Genetic parameters, correlation and path coefficient investigation of yield accrediting characters in Indian mustard (*Brassica juncea* l. Czern. & coss)

Comment [MSK1]: May be revised

ABSTRACT

Indian mustard (*Brassica juncea L. Czern. & Coss*) is a natural amphidiploid which is the greatest pre-dominating crop of oilseed *Brassica* group. A study was undertaken to estimate the genetic variability, correlation and path coefficient analysis of yield and its contributing traits in 75 mustard cultivars grown in Randomized Block Design with two replications. The analysis of variance were highly significant for all the characters investigated. All thirteen characters were showed higher values of phenotypic coefficients of variation than genotypic coefficients of variation. The higher heritability in broad sense was estimated for all the characters. High value of heritability indicates that it may be due to higher contribution of genotypic components. High heritability coupled with high genetic advance as percent of means were recorded for days to 50% flowering, plant height (cm), number(s) of secondary branches per plant, length of main raceme (cm), siliquae length (cm), seed yield per plant (g), yield per plot (g), harvest index and biological yield that indicated predominance of additive gene action in the inheritance of these traits. The higher direct positive genotypic and phenotypic correlations for the biological yield, numbers of primary branches, numbers of siliquae on main raceme and number of secondary branches was documented. Whereas, days to maturity and siliquae length showed direct negative correlations with grain yield. Seventy-five varieties, included in study were grouped into 6 clusters. The maximum inter cluster D^2 value indicated that genotypes of cluster III and IV are not so closely related while the genotypes of cluster I and III are closely related. It is apparent therefore; the genotypes of various clusters differ so significantly with regards to their relative genetic distance as indicated from the high variation of D^2 values. This makes it clear that the genotypes included in these clusters have a wide range of genetic diversity and may be used in a mustard hybridization programme to develop higher yielding cultivars.

Key words: Genetic variability, correlation, path analysis and Indian mustard

INTRODUCTION

Comment [MSK2]: Shorten introduction

Indian mustard (*Brassica juncea L. Czern. & Coss*)is a natural amphidiploid (2n = 36, AABB genome) which is the greatest pre-dominating crop of oilseed *Brassica* group. It is self-pollinated with some degree of cross-pollination and with a physical genome size of 920 Mb (Yang *et al.*, 2016). It is the most significant oilseed crop of India having substantial economic, nutritional, and industrial applications (Shyam *et al*., 2019; Thakur *et al.*, 2020; Egorova *et al*., 2021; Treccarichi *et al*., 2022). Tropical and subtropical areas both cultivate mustard crop. Mustard is primarily cultivated throughout Asia, specifically in China, India, and Pakistan. Furthermore, rapeseed and mustard are also grown in Europe, Canada, and the former Soviet Union, but the cultivars planted there differ from those grown in India. The oil content varies slightly depending on the type of oil used (Shyam *et al*., 2021a; Shyam *et al*., 2021b; Shyam *et al*., 2021c; Yadav *et al*., 2022). Depending upon the quality of seed, oil content can be ranged between 30% to 49% (GoI, 2021) in mustard. India is the fourth-largest contributor of oilseeds in the world and Rapeseed and mustard contributes about 28.6% of total oil seeds production. The output of mustard seeds, which is grown in Rabi (winter-sown) season, stood at 85 lakh tonnes in the previous year (COOIT). Mustard seed production is estimated at 109.5 lakh tonnes in 2021-22. The area under coverage has been pegged at 87.44 lakh hectares while the average yield is seen at 1,270 kg ha^{-1}. Mustard is an important cash crop for farmers in Rajasthan, Haryana, Madhya Pradesh, and Uttar Pradesh, among others. Rajasthan is the largest producing state in the country (Central Organization for Oil Industry & Trade, 2022).

Indian mustard yield and its constituents are quantitative in nature, thus learning more about the type, scope, and effects of genetic variability on the environment may be proved obliging. Because they reflect environmental changes if genetic makeup is known and, in most situations, predictions can be made in advance, interactions between genotypes and environments are particularly fascinating. Therefore, it is more reasonable to assess heritability that considers the genotype environment interaction variation for the overall variance when predicting genetic advance as a result of selection (Yadav *et al*., 2005; Tripathi *et al*., 2015; Bafra *et al*., 2017; Shyam *et al*., 2021d; Shyam *et al*., 2022a). Genotypes, which can adjust its phenotypic state in response to environmental fluctuations in such a way that it gives maximum stable economic return, can be termed as well "buffered" or stable. It is necessary to identify the stable genotypes suitable for wide range of environmental conditions (Wu *et al*.,2006; Escobar *et al*., 2011; Jeromela *et al*., 2011; Zhang *et al*., 2013; Shyam *et al*., 2022b).

Different yield-contributing features are associated with grain yield in Indian mustard. Additionally, these characteristics are related to one another (Ali *et al*., 2003; Khan and Khan, 2003;). As a result, a complicated connection is established between many contributing features and grain yield. Through path coefficient, the intricate web of such a relationship is further simplified for analysis (Akbar *et al*., 2003, 2007). The path coefficient breaks the correlation coefficient of the yield with its contributing traits into direct and indirect effects (Aytaç and Kinaci, 2009). Estimates of genetic variability, heritability and genetic advance facilitated selection may help to devise efficient selection criteria (Sadat *et al*., 2010).

The presence of high-genetic diversity in the germplasm material provides the basis for plant breeding and developing new cultivars and assists in selecting desirable agronomic traits (Govindaraj *et al*., 2015;). The extent and amount of genetic diversity present among available germplasm are of greatest importance while formulating any breeding program (Sharma *et al*., 2020; Tiwari et al., 2017). The loss of genetic diversity is a universal phenomenon for all crops and almost all the cultivated varieties of Indian mustard have a narrow genetic base (Srivastava and Singh 2002; Chauhan *et al*., 2008; Bafra *et al*., 2017). Further, the identification and selection of genetically diverse parents are the most vital criteria for hybrid breeding programmes (Banga *et al*., 2015).

