

Assessment of genetic variation for seed yield and quality attributing characters in Indian rapeseed and mustard

ABSTRACT

During *Rabi* 2019-20 and 2020-21, a set of five yellow sarson, five toria and ten Indian mustard genotypes were used to analyse and estimate the genetic variability for seed quality and yield attributing traits. A wide range of variations among genotypes for seed quality and yield-related characters were observed. In the majority of the characters, environment and genotype-environment interaction variation was found significant. The highest GCV, PCV, and heritability coupled with high genetic advance were observed for the seed yield per hectare and germination index. Among the yellow sarson genotypes B9 (highest yielder), BNYS-1 and BNYS-2; among the toria lines TS-46 (highest yielder), Jeuti, TS-38 and TS-67 and among the Indian mustard genotypes JMM-TM2-36 (highest yielder), NRCHB-101, TM-2 and JMM-TM2-34 were found superior for the seed quality and yield attributing parameters. Genetic diversity based on seed quality traits showed five distinct clusters among the 20 rapeseed and Indian mustard genotypes.

Keywords: Genetic variation, seed quality, genetic diversity, heritability, rapeseed and mustard

Introduction

The oilseed *Brassica* collectively known as rapeseed-mustard is amongst the oldest cultivated plants in human civilization. The cultivated mustard is an ancient crop of the New World which originated in Asia, Europe and perhaps Africa, where it was cultivated in 1200 B.C (Shathi *et al.* 2012). The *Brassicaceae* family, which is comprised of about 350 genera and 3500 species, falls under the ten most economically dominant plant families having a wide range of agronomic traits (Rich 1991; Christopher *et al.* 2005). Indian mustard [*Brassica juncea* (L.) Czern & Coss.] and Indian rapeseed (*Brassica rapa* L.) group having chromosome number $2n = 36$ (mustard) and $2n = 20$ (rapeseed) is ranked as the third most important edible *Rabi* oilseed crop in the world after soybean and palm oil. The oil and protein content of rapeseed and mustard ranged from 38-42% and 24% respectively (Gupta *et al.* 2018). Globally, India ranks second after Canada in acreage (19.81%) and ranks fourth after Canada, European Union and China in production (10.37%) according to the annual report of DRMR (2021). Rapeseed-mustard plays an important role in Indian national economy as it contributes 27 % of the total oilseed production accounting for about 14% of world production and 22.5% of the world area under rapeseed mustard (Roy *et al.* 2018). In Assam, rapeseed-mustard is grown in an area of 2.95 lakh hectare i.e., 85.5% of total oilseeds crop area with a production of 1.995 lakh tonnes and average productivity of 698

Kg/ha. In the northeastern hill region, rapeseed and mustard among the *Rabi* oilseeds can play a significant role in boosting oilseed production[24-27].

As an oil seed crop, seed yield in rapeseed mustard is considered as the most important trait. Moreover, the seeds of rapeseed-mustard are a rich source of several nutritionally important macromolecules like proteins, oil, amino acids and possess anticancer, and antioxidant properties (Poisson *et al.* 2019). However, it is highly influenced by genotype and environmental interaction. Therefore, for efficient selection of genotypes for seed quality and yield-associated traits, knowledge of the association of seed yield with its component traits is desirable. Also, the success of any breeding programme is influenced by the availability of genetic variability or diversity present in the breeding material, since variation provides scope for selection and, the efficiency of selection depends on the heritability of the concerned traits. The heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into the next generations (Kumar *et al.* 2013; Malek *et al.* 2014). Hence, the present investigation evaluated twenty rapeseed and Indian mustard genotypes for seed quality and yield traits to estimate the genetic variability and diversity present among the traits.

