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Selection of promising rapeseed mutants on the basis of morphology and yield attributes

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Abstract

The experiment was conducted to find out the best rapeseed mutants by observing their morphology and yield attributes. Seven mutant lines (RL-11, RL-12, RL-13, RL-14, RL-15, RL-16 and RL-17) with two checks (Binasarisha-9 and BARI Sharisha-14) were evaluated in this experiment. The experiment was conducted in RCBD design with three replications. High level of genetic diversity was observed among the mutant lines and the check varieties. Among the mutants RL-12, RL-14 and RL-17 proved their performance better in terms of morphology and yield attributes. These three mutant lines showed the highest yield and other yield attributes performance over the two check varieties. From this study it was revealed that these three mutants can be further used in genetic improvement of rapeseed.

Keywords: Rapeseed, mutant, genetic diversity, siliqua, significant

Introduction

Rapeseed (*Oleiferous brassica*) is an important oil seed crop in Bangladesh. It is the second most important edible oil crop in the world. *Brassica* oil crop is the most important group that supplies major edible oil in Bangladesh. Its national average seed yield is 1.14 ton ha⁻¹ only (BBS, 2018) [2]. Domestic oilseed production can hardly meet 15% demand but its contribution to industrial, agricultural and medicinal sectors is significantly increasing. In Bangladesh, there is little scope of horizontal expansion of the rapeseed cultivation, in this regard, attempt should be made to increase the yield per unit area within the shortest possible time. Seed yield itself is a product of interaction of many component traits which influence yield directly or indirectly. By creating genetic variability we can achieve higher seed yield with desired agronomic traits. Induced mutations have generated a vast amount of genetic variability and are now widely used for the development of genes controlling important traits and understanding the functions and mechanisms of actions of these genes in plants (Liang, 2009) [8]. Using mutation breeding, genetic improvement of any yield attributes either qualitative or quantitative trait, has been successfully achieved in rapeseed-mustard (Seyis *et al.*, 2006; Spasibionek, 2006; Zhao *et al.*, 2009; Malek *et al.*, 2012) [18, 18, 20, 10]. Furthermore, mutation breeding requires less time to develop crop cultivars as compared to the conventional breeding (Manjaya, 2009) [11]. Availability of genetic diversity and genetic variation is the heart of any breeding program which plays a critical role in developing well-adapted and improved crop varieties. Induced mutagenesis has played a vital role in germplasm strengthening and the development of high yielding varieties (Choudhary *et al.*, 2016) [4]. Kharkwal *et al.* (2004) [7] reported that among the mutant varieties, 89% have been developed worldwide using physical mutagens like X-rays, gamma rays, thermal and fast neutrons and with gamma rays alone accounting for the development of 60% of the mutant varieties. For an effective breeding program for crop variety development through hybridization, the analysis of genetic diversity is one of the useful tools and plays a fundamental role in identification of parents (Mazid *et al.*, 2013) [12]. This study investigated the morphology, seed yield and yield components variability among 7 rapeseed mutants along with two check varieties (Binasarisha-9 and BARI sarisha-14).

Materials and Methods

Experiment material

Seven mutant lines (RL-11, RL-12, RL-13, RL-14, RL-15, RL-16 and RL-17) and two checks (Binasarisha-9 and BARI Sarisha-14) were used as plant material for evaluation in this experiment. To create genetic variations, seeds of popular variety Binasarisha-9 were irradiated at Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh.

Design of experiment

The experiment was conducted in randomized complete block design with three replications at farm of BINA sub-station, Gopalganj during 2019-2020. Seeds were sown on 25 November in BINA sub-station, Gopalganj. Unit plot size was 5.4 m² (3×1.8 m) with 25 cm row to row spacing and 6-8 cm from plant to plant within rows.

Experimental management

Recommended production packages i.e., application of fertilizers, weeding, thinning, irrigation, application of pesticide etc. were followed to ensure normal plant growth and development of the plants in each plot.

Data collection parameters

Data were taken on morphological yield contributing characters such as plant height (avg. of 10 randomly selected representative plants), branches/plant (avg. of 10 randomly selected representative plants) and yield attributes like siliqua length (avg. of 10 randomly selected siliqua of 10 representative plants), siliqua/plant (avg. of 10 randomly selected representative plants), seeds/siliqua (avg. of 10 randomly selected siliqua of 10 representative plants) and 1000 seed weight (from each experimental plot 1000 seed counted and weighted). All the data were collected from each plot at maturity.