Genetic diversity among individuals or populations can be determined using morphological (Vaishnava *et al*., 2006; Alie *et al*., 2009; Singh *et al*., 2010; Bafra *et al*., 2017; Mishra *et al*., 2021), biochemical (Shyam *et al*., 2019;Sharma *et al*., 2021;Shyam *et al*., 2022b; Shyam*et al*., 2022c), and molecular approaches (Mohammadi and Prasanna, 2003;Bagel *et al*., 2020; Rajpoot *et al*., 2020; Shyam *et al*., 2020; Mishra *et al*., 2020; Thakur *et al*., 2020; Makwana *et al*., 2021; Pramanik *et al*., 2021; Singh *et al*., 2021; Verma *et al*., 2021;Asati *et al*., 2022; Mishra *et al*., 2022a; Mishra *et al*., 2022b; Rajpoot *et al*., 2022; Shyam *et al*., 2022d; Tomar *et al*., 2022; Tripathi *et al*., 2022; Tripathi *et al*., 2023). It is now possible to quantify the magnitude of diversity among germplasm for use in breeding programme evaluation by employing biometrical methods like multivariate analysis (Rao, 1952) based on Mahalanobis (1936), D^2 statistics, and Ward's no-hierarchical squared Euclidean distance method. The present study was conducted to accomplish the presence of the genetic variability and diversity among various Indian mustard genotypes for yield accrediting traits.

MATERIALS AND METHODS

The current investigation was undertaken on a total of 75 Indian mustard genotypes (Table 1) acquired from the Zonal Agricultural Research Station, Morena, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya (RVSKVV), Gwalior, India (AICRP on Rapeseed and Mustard). All the genotypes were grown in randomized block design with two replications in Rabi 2021at the experimental field of Department of Genetics & Plant Breeding, College of Agriculture, RVSKVV, Gwalior, India. Each genotype was planted in a plot of one row of 2 meter length with an arrangement of 30 cm apart between rows and 15 cm plant to plant. The crop was enchanted with protective irrigations and recommended packages of practices right through the growing season. Five arbitrarily chosen plants from each treatment were marked for taking the observations for the parameters, *viz*., plant height (cm), numbers of primary and secondary branches per plant, days to 50 percent flowering, days to maturity, length of the main raceme (cm), numbers of silique per the main raceme, numbers of silique per plant, silique length (cm), test weight (g), seed yield per plant (g), biological yield and harvest index (%) for analysis of mean performance.

The mean values of each genotype were employed for statistical analysis. Genotypic (GCV) and phenotypic coefficient of variation (PCV) was computed as per formula given by Burton (1952); heritability in the broad sense (h2) as proposed by Burton and De (1953) and genetic advance as per the method designated by Johnson *et al.* (1955). Genotypic and phenotypic correlations were calculated by way of the formula described by Weber and Moorthy (1952) and Miller (1958). The portion of direct and indirect donations of different traits to the total correlation coefficients with yield was evaluated through path coefficient analysis as suggested by Wright (1921,1935)and suggested by Dewey and Lu (1959). The genetic divergence was estimated using Mahalanobis D^2 statistic following Rao (1952). Inter and intra-cluster distances were calculated by Tocher's method as suggested by Rao (1952) to form the clusters.

RESULTS AND DISCUSSION

Comment [MSK3]: Paper needs bifurcation as it is too lengthy

Prediction of genetic variability in a crop is a goal since hybrids between lines of diverse backgrounds usually; exhibit better heterosis than those between closely related parents (Tripathi *et al*., 2015; Bafra *et al.*, 2017). Selection of genetically dissimilar parents for hybridization is a main aim of any crop improvement programme to accomplish anticipated segregates. The analysis of variance revealed considerable genetic differences for each of the investigated traits advised that there was genetic divergence among genotypes (Table 2). This demonstrates that the available gene pool for yields and its components has enough selection space for promising lines. For most of the traits, for instance days to 50% flowering, days to maturity, plant height (cm), number(s) of primary and secondary branches per plant, length of main raceme(cm), number(s) of siliquae on main raceme, test weight (g), siliquae length(cm), seed yield per plant(g), harvest index and biological yield, a vast range of variation was documented. Thus, it suggests that there is a lot of scope for choosing various quantitative traits to improve Indian mustard. Estimates of PCV and GCV showed greater values for traits such as seed yield per plant(g), biological yield, number(s) of siliquae on main raceme and number(s) of secondary branches per plant (Table 3). Similar results for many characteristics of Indian mustard were also addressed by Singh (2004) and Yadav *et al*. (2011).

The whole range of heritable variation is not displayed by the coefficient of variation. When heritability and genetic progress are assessed together, the accuracy of the determination could be increased. Heritability and genetic advancement are crucial factors to consider while analyzing the potential for trait improvement through selection. Heritability alone is less beneficial in guesstimating the gain under selection than estimates of high heritability combined with rapid genetic advance.

When developing a sound selection criterion for analyzing the degree of reciprocal interaction among different attributes, the measurement of correlation coefficients would be helpful. This information may be utilized to practice both indirect selection and forecast the corresponding response to direct selection. Like any crop, in Indian mustard, seed yield is highly variable and complex due to an array of interrelated contributing characters. Direct selection for yield may therefore be ineffective. The intricacy of the trait has highlighted the significance of the component approach in creating an effective breeding programme aimed at yield enhancement. Additionally, it has been suggested that rather than specific genes for yield *per se*, there may be genes for the many components that are available. When examining the genetic basis of the relationship between two qualities, Falconer (1960) argued that pleiotropy or full linkage could be answerable for the linear association. When a gene has pleiotropy or linkage, it has a general influence on both aspects (positive correlation), but other genes tend to boost one feature while decreasing the other (negative correlation).

In the present experimentation, the phenotypic and genotypic correlation coefficients between different traits were computed (Table4; Table 5). Genotypic correlation coefficients were found to be higher than phenotypic correlation coefficients for most of the traits, signifying a substantial inherent link between several traits that was masked by environmental factors in terms of phenotypic representation. In general, it was found that phenotypic correlation coefficients were higher than genotypic correlation coefficients. Comparable outcomes were reported by Larik and Rajput (2000), Baghel *et al*. (2020), Rajpoot *et al*. (2020), Verma *et al.* (2021) and Shyam *et al.* (2022a) in Indian mustard. According to Tahira *et al.* (2011), most of the traits and the seed yield per plant had significant and positive correlations, with phenotypic correlation coefficients being higher than genotypic correlation coefficients.