Materials and Methods

The present study was carried out in the experimental plot of the Department of Plant Breeding & Genetics (PBG), Assam Agricultural University (AAU), Jorhat (26°44' North latitude, 94°10' East longitude, elevation 91 m above mean sea level; www.aau.ac.in) during the *Rabi* season of 2019-20 and 2020-21. Twenty genotypes selected for the experiment were five yellow sarson (B9, YSH-401, JYS-14-2, BNYS-1 and BNYS-2), five toria (TS-38, TS-67, TS-46, M-27 and Jeuti) and ten Indian mustard genotypes (JMM-TM2-15, JMM-TM2-34, JMM-TM2-36, JMM-TM2-263, JMM-TM2-4, JMM-TM2-44, JMM-TM2-41, PM 27, TM2 and NRCHB-101) which were collected from the Department of PBG, AAU, Jorhat.

The seeds of all twenty genotypes were sown on 19th November 2019 and on 22nd November 2020 in randomized block design in three replications. The agronomic practices were followed according to the standard package and practices.

Yield attributing characters viz. seeds per siliqua (SPS), thousand seed weight (TSW), Seed yield per hectare (SYPH) were recorded as per standard procedures. The seed quality parameters viz. seedling length (SL), seedling dry weight (SDW) were recorded and

pure live seed percentage (PLS), Germination index (GI), Germination percentage (GP), Seed vigour index-I (SVI-I), Seed vigour index-II (SVI-II) were estimated using standard formula for the two seasons. However, the oil content was recorded for only a single season i.e., 2019-20 and was determined using Near Infrared Reflectance Spectroscopy (NIRS). The working samples of dried and cleaned seeds were sent to ICAR-Indian Institute of Oilseeds Research, Hyderabad for the estimation of seed oil content.

Statistical methods viz. pooled analysis of variance of the two environments (years) for each character was performed, following Gomez and Gomez (1984). Genotypic variances (σ^2_g), phenotypic variance (σ^2_p) and environmental variance (σ^2_e) were computed as given by Singh and Chowdhury (1985). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated from these variances following Burton and Devane (1953). Heritability (h^2) in broad sense was calculated by using the formula suggested by Burton and Devane (1953). The genetic advance was estimated following Allard (1960) then expressed as percentage of the grand mean. Genetic diversity was carried out by cluster analysis using Euclidean distances followed by the method UPGMA (unweighted pair group method with arithmetic mean) given by Sokal and Michener (1958).

Meteorological data viz. temperature, relative humidity, rainfall and bright sunshine hours were obtained from the Department of Agro-meteorology, AAU, Jorhat during the crop period.

Results and Discussion

The pooled analysis of variance over two years i.e., two environments showed high genotypic differences for all the characters. Among yellow sarson, variation was observed for few traits whereas among toria difference was observed only for seeds per siliqua, however, great differences were found between yellow sarson and toria though they belong to the same species. Variation was also observed between mustard and rapeseed for all the traits except for seed vigour parameters indicating both to be alike for vigour parameters. The effect of environments and genotype-environment interactions was found to be varied only for seed yield per hectare and seed numbers per siliqua. Analysis of variance for oil content also showed high variation among all the genotypes.

GCV, PCV, heritability in broad sense, expected genetic advance as a percentage of mean and ranges of pooled mean were assessed from the pooled data which revealed higher

PCV than GCV (Table 1; Fig. 1) indicating the clear influence of environmental factors on the traits. Similar results were also recorded by Prasad and Patil (2018) and Pandey *et al.* (2020). The highest GCV and PCV were exhibited by seed yield per hectare (44.26% and 45.26% respectively) followed by germination index (33.47% and 33.64% respectively). Moderate GCV and PCV were observed in SVI-II (13.95% and 15.33% respectively), number of seeds per siliqua (11.45% and 15.63% respectively), seedling dry weight (11.23% and 13.26% respectively), SVI-I (10.49% and 12.13% respectively), germination percentage (10.32% and 10.59% respectively) and pure live seed percentage (10.32% and 10.59% respectively). The remaining traits showed low GCV and PCV which included thousand seed weight (8.70% and 8.99% respectively), oil content (4.44% and 4.49% respectively). For seedling length, GCV (9.81%) was low but PCV was moderate (10.57%). Low GCV and PCV were also reported by Yadav *et al.* (2021) for oil content and Ray *et al.* (2019) for thousand seed weight.

