Genetic Variability, Standardized Multiple Linear Regression and Principal Component Analysis to Determine Some Important Sesame Yield Components

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ABSTRACT

Sesame is an important commodity in supporting various industries such as low saturated fat oil producing and are often able to adapt under stressed grown conditions. Breeding sesame is undertaken to increase production and is possible by radiation induced polygenic characteristic changes with a gamma rays source. The study aims to identify the effectiveness of genetic variability, standardized multiple linear regression, and principal component analysis to determine some important sesame yield components for indirect selection. Eighteen sesame mutant lines (black and white types) were studied for eleven quantitative traits. Two sesame types were irradiated with eight doses (100-800 Gy) of gamma rays individually. Variability studies on seed yield and yield components are important raw material of high productivity for all studied traits. Standardized multiple linear regression analysis is the most effective way to provide information of relationship between seed yield and yield components in sesame mutant lines for indirect selection.

Keywords: genetic variability; indirect selection; seed yield; sesame

INTRODUCTION

Sesame (*Sesamum indicum* L.) is the most important ancient oilseeds crop known to mankind (Ashri, 1994) and grows well in tropical and subtropical climates, highly tolerant to drought and various agro climatic regions (Weiss, 1971; Tripathi et al., 2014). Sesame is an important commodity supporting various industries and produce oil which is low in saturated fat (Suja, Jayalekshmy, & Arumughan, 2004). Sesame is normally self-pollinated species and a composite of various homozygous individuals in populations (Furat & Uzun, 2010).

The achievement in sesame genetic improvement requires the availability and accessibility of genetic variability of target traits.

Induced mutation is an important way to foster additional variability in inherited traits and yield improvement of the plant in breeding program (Begum & Dasgupta, 2014). Irradiation with gamma rays of seeds can increase mutation frequency and widen the mutation spectrum (Micke, 1996).

The knowledge of genetic variability is of immense value for planning efficient breeding program to improve the yield potential of the lines (Narayanan & Murugan, 2013). The understanding of relationship between seed yield and yield components is crucial for selection process of breeding program (Biabani & Pakniyat, 2008; Siva, Krishna, & Venkateswarlu, 2013), therefore this study aims to identify the effectiveness of genetic variability, standardized multiple linear regression, and principal component analysis to determine some important sesame yield components for indirect selection of yield.

MATERIALS AND METHODS

Plant Materials

Eighteen sesame (*Sesamum indicum* L.) mutant lines M_4 generations (black and white types) were studied for eleven quantitative traits. Homogeneous seeds of each of two sesame types were treated with eight doses (100-800 Gy) of gamma rays individually. In M_2 generations, the populations were selected on salinity tolerance at 6 g L^{-1} NaCl. Survival individual plants were harvested together for each doses to produce M_3 seed materials. The M_4 generations were than exploited to determine the important characteristic for yields. A field experiment was conducted in Sleman, Yogyakarta (7°16' N; 110°21' E), altitude of 193 m above sea level (masl), in March-August 2015. The lines were sown on Inceptisol which

contained of 9.73 % clay, 33.63 % silt and 56.64 % sand, with the soil pH was 6.34.

Each line was grown in four rows of 5 m length at a distance of 50 cm between the rows and 25 cm between the plants within the rows. Sesame was sown at two seeds per hole to ensure adequate crop stand. Increasing soil humidity was provided by means of furrow irrigation. Two t ha^{-1} organic fertilizers, a dose of 100 kg ha^{-1} nitrogen, potassium, and phosphorus was applied at sowing.

Data Collection and Analysis

Quantitative observations were recorded on ten yield related components including plant height (x_1), number of primary branches (x_2), number of secondary branches (x_3), number of nodes per plant (x_4), number of nodes to first flower (x_5), stem height from base to first branch (x_6), stem height from base to first capsule (x_7), number of capsules per plant (x_8), biomass yield per plant (x_9), 1000-seed weight (x_{10}) and seed yield per plant (y). Trait selection and measurement techniques were based on descriptors of sesame according to IPGRI & NBPGR (2004).

