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EFFECT OF DROUGHT STRESS ON GAS EXCHANGE CHARACTERISTICS OF FOUR SOYBEAN GENOTYPES

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A. U. AHMED[3] AND M. S. A. KHAN[1]

Abstract

An experiment was conducted in a venylhouse at the environmental stress site of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur during September to December 2012 to determine the changes of photosynthesis and some related traits under drought stress in soybean genotypes. Four studied genotypes viz. Shohag, BARI Soybean 6 and BD2331 (relatively stress tolerant) and BGM2026 (susceptible) were tested against two water regimes such as water stress and non-stress. Results indicated that gas exchange characteristics were positively correlated with plant growth. Photosynthesis and stomatal conductance showed more reduction in susceptible genotypes than the tolerant ones. Transpiration rate was found minimal in tolerant genotypes. Changes in leaf growth attributes of the four selected genotypes were compared under drought (water) stress conditions which is one of the major plant parts related to gas exchange. Generally, drought stress decreased the leaf area more in susceptible genotype than tolerant genotype. From the result, genotype BGM2026 which recorded the lowest photosynthesis, stomatal conductance, leaf area but highest transpiration rate was considered as drought susceptible whereas BARI Soybean-6, Shohag and BD2331 were more drought stress tolerant which have better mechanisms of drought tolerance.

Keywords: Soybean, drought, photosy on thesis, transpiration, stomabal conductance.

Introduction

Drought stress is one of the serious environmental factors affecting plant growth, development, yield and quality. It induces various physiological and biochemical adaptations in plants. Among physiological processes gas exchange processes is one of the most important processes and this process of tolerant and susceptible genotypes responded dissimilarly under stress conditions. Lawlor and Cornic (2000) and Zhu (2002) reported that drought affects the morpho-physiological, biochemical and molecular processes in plants resulting in growth inhibition, stomata closure with consecutive reduction of photosynthesis, transpiration, decrease in chlorophyll content and inhibition of photosynthesis and protein changes to cope with osmotic changes in their tissues. The productivity of the crop may be related to physiological attributes like transpiration rate,

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photosynthetic rate etc. Water stress inhibits cell enlargement more than cell division. It reduces plant growth by affecting photosynthesis, respiration, translocation, ion uptake, carbohydrates and nutrient metabolism and growth promoters (Farooq *et al*., 2009). Drought reduces leaf expansion (Alves and Setter, 2004), accelerates leaf senescence (De Souza *et al*., 1997) and leads to death of leaf tissue. The adaptive potential of some plant species reducing water losses were achieved by closing of stomata and reduction in the transpiration rate (Tardieu and Davies, 1996). Hence, measurement of transpiration rate is an excellent tool to assess drought tolerant capacity of crop plants. Soybean is one of the sensitive crop to several abiotic stress as compared to many other legumes though variability in tolerance among its genotypes is very common (Silveria *et al.*, 2003). Among different stresses one of the most important stresses that affects plant growth is drought stress. This study was, therefore, initiated to determine the changes of photosynthesis and some related traits in soybean under drought stress situation.

Materials and Method

A pot experiment in a vinyl house was conducted at the Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur during September to December 2012. Three relatively water stress tolerant (Shohag, BARI Soybean 6 and BD2331) and one susceptible (BGM 2026) genotypes, selected from the previous experiment, were used in this study to determine the changes of photosynthesis and some related traits in soybean under drought stress at vegetative and pod development stages. Seeds of tolerant genotypes and susceptible genotypes were sown in plastic pots (24 cm internal diameter and 30 cm height). The pot was filled with mixture of soil and cow dung at a ratio of 4:1. Pot contained 12.0 kg of soil which was equivalent to 9 kg oven dry soil and holds about 28% moisture at field capacity (FC). Soil used in the pot was sandy loam. Fertilizer rates of 70 mg N, 35 mg P, 180 mg K and 20 mg S pot^{-1} in the form of urea, triple super phosphate, muriate of potash and gypsum was added and well mixed with the soil before pouring into the pots. Six seeds pot^{-1} were sown on 3 September, 2012. After seedling establishment two uniform and healthy plants pot^{-1} were allowed to grow. Two watering treatments of the plants viz. drought stress i.e. water stress (50% water of the FC) and non-stress i.e. control (80% water of FC) were applied at 21 days after emergence (DAE) and maintained throughout the growing season. The pots were arranged in a completely randomized design under Factorial arrangement with four replications (two plants pot^{-1} considered as one replication). There were four genotypes and two water regimes treatments (hereafter referred to as non-stress and water stress treatments) were included as variable treatments. Weeding and spraying were done as normal management practices for all the treatments. Some growth parameters such as leaf area, leaf weight, transpiration rate and gas exchange was measured which are described below:

Data collection

Leaf growth measurement

Leaf samples were taken to determine leaf biomass accumulation at vegetative and pod development stages. At each sampling, leaves of two plants pot^{-1} were removed and leaf area $plant^{-1}$ was measured by an automatic leaf area meter (AAM-8, Hayashi-denko, Japan). Leaves were oven dried at 70^0 C to a constant weight and dry weight taken. Specific leaf area (SLA) and specific leaf mass (SLM) were also measured.

Specific leaf area: Specific leaf area (SLA) is the ratio of leaf area to leaf dry weight. It is used to understand the quantity of plant tissue employed for photosynthesis per unit of leaf tissue. It was determined by the following formula:

$$SLA = \frac{\text{Leaf area}}{\text{Leaf dry weight}} \ (cm^2\ g^{-1})$$

Specific leaf mass: The specific leaf mass (SLM) indicates the leaf thickness, and it was determined by the following formula:

$$SLM = \frac{\text{Leaf dry weight}}{\text{Leaf area}} \ (g\ cm^{-2})$$

The transpiration rate and leaf gas exchange was measured at the pod development stage using a portable photosynthesis system (LICOR-6200).

The data were analyzed by MSTAT-C statistical package program. The difference between the treatments means were compared by Least Significant Difference (LSD) test (Gomez and Gomez, 1984). Functional relationship between stomatal conductance and photosynthesis was established through correlation and regression analyses by using Excel program.

Results and Discussion

Photosynthesis

Photosynthesis rate of four soybean genotypes grown under non-stress and water stress environment are presented in Fig. 1. Plants grown under water stress condition showed less photosynthesis than that grown under non-stress condition. Kawamitsu *et al*. (2000) reported that drought stress decreased the rate of photosynthesis in an intertidal algae and a land plant. Purwanto (2003) also reported that photosynthetic rate decreased as water stress was increased. Photosynthetic reduction due to drought was caused by a decrease in leaf expansion, impaired photosynthetic machinery, pre-mature leaf senescence and

associated reduction in food production (Wahid and Rasul, 2005). The differences in photosynthesis between the non-stressed and water stressed plants were observed in all the genotypes but the difference was higher in BGM2026 than that of other genotypes. Photosynthetic rate ranged from 26.87 to 29.81 and 17.14 to 22.06 µmol CO_2 m^{-2} s^{-1} under non-stress and water stress conditions, respectively. The highest photosynthesis rate was observed in BARI Soybean 6 under non-stress condition followed by BGM2026 though the reduction percent was higher in BGM2026 (40.48%). The other three genotypes (BARI Soybean 6, Shohag and BD2331) showed 25.97, 27.94 and 28.5% reduction, respectively. The decreased photosynthesis under stress might be attributed partly due to reduced stomatal conductance (Nagy and Galiba, 1995), lowered transporation of photosyntahte (Hagemayer, 1997), reduction in protein concentration (Sibole *et al*., 1998), decline in photosynthetic pigment concentration (Kolchevskii *et al*., 1995), reduced carboxylase activity (Hagemayer, 1997) and inhibition of the light reaction mechanism (Unger, 1991). Drought stress may reduce plant photosynthesis by reducing leaf area, closing of stomata, and reducing the activity of dehydrated protoplasmic machinery (Boyer, 1976). Drought stress caused changes in photosynthetic pigments and components (Anjum *et al*., 2003), damaged photosynthetic apparatus (Fu and Huang, 2001) and diminished activities of Calvin cycle enzymes, which are important factors for reducing crop yield (Monakhova and Chernyadev, 2002). The less reduction of photosynthesis under stress condition was obviously helpful for maintaining better growth.

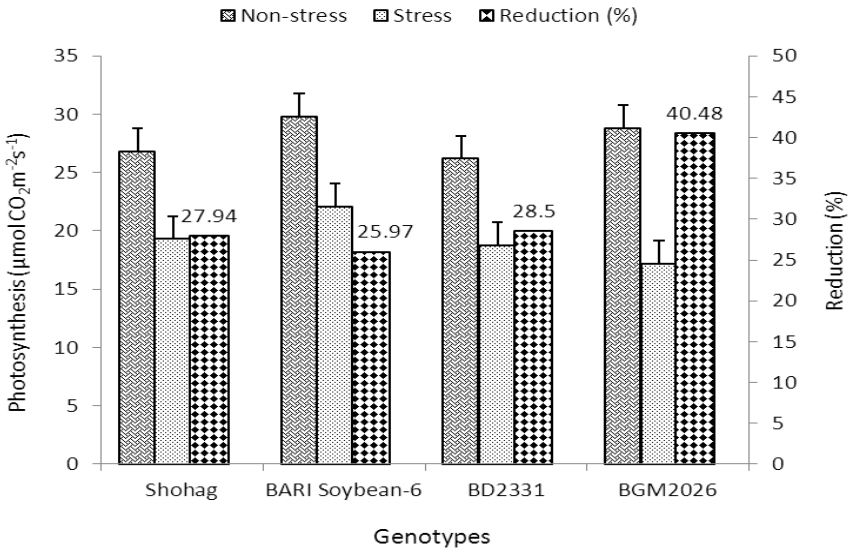

Fig.1 Photosynthesis rate and reduction (%) in four soybean genotypes grown under non-stress and water stress conditions at pod development stage. Vertical bars represent $LSD_{(0.05)}$ value.

Stomatal conductance

Stomatal conductance indicated the degree of exchange of CO_2 and water vapor between ambient and inner leaf. Stomatal conductance decreased very quickly as soil dried (Atteya, 2003). Water stress condition significantly decreased the stomatal conductance of leaves in all the genotypes studied (Fig. 2). Decreased stomatal conductance due to water stress also observed in soybean leaves by Makbul *et al*. (2011). They reported that exposure to drought stress resulted in decreasing in stomatal conductance of 42% in drought stressed leaves as compared to the unstressed leaves. To survive over an extended drought period, it is important for the soybean leaves to adjust its stomatal conductance to prevent excessive water loss (Ku *et al*., 2013). Stomatal conductance ranged from 0.284 to 0.498 and 0.033 to 0.091 mol water m^{-2} s^{-1} under non-stress and water stress conditions, respectively. BARI Soybean 6 showed higher stomatal conductance followed by genotype BGM2026 under non-stress environment but the highest reduction in stomatal conductance occurred in BGM2026. The stomatal conductance of BGM2026 was 0.033 mol water m^{-2} s^{-1} which was much less than that of other three genotypes. The higher reduction of stomatal conductance in BGM2026 due to water stress might be attributed to the lower leaf water potential and a reduction in leaf relative water content, which resulted in loss of turgor vis a vis to reduced photosynthetic rate. In this study, stomatal conductance declined by 78.52 to 93.22% due to water stress. Stomatal conductance was decreased under water stress, and plants grown under drought condition had lower stomatal conductance in order to conserve water (Purwanto, 2003).