The genotypic and phenotypic associations between seed yield per plant and the length of the main raceme and the numbers of siliquae on it were both significantly and positively (r= 0.575 and r= 0.574, respectively) correlated. Therefore, selection based on any of these traits, alone or in combination, will lead to the discovery of genotypes with higher yields. These results are in accordance with findings of Khan *et al.* (2013), who found that plant height, dry matter yield, numbers of seeds per siliquae, days to flowering, raceme length, and test weight were significantly and positively correlated with seed yield. The oil content, plant height, days to flowering, days to maturity, numbers of siliquae per plant, numbers of seeds per siliquae and 1000-seed weight were found to have positive and significant correlations with seed yield in the experiment of Sandhu and Gupta (1996). According to Kumar *et al.* (1999), seed yield was positively connected with plant height, numbers of primary and secondary branches per plant, numbers of siliquae on the main shoot and the numbers of siliquae per plant with 1,000-seed weigh and harvest index. Singh (2004) found a positive link between seed yield per plant and numbers of branches per plant, height of the plant, numbers of siliquae on the main raceme, length of the main raceme, number of seeds per siliquae and weight of the seeds. Chaudhary *et al.* (2003) found substantial and positive association between the numbers of seeds produced per plant and the numbers of siliquae per plant, biological yield, oil content and harvest index. Seed yield was significantly and positively correlated with days to 50% flowering, days to maturity, plant height, numbers of primary and secondary branches, length of main shoot, numbers of siliquae on main shoot, numbers of seeds per siliquae and 1000-seed weightin investigation of Kumar *et al.* (2007). Gupta *et al.* (2010) observed that plant height, harvest index, days to maturity, numbers of siliquae on the main axis, 1000-seed weight and numbers of principal branches were all positively and substantially corelated with seed yield. Moreover,Baghel*et al.* (2020) investigated that majority of the traits and the seed yield per plant had considerable and positive correlations with phenotypic correlation coefficients being greater than genotypic correlation coefficients. According to Singh *et al.* (2010), there is a positive and significant correlation between plant height, numbers of seeds per siliquae, weight of 1000 seeds, oil content, numbers of days to flowering, numbers of days to maturity, the length of the major raceme, and biological yield.

The breeder would be able to select the breeding tactic to be employed based on the estimates of genotypic and phenotypic correlations so that the advantageous correlation could be utilized and the unfavorable ones adjusted by creating new variability to generate new recombinants. In contrast, if linkage is involved, special breeding programmes are needed to break these links. If negative association between characters is instigated by pleiotropic effects, it would be extremely tough to get the suitable recombinants. Recurrent selection programmes have been revealed to break undesirable correlations by Miller (1958), whereas a breeding programme that uses yield, plant or field as the selection method would be beneficial if physical features are strongly associated with yield. Thus, it became clear from correlation studies in the current study that seven traits *viz*., days to 50% flowering, numbers of secondary branches per plant, length of the main raceme, numbers of siliquae on the main raceme, test weight, biological yield and seed yield per plant are crucial for improving Indian mustard. Furthermore, two of these traits *i. e*., length of the main raceme and numbers of siliquae on the main raceme have the highest correlation coefficient, making them the most significant characters.

Although correlation coefficients are helpful in identifying the relationships between several characters on complex attributes like yield, nevertheless, such investigations may not deliver a precise depiction of the relative significant of direct and indirect effects of each contributing characters. Path coefficient analysis splits the correlation coefficient into the direct and indirect effects of a set of independent variables on the dependent variable and recognizes the constituent qualities on which breeding programme that aim to increase yield may be based (Wright, 1921; Dewey and Lu, 1959). The length of the main raceme, days to 50% flowering, thousand seed weight, numbers of secondary branches per plant and biological yield towards seed yield, all disclosed substantial positive direct donations from siliquae in the results of the genotypic and phenotypic path coefficient (Table 6; Table 7). Days to flowering, maturity, plant height, oil content, test weight, and major branches all have a direct impact on seed yield (Kumar and Shrivastava, 2000). Numberof primary branches, days to flowering, 1000-seed weight, and numbers of seeds per siliquae were found to have a direct impact on seed output (Sadat*et al.*, 2010). Comparable results were also documented by Gangapur *et al.* (2009), Gupta *et al.* (2010) and Shyam *et al.* (2021a). According to Singh *et al.* (2013), most characters had a direct effect on seed yield while days to 50% flowering indicated an indirect effect. Singh *et al.* (2014) confirmed a direct relationship between plant branch count, siliquae count on the main raceme, siliquae count per plant, plant height, oil content, days to maturity, test weight and seed production. Badra *et al.* (2001) and Singh and Singh (2004) also investigated an indirect relationship between plant height, seeds per siliquae, primary branches, siliquae per plant and days to maturity. Indirect effects on siliquae per plant, plant height, branches per plant, seeds per siliquae, oil content, test weight, and days to flowering were noted by Akbar *et al.* (2003) *via* biological yield. Most characteristics had a direct effect on seed yield and an indirect effect on the numbers of days to 50% blooming in the experiment of Singh *et al.* (2013). Biological yield per plant revealed the trait's highest indirect influence, while days to 50% flowering showed the most beneficial direct effect in the research of Devi (2018).

The percent contribution of thirteen different characters towards the expression of genetic divergence revealed that numbers of siliquae on main raceme contributed maximum divergence (37.63%) tracked by days to maturity, biological yield, plant height (cm), length of main raceme (cm), seed yield per plant (g), days to 50% flowering, harvest index, test weight (g), numbers of seeds per siliquae and numbers of primary branches per plant. Whilst the numbers of secondary branches per plant (0.04%) and siliquae length (cm) (0.04%) donated lowest in the genetic divergence (Table 8). These findings are parallel with the results of Mahto (1996).

It has been discovered that the number of agricultural plants with various breeding systems and geographical dispersion are determined by the D^2 static, may be directly associated. Greater diversity than a difference in location may result from genetic drift and selection in various environments. Crop species use their understanding of genetic divergence to choose their parents since this idea facilitates the differentiation of well-defined populations (Aunwinithul, 2004). It was possible to deduce from the clustering pattern that there was enough divergence to permit the establishment of distinct clusters. A potent approach for assessing genetic divergence among the choices from the same geographic region is the Mahalanobis D^2 analysis of quantitative traits. Seventy-five genotypes, included in this investigation were grouped into 6 clusters. A total of 53 genotypes fell into cluster I, 14 genotypes in cluster II, 5 genotypes in cluster IV and 1 each in cluster III, V and VI (Table 9). Similar outcomes were also seen in studies of Ghosh and Gulati (2002), Aunwinithul *et al*. (2004), Goswami and Behl (2006), Malik *et al*. (2006), Doddabhimappa *et al.* (2010), Singh *et al.* (2010), Goyat *et al*. (2012), Khan *et al.* (2013), Kumar et al. (2013), Shekhawat *et al*. (2014),Singh*et al*. (2021) and Nandi *et al.* (2021).

