

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.911.162>

Genetic Variability, Association and Path Analysis in Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] for Yield and its Component Traits

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ABSTRACT

A field experiment was conducted to estimate the genetic variability, trait association and path coefficient analysis among the Indian mustard genotypes during *rabi*, 2019. Analysis of variance revealed the mean sum of squares due to genotypes was highly significant for all the characters studies indicating the existence of ample variability among the genotypes studied. The high GCV and PCV observed for number of siliquae per plant and secondary branches per plant indicated the influence of environment on the expression of these characters were at minimum level. High heritability was recorded for character 1000-seed weight and siliqua length, moderate heritability observed for days to 50% flowering and days to physiological maturity revealed the presence of additive gene action and minimum influence of environment in expression of these characters. High heritability estimates in broad sense coupled with low genetic advance as percent of mean was observed for siliqua length and 1000-seed weight indicated presence of non-additive gene action and provide limited scope for improvement through selection. Results of genotypic and phenotypic correlation coefficient revealed that seed yield per plant had significant positive correlation with plant height at genotypic level. However, seed yield per plant recorded negative correlation with days to 50% flowering at both levels but was significant at genotypic level.

Keywords

Indian mustard,
Path coefficient
analysis,
Brassica juncea

Article Info

Accepted:

12 October 2020

Available Online:

10 November 2020

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the most important oilseed crops and stands second in both acreage and production of rapeseed and mustard in Asia. In India, Rapeseed and mustard occupied second position among the oilseed crops with

an area and production of 6.23 million hectares and 9.34 million tons, respectively during 2018-19 (Anon, 2019). Prominent states growing mustard in India are Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh and Gujarat which contribute more than 80 per cent in area and production.

Every breeder's first and foremost objective is to enhance the productivity through the varietal development programme which totally depends upon the genetic variability present in the available germplasm/breeding material of a particular crop. The assessment of various genetic parameters like genotypic coefficient of variance, phenotypic coefficient of variance, heritability and genetic advance are pre-requisite for the effective selection programme. Seed yield is a complex character and is usually controlled by non-additive gene actions and it is not only influenced by a few morphological characters which are governed by many genes, but also environment to a great extent.

Understanding the association between yield and its components is of paramount importance for making the best use of these relationships in selection (Sarawgi *et al.*, 1997). The path coefficient analysis helps breeders to explain direct and indirect effects, and hence been extensively used in breeding experiments in different crop species (Ali *et al.*, 2003; Akbar *et al.*, 2003). Therefore, the present investigation was undertaken to assess the genetic variability, trait association, and path coefficient analysis in Indian mustard.

Materials and Methods

Experimental material and location

The experimental material consisted of 38 mustard genotypes including checks. These genotypes were evaluated during *rabi* 2019-20 at the experimental block, College of Agriculture, Bheemaranagudi, University of Agricultural Sciences Raichur following randomized block design with three replications. Each genotype was sown in three rows of 3 m length with row to row and plant to plant spacing of 0.45 m and 0.10 m respectively. All the recommended packages of practices were followed to raise a healthy

crop. Data on 10 traits were recorded on five randomly selected competitive plants from each genotype.

Statistical analysis

The statistical data of sampled plants were averaged to get mean values. The character means for each replication were then utilized for various statistical analyses following standard usual statistical procedure adopted to calculate mean, range, standard error, coefficient of variation and critical difference using Windostat version 9.2. Based on means and variances, different genetic parameters were calculated.

The analysis of variance (ANOVA) was calculated as per the procedure given by Panse and Shuklatme (1967). Phenotypic and genotypic variances were estimated by using the formula given by Johnson *et al.*, (1955). Genotypic and phenotypic coefficients of variation were estimated by using the formula (Burton, 1952). Broad sense heritability was calculated by using the formula suggested by Singh and Chaudhary (1985). Genetic advance was estimated by using the formula recommended by Allard (1960). Genetic advance in per cent of mean was estimated by the formula given by Comstock and Robinson (1952).

Results and Discussion

Analysis of variance

Analysis of variance (ANOVA) revealed that the mean sum of squares due to genotypes were highly significant for all the characters studies indicating the existence of ample variability among the genotypes studied (Table 1). This finding was in confirmation with the findings of Singh *et al.*, (2013), Tripathi *et al.*, (2013) and Shekhawat *et al.*, (2014).