Data of seed yield and yield components were used to study the relationship. Statistical parameters such as mean, standard deviation, variance and coefficient of variation were described by Steel & Torrie (1980). Homogeneity test of variances and the statistical significance of correlations were analyzed according to Gomez & Gomez (1984). Genetic variability for all properties was calculated from the phenotypic and genotypic coefficient of variation (Singh & Chaudhary, 1979). The genotypic coefficient of variation (GCV) was divided into three major categories: high (GCV > 14.5 %), moderate (5 % < GCV ≤ 14.5 %) and small (GCV ≤ 5 %). The phenotypic coefficient of variation (PCV) was divided into three major categories: high (PCV > 50 %), moderate (25 % < PCV ≤ 50 %) and small (0 % < PCV ≤ 25 %) (Johnson, Robinson,

& Comstock, 1955). Broad sense heritability (H) was divided into three major categories: high (H > 50 %), moderate (20 % < H ≤ 50 %) and small (H ≤ 20 %) (Knight, 1979). To see the pattern of the relationship between the characteristics using a correlation analysis was examined based on t-test (Singh & Chaudhary, 1979; Falconer, 1981; Kearsey & Pooni, 1996). Standardized multiple linear regression analysis followed by Montgomery, Peck, & Vining (2012). Principal component analysis was also carried out, as proposed by Jeffers (1967). Analysis of variance and correlation between characteristics with a correlation coefficient was processed using SAS software facility (Littell, Milliken, Stroup, Wolfinger, & Schabenberger, 2006).

RESULTS AND DISCUSSION

Genetic parameters for quantitative traits observed among the eighteen sesame mutant lines are presented in Table 1. The largest variation was observed for plant height (x_1), stem height from base to first capsule (x_7), number of capsules per plant (x_8), biomass yield per plant (x_9) and seed yield per plant (y). High genetic variability of plant population is very important for plant breeding program. Genetic variability is the most important raw material for developing new varieties to sustain level of high productivity.

The genotypic variance presented ranging between 0.12 (1000-seed weight) to 3970.10 (number of capsules per plant) (Table 1). High estimations of genotypic variance were recorded for plant height, number of capsules per plant, and biomass yield per plant. The phenotypic variance for sesame mutant lines was highest in the number of capsules per plant, followed by plant height, and biomass yield per plant. The lowest phenotypic variance was recorded by 1000-seed weight.

Table 1. Genetic parameters for quantitative traits in sesame mutant lines

Traits	Mean±SE	Range	Variance	σ_g^2	σ_f^2
Plant height (x_1)	202.83±0.012	73-276	**816.80**	147.67	832.70
Number of primary branches (x_2)	4.68±0.164	0-12	4.96	2.00	4.51
Number of secondary branches (x_3)	5.07±0.088	0-22	19.13	7.39	18.42
Number of nodes per plant (x_4)	23.26±0.057	8-38	30.64	7.65	32.00
Number of nodes to first flower (x_5)	5.44±0.105	3-27	7.11	15.64	17.09
Stem height from base to first branch (x_6)	10.50±0.048	1-42	39.19	10.58	32.61
Stem height from base to first capsule (x_7)	53.52±0.026	15-102	**225.16**	62.93	194.35
Number of capsules per plant (x_8)	140.34±0.004	3-540	**9911.10**	3970.10	10636.10
Biomass yield per plant (x_9)	111.26±0.006	3-410	**4730.62**	996.16	4907.46
1000-seed weight (x_{10})	3.56±0.375	1.59-16.32	0.41	0.12	0.44
Seed yield per plant (y)	24.53±0.012	1.46-156.53	237.08	81.07	263.81

Table 1 (Continued)

Traits	GCV (%)	PCV (%)	H (%)
Plant height (x_1)	5.99 (moderate)	14.23 (small)	17.73 (small)
Number of primary branches (x_2)	**30.16** (high)	45.34 (moderate)	44.33 (moderate)
Number of secondary branches (x_3)	**53.64** (high)	**84.60** (high)	40.12 (moderate)
Number of nodes per plant (x_4)	11.91 (moderate)	24.34 (small)	23.92 (moderate)
Number of nodes to first flower (x_5)	**72.66** (high)	**75.97** (high)	91.49 (high)
Stem height from base to first branch (x_6)	**30.96** (high)	**54.40** (high)	32.45 (moderate)
Stem height from base to first capsule (x_7)	**14.82** (high)	26.05 (moderate)	32.38 (moderate)
Number of capsules per plant (x_8)	**44.90** (high)	**73.49** (high)	37.33 (moderate)
Biomass yield per plant (x_9)	**28.37** (high)	**62.96** (high)	20.30 (moderate)
1000-seed weight (x_{10})	9.83 (moderate)	18.53 (small)	28.23 (moderate)
Seed yield per plant (y)	36.68 (high)	66.19 (high)	30.73 (moderate)

Remarks: Numbers in bold are associated with the effectiveness of some indirect selection analysis to determine some important sesame yield components; σ_g^2 = genotypic variance; σ_f^2 = phenotypic variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; H = broad sense heritability.

