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IMPROVEMENT OF COTTON YIELD AND FIBER QUALITY PARAMETERS IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.) GENOTYPES THROUGH CHEMICAL MUTAGEN

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ABSTRACT

Eight mutant lines developed through mutation breeding technique using chemical mutagen along with parent line (Sadori) were evaluated at NIA, experimental farm. Quantitative and qualitative traits were analyzed statistically. The chemical mutagen Ethyle Methane Sulphonate (EMS) was used at the rate of 0.03%. The mutant lines (viz. NIA-M5, NIA-M10, NIA-M16, NIA-M20, NIA-M23, NIA-M29, NIA-M33 and NIA-M35) with parent Sadori were included in this study. The results revealed that three mutants (NIA-M20, NIA-M35 and NIA-M5) took (7.2%, 8.1% and 8.1%) higher plant height than parent (111 cm), two mutants (NIA-M5 and NIA-M20) obtained (36.8% and 42.1%) more sympodial branches plant^{-1} than parent (19.0). Three mutants (NIA-M20, NIA-M5 and NIA-M10) produced (16.8%, 22.4.0% and 25.4%) more number of bolls plant^{-1} than parental line (67.0). Five mutants (NIA-M5, NIA-M35, NIA-M20, NIA-M23 and NIA-M29) had higher fiber length (mm) (10.2%, 8%, 5.7%, 5% and 4.0%) as compared parent Sadori (28.0 mm). Two mutants (NIA-M20 and NIA-M29) showed higher fiber strength (g/tex) (5.5% and 8.3%) than parent (34.4%). Two mutants (NIA-M5 and NIA-M20) produced higher seed-cotton yield kg ha^{-1} (24.0% and 25.4%) over parent Sadori (3563 kg ha^{-1}). The selected mutant lines on the basis of higher seed-cotton yield (kg ha^{-1}) and enhanced fiber length (mm) compared to parent (Sadori) will be promoted in preliminary yield trials. Heritability and genetic advance were noted for early days to maturity, higher plant height (cm), sympodial branches plant^{-1}, length fiber (mm), bolls plant^{-1} and seed-cotton yield (kg ha^{-1}).

Keywords: cotton, fiber length, mutant, mutagen, yield

INTRODUCTION

Cotton is considered as life line of economy of Pakistan. It has a 0.8 percent share in GDP and contributes 4.5 percent in agriculture value addition (Economic Survey Report-2018-19). Mutation breeding is one of the most effective ways of inducing substantial genetic variability in plant species with desirable traits in the new mutant lines (Mei *et al.,* 2007). The beneficial point mutations from this mutagen have resulted in the improvement of yield, quality, biotic, or abiotic tolerance of plants worldwide (IAEA, 2015).The use of induced mutation in crop upgrading has proven to be a successful approach to develop yield and quality (Bibi *et al.,* 2009). The effectiveness of mutagenesis is considered feasible method to develop hereditary difference mainly in field crops (Hussain *et al*., 1982; Auld *et al*., 1998). Mutagenesis has been valuable to control the cotton genome for development of quantitative and qualitative characters (Bhat and Dani, 1990). Valuable variations induced by chemical mutagen is considered useful in by passing the prolonged evolution of inclusion of exotic genes to get better fibre quality traits in cotton (Andy *et al*., 2004). The ethyl methane sulphonate (EMS) stimulate mutagenic efficiency and capability was noted to be genotype and mutagen reliant (Giri and Aprao, 2011). Inducing genetic distinction, mutations have been used successfully in a number of crops for breeding of agronomically important traits. Conventional mutation techniques have generally been used to improve cotton yield, fiber quality, insect pests and disease conflict in field crops. Mainly, some inexpensively important field crops viz. barley, wheat, and cotton mutant varieties which take up the majority of farm fields (Maluszynski *et al*., 1995). One way to induce mutation is through the use of chemical mutagens. The EMS is a

