Assessment of Genetic Variability for Seed Yield and Related Traits in Some Mutant and Non-mutant Lines of Indian Mustard (*Brassica juncea* L.)

Abstract

A study was conducted to evaluate the genetic variability for seed yield and related traits in 29 genotypes of Indian mustardduring*Rabi* 2019-20 and *Rabi* 2020-21 at Experimental Farm, Department of Plant Breeding and Genetics, AAU, Jorhat. The genotypes comprised of 21 M_{4-5} mutant lines developed by gamma irradiation of the parent varieties TM-2 and PM-27, 5 newly developed F_{6-7} lines, and 3 check varieties (TM-2, PM-27 and NRCHB-101). Pooled analysis of variances over the years revealed significant variation for most of the characters observed. The characters seed yield per plant, number of primary branches per plant and number of secondary branches per plant exhibited moderate genetic variation. Moderate heritability coupled with high genetic advance was observed for number of secondary branches per plant whereas, number of primary branches per plant showed high heritability with moderate genetic advance. The genotypes JMM-TM2-17, JMM-TM2-15, JMM-TM2-34, JMM-TM2-10, JMM-PM27-1, JM13-6 and the variety NRCHB-101 were found promising for most of the yield attributing characters. The mutant line JMM-TM2-28 and recombinant line JM13-4 may be exploited for the development of early-maturing mustard varieties.

Key words:*Brassica juncea*, mutant lines, genetic variability, seed yield, early maturity.

Introduction

Oilseeds form the second-largest agricultural commodity after cereals and play a vital role in the Indian agricultural economy. In India, oilseed brassicas, also referred to as rapeseed-mustard, ranks second after soyabean and account for 24 percent of oilseeds acreage and 25 percent of total oilseed production in the country (Jat *et al.*, 2019). Rapeseed-mustard comprises of different species of the family Brassicaceae viz., *Brassica juncea* (Indian mustard), *Brassica rapa* L. var. toria (Toria), *Brassica rapa* L. var. yellow sarson (Yellow sarson), *Brassica rapa* L. var. brown sarson (Brown sarson), *Brassica napus* L. (Gobhi sarson), *Brassica carinata* A. Braun (Karan rai / Ethiopian mustard), *Brassica nigra* (Black mustard) and *Eruca sativa* (Taramira). Indian mustard is an amphidiploid (2n = 36, AABB) derived from the interspecific cross between *Brassica rapa* (2n = 20, AA) and *Brassica nigra* (2n = 16, BB).It grows well under well-conserved moisture conditions with cool, dry weather during the growing period and dry clear weather at the time of maturity. Young and tender parts of the plants are used as leafy vegetables and the stems and leaves as green fodder. Its oil is used for various purposes such as cooking, frying, preparation of pickles, medicines, hair oils, and in the tannery industry. The oil meal is used as cattle feed and manure. In India, rapeseed-mustard crops occupy 6.86 million hectares, produce 9.12 million tonnes of oilseeds with average productivity of 1331 kg/ha as in 2019-20(DACFW, 2020). Rajasthan, Madhya Pradesh, Uttar Pradesh, Haryana, West Bengal, and Assam contribute 86.72 percent of the area and 89.53 percent of production. In Assam, rapeseed-mustard are cultivated in 0.29 million hectares (4.30% of Indian acreage) produces 0.23 million tonnes (2.47% production) with an average yield of 773 kg/ha as in 2019-20 (DACFW,2020). Being a major Rabi crop, it has high potential to increase edible oil production with low production cost.In Assam, though toria is widely grown due to its short duration, the yield potential of toria is lower than that of Indian mustard. Therefore, the development of short-duration superior Indian mustard varieties is important to increase the oilseed production in the state. Towards this objective, efforts were made to develop some genotypes of Indian mustard by induction of mutations and by inter-varietal hybridization. In this experiment, the genetic variability in the mutant and non-mutant breeding lines of Indian mustard for seed yield and related traits was studied for further advancement of the lines.

Materials and Methods

The experiments were conducted during *Rabi* 2019-20 and *Rabi* 2020-21at the experimental farm of the Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat, Assam.Twenty-nine entries (Table 1) comprising of twenty-one M_4 mutant lines developed by gamma irradiation of the parent lines TM-2 and PM-27, five newly developed F_6 lines and three check varieties (TM-2, PM-27 and NRCHB-101) of Indian mustard were sown in randomized block design with three replications.

