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RESEARCH ARTICLE

Unravelling genetic variability, correlation and path analysis to uncover key traits for drought tolerance in Indian mustard (*Brassica juncea* L.)

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Abstract

In the current era of continuously shifting environmental conditions, drought remains a major abiotic constraint, significantly impacting crop growth and productivity. This study assessed genetic variability and trait associations and effects in 65 Indian mustard genotypes under normal and drought stress conditions to identify key traits for drought tolerance. These genotypes were analyzed in randomized block design with three replications under irrigated and drought stress conditions for two consecutive years *Rabi* 2020-21 and 2021-22 at the Instructional research farm, SKRAU, Bikaner. Analysis of variance were found to be highly significant for all the traits analyzed over years and environments, suggesting the existence of significant genetic variation for these traits in the present germplasm. High heritability along with high genetic advance were observed for number of primary branches, number of secondary branches, number of siliqua per plant, test weight, harvest index, seed yield per plant, root diameter, membrane stability index, leaf water potential and proline content under both the conditions, suggesting the predominance of additive gene effects, hence these traits can be efficiently improved through direct selection. Seed yield per plant showed significant positive associations with most traits, except plant height and root diameter and a negative association with leaf water potential under drought stress, suggesting these traits as key targets for selection to enhance yield under limited moisture. Path analysis indicated that HI and BYPP were the most critical determinants of SYPP under drought stress, while other traits contributed mainly through indirect effects, underscoring the pivotal role of HI-mediated pathways in yield enhancement.

Keywords: correlation; genetic advance; heritability; Indian mustard; variability

Introduction

Oilseed crops are next to cereals in production of agricultural commodities in India, occupying a place of vital importance in Indian economy. Rapeseed-mustard occupies the first position among the edible oilseed production in India, contributing to 33.24 % of total oilseeds production, with a record production of 13.16 million tonnes (1). Among the different *Brassica* species, *Brassica juncea* (Indian mustard) holds significant importance as a primary edible oilseed crop in India, occupying a substantial area of cultivation. *B. juncea* is a natural amphidiploid (AABB; 2n = 36) from the interspecific cross between two diploid species, namely *B. campestris* (AA; 2n = 20) and *B. nigra* (BB; 2n = 16), followed by spontaneous chromosome doubling (2, 3). Under the changing climatic scenario, plants are encountered with various biotic and abiotic stresses (4). Among all the various abiotic stresses that leads to a decline in crop productivity, drought is the most devastating one and the most recalcitrant to breeders' efforts (5, 6). Nearly, 37 % area of rapeseed-mustard is under rainfed cultivation where the crops are mostly grown on conserved soil moisture with one supplemental irrigation in the Indian subcontinent (7). *Brassica* crops are the most susceptible to drought that limits their survival and growth (8). Therefore, occurrence of drought is a usual feature during the crop growth period especially at reproductive phases of growth in *Brassica* species, when the seed yield is reduced drastically.

The existence of genetic variability within the population is of paramount importance to a breeder to develop varieties with desirable traits such as resistance to biotic and abiotic stresses, improved quality as well as wide adaptability (9, 10). Analysis of variability parameters for various traits and realization of association between yield and its attributing traits are basic and foremost endeavour to determine the benchmark for plant selection (11). Despite its importance, genetic improvement in *B. juncea* is constrained by its limited genetic diversity, a characteristic of its amphidiploid nature. This narrow genetic variability hampers efforts to improve yield, stress tolerance and adaptability, critical for addressing climate change and rising demand for edible oils (12). Therefore, the present study was undertaken to estimate the magnitude of genetic variability among the genotypes and to determine the desirable traits for drought tolerance that can be incorporated in elite varieties for improving their performance under drought stress conditions in Indian mustard.

Materials and Methods

The present investigation was carried out at the Instructional research farm, College of Agriculture, SKRAU, Bikaner during the *Rabi* season of two successive years 2020-2021 and 2021-2022. The experimental material comprised of 65 genotypes of Indian mustard (*B. juncea*) procured from ICAR-DRMR, Bharatpur; ARS, Sri Ganganagar and ARS, Bikaner. The experiment was laid in randomized block design with three replications under two soil moisture regimes i.e., normal sown and drought stress. Pre-sowing irrigation was applied to both the fields. The normal irrigated environment received four irrigations - first at vegetative stage (30 DAS), second at pre-flowering stage (45 DAS), third at post-flowering stage (65 DAS) and fourth at pod setting stage (80 DAS). The drought stress environment was created by withholding irrigation after germination. The restricted moisture trials received only two post-germination irrigations - first at pre-flowering stage (40-45 DAS) and second at pod setting stage (80 DAS). Each environment was separated by at least 5 m to avoid experimental error. The genotypes were raised in paired rows of 3 m length with a spacing of 45 cm between rows and 15 cm between plants. All the recommended package of practices were followed during the crop growth period (13).

Data were recorded on 5 randomly selected plants per genotype in each replication and averaged during both the Rabi seasons. Observations were obtained for twelve agro-morphological traits viz., days to 50 % flowering (DTF), days to maturity (DTM), plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), siliqua length (SL), number of seeds per siliqua (SPS), number of siliqua per plant (NSPP), test weight (TW), biological yield per plant (BYPP), harvest index (HI), seed yield plant (SYPP); four physiological traits i.e., root length (RL), root diameter (RD), membrane stability index (MSI), leaf water potential (LWP) and a biochemical parameter i.e., proline content (PC) (13). The data were subjected to analysis of variance by Panse and Sukhatme (14); estimation of genetic variability parameters by Burton and Devane (15), Johnson et al. (16) and Hanson et al. (17), analysis of phenotypic correlation coefficient by Singh and Chaudhary (18) and path coefficient analysis by Dewey and Lu (19) using INDOSTAT v7.1 software.

Results and discussion

Analysis of variance (ANOVA)

The ANOVA revealed highly significant differences among the genotypes for all the seventeen traits under both the conditions (Table 1). Variance due to genotypes were found to be highly significant for all the 17 characters thereby, indicating the presence of wide spectrum of variability in the genotypes selected for this study. Similar findings were also reported earlier in various studies (20-22).

Genetic variability parameters

Assessment of genetic diversity in crop plants aids in crop improvement strategies. The phenotype of an individual is determined by the genotype and environment along with their interaction. Parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) determine that whether the traits are under genetic control or influenced by the environment. In the present study, it was observed that the magnitude of PCV was found slightly higher than their corresponding GCV for all the analyzed traits under both the sowing conditions, indicating a greater contribution of genotypic variance to the total phenotypic variance and the effect of environment is minimal.

The analysis of coefficient of variation depicted high magnitude of GCV and PCV for PC (66.47 %, 66.61 %), LWP (29.73 %, 31.38 %) and RD (20.04 %, 23.89 %) under recommended irrigation conditions. The moderate estimates of GCV and PCV

Table 1. Analysis of variance for 17 characters in Indian mustard (*Brassica juncea* L.) under normal sown and drought stress conditions

Source of variation	Mean sum of squares					
	Genotype		Replication		Error	
	d.f. = 64		d.f. = 2		d.f. = 128	
SC	NS	DS	NS	DS	NS	DS
DTF	39.73**	40.65**	0.20	1.68	1.17	1.08
DTM	85.05**	71.51**	2.47	0.10	2.58	2.05
PH	670.05**	604.63**	129.37	73.76	95.76	78.21
NPB	3.47**	1.75**	0.48	0.64	0.42	0.43
NSB	9.75**	4.69**	0.19	1.62	1.28	0.94
SL	0.38**	0.43**	0.40	0.37	0.23	0.15
SPS	7.91**	6.75**	0.25	0.77	1.25	1.35
NSPP	28321.87**	22029.56**	8125.45	1356.08	3380.52	2050.09
TW	1.19**	1.4**	0.05	0.01	0.03	0.02
BYPP	404.13**	309.66**	31.18	51.10	43.91	26.59
HI	32.38**	50.19**	0.57	0.15	2.14	1.98
SYPP	41.38**	55.02**	0.52	2.96	2.66	1.73
RL	7.55**	16.62**	3.10	0.42	1.02	1.78
RD	0.54**	0.4**	0.01	0.05	0.05	0.05
MSI	183.61**	238.67**	10.93	1.86	5.77	2.90
LWP	14.61**	19.63**	0.19	0.65	0.14	0.21
PC	18.69**	22.11**	0.01	0.01	0.01	0.01

SC: sowing condition; NS: normal sown; DS: drought stress trait details are given in Materials and Methods.