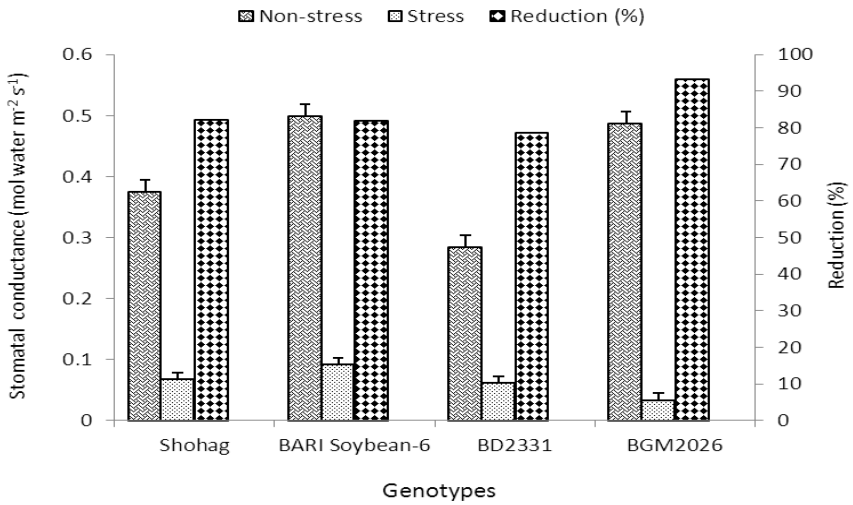

Fig. 2 Stomatal conductance and reduction (%) in four soybean genotypes grown under non-stress and water stress conditions at pod development stage. Vertical bars represent $LSD_{(0.05)}$ value.

Stomatal conductance and photosynthetic rate of soybean genotypes showed a strong positive relationship (r=0.97; Fig. 3). A linear relationship between stomatal conductance and photosynthetic rate was observed at pod development stage indicating that higher the stomatal conductance greater was the photosynthetic rate. Ashraf and Iram (2005) reported that higher stomatal conductance in plants increased CO_2 diffusion into leaf thereby favoring higher photosynthetic rate. However, both variables declined considerably under water deficit stress condition. Similar result was found in *Phaseolus vulgaris* and *Sesbania aculeate* by Ashraf and Iram (2005). Mafakheri *et al*. (2010) also reported that plants grown under drought condition had a lower stomatal conductance in order to conserve water and consequently, the CO_2 fixation was reduced vis a vis photosynthetic rate decreased considerably.

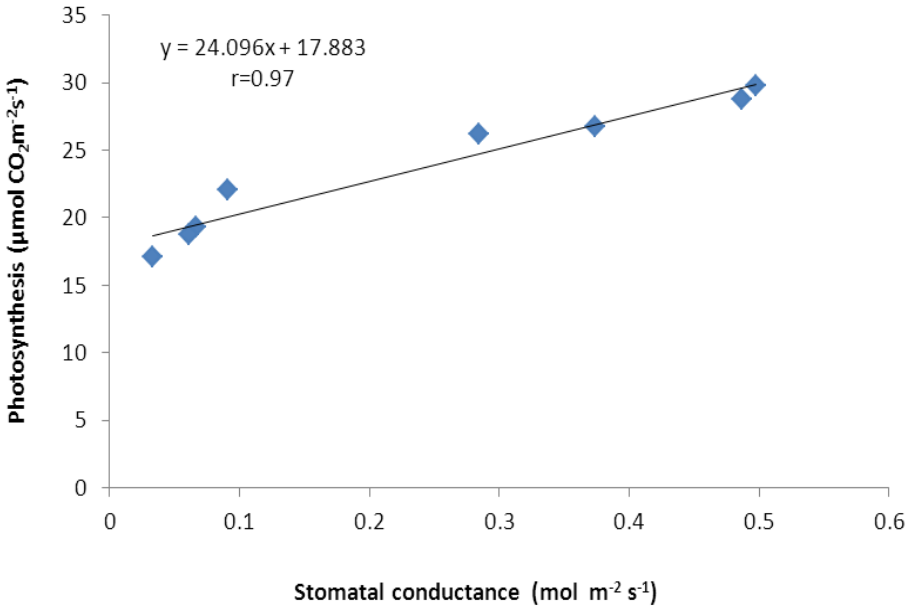

Fig. 3 Relationship between stomatal conductance and photosynthesis at pod development stage.

Transpiration rate

The effect of drought stress on transpiration rate was similar to that on photosynthesis. Transpiration rate in all the four soybean genotypes decreased with water stress (Fig. 4). Under water stress condition, genotype BGM2026 showed higher transpiration rate than the other genotypes. The reduction in transpiration rate was higher in BARI Soybean-6 followed by Shohag while that was the least in the genotype BGM2026 (Fig. 4). Transpiration rate was 21, 31

and 15% lower in Shohag, BARI Soybean-6 and BD2331, respectively than the genotype BGM2026. Genotypes Shohag, BARI Soybean 6 and BD2331 presumably conserved more water than BGM2026. Transpiration rate ranged from 10.3 to 12.09 mmol water m^{-2} s^{-1} under non-stress and 2.52 to 3.35 mmol water m^{-2} s^{-1} under water stress conditions. In response to the water stress, the highest reduction in transpiration rate was observed in BARI Soybean 6 (78.38%), while the lowest in BGM2026 (72.29%) but close to BD2331 (72.71%). Islam *et al*. (2004) reported that the decrease in transpiration under stress conditions may be considered as a drought avoidance mechanism in French bean.

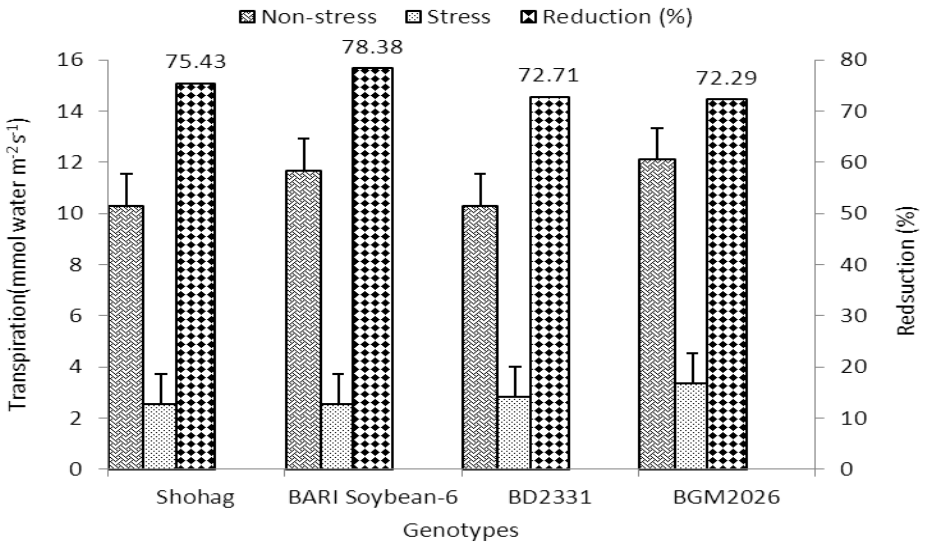

Fig. 4. Transpiration rate and reduction (%) in four soybean genotypes grown under non-stress and water stress conditions at pod development stage. Vertical bars represent $LSD_{(0.05)}$ value.

Avoidance of drought can be realized minimizing water loss by reduction of stomatal conductance or the transpiring leaf surface (Van den Boogaard *et al*., 1996). Leaf water use efficiency may be positively correlated with yield when water is a limiting factor for crop growth (Condon *et al*., 1990). The higher value of water use efficiency at the leaf level resulted from lower rates of transpiration rather than from higher rates of photosynthesis (Van den Boogaard *et al*., 1996).

Leaf growth attributes

Leaf area is the expression of cumulative cell expansion and division during leaf growth and plasticity in leaf area could be a means by which plants control water use under stress conditions. Leaf area of soybean genotypes subjected to drought

stress was significantly lower than those that were not exposed to drought stress. Barrios *et al*. (2005) reported that leaf area of dry beans reduced when the plants expose to drought stress. In this experiment, leaf area in the four genotypes was strongly reduced by water stress (Tables 1 and 2). At vegetative stage, leaf areas of stressed plants were 87, 89, 88 and 74% of that of non stress plants of Shohag, BARI Soybean 6, BD2331 and BGM2026, respectively (Table 1). On the contrary, at pod development stage, the areas of water stressed plants were 71, 72, 70 and 55% (Table: 2) of that of non-stressed of Shohag, BARI Soybean 6, BD2331 and BGM2026, respectively which indicated that the expansion of newer leaves was less under water stress condition compared to non-stress condition. Similar results were observed by Ocampo and Robles (2000) in mungbean. The reduction in leaf area as a result of drought stress is considered to be a drought adaptive mechanism whereby plant avoids becoming dehydrated. With the reduction of leaf area transpiration losses would also be minimized (Purwanto, 2003).

Table 1. Leaf area (LA), specific leaf area (SLA) and specific leaf mass (SLM) of four soybean genotypes at vegetative stage under two water regimes

Genotypes	LA (cm^2)		SLA ($dm^2\ g^{-1}$)		SLM ($g\ dm^{-2}$)	
	Non-stress	Water stress	Non-stress	Water stress	Non-stress	Water stress
Shohag	651.52	569.16	3.25	3.21	0.306	0.314
BARI Soybean 6	717.2	642.8	3.26	3.25	0.306	0.322
BD 2331	625.6	552.7	3.23	3.19	0.308	0.313
BGM 2026	711.12	526.31	3.15	3.09	0.316	0.323
$LSD_{(0.05)}$ S	**		NS		NS	
G	24.69		NS		NS	
SxG	34.91		NS		NS	
CV%	3.91		3.99		5.77	

S=Stress, G=Genotypes, ** significant at 5% levels of probability, NS=not significant.