Broad-sense heritability (Table 1; Fig. 1) was noted highest for germination index (98.97), followed by oil content (97.98), germination percentage (95.05), pure live seed percentage (95.05), seed yield per hectare (94.36), thousand seed weight (93.72), seedling length (86.09) and SVI-II (82.86). SVI-I (74.82), seedling dry weight (71.81) and number of seeds per siliqua (53.66) exhibited moderate heritability. Traits with high heritability can be assessed for the selection of suitable genotypes to be used for a breeding programme.

High genetic advance as percent of mean (Table 1; Fig. 1) was observed for seed yield per hectare (88.58), germination index (68.59). Moderate genetic advance was observed for SVI-II (26.16), germination percentage (20.73) and pure live seed percentage (20.73). However, seedling dry weight (19.61), seedling length (18.75), SVI-I (18.69), thousand seed weight (17.36), number of seeds per siliqua (17.28) and oil content (9.06) showed low genetic advance. Similar observations were recorded by Maurya (2019) for germination percentage showing moderate genetic advance with high heritability for SVI-I. High heritability coupled with high genetic advance was observed for seed yield per hectare and germination index, also reported by Uzair *et al.* (2016) for seed yield per hectare, indicating the effect of additive gene action in the inheritance of these characteristics (Johnson *et al.* 1955).

Oil content, the economically most important trait exhibited lowest GCV and PCV and genetic advance but very high heritability. Whereas seed yield per hectare and

germination index showed high GCV and PCV coupled with high heritability and genetic advance. Similar findings were reported by many researchers (Yadav *et al.* 2021; Maurya 2019; Patel *et al.* 2019 and Prasad and Patil 2018).

Genotypes exhibited a wide range of variation (Table 2) in mean performance for seed quality and seed yield-related characters. Among the yellow sarson genotypes, B9 was the highest yielder followed by YSH-401 and JYS-14-2. Among toria, TS-46 was found to be the highest yielder, followed by M-27, Jeuti and TS-67 and among the Indian mustard lines, JMM-TM2-36 was the highest yielder followed by JMM-TM2-263 and JMM-TM2-4.

Mean performance values were evaluated separately for yellow sarson, toria and Indian mustard as shown in Table 3. The observations indicated that yellow sarson was significantly superior to toria for seeds per siliqua, 1000-seed weight and oil content. The toria genotypes were superior to the yellow sarson for seed yield, and all the seed quality traits including germination percentage. The Indian mustard genotypes were superior to the rapeseed genotypes for seed yield, seed weight, seedling length and seedling dry weight, but inferior for all other seed quality traits. Seed yield was 805 kg/ha for Indian mustard, 486 kg/ha for toria and 435 kg/ha for yellow sarson. Number of seeds per siliqua was higher in yellow sarson than in toria and Indian mustard. Similarly, oil content was observed to be significantly higher in yellow sarson (40.7%) than in toria (39.1%) and Indian mustard (33.3%). The germination percentage was below the certification standard in Indian mustard.

Table 1: Estimates of genetic parameters for seed yield and quality traits in rapeseed and mustard

Characters	Mean	SE (Mean)	Range		GCV %	PCV %	Heritability %	Genetic advance (%)
			Lowest	Highest				
Seeds per siliqua (nos.)	15.96	0.70	11.67	18.78	11.45	15.63	53.66	17.28
Thousand seed weight (g)	3.28	0.07	2.81	3.98	8.70	8.99	93.72	17.36
Oil content (%)	36.61	0.24	32.20	41.39	4.44	4.49	97.98	9.06
Seed yield per ha (Kg)	627.94	26.17	378.33	896.18	44.26	45.26	94.36	88.58
Pure live seed percentage	85.32	2.01	67.00	96.33	10.32	10.59	95.05	20.73
Germination index	16.34	0.56	8.65	23.88	33.47	33.64	98.97	68.59
Germination percentage	85.32	2.01	67.00	96.33	10.32	10.59	95.05	20.73
Seedling length (cm)	12.71	0.50	10.51	15.00	9.81	10.57	86.09	18.75
Seedling dry weight (mg)	14.50	1.02	11.33	18.48	11.23	13.26	71.81	19.61
Seed vigour index-I (based on seedling length)	1081.03	65.77	857.09	1253.69	10.49	12.13	74.82	18.69
Seed vigour index-II (based on dry seedling weight)	1246.58	79.10	851.40	1546.50	13.95	15.33	82.86	26.16