Phenological and morphological observations

A total of fourteen quantitative characters viz., days to 50% flowering in days (DF), days to maturity in days (DM), plant height at maturity in cm(PH), number of primary branches per plant (PBN), number of secondary branches per plant (SBN), main shoot length in cm (MSL), number of siliquae on main shoot (SMS), siliqua density on main shoot (SD), number of seeds per siliqua (SPS), number of flowers on terminal main shoot (TF), number of siliqua on terminal main shoot (TS), 1000-seed weightin g (TSW), percent oil content (OC) and total seed weight in g (SYP) were recorded.

Table 1. List of genotypes used in the study

Sl. No.	Line No.	Designation	Sl. No.	Line No.	Designation
	Mutant lines of TM-2			**Mutant lines of PM-27**	
1	15	JMM-TM2-15	**20**	1	JMM-PM27-1
2	17	JMM-TM2-17	**21**	11	JMM-PM27-11
3	38	JMM-TM2-38		**Newly-developed lines**	
4	34	JMM-TM2-34			
5	20	JMM-TM2-20	**22**		JM13-2
6	47	JMM-TM2-47	**23**		JM13-3
7	160	JMM-TM2-160	**24**		JM13-4
8	1	JMM-TM2-1	**25**		JM13-5
9	4	JMM-TM2-4	**26**		JM13-6
10	51	JMM-TM2-51		**Check varieties**	
11	22	JMM-TM2-22	**27**		TM-2
12	73	JMM-TM2-73	**28**		NRCHB-101
13	208	JMM-TM2-208	**29**		PM-27
14	28	JMM-TM2-28			
15	14	JMM-TM2-14			
16	23	JMM-TM2-23			
17	27	JMM-TM2-27			
18	10	JMM-TM2-10			
19	2	JMM-TM2-2			

Source of experimental materials: Dept. of Plant Breeding & Genetics, AAU, Jorhat.

Statistical analysis

Analysis of variance for individual characters in each environment (year) was done for randomized block design based on plot mean values following standard statistical procedures. Pooled analysis of variance of the two environments (years) for each character was carried out following Gomez and Gomez (1984). Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), and environmental variance (σ^2_e) were computed following Burton and Devane (1953). Heritability in broad-sense was estimated following Singh and Chaudhary (1979). The expected genetic advance was calculated for each character following Allard (1960), which was then expressed as percent of grand mean.

Results and discussion

Mean performance

The pooled analysis of variance of the two years showed that the effect of environments (years) was significant for all the characters except days to maturity and 1000-seed weight. Highly significant variation due to genotypes for all the characters was observed. This indicated the presence of good range of genetic variation in the populations for seed yield and yield-related traits. Significant genotype x year interactions were observed for all characters except days to 50% flowering and oil content. Similar significantgenotype x environment interactions were reported for various traits by Brar *et al.* (2007) and Gupta *et al.* (2021).

The mean performances of the genotypes are presented in Table 2 and 3. Over both the years, JM13-6 was found to be the tallest genotype (156.58 cm), with high number of siliquae on main shoot (46.17) and siliqua density (0.72/cm). JMM-TM2-15 was found to be the earliest in maturity (102.17days) with the highest number of siliquae on terminal shoot (14.93) and high seed yield per plant (12.96 g). JM13-2 was the earliest in days to 50% flowering (46.77 days). The highest number of primary branches per plant was observed in JMM-TM2-28 (7.90), while the highest number of secondary branches per plant was observed in JMM-TM2-4 (11.40). The longest main shoot was exhibited by JMM-TM2-10 (69.51cm), and the maximum number of flowers on terminal main shoot was observed in JMM-TM2-22 (18.9). The highest mean value for 1000-seed weight was recorded in JM13-3 (4.28 g) while, the highest oil content was exhibited by the variety NRCHB-101 (38.74%). Thus, the genotypes JMM-TM2-17, JMM-TM2-15, JMM-TM2-34, JMM-TM2-10, JMM-PM27-1, JM13-6, and NRCHB-101 were promising compared to the check varieties for all the characters except for oil content.