The intra cluster divergence was found to range between 22.17 for cluster I and 30.85 for cluster IV.It is ranged from 0.00 to 30.85. Cluster IV showed maximum intra cluster D^2 value (D^2 = 30.85), cluster II (D^2 = 24.32) and cluster I (D^2 =22.17) whereas clusters III and IV showed zero value for Intra cluster distance. (Table9). The substantial genetic divergence of the genotypes led to the highest intra-cluster dispersion. There is virtually little probability of creating desirable types by removing genotypes from clusters that are like them and have low intra-cluster divergence values (Singh *et al.*, 2021). Therefore, it might make sense to test crossovers between types from clusters that are farther apart than usual. In order to further produce high yielding Indian mustard varieties, the little diversity and selection of parents within the cluster having a higher mean for a certain characteristic may be helpful.

Maximum inter cluster D^2 value (56.23) was recorded between clusters II and VI, whereas the minimum average inter cluster D^2 value (27.97) was recorded between cluster I and III. The maximum inter cluster D^2 value indicated that varieties of cluster III and IV are not so closely related whereas the varieties of cluster I and III are closely related (Table 10). It is apparent therefore; the varieties of various clusters differ so significantly with regards to their relative genetic distance as indicated from the high variation of D^2 values. This makes it clear that the genotypes included in these clusters have a wide range of genetic diversity and may be used in a mustard hybridization programme to increase seed yield. Cluster means showing importance of grouped characters was noted wide range of variation for all the characters under study. Maximum cluster mean estimated for number of siliquae on main raceme cluster III showed maximum value (222.50) and cluster V showed minimum value (71.50), length of main raceme cluster IV showed maximum (117.40) and cluster VI had minimum (72.50) cluster mean values, while for seed yield per plant was found maximum in cluster IV (21.45) and while minimum value was noticed for cluster I (9.03) (Table 11). These findings confirm in earlier studies of Sandhu *et al.*, (2001) and Ghosh and Gulati (2002). Based on these traits superior genotypes are selected and used in hybridization programme as a donor parent. Inter-crossing of genotypes involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield.

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Table 1 List of mustard genotypes with their parentage/ source

S. No.	Genotypes	Parentage/ Sources
1.	RB-50	Laxmi X RH-9617
2.	Pusa Bold	Varuna x BIC1780
3.	Varuna	Selection from Varansi Local
4.	Rohini	Selection from natural population of Varuna
5.	Kranti	Selection for Varuna
6.	RH- 725	CCSHAU Hisar
7.	Maya	Varuna x KRV 11
8.	Vardan	Derived through biparental mating involving Varuna, Keshari, CSU 10 and IB 1775, IB 1786, IB 1866
9.	Vasundhara	RH 839 x RH 30
10.	Swarn Jyoti	Selection from germplasm line RC 1670
11.	Pusa Jagannath	Varuna x Synthetic juncea
12.	PusaJaiKisan	Somaclone of Varuna
13.	Albeli	ZARS, Morena, RVSKVV, Gwalior
14.	Sej-2	Derived from a cross of B. juncea to a amphidiploid
15.	Shraddha	ZARS, Morena, RVSKVV, Gwalior
16.	DMH 1	CMS based hybrid
17.	L-4	Canada
18.	JMWR-908-1	ZARS, Morena, RVSKVV, Gwalior
19.	RGN-73	RGN 8 x Pusa Bold
20.	NRC-HB-101	BL 4 x Pusa Bold
21.	NRC-HB-506	(MJA 05 x MJR 1)
22.	RVM-3	ZARS, Morena
23.	RH-749	RH-781 xRH-9617
24.	NRC DR-2	MDOC 43 x NBPGR 36
25.	DRMR IJ-31	HB 9908 x HB 9916
26.	China	ZARS, Morena, RVSKVV, Gwalior
27.	GSL-1	Punjab agricultural university, Ludhiana
28.	GSC-7	Punjab agricultural university, Ludhiana
29.	PC-5	ZARS, Morena, RVSKVV, Gwalior
30.	PC-6	ZARS, Morena, RVSKVV, Gwalior
31.	RP-9	ZARS, Morena, RVSKVV, Gwalior
32.	Kiran	ZARS, Morena, RVSKVV, Gwalior
33.	JTC-1	ZARS, Morena, RVSKVV, Gwalior
34.	JM-1	Pusa Bold x L 6
35.	JM-2	MutantofRL9
36.	JM-3	Varuna x YRT 3
37.	RVM-1	ZARS, Morena
38.	RVM-2	Selection from Chambal growing region
39.	PM-25	Sej-8 x Pusa Jagannath
40.	PM-26	VEJ Open x PusaAgrani
41.	PM-27	Derived from the cross [(Divya x Pusa Bold) x (PR 666EPS) x PR 704EPS-2 x B85)]
42.	PM-28	SEJ8 x PUSA JAGANNATH
43.	PM-30	Bio 902 x ZEM 1
44.	Pusa Vijay	Synthetic *Brassica juncea* x VSL 5
45.	JMM-927	ZARS, Morena, RVSKVV, Gwalior
46.	JMM-991	ZARS, Morena, RVSKVV, Gwalior
47.	RMM-10-01-01	ZARS, Morena, RVSKVV, Gwalior

48.	RMM-12-01-18	ZARS, Morena, RVSKVV, Gwalior
49.	RMM-12-03-18	ZARS, Morena, RVSKVV, Gwalior
50.	WRR-5	White rust resistant advance breeding lines, DRMR, Bharatpur
51.	WRR-6	White rust resistant advance breeding lines, DRMR, Bharatpur
52.	WRR-7	White rust resistant advance breeding lines, DRMR, Bharatpur
53.	WRR-8	White rust resistant advance breeding lines, DRMR, Bharatpur
54.	WRR-9	White rust resistant advance breeding lines, DRMR, Bharatpur
55.	WRR-10	White rust resistant advance breeding lines, DRMR, Bharatpur
56.	WRR-11	White rust resistant advance breeding lines, DRMR, Bharatpur
57.	WRR-12	White rust resistant advance breeding lines, DRMR, Bharatpur
58.	WRR-13	White rust resistant advance breeding lines, DRMR, Bharatpur
59.	WRR-14	White rust resistant advance breeding lines, DRMR, Bharatpur
60.	WRR-15	White rust resistant advance breeding lines, DRMR, Bharatpur
61.	WRR-16	White rust resistant advance breeding lines, DRMR, Bharatpur
62.	WRR-17	White rust resistant advance breeding lines, DRMR, Bharatpur
63.	WRR-18	White rust resistant advance breeding lines, Bharatpur
64.	WRR-19	White rust resistant advance breeding lines, DRMR, Bharatpur
65.	WRR-20	White rust resistant advance breeding lines, DRMR, Bharatpur
66.	WRR-21	White rust resistant advance breeding lines, DRMR, Bharatpur
67.	WRR-22	White rust resistant advance breeding lines, DRMR, Bharatpur
68.	WRR-25	White rust resistant advance breeding lines, DRMR, Bharatpur
69.	WRR-26	White rust resistant advance breeding lines, DRMR, Bharatpur
70.	WRR-27	White rust resistant advance breeding lines, DRMR, Bharatpur
71.	WRR-28	White rust resistant advance breeding lines, DRMR, Bharatpur
72.	WRR-29	White rust resistant advance breeding lines, DRMR, Bharatpur
73.	WRR-30	White rust resistant advance breeding lines, DRMR, Bharatpur
74.	WRR-31	White rust resistant advance breeding lines, DRMR, Bharatpur
75.	WRR-32	White rust resistant advance breeding lines, DRMR, Bharatpur