Specific leaf area (SLA) is an indirect measure of leaf thickness. SLA was not significantly affected during water stress at vegetative stage, though affected at pod development stage. Specific leaf area was slightly higher in non-stress condition, whereas specific leaf mass was higher in water stress condition. Coasta-Franca *et al*. (2000) reported that SLA was not significantly affected during 10 days drought in *Phaseolus vulgaris*. Mondal and Paul (1992) also reported that pre-flowering SLA of the irrigated plants of mustard was significantly higher than that of the rainfed mustard plants. The slightly lower SLA under water stress condition revealed that leaves were to some extent thick

compared to that of non-stress condition. Specific leaf mass (SLM) was significantly affected during water stress at pod development stage. SLM indicates amount of photosynthetic tissues in a unit leaf area increased in response to water stress. An increase in SLM suggests that the water stressed plants may have accumulated dry matter in the leaves more when encountered water stress which is considered as an adaptive strategy to cope with the water stress situation. Higher SLW means high ratio of leaf weight to leaf area and it is indicative of plant ability to reduce water loss (Purwanto, 2003). According to Nobel (1980), increases in rate of photosynthesis have been correlated with increase in specific leaf mass.

Table 2. Leaf area (LA), specific leaf area (SLA) and specific leaf mass (SLM) of four soybean genotypes at pod development stage under two water regimes

Genotypes		LA (cm^2)		SLA ($dm^2\ g^{-1}$)		SLM ($g\ dm^{-2}$)	
		Non-stress	Water stress	Non-stress	Water stress	Non-stress	Water stress
Shohag		1040.8	745.12	3.14	3.02	0.318	0.332
BARI Soybean 6		1093.24	792.66	3.21	3.03	0.311	0.330
BD 2331		982.37	687.65	3.11	2.97	0.320	0.336
BGM 2026		1126.21	624.75	3.25	2.91	0.307	0.342
	S	**		**		**	
$LSD_{(0.05)}$	G	54.15		NS		NS	
	SxG	76.58		NS		NS	
CV%		4.95		4.6		4.41	

S=Stress, G=Genotypes, ** significant at 5% levels of probability, NS=not significant.

Conclusion

It is clear from this study that drought stress tolerance of genotypes Shohag, BARI Soybean 6, BD2331 was associated with higher photosynthetic efficiency and stomatal conductance, maintaining higher leaf area and lower transpiration rate and genotype BGM2026 showed lower tolerance to drought stress.

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EFFECT OF DROUGHT STRESS ON AGRO-MORPHOLOGICAL TRAITS OF LENTIL (*Lens culinaris* Medik.) RECOMBINANT INBRED LINES

M. H. RAHIMI[1], S. HOUSHMAND[2], M. KHODAMBASHI[2]
B. SHIRAN[2] AND S. MOHAMMADY[2]

Abstract

To evaluate the effect of drought stress on agro-morphological traits of lentil, an experiment was conducted using 168 F6:7 inbred lines along with their parents in RCB design with three replications. Analysis of variance revealed significant differences among lines in terms of all studied characters in both normal and stress conditions. Comparing with non-stress condition, drought stress reduced pod weight per plant, seed yield and pod number per plant to 54%, 45.3% and 42.2%, respectively. Correlation coefficient of biological yield, pod number per plant, pod weight per plant and harvest index (HI) with seed yield was positive and significant. Stepwise regression analysis showed that biological yield, HI, pod weights per plant and leaf length determined 87.6% of seed yield variations and biological yield had the most function. Maximum values of genotypic and phenotypic coefficient of variations were observed for seed yield, pod weight per plant and pod number per plant. The highest values of heritability found in leaf width (h^2= 0.77), seed diameter (h^2= 0.69) and plant height (h^2= 0.66). Evaluation of stress tolerance index (STI) showed that lines 125 and 160 were the most tolerant lines, which could be recommended for cultivation in areas that subject to terminal drought stress.

Keywords: lentil, drought stress, recombinant lines, genotypic parameters, yield components.

Introduction

Legumes are being commonly cultivated in the arid and semi-arid regions in the world. The crops have been considered as a part of important human diet especially in the developing countries (Wang *et al.*, 2003). Lentil (*Lens culinaris* Medik.) is an annual diploid self-pollinated legume species that is used in human diet and animal feed as well owing to high protein (up to 28%), micro-nutrient of iron, zinc and beta-carotene (Sarker *et al.*, 2003; Erskine and Sarker, 2004). FAO (2013) reported that world production of lentil was 4.9 million tons with an average yield of 970 kg/ha. The area harvested of lentil in Iran was about 120000 ha with a yield average of 608.33 kg/ha (FAO, 2013). Although lentil originated from Mediterranean areas, it is adapted to hot and semi-arid areas and is

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cultivated in Eastern Asia, North Africa, Indian subcontinent, North America, South America and Australia (Muehlbauer, 2009).

Agro-morphological traits are very important in crop improvement programs. Breeding for these characters along with the crop adaptation, agronomic performance, market value and demands for special uses are the major factors that improve the breeding goals of a crop (Saha *et al.*, 2013). Plant breeders use morphological characters such as plant height, pod number, length and width of leaf, days to flowering, days to maturity, etc. and seed yield as selection criteria (Bayoumi, 2008).

Drought stress is a common concern for successful crops production in many areas of the world. This abiotic stress accrues when the combination of physical and environmental factors cause the inner tension in plant and reduce the yield (Blum, 2002). Water deficit affects almost all morphological and physiological traits that related to growth and decreased even 50% crop yield (Wang *et al*., 2003). Lentil which is mostly grown as a rainfed crop often faces terminal moisture stress in arid regions that led to early maturity and low yield. Yield of lentil in Iran is less than average of the world because it is cultivated after downfall season with low humidity. In Mediterranean environments, lentil is subjected to periodic drought stress during the growth season, too (Silim *et al.*, 1993). According to Oweis *et al*. (2004) drought stress reduced 6 to 54 percentage of lentil yield and production functions relating lentil yield with field water supply under supplemental and rainfed conditions. As a result, drought is considered as the main barrier of lentil yield (Fouad *et al.*, 2011).

In order to develop genotypes resistant to drought, it is necessary for breeder to identify the lentil genotypes with high yield and resistant in confrontation to drought stress. Knowledge of genetic diversity, which exists among different lines of lentil for yield and its components, promotes the program of plant breeding. So far, genetic diversity among lentil genotypes in drought prone-areas has not been studied enough (Kumar *et al.*, 2012). Therefore, special attention was paid on genetic diversity of cultivated genotypes of lentil in drought prone area for attempting a programmatic breeding program. The objectives of present study were to investigate the genetic diversity related to biological yield, pod number per plant, pod weight per plant, 100 grain weight, plant height, leaf length, leaf width, seed diameter and harvest index (HI) of lentil genotypes under normal and drought stress conditions.

Materials and Method

Plant material

In this study, agro-morphological traits were evaluated in 168 lines of a F6:7 population with their parents. This population was generated from cross between

L3685 (a small seeded line as female parent) and Ghazvin (a large seeded line as male parent).

Field experiment

The experiment was conducted in the research field of Shahrekord University, Shahrekord, Iran during the period from March to June 2013 in a Randomized Complete Block Design (RCBD) with three replications. The experiment was carried out at two irrigation levels (normal and drought stress at flowering stage). Each plot consisted of one row of 150 cm long and 25 and 10 cm space between rows and within rows, respectively. Lentil lines were sown on 07 March, 2013. Weeding and other management practices were done when necessary. Drought stress was imposed by cutting irrigation at 50% flowering stage of the crop. When the plants of each line showed drought stressed symptom, five plants from each line were selected randomly. The plants were harvested on 30 July, 2013, then some traits such as biological yield (g), pod number per plant, pod weight per plant (g), 100-grain weight (g), plant height (cm), leaf length, leaf width (cm), seed diameter (mm), HI (%) and seed yield per plant (g) were measured.

Statistical analysis

Analysis of variances was performed using SAS 9.2 software (SAS Institute, 2008). LSD test was used for mean comparison. Reduction percentage in the mean value of each trait due to drought stress was calculated as follow:

$$C = \frac{\overline{X}_{ns} - \overline{X}_{ds}}{\overline{X}_{ns}}$$

Where $\overline{X}_{ns}$ and $\overline{X}_{ds}$ are the means of traits in normal and stress conditions, respectively. For understanding relationships between traits with seed yield, Pearson correlation coefficient and Stepwise regression analysis were used. Broadsence heritability was estimated with genetic variance to phenotypic variance ratio ($\frac{\delta_g^2}{\delta_p^2}$) (Falconer, 1996). For evaluating tolerance in the studied lines, STI (Stress Tolerance Index) were computed as follow (Fernandez, 1992):

$$STI = \frac{Y_{pi} * Y_{si}}{\bar{Y}_p^2}$$

where Y_{Pi} and Y_{Si} are the seed yield of lines in normal and stress conditions, respectively, and $\bar{Y}_n$ is the mean of all lines in normal conditions.

Results and Discussion

Results of analysis of variance showed that significant differences exist in terms of all studied traits between normal and stress condition and also among studied lines (Table 1) as well as, interaction effect of line × environment for all traits. It indicates that not only the levels of irrigation had different effects on characters, but studied lines had also different reactions to terminal drought stress. These results reveal the high values of genetic diversity. Bayoumi (2008) in a study of effect of different irrigations on 27 genotypes of lentil stated that high genetic diversity existed in terms of studied traits and effect of line × environment. Kumar *et al.* (2012) observed high diversity for biological yield, seed yield and HI in 43 genotypes of lentil in drought stress condition. Based on coefficient of variations (CV), it could be stated that experiment had carried out with acceptable accuracy. Leaf width and biological yield had the highest and the lowest CV values, respectively. Table 2 shows the percentage reduction of traits mean in normal and drought condition. The results revealed that drought stress decreased all the traits except for leaf width (Table 2). With the view to %reduction, it was clear that reaction of characters due to drought stress was different. It was observed from Table 2 that water deficient had the highest effect on pod weight per plant, seed yield and pod number per plant, so as to reduce them 54%, 45.3% and 42.2%, respectively. Traits associated to leaf (length and width of leaf) had the minimum unaffected from stress. Hosseini *et al.* (2011) pointed out that irrigating in flowering stage increased 52% seed yield of lentil compared to condition without irrigation. Drought stress or water deficient had significant impact on yield and its components and in a study of Panahyan-e-Kivi *et al.* (2009) drought stress reduced the pod number per plant, seed number per pod and 100 grain weight.