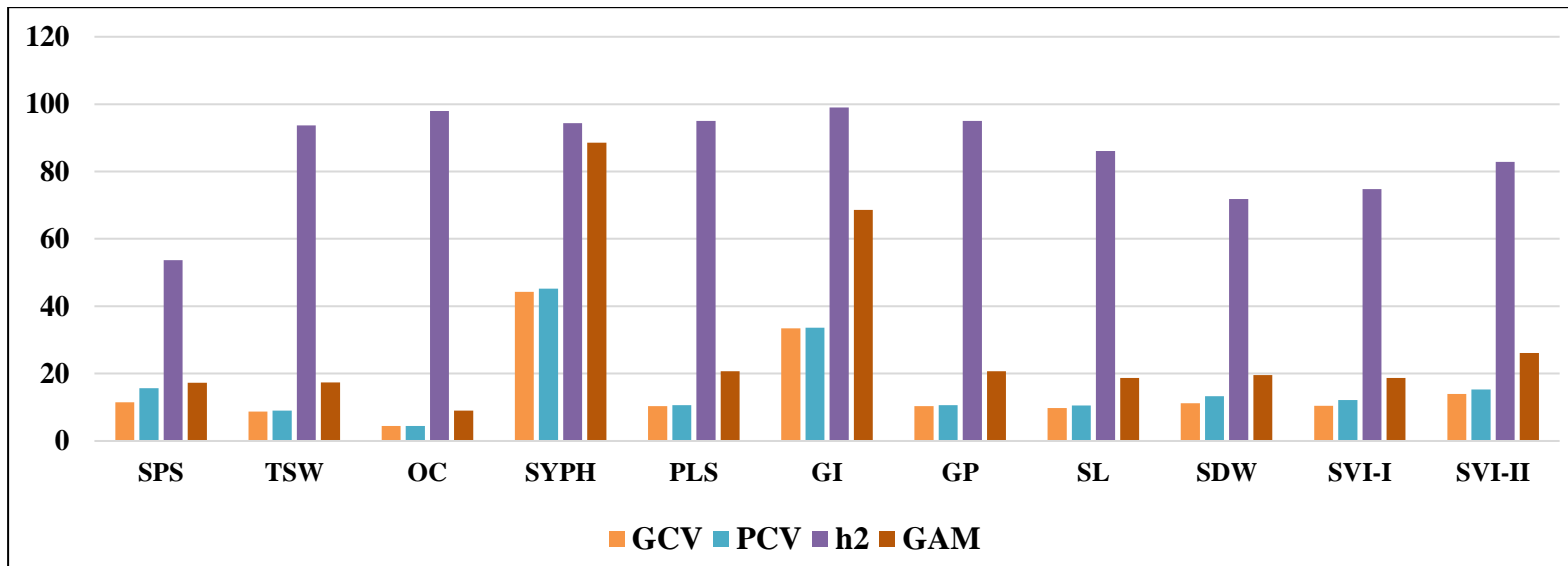


Fig. 1. Graphical representation of genetic parameters of seed quality and yield attributing traits in rapeseed and Indian mustard from pooled data

SPS= Seeds per siliqua, **TSW**= Thousand seed weight, **OC**= Oil content, **SYPH**= Seed yield per hectare, **PLS**= Pure live seed percentage, **GI**= Germination index, **GP**= Germination percentage, **SL**= Seedling length, **SDW**= Seedling dry weight, **SVI-I**= Seed vigour index-I, **SVI-II**= Seed vigour index-II