Table 2 Analysis of variance for different traits in Indian mustard

Source of Var.	Df	DF	DM	PH	PB	SB	LMR	SMR	S/SL	SL	TSW	BY	HI	SYPP
Replication	1	26.45	23.20	235.35	12.90	6.82	6.82	20.16	0.3260	0.5400	1.6030	37.5000	62.39	0.272
Treatment	74	125.39**	774.85**	2291.60**	5.684**	31.801**	31.801**	7094.7**	4.004**	0.637**	0.971**	543.1**	156.21**	35.229**
Error	74	3.73	4.949	51.105	2.501	3.218	3.218	32.49	1.65	0.137	0.081	5.864	8.577	0.323

DF= Days to 50% Flowering, **DM=** Days to maturity, **PH=** Plant height (cm), **PB=** Numbers of primary branches/ plants**, SB=** Numbers of secondary branches/ plants**, LMR=** Length of main raceme (cm), **SMR=** Numbers of siliquae on main raceme**, S/SL=** Numbers of seed per siliquae, **SL=** Siliquae length (cm), **TSW=** Test weight (g), **BY=** Biological yield, **HI=** Harvest Index**, SSYP=** Seed yield per plant (g)

Table 3 Estimation of GCV, PCV, heritability and genetic advance for different quantitative characters

Observations	**Range**		**Grand Mean**	**Coefficient of variation**		**h² (bs)**	**Gen. Adv as 5% of Mean**
	Min	**Max**		**GCV**	**PCV**		
DF	41	75.5	52.5533	14.841	15.066	0.97	30.113
DM	106	184	145.6867	13.467	13.511	0.994	27.654
PH	93.34	245.84	178.7997	18.719	18.932	0.978	38.13
PB	4.5	13.5	8.32	15.163	20.263	0.56	23.374
SB	6	23	11.1067	34.037	35.902	0.899	66.474
LMR	59	142.5	89.5733	21.292	21.517	0.979	43.401
SMR	65	294	144.42	41.146	41.241	0.995	84.566
S/SL	11	18	12.7667	8.497	11.084	0.588	13.419
SL	3.75	6.5	4.98	10.037	11.339	0.784	18.304
TSW	3.68	6.25	4.8086	13.871	14.492	0.916	27.351
BY	16	95	35.26	46.482	46.735	0.989	95.234
HI	15.07	55.62	30.8091	27.887	28.685	0.945	55.847
SSYP	4.85	27.68	10.1947	40.979	41.168	0.991	84.029

Table 4 Estimation of correlation coefficient at genotypic level in Indian mustard

Characters	DF	DM	PH	PB	SB	LMR	SMR	S/SL	SL	TSW	BY	HI	SSYP
DF	**1.000**	0.0936	0.0774	0.0721	-0.0240	-0.1130	-0.1080	0.1887	0.0779	-0.011	0.3182*	-0.2860	0.0939
DM		**1.0000**	-0.0310	0.1287	-0.0380	-0.0620	0.0459	0.1853	0.1971	-0.039	0.0693	-0.3628*	-0.16
PH			**1.0000**	0.0302	-0.1360	0.1414	0.0584	0.1154	-0.086	0.1511	0.1225	-0.0730	0.0888
PB				**1.0000**	0.5699**	0.0981	0.4166**	0.2086	-0.069	0.192	0.6593**	-0.1700	0.5908**
SB					**1.0000**	0.3024*	0.2661	-0.14	-0.135	-0.049	0.3757*	0.1124	0.5405**
LMR						**1.0000**	0.0569	-0.071	-0.018	0.1958	0.1247	0.0764	0.2247
SMR							**1.0000**	0.2608	0.1284	0.1047	0.4849*	-0.0720	0.5882**
S/SL								**1.0000**	0.5946**	-0.016	0.1158	-0.2130	0.0154
SL									**1.0000**	-0.005	-0.128	0.0230	-0.1140
TSW										**1.0000**	0.2469	0.1752	0.2926
BY											**1.0000**	-0.4476*	0.7303**
HI												**1.0000**	0.2182
SSYP													**1.0000**

Table 5 Estimation of correlation coefficient at phenotypic kevel in Indian mustard

Characters	DF	DM	PH	PB	SB	LMR	SMR	S/SL	SL	TSW	BY	HI	SYPP
DF	**1.0000**	0.0949	0.0765	0.0640	-0.0220	-0.1120	-0.1060	0.1356	0.0690	-0.0160	0.3155*	-0.2740*	0.0960
DM		**1.0000**	-0.0330	0.0957	-0.0330	-0.0600	0.0448	0.1417	0.1832	-0.0350	0.0686	-0.3510**	-0.1590
PH			**1.0000**	0.0121	-0.1360	0.1360	0.0581	0.0945	-0.0670	0.1462	0.1155	-0.0660	0.0858
PB				**1.0000**	0.4125**	0.0877	0.3085**	0.1691	-0.015	0.1354	0.5027**	-0.1370	0.4422**
SB					**1.0000**	0.2888*	0.2519*	-0.1120	-0.099	-0.0480	0.3587**	0.0949	0.5040**
LMR						**1.0000**	0.0569	-0.0530	-0.014	0.1852	0.1204	0.0789	0.2223
SMR							**1.0000**	0.2038	0.1115	0.0993	0.4823**	-0.0700	0.5848**
S/SL								**1.0000**	0.4444**	-0.0180	0.0874	-0.1610	0.0110
SL									**1.0000**	-0.0160	-0.1210	0.0235	-0.1080
TSW										**1.0000**	0.2398*	0.1651	0.2829*
BY											**1.0000**	-0.4480**	0.7247**
HI												**1.0000**	0.2218
SYPP													**1.0000**