Genetic parameters

The estimates of phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance as percent of mean help to formulate an effective method for selection in genetic improvement (Swetha *et al.*, 2019). In the present study, the genetic parameters were estimated from the pooled analysis over the two years to determine the magnitude and nature of genetic variation present in the materials (Table4). Moderate genotypic coefficient of variation was observed in the number of primary branches per plant (18.30%), number of secondary branches per plant (18.23%), and seed yield per plant (10%). The highest phenotypic coefficient of variation was observed for number of primary branches per plant (27.72%), followed by number of secondary branches per plant (22.46%). Similar result was reported by Rout *et al.* (2019) for seed yield per plant, Swetha*et al.* (2019) for number of siliquae on main shoot and number of siliquae on terminal main shoot. Pandey *et al.* (2020) also reported high estimates of PCV and GCV for secondary branches per plant and primary branches per plant and moderate estimates of PCV and GCV for number of seeds per siliqua, siliquae on main raceme, seed yield per plant, and plant height.The characters oil content (82.5%) and 1000-seed weight (74.6%) exhibited high heritability indicated the presence of high amount of genetic effects. High heritability along with genetic advance as percent of means can effectively predict the response to selection (Singh *et al.*, 2019). Similar results were reported by Swetha *et al.* (2019); Tripathi *et al.* (2019); Singh *et al.* (2011); Acharya and Pati (2008) and Singh *et al.* (2003). Moderate heritability was observed for plant height (68.86 %), number of secondary branches per plant (65.84 %), number of siliquae on terminal shoot (59.21 %), number of siliquae on main shoot (52.96 %), siliqua density (52.68 %), seed yield per plant (44.75 %), days to maturity (44.34 %), number of primary branches per plant (43.58 %), and number of flowers on terminal shoot (40.76 %). Rout *et al.* (2019) also reported moderate heritability for seeds per siliqua and seed yield per plant. High estimate of genetic advance as percent of means was observed for number of secondary branches per plant (30.47%). Number of primary branches per plant showed

Table 2. Mean values for quantitative characters in Indian mustard

Genotypes	DF	DM	PH	PBN	SBN	MSL	SMS
JMM-TM2-15	47.33	102.17	132.92	4.30	8.43	60.88	36.67
JMM-TM2-17	46.50	103.17	135.18	7.27	7.40	67.59	40.27
JMM-TM2-38	48.83	104.50	121.54	4.50	8.37	55.81	30.20
JMM-TM2-34	48.67	104.83	132.95	5.17	10.57	65.90	41.50

JMM-TM2-20	50.00	107.67	137.77	4.03	7.13	69.46	38.13
JMM-TM2-47	48.33	105.50	121.64	3.70	6.50	62.08	35.80
JMM-TM2-160	49.00	105.33	120.14	4.27	7.77	60.18	32.63
JMM-TM2-1	50.67	106.00	141.74	4.93	7.63	65.60	39.13
JMM-TM2-4	49.17	103.50	130.76	4.83	11.40	62.51	37.13
JMM-TM2-51	48.50	107.17	117.87	4.17	6.47	55.08	35.30
JMM-TM2-22	48.33	106.17	142.60	4.40	6.47	67.78	37.67
JMM-TM2-73	49.83	107.17	129.43	4.43	8.70	63.36	37.27
JMM-TM2-208	50.17	105.33	141.68	4.60	6.90	67.95	40.10
JMM-TM2-28	48.67	105.00	140.83	7.90	8.83	67.09	41.60
JMM-TM2-14	47.33	105.17	124.57	3.87	7.03	57.14	32.40
JMM-TM2-23	48.33	104.33	128.87	4.13	8.10	61.46	34.97
JMM-TM2-27	50.33	105.17	135.73	4.30	8.57	65.33	34.83
JMM-TM2-10	50.83	107.00	150.94	4.87	8.20	69.51	39.17
JMM-TM2-2	50.50	106.83	142.44	4.40	10.93	58.84	36.77
JMM-PM27-1	49.33	104.67	139.18	4.93	9.38	61.13	39.07
JMM-PM27-11	51.17	105.50	146.84	4.33	8.80	63.29	39.93
JM13-2	42.33	105.67	132.58	4.30	7.33	62.41	39.35
JM13-3	51.17	107.00	144.35	4.70	6.63	62.54	36.83
JM13-4	47.00	104.00	139.99	4.10	6.03	66.53	39.27
JM13-5	51.50	107.83	144.60	4.17	7.00	62.67	40.57
JM13-6	54.17	108.00	156.58	4.60	8.30	66.11	46.17
TM-2	52.17	109.50	140.18	4.47	5.74	56.58	38.33
NRCHB-101	52.50	106.17	144.97	3.93	6.30	68.56	39.70
PM-27	50.67	104.67	138.97	4.30	5.13	59.45	38.63
Mean	49.43	105.69	136.48	4.61	7.80	63.20	37.91
SE(mean)	1.58	0.97	2.47	0.31	0.51	1.87	0.96
CD 5%	1.10	2.72	6.92	0.86	1.43	5.23	2.70
CD 1%	1.46	3.59	9.14	1.14	1.89	6.92	3.56
CD 5% (Yrs)	1.16	NS	1.82	0.23	0.38	1.37	0.71