**Significant at 1 % level of significance.

were manifested by MSI (16.04 %, 16.70 %), NSPP (15.87 %, 19.34 %), HI (15.49 %, 16.76 %), NPB (15.20 %, 18.62 %), NSB (13.93 %, 17.21 %), SYPP (13.40 %, 14.90 %), TW (13.03 %, 13.44 %) and RL (10.70 %, 13.54 %). In contrast to this, when plants were irrigated at only pre-flowering and pod setting stage, the traits viz., PC (57.22 %, 57.37 %), MSI (26.83 %, 27.50 %), LWP (23.24 %, 24.52 %) and SYPP (21.34 %, 22.36 %) had the highest GCV and PCV. The characters such as NSPP (19.90 %, 22.85 %), HI (19.64 %, 20.97 %) and RD (17.70 %, 21.80 %) showed moderate GCV and high PCV (Table 2). These findings indicated the existence of wide range of genetic variability for the traits having high to moderate values of GCV and PCV, thereby providing a greater scope for further improvement through simple selection. Earlier findings reported that these traits are considered as major yield contributing traits (22-24). Similar outcomes pertaining to the presence of high to moderate genetic variability were also observed by former researchers (20, 24-26). The occurrence of low GCV and PCV values for a character indicated the presence of limited variability for these traits among the tested accessions. Therefore, the improvement of these characters cannot be achieved effectively through mere selection (10, 20, 27-29).

The detection of significant genetic variability suggests the existence of genetic variation in the germplasm pool but does not provide any idea about the range of genetic variability within a particular population. The estimation of broad sense heritability provides information on the relative magnitude of genetic and environmental variation present in a crop population. In the present study, the heritability estimates recorded high magnitude for PC (99.60 %), TW (94.10 %), MSI (92.30 %), DTM (90.30 %), LWP (89.80 %), DTF (86.60 %), HI (85.40 %), SYPP (81 %), BYPP (74.90 %), RD (70.40 %), NSPP (67.30 %), NPB (66.60 %), NSB (65.50 %) and RL (62.40 %) under recommended irrigation conditions (Fig. 1). The traits viz., number of seeds per siliqua (56.90 %), plant height (51.50 %) and siliqua length (31.70 %) display moderate heritability. However, under restricted (two) irrigation conditions, high heritability was manifested by PC (99.50 %), TW (95.70 %), MSI (95.20 %), DTF (91.40 %), SYPP (91 %), DTM (90.40 %), LWP (89.90 %), HI (87.70 %), BYPP (76.70 %), NSPP (75.80 %), RL (73.70 %), RD (65.90 %), PH (64 %) and NSB (63.80 %). Moderate values of heritability were observed for NPB (57.10 %), SPS (54.30 %) and SL (37.70 %) (Fig. 2). High heritability for one or more of the studied traits were also reported in earlier studies (5, 18, 30, 31). These findings depicted that the major proportion of the observable phenotypic variance of these traits were due to the genotypes and they can be easily improved through individual plant selection due to its high heritability value and better response to selection.

Table 2. Estimates of genetic variability parameters for 17 characters studied among 65 genotypes of Indian mustard (*Brassica juncea* L.) under normal sown and drought stress conditions

Trait	GCV (%)		PCV (%)		Heritability (%)		GA (k=2.06)		GA as % of mean	
	NS	DS	NS	DS	NS	DS	NS	DS	NS	DS
DTF	6.43	7.45	6.91	7.79	86.60	91.40	6.66	7.25	12.34	14.67
DTM	3.58	3.50	3.76	3.68	90.30	90.40	10.00	9.41	7.00	6.85
PH	7.12	7.78	9.92	9.72	51.50	64.00	20.31	21.35	10.50	12.82
NPB	15.20	14.57	18.62	19.28	66.60	57.10	1.66	1.12	25.55	22.68
NSB	13.93	14.02	17.21	17.55	65.50	63.80	2.77	2.04	23.23	23.07
SL	5.63	6.91	10.00	11.25	31.70	37.70	0.36	0.41	6.54	8.73
SPS	9.32	11.26	12.35	15.27	56.90	54.30	2.50	2.36	14.48	17.10
NSPP	15.87	19.90	19.34	22.85	67.30	75.80	164.99	154.12	26.84	35.69
TW	13.03	16.20	13.44	16.56	94.10	95.70	1.25	1.36	26.04	32.64
BYPP	9.53	10.97	11.01	12.53	74.90	76.70	22.40	19.98	17.00	19.80
HI	15.49	19.64	16.76	20.97	85.40	87.70	6.38	7.85	29.50	37.88
SYPP	13.40	21.34	14.90	22.36	81.00	91.00	7.01	8.72	24.84	41.94
RL	10.70	13.09	13.54	15.24	62.40	73.70	2.90	4.63	17.40	23.15
RD	20.04	17.70	23.89	21.80	70.40	65.90	0.64	0.61	34.65	29.60
MSI	16.04	26.83	16.70	27.50	92.30	95.20	15.59	18.11	31.74	53.91
LWP	29.73	23.24	31.38	24.52	89.80	89.90	4.02	4.92	58.02	45.40
PC	66.47	57.22	66.61	57.37	99.60	99.50	5.13	5.54	136.63	117.57

SC: sowing condition; NS: normal sown; DS: drought stress. Trait details are given in Materials and Methods.

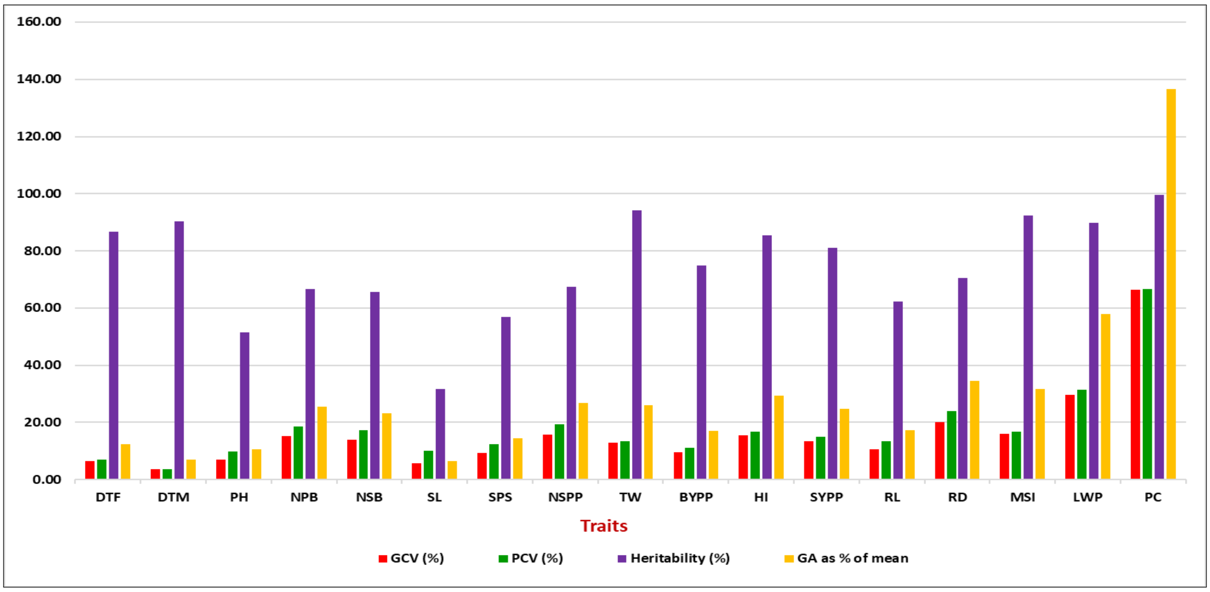

Fig. 1. Graphical representation of inheritance of 17 characters in Indian mustard under normal sown conditions.

