EVALUATION OF INDUCED GENETIC VARIABILITY IN GAMMA RAY IRRADIATED RAPESEED MUTANTS

M.S.H. Bhuiyan[1]*, R.M. Emon[1], M.K. Khatun[1], M.A. Malek[2] and N.A. Khan[3]

Abstract

Bangladesh is suffering from a severe lack of edible oil. As a result, we import oil and oilseeds to overcome the shortage. To select the superior rapeseed mutants an experiment was conducted with thirteen mutants following randomized complete block design. The mutants showed significant genetic variation for most of the characters. Phenotypic variations were higher than genotypic variances for the majority of the traits, the high genotypic coefficient of variation value was also observed for seed yield, number of seeds siliqua^{-1} and number of siliqua plant^{-1}. Number of seeds siliqua^{-1} exhibited the highest value of heritability followed by plant height while siliqua length exhibited the lowest value of heritability. Path co-efficient analysis revealed that number of branch plant^{-1}, siliqua length, number of siliqua plant^{-1}, and number of seed siliqua^{-1} had a direct positive effect on yield. Considering the yield performance genotypes RNM-8, RNM-18, RNM-20 and RNM-33 might be recommended for future varietal improvement program of rapeseeds.

Key words: Rapeseed, Mutants, Genetic Variability, Correlation coefficient, Path coefficient analysis and Yield performance

Introduction

Mustard (*Brassica napus*) a member of the Brassicaceae family, is the most important edible oil crop in Bangladesh. We need to spend a significant amount of foreign currency to import edible oil. After soybeans and groundnuts, mustard is one of the most important oil crops in the world (www.fao.org). Mustard oil meets the country's one-third edible oil demand as noted by Ahmed (2008). It is used as a condiment, salad, green manure, fodder crop, and the leaf and stem are used as a vegetable in the many mustard cultivating regions. Its oil is also utilized as a green biofuel, an ingredient in animal feed and a key component in a variety of chemical and pharmaceutical applications (Huang *et al.,* 2016). After oil extraction, the by product from rapeseeds provides a protein-rich (38-44%) animal feed. Oilseed rape may be regarded as an alternate source of protein instead of soya in subtropical monsoon region such as Bangladesh, due to its nutritional benefits. This meal has a good amino acid profile, with a high concentration of sulfur containing amino acids, methionine and cysteine. Furthermore, the meal is high in minerals including calcium, magnesium, and phosphorus, as well as vitamins B4 and E (Bocianowski *et al.,* 2011).

[1]Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, BAU Campus, Mymensingh-2202
[2]Director (Research), Bangladesh Institute of Nuclear Agriculture, BAU Campus, Mymensingh-2202
[3]Biotechnology Division, Bangladesh Institute of Nuclear Agriculture, BAU Campus, Mymensingh-2202
*Corresponding author's email: saikat.ag88@gmail.com

Meeting the ever-increasing demand for high-quality human food and animal feed is a challenge for academics, farmers and food producers. Variety plays an important role for the yield of mustard, because different varieties perform differently for their genotypic characters. Improved variety is the first and foremost requirement for initiation and acceleration crop production program. High yielding varieties (HYVs) can contribute to getting optimum yield as well as the highest percentage of oil. The presence of genetic variability in the gene pool for high yielding diverse economic features is required for the development of a successful breeding program. Induced mutation is a common source of creating genetic variation. The most common method of mutation induction is gamma rays, which account for 64% of all radiation-induced mutant types. Induced mutation has been employed to improve a variety of crops, including oilseeds, with great success. More variability of rapeseed germplasms can be created via mutagenesis (Amosova *et al.,* 2019). Understanding the level of variability existing in a population is critical to determine the best breeding approach for improving trait (s). Traits connected with yield component, can be employed as the greatest guidance for successful indirect selection for yield improvement. With genetic variability, there must be a thorough knowledge of inheritance, kind of gene action and the relative magnitude for most of yield contributing characters. So in the context of the above mentioned situation, the present work was undertaken to select elite mutant genotypes to utilize in future breeding programs.

Material and Methods

Plant Materials and Experimental Design

The studied mutants were derived from a gamma ray irradiated local rapeseed germplasm collected from Nachol (Rajshahi). The list of mutants derived from collected germplasm is given in Table 1. The experiment was carried out at BINA Headquarters farm, Mymensingh following a randomized complete bock design (RCBD) with 3 replications in 2019.