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common, powerful, and most effective chemical mutagen, especially recommended using when mutation is introduced to the seed materials, since the application and the monitoring of the outcome of mutations are relatively easy. Usually EMS in plants; causes point mutations, on the other hand, loss of a chromosome segment or deletion can also occur in lesser extent (Okagaki *et al.,* 1991). It is significant to optimize the best probable condition to create large number of mutants having good seed germination for segregation without harmful genetic damages. Besides the wide use of mutagenesis to obtain genetic variation for plant breeding purposes, the generation of induced mutations is also applied with intentions for altering gene function with changed phenotype in basic research. The purpose was to confirm a function of a candidate gene, especially for the elucidation of biochemical, developmental, and disease resistance mechanisms (Coen and Meyerowitz, 1991). The use of chemical mutagenesis combined with modern plant breeding practices has a great potential for the future in the area of crop improvement (Percy *et al*., 2015). Presence of genetic variability, interrelationship and heritability of the characters provides a chance to the breeder to choose a perfect genotype directly or indirect choice of specific trait (Sadat *et al*., 2010).

MATERIALS AND METHODS

The commercial cotton variety Sadori was treated with EMS. The cotton seed was soaked with distilled water for eighteen hours and then soaked in 0.03% EMS solution for four hours and sown in the field. The experiment was conducted on a RCBD design with three replicates. Net plot size was maintained at 6.1 x 6.1m^2 (eight rows of 6.09 meters). Out of eight rows, six were harvested for taking yield data. Intercultural practices like thinning, weeding, inter-culturing, fertilizer and insecticide application applied as per schedule. The data were noted on plant height (cm), sympodial branches plant^{-1}, fiber length (mm), number of bolls plant^{-1}, fiber strength (g/tex), and seed-cotton yield (kg ha^{-1}). Lint samples were weighed and lint percentage was computed by using the following formula: Ginning out turn percentage (GOT %) = Weight of lint in a sample/ Weight of seed-cotton in a sample × 100. The data were analyzed statistically, for LSD at $P<0.05$ after ANOVA using statistical software, Statistix. The following formula was used to estimate Heritability and Genetic Advance:

H^2 (%) = $\delta 2g / \delta 2t$ x 100

Where h^2 = Heritability in broad sense, $\delta 2g$= induced genotypic variance and $\delta 2t$= Total phenotypic variance calculated from mutagen treated population.

GA (%) =K x δp x H

Where, GA= Genetic Advance, K= 2.06 constant for selection differential δp= phenotypic standard deviation of the mean performance of the mutated population and H=Heritability coefficient. The GA was expressed and percentage of the mean for the purpose of comparison.

RESULTS AND DISCUSSION

Mean squares from ANOVA for the studied characters are given in the Table 1. The data showed that mutant lines were highly significant at $P\leq0.05$ for plant height (cm), sympodial branches plant^{-1}, fiber length (mm), number of bolls plant^{-1}, fiber strength (g/tex), and seed-cotton yield (kg ha^{-1}) representing the survival of substantial genetic unevenness along with mutant lines for different traits except that ginning out turn% value which was non-significant. These results specify that the studied material is useful as genetic resources for variety development and also can be utilized for further breeding program (Faiza *et al*., 2017). The improving cotton and other major crops through the use of chemically induced mutants have been highly successful grown across the world (Auld *et al*., 1998). Chemical based mutagenesis like ethyle methane sulphonate was successful in developing change within-boll yield character as well as fiber quality parameters (Nino Brown *et al.,* 2015). The mutagenic agents like gamma rays and EMS, proved to be highly efficient in inducing an immense amount of variability for particular trait that to in favorable direction (Patil *et al.,* 2018).

Plant height (cm)

The data concerning plant height (cm) revealed that mutant lines mean squares were highly significant ($P<0.05$%). Results indicated that three mutants (NIA-M20, NIA-M35 and NIA-M5) showed increase in (7.2%, 8.1% and 8.1%) plant height over parent (111 cm) (Table 1). Computations revealed 0.4352 (GCV), 21.4722 (PCV), 0.0268 (h^2 BS) and 0.101609 (G.A as %

of mean) (Table 3) Mutagenic treatment has improved the plant height (cm) for the highest phenotypic and genetic coefficients of variation; heritability and genetic advance (Siddiqui *et al.,* 2009).