Table 2: Mean values of the genotypes for quantitative traits related to seed quality and yield attributing parameters

Genotypes	Seeds per siliqua	1000 seed weight (g)	Seed yield (Kg/ha)	Oil content (%)	Pure live seed (%)	Germination index	Germination %	Seedling length (cm)	Seedling DW (mg)	SVI-I	SVI-II
B9	17.70	3.47	471	40.62	90.33	19.57	90.33	10.76	12.44	972	1354
YSH-401	18.46	2.94	467	40.10	88.00	20.32	88.00	10.51	11.33	924	997
JYS-14-2	18.36	3.14	438	40.23	83.67	18.61	83.67	11.13	12.47	931	1043
BNYS-1	17.43	3.23	419	41.39	94.00	21.35	94.00	10.89	12.91	981	1185
BNYS-2	18.78	3.39	378	41.33	92.00	20.55	92.00	10.64	14.12	1026	1335
TS-38	17.16	3.16	445	38.95	95.67	22.48	95.67	12.85	13.23	1231	1266
TS-67	15.40	3.08	475	39.22	95.00	22.53	95.00	13.17	14.99	1254	1422
TS-46	16.16	3.17	551	39.26	96.00	23.46	96.00	12.59	13.87	1209	1331
M-27	16.90	3.17	486	39.00	92.00	22.13	92.00	12.74	13.92	1172	1279
Jeuti	14.46	3.13	475	39.23	96.33	23.88	96.33	12.97	15.22	1249	1465
JMM-TM2-15	14.13	3.72	791	32.96	77.00	9.32	77.00	13.36	15.20	1034	1171
JMM-TM2-34	14.14	3.52	823	33.32	83.33	12.19	83.33	14.31	18.48	1193	1547
JMM-TM2-36	14.26	2.81	896	33.68	71.00	10.17	71.00	12.06	14.79	857	1049
JMM-TM2-263	15.10	3.00	857	32.21	73.33	10.64	73.33	14.07	13.93	1032	1021
JMM-TM2-4	17.72	3.52	851	32.30	85.00	12.03	85.00	12.76	15.33	1080	1300
JMM-TM2-44	15.69	3.57	812	34.53	67.00	8.65	67.00	13.59	15.98	918	1074
JMM-TM2-41	16.21	2.85	824	32.20	73.67	11.36	73.67	14.16	11.58	1040	851
PM 27	11.67	3.36	777	34.08	82.00	12.67	82.00	12.53	15.89	1034	1299
TM-2	12.75	3.34	769	33.08	87.67	12.39	87.67	14.07	16.39	1238	1438
NRCHB-101	16.64	3.98	655	34.49	83.33	12.56	83.33	15.00	18.01	1245	1504
Mean	15.96	3.47	628	36.61	85.32	16.34	85.32	12.71	14.50	1081	1247
SE(m)	0.70	0.07	26	0.24	2.01	0.56	2.01	0.50	1.02	66	79
CD5%	1.98	0.21	74	0.68	5.68	1.58	5.68	1.42	2.89	186	224

Table 3: Mean values of Toria, Yellow sarson and Indian mustard for quantitative traits related to seed quality and yield attributing parameters

Crop type	Seeds per siliqua	1000 seed weight (g)	Seed yield (Kg/ha)	Oil content (%)	Pure live seed (%)	Germination index	Germination %	Seedling length (cm)	Seedling dry weight (mg)	Seed vigour Index-I	Seed vigour Index-II
Toria	16.02	3.14	486.00	39.13	95.00	22.89	95.00	12.86	14.24	1223	1353
Yellow sarson	18.14	3.23	434.76	40.73	89.60	20.08	89.60	10.79	12.65	967	1183
Mustard	14.83	3.37	805.39	33.28	78.33	11.20	78.33	13.59	15.56	1067	1225
CD5%	0.89	0.09	8.94	0.37	2.54	0.70	2.54	0.63	1.29	83	100
CD1%	1.18	0.12	11.89	0.50	3.38	0.94	3.38	0.84	1.72	111	133