Table 1. List of rapeseed genotypes used in this study

Genotype	Doses of gamma rays	Source	Genotype	Doses of gamma rays	Source
RNM-3	500 Gy	BINA	RNM-22	700Gy	BINA
RNM-5	500 Gy	BINA	RNM-27	700Gy	BINA
RNM-7	600 Gy	BINA	RNM-33	700Gy	BINA
RNM-8	600 Gy	BINA	RNM-35	700Gy	BINA
RNM-10	600 Gy	BINA	RNM-66	700Gy	BINA
RNM-18	800Gy	BINA	BARI Sarisha-14	Check	BINA
RNM-20	800Gy	BINA	Nachoal (Local)	Parent	BINA
RNM-21	700Gy	BINA			

The unit plot size was 10 m with 10 rows and line to line and plant to plant distances were 30 cm and 5 to 7cm, respectively. The recommended fertilizers and cultural practices

were done to maintain a healthy crop growth. The harvesting was done separately for each genotype when 80% of plants were matured.

Data Collection

The data were recorded from 10 randomly selected plants for days to maturity, plant height (cm), number of branches plant[-1], number of siliquae plant[-1], siliqua length (cm), number of seeds siliqua[-1], and seed yield.

Statistical Analysis

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.,* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhury (1985). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Correlation coefficient analysis was done by the formula proposed by Miller *et al.,* (1958). Path coefficient analysis was performed according to the method described by Dewey and Lu (1959).

Result and Discussion

The analysis of variance (ANOVA) revealed the existence of significant variations for days to maturity, plant height, number of siliquae plant[-1], number of seeds silique[-1] and seed yield among 15 rapeseed genotypes (Table 2). This suggests that there is an opportunity for the genetic improvement of rapeseed for these traits by using mutation techniques.

Table 2. Estimation of genetic parameters for 11 characters among 15 genotypes in rapeseed

Traits	GMS	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	$h^2 b$	GA	GA(%)
Maturity	24.85**	3.5	17.7	2.24	4.99	20.18	1.79	2.08
Plant height (cm)	196.38*	34.09	128.19	6.12	11.87	26.60	6.2	6.5
Number of branch plant[-1]	0.89	0.11	1.12	7.26	22.93	10.03	0.22	4.74
Number of siliqua plant[-1]	605.26**	66.88	471.49	11.57	30.73	14.19	6.3	8.9
Siliqua length	0.55	0.04	0.56	1.18	14.36	9.66	0.105	2.14
Number of seed siliqua[-1]	4.89**	8.14	14.42	13.42	17.85	56.49	4.42	20.78
Yield (kg/ha)	163724*	26024.2	111674.28	13.13	27.21	23.3	60.42	13.06

** = Significant at 1%; * = Significant at 5%.

GMS = Genotypic mean sum of Square, $\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, GCV = Genotypic coefficient of variation and PCV = Phenotypic coefficient of variation $h^2 b$ = heritability and GA= Genetic advance.

The higher phenotypic variance ($\sigma^2 p$) compared to the genotypic variance ($\sigma^2 g$) for the studied traits indicates the prevalence of environmental effect on the phenotypic expression of these traits (Table 2). The higher $\sigma^2 g$ was found for seed yield (kg ha^{-1}), number of siliquae plant[-1] and plant height followed by number of seeds siliquae[-1] and maturity period, where as lower $\sigma^2 g$ was found for siliqua length followed by number of