Sympodial branches (plant^{-1})

The boll bearing branch which is called sympodial branch; is an important quantitative character that contributes to seed-cotton yield (Naimatullah *et al*., 2017). The sympodial branches per plant exposed that mutant lines mean squares were highly significant (Table 1). Two mutants (NIA-M5 and NIA-M20) number of increase (36.8 and 42.1%) sympodial branches plant^{-1} than parent (19.0). Data perusal revealed -0.1853(GCV), 21.5187 (PCV), -0.0861 (h^2 BS) and -0.022809 (G.A as % of mean (Table 3) (Faiza *et al*., 2017).

Fiber length (mm)

The analysis of variance depicted that mutant lines mean squares also remained highly significant for fiber length (mm). Five mutants (NIA-M5, NIA-M35, NIA-M20, NIA-M23 and NIA-M29) had higher fiber length (mm) (10.2%, 8%, 5.7%, 5% and 4.0%) as compared to parent line (28.0 mm) (Table 1). Data perusal revealed 3.9395 (GCV), 7.452 (PCV), 0.528614 (h^2 BS) and 5.32549 G.A as % of mean. (Maluszynski *et al*., 1995).

Bolls (plant^{-1})

Boll weight is also imperative character which contributes to enhance seed-cotton yield. The mutagenic agent EMS, confirm to be highly proficient in inducing vast amount of variability for particular trait in positive direction. Numerous mutants were found to be better to the parents. (Patil *et al.,* 2018). The bolls plant^{-1} regarding mutant lines mean square were highly significant. Three mutants (NIA-M20, NIA-M5 and NIA-M10) show increase (16.8%, 22.4.0% and 25.4%) number of bolls plant^{-1} than parental line (67.0) (Table 1). Data also revealed 0.36 (GCV), 123.03 (PCV), 0.00292 (h^2 BS) and 0.05557 (G.A as % of mean) (Table 3). The breeder can choose a perfect genotype directly or indirectly (Sadat *et al*., 2010).

Fiber strength (g/tex)

The fiber strength (gram/tex) showed that mutant lines were highly significant (P<0.05%). Two mutants (NIA-M20 and NIA-M29) showed higher fiber strength (g/tex) increase over (5.5% and 8.3%) than parental line (34.4%). Data perusal revealed 4.56 (GCV), 14.0 (PCV), 0.33 (h^2 BS) and 2.51 G.A as % of mean (Table 3). Ethyl methane sulphonate treatment can bring successful in improvement of fiber quality parameters especially HVI length and strength. (Deepika, *et al.,* 2016).

Table 1. Mean square for agronomic traits of cotton mutant lines

Source	**DF**	**Plant height (cm)**	**Sympodial branches (plant^{-1})**	**No, of bolls (plant^{-1})**	**Fiber length (cm)**	**Fiber strength (g/tex)**	**Ginning out turn (%)**	**Seed-cotton yield (kg ha^{-1})**
Rep.	02	0.4815	0.1481	7.000	0.10815	0.6604	2.36259	46391
Mutant	12	22.3426**	21.1481**	123.750**	4.39870**	15.3315**	0.94176ns	315024**
Error	24	1.3148	1.3565	7.667	0.10231	0.2195	0.73134	18943
Total	38							

** = Highly significant ns= Non-significant

Table 2. Mean performance of upland cotton mutant lines for yield and fiber quality traits

Mutant	**Plant height (cm)**	**Sympodial branches (plant^{-1})**	**No, of bolls (plant^{-1})**	**Fiber length (mm)**	**Fiber strength (g/tex)**	**Ginning out turn (%)**	**Seed-cotton yield (kg ha^{-1})**
NIA-M5	119ab	26a	82ab	30.9a	35c	38.0 a	4421a
NIA-M-10	118bc	21bcd	78bc	27.2f	34e	37.8a	3899b
NIA-M-16	117c	20cd	69d	27.8e	33f	37.9a	3823bc
NIA-M-20	120a	27a	84a	29.6	36b	38.8a	4468a
NIA-M-23	117c	22b	76c	29.4c	35c	38.9a	3915b
NIA-M-29	117c	21bcd	68d	29.2c	37a	38.7a	3620cd
NIA-M-33	118bc	21bc	75c	28.4d	29.4	37.7a	3727bcd
NIA-M-35	120a	23b	69d	30.2b	35cd	39.0a	3762bcd
Parent	111d	19d	67d	28.0de	34de	38.9a	3563d