Genotypic and phenotypic coefficient of variation

Genetic parameters of variation for seed yield and its components in Indian mustard are presented in Table 2. Genotypic coefficient of variation and phenotypic coefficient of variation were categorized as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Sivasubramaniam and Madhavamenon (1973). Phenotypic coefficients of variation (PCV) in general, were higher in magnitude than the genotypic coefficient of variation (GCV) indicating that all characters under investigation were influenced by environmental factors. Characters, siliquae per plant (38.71%, 56.39%) and secondary branches per plant (20.03%, 38.16%) recorded the high GCV and PCV estimates while, days to physiological maturity exhibited lower magnitude of coefficient at both GCV (04.74%) and PCV (06.21%) levels. The high GCV and PCV estimates indicated that the minimum influence of environment and lower magnitude of GCV and PCV revealed the fixation of recessive genes and thus increasing homozygosity within the genotype and breeders should go for source having high variability for improvement of these characters. Earlier, high GCV and PCV estimates were reported by Akbari and Niranjana (2015) for siliquae per plant, Lodhi *et al.*, (2014), Singh *et al.*, (2013) and Tripathi *et al.*, (2013) for secondary branches per plant. Similarly, low GCV and PCV estimates for days to physiological maturity were reported by Singh *et al.*, (2013), Lodhi *et al.*, (2014) and Semahegn and Tesfaye (2016).

The moderate estimates of GCV and PCV were recorded for siliqua length (12.72%, 15.10%) and 1000-seed weight (16.98%, 17.72%). These results are in confirmation with the results obtained by Lodhi *et al.*, (2014) and Singh *et al.*, (2013) for siliqua

length and Yadava *et al.*, (2011) and Singh *et al.*, (2013) for 1000-seed weight.

The characters days to 50% flowering (08.54%, 10.51%), plant height (09.01%, 14.45%) and seeds per siliqua (09.64%, 15.95%) recorded low and moderate GCV and PCV estimates, respectively. Character primary branches per plant registered a moderate and high GCV (14.85%) and PCV (29.86%) estimates, respectively. Earlier, Hussain *et al.*, (2016) reported low GCV and moderate PCV estimates while Lodhi *et al.*, (2014) and Singh *et al.*, (2013), respectively reported low GCV and moderate PCV estimates for days to 50% flowering. Similarly, Hussain *et al.*, (2016), Lodhi *et al.*, (2014) and Semahegn and Tesfaye (2016) reported low GCV whereas, Singh *et al.*, (2016) and Tripathi *et al.*, (2013) reported moderate PCV estimates for plant height. Hussain *et al.*, (2016), Singh *et al.*, (2013) and Yadava *et al.*, (2011) observed low GCV whereas, moderate PCV estimates were reported by Lodhi *et al.*, 2014, Singh *et al.*, (2013) and Tripathi *et al.*, (2013).

Moderate GCV and high PCV estimates were registered for number of primary branches and seed yield per plant. These results agree with Lodhi *et al.*, (2014) and Singh *et al.*, (2013) for number of primary branches. Singh *et al.*, (2013) reported moderate GCV and high PCV estimates and Hussain *et al.*, (2016) moderate GCV and Tripathi *et al.*, (2013) high PCV for seed yield per plant.

Heritability and genetic advance

An attempt was made to estimate the heritability in broad sense by variance component analysis in the present investigation. The prediction regarding this aspect was made based on percentage *viz.*, low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966). High heritability was recorded for 1000-seed

weight (91.80%) followed by siliqua length (71.00%). Higher heritability values revealed the presence of additive gene action and minimum influence of environment in expression of these characters. Selection based on these characters would be more effective compared to other characters, as it is an exploitable amount of variation. These findings are in line with the results of Singh *et al.*, (2013) for both the characters, Tripathi *et al.*, (2013) for 1000-seed weight and Lodhi *et al.*, (2014) for siliqua length.