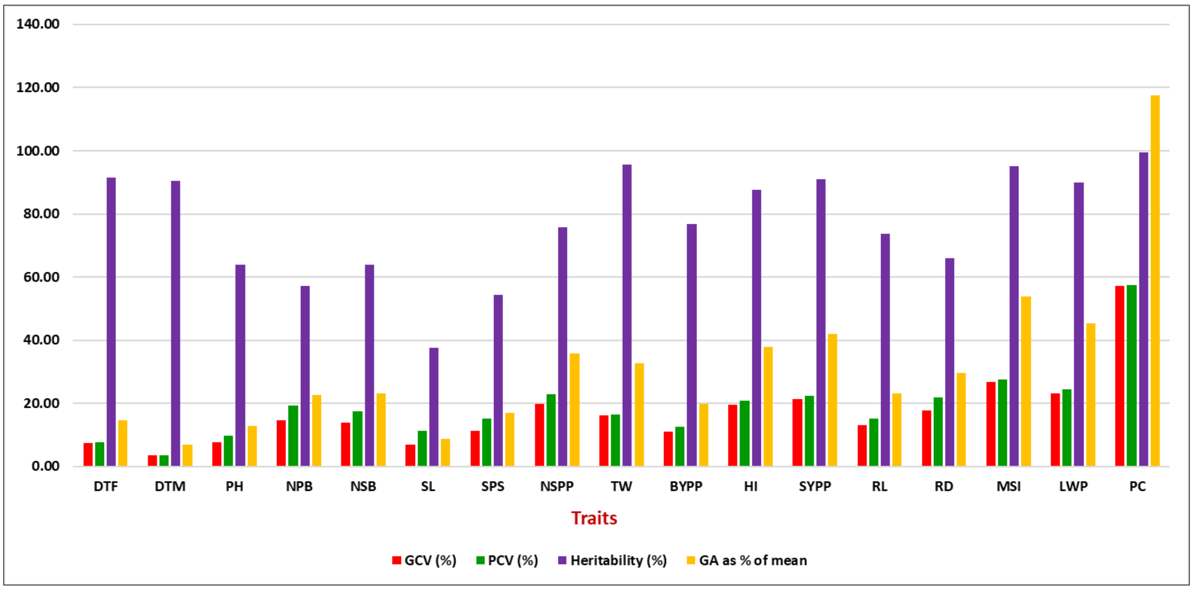

Fig. 2. Graphical representation of inheritance of 17 characters in Indian mustard under drought stress conditions.

Genetic advance under selection is the improvement in mean genotypic value of selected population over that of base population. It determines the expected genetic gain under a particular selection pressure. The analysis of magnitude of genetic advance as percent of mean depicted that characters such as PC (136.63 %), LWP (58.02 %), RD (34.65 %), MSI (31.74 %), HI (29.50 %), NSPP (26.84 %), TW (26.04 %), NPB (25.55 %), SYPP (24.84 %) and NSB (23.23 %) had high GA as percentage of mean under recommended irrigation conditions. Traits viz., RL (17.40 %), BYPP (17 %), SPS (14.48 %), DTF (12.34 %) and PH (10.50 %) had moderate GA, whereas low GA as percent of mean was observed for DTM (7 %) and SL (6.54 %). In contrast, under limited irrigation conditions, high GA as percent of mean was displayed by PC (117.57 %), MSI (53.91 %), LWP (45.40 %), SYPP (41.94 %), HI (37.88 %), NSPP (35.69 %), TW (32.64 %), RD (29.60 %), RL (23.15 %), NSB (23.07 %) and NPB (22.68 %). Characters like BYPP (19.80 %), SPS (17.10 %), DTF (14.67 %) and PH (12.82 %) showed moderate GA, whereas SL (8.73 %) and DTM (6.85 %) had low GA as percent of mean. Similarly, previous studies have reported high genetic advance as a percentage of the mean for the number of siliquae per plant (31) as well as for seed yield per plant, number of siliqua per plant, number of secondary branches and test weight (32). The consistency of these findings across different studies highlights the stability of additive genetic effects controlling these traits in Indian mustard. Among them, the number of siliquae per plant and branching traits directly contribute to reproductive sink capacity, while test weight reflects seed size and density, thereby exerting a strong influence on yield potential.

However, the estimates of heritability and genetic advance alone do not clearly depict the real insight of genetic improvement. Heritability along with genetic advance is more reliable in predicting the effectiveness of selection on the phenotypic expression of a trait rather than the heritability estimates alone (14). In the present study, high heritability combined with high genetic advance was recorded for NPB, NSB, NSPP, RD, SYPP, HI, TW, MSI, LWP and PC under both conditions, while for RL, this association was observed only under drought stress. The results depicted the preponderance of additive gene effects in the genotypic variation of these traits and they can be improved through simple or progeny selection methods (5, 8, 10). Existing literatures reported high heritability in conjugation with high genetic advance for harvest index, secondary branches per plant, number of siliqua per plant, seed yield per plant and for test weight (22, 26, 27, 32-34). The high GAM coupled with substantial heritability estimates suggests that these yield-attributing traits can be effectively improved through direct selection.

The presence of high heritability coupled with moderate to low genetic advance for a character is an indication of involvement of non-additive gene action in their genetic control. The high magnitude of heritability of these traits could be due to favourable influence of environment on their phenotypic expression rather than the genotype. Hence, the selection for such traits may not be rewarding. For improvement of such traits, the breeder might resort to diallel selective mating or reciprocal recurrent selection (33, 34).

Correlation analysis

The potential productivity of a crop is manifested in terms of seed yield. Seed yield per plant (SYPP) in Indian mustard is a highly complex trait governed by multiple genetic and environmental factors and direct selection for yield is often inefficient due to its low heritability (35). The estimation of correlation quantifies the degree of genetic and non-genetic association between traits thus, allowing the indirect selection through component character with high heritability (36). In the present study, phenotypic correlation analysis provided insights into the association of SYPP with its component traits under both normal and drought stress conditions, thereby identifying the most reliable characters for indirect selection. Under normal sown conditions (Table 3 and Fig. 3), SYPP exhibited significant and positive associations with HI (0.7659**), NSPP (0.6323**), NSB (0.6088**), NPB (0.591**), DTF (0.5672**), TW (0.4838**), DTM (0.3571**), MSI (0.2891**), SPS (0.1564*) and RL (0.1509*) under normal sown condition. These results suggest that improvement in these traits may lead to a corresponding increase in seed yield, emphasizing their potential as effective selection indices. The strong association of HI and branching traits with SYPP particularly highlights their role in enhancing source-sink balance and assimilate partitioning efficiency.