Study of correlation is a useful tool for determination of extent and direction of the relationship between different variables with seed yield (Gashaw *et al.*, 2007). According to the results, a positive and significant correlation between biological yield, pod weight per plant, pod number per plant and HI were observed in both the conditions (Table 3). Plant height had a positive and significant correlation with seed yield only in normal condition. This result is compatible with Sarker *et al.* (2003). It revealed from Table 3 that a significant positive correlation exists between leaf width and grain yield in normal condition; while correlation of leaf length with grain yield under drought stress condition was negative and significant. Kumar *et al.* (2012) observed significant and positive correlations between seed yield with seedling vigour, number of pods per plant, biological yield, HI and chlorophyll content under drought stress condition. In the present study, the seed diameter had negative correlation with grain yield in drought condition (Table 3).

Table 1. Analysis of variances for yield and other traits in a F6:7 population of lentil under different irrigation treatments

S.O.V	df	MS (Mean Square)									
		BY	PH	LL	LW	NP	WP	GW	HI	SD	SY
Irrigation	1	1593.10**	5124.27**	0.19*	0.06*	200108.48**	89.54**	55.05**	7290.50**	47.96**	234.76**
Error 1	4	0.04	4.59	0.005	0.007	24.97	0.001	0.002	0.27	0.16	0.006
Line	169	20.10**	47.09**	0.34*	0.037**	3158.59**	1.05**	0.66**	145.57**	0.52**	3.53**
Line × Stress	169	5.42**	7.88**	0.26**	0.03**	788.24**	0.48**	0.16**	36.16**	0.09**	1.10**
Error 2	676	0.02	1.19	0.03	0.01	11.91	0.002	0.006	0.36	0.004	0.006
CV%	--	1.72	4.64	7.03	10.21	6.59	6.11	3.83	3.33	1.93	4.96

ns, * and **: Non-significant, significant at the 0.05 and 0.01 probability level, respectively.

BY= Biological Yield; PH: Plant Height; LL= Leaf Length; LW= Leaf Width; NP= Number of Pods, WP= Weight of Pods; GW= 100 Grains Weight; HI= Harvest Index; SD= Seed Diameter and SY= Seed Yield.

Table 2. Mean of agro-morphological traits in a F6:7 population of lentil under normal (N) and water deficit stress (S) conditions and percent of reduction (%R)

	BY	PH	LL	WL	NP	WP	GW	HI	SD	SY
N	9.66 a	25.76 a	2.72 a	1.01 a	66.31 a	1.10 a	2.39 a	21.94 a	3.81 a	2.12 a
S	7.16 b	21.28 b	2.70 b	0.99 b	38.30 b	0.50 b	1.93 b	16.20 b	3.25 b	1.16 b
%R	25.87	17.40	0.95	1.63	42.25	54.00	19.42	25.69	14.78	45.30

BY= Biological Yield; PH: Plant Height; LL= Length of Leaf; WL= Width of Leaf; NP= Number of Pods, WP= Weight of Pods; GW= 100 Grains Weight; HI= Harvest Index; SD= Seed Diameter and SY= Seed Yield.

Table 3. Correlation coefficient between agro-morphological traits with yield in a F6:7 population of lentil under normal (above diameter) and water deficit stress (below diameter) conditions

	BY	PH	LL	WL	NP	WP	GW	HI	SD	SY
BY	1	0.25**	-0.05	0.06	0.91**	0.83**	0.07	0.70**	-0.02	0.92**
He	0.12	1	0.04	-0.007	0.26**	0.17*	0.01	0.20**	-0.02	0.22**
LL	-0.71**	0.18*	1	0.64**	-0.08	-0.15*	0.05	0.15	0.02	0.10
WL	-0.25**	-0.15*	0.58**	1	0.07	-0.16*	0.17*	0.28**	0.05	0.23**
NP	0.89**	0.10	-0.75**	-0.26**	1	0.66**	0.07	0.64**	-0.07	0.83**
WP	0.80**	0.13	-0.62**	-0.51**	0.67**	1	0.03	0.33**	0.03	0.60**
GW	0.05	0.003	0.19*	0.68**	0.05	0.03	1	0.10	0.06	0.08
HI	0.75**	0.05	-0.44**	0.09	0.68**	0.41**	0.12	1	-0.05	0.90**
SD	-0.12	-0.11	0.05	0.03	-0.13	-0.05	0.06	-0.18*	1	-0.03
SY	0.90**	0.07	-0.54**	0.0004	0.80**	0.59**	0.10	0.95**	-0.17*	1

BY= Biological Yield; PH: Plant Height; LL= Length of Leaf; WL= Width of Leaf; NP= Number of Pods, WP= Weight of Pods; GW= 100 Grains Weight; HI= Harvest Index; SD= Seed Diameter and SY= Seed Yield.

According to the results of the regression analysis (Table 4), 10 independent variables were introduced to model in four steps, and finally 87.6% of yield changes were determined by the biological yield, HI, pod weight per plant and leaf length as input variables.

Table 4. Indicators of Stepwise regression of traits in yield (g/per plant)

Step	R (Multiple correlation coefficient)	(R^2) Determination coefficient	(R^2 Ad) Modified determination coefficient	(Std. Error)
1	0.878	0.772	0.772	0.35
2	0.930	0.866	0.866	0.18
3	0.933	0.871	0.871	0.17
4	0.983	0.876	0.876	0.15

The results of ANOVA for validating of final model showed that the model was significant (Table 5).

Table 5. Results of stepwise regression analysis for seed yield (per plant)

ANOVA

Model	S.O.V	Sum of Squares	df	Mean Square	F	Significant level
	Regression	998.457	4	249.614	10261.747	0.000
4	Residual	24.690	1015	0.024		
	Total	1023.147	1019			

According to Table 5, equation derived from stepwise regression for seed yield was as follow:

Seed Yield = -2.738 + 0.423 (BY) + 0

Seed Yield = -2.738+0.423 (BY) + 0.057 (HI) -0.412 (WP) + 0.191 (LL), R^2 = 0.876

Where BY is biological yield, HI is harvest index, WP is pod weight pre plant and LL is leaf length.

In accordance to Standardized regression coefficients (Table 6), biological yield determine more yield changes in comparison with other variables. After it, HI and pod weight per plant were considered as positive and negative factors, respectively, to achieve high yield. It seemed that biological yield and pod weight could be used as main keys for indirect selection. Aghili *et al.* (2012) used stepwise regression and reported that increasing in biological yield would have desirable effect on seed yield. Tadayyon *et al.* (2011) stated that using standard multiple regression analysis it could be useful to investigate the relationship

between yield and 100-seed weight, number of seeds per pod and number of pods per plant highly affected seed yield.

Table 6. Coefficient and indicators of stepwise regression related to measured traits on seed yield (per plant)

Model	Regression coefficient	Std. Error	Standardized regression coefficients	t-Test	Significant level
Intercept	-2.738	0.057		-48.392	0.000
Biological Yield	0.423	0.012	1.018	36.751	0.000
Harvest Index (%)	0.057	0.002	0.349	36.337	0.000
Weight of Pods Per Plant	-0.412	0.024	-0.241	-17.207	0.000
Length of leaf	0.191	0.014	0.067	13.838	0.000

The estimation of genetic variance (Vg), phonotypic variance (Vp), genotypic coefficient of variation (CVg) and phonotypic coefficient of variation (CVp) from ANOVA were showed in Table 7. It was observed that the values of Vp and CVp were more than in contrast to values that related to Vg and CVg in all traits. This is proved more contributions of environment in expression of these characters (Makeen *et al.,* 2007).

Maximum values of CVg were observed for seed yield (38.84%), pod weight per plant (38.47%) and pod number per plant (38%). In contrast, the highest values of CVp were in pod weight per plant (63.19%), seed yield (53.75%) and pod number per plant (49.33). High values of CVg and CVp for seed yield and pod number per plant were reported by Sadiq *et al.* (2000) and Sarwar *et al.* (2013).

Table 7. Estimates of variance components, coefficient of variation and heritability in a F6:7 population of lentil under normal and water deficit stress conditions

Traits	Vg	Vp	CVg%	CVp%	h^2
Biological Yield	2.45	4.27	18.59	24.56	0.57
Height	6.54	9.96	10.87	13.41	0.66
Length of Leaf	0.01	0.12	4.26	12.78	0.11
Width of Leaf	0.06	0.07	23.75	27.02	0.77
Number of Pods	395.06	665.75	38.00	49.33	0.59
Weight of Pods	0.10	0.26	38.47	63.19	0.37
100 Grains Weight	0.08	0.14	13.36	17.36	0.59
Harvest Index	18.24	30.53	23.54	30.46	0.60
Seed Diameter	0.07	0.10	7.59	9.16	0.69
Seed Yield	0.41	0.78	38.84	53.75	0.52

Vg = Genetic variance, Vp= Phenotypic variance, CVg% = Genotypic coefficient of variation, CVp% = Phenotypic coefficient of variation, h^2 = Heritability.

Maximum heritability was in leaf width (h^2= 0.77), seed diameter (h^2= 0.69) and height (h^2= 0.66) that indicated the low environmental effect on them in contrast to other traits. Such traits could be used as powerful tools for selecting of lentil genotypes. Heritability for seed yield was 0.52. For other traits moderate heritability were estimated except leaf width. According to Younis *et al.* (2008) high heritability exists in seed yield, HI and days to flowering. Tyagi and Khan (2010) stated that pod number per plant, 100-seed weight, HI and seed yield had high heritability.

Stress Tolerance Index (STI) introduced by Fernandez (1992) is a perfect tool to select, determine and identify the genotypes that have the maximum yield in normal and stress conditions. STI index revealed that the studied lines had high diversity in reflected to terminal drought stress (Table 8). While Lines 160 and 125 in normal condition and lines 125 and 63 in stress condition had maximum values of seed yield, lines 93 and 98 had the lowest productivity in both conditions. Seed yield of L3685 was more than Ghazvin in both conditions. L3685 parent was also more tolerant to other parent (Ghazvin). In accordance with Table 5, it revealed that lines 125 and 160 were the most tolerant lines comparing to other lines. Therefore to cultivate in the area where lentil lines faces terminal drought stress, these lines might be recommended. On other hand, lines 93 and 98 were the most sensitive to drought stress.

Conclusion

Drought stress caused the significant reduction in yield and its components. Results indicated that considerable variations exist related to biological yield, pod number per plant, pod weight per plant, 100-grain weight, plant height, leaf length, leaf width, seed diameter and harvest index among the lentil lines. These characters could be used for screening to drought stress tolerance of lentil. The results showed that biological yield, number and weight of pods were the main keys for indirect selection for resistance to water deficient. Two lines (125 and 160) have been found that had remarkable resistance to drought stress.

Table 8. Stress Tolerance Index (STI) in a F6:7 population of lentil under normal (Yp) and water deficit stress (Ys).

