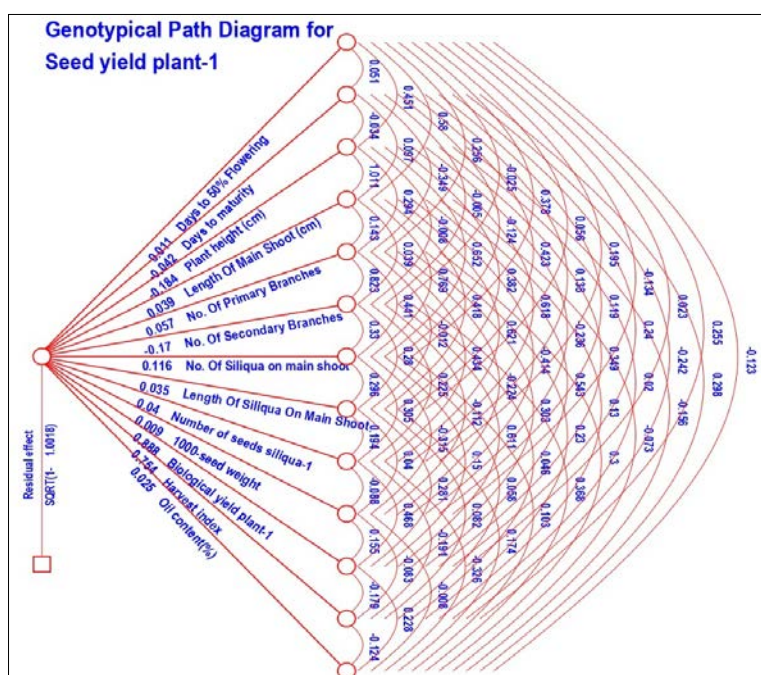


Fig 5: Genotypical path diagram for seed yield plant⁻¹

Table 3: Genetic Parameters of variation

Parameters	DFE	DM	PH	LMS	NPB	NSB	NSMS	LSMS	NSS	TAW	BYP	HI	OC	SYP
GCV	11.595	13.632	12.384	7.571	7.826	21.906	10.222	3.885	9.321	19.778	17.977	14.553	7.244	20.342
PCV	11.667	13.655	12.499	9.195	10.189	24.312	11.156	4.731	9.549	20.039	18.785	15.847	7.262	20.39
ECV	2.25	1.381	2.932	9.038	11.301	18.266	7.74	4.677	3.592	5.581	9.439	10.863	0.88	2.412
h ² (Broad Sense)	0.988	0.997	0.982	0.678	0.59	0.812	0.84	0.674	0.953	0.974	0.916	0.843	0.995	0.995
Genetic Advancement 5%	10.743	34.931	39.096	9.033	0.602	3.544	6.974	0.26	1.852	1.744	31.942	5.808	5.787	7.836
Gen. Adv as % of Mean 5%	23.736	28.033	25.276	12.842	12.383	40.66	19.295	6.572	18.743	40.212	35.44	27.532	14.886	41.807

Table 4: Genotypic path coefficient

	DFE	DM	PH	LMS	NPB	NSB	NSMS	LSMS	NSS	TAW	BYP	HI
DFE	0.0108	0.0006	0.0049	0.0063	0.0028	-0.0003	0.0041	0.0006	0.0021	-0.0014	0.0003	0.0028
DM	-0.0022	-0.0424	0.0014	-0.0041	0.0148	0.0002	0.0053	-0.0179	-0.0059	-0.0050	-0.0102	0.0103
PH	-0.0830	0.0063	-0.1841	-0.1862	-0.0541	0.0015	-0.1200	-0.0704	-0.1137	0.0435	-0.0644	-0.0036
LMS	0.0227	0.0038	0.0395	0.0391	0.0056	0.0015	0.0301	0.0163	0.0243	-0.0162	0.0212	0.0051
NPB	0.0145	-0.0197	0.0166	0.0081	0.0565	0.0465	0.0250	-0.0007	0.0245	-0.0126	0.0171	0.0130
NSB	0.0042	0.0008	0.0014	-0.0067	-0.1397	-0.1697	-0.0561	-0.0476	-0.0382	0.0190	-0.1037	-0.0079
NSMS	0.0437	-0.0144	0.0754	0.0890	0.0511	0.0382	0.1157	0.0342	0.0353	-0.0365	0.0174	0.0067
LSMS	0.0020	0.0148	0.0134	0.0146	-0.0004	0.0098	0.0103	0.0350	0.0068	0.0014	0.0098	0.0029
NSS	0.0078	0.0055	0.0247	0.0248	0.0173	0.0090	0.0122	0.0078	0.0400	-0.0035	0.0187	-0.0076
TAW	-0.0012	0.0011	-0.0022	-0.0038	-0.0021	-0.0010	-0.0029	0.0004	-0.0008	0.0092	0.0014	-0.0008
BYP	0.0208	0.2129	0.3104	0.4821	0.2688	0.5430	0.1335	0.2498	0.4156	0.1375	0.8883	-0.1587
HI	0.1919	-0.1826	0.0149	0.0979	0.1732	0.0349	0.0434	0.0619	-0.1437	-0.0626	-0.1347	0.7541
OC	-0.0031	0.0076	-0.0040	-0.0019	0.0076	0.0094	0.0026	0.0044	-0.0083	-0.0002	0.0058	-0.0032

Conclusion

The investigation the traits such as SYP, TAW and NSB depicted high GCV coupled with high PCV making selection beneficial for these traits. The difference between GCV and PCV was negligible predicting inconsequential environmental influence. Further important traits such as DFE, DM, NSB, TAW, BYP, HI, SYP exhibited very high heritability coupled with high genetic advance indicating the existence of additive gene action. Traits namely LMS, BYP, NSS and NSB exposed significant positive association with the trait SYP. In the path coefficient study it was prevalent that the traits such as BYP, followed by HI, NSMS, NPB, NSS, LMS, LSMS, OC, DFE and TAW had gradual positive direct effect on the trait SYP. In the study important yield and yield contributive traits unveiled high inheritance with additive gene action and showed positive and direct association which will be providing a set of strictures for the traits for competent selection.

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