Interestingly, under drought stress conditions (Table 3 and Fig. 4), the association pattern of SYPP with component traits was altered, with stronger positive correlations observed

Table 3. Phenotypic correlation coefficient among 17 characters studied among 65 genotypes of Indian mustard (*Brassica juncea* L.) under normal sown and drought stress conditions

Trait	SC	DOF	DOM	PH	NPB	NSB	SL	SPS	NSPP	TW	BYPP	HI	RL	RD	MSI	LWP	PC
DTF	NS	1	04231**	01739*	08642**	07857**	01039	00661	03850**	03466**	01606*	04108**	00796	00033	02424**	02822**	03169**
	DS	1	04025**	02294**	08091**	07500**	01958**	01265	05432**	05787**	03267**	06355**	02949**	-00022	03377**	00569	03736**
DTM	NS		1	00119	03065**	02920**	00606	00179	01982**	00694	00501	02874**	-01979**	01142	01887**	02433**	00197
	DS		1	0083	02975**	03585**	01428*	00582	01877**	02375**	00842	04349**	01411*	0061	02941**	01387	02040**
PH	NS			1	00757	01072	00102	00427	00716	01144	02550**	-02332**	00978	-01711*	01162	03064**	04529**
	DS			1	01774*	01619*	02629**	02236**	02448**	02301**	03685**	-0042	00786	-01311	02657**	01104	04739**
NPB	NS				1	08306**	01043	00764	04131**	03925**	01828*	04129**	00781	-00044	02545**	02245**	03367**
	DS				1	08334**	01601*	01134	05191**	05586**	03050**	05693**	02589**	00816	03851**	00058	03451**
NSB	NS					1	01265	00472	04244**	03704**	02242**	04080**	01161	00026	01908**	02448**	03000**
	DS					1	00982	01215	04841**	04915**	03406**	05908**	01808*	00157	03653**	00497	03966**
SL	NS						1	01943**	0066	03219**	00267	00544	01053	00949	01394	00409	01631*
	DS						1	02331**	00793	03013**	01526*	01026	0093	00598	03025**	-00616	02716**
SPS	NS							1	00886	01499*	01081	00516	01950**	01445*	01675*	-01431*	00112
	DS							1	01717*	02036**	02531**	00494	02045**	-00055	01873**	-01265	01686*
NSPP	NS								1	04290**	01318	04634**	01740*	0083	00736	00312	01242
	DS								1	04444**	03845**	04574**	02210**	-00034	03624**	-00304	04486**
TW	NS									1	00301	03408**	00921	00921	02403**	01870**	03465**
	DS									1	03073**	05013**	00903	00903	03174**	00378	03580**
BYPP	NS										1	-04619**	01668*	01668*	00301	01431*	02710**
	DS										1	-01553*	01609*	01609*	03073**	-01063	04294**
HI	NS											1	00328	00328	02367**	-00175	-00632
	DS											1	01978**	01978**	03461**	-00407	01614*
RL	NS												1	02123**	00811	00145	01605*
	DS												1	02541**	01429*	-00419	02258**
RD	NS													1	-00984	-01797*	-00818
	DS													1	-01328	00181	-00424
MSI	NS														1	03701**	02015**
	DS														1	01254	03870**
LWP	NS															1	03072**
	DS															1	01193
PC	NS																1
	DS																1
SYPP	NS	05672**	03571**	-00711	0591**	06088**	00698	01564*	06323**	04838**	02056**	07659**	01509*	00761	02891**	00794	01138
	DS	07639**	04611**	01538*	06914**	07199**	01823**	01844**	06311**	06318**	03801**	08501**	02734**	-0027	04912**	-0095	03731**

SC: sowing condition; NS: normal sown; DS: drought stress. Trait details are given in Materials and Methods.

*Significant at 5 % level of significance.

**Significant at 1 % level of significance.

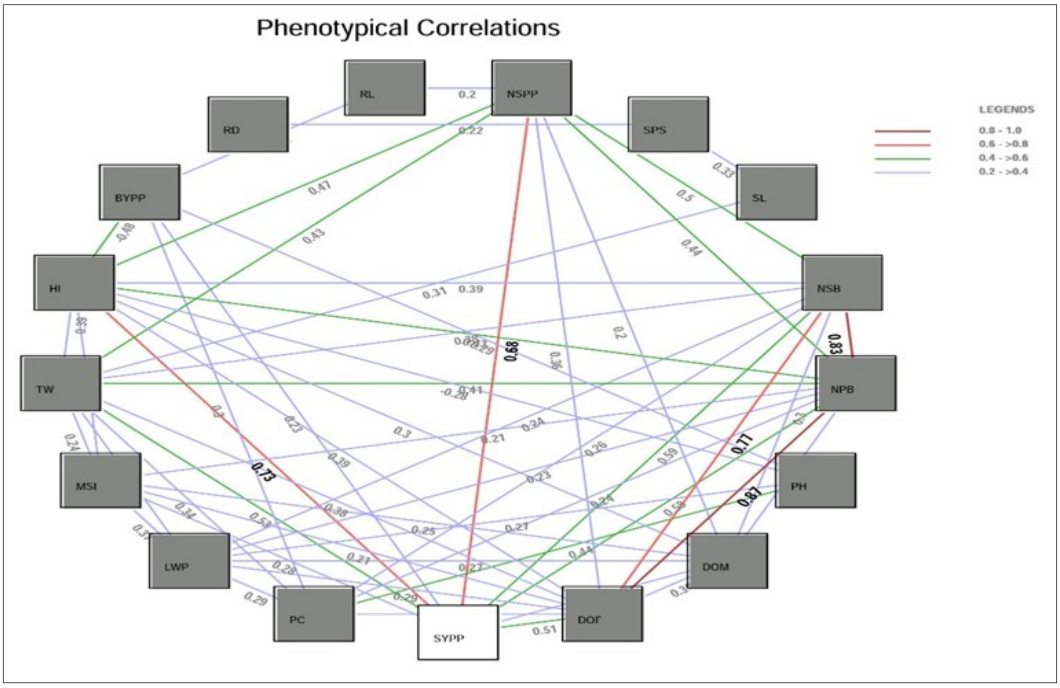

Fig. 3. Phenotypic correlation between yield and its related traits in 65 genotypes of Indian mustard under normal sown conditions.

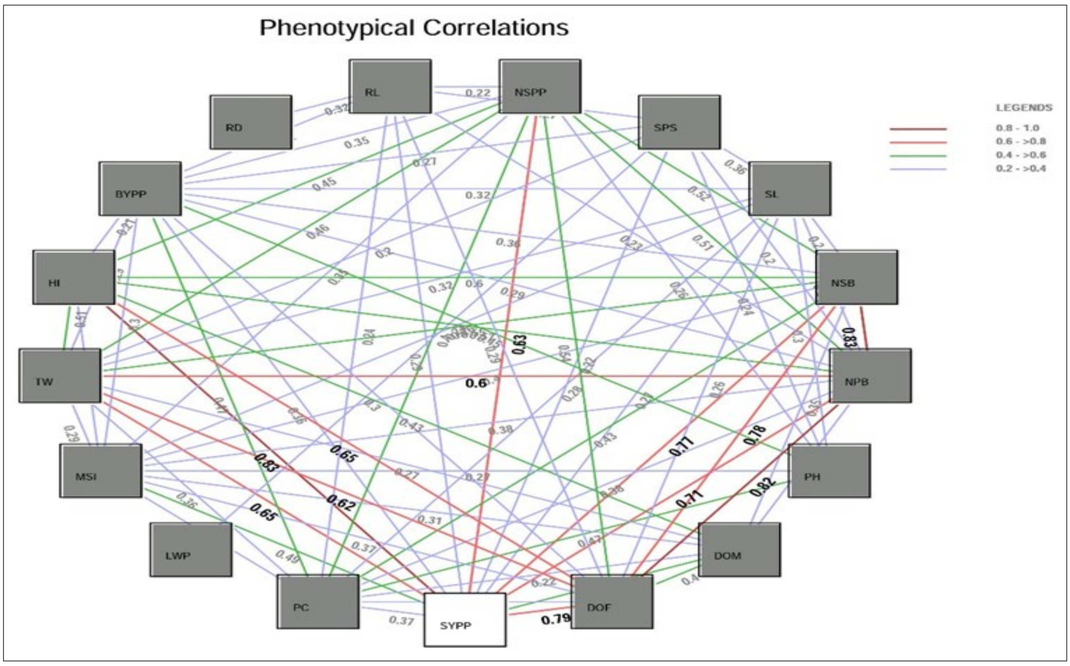

Fig. 4. Phenotypic correlation between yield and its related traits in 65 genotypes of Indian mustard under drought stress conditions.