DF= Days to 50% Flowering, **DM=** Days to maturity, **PH=** Plant height (cm), **PB=** Numbers of primary branches/ plants**, SB=** Numbers of secondary branches/ plants**, LMR=** Length of main raceme (cm), **SMR=** Numbers of siliquae on main raceme**, S/SL=** Numbers of seed per siliquae, **SL=** Siliquae length (cm), **TSW=** Test weight (g), **BY=** Biological yield, **HI=** Harvest Index**, SSYP=** Seed yield per plant (g)

Table 6 Path coefficient analysis showing the direct and indirect effect of different characters on the seed yield at genotypic level in Indian mustard

Character	DF	DM	PH	PB	SB	LMR	SMR	S/SL	SL	TSW	BY	HI
DF	**0.0080**	0.0008	0.0006	0.0006	-0.0002	-0.0009	-0.0009	0.0015	0.0006	-0.0001	0.0026	-0.0023
DM	0.0016	**0.0166**	-0.0005	0.0021	-0.0006	-0.0010	0.0008	0.0031	0.0033	-0.0007	0.0012	-0.0060
PH	0.0014	-0.0005	**0.0176**	0.0005	-0.0024	0.0025	0.0010	0.0020	-0.0015	0.0027	0.0022	-0.0013
PB	-0.0024	-0.0043	-0.0010	**-0.0334**	-0.0191	-0.0033	-0.0139	-0.0070	0.0023	-0.0064	-0.0221	0.0057
SB	-0.0018	-0.0028	-0.0101	0.0424	**0.0744**	0.0225	0.0198	-0.0104	-0.0100	-0.0036	0.0279	0.0084
LMR	-0.0051	-0.0028	0.0064	0.0044	0.0136	**0.0450**	0.0026	-0.0032	-0.0008	0.0088	0.0056	0.0034
SMR	-0.0193	0.0082	0.0104	0.0745	0.0476	0.0102	**0.1787**	0.0466	0.0230	0.0187	0.0867	-0.0128
S/SL	0.0094	0.0092	0.0057	0.0104	-0.0069	-0.0035	0.0129	**0.0496**	0.0295	-0.0008	0.0057	-0.0106
SL	-0.0045	-0.0114	0.0050	0.0040	0.0078	0.0010	-0.0074	-0.0343	**-0.0576**	0.0003	0.0074	-0.0013
TSW	0.0008	0.0028	-0.0108	-0.0137	0.0035	-0.0140	-0.0075	0.0011	0.0003	**-0.0714**	-0.0176	-0.0125
BY	0.2951	0.0642	0.1136	0.6115	0.3484	0.1156	0.4497	0.1074	-0.1187	0.2290	**0.9274**	-0.4152
HI	-0.1893	-0.2404	-0.0481	-0.1123	0.0745	0.0507	-0.0476	-0.1411	0.0153	0.1161	-0.2967	**0.6628**
SYPP	0.0939	-0.1604	0.0888	0.5908	0.5405	0.2247	0.5882	0.0154	-0.1144	0.2926	0.7303	0.2182

Table 7 Path coefficient analysis showing the direct and indirect effect of different characters on the seed yield at phenotypic level in Indian mustard

Character	DF	DM	PH	PB	SB	LMR	SMR	S/SL	SL	TSW	BY	HI
DF	**0.0109**	0.0010	0.0008	0.0007	-0.0002	-0.0012	-0.0012	0.0015	0.0008	-0.0002	0.0034	-0.0030
DM	0.0006	**0.0064**	-0.0002	0.0006	-0.0002	-0.0004	0.0003	0.0009	0.0012	-0.0002	0.0004	-0.0022
PH	0.0015	-0.0006	**0.0196**	0.0002	-0.0027	0.0027	0.0011	0.0019	-0.0013	0.0029	0.0023	-0.0013
PB	-0.0004	-0.0006	-0.0001	**-0.0065**	-0.0027	-0.0006	-0.0020	-0.0011	0.0001	-0.0009	-0.0033	0.0009
SB	-0.0012	-0.0018	-0.0076	0.0231	**0.0559**	0.0161	0.0141	-0.0063	-0.0055	-0.0027	0.0201	0.0053
LMR	-0.0053	-0.0028	0.0064	0.0042	0.0137	**0.0473**	0.0027	-0.0025	-0.0007	0.0088	0.0057	0.0037
SMR	-	0.0082	0.0106	0.0565	0.0461	0.010	**0.183**	0.037	0.020	0.018	0.088	-

	0.0194					4	**0**	3	4	2	3	0.0129
S/SL	0.0028	0.0029	0.0020	0.0035	-0.0023	-0.0011	0.0042	**0.0207**	0.0092	-0.0004	0.0018	-0.0033
SL	-0.0026	-0.0070	0.0026	0.0006	0.0038	0.0005	-0.0043	-0.0170	**-0.0382**	0.0006	0.0046	-0.0009
TSW	0.0011	0.0024	-0.0102	-0.0095	0.0034	-0.0130	-0.0070	0.0012	0.0011	**-0.0701**	-0.0168	-0.0116
BY	0.2876	0.0625	0.1053	0.4584	0.3271	0.1098	0.4398	0.0797	-0.1107	0.2187	**0.9117**	-0.4084
HI	-0.1796	-0.2298	-0.0434	-0.0895	0.0622	0.0517	-0.0460	-0.1053	0.0154	0.1082	-0.2936	**0.6554**
SYPP	0.0960	-0.1592	0.0858	0.4422	0.5040	0.2223	0.5848	0.0110	-0.1082	0.2829	0.7247	0.2218

DF= Days to 50% Flowering, **DM=** Days to maturity, **PH=** Plant height (cm), **PB=** Number of primary branches/ plants**,** **SB=** Number of secondary branches/ plants**, LMR=** Length of main raceme (cm), **SMR=** Number of siliquae on main raceme**,** **S/SL=** Number of seed per siliquae, **SL=** Siliquae length (cm), **TSW=** Test weight (g), **BY=** Biological yield, **HI=** Harvest Index**, SSYP=** Seed yield per plant (g)

Table 8 Individual character's percentage contribution to genetic divergence

Source	**Contribution %**
Days to 50% flowering	2.36
Days to maturity	27.80
Plant height (cm)	7.64
Numbers of primary branches per plant	0.08
Numbers of secondary branches per plant	0.04
Length of main raceme (cm)	5.98
Numbers of siliquae on main raceme	37.63
Numbers of seeds per siliquae	0.09
Siliquae length(cm)	0.04
Test weight (g)	0.72
Biological Yield	12.43
Harvest Index	1.12
Seed Yield per Plant (g)	4.07
Total	**100.00%**