Cluster analysis based on seed quality traits reported formation of five distinct clusters among the 20 rapeseed and Indian mustard genotypes (Table. 4). Cluster-I and Cluster-II represents Rapeseed (toria and yellow sarson respectively) whereas, Cluster-III, Cluster-IV and Cluster-V are that of Indian mustard (Figure 2). Cluster-I comprised of five toria genotypes which were TS-67, Jeuti, M-27, TS-38 and TS-46. Cluster-II included all the five yellow sarson genotypes under study which were B9, BNYS-2, BNYS-1, YSH-401 and JYS-14-2. Cluster-III consisted of six Indian mustard genotypes viz., JMM-TM2-15, PM 27, JMM-TM2-4, NRCHB-101, JMM-TM2-34 and TM-2. Cluster-IV comprised of two Indian mustard genotypes which were JMM-TM2-263 and JMM-TM2-41. Similarly, the two genotypes under Cluster-V were of Indian mustard viz., JMM-TM2-36 and JMM-TM2-44. Singh *et al.* (2013) conducted a similar experiment which comprised of fifty diverse genotypes including twelve of exotic origin and thirty-eight from different states of India and reported five clusters.

Table 4: Grouping of genotypes based on seed quality characters in different clusters

Cluster	No. of genotypes	Genotypes
Cluster I	5	TS-67, Jeuti, M-27, TS-38, TS-46
Cluster II	5	B9, BNYS-2, BNYS-1, YSH-401, JYS-14-2
Cluster III	6	JMM-TM2-15, PM 27, JMM-TM2-4, NRCHB-101, JMM-TM2-34 and TM-2
Cluster IV	2	JMM-TM2-263 and JMM-TM2-41
Cluster V	2	JMM-TM2-36 and JMM-TM2-44

Cluster means for the seed quality traits of the 20 genotypes of rapeseed and Indian mustard evaluated during 2019-20 and 2020-21 are depicted in Table 5. It was observed that the genotypes from Cluster-I exhibited highest percentage of germination and pure live seed along with highest range for germination index and seed vigour index-I. The genotypes in Cluster-II displayed highest percentage for oil content. Highest values for seed vigour index-II and seedling dry weight were represented in Cluster-III. Cluster-IV exhibited the highest measurement for seedling length. However, the genotypes under Cluster-V were revealed to have the lowest values for germination percentage, germination index, seed vigour index-I and pure live seed percentage.