for HI (0.8501**), DTF (0.7639**), NSB (0.7199**), NPB (0.6914**), TW (0.6318**), NSPP (0.6311**), MSI (0.4912**), DTM (0.4611**), BYPP (0.3801**), PC (0.3731**), RL (0.2734**), SPS (0.1844**), SL (0.1823**) and PH (0.1538*). The magnitude of correlation for HI and DTF under stress conditions was higher compared to normal conditions, indicating that these traits play a critical role in yield stability under moisture-limited environments. Furthermore, additional significant associations of SYPP with PC, SL and PH were observed under stress, reflecting their adaptive contribution to drought tolerance.

Previous studies have similarly reported a positive relationship of SYPP with TW, SL, DTM, PH and branching traits, reinforcing the current findings (8, 34). The contrasting observation that SYPP correlated positively with nearly all yield-attributing traits under drought stress, except SL, suggests that under stress, multiple traits act in coordination to sustain yield performance. This aligns with the reports of earlier researchers who emphasized the importance of simultaneous selection for yield components in stressed environments (4, 37).

Overall, the results demonstrate that SYPP improvement in Indian mustard can be achieved more effectively by indirect selection through HI, branching traits, siliqua-related traits and TW, especially under stress conditions where these characters show enhanced association with yield. The presence of mutual and positive inter-relationships among component traits further implies that selection for one trait may result in correlated improvement in others, thereby enhancing overall breeding efficiency. Thus, incorporating these key traits into breeding programs will accelerate the development of high-yielding and stress-resilient mustard genotypes.

Path analysis

The results of correlation analysis alone may be misleading, as apparent associations between traits can arise due to their mutual dependence on a third variable. Path coefficient analysis overcomes this limitation by partitioning correlations into direct and indirect effects, thereby providing precise insights into trait contributions and guiding effective selection for yield improvement. Path analysis at the phenotypic level in Indian mustard revealed the magnitude of direct and indirect effects of various yield-attributing traits on seed yield per plant (34). As depicted from Table 4, among the traits studied, HI (1.0528) exerted the highest positive direct effect on seed yield per plant under normal sown conditions, followed by BYPP (0.6865) and NSPP (0.0559). This suggests that these three traits were the most important contributors to seed yield at the phenotypic level. Moderate positive direct effects were also contributed by SPS (0.0254) and MSI (0.0151). On the contrary, traits such as DTF (-0.0162), TW (-0.0158), PC (-0.0120) and SL (-0.0096) exhibited negative direct effects on SYPP, indicating their limited role in direct improvement of yield. Root-related traits viz., RL (-0.0091 and RD (-0.0007) also had negligible or unfavourable direct effects under irrigated conditions (Fig. 5). In addition to the direct contributions, several traits showed substantial indirect effects via major yield-contributing traits. NPB and NSPP exerted strong positive indirect effects on SYPP through HI and BYPP; DTM had negligible direct effect (0.0049) but contributed indirectly through HI (0.3025) and BYPP (0.0344); SPS and MSI also enhanced yield indirectly via HI and NSPP. Despite its negative direct effect, DTF influenced yield indirectly through HI (0.4325) and BYPP (0.1103). The coefficient of determination (R^2 = 0.9875) indicated that the set of characters included in the model explained about 98.75 % of the total variation in seed yield per plant, with a residual effect of 0.1120. Overall, the study clearly indicated that harvest index, biological yield per plant and number of siliquae per plant are the most important determinants of seed yield per plant in Indian mustard under normal sown conditions. Therefore, selection strategies emphasizing these traits would be highly effective for yield improvement (32, 37).

However, under drought stress sown conditions (Table 5), the highest positive direct effect on SYPP were observed via HI (0.9233) and BYPP (0.5196). Other traits with positive but small direct effects included NSPP (0.0083), TW (0.0047), SL (0.0045), SPS (0.0042) and MSI (0.0035). Traits viz., NSB (-0.0362), DTF (-0.0059), PC (-0.0053), PH (-0.0052) and RD (-0.0188) had negative direct effects on SYPP, thus limiting their direct contribution to yield under stress. A large part of the yield variation was also explained through indirect effects via HI and BYPP (Fig. 6). For instance, NPB and NSPP recorded strong indirect contributions to SYPP via HI (0.5256 and 0.4223, respectively); DTM though showing a small direct effect (0.0196), contributed indirectly through HI (0.4015) and BYPP (0.0437); DTF despite its negative direct effect, showed a substantial positive indirect effect via HI

Table 4. Path coefficient analysis depicting the direct and indirect effect of yield attributing traits on seed yield per plant at phenotypic level under normal sown conditions in Indian mustard (*Brassica juncea* L.)

Trait	DTF	DTM	PH	NPB	NSB	SL	SPS	NSPP	RL	RD	BYPP	HI	TW	MSI	LWP	PC
DTF	-0.0162	-0.0068	-0.0028	-0.0140	-0.0127	-0.0017	-0.0011	-0.0062	-0.0013	-0.0001	-0.0026	-0.0066	-0.0056	-0.0039	-0.0046	-0.0051
DTM	0.0021	0.0049	0.0001	0.0015	0.0014	0.0003	0.0001	0.0010	-0.0010	0.0006	0.0002	0.0014	0.0003	0.0009	0.0012	0.0001
PH	0.0003	0.0000	0.0016	0.0001	0.0002	0.0000	0.0001	0.0001	0.0002	-0.0003	0.0004	-0.0004	0.0002	0.0002	0.0005	0.0007
NPB	0.0261	0.0093	0.0023	0.0302	0.0251	0.0031	0.0023	0.0125	0.0024	-0.0001	0.0055	0.0125	0.0118	0.0077	0.0068	0.0102
NSB	-0.0037	-0.0014	-0.0005	-0.0039	-0.0047	-0.0006	-0.0002	-0.0020	-0.0005	0.0000	-0.0011	-0.0019	-0.0018	-0.0009	-0.0012	-0.0014
SL	-0.0010	-0.0006	-0.0001	-0.0010	-0.0012	-0.0096	-0.0019	-0.0006	-0.0010	-0.0009	-0.0003	-0.0005	-0.0031	-0.0013	-0.0004	-0.0016
SPS	0.0017	0.0005	0.0011	0.0019	0.0012	0.0049	0.0254	0.0023	0.0050	0.0037	0.0028	0.0013	0.0038	0.0043	-0.0036	0.0003
NSPP	0.0215	0.0111	0.0040	0.0231	0.0237	0.0037	0.0050	0.0559	0.0097	0.0046	0.0074	0.0259	0.0240	0.0041	0.0017	0.0069
RL	-0.0007	0.0018	-0.0009	-0.0007	-0.0011	-0.0010	-0.0018	-0.0016	-0.0091	-0.0019	-0.0015	-0.0003	-0.0008	-0.0007	-0.0001	-0.0015
RD	0.0000	-0.0001	0.0001	0.0000	0.0000	-0.0001	-0.0001	-0.0001	-0.0001	-0.0007	0.0000	0.0000	0.0000	0.0001	0.0001	0.0001
BYPP	0.1103	0.0344	0.1750	0.1255	0.1539	0.0183	0.0742	0.0905	0.1145	0.0171	0.6865	-0.3171	0.1125	0.0207	0.0983	0.1860
HI	0.4325	0.3025	-0.2455	0.4347	0.4296	0.0573	0.0544	0.4878	0.0345	0.0550	-0.4863	1.0528	0.3587	0.2492	-0.0185	-0.0665
TW	-0.0055	-0.0011	-0.0018	-0.0062	-0.0058	-0.0051	-0.0024	-0.0068	-0.0015	-0.0004	-0.0026	-0.0054	-0.0158	-0.0038	-0.0030	-0.0055
MSI	0.0037	0.0028	0.0018	0.0038	0.0029	0.0021	0.0025	0.0011	0.0012	-0.0015	0.0005	0.0036	0.0036	0.0151	0.0056	0.0030
LWP	0.0001	0.0001	0.0001	0.0001	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.0001	0.0003	0.0001
PC	-0.0038	-0.0002	-0.0055	-0.0041	-0.0036	-0.0020	-0.0001	-0.0015	-0.0019	0.0010	-0.0033	0.0008	-0.0042	-0.0024	-0.0037	-0.0120
SYPP	0.5672	0.3571	-0.0711	0.5910	0.6088	0.0698	0.1564	0.6323	0.1509	0.0761	0.2056	0.7659	0.4838	0.2891	0.0794	0.1138