Line	Yp (g per Plant)	Ys (g per plant)	STI	Line	Yp (g per Plant)	Ys (g per plant)	STI
1	2.73	1.75	1.06	**51**	2.18	1.46	0.71
2	2.62	1.96	1.15	**52**	0.64	0.55	0.08
3	2.25	2.01	1.01	**53**	1.30	0.43	0.13
4	0.66	0.37	0.05	**54**	3.66	1.63	1.33
5	2.18	1.39	0.68	**55**	2.28	0.32	0.16
6	1.54	1.36	0.47	**56**	2.37	1.65	0.87

Table 8. Cont'd

Line	Yp (g per Plant)	Ys (g per plant)	STI	Line	Yp (g per Plant)	Ys (g per plant)	STI
7	1.93	0.84	0.36	**57**	1.83	0.53	0.22
8	1.23	1.14	0.31	**58**	2.32	1.05	0.54
9	1.85	1.35	0.56	**59**	4.67	1.26	1.31
10	2.43	1.96	1.06	**60**	2.44	0.61	0.33
11	2.92	2.55	1.66	**61**	2.51	1.19	0.67
12	1.55	1.22	0.42	**62**	1.49	0.51	0.17
13	1.71	1.52	0.58	**63**	2.25	0.75	0.37
14	1.27	0.75	0.21	**64**	1.84	0.50	0.21
15	2.49	1.52	0.84	**65**	1.59	0.83	0.29
16	0.77	0.43	0.07	**66**	1.87	1.38	0.57
17	2.10	1.38	0.64	**67**	1.15	0.56	0.14
18	2.03	1.76	0.80	**68**	1.50	0.54	0.18
19	1.13	0.72	0.18	**69**	3.13	2.23	1.55
20	0.86	0.43	0.08	**70**	1.18	0.84	0.22
21	0.71	0.34	0.05	**71**	2.85	1.87	1.19
22	1.37	0.96	0.29	**72**	2.51	1.48	0.83
23	1.34	0.94	0.28	**73**	2.07	1.71	0.79
24	1.17	0.69	0.18	**74**	3.15	1.19	0.84
25	1.06	0.66	0.15	**75**	3.56	0.62	0.49
26	1.94	1.01	0.44	**76**	1.41	1.10	0.35
27	2.04	1.12	0.51	**77**	2.07	1.43	0.66
28	0.91	0.51	0.10	**78**	1.80	1.29	0.52
29	1.47	0.76	0.25	**79**	4.77	1.81	1.93
30	1.24	0.74	0.21	**80**	3.76	1.36	1.14
31	0.76	0.54	0.09	**81**	3.69	2.35	1.94
32	1.24	0.93	0.26	**82**	4.36	1.40	1.36
33	1.25	0.49	0.14	**83**	1.66	0.42	0.15
34	1.97	1.33	0.58	**84**	2.45	1.28	0.70
35	2.71	0.67	0.41	**85**	1.37	0.67	0.20
36	2.38	1.98	1.05	**86**	1.59	1.91	0.68
37	2.22	1.25	0.62	**87**	2.73	1.33	0.81
38	1.65	1.04	0.38	**88**	1.74	1.20	0.46
39	1.85	1.16	0.48	**89**	1.57	1.12	0.39
40	1.44	0.73	0.23	**90**	0.62	0.33	0.05
41	1.49	0.85	0.28	**91**	1.04	0.54	0.12
42	2.89	1.64	1.06	**92**	0.77	0.43	0.07

Table 8. Cont'd

Line	Yp (g per Plant)	Ys (g per plant)	STI	Line	Yp (g per Plant)	Ys (g per plant)	STI
43	2.52	0.88	0.50	**93**	0.52	0.32	0.04
44	2.21	1.05	0.52	**94**	0.76	0.73	0.12
45	1.60	1.45	0.52	**95**	1.14	0.58	0.15
46	2.16	1.45	0.70	**96**	2.15	1.80	0.86
47	1.09	0.74	0.18	**97**	1.45	1.38	0.45
48	4.66	2.84	2.95	**98**	0.52	0.22	0.03
49	2.76	1.20	0.74	**99**	0.87	0.65	0.13
50	1.77	1.31	0.52	**100**	0.75	0.57	0.10
101	1.10	0.55	0.13	**136**	3.51	1.03	0.81
102	1.45	1.26	0.41	**137**	2.35	1.06	0.55
103	4.18	2.76	2.57	**138**	4.52	1.33	1.34
104	4.51	0.96	0.97	**139**	2.20	1.32	0.65
105	0.65	0.57	0.08	**140**	1.94	0.92	0.40
106	1.93	1.58	0.68	**141**	2.05	0.94	0.43
107	3.75	1.10	0.92	**142**	3.33	1.02	0.75
108	2.73	1.89	1.15	**143**	2.03	1.67	0.75
109	1.85	1.65	0.68	**144**	2.00	0.52	0.23
110	1.12	0.79	0.20	**145**	4.32	1.86	1.79
111	0.84	0.75	0.14	**146**	3.10	0.65	0.45
112	1.12	0.56	0.14	**147**	2.95	0.72	0.47
113	2.46	1.84	1.01	**148**	3.76	1.41	1.18
114	2.72	1.20	0.73	**149**	3.03	2.67	1.80
115	1.23	0.83	0.23	**150**	2.45	1.51	0.83
116	2.27	1.11	0.56	**151**	3.44	0.54	0.42
117	1.64	0.98	0.36	**152**	2.25	1.12	0.56
118	1.36	0.99	0.30	**153**	1.93	1.14	0.49
119	1.73	1.95	0.75	**154**	1.32	1.37	0.40
120	1.74	0.77	0.30	**155**	1.01	1.03	0.23
121	2.09	1.81	0.84	**156**	3.14	1.70	1.19
122	2.13	1.08	0.51	**157**	2.27	0.88	0.44
123	1.52	0.95	0.32	**158**	1.98	1.12	0.49
124	1.54	1.62	0.56	**159**	2.95	1.52	1.00
125	5.86	2.93	3.83	**160**	7.11	1.93	3.06
126	1.42	0.78	0.25	**161**	2.87	1.34	0.86

Table 8. Cont'd

Line	Yp (g per Plant)	Ys (g per plant)	STI	Line	Yp (g per Plant)	Ys (g per plant)	STI
127	1.55	0.98	0.34	**162**	2.61	1.77	1.03
128	1.45	0.84	0.27	**163**	2.09	1.38	0.65
129	4.93	2.30	2.53	**164**	1.46	1.16	0.38
130	3.34	2.10	1.56	**165**	2.09	1.23	0.58
131	2.43	1.62	0.88	**166**	2.05	0.94	0.43
132	0.87	0.64	0.12	**167**	1.16	0.43	0.11
133	0.76	0.47	0.08	**168**	1.15	0.84	0.21
134	1.35	0.77	0.23	**Ghazvin**	1.85	0.86	0.36
135	2.67	0.95	0.56	**L-3685**	2.53	1.53	0.86

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INFLUENCE OF SUCROSE AND ALUMINIUM SULPHATE ON VASE LIFE OF CUT HIPPEASTRUM FLOWER (*Hippeastrum hybridum* Hort.)

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Abstract

An experiment with Hippeastrum flower (*Hippeastrum hybridum* Hort.) cv. 'Apple Blossom' comprising three sucrose concentrations viz. 0 (control), 2 and 4 % and five aluminium sulphate concentrations viz. 0 (control), 0.25, 0.50, 0.75 and 1.0 mM at the Horticulture Laboratory of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh during the period from April 01 to April 30, 2009. The experiment was laid out in a Completely Randomized Design (CRD) with three replications. Sucrose, aluminium sulphate and their combinations had significant influence on most of the parameters studied. Transpiration loss and water uptake ratio decreased significantly with the increased sugar levels and aluminium sulphate upto 0.75 mM beyond which they were increased. Transpiration loss and water uptake ratio was found minimum in the vase solution containing 4% sucrose (0.78) and 0.75 mM aluminium sulphate (0.80), which ultimately resulted in an enhanced vase life (9.2 days for sucrose and 9.11 days for aluminium sulphate) of cut Hippeastrum flower. A linear relationship between water uptake and vase life of flowers was found (y = 0.056x + 5.791). Sucrose 4% and aluminium sulphate 0.75 mM in combination gave maximum total water uptake, maximum days to onset of deterioration, the highest average fresh weight of single scape at 6^{th} and 10^{th} day after setting the trial. Transpiration loss and solution uptake ratio was found maximum in the combination of 4% sucrose and 0.75 mM aluminium sulphate (0.48) with the longest vase life of 10.33 days of cut Hippeastrum flower cv. 'Apple Blossom'.

Keywords: Sucrose, aluminium sulphate, transpiration loss, vase life, Hippeastrum flower and *Hippeastrum hybridum* Hort.

Introduction

Hippeastrum (*Hippeastrum hybridum* Hort.), a member of Amaryllidaceae family is one of the finest flowering bulbous plants. The genus Hippeastrum consists of 75 species and more than 300 cultivars (Bhattacharjee and De, 2010).The flowers are typically arranged in umbels at the apex of leafless flowering stem, called a

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scape. The flowers are spectacular having various shades of bright colour and wide range of variation exists in cultivars developed by hybridization. It is a well known pot and garden plants. It is also popular as cut flowers because of their large size, attractive colour, and good keeping quality. The flowers can be used to beautify the garden and decorate the verandah and also for great demand as cut flowers in floriculture trade (Datta *et al*., 2008).

Vase life of the Hippeastrum flower varies from 10-15 days depending on the number of flower per scape, environment and change of water. Sucrose and aluminium sulphate are used as preservatives in vase solution for prolonging the vase life of cut flowers (Gowada, 1990; Gowada and Murthy, 1994; Gowada and Gowada, 1990). Sucrose is the most widely used floral preservatives that maintain the pool of dry matter and respirable substrates in floral petals and exogenous sucrose replaces the depleted endogenous carbohydrates utilized during post harvest life of cut flowers (De and Bhattacharjee, 2006). Treatment with sucrose promoted unfolding petals, suppresses the decrease in fresh dry weight of cut flowers and inhibition on the occurrence of petals senescence (Ichimura *et al*., 2003).

Aluminium sulphate, a germicide, has been found to reduce petal pH to stabilize the anthocyanin of petals to acidify the holding solution, to reduce bacterial and fungal growth (Halevy and Mayak, 1981) and it is reported that aluminium sulphate extended vase life and improved water relation of cut rose flowers by antimicrobial effect (Ichimura and Ueyama, 1998). Farhat *et al*. (2014) reported that sucrose in combination with aluminium sulphate is better for improving vase life in rose. Several attempts have also been made to study the effect of some germicide and sugars on longevity and keeping quality to tube rose (Pathak *et al.*, 1979). There has been reported that the Hippeastrum cut flower remains fresh for a longer period if it is kept in 3 percent sugar solution (Jana, 1979).