Table 9 Distribution of seventy-five Indian mustard genotypes by Tocher's method

Cluster No.	**Name of genotypes**	**Numbers of genotypes**
I	RB-50, Pusa Bold, Rohini, Kranti, RH-725, Maya,Vardan, Vasundhara, Swarn Jyoti, DMH1, JMWR-908-1, NRC-HB-101 , NRC-HB-506, RVM-3, RH-749, NRC DR-2, DRMR IJ-31, CHINA, GSL-1, GSC-7, PC-5, PC-6, RP-9, JTC-1, JM-1, JM-2 , RVM-1, RVM-2, PM-25, PM-26, PM-27, PM-30, Pusa Vijay, JMM-927, WRR-5, WRR-6, WRR-7, WRR-8, WRR-9, WRR-10, WRR-13, WRR-14, WRR-15, WRR-16, WRR-17, WRR-18, WRR-19, WRR-25, WRR-26, WRR-27, WRR-28, WRR-29, WRR-30, WRR-32	53
II	Pusa Jagannath, PusaJaiKisan, Albeli, Sej-2, Shraddha, RGN-73, JMM-991, RMM-12-03-18, WRR-11, WRR-12, WRR-20, WRR-21, WRR-22, WRR-31	14
III	Varuna	1
IV	L-4, JM-3, PM-28, RMM-10-01-01, RMM-12-01-18	5
V	KIRAN	1
VI	RP-9	1

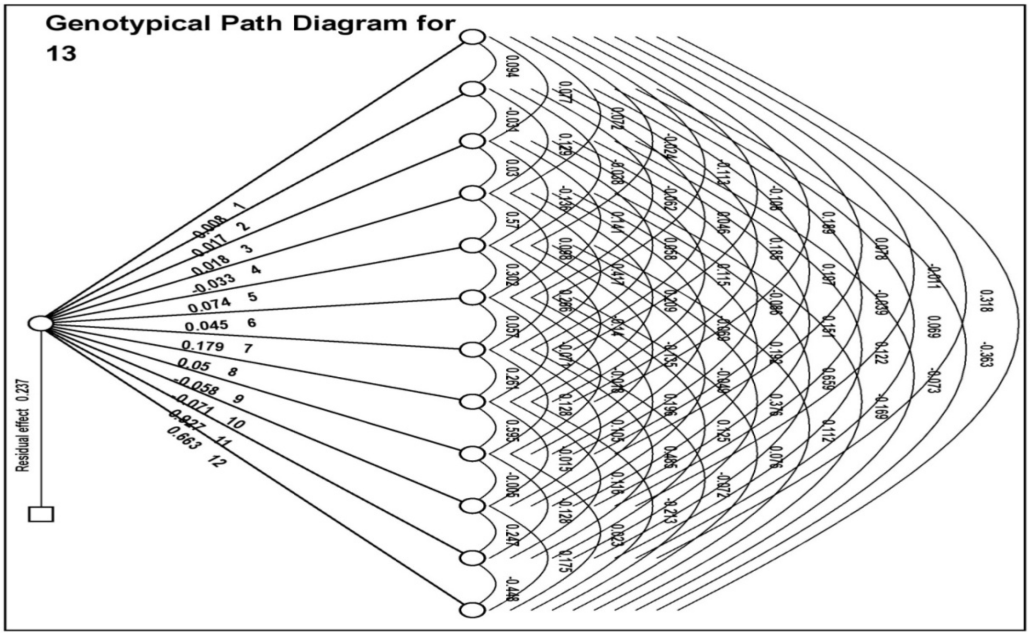
Table10. Inter and intra-cluster distance in Indian mustard

Cluster	**Cluster I**	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**
Cluster I	**22.17**	29.68	27.97	42.01	43.14	43.76
Cluster II		**24.32**	43.71	44.27	46.40	56.23
Cluster III			**0.00**	42.14	52.04	29.93
Cluster IV				**30.85**	51.73	38.74
Cluster V					**0.00**	51.63
Cluster VI						**0.00**

Table 11 Cluster mean in Indian mustard

Cluster	**DF**	**DM**	**PH**	**PB**	**SB**	**LMR**	**SMR**	**S/SL**	**SL**	**TSW**	**BY**	**HI**	**SYPP**
Cluster I	51.72	153.04	179.70	8.10	10.39	88.83	139.22	12.97	5.10	4.76	31.43	30.23	9.03
Cluster II	52.75	118.79	171.51	8.07	10.93	84.79	117.29	12.18	4.73	4.82	30.46	34.47	9.66
Cluster III	43.00	178.50	162.99	8.00	10.50	89.00	222.50	11.00	4.75	5.10	38.50	25.94	9.98
Cluster IV	53.90	127.20	186.20	10.30	17.70	117.40	245.80	12.20	4.60	5.07	68.30	31.98	21.45
Cluster V	75.50	159.50	188.32	8.50	9.00	74.50	71.50	12.50	4.25	5.90	93.50	15.06	14.07
Cluster VI	74.00	178.50	202.34	13.50	21.50	72.50	288.00	15	4.75	4.41	78.50	24.83	19.47

DF= Days to 50% Flowering, **DM=** Days to maturity= Plant height (cm), **PB=** Number of primary branches/ plants**, SB=** Number of secondary branches/ plants**, LMR=** Length of main raceme (cm), **SMR=** Number of siliquae on main raceme**, S/SL=** Number of seed per siliquae, **SL=** Siliquae length (cm), **TSW=** Test weight (g), **BY=** Biological yield, **HI=** Harvest Index**, SSYP=** Seed yield per plant (g)


Genotypical Path Diagram for 13
Residual effect 0.237
0.008 1
0.017 2
0.018 3
-0.033 4
0.074 5
0.045 6
0.179 7
0.05 8
-0.058 9
-0.071 10
-0.027 11
0.663 12
0.094
-0.034
0.03
0.57
0.302
0.057
0.261
0.595
-0.006
0.247
-0.448
0.077
0.129
-0.136
0.088
0.285
-0.077
0.128
-0.015
-0.128
0.175
0.072
-0.038
0.141
0.417
0.14
-0.018
0.105
0.118
0.023
-0.024
-0.052
0.058
0.209
-0.135
0.196
0.406
-0.213
-0.113
0.046
0.115
0.069
-0.046
0.125
-0.072
-0.106
0.185
-0.086
0.194
0.376
0.076
0.189
0.187
0.151
0.659
0.112
0.078
-0.039
0.122
-0.169
-0.011
0.069
-0.073
0.318
-0.363
-0.286