branch plant[-1]. The results indicate the presence of high genetic variability for these traits. There were differences between PCV and GCV for almost all characters. Highest GCV (13.13) and PCV (27.21) were shown for seed yield followed by number of siliqua plant[-1] and number of seed siliqua[-1]. It's indicating that a greater amount of genetic variability is present for this characters which provide greater scope for selection followed by number of branch plant[-1] and plant height. Lowest values GCV (1.18) and PCV (14.36) were obtained from siliqua length followed by maturity values indicating the limited scope for improvement by selection. For maturity period lowest GCV and PCV were also observed by Aradhana *et al.,* (2003) and Bhuiyan *et al.,* (2019). Broad sense heritability estimates ranged from 9.66 to 56.49% for all characters. Highest values were obtained from number of seed siliqua[-1], plant height and maturity and lowest value was found for the siliqua length. In order to estimate the selection effects, heritability accompanied with genetic advance is rather useful than heritability alone. Heritability and genetic advance were maximum for seed yield (kg ha^{-1}), number of seed siliqua[-1] and plant height. Thus suggests that these traits under additive genetic control and selection might be effective for these traits. Like this study Zare and Sharafzadeh (2012) also found low broad sense heritability for siliqua length in rapeseed. High heritability with high genetic advance for number of siliquae plant[-1] reported by Sadat *et al.,* (2010) also support our result. High heritability for number of seeds per siliqua was observed by Yadava *et al.,* (1993). Aytac and Kinaci (2009) mentioned the high heritability and genetic advance for seed yield selection for this character would be effective. Yield is a complex trait and controlled by polygene's and very often influenced by environment. Therefore, phenotypic selection based only on yield is not effective. Correlation and path co-efficient pave the way to select plant for breeding purpose by the plant breeders. Genotypic and phenotypic correlation coefficients among 6 characters are presented in Table 3.

Table 3. Genotypic (r_g) and phenotype (r_p) correlation coefficients among different pairs of yield and yield contributing characters for different genotype of mustard

Traits		PH	NBP	NSP	SL	NSS	Yield
DM	r_g	0.5896**	-0.1948	-0.3974	-0.087**	0.4938**	0.4544**
	r_p	0.5485**	-0.2798	-0.03	-0.5596**	0.6391**	0.3947**
PH	r_g		0.2145	0.5389*	-0.5674	0.6765	0.1978
	r_p		0.1776	0.3702 *	-0.1656	0.5772 **	0.1883
NBP	r_g			0.0684**	0.766**	0.6668**	0.134**
	r_p			0.4843**	0.6901**	0.4823 **	0.5456 **
NSP	r_g				0.3333	0.1064	0.463**
	r_p				0.1961	0.0741	0.806**
SL	r_g					0.8552 **	0.0528 **
	r_p					0.2624 **	0.8111 **
NSS	r_g						0.994 **
	r_p						0.604 **

** = Significant at 1%; * = Significant at 5%.

DM = Days to maturity, PH = Plant height (cm), NBP = Number of branches per plant, NSP = Number of siliqua per plant, NSS = Number of seed per siliqua, SL = Siliqua length

In most instances, there was a close agreement between genetic correlations and phenotypic correlations. The genotypic correlations were higher than phenotypic correlations for all the studied traits that indicate the minimum influence of environments for the expression of those characters. Seed yield had a highly significant positive correlation with days to maturity, number of branches plant[-1], number of siliqua plant[-1], siliqua length and number of seeds silique[-1].

Among these, number of seeds siliqua[-1] and number of siliqua plant[-1] have highly significant and strong positive correlation with seed yield at both levels suggests the high degree of association between these traits. Malik *et al.,* (200) and Jeromela *et al.,* (2007) reported positive correlation between siliqua plant[-1] and seed yield. Rameeh (2015) reported that number of seeds siliqua[-1] was positively correlated with seed yield. As genetic correlation coefficient was higher than phenotypic correlation coefficient, it reveals that the apparent association of two characters is mainly due to genetic effects. The direct and indirect effects of yield contributing traits on seed yield were analyzed by path analysis. Seed yield per plant was considered as effect (dependent variable) while remaining traits were treated as causes (independent variables) and shown in Table 4.

Table 4. Path coefficient analysis showing indirect effects of different characters on yield of mustard

Traits	DM	PH	NBP	NSP	SL	NSS	r_g with Yield
DM		-0.288	0.025	0.510	0.698	0.997	-0.17
PH	-0.323		0.007	0.408	0.282	0.913	0.01*
NBP	0.294	0.075		-0.620	0.212	-0.927	-0.06
NSP	0.744	0.531	0.079		0.651	1.681	0.03**
SL	0.849	0.389	0.102	-0.465		-0.360	-0.21**
NSS	0.486	0.394	0.039	0.557	0.469		0.014**
Residual Effect = 0.211							