Maturity period was counted when approximately 70% siliqua of each plot turned into yellowish brown color. Plot seed yield was taken after proper drying of seeds. At first seed yield was taken from all the experimental plots (5.4 m² unit area) and converted into ton ha⁻¹.

Data analysis

The data were compiled and tabulated in proper form for statistical analysis. Analysis of variance was done following the experimental design with the help of the computer package Statistix 10. Later the means were separated through Least Significance Difference (LSD) test at 5% level of significance was used to compare mean differences among the treatments (Gomez & Gomez, 1984)^[5].

Results and Discussion

A significant variation was observed on the plant height among the mutants and check varieties. Among the mutants, RL-14 produced the tallest plant (87.33 cm). It is statistically similar with Binasarisha-9 (84.40 cm) but shows significant difference with BARI Sarisha-14 (56.33 cm) (Table 1). On the other hand, RL-16 (68.13 cm) produced the shortest plant (Table 1). Plant height may vary due to the genetic effects present among the genotypes and as well as the proper agronomic management. Medium size plants are more likely to produce greater number of branches, number of siliqua per plant and number of seeds per siliqua that leads to higher yield of rapeseed (Javed *et al.*, 2003)^[6]. Seyis *et al.* (2006)^[16] showed that induced mutation through gamma rays played a significant role in the alteration of plant architecture in rapeseed-mustard. Number of branches per plant is the important morphological parameters contributing to yield. A significant variation was found on the number of branches per plant among the mutant lines (Table 1). Mutant RL-15 produced the highest number of branches (7.93) followed by RL-11 (7.40) and RL-12 (7.27) while Binasarisha-4 produced the lowest number (3.40). Genotypes with more branches and siliqua/plant have also been reported in oilseed *Brassica* (Chauhan and Kumar 1986, Naz and Islam 1979, Shah *et al.* 1990, Javed *et al.* 2003, Malek and Monshi 2009)^[3, 14, 17, 9, 6] as a consequence of mutagenesis. Binasarisha-9 produced the highest siliqua length (7.33 cm) and BARI Sarisha-14 produced the lowest (4.11 cm). Among the mutants RL-11 produced the highest siliqua length (5.63 cm) followed by RL-15 (5.11 cm) and RL-12 (5.05 cm). RL-17 produced the highest no. of siliqua/plant (112.73) followed by RL-12 (100.33) and the lowest no. of siliqua/plant produced by BARI Sarisha-14 (31.87). There is significant difference among the mutant lines than the mother Binasarisha-9 in producing no. of siliqua/plant. Binasarisha-9 produced the highest no. of seeds/siliqua (25.80) followed by BARI Sarisha-14 (23.47). Among the mutant lines the highest no. of seeds/siliqua produced by RL-16 (18.73) and the lowest one produced by RL-11 (14.00). Spasibionek (2006)^[18] reported similar type of results and found positive and significant correlation in number of seeds per siliqua. Binasarisha-9 produced the highest 1000 seed weight (2.90 gm.) followed by RL-16 (2.86 gm.) and lowest one produced by RL-14 (2.12 gm.) (Table 1). Javed *et al.* (2003)^[6] demonstrated that number of seeds per siliqua and 1000 seed weight directly influenced the seed yield in rapeseed and mustard. Improvement in seed size i.e., obtaining bold-seeded mutants has also been achieved earlier through induced mutations in oilseed *Brassica* by Malek *et al.* (2012)^[12] which confirm the present results.

Table 1: Different yield contributing characters of rapeseed mutants with check varieties