Table 2. Genotypic and phenotypic correlation coefficient for seed yield and yield components in sesame mutant lines

Traits	Correlation	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	x_{10}	y
x_1	Genotypic	1										
	Phenotypic	1										
x_2	Genotypic	0.012	1									
	Phenotypic	0.021	1									
x_3	Genotypic	-0.045	0.679**	1								
	Phenotypic	-0.066*	0.665**	1								
x_4	Genotypic	0.280	-0.071**	0.051**	1							
	Phenotypic	0.329**	-0.056*	0.041	1							
x_5	Genotypic	-0.001	0.085**	0.078**	-0.060	1						
	Phenotypic	-0.002	0.199**	0.187**	-0.177**	1						
x_6	Genotypic	0.176	-0.086**	-0.217**	-0.153	0.003	1					
	Phenotypic	0.216**	-0.070*	-0.181**	-0.159**	0.001	1					
x_7	Genotypic	0.470	0.264**	0.026**	-0.129	0.345**	0.417**	1				
	Phenotypic	0.584**	0.220**	0.022	-0.136**	0.123**	0.425**	1				
x_8	Genotypic	-0.014	0.409**	0.534**	0.107	0.414**	-0.239**	-0.076**	1			
	Phenotypic	-0.020	0.408**	0.544**	0.136**	0.177**	-0.291**	-0.091**	1			
x_9	Genotypic	0.071	0.417**	0.525**	0.305	0.367**	-0.297**	-0.087**	1.011*	1		
	Phenotypic	0.076**	0.301**	0.387**	0.280**	0.114**	-0.262**	-0.075**	0.733**	1		
x_{10}	Genotypic	0.059	-0.112	-0.026	0.134	0.464	-0.114	-0.063	0.175	0.177	1	
	Phenotypic	0.077**	-0.097**	-0.024	0.148**	0.173**	-0.121**	-0.065*	0.153**	0.214**	1	
y	Genotypic	0.074	**0.334****	**0.344****	0.178	**0.352****	-0.201**	-0.017	0.730	0.614	**0.177****	1
	Phenotypic	**0.102****	**0.307****	**0.324****	**0.209****	**0.139****	-0.226**	-0.018	**0.675****	**0.782****	**0.187****	1

Remarks: * Significant at $p \leq 0.05$, ** Significant at $p \leq 0.01$; Numbers in bold had positively and significantly correlated with sesame seed yield per plant; x_1 = plant height (cm); x_2 = number of primary branches; x_3 = number of secondary branches; x_4 = number of nodes per plant; x_5 = number of nodes to first flower; x_6 = stem height from base to first branch (cm); x_7 = stem height from base to first capsule (cm); x_8 = number of capsules per plant; x_9 = biomass yield per plant (g); x_{10} = 1000-seed weight (g); y = seed yield per plant (g).

The phenotypic and genotypic coefficient of variation (Table 1) were the highest for number of secondary branches (x_3), number of nodes to first flower (x_5), stem height from base to first branch (x_6), number of capsules per plant (x_8), biomass yield per plant (x_9), and seed yield per plant (y). Higher genotypic coefficient of variation suggested that these characteristics were under the influence of genetic control. These results are in agreement with those of Parameshwarappa, Palakshappa, Salimath, & Parameshwarappa (2009). High heritability was observed for number of nodes to first flower. This indicates that less influence of environment in expression of this characteristic. Moderate heritability was recognized in all quantitative characteristics except plant height (small) and number of nodes to first flower (high) which indicating that these characteristics were governed by gene action.

Correlation coefficients in sesame mutant lines are given in Table 2. In general, they indicated the effect of environmental factors. Genotypic and phenotypic correlation in sesame seed yield plant^{-1} had positively and significantly correlated with number of primary branches (x_2), number of secondary branches (x_3), number of nodes to first flower (x_5), and 1000-seed weight (x_{10}) (Table 2). It had negatively and significantly correlated with stem height from base to first branch (cm). Our results agreed with similar positive correlation observed by Akbar, Rabbani, Shinwari, & Khan (2011).

The purpose of multiple linear regressions is to predict a single variable from one or more independent variables. The results of fitting a multiple linear regression model are showed in Table 3. Standardized multiple linear regression analysis was strongly associated seed yield with number of number of primary branches (x_2), number of secondary branches (x_3), number of capsules per plant (x_8), and biomass yield per plant (x_9). Standardized multiple linear regressions provide a powerful method to analyze multivariate data.

The principal component analysis after varimax rotation method in sesame mutant lines is given in Table 4. Factor loadings (greater than 0.5) were considered important for interpretation of data. Factor 1 was strongly associated with number of primary branches (x_2), number of secondary branches (x_3), number of capsules per plant (x_8), biomass yield per plant ($x9$) and seed yield per plant (y). These variables had positive and indicates the direction of the relationship between the factor and the variable in factor 1. Factor 2 consisted of plant height, stem height from base to first branch, stem height from base to first capsule and are associated with quantitative traits. Again all these variables had positive loadings. These types of traits might be influenced by the same gene or genes and therefore could be beneficial for suitable sesame lines screening. Factor 3 was strongly associated with number of nodes per plant. Factor 4 was strongly associated with number of nodes to first flower and 1000-seed weight. Four principal component axes were required to provide a useful separation of the lines and these traits would be effective for the identification of best sesame mutant lines.