Despite the importance of Hippeastrum as well known cut flower, very few research works have been done on vase life of cut Hippeastrum scapes using sucrose and aluminium sulphate. The present investigation was therefore, undertaken to find out the optimum concentration of sucrose and aluminium sulphate for enhancing vase life and keeping quality of cut Hippeastrum flower.

Materials and Method

The experiment was conducted at the Horticulture laboratory of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur during 01 April to 30 April, 2009 to observe the effect of different concentrations of sucrose and aluminium sulphate on post harvest physiology of Hippeastum flower cv. Apple Blossom in vase under normal room temperature ($30^0C \pm 2^0C$). The experiment was laid out in a Completely Randomized Design (CRD) with

three replications. There were 15 treatment combinations comprising three concentrations of sucrose viz. S_0 = 0% (control), S_1 = 2% and S_2 = 4% and five concentrations of aluminium sulphate viz. A_0 = 0% (control), A_1 = 0.25 mM, A_2 = 0.50 mM, A_3 = 0.75 mM and A_4 = 1.0 mM.

Forty five conical flasks (500 ml each) were filled with 300 ml distilled water for both sucrose (0, 2 and 4%) and different concentration of aluminium sulphate (0, 0.25, 0.50, 0.75 and 1.0 mM) on respective conical flask and dissolved it by hand shaking. The plants of Hippeastrum cv. Apple Blossom were grown in the Horticulture Research Field of BSMRAU following the recommended package of production techniques. Hippeastrum floral scapes were harvested when the buds were fully elongated but not full open. The floral scapes were harvested early in the morning and were immediately placed in water. During harvesting, the scapes were cut horizontally in uniform length of 30 cm by sharp knife. Then the floral scapes were trimmed by about 2 cm under water again prior to place them in holding solution After harvesting, the scapes were carried out to the Horticulture laboratory and fresh weight was measured. Two floral scapes were used for each treatment consisting of a 500 ml conical flask containing 300 ml vase solution of given concentrations. The conical flasks were kept at room temperature of $30^0C \pm 2^0C$ with 65- 80% relative humidity and adequate aeration. Data were recorded on every day based on the following parameters. Water uptake, transpiration loss of water and fresh weight was determined on alternate days.

a) **Water uptake (g):** The difference in weight between consecutive measurements of the conical flask + solution (without floral scape) represented the water uptake.
b) **Transpiration loss of water (g):** The difference in weight between consecutive measurements of the conical flask + solution + floral scape represented the transpiration loss of water.
c) **Fresh weight of floral scape:** The difference between the weight of conical flask + solution + floral scape and the weight of conical flask + solution represented the fresh weight of scape on that particular day.
d) **Days taken to deterioration started:** Days counted when the petals of the flowers started to dry.
e) **Vase life (days):** Wilting or fading of 50 percent of the flowers per scape was considered the end of the vase life of the floral scape.

All the recorded data were statistically analyzed through partitioning the total variance with the help of computer based MSTAT C Program. The difference between treatments means were compared by Duncan's Multiple Range Test (DMRT) (Gomez and Gomez, 1984).

Results and Discussion

A. Effect of sucrose

Water uptake

Total water uptake for a period of 10 days by the floral scape differed significantly due to sucrose levels (Table 1).The scape held in 4% sucrose had the maximum water uptake (57.08 g) closely followed by the scape held in 2% sucrose and the scapes held in control had the minimum water uptake. Sugars play an important role in flower development, either as an energy source for respiration or as osmotically active substances, which aid in maintaining the turgidity of the expanding corollas. Sucrose improves water absorption from the vase solution which made a better water balance by maintaining turgidity and flower freshness (Reddy and Singh, 1997) and saves from early wilting resulting in enhanced vase life. This result is in agreement with the findings of Shobha and Gowda (1994) in calendula; Reddy *et al*. (1994) in gladiolus and Singh *et al*. (1994) in tuberose. The minimum water uptake of 45.10 g by the scape was recorded in control (without sucrose).

Transpiration loss of water

Water loss from the flower tissue by transpiration during the experimental period was influenced significantly by sucrose (Table 1). The scape held in solution without sucrose, with lower water uptake, recorded the highest water loss at 10 days (60.46 g) and those held in solution with 4% sucrose recorded the lowest water loss at 10 days (42.27 g). This might be due to the fact that sugar helped reduce moisture stress in cut Hippeastrum flowers by affecting stomatal closure, preventing water loss due to transpiration. The findings of the experiment corroborate the results of Khondakar and Mozumder (1985) in tuberose and Gowda (1986) in China aster.

Transpiration loss and water uptake ratio

The ratio of transpiration loss and water uptake is an indication of water balance in the flower scape. The transpiration loss and water uptake ratio was affected significantly by sucrose (Table 1). The ratio was found the highest (1.36) for the scape held in distilled water only (control) and it was the lowest (0.78) for the scape held in vase solution with 4% sucrose. The lowest transpiration loss and water uptake ratio was found in sucrose solution because it increased water uptake and decreased water loss due to transpiration by regulating stomatal opening. This is in agreement with Gupta *et al.* (1994) who reported that 4% sucrose solution significantly reduced the ratio in gladiolus cut flowers.

Days to onset of deterioration

Days to onset of deterioration was not significantly influenced by sucrose level (Table 1). However, the longest duration to onset of deterioration (7.9 days) was

observed in floral scape which holds 4% sucrose solution followed by 2% sucrose solution. The earliest deterioration (5.7 days) of floral scape was commenced in control. The onset of deterioration started when turgor of cut flowers was reduced by water deficit. This is in agreement with Khondakar and Mozumder (1985) who reported that the tuberose cut flowers retained their freshness for longer periods when higher concentrations of sucrose (3%) were used. The treatment was also effective in retarding the abscission rate of the petals of the flowers.

Vase life

The vase life of the floral scape was affected significantly by sucrose levels (Table 1). The floral scape placed in 4% sucrose lasted for 9.2 days, while those in solution without sucrose lasted for only 7.00 days. The extended vase life might be due to water balance in cut Hippeastrum flowers as affected by sucrose in vase solution. Sugar also serves as a building block needed for the growth processes associated with flower opening and provides sufficient intercellular carbohydrate reserves to ensure an optimum vase life. These results are in agreement with previous workers who reported that sucrose was better than distilled water for preserving cut flowers of gladiolus cv. Priscilla and Moana (Garibaldi and Dembrogio, 1989). Treatment with 6% sucrose maintained vase life of gladiolus for up to 11 days, which was better than that of distilled water was also reported by Anserwadekar and Patil (1986).

Table1. Main effect of sucrose on postharvest physiology and quality of Hippeastrum flower

Treatment (Sucrose)	Total water uptake in 10 days(g/scape)	Transpiration loss in 10 days (g/scape)	Transpiration loss and water uptake ratio	Days to onset of deterioration	Vase life (days)
S_0 (Control)	45.10 b	60.46 a	1.36 a	5.7	7.0 b
S_1 (2%)	48.25 ab	49.72 b	1.05 b	6.4	8.2 b
S_2 (4%)	57.08 a	42.27 b	0.78 b	7.9	9.2 a
Level of significance	**	**	**	ns	**
CV (%)	5.11	4.54	7.57	16.53	14.54

Means in the same column followed by different letters are significantly different by DMRT. ** indicates significant at 1% level and 'ns' indicates non-significant

B. Effect of aluminium sulphate

Water uptake

Different levels of aluminium sulphate influenced significantly on water uptake of the floral scape (Table 2). The scapes held in 0.75 mM $Al_2(SO_4)_3$ had the

highest water uptake (61.90 g), while those held in a solution without $Al_2(SO_4)_3$ (control) had the minimum water uptake (41.18 g). At higher conc. of aluminium sulphate (1.0 mM), water uptake declined due to phyto toxicity in vase solution which causes chlorophyll degradation, chlorophyll fluorescence and increase in membrane permeability. Water absorbed by cut flowers is inversely related to the degree of vascular blockage. Since $Al_2(SO_4)_3$ acts as a germicide, thereby encouraging continuous water transport through the cut stem by inhibiting the vascular blockage and delaying the increase in membrane permeability. This corroborates the result of Shobha and Gowda (1994) in cut calendula flowers.

Transpiration loss of water

In case of $Al_2(SO_4)_3$, the maximum water loss (55.56 g) was observed in the scapes which held in solution without $Al_2(SO_4)_3$ and the minimum water loss (47.11 g) were found in 0.75 mM $Al_2(SO_4)_3$ solution (Table 2). The results are in close conformity with the findings of Shobha and Gowda (1994), who reported that the transpiration loss in cut calendula flowers was affected by accumulation of $Al_2(SO_4)_3$ both in the transpiring tissue and water content.

Transpiration loss and water uptake ratio

Transpiration loss and water uptake ratio (1.36) was found the highest from the scapes held in solution without aluminium sulphate (Table 2). Addition of $Al_2(SO_4)_3$ reduced the ratio either by improving the water uptake or reducing the water loss by transpiration, thus improving the water balance in the tissue. The ratio was found the lowest (0.80) from the scape held in solution containing 0.75 mM $Al_2(SO_4)_3$.

Days to onset of deterioration

Days to onset of deterioration of Hippeastrum cut flower was significantly influenced by different levels of $Al_2(SO_4)_3$ (Table 2). Flowers on scapes took the maximum days (7.4) for starting the deterioration at 0.75 mM $Al_2(SO_4)_3$ which was closely followed by (7.1 days) at 1.0 mM $Al_2(SO_4)_3$. The minimum days (5.9) for deterioration of flowers were starting in control. One of the major requirements for an increased vase life i.e. delays in deterioration of cut flowers is that water uptake should not be hindered. Some workers reported that stem blockage is the major cause of water deficit and wilting of cut flowers (Rogers, 1973). Since $Al_2(SO_4)_3$ increases the water uptake, it might act to inhibit vascular blockage by suppressing microbial growth.

Vase life

$Al_2(SO_4)_3$ had no significant effect on vase life of Hippeastrum cut flowers (Table 2). However, the floral scape held in 0.75 mM $Al_2(SO_4)_3$ had the

maximum vase life (9.11 days), which was closely followed by 8.67 days at 1.0 mM $Al_2(SO_4)_3$ solution and 7.78 days at 0.50 mM $Al_2(SO_4)_3$. The minimum vase life (7 days) for the scape was found in distilled water. The extension of vase life by $Al_2(SO_4)_3$ as observed in the present investigation, accords with previous results obtained in narcissus flowers (Goszczynska *et al.*, 1989) and tuberose (Gowda, 1990). Aluminium sulphate acts as a germicide, and improves water uptake by cut calendula (Shobha and Gowda, 1994) and gladiolus (Gowda and Murthy, 1994) and thereby maintains the fresh weight. It is possible that $Al_2(SO_4)_3$ delays senescence of Hippeastrum flowers by increasing water uptake and maintaining a higher fresh weight, leading to enhanced vase life.