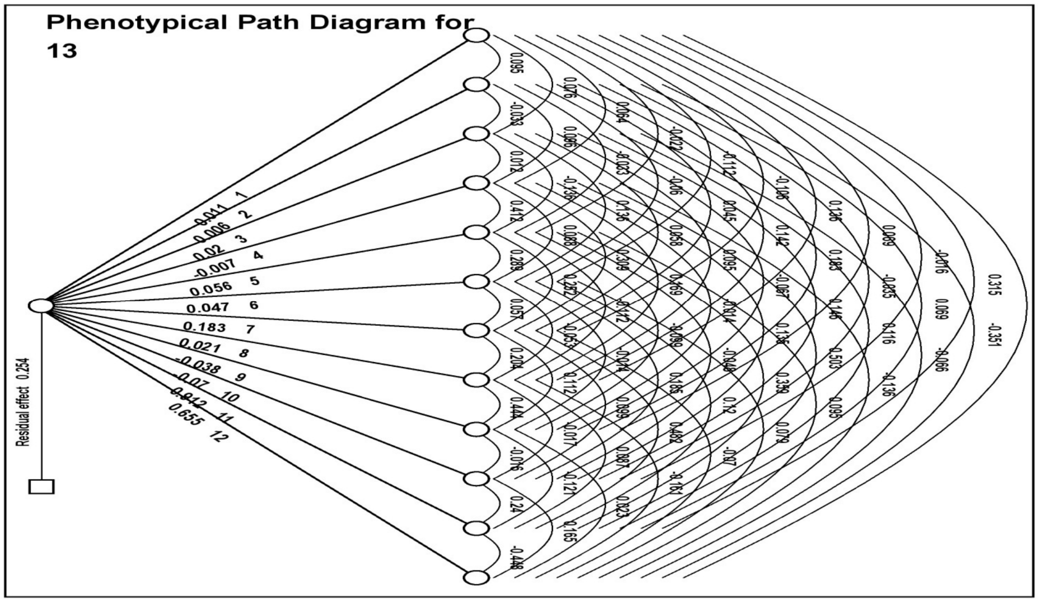

Phenotypical Path Diagram for 13
Residual effect 0.254
0.011 1
0.006 2
0.02 3
-0.007 4
0.056 5
0.047 6
0.183 7
0.021 8
-0.038 9
-0.07 10
-0.012 11
0.655 12
0.095
-0.033
0.012
0.412
0.289
0.057
0.204
0.444
-0.016
0.24
-0.448
0.076
0.095
-0.135
0.088
0.262
-0.063
0.112
-0.017
-0.121
0.165
0.064
-0.023
0.136
0.309
0.112
-0.014
0.099
0.087
0.023
-0.022
-0.06
0.058
0.169
-0.098
0.185
0.482
-0.161
-0.112
0.045
0.095
0.014
-0.048
0.12
-0.07
-0.106
0.142
-0.067
0.136
0.359
0.079
0.136
0.183
0.146
0.505
0.095
0.089
-0.035
0.116
-0.136
-0.016
0.069
-0.066
0.315
-0.351
-0.274

Fig. 1 Path Diagram at genotypic and phenotypic level in Indian mustard

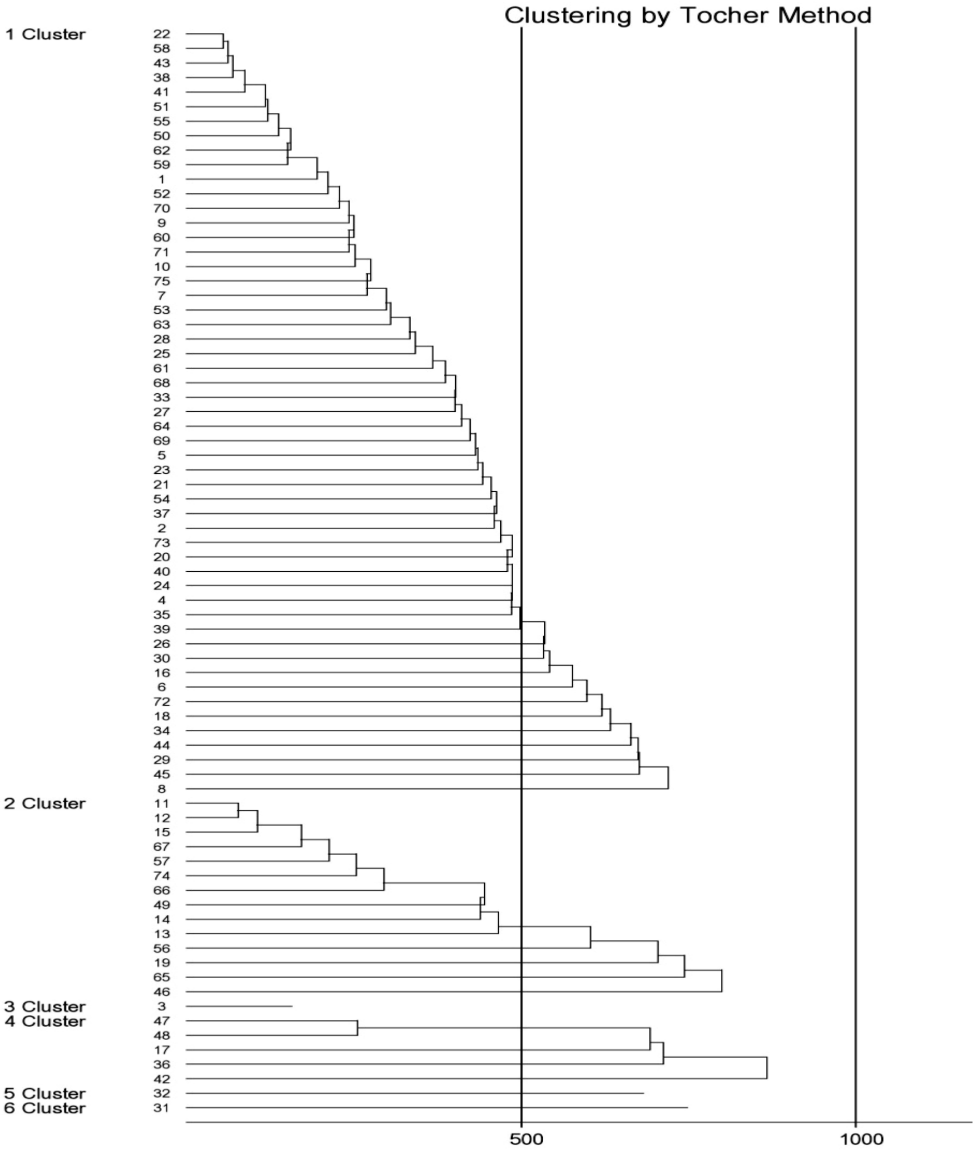


Fig. 2 Cluster Diagram in Indian mustard