The moderate heritability was observed for the character days to 50% flowering (66.00%) and days to physiological maturity (58.30%). However, the characters, siliqua per plant (47.10%), plant height (38.90%), seeds per siliqua (36.50%), secondary branches per plant (27.60%), primary branches per plant (24.70%) and seed yield per plant (16.70%) registered lower estimates of heritability. Lower heritability estimates indicate that these characters are governed by poly genes and progress in selection for these characters is generally slow as environmental influence is more in expression of such characters. These results are in confirmation with results of Hussain *et al.*, (2016) and Tripathi *et al.*, (2013) for days to 50 % flowering and Lodhi *et al.*, (2014) and Tripathi *et al.*, (2013) for days to physiological maturity. Similarly, Yadava *et al.*, (2011) observed lower estimates of heritability for siliqua per plant, plant height, seeds per siliqua, secondary branches per plant, primary branches per plant and seed yield per plant. Hussain *et al.*, (2016) reported lower estimates of heritability for plant height and siliqua per plant. Lower heritability estimates were reported by Singh *et al.*, (2013) for primary and secondary branches per plant.

The heritability value alone provides no information on the amount of genetic improvement that would be possible from

selection of superior genotypes and character exhibiting high heritability may not necessarily give high genetic advance. Therefore, knowledge about genetic advance coupled with heritability is most useful. The magnitude of genetic advance as percentage of mean was categorized as high (>20%), moderate (10% - 20%) and low (< 10%). Genetic advance as percentage of mean was observed high for siliqua per plant (207.22%) and moderate level for plant height (15.69%). While, rest of the characters *viz.*, days to 50% flowering (07.15%), days to physiological maturity (06.69%), secondary branches per plant (02.12%), seed yield per plant (01.86%), seeds per siliqua (01.33%), 1000-seed weight (01.27%), siliqua length (01.02%) and primary branches per plant (0.54%) recorded lower estimates. Earlier, Semahegn and Tesfaye (2016) reported lower estimates of GAM for days to 50% flowering, primary branches per plant, secondary branches per plant and seed yield per plant, Tripathi *et al.*, (2013) for days to 50% flowering and days to physiological maturity and moderate GAM for plant height. Lower estimates of GAM for were also reported by Hussain *et al.*, (2016) for days to physiological maturity, siliqua length and 1000-seed weight, Tiwari *et al.*, (2017) reported low and high GAM estimates respectively, for seeds per siliqua and siliqua per plant.

Panse and Shukatme (1954) stated that if non-additive gene action is involved in controlling a character, then character will show high heritability but low genetic advance whereas, if governed by additive gene action, heritability and genetic advance would be high. In the present investigation, high heritability estimates in broad sense coupled with low genetic advance as percent of mean was observed for siliqua length and 1000-seed weight indicating the presence of non-additive gene action and provide limited scope for

improvement through selection while, siliquae per plant recorded low heritability and high genetic advance as percent of mean.

Moderate estimates of heritability with lower genetic advance as percentage of mean values were recorded for days to 50 % flowering, days to physiological maturity. Plant height registered low heritability and moderate genetic advance as percentage of mean. Heritability and genetic advance as percentage of mean values for primary branches, secondary branches, seeds per siliqua and seed yield per plant were low. The results of present investigation are in line with findings of Swarnakar *et al.*, (2002) for days to 50% flowering, Lodhi *et al.*, (2014) for days to physiological maturity, Singh *et al.*, (2011) for plant height, Singh *et al.*, (2013) and Kumar *et al.*, (2013) for primary branches per plant, Singh *et al.*, (2013) and Mohan (2017) for secondary branches per plant, Kumar and Singh (2013) for seeds per siliqua, Singh *et al.*, (2013) for siliqua length and Semahegn and Tesfaye (2016) for 1000-seed weight.

Phenotypic and genotypic correlation coefficients

Correlation coefficient analysis is a statistical measure which is used to find out the degree and direction of association between two or more variables. Information on the degree and magnitude of association between characters is of prime importance for the breeder to initiate any selection plan. Phenotypic and genotypic correlation coefficients for all possible combination of characters are presented in (Table 3). In general, the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients.