Table 2. Main effect of aluminium sulphate on postharvest physiology and quality of Hippeastrum flower

Treatment ($Al_2(SO_4)_3$ in mM)	Total water uptake in 10 days(g/scape)	Transpiration loss in 10 days (g/scape)	Transpiration loss and water uptake ratio	Days to onset of deterioration	Vase life (days)
Control (A_0)	41.18 c	55.56 a	1.36 a	5.9 b	7.00
A_1 (0.25)	46.41 c	52.59 ab	1.14 b	6.1 ab	7.22
A_2 (0.50)	55.54 b	50.34 bc	0.94 cd	6.5 ab	7.78
A_3 (0.75)	61.90 a	47.11 c	0.80 d	7.4 a	9.11
A_4 (1.00)	45.69 c	48.48 bc	1.09 bc	7.1 ab	8.67
Level of significance	**	**	**	**	ns
CV (%)	5.11	4.54	7.57	16.53	14.54

Means in the same column followed by different letters are significantly different by DMRT. ** indicates significant at 1% level and 'ns' indicates non-significant

C. Interaction effect of sucrose and aluminium sulphate

Water uptake

Interaction of sucrose and $Al_2(SO_4)_3$ had significant influence on water uptake (Table 3). The scapes held in distilled water (without sucrose and $Al_2(SO_4)_3$) recorded a lower water uptake (39.80 g). On the other hand, the scapes held in the vase solution containing 4% sucrose and 0.75 mM $Al_2(SO_4)_3$ had the highest water uptake (76.60 g), closely followed by those held in 4% sucrose and 0.50 mM $Al_2(SO_4)_3$ vase solution (65.77 g). This result is in full agreement with the findings of Gowda and Gowda, (1990) in gladiolus and Mukhopadhyay (1982) in cut tuberose.

Transpiration loss of water

Interaction of sucrose and aluminium sulphate affected significantly the water loss by transpiration of the scape kept in vase solution (Table 3). The maximum

water loss (67.83 g) was observed in vase solution containing distilled water (control) and the minimum water loss (36.83 g) was found in solution containing 4% sucrose and 0.75 mM $Al_2(SO_4)_3$. It is clear from the above results that different concentrations of sucrose and $Al_2(SO_4)_3$ proved effective in increasing the water uptake and enhancing vase life and decreasing water loss when these solutions were used singly. But in combination their solutions were found more effective in maintaining an increased pattern of water uptake and decreasing water loss by transpiration.

Transpiration loss and water uptake ratio

Interaction of sucrose and $Al_2(SO_4)_3$ significantly influenced the ratio of transpiration loss and water uptake (Table 3). The scapes which recorded the highest water uptake, held in sucrose 4% with 0.75 mM $Al_2(SO_4)_3$ had the lowest ratio (0.48), while those held in distilled water only had the highest ratio (1.71). Solutions of sucrose and $Al_2(SO_4)_3$ alone and in combination were found effective in maintaining a decrease in the ratio of transpiration loss and water uptake in the present study were also supported by Shobha and Gowda (1994) in cut calendula flowers.

Days to onset of deterioration

The interaction effect of sucrose and aluminium sulphate had significant effect on days to onset of deterioration (Table 3). The maximum days (8.0) was taken for starting of deterioration of cut Hippeastrum flower by the combination of 4% sucrose and 0.75 mM $Al_2(SO_4)_3$, which was closely followed by 7.7 days at 2% sucrose and 0.75 mM $Al_2(SO_4)_3$. The minimum days for starting the deterioration of flower (5.8 days) in control. Similar results were found by Shobha and Gowda (1994) in calendula flowers who observed that the relative contribution of the petals to the large accumulation of 0.75 mM $Al_2(SO_4)_3$ and sucrose resulted in extending the longevity of the shoots with flowers.

Vase life

The vase life of floral scape was varied significantly by the combined effect of sucrose and aluminium sulphate (Table 3). The scapes held in a solution with 4% sucrose and 0.75 mM $Al_2(SO_4)_3$ had the maximum vase life (10.33 days), while those held in a solution without sucrose and aluminium sulphate had the minimum vase life (7 days). Solution of sucrose and $Al_2(SO_4)_3$ in combination were found effective in extending the vase life of cut flowers. This might be due to a synergistic effect of sucrose and $Al_2(SO_4)_3$ which improved water balance and osmotic potential, since sugar had been observed to reduce moisture stress in cut flowers by affecting stomatal closure, preventing transportation and water loss. The findings of the present study are further supported by Gowda and

Gowda, (1990) in gladiolus, Mukhopadhyay (1982) in tuberose and Gowda (1990) in tuberose.

Table 3. Interaction effect of sucrose and aluminium sulphate on post-harvest physiology and quality of Hippeastrum flower

Treatment	Total water uptake in 10 days(g/scape)	Transpiration loss in 10 days (g/scape)	Transpiration loss and water uptake ratio	Days to onset of deterioration	Vase life (days)
S_0 x A_0	39.80 f	67.83 a	1.71 a	5.8 cd	7.00 c
S_0 x A_1	46.00 ef	62.13 b	1.36 b	6.3 a-c	8.00 bc
S_0 x A_2	46.43 ef	58.50 bc	1.26 bc	7.0 a-c	8.70 a-c
S_0 x A_3	53.00 cde	58.20 bc	1.10 cd	7.5 a-c	9.33 ab
S_0 x A_4	40.27 f	55.63 cd	1.39 b	6.4 a-c	8.65 a-c
S_1 x A_0	41.50 f	54.93 cd	1.33 b	6.0 a-d	8.00 a-c
S_1 x A_1	46.07 ef	51.80 de	1.12 cd	6.7 a -c	8.67 a-c
S_1 x A_2	54.43 cd	49.07 ef	0.90 fg	6.8 a-c	8.68 bc
S_1 x A_3	56.10 c	46.30 fg	0.83 gh	7.7 ab	9.53 ab
S_1 x A_4	43.17 f	46.50 fg	1.08 de	6.0 a-d	8.00 a-c
S_2 x A_0	42.23 f	43.90 g	1.04 def	6.6 d	8.80 a-c
S_2 x A_1	47.17 def	43.83 g	0.93 efg	6.3 cd	8.00 bc
S_2 x A_2	65.77 b	43.47 g	0.66 h	6.7 a-c	8.64 bc
S_2 x A_3	76.60 a	36.83 h	0.48 i	8.0 a	10.33 a
S_2 x A_4	53.63 cde	43.30 g	0.81 gh	6.7 b-d	8.67 a -c
Level of significance	**	**	**	*	**
CV (%)	5.11	4.54	7.57	16.53	14.54

Means in the same column followed by different letters are significantly different by DMRT. ** indicates significant at 1% level * indicates significant at 5% level.

S_0 = 0% Sucrose (distilled water)
S_1 = 2% Sucrose
S_2 = 4% Sucrose

A_0 = 0 mM aluminium sulphate (distilled water)
A_1 = 0.25 mM aluminium sulphate
A_2 = 0.50 mM aluminium sulphate
A_3 = 0.75 mM aluminium sulphate
A_4 = 1.0 mM aluminium sulphate

Fresh weight

The fresh weight of floral scape on any observation day during the vase life period was not affected by sucrose (Fig. 1) but was affected by aluminium sulphate (Fig. 2). The scape held in 2% sucrose showed the maximum increase in weight (84.19 g) at 4^{th} day after setting the trial, while those held in solutions without sucrose showed the minimum weight per scape (80.32 g) at the same day.

Aluminium sulphate had significant effect on fresh weight of flower scape at 6th and 10th days of vase life (Fig. 2). The scapes held in 0.75 mM $Al_2(SO_4)_3$ solution showed the highest increment of weight on every observation day during the vase period. The maximum fresh weight (93.28 g) was obtained at 4th day of the observation trial and it was gradually decreased at 6th and 10th day of vase life.

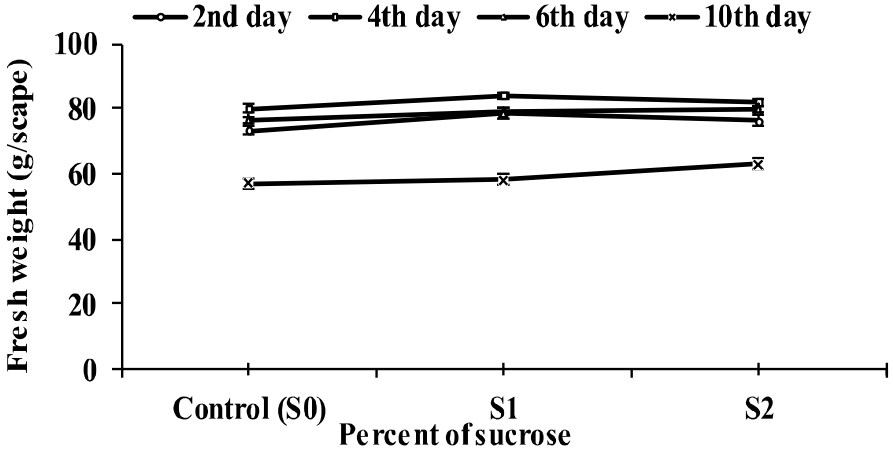

Fig.1. Effect of different conc. of sucrose on fresh weight of Hippeastrum cut flower at different days of vase life.

S_0 = 0% sucrose, S_1 = 2% sucrose and S_2 = 4 % sucrose

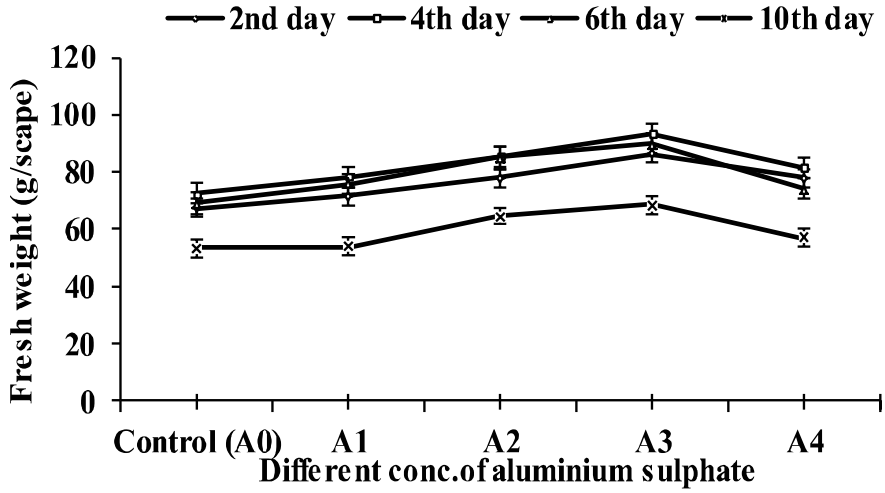

Fig.2. Effect of different conc. of aluminium sulphate on fresh weight of Hippeastrum cut flower at different days of vase life.