Table 3. Mean values for quantitative characters in Indian mustard

Genotypes	SD	SPS	TF	TS	TSW	OC	SYP
JMM-TM2-15	0.61	13.87	16.63	14.40	4.05	35.28	12.96
JMM-TM2-17	0.61	11.47	17.20	13.60	4.08	35.34	9.54
JMM-TM2-38	0.56	12.80	15.30	10.33	3.30	36.84	9.59
JMM-TM2-34	0.65	11.83	18.53	14.93	3.63	35.53	10.01
JMM-TM2-20	0.56	11.17	15.70	11.30	3.53	35.83	7.41

JMM-TM2-47	0.59	14.17	17.23	12.03	3.43	36.95	8.65
JMM-TM2-160	0.54	12.63	16.83	12.23	3.14	36.36	8.33
JMM-TM2-1	0.64	12.40	17.27	12.50	3.51	36.32	10.23
JMM-TM2-4	0.61	12.43	18.47	13.23	3.41	35.58	9.36
JMM-TM2-51	0.65	12.10	18.73	13.40	3.40	36.60	9.14
JMM-TM2-22	0.59	13.60	18.90	12.56	3.37	35.19	8.30
JMM-TM2-73	0.60	12.43	18.27	13.93	3.77	36.22	9.91
JMM-TM2-208	0.60	12.37	16.67	11.27	3.74	35.10	10.01
JMM-TM2-28	0.63	12.70	17.73	12.33	3.58	34.59	10.63
JMM-TM2-14	0.57	13.27	16.17	10.80	3.18	36.25	9.31
JMM-TM2-23	0.58	12.67	16.67	10.93	3.52	36.70	8.92
JMM-TM2-27	0.55	13.00	17.03	11.87	3.14	37.04	9.70
JMM-TM2-10	0.57	11.87	18.10	12.93	3.53	36.58	11.99
JMM-TM2-2	0.63	11.63	17.63	13.10	3.24	35.07	8.72
JMM-PM27-1	0.65	13.60	17.63	14.27	3.54	35.31	8.80
JMM-PM27-11	0.63	13.07	17.73	12.00	3.78	37.21	10.94
JM13-2	0.66	10.73	17.80	12.53	3.17	36.73	9.03
JM13-3	0.60	12.53	17.13	12.47	4.28	37.12	9.37
JM13-4	0.61	12.93	15.93	11.37	4.01	36.79	10.45
JM13-5	0.66	12.53	17.53	12.53	3.33	36.96	10.65
JM13-6	0.72	11.87	17.37	12.27	3.95	36.72	10.19
TM-2	0.69	12.80	17.17	11.87	3.70	36.63	9.40
NRCHB-101	0.59	13.37	17.43	11.67	4.11	38.74	10.49
PM-27	0.64	12.30	16.53	10.97	3.40	38.13	9.14
Mean	0.61	12.56	17.29	12.40	3.58	36.33	9.69
SE(mean)	0.02	0.34	0.46	0.52	0.11	0.39	0.56
CD 5%	0.06	0.96	1.28	1.45	0.30	1.10	1.58
CD 1%	0.07	1.27	1.69	1.92	0.40	1.46	1.86
CD 5% (Yrs)	0.01	0.25	0.34	0.71	NS	0.29	0.37

moderate genetic advance (24.89 %). Singh (2020), Kumar *et al.* (2020) and Tiwari *et al.* (2017) also reported high genetic advance for number of secondary branches per plant. High heritability coupled with high genetic advance indicates additive gene effects (Panse, 1957, Phukan *et al.* 2023) and therefore simple selection methods can be easily employed for improvement. High heritability with low genetic advance was observed for oil content and 1000-seed weight, which indicates the presence of non-additive genetic effects in the inheritance of these traits and for improvement programme, biparental mating could be effective.