Days to 50% flowering registered significant positive correlation with days to physiological

maturity (0.543: 0.842), number of primary branches per plant (0.345: 0.745) and number of secondary branches per plant (0.422: 0.972) at both genotypic and phenotypic levels. However, it exhibited significant but negative correlation with Seeds per siliqua (0.212) and Seed yield per plant (-0.705) at phenotypic and genotypic levels, respectively. Days to physiological maturity registered significant positive correlation with primary branches per plant (0.350) at phenotypic level and with Secondary branches per plant (0.390: 0.950) at both genotypic and phenotypic levels.

Plant height registered significant positive correlation with primary branches per plant (0.344) and seed yield per plant (0.708) at genotypic level only. Primary branches per plant registered significant positive correlation with secondary branches per plant (0.793), siliquae per plant (0.295) and siliqua length (0.299) at phenotypic level and significant but negative correlation with seed yield per plant (-0.344) at genotypic level only. Secondary branches per plant registered significant positive correlation with siliquae per plant (0.347) and siliqua length (0.351) at phenotypic level and significant but negative correlation with seed yield per plant (-0.760) at genotypic level only.

Siliquae per plant registered significant negative correlation with siliqua length (-0.280: -0.694) and 1000-seed weight (-0.368: -0.600) at both phenotypic and genotypic levels and with seeds per siliqua (-0.515) at genotypic level only. Seeds per siliqua plant registered significant positive correlation with siliqua length (0.567: 0.780) at phenotypic and genotypic levels and only at phenotypic level with 1000-seed weight (0.206). Siliqua length registered significant positive correlation with 1000-seed weight (0.551: 0.682) at both phenotypic and genotypic levels.

Table.1 Analysis of variance for seed yield and its component traits in Indian mustard genotypes

Source of Variation	Degrees of freedom	Mean Sum of Squares									
		Days to 50% flowering (d)	Days to physiological maturity (d)	Plant height (cm)	Primary branches per plant (no.)	Secondary branches per plant (no.)	Siliquae per plant (no.)	Seeds per siliqua (no.)	Siliqua length (cm)	1000-seed weight (g)	Seed yield per plant (g)
Genotype	2	64.10**	67.24**	682.98**	1.69**	21.61**	88510.35**	5.47**	1.18**	1.28**	38.89*
Replication	37	32.31	134.53	963.05	2.03	627.96	72216.05	0.04	0.49	0.13	94.88
Error	74	09.37	12.94	234.90	0.85	10.09	24092.31	2.00	0.14	0.03	24.25

Note: * and ** significant at 5 and 1 per cent level of probability, respectively

Table.2 Genetic variability parameters for seed yield and its component traits in Indian mustard genotypes

Genetic Parameter	Range		Mean	Coefficient of variation			Heritability (broad sense)	Genetic Advancement	Genetic Advance as per cent of mean
	Minimum	Maximum		GCV	PCV	ECV			
Days to 50% flowering (d)	43.00	60.00	49.96	08.54	10.51	06.13	66.00	14.31	07.15
Days to physiological maturity (d)	80.00	98.00	89.68	04.74	06.21	04.01	58.30	07.46	06.69
Plant height (cm)	108.00	168.00	135.62	09.01	14.45	11.30	38.90	11.57	15.69
Primary branches per plant (no.)	02.00	05.00	03.56	14.85	29.86	25.91	24.70	15.22	0.54
Secondary branches per plant (no.)	06.00	17.00	09.78	20.03	38.16	32.47	27.60	21.67	02.12
Siliquae per plant (no.)	209.00	1089.00	378.54	38.71	56.39	41.00	47.10	54.74	207.22
Seeds per siliqua (no.)	07.00	14.00	11.14	09.64	15.95	12.71	36.50	11.99	01.33
Siliqua length (cm)	01.40	05.32	04.63	12.72	15.10	08.13	71.00	22.07	01.02
1000-seed weight (g)	01.40	04.88	03.80	16.98	17.72	05.07	91.80	33.52	01.27
Seed yield per plant (g)	04.56	20.10	11.36	19.43	47.49	43.33	16.70	16.38	01.86

Note: GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation and ECV= Environmental coefficient of variation

Table.3 Phenotypic and genotypic correlation coefficients for seed yield and its component traits in Indian mustard genotypes