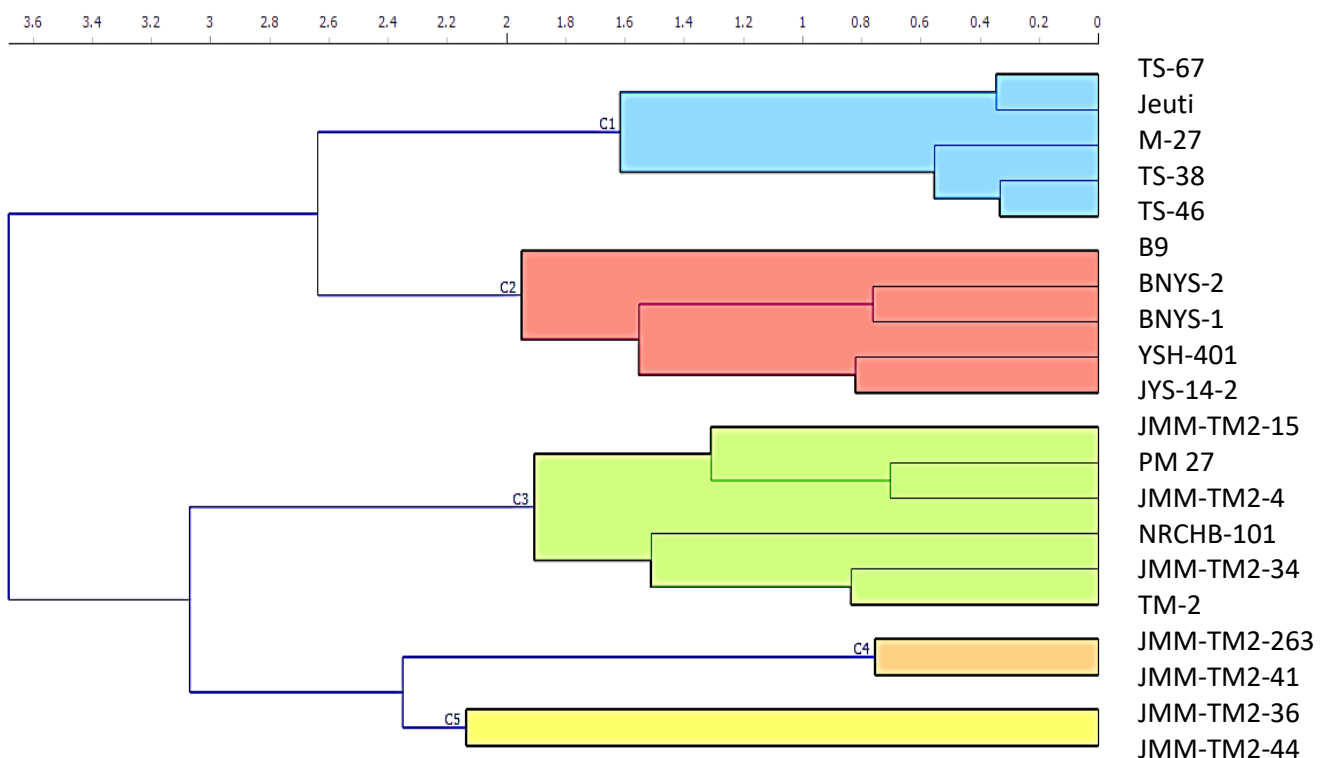


Fig. 2. Hierarchical clustering of the 20 genotypes of rapeseed and indian mustard using euclidean distances followed by UPGMA based on seed quality parameters

Table 5: Cluster mean performance for seed quality traits of the 20 genotypes of rapeseed and Indian mustard evaluated during 2019-20 and 2020-21

Cluster No.	GP (%)	GI	SVI-I	SVI-II	SL	SDW	PLS (%)	OC (%)
I	95.00	22.89	1222.76	1.35	12.86	0.014	95.00	39.13
II	89.60	20.08	966.80	1.18	10.79	0.013	89.60	40.73
III	83.06	11.86	1137.56	1.38	13.67	0.017	83.06	33.37
IV	73.50	11.00	1036.05	0.94	14.12	0.013	73.50	32.20
V	69.00	9.41	887.62	1.06	12.83	0.015	69.00	34.10

Conclusion

Presence of high significant differences among genotypes for most of the important traits indicated the existence of diversity among the genotypes. The presence of considerable variation among the genotypes for seed quality and yield attributing characters revealed scope for further investigation. Heritability and genetic advancement indicated that the nature of action and reliability of those characters for selection can emerge as ideal traits for improvement through selection. The study identified three significantly superior yellow sarson genotypes viz., BNYS-1, BNYS-2 and B9; four toria genotypes viz., Jeuti, TS-46, TS-38 and TS-67 and three Indian mustard genotypes viz., NRCHB-101, TM-2, and JMM-TM2-34 based on all the seed quality and yield attributing parameters under study. Therefore, these genotypes could be considered for further evaluation and recommendation. The genotypes which were identified as high yielders are

B9, YSH-401 and JYS-14-2 among the yellow sarson genotypes, TS-46, M-27, Jeuti and TS-67 among the toria genotypes and JMM-TM2-36, JMM-TM2-263 and JMM-TM2-4 among the Indian mustard genotypes. From the diversity analysis it was observed that the genotypes of yellow sarson, toria and Indian mustard were grouped into distinct clusters without any combination between them. The characters or traits taken into account are specific to a particular cluster and there is no intermingling of morphological trait.

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