Conclusion

In crop improvement programmes, mutation breeding has been playing an important role in development of promising cultivar within a short period of time (Gaul, 1961; Manjaya, 2009). Among the different mutagenic agents, irradiation has been successfully used for induced mutation breeding in various crops (Song and Kang, 2003, Malek *et al*., 2012). In the present investigation, it was observed that all the genotypes showed better results than the check varieties. For the advancement of the lines as early-maturing, the mutant line JMM-TM2-28 and recombinant line JM13-4 canbe exploited which is the primary goal of improvement of mustard in Assam.

Authors' contribution:

Conceptualization of research (PKB, SAD); Designing of the experiments (PKB, SAD); Contribution of experimental materials (PKB, SAD); Execution of field/ lab experiments and data collection (SAD); Analysis of data and interpretation (PKB, SAD); Preparation of manuscript (SAD, PKB, AP).

Declaration:

The authors declare no conflict of interest.

References:

Acharya N.N. and Pati P. 2008. Genetic variability, correlation and path analysis in Indian mustard (*Brassica juncea* L.). Environment and Ecology, **26**: 2165-2168.

Allard R.W. 1960. *In*: Principles of Plant Breeding. John Willey and Sons. Inc. New York.

Brar K.S, Mittal V.P. and Singh P. 2007. G×E interaction and stability of elite strains in Indian mustard (*Brassica juncea*Czern&Coss.). Crop Improvement, **34**(1):33-36.

Burton G.W. and Devane D.E. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy journal, **45**(10): 478-481.

DACFW 2020. Agricultural Statistics at a Glance (2020), Department of Agriculture, Cooperation and Farmers Welfare, Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare, Government of India. (https://eands.dacnet.nic.in/)

DRMR 2021. AICRP on Rapeseed-Mustard, Project Coordinator's Report 2020-21. Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan. (https://www.drmr.res.in/aicrp2021/DRMR-PC-Report-2021.pdf)

Gomez K.A. and Gomez A.A. 1984. *In*: Statistical procedures for agricultural research. John Wiley & Sons, New York.

Gaul H. 1961. Use of induced mutants in seed propagated species. *In*: Mutation and Plant Breeding. Nat Acad Sci, Nat Res Council USA ,206-252

Manjaya J.G. 2009. Genetic Improvement of Soybean Variety VLS-2 through Induced Mutations. *In*: Induced Plant Mutations in Genomics Era. Food and Agriculture Organization of the United States, 106-110

Song H.S, Kang S.Y. 2003. Application of Natural Variation and Induced Mutation in Breeding and Functional Genomics: Papers for International Symposium; Current Status and Future of Plant Mutation Breeding. Korean J Breed Sci., **35**(1): 24-34

Malek M.A., Begum H.A., Begum M., Sattar M.A., Ismail M.R. and Rafii M.Y. 2012. Development of two high yielding mutant varieties of mustard [Brassica juncea (L.) Czern.] through gamma rays irradiation. Australian Journal of Crop Science, **6**(5):922-927

Gupta M., Yadav R.D.S., Vimal S.C., Katiyar D. and Bhati J. 2021. Stability behaviour in Indian mustard (*Brassica juncea* L.). The Pharma Innovation Journal, **10**(4): 802-806

Jat R.S., Singh V.V., Sharma P. and Rai P.K. 2019. Oilseed brassica in India: Demand, supply, policy perspective and future potential. OCL, **26**: 8.

Kumar S.N., Janeja H.S., Talerkar N., Nandini D. and Kahan, F. 2020. Evaluation of germplasm for variability in breeding and seed yield traits in *Brassica juncea* (L.). Plant Cell Biotechnology and Molecular Biology, **20**(23-24): 1402-1407.