R^2 = 0.9875; residual effect = 0.1120.

Table 5. Path coefficient analysis depicting the direct and indirect effect of yield attributing traits on seed yield per plant at phenotypic level under drought stress conditions in Indian mustard (*Brassica juncea* L.)

Trait	DOF	DOM	PH	NPB	NSB	SL	SPS	NSPP	RL	RD	BYPP	HI	TW	MSI	LWP	PC
DTF	-0.0059	-0.0024	-0.0013	-0.0048	-0.0044	-0.0012	-0.0007	-0.0032	-0.0017	0.0000	-0.0019	-0.0037	-0.0034	-0.0020	-0.0003	-0.0022
DTM	0.0079	0.0196	0.0016	0.0058	0.0070	0.0028	0.0011	0.0037	0.0028	0.0012	0.0016	0.0085	0.0047	0.0058	0.0027	0.0040
PH	-0.0012	-0.0004	-0.0052	-0.0009	-0.0008	-0.0014	-0.0012	-0.0013	-0.0004	0.0007	-0.0019	0.0002	-0.0012	-0.0014	-0.0006	-0.0025
NPB	0.0237	0.0087	0.0052	0.0292	0.0244	0.0047	0.0033	0.0152	0.0076	0.0024	0.0089	0.0166	0.0163	0.0113	0.0002	0.0101
NSB	-0.0271	-0.0130	-0.0059	-0.0301	-0.0362	-0.0036	-0.0044	-0.0175	-0.0065	-0.0006	-0.0123	-0.0214	-0.0178	-0.0132	-0.0018	-0.0143
SL	0.0009	0.0006	0.0012	0.0007	0.0004	0.0045	0.0011	0.0004	0.0004	0.0003	0.0007	0.0005	0.0014	0.0014	-0.0003	0.0012
SPS	0.0005	0.0002	0.0009	0.0005	0.0005	0.0010	0.0042	0.0007	0.0009	0.0000	0.0011	0.0002	0.0009	0.0008	-0.0005	0.0007
NSPP	0.0045	0.0016	0.0020	0.0043	0.0040	0.0007	0.0014	0.0083	0.0018	0.0000	0.0032	0.0038	0.0037	0.0030	-0.0003	0.0037
RL	0.0022	0.0010	0.0006	0.0019	0.0013	0.0007	0.0015	0.0016	0.0074	0.0019	0.0012	0.0015	0.0007	0.0011	-0.0003	0.0017
RD	0.0000	-0.0011	0.0025	-0.0015	-0.0003	-0.0011	0.0001	0.0001	-0.0048	-0.0188	0.0030	-0.0014	0.0001	0.0025	-0.0003	0.0008
BYPP	0.1698	0.0437	0.1915	0.1585	0.1770	0.0793	0.1315	0.1998	0.0836	-0.0825	0.5196	-0.0807	0.1598	0.1597	-0.0552	0.2231
HI	0.5867	0.4015	-0.0388	0.5256	0.5455	0.0948	0.0456	0.4223	0.1826	0.0688	-0.1434	0.9233	0.4628	0.3195	-0.0375	0.1490
TW	0.0027	0.0011	0.0011	0.0026	0.0023	0.0014	0.0010	0.0021	0.0004	0.0000	0.0014	0.0023	0.0047	0.0015	0.0002	0.0017
MSI	0.0012	0.0010	0.0009	0.0014	0.0013	0.0011	0.0007	0.0013	0.0005	-0.0005	0.0011	0.0012	0.0011	0.0035	0.0004	0.0014
LWP	0.0000	-0.0001	-0.0001	0.0000	0.0000	0.0000	0.0001	0.0000	0.0000	0.0000	0.0001	0.0000	0.0000	-0.0001	-0.0007	-0.0001
PC	-0.0020	-0.0011	-0.0025	-0.0018	-0.0021	-0.0014	-0.0009	-0.0024	-0.0012	0.0002	-0.0023	-0.0008	-0.0019	-0.0020	-0.0006	-0.0053
SYPP	0.7639	0.4611	0.1538	0.6914	0.7199	0.1823	0.1844	0.6311	0.2734	-0.0270	0.3801	0.8501	0.6318	0.4912	-0.0950	0.3731

R^2 = 0.9925; residual effect = 0.0864.