Table 3. Standardized multiple linear regression analysis in sesame mutant lines

Traits	Regression coefficient	Standard Error	*t*-value	*P*-value
Plant height (x_1)	0.017	0.012	1.40	0.1615
Number of primary branches (x_2)	0.554	0.164	3.39	**0.0007**
Number of secondary branches (x_3)	-0.377	0.088	-4.27	**<.0001**
Number of nodes per plant (x_4)	-0.022	0.057	-0.39	0.6985
Number of nodes to first flower (x_5)	0.126	0.105	1.20	0.2306
Stem height from base to first branch (x_6)	-0.071	0.048	-1.47	0.1416
Stem height from base to first capsule (x_7)	0.013	0.026	0.51	0.6105
Number of capsules per plant (x_8)	0.037	0.004	8.60	**<.0001**
Biomass yield per plant (x_9)	0.136	0.006	23.43	**<.0001**
1000-seed weight (x_{10})	0.002	0.375	0.00	0.9961

Remarks: Numbers in bold significant at $p \leq 0.01$ and are strongly associated with seed yield

Table 4. Principal component analysis after varimax rotation method in sesame mutant lines

Traits	Factors				Communality
	1	2	3	4	
Plant height (x_1)	0.045	**0.781**	0.429	0.149	0.819
Number of primary branches (x_2)	**0.746**	0.180	-0.268	-0.290	0.744
Number of secondary branches (x_3)	**0.792**	-0.031	-0.184	-0.217	0.709
Number of nodes per plant (x_4)	0.134	0.014	**0.801**	0.121	0.674
Number of nodes to first flower (x_5)	0.242	0.145	-0.602	**0.502**	0.695
Stem height from base to first branch (x_6)	-0.278	**0.625**	-0.179	-0.113	0.512
Stem height from base to first capsule (x_7)	0.069	**0.896**	-0.117	-0.043	0.823
Number of capsules per plant (x_8)	**0.831**	-0.157	0.093	0.201	0.766
Biomass yield per plant (x_9)	**0.761**	-0.103	0.304	0.321	0.786
1000-seed weight (x_{10})	0.018	-0.048	0.053	**0.824**	0.684
Seed yield per plant (y)	**0.731**	-0.042	0.254	0.330	0.710
Variance	3.150	1.897	1.507	1.367	

Remarks: Numbers in bold are those with factor loadings greater than 0.5. Factor 1 = x_2, x_3, x_8, x_9, y; Factor 2 = x_1, x_6, x_7; Factor 3 = x_4; Factor 4 = x_5, x_{10}.

Table 5. The effectiveness of some indirect selection analysis to determine some important sesame yield components

Traits	Indirect selection analysis						
	Variance	GCV (%)	PCV (%)	r_g	r_p	Standardized multiple linear regression	PCA
Plant height (x_1)	*				*		
Number of primary branches (x_2)		*		*	*	*	*
Number of secondary branches (x_3)		*	*	*	*	*	*
Number of nodes per plant (x_4)					*		
Number of nodes to first flower (x_5)		*	*	*	*		
Stem height from base to first branch (x_6)		*	*				
Stem height from base to first capsule (x_7)	*	*					
Number of capsules per plant (x_8)	*	*	*		*	*	*
Biomass yield per plant (x_9)	*	*	*		*	*	*
1000-seed weight (x_{10})				*	*		

Remarks: * associated with this trait. GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, r_g = genotypic correlation coefficient, r_p = phenotypic correlation coefficient, PCA = principal component analysis

The comparison of several ways to construct indirect selection in determining some important sesame yield components is shown in Table 5. The effectiveness of some indirect selection method to determine some important components of sesame yield can be judged by comparing the explainable effect of traits on seed yield per plant. Standardized multiple linear regression analysis provides similar information to principle component analysis (Table 5). Due to the simplicity and easy to be understood, standardized multiple linear regression is the most effective way in providing information about the relationship of seed yield and yield components in sesame mutant lines for indirect selection. This analysis can decide minimum number of characteristics, which are probably effective in improving yield, and will help breeders to handle the number of characteristics in the selection procedure.

CONCLUSION

Standardized multiple linear regression analysis is the most effective way to obtain information about the relation of seed yield and yield components in sesame mutant lines for indirect selection. This study indicated that the improvement of variability in yield and important

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yield components could be generated through induced mutagenesis.

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