Table 3. Analysis of variance Error/Env, Grand Mean (GM), Genotypic Variance (GCV), Phenotypic Variance (PCV), Heritability (h^2) and Genetic Advance (GA)

Mutant lines plant characters	**Mean M.S**	**Error M.S**	**Grand Mean (GM)**	**Genotypic Variance (GCV)**	**Phenotypic Variance (PCV)**	**Heritability (h^2)**	**Genetic advance (GA)**
Plant height (cm)	22.3426	21.037	117.48	0.4352	21.4722	0.0268	0.101609
Sympodial branches (plant^{-1})	21.1481	21.704	22.259	-0.1853	21.5187	-0.0861	-0.22809
No, of bolls (plant^{-1})	123.750	122.67	74.222	0.36	123.03	0.00292	0.05557
Fiber length (mm)	4.39870	1.6370	28.963	0.916	2.5536	0.35896	2.51727
Fiber strength (g/tex)	15.3315	3.513	34.441	3.9395	7.452	0.528614	5.32549
Ginning out turn (%)	0.94176	11.7015	38.419	-3.5877	8.1172	-0.44190	-4.16597
Seed-cotton yield (kg ha $^{-1}$)	315024	303083	3910.8	3980.33	307063.33	0.012962	0.233445

Ginning out turn %

Mean values for ginning out turn % of cotton is presented in Table 1. The analysis of variance for GOT % depicted non-significant variation among the mean values at *P*<0.05% level of probability. The mean values revealed that two mutant lines took increase over parental line. Data perusal revealed -3.5877 (GCV), 8.1172 (PCV), -0.44190 (h^2 BS) and -4.16597 (G.A as % of mean). Efficiency and capability was found to be genotype and mutagen reliant Giri and Aprao, (2011) agreed with our results given in Table 3.

Seed-cotton yield (kg ha^{-1})

The results for seed-cotton yield (kg ha^{-1}) given in theTable 1 revealed that mutant lines mean square were highly significant at *P*<0.05%. Two mutants (NIA-M5 and NIA-M20) produced higher seed-cotton yield (kg ha^{-1}) (24.0% and 25.4%) over parental line (3563 kg ha^{-1}). Muthusamy and Jaybalan (2011) and Khan *et al.* (2014) also stated that chemical mutagen induces positive mutation to increase seed-cotton yield (plant^{-1}). Data revealed 3980.33 (GCV), 307063.33 (PCV), 0.0129 (h^2 BS) and 0.233445 (G.A as % of mean) (Table 3). Valuable variations induced by chemical mutagen are considered as useful tool in by passing the prolonged progression of insertion of foreign genes to get better seed-cotton yield and improved quality in cotton. These results are also comparable with the findings of Andy *et al*. (2004).

CONCLUSION

In this experiment, genetic variation produced and confined by selection of the treated cotton variety Sadori with EMS. Five mutants (NIA-M5, NIA-M35, NIA-M20, NIA-M23 and NIA-M29) had produced higher fiber length (30.9, 30.2, 29.6, 29.4 and 29.2 mm, respectively) than parental line (28.0 mm). Two mutants (NIA-M5 and NIA-M20) produced higher seedcotton yield kg ha^{-1} (4468.3 and 4420.7) than parental line (3563.3). These mutant lines showed their superior genetic variation and boost cotton yield kg ha^{-1} and fiber length (mm).

AUTHOR'S CONTRIBUTION

Z. A. Deho: Writing of research paper

S. Abro: Provided technical support

M. Rizwan: Critical review

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