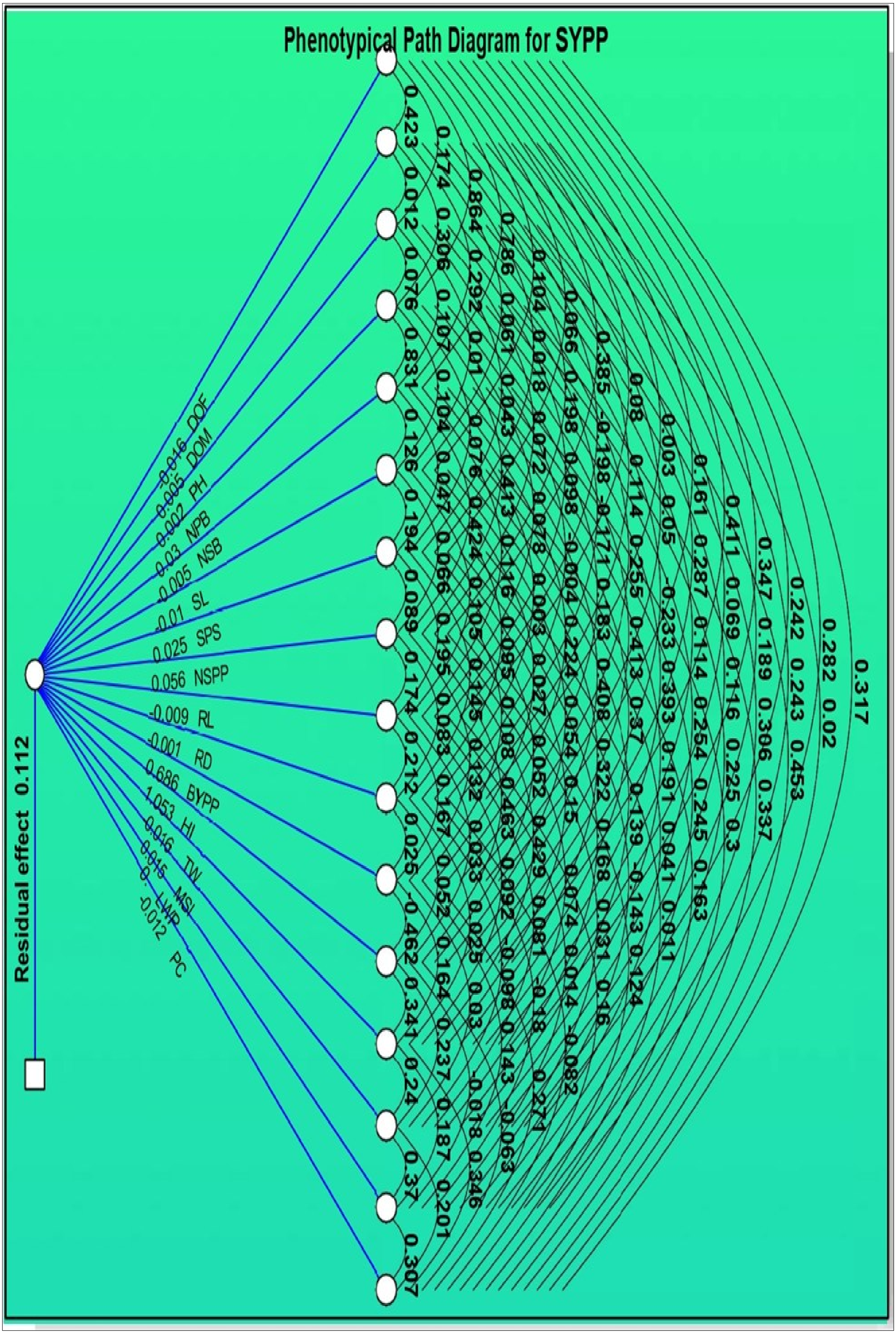

Fig. 5. Phenotypic path diagram for seed yield per plant in 65 genotypes of Indian mustard under normal sown conditions.

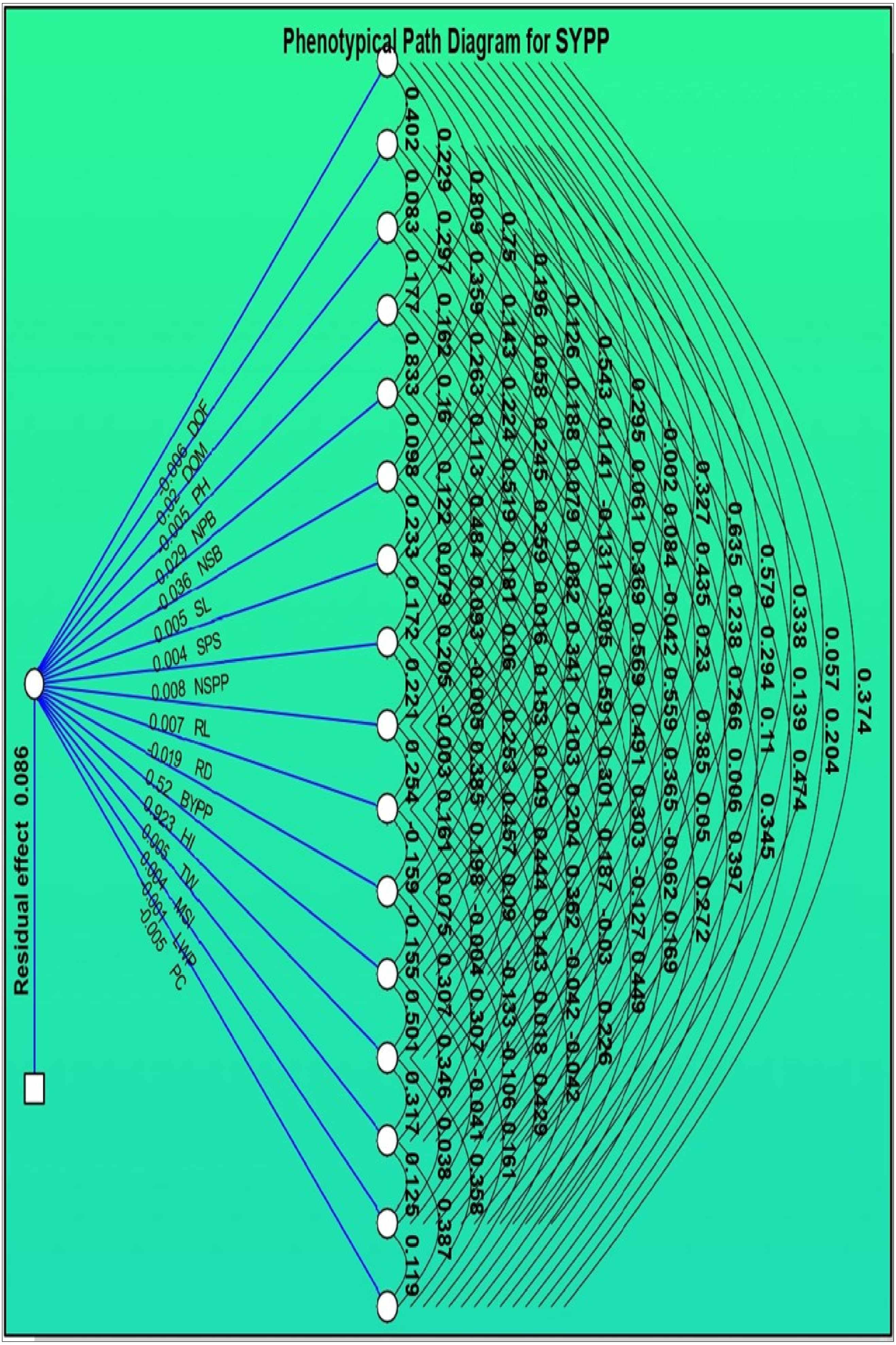

Fig. 6. Phenotypic path diagram for seed yield per plant in 65 genotypes of Indian mustard under drought stress conditions.

(0.5867) and BYPP (0.1698). MSI, with a minor direct effect (0.0035), contributed positively through HI (0.3195); RL also enhanced yield indirectly via HI and BYPP, despite its small direct contribution (0.0074). The model accounted for 99.25 % (R^2 = 0.9925) of the variability in SYPP, with a residual effect of 0.0864, indicating that most of the variation was explained by the characters included. These results emphasize the central role of HI as a yield mediator under stress and highlight BYPP as a complementary selection criterion. Such insights are consistent with earlier studies where HI and BYPP has been identified as a key yield determinant under abiotic stress (38, 39). Therefore, in drought-prone environments, selection strategies focusing on HI and BYPP, along with component traits influencing them indirectly, may offer a promising route for yield enhancement in Indian mustard.

Conclusion

The analysis of variance confirmed substantial genetic variability among the experimental material. Key traits such as proline content, leaf water potential, root diameter, membrane stability index, number of primary and secondary branches per plant, number of siliquae per plant and seed yield per plant exhibited high variability parameters, indicating control by additive genetic variance. These traits can be effectively improved through simple or progeny selection methods. Moreover, selecting traits that show a significant positive correlation and direct effect on seed yield per plant will facilitate the development of resilient, high-yielding genotypes for sustainable mustard cultivation in future breeding programs. Overall, this study indicates that selection focused on HI, BYPP and NSPP, together with supporting physiological traits such as MSI and root traits, would be effective for improving seed yield in Indian mustard under drought conditions.