**, * indicates significant at the 0.01 and 0.05 level, respectively.
DM = Days to Maturity, PH= Plant height (cm), NBP= Number of primary branches plant[-1]
NSP= Number of siliqua plant[-1], SL= Siliqua length, NSS= Number of seed siliqua[-1]

The results showed that number of siliqua plant[-1] had maximum direct effect (Fig. 1) followed by number of seeds siliqua[-1] on seed yield. Number of siliqua plant[-1] had a positive indirect effect to all the traits and finally this trait had a highly significant positive correlation with number of seeds siliqua[-1].
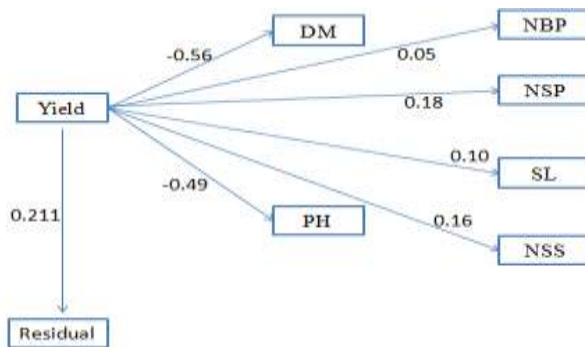

Fig. 1. Path coefficient analysis showing direct and effects of different characters on yield of mustard

Similarly, number of seeds siliqua[-1] had a positive indirect effect via all the traits and have strong positive correlation with number of siliqua plant[-1]. These results indicate that the correlation is mainly due to the direct effect of a character and it was realized via indirect positive and negative effects. It reveals the true relationship between them and direct selection for this trait will be rewarding for the genetic improvement of yield. Sharafi *et al.,* (2015) found the number of siliqua plant[-1] had the highest direct effect on seed yield. They also reported that number of seeds siliqua[-1] had direct positive effect on yield per plant. On the contrary, a negative direct effect for seeds siliqua[-1] on seed yield per plant has been reported by Basalma (2008). The value of residual effect was 0.211. It indicated that beside the component characters, there was an influence of some other attributes (approx. 21.1%) on seed yield.
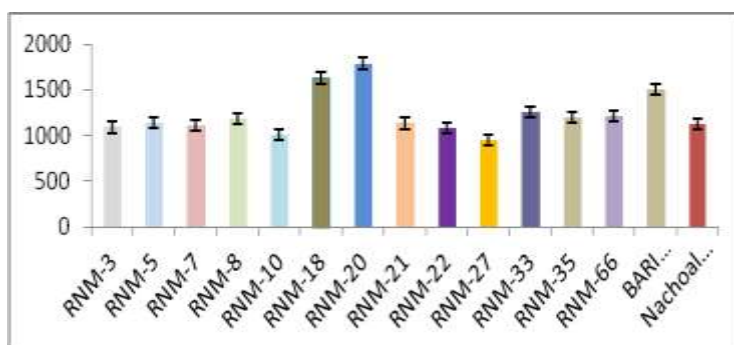

Fig. 2. Yield performance of rapeseed mutants and varieties

The mutants RNM-20 produced the highest seed yield of 1789 kgha[-1] followed by RNM-18 (1630 kgha[-1]) and BARI Sarisha-14 (1505) (Fig. 2). Lowest seed yield was reported from RNM-10 and RNM-27. Mother variety Nachoal (Local) produced the yield of 1127 kg ha^{-1}. In rapeseed-mustard and other oilseed mutants having higher seed yield over mother varieties also reported by Akter *et al.,* 2020 and Mondal *et al.,* 2020.

Conclusion

By selecting high yielding genotypes, there is a lot of room to increase production. We know that yield attribute characteristics like siliqua plant[-1] and seeds siliqua[-1] might improve seed yield. Various genotypes differ in their yield regulating characteristics which play an essential role in yields of rapeseed and mustard. It was observed that among the mutants and mother variety mutants RNM-8, RNM-18, RNM-20 and RNM-33 performed better for seed yield and yield contributing characters which can be selected for further multi locational yield trials. Moreover, this study suggests that for rapeseed or mustard improvement breeding program, researcher needs to consider the characters like seed siliqua[-1] and siliqua plant[-1]. It also concludes that gamma rays irradiation can be fruitfully applied to induce mutations in rapeseed with higher seed yield and other improved agronomic traits.