Character		Days to physiological maturity	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seeds per siliqua	Siliqua length	1000-seed weight	Seed yield per plant
Days to 50% flowering	P	0.543***	-0.079	0.345**	0.422**	0.083	-0.212*	0.032	0.024	-0.298
	G	0.842**	-0.213	0.745**	0.972**	0.245	-0.219	0.066	0.009	-0.705**
Days to physiological maturity	P		0.158	0.350**	0.390**	0.070	-0.079	0.088	0.117	-0.150
	G		0.224	1.084	0.950**	0.158	-0.0003s	0.202	0.172	-0.115
Plant height	P			0.058	-0.003	-0.04	0.041	0.078	-0.02	0.304
	G			0.344*	-0.163	-0.113	0.036	0.111	-0.019	0.708**
Primary branches per plant	P				0.793**	0.295**	0.071	0.299**	0.029	0.319
	G				1.030	0.228	-0.144	0.272	0.071	-0.344*
Secondary branches per plant	P					0.347**	0.155	0.351***	0.088	0.254
	G					0.010	-0.064	0.345*	0.195	-0.760**
Siliquae per plant	P						-0.092	-0.280**	-0.368**	0.452
	G						-0.515**	-0.694**	-0.600**	0.32
Seeds per siliqua	P							0.567**	0.206*	0.241
	G							0.780**	0.318	-0.062
Siliqua length	P								0.551**	0.036
	G								0.682**	-0.188
1000-seed weight	P									0.021
	G									0.017

Note: P= Phenotypic level, G= Genotypic level, * and ** significant at 5 and 1 per cent level of probability, respectively

Table.4 Phenotypic path matrix for seed yield and its component traits in Indian mustard genotypes

Character	Days to 50% flowering	Days to physiological maturity	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seeds per siliqua	Siliqua length	1000-seed weight
Days to 50% flowering	-0.288	-0.156	0.022	-0.099	-0.127	-0.023	0.061	-0.009	-0.007
Days to physiological maturity	-0.118	-0.219	-0.034	-0.076	-0.085	-0.015	0.017	-0.019	-0.025
Plant height	-0.026	0.052	0.331	0.019	-0.001	-0.013	0.013	0.025	-0.006
Primary branches per plant	0.118	0.120	0.019	0.345	0.273	0.101	0.024	0.103	0.009
Secondary branches per plant	0.033	0.029	-0.002	0.060	0.076	0.026	0.011	0.026	0.006
Siliquae per plant	0.036	0.030	-0.017	0.128	0.151	0.435	-0.040	-0.121	-0.16
Seeds per siliqua	-0.052	-0.019	0.010	0.017	0.038	-0.022	0.246	0.139	0.050
Siliqua length	-0.008	-0.024	-0.021	-0.082	-0.096	0.077	-0.156	-0.276	-0.152
1000-seed weight	0.007	0.035	-0.006	0.008	0.026	-0.112	0.062	0.168	0.305
Seed yield per plant	-0.298	-0.150	0.304	0.319	0.254	0.452	0.241	0.036	0.021
r value	0.086	0.032	0.100	0.110	0.019	0.196	0.059	-0.010	0.006

In the present investigation, seed yield per plant registering significant and positive correlation only with plant height at genotypic level indicates that direct selection for seed yield would be effective. This finding agrees with results of Akbari and Niranjana (2015) and Afrin *et al.*, (2011).

However, seed yield per plant recording negative correlation with days to 50% flowering at both levels signifies the fact that early flowering leads early maturity and reducing the duration of photosynthates accumulation in the plants and resulting in reduced yield levels. Previously, Shekhawat *et al.*, (2014) reported negative correlation between seed yield per plant and days to 50% flowering at genotypic level. Character, days to 50% flowering registered significant positive correlation with days to physiological maturity at both genotypic and phenotypic level indicating that earlier the flowering shorter would be maturity duration. These results confirm the earlier findings of Ara *et al.*, (2013), Bind *et al.*, (2014) and Shekhawat *et al.*, (2014).