Panse V.G. 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet, **17**(2): 318-328.

Phukan A., Sarma R.N., Das R. and Barua P.K. 2023. Genetic analysis of adaptive and physiological traits in response to high temperature stress in rapeseed. Indian J. Genet. Plant Breed., **83**(2): 224-234.

Rout S., Sur B., Sadhu S., Ghimiray T.S., Mondal H.A., Hijam L.,Chakraborty M. and Roy S.K. 2019. Traits association, cause and effect analyses in Indian mustard [*Brassica juncea* (L.) Czern&Coss]. Electronic Journal of Plant Breeding, **10**(4): 1482-1494.

Singh J. 2020. Correlation and path studies for seed yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern&Coss.]. Int. J. Curr. Microbiol. App. Sci., **9**(09): 620-626.

Singh M., Srivastava R.L., Prasad L. and Dixit R.K. 2003. Studies on heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Advances in Plant Sciences, **16**(1): 263-266.

Singh R.K. and Chaudhary B.D. (1979). *In*: Biometrical method in quantitative genetic analysis 2nd edition, Kalyani Publishers, Ludhiana, New Delhi, India.

Singh T., Kumar M. and Pathania M. 2011. Genetic variability and character association analysis over environments in Indian mustard (*Brassica juncea* (L.) Czern&Coss). Indian Journal of Agricultural Research, **45**(1): 30-37.

Singh V.K., Sen R., Kumar N., Saini R.K. and Singh S.P. 2019. Genetic variability parameters studies in mustard (*Brassica juncea*Czern&Coss). Journal of Pharmacognosy and Phytochemistry, **8**(4): 2142- 2144.

Swetha M., Janeja H.S., Singh H., Sravani M., Rajaneesh K. and Madakemohekar A.H. 2019. Genetic evaluation of Indian mustard (*Brassica juncea* L.) genotypes for yield and quality parameters. Plant Archives, **19**(1): 413- 417.

Tiwari A.K., Singh S.K., Tomar A. and Singh M. 2017. Heritability, genetic advance and correlation coefficient analysis in Indian mustard (*Brassica juncea* (L.) Czern&Coss). Journal of Pharmacognosy and Phytochemistry, **6**(1): 356-359.

Tripathi A., Singh M. and Tomar A. 2019. Selection parameter analysis in Indian mustard (*Brassica juncea*) germplasm under normal sown condition. Journal of Pharmacognosy and Phytochemistry, **8**(1): 1551-1553.

Table 4. Genetic parameters for different characters in Indian mustard estimated from the pooled analysis of variance over two years

Characters	Mean	Range	GCV (%)	PCV (%)	h^2 (%)	GAM (%)
Days to 50% flowering	49.43±1.58	42.33-54.17	3.14	5.00	48.92	4.52
Days to maturity	105.69±0.97	102.17-109.50	1.21	1.73	48.34	1.73
Plant height (cm)	136.48±2.47	117.87-156.58	6.67	8.03	68.86	11.40
Number of primary branches/plant	4.61±0.31	3.70-7.90	18.30	27.73	43.58	24.89
Number of secondary branches/plant	7.80±0.51	5.13-11.40	18.23	22.46	65.84	30.47
Main shoot length (cm)	63.20±1.87	55.08-69.51	5.86	9.88	35.13	7.15
Number of siliquae on main shoot	37.91±0.96	30.20-46.17	7.96	10.93	52.96	11.93
Siliqua density (no./cm)	0.61±0.02	0.54-0.72	6.19	8.53	52.68	9.25
Seeds per siliqua	12.56±0.34	10.73-14.17	5.68	7.28	60.82	9.13
Number of flowers on terminal main shoot	17.29±0.46	15.30-18.90	4.38	6.86	40.76	5.76
Number of siliquae on terminal main shoot	12.40±0.52	10.33-14.93	8.17	10.62	59.21	12.95
1000-seed weight (g)	3.58±0.11	3.14-4.28	8.37	9.69	74.57	14.89
Oil content (%)	36.33±0.39	34.59-38.74	2.36	2.59	82.54	4.41
Seed yield/plant (g)	9.69±0.56	7.41-12.96	10.00	14.95	44.75	13.78