Mutants/Varieties	Plant height (cm)	Branches/plant (no.)	Siliqua length (cm)	Siliqua/plant (no.)	Seeds/siliqua (no.)	1000 seed weight (gm.)
RL-11	74.27abc	7.40ab	5.63b	71.93abc	14.00c	2.79a
RL-12	78.27abc	7.27abc	5.05bc	100.33ab	15.53bc	2.77a
RL-13	73.40bc	5.87c	4.34de	74.27abc	17.13bc	2.35bc
RL-14	87.33a	6.93abc	4.74cde	77.53ab	14.67bc	2.12c
RL-15	68.93cd	7.93a	5.11bc	83.40ab	15.33bc	2.61ab
RL-16	68.13cda	6.00bc	4.92cd	72.53abc	18.73b	2.86ab
RL-17	71.27c	6.87abc	4.53cde	112.73a	14.47bc	2.75ab
Binasarisha-9	84.40ab	3.40d	7.33a	61.20bc	25.80a	2.90a
BARI Sarisha-14	56.33d	3.80d	4.11e	31.87c	23.47a	2.64ab
CV (%)	10.27	13.15	7.32	32.27	15.12	8.74

Plant height showed significant correlation with no. of siliqua/plant and yield. Both no. of siliqua/plant and yield

were significant at 5% level. Other yield contributing characters had non-significant correlation with plant height.

Plant height had negative non-significant correlation with no. of seeds/siliqua and 1000 seeds weight that means plant height had no positive influence on those parameters (Table 2). No. of branches/plant showed significant correlation with no. of siliqua/plant and no. of seeds/siliqua at 1% level. No. of branches/plant had negative significant correlation with no. of seeds/siliqua and with other yield contributing characters it had non-significant correlation. Siliqua length showed non-significant correlation with all the yield contributing characters. No. of siliqua/plant showed significant correlation with yield at 1% level and showed negative non-significant

correlation with no. of seeds/siliqua and 1000 seeds weight. No. of seed/siliqua showed non-significant correlation with 1000 seeds weight and negative non-significant correlation with yield. 1000 seeds weight showed non-significant correlation with yield (Table 2). Seed yield was significantly and positively correlated with number of siliqua/plant, 1000 seed weight, straw yield, plant height, biological yield and harvest index which implies that seed yield would increase with the increase of these yield attributes. It was also reported by Zehra *et al.* (2009) [19].

Table 2: Correlation between different yield contributing characters and yield of rapeseed mutants and check varieties

	P.H.	Br./P	Siliqua L.	Siliqua/P.	Seeds/S.	1000S.w.	Yield
P.H.	1.0000						
Br./P	0.1433 ^{NS}	1.0000					
Siliqua L.	0.4179 ^{NS}	-0.3017 ^{NS}	1.0000				
Siliqua/P.	0.5046*	0.5858**	-0.0967 ^{NS}	1.0000			
Seeds/S.	-0.0703 ^{NS}	-0.7434**	0.3407 ^{NS}	-0.3741 ^{NS}	1.0000		
1000S.w.	-0.2811 ^{NS}	-0.1873 ^{NS}	0.4242 ^{NS}	-0.1027 ^{NS}	0.1383 ^{NS}	1.0000	
Yield	0.5239*	0.2702 ^{NS}	0.1957 ^{NS}	0.6263**	-0.1844 ^{NS}	0.0795 ^{NS}	1.0000

NS-Non Significant; *-Significant at 5% level; **- Significant at 1% level

P.H.-Plant height; Br/P-Branches/Plant; Siliqua L.-Siliqua Length; Siliqua/P-Siliqua/Plant; Seeds/S-Seeds/Siliqua; 1000S.w.-1000 Seeds Weight.

Among the mutant lines, RL-12 produced the highest seed yield (0.88 ton/ha) followed by RL-14 (0.66 ton/ha) and RL-17 (0.64 ton/ha). The lowest seed yield produced by BARI Sarisha-14 (0.41 ton/ha) (Fig. 1). The results are supported with the findings of Javed *et al.* (2003) [6], Seyis *et al.* (2006) [16] and Zhao *et al.* (2009) [20] who obtained considerable genotypic variability for seed yield. Mostofa *et al.* (2016) [13] reported that production of higher yield by different varieties might be due to the contribution of cumulative favorable effects of the crop characteristics *viz.*, number of branches/plant, siliqua/plant and seeds/siliqua.