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Authors' contributions

SG drafted the manuscript. SR participated in the sequence alignment. SG and AKS participated in the design of the study and performed the statistical analysis. SG, RK, SB, URG and AK conceived the study and participated in its design and coordination. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

1. ICAR-Directorate of Rapeseed-Mustard Research (DRMR). Annual report 2023-24. Bharatpur, Rajasthan: ICAR-DRMR; 2024.
2. Morinaga T. Interspecific hybridization in *Brassica*: the cytology of F1 hybrids of *B. juncea* and *B. nigra*. Cytologia. 1934;6(1):62-7. https://doi.org/10.1508/cytologia.6.62
3. Nagaharu U. Genome analysis in *Brassica* with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. Jpn J Bot. 1935;7:389-52.
4. Rejeb IB, Pastor V, Mauch-Mani B. Plant responses to simultaneous biotic and abiotic stress: molecular mechanisms. Plants. 2014;3 (4):458-75. https://doi.org/10.3390/plants3040458
5. Tuberosa R, Salvi S. Genomics-based approaches to improve drought tolerance of crops. Trends Plant Sci. 2006;11(8):405-12. https://doi.org/10.1016/j.tplants.2006.06.003
6. Mohammadkhani N, Heidari R. Effects of drought stress on soluble proteins in two maize varieties. Turk J Biol. 2008;32:23-30. https://doi.org/10.2478/v10020-008-0029-8
7. Choudhary RL, Jat RS, Singh HV, Meena MK, Meena VD, Rai PK. Effect of superabsorbent polymer and plant bio-regulators on growth, yield and water productivity of Indian mustard (*Brassica juncea* L.) under different soil moisture regimes. J Oilseed Brassica. 2023;14(1):11-9.
8. Zhang X, Lu G, Long W, Zou X, Li F, Nishio T. Recent progress in drought and salt tolerance studies in *Brassica* crops. Breed Sci. 2014;64(1):60-73. https://doi.org/10.1270/jsbbs.64.60
9. Ali Z, Maryam H, Saddique MAB, Ikram RM. Exploiting genetic diversity in enhancing phenotypic plasticity to develop climate-resilient cotton. Genet Resour Crop Evol. 2023;70(5):1305-20. https://doi.org/10.1007/s10722-023-01554-3
10. Salgotra RK, Chauhan BS. Genetic diversity, conservation and utilization of plant genetic resources. Genes. 2023;14(1):174-93. https://doi.org/10.3390/genes14010174
11. Immanuel SC, Pothiraj N, Thiyagarajan K, Bharathi M, Rabindran R. Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). Afr J Biotechnol. 2011;10(17):3322-34. https://doi.org/10.5897/AJB10.2575
12. Panjabi P, Yadava SK, Kumar N, Bangkim R, Ramchiary N. Breeding *Brassica juncea* and *B. rapa* for sustainable oilseed production in the changing climate: progress and prospects. In: Genomic designing of climate-smart oilseed crops. Cham: Springer; 2019. p. 275-369. https://doi.org/10.1007/978-3-319-93536-2_6
13. Indian Council of Agricultural Research. Rapeseed and mustard. In: Prasad R, editor. Textbook of field crops production: Vol. II. Rabi crops. New Delhi: ICAR; p. 339-50.
14. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 4th ed. New Delhi: ICAR; 1985.
15. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1952;45 (10):478-81. https://doi.org/10.2134/agronj1953.00021962004500100005x
16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-8. https://doi.org/10.2134/agronj1955.00021962004700070009x
17. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. Agron J. 1956;48 (6):268-72. https://doi.org/10.2134/agronj1956.00021962004800060008x
18. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. 3rd ed. Ludhiana: Kalyani Publisher; 1985. p. 69-78.
19. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51:515-51. https://doi.org/10.2134/agronj1959.00021962005100090002x
20. Rai PK, Gurjar SAN, Singh VV, Singh S. Assessment of genetic variation among drought tolerant recombinant inbred lines (RILs) of

Indian mustard (*Brassica juncea* L.). J Oilseed Brassica. 2017;81 (2):143-50.

21. Rout S, Kerkhi SA, Gupta A. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard (*Brassica juncea*). J Pharmacogn Phytochem. 2019;8(3):4119-23.
22. Patel PB, Patel PJ, Patel JR, Patel PC. Elucidation of genetic variability and inter-relationship studies for seed yield and quality traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Electron J Plant Breed. 2021;12(2):589-96. https://doi.org/10.37992/2021.1202.083
23. Kardam DK, Singh VV. Correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czern & Coss] grown under rainfed condition. J Spices Aromat Crops. 2005;14(1):56-60.
24. Lakra A, Tantuway G, Tirkey AE, Srivastava K. Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss). Int J Curr Microbiol Appl Sci. 2020;9(1):2556-63. https://doi.org/10.20546/ijcmas.2020.901.290
25. Saroj R, Soumya SL, Singh S, Sankar SM, Chaudhary R, Saini N, et al. Unraveling the relationship between seed yield and yield-related traits in a diversity panel of *Brassica juncea* using multi-traits mixed model. Front Plant Sci. 2021;12:6519-36. https://doi.org/10.3389/fpls.2021.651936
26. Jat L, Rai SK, Choudhary JR, Bawa V, Bharti R, Sharma M, et al. Phenotypic evaluation of genetic diversity of diverse Indian mustard (*Brassica juncea*) genotypes using correlation and path analysis. Int J Bio-resour Stress Manag. 2019;10(5):467-71. https://doi.org/10.23910/IJBSM/2019.10.5.2000a
27. Ray J, Singh OP, Pathak VN, Verma SP. Assessment of genetic variability, heritability, genetic advance and selection indices for yield contributing traits in Indian mustard (*Brassica juncea*). Int J Chem Stud. 2019;7(4):1096-9.
28. Pandey SK, Srivastava KK, Negi S, Khan NA, Singh RK. Variability, trait relationship and path analysis for seed yield and seed quality parameters in Indian mustard (*Brassica juncea* L.). J Oilseed Brassica. 2020;11(1):69-76.
29. Pawar PD, Nair B, Charjan SU, Manoj Kumar D. Evaluation of induced genetic variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.). J Soils Crops. 2018;28(1):115-20.
30. Khulbe RK, Pant DP, Naveen S. Variability, heritability and genetic advance in Indian mustard [*Brassica juncea* L.]. Crop Res (Hisar). 2000;20(3):551-2.
31. Mohan S, Yadav RK, Tomar A, Singh M. Utilization of selection parameters for seed yield and its contributed traits in Indian mustard (*Brassica juncea* L.). Pharma Innov J. 2017;6(8):306-9.
32. Akabari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). Int J Agric Sci. 2015;11 (1):35-9. https://doi.org/10.15740/HAS/IJAS/11.1/35-39
33. Lodhi B, Thakral NK, Ram A, Singh A. Genetic variability, association and path analysis in Indian mustard [*Brassica juncea* (L.)]. J Oilseed Brassica. 2014;5(1):26-31.
34. Meena RL, Chauhan JS, Singh KH, Rathore SS. Genetic variability and correlation analysis in Indian mustard [*Brassica juncea* (L.)] under drought stress. Indian J Plant Genet Resour. 2015;28(3):329-34. https://doi.org/10.5958/0976-1926.2015.00044.3
35. Gupta S, Upadhyay S, Koli GK, Rathi SR, Bisen P, et al. Trait association and path analysis studies of yield attributing traits in rice (*Oryza sativa* L.) germplasm. Int J Bio-resour Stress Manag. 2020;11(6):508-17.
36. Hallauer AR, Miranda Filho JB. Quantitative genetics in maize breeding. 2nd ed. Ames: Iowa State University Press; 1988. p. 468.
37. Singh M, Singh VV. Physiological approaches for breeding drought tolerant *Brassica* genotypes. SABRAO J Breed Genet. 2018;50(3):360-72.
38. Kumar R, Gaurav SS, Jayasudha S, Kumar H. Study of correlation and path coefficient analysis in germplasm lines of Indian mustard (*Brassica juncea* L.). Agric Sci Dig. 2016;36(2):92-6. https://doi.org/10.18805/asd.v36i2.10625
39. Singh T, Gupta SK, Dhillon L, Sheera A. Correlation and path coefficient studies for yield-related traits in F2 population of Indian mustard (*Brassica juncea* L.). J Oilseed Brassica. 2024;15(2):262-7.

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