Plant height and primary branches per plant have significant and positive correlation at genotypic level indicating the taller the plant more will be the branches. These results are in accordance with findings of Bind *et al.*, (2014), Akbari and Niranjana (2015) and Afrin *et al.*, (2011). Significant and positive association between seeds per siliqua and siliqua length revealed the fact that larger the siliqua length greater will be seed number. 1000-seed weight and siliqua length have significant and positive correlation at genotypic and phenotypic level.

These findings are in accordance with reports of Bind *et al.*, (2014) at genotypic and phenotypic levels and Tantuway *et al.*, (2018) at genotypic level only.

Phenotypic path coefficient analysis

Direct effects

Results of phenotypic path coefficient exhibited positive direct contribution of plant height (0.331), primary branches per plant (0.345), siliquae per plant (0.435), seeds per siliqua (0.246) and 1000-seed weight (0.305) towards seed yield per plant (Table 4). These results indicate the importance of these characters in governing seed yield per plant. The positive direct contribution of these characters observed for seed plant in this study are in confirmation with findings of Mahak *et al.*, (2011) for plant height; Bind *et al.*, (2014) for seeds per siliqua; Mahak *et al.*, (2011) and Bind *et al.*, (2014) for 1000-seed weight; Bind *et al.*, (2014) for primary branches per plant.

Characters, days to 50% flowering, days to physiological maturity and siliqua length had negative direct effect on seed yield per plant. These results are in confirmation with findings of, Shekhawat *et al.*, (2014) for days to 50% flowering; Bind *et al.*, (2014) and Mahak *et al.*, (2011) for days to physiological maturity and Iqbal *et al.*, (2014) for siliqua length.

Indirect effects

Days to flowering exhibited highest positive effect *via* primary branches per plant (0.118) and lowest *via* 1000-seed weight (0.007). Similarly, highest negative effect was exhibited *via* siliqua length (-0.008) and lowest *via* days to physiological maturity (-0.118) Days to physiological maturity exhibited highest positive effect *via* number of primary branches per plant (0.120) and lowest *via* number of secondary branches per plant (0.029). Similarly, highest negative effect *via* siliqua length (-0.024) and lowest *via* days to 50% flowering (-0.156) was

recorded. Plant height recorded highest positive effect *via* days to 50% flowering (0.022) and lowest *via* seeds per siliqua (0.010). Highest negative effect was revealed by secondary branches per plant (-0.002) and lowest by days to physiological maturity (-0.034).

Number of primary branches exhibited highest positive effects *via* siliquae per plant (0.128) and lowest *via* 1000-seed weight (0.008) and highest negative effect *via* days to physiological maturity (-0.076) and lowest *via* days to 50% flowering (-0.099). Number of secondary branches exhibited highest positive effect *via* primary branches per plant (0.273) and lowest *via* 1000-seed weight (0.026).

Highest negative effect was exhibited by plant height (-0.001) and lowest by days to 50% flowering (-0.127). Number of siliquae per plant exhibited highest positive effect *via* siliqua length (0.077) and lowest *via* number of secondary branches (0.026) and highest negative effect *via* plant height (-0.013) and lowest *via* 1000-seed weight (-0.112).

Seeds per siliqua showed highest positive effect *via* 1000-seed weight (0.062) and lowest *via* number of secondary branches (0.011) similarly, highest negative effect *via* number of siliquae per plant (-0.040) and lowest *via* siliqua length (-0.156). Siliqua length exhibited highest positive indirect effect *via* 1000-seed weight (0.168) and lowest *via* plant height (0.025) and highest negative effect by days to 50% flowering (-0.009) and highest by number of siliquae per plant (-0.121). 1000-seed weight exhibited highest positive effect *via* seeds per siliqua (0.050) and lowest *via* secondary branches per plant (0.006) and highest negative effect *via* number of siliquae per plant (-0.16) and lowest *via* days to 50% flowering (-0.007) (Table 4).

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How to cite this article:

Saikrishna Akoju, B. Arunkumar, P. H. Kuchanur, Hasan Khan and Ayyanagouda Patil. 2020. Genetic Variability, Association and Path Analysis in Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] for Yield and its Component Traits. *Int.J.Curr.Microbiol.App.Sci.* 9(11): 1373-1384. doi: <https://doi.org/10.20546/ijemas.2020.911.162>