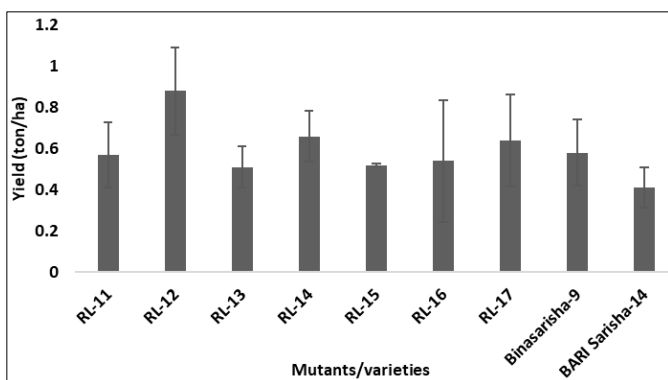


Fig 1: Seed yield (ton/ha) of rapeseed mutants with check variety.

Yield is a complex quantitative character governed by large number of genes and is greatly affected by environmental fluctuations. Seed yield is the most important character for considering as a promising variety of a particular crop. Among the mutant lines, the yield of RL-12, RL-14 and RL-17 increased over the check variety Binasarisha-9 and others are decreased. RL-12 showed the highest yield increase (51.72%) over Binasarisha-9 (Fig. 2). RL-13 showed the highest decrease of yield (-12.06%) from Binasarisha-9. Mutants having higher seed yield over mother variety were also reported earlier in rapeseed-mustard (Radoev *et al.*, 2008; Barve *et al.*, 2009; Malek *et al.*, 2012) [15, 1, 12].

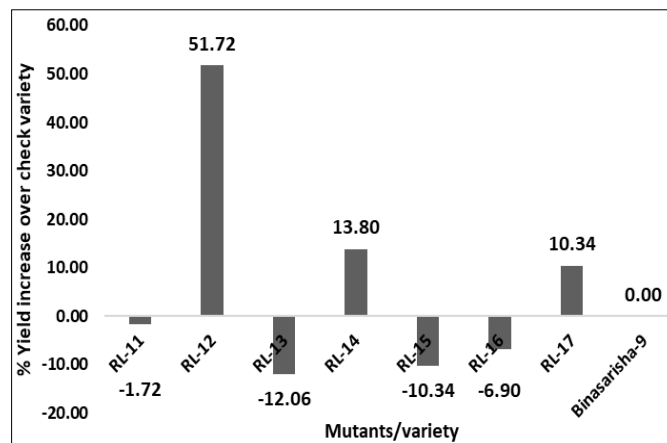


Fig 2: Increase of yield of mutant lines over Binasarisha-9.

All the mutant lines showed the positive yield increase over the check variety BARI sarisha-14 (Fig. 3). Here RL-12 shows the highest % yield increase (114.63%). RL-14 showed the lowest increase (13.79%) of yield over the check variety BARI sarisha-14 among the mutant lines. All the mutant lines showed their yield potentiality over BARI sarisha-14 (Fig. 3).

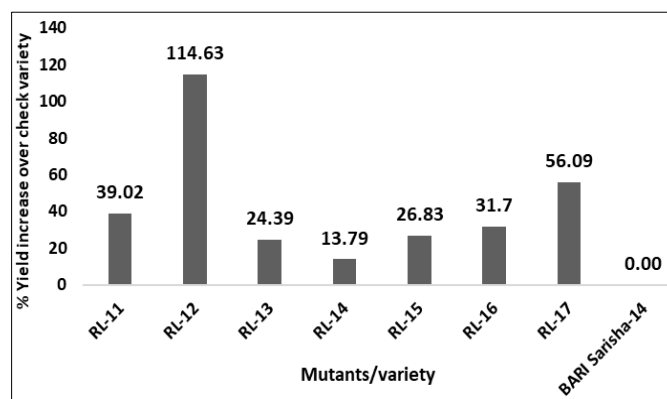


Fig 3: Increase of yield of mutant lines over BARI sarisha-14.

Conclusion

The mutants showed variation of different morphological and yield contributing characters among them from their mother plant Binasarisha-9. Among the mutants RL-12, RL-14 and RL-17 showed better performance for seed yield and yield contributing character like no. of siliqua/plant and proved as promising lines to be mutant varieties. These three lines showed significant correlation with all the yield contributing characters. This suggests that gamma rays irradiation can be fruitfully applied to develop mutants with higher seed yield and other improved agronomic traits in oleiferous *Brassica*. RL-12, RL-14 and RL-17 also showed yield increase over Binasarisha-9 and BARI sarisha-14. This study indicated that these lines showed presence of high level of genetic diversity and can be recommended as variety or used in further genetic improvement of rapeseed.

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