6

References

Ahmed, M. 2008. Results of farm level socio-economic study on mustard production. Bangladesh J. Agril. Res. 13(1): 20-23.

Akter, S.E., Malek, M.A., Hossain, B.M., Akondo, R.I., Islam, M. and Bhuiyan, M.S.H. 2020. Selection of promising rapeseed mutants on the basis of morphology and yield attributes. International Journal of Chemical Studies, 8(3): 2171-2174.

Aytac, Z. and Kinaci, G. 2009. Genetic variability and association studies of some quantitative characters in winter rape seed (*Brassica napus* L.). African J. Biotech. 8(15): 3547-3554.

Aradhana, J.C. and Singh, J.P. 2003. Studied on genetic variability in tomato. Prog Hort 35: 179-182.

Basalma, D. 2008. The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus ssp. oleifera* L.) cultivars. Res. J. of Agric. Bio. Sci. 4(2): 120-125.

Bhuiyan, M.S.H., Malek, M.A., Sarkar, M.A., Islam, M. and Akram, W.M. 2019. Genetic variance and performance of sesame mutants for yield contributing characters. Malaysian Journal of Sustainable Agriculture, 3(2): 27-30.

Bocianowski, J. and Liersch, A. 2021. Multi-environmental evaluation of winter oilseed rape genotypic performance using mixed models. Euphytica . 217:80.

Burton, G.W. 1952. Quantitative inheritance in grass pea. Proc. of the 6th Int. Grassland Cong. Pennsylvania, USA. 1952; pp. 277-283.

Dewey, D.R. and Lu, K.A. 1959. Correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron. J. 51: 515-518.

Dong, Y.S., Zhuang, B.C., Zhao, L.M., Sun, H. and He, M.Y. 2001. The genetic diversity of annual wild soybeans grown in China. *Theor. Appl. Genet*., 103(1): 98-103.

FAO (Food and Agriculture Organization). Production Year Book. Food and Agriculture Organization of the United Nations, Rome. Italy. 2012; www.fao.org.

Huang, X.Q., Huang, T., Hou, G.Z., Li, L., Hou, Y. and Lu, Y.H. 2016. Identification of QTLs for seed quality traits in rapeseed (*Brassica napus* L.) using recombinant inbreed lines (RILs). Euphytica 210:1.

Jeromela, M.A., Marinkovic, R., Mijic, A. and Zdunic, M.Z. 2007. Interrelation between oil yield and other quantitative traits in rapeseed (*Brassica napus* L.). Sci. J. Agri. 8(2): 165-170.

Johnson, H.W., Robinson, H.F., Comstoc, R. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J. 1955; 47: 314-318.

Malik, M.A., Khan, A.S., Khan, M.A.S., Khan, B.R. and Mohamand, A.S. 2000. Study of correlation among morphological parameters in different varieties/accessions of Brassica species. Pakistan J. Biol. Sci. 3(7): 1180-1182.

Miller, P.A., Williams, J.C., Robinson, H.F., Comstock, R.E. 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J. 50: 126-131.

Mondal, M.M.A. and Bhuiyan, M.S.H. 2020. Morphological and reproductive characterization of developed mutants in groundnut. International Journal of Advanced Geosciences, 8(1): 21-26.

Ram, H.H. and Hari, G.S. 1998. Crop Breeding and Genetics. Kalyani Publishers, New Delhi-1 10002, p381.

Sadat, H.A., Nematzadeh G.A., Jelodar N.B., Chapi O.G. 2010. Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.). African J. Agric. Res. 5(15): 1958-1964.

Sharafi, Y., Majidi, M.M., Jafarzadeh, M., Mirlohi, A. 2015. Multivariate analysis of genetic variation in winter rapeseed (*Brassica napus* L.) cultivars. Journal of Agricultural Science and Technology. 17(5): 1319-1331.

Singh, R.K & Chaudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India. p.56.

Zare, M. & Sharafzadeh, S. 2012. Genetic variability of some rapeseed (*Brassica napus* L.) cultivars in Southern Iran. African J. Agric. Res. 7(2): 224-229.

Yadava, Y.P., Singh, H. and Singh, D. 1993. Gene action for seed yield and its attributes under research. Indian J. Genet. Plant Breeding. 6(1): 168-172.