A_0 = 0 mM $Al_2(SO_4)_3$, A_1= 0.25mM $Al_2(SO_4)_3$, A_2 = 0.50 mM $Al_2(SO_4)_3$, A_3 = 0.75 mM $Al_2(SO_4)_3$, A_4 = 1.0 mM $Al_2(SO_4)_3$

Table 4. Interaction effect of sucrose and aluminium sulphate on fresh weight of Hippeastrum flower scape at different days in vase solution

Treatment	Average fresh weight (g /scape)				
	1st day	2nd day	4th day	6th day	10th day
S_0 x A_0	55.70	62.80	68.80	66.03 b	49.93 cde
S_0 x A_1	71.53	76.80	86.23	82.00 ab	60.43 b-e
S_0 x A_2	71.47	77.33	87.27	89.57 ab	68.17 ab
S_0 x A_3	76.13	82.20	87.50	82.57 ab	62.00 bcd
S_0 x A_4	62.10	68.23	71.80	64.07 b	45.27 e
S_1 x A_0	61.43	70.43	74.50	72.10 ab	56.10 b-e
S_1 x A_1	64.87	69.37	73.60	68.50 ab	46.97 de
S_1 x A_2	73.33	80.47	88.73	88.27 ab	64.97 bc
S_1 x A_3	81.47	88.40	96.07	89.70 ab	62.17 bcd
S_1 x A_4	78.50	84.93	88.03	77.90 ab	60.90 b-e
S_2 x A_0	60.80	68.47	74.63	69.60 ab	54.13 b-e
S_2 x A_1	62.93	68.93	74.90	77.17 ab	54.50 b-e
S_2 x A_2	70.83	75.97	80.60	77.37 ab	60.93 b-e
S_2 x A_3	80.53	88.83	96.27	96.80 a	80.80 a
S_2 x A_4	73.47	80.53	84.77	80.37 ab	65.13 bc
Level of significance		ns	ns	**	**
CV (%)		14.04	13.34	12.66	13.02

Means in the same column followed by different letters are significantly different by DMRT. ** indicates significant at 1% level and 'ns' indicates non-significant.

S_0 = 0% sucrose A_0 = 0 mM $Al_2(SO_4)_3$ A_3 = 0.75 mM $Al_2(SO_4)_3$

S_1 = 2% sucrose and A_1= 0.25mM $Al_2(SO_4)_3$ A_4 = 1.0 mM $Al_2(SO_4)_3$

S_2 = 4 % sucrose A_2 = 0.50 mM $Al_2(SO_4)_3$

The interaction effect of sucrose and $Al_2(SO_4)_3$ had significant influence on the fresh weight of floral scapes at 6th and 10th day of vase life but no significant effect on fresh weight at 2nd and 4th day of vase life (Table 4). The scapes held in vase solutions without sucrose and $Al_2(SO_4)_3$ had lower fresh weight on any day of vase life, while those held in the solution containing 4% sucrose and 0.75 mM $Al_2(SO_4)_3$ showed a weight increment of about 10 per cent over the initial weight on the 4th day of vase life. The scapes held in distilled water were increased in fresh weight slightly, but about 9.55% over the original weight, which then declined compared to the original weight after the 4th day of vase life. The scapes held in 4% sucrose and 0.75 mM $Al_2(SO_4)_3$ maintained their fresh weight well

above the original weight even up to the 10th day of vase life. Floral scapes held in 4% sucrose and 0.75 mM $Al_2(SO_4)_3$ vase solution maintained their fresh weight above initial weights even on the 6th day of vase life, while those held in distilled water lost their fresh weight gains in comparison with their initial weight on the 6th day. These results indicated that $Al_2(SO_4)_3$ helps flower scape maintain their fresh weight. The results of the experiment supports other published reports that $Al_2(SO_4)_3$ and sucrose increased cut flower life, by increasing the water uptake and maintaining higher fresh weight of cut gladiolus and calendula flowers (Gowda and Murthy, 1994; Shobha and Gowda, 1994).

Relationship between water uptake and vase life of flowers.

There exhibited a linear relationship between vase life of cut Hippeastrum flowers and water uptake as indicated by the following equation: y = 0.056x + 5.791, (R^2 = 0.5433). The regression line stated that the vase life of hippeastrum flower increased at the rate of 0.056 day for per unit change of water uptake. The R^2 value indicated that 54.33% vase life of Hippeastrum cut flower was due to water uptake.

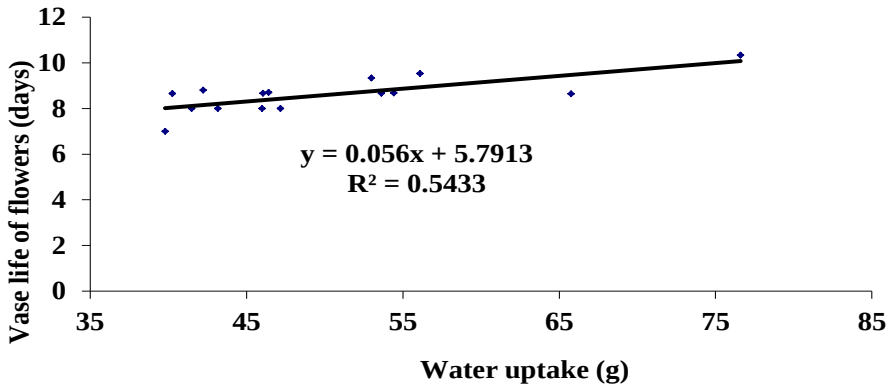

Fig. 3. Relationship between water uptake and vase life of Hippeastrum cut flower.

Conclusion

The results of the present experiment suggests that vase solution containing 4% sucrose and 0.75 mM aluminium sulphate can be used for prolonging the vase life of cut Hippeastrum flower cv. Apple Blossom.

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STUDY ON MORPHO-PHYSIOLOGICAL TRAITS IN SPRING WHEAT (*Triticum aestivum* L.) UNDER RAINFED CONDITION

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A. A. KHAN[4] AND J. RAHMAN[5]

Abstract

Nine morphological and physiological traits were taken to assess genetic parameters, association between the traits and grain yield and partition correlation of yield with other traits, which were purposefully considered as the important strategy for the investigation. Therefore, the main objective of the present investigation was to find out suitable morpho-physiological traits that could be invariably used for the yield improvement of spring wheat grown under drought stress condition. Thirty wheat diverse genotypes were evaluated under drought stress field condition in Alpha Lattice Design with three replications. The study revealed wide range of variability and high broad sense heritability for most of the traits (early ground coverage, canopy temperature, peduncle length, relative water content, number of spikes per m^2 and 1,000-grain weight). Genetic advance in percent of mean suggested that there is enough scope for further improvement of genotypes for the characters studied. Correlation studies exhibited that grain yield was positively and significantly associated with early ground coverage and 1000-grain weight. The path analysis also revealed a maximum direct effect on grain yield contributed by 1000-grain weight. Early ground coverage and 1000-grain weight had a significant and spikes per m^2 had positive indirect effect on grain yield. Therefore, these three traits were found to be most important for wheat breeding under drought stress. As these traits can be evaluated quickly and easily, hence breeders can choose these traits for selecting potential wheat genotypes for further breeding programs.

Keywords: Correlation, Morpho-Physiological Traits, Path analysis, Spring Wheat.

1. Introduction

Wheat (*Triticum aestivum* L.) is economically one of the most important cereal crops in the world. Genetic improvement in wheat yields in dry areas has not been as easy as in more favorable environments or where water is not a limiting factor (Richards *et al.*, 2001). Customarily, drought severely limits wheat productivity in many locations across the globe. Some estimates obviously

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indicate that approximately 50% of the 230 million hectares are being cultivated annually with wheat in the world which is regularly affected by drought (Pfeiffer *et al*., 2005). In dry environments wheat production can be depressed by 50-90% of the crop potential (Oliveras-Villegas *et al*., 2007). Additionally, climate change scenarios predict an increase of aridity in the future and certainly water will become an increasingly scarce commodity.

Though Bangladesh is a land of abundant rainfall but drought is very familiar to wheat cultivars. North-western region namely, Barind tract is one of the largest drought affected area of Bangladesh (Brammer, 1999). Besides, each year north-western region of Bangladesh comprising of 16 districts are also being affected by different levels of drought stress. Farmers' livelihoods of those areas largely depend on rainfed agriculture which is recurrently affected by drought. A joint Bangladesh-FAO soil survey project indicated that 2.3 million hectares of land are physically suitable for wheat under rainfed condition (Begum, 1998).

Undoubtedly, the improvement of drought tolerance is the principal goal in the wheat breeding programs for a long time, since a water deficit in grain filling stage is common in many wheat growing regions of the world. The conventional breeding approach under Wheat Research Centre, BARI has given much emphasis on selecting high yielding advanced lines under optimum growing conditions. Wheat breeding only for yield potential is not the best approach for improving yield under drought conditions as the existing climatic situation is being changed in an irregular and erratic fashion particularly concerning drought. For strengthening wheat improvement program some drought related adaptive traits, for instance relative water content (RWC), canopy temperature, leaf glaucosity/waxiness etc. have been considered for breeding drought tolerant wheat in many wheat growing countries.

Apparently, morpho-physiological traits for growth and development have the greatest impact on the adaptation of plants to the target environments with the aim of achieving a maximum productivity. Selection criteria based on morphological, physiological and biochemical traits have been suggested for screening drought tolerance in wheat. Plant traits, like, water-use efficiency and harvest index (Araus *et al.,* 2002), canopy temperature (Oliveras-Villegas *et al*., 2007), leaf area, number of grains, grain yield and biological yield (Gupta *et al*., 2001), RWC % (Merah, 2001), peduncle length (Kaya *et al*., 2002), flag leaf chlorophyll content at grain filling stage (Reynolds *et al.,* 2007a) and early ground coverage (Rana *et al*., 2007) were considered as important drought adaptive traits in wheat. Selection for one trait may or may not offer the chance for a success for other traits, therefore, more than one trait should be considered in selection process. Moreover, preliminary selection of morpho-physiological drought adaptive traits is very important for next generations judicious and careful selection and consequently confirm the outstanding drought tolerant wheat genotypes through appropriate breeding program. Therefore, success of

such breeding programs mainly depends on the suitable plant morpho-physiological traits, which might be considered as the main contributing parameters for drought tolerance in advanced generations. Here, different genetic parameters like coefficient of variation, heritability, genetic advances etc. have been estimated on the morpho-physiological traits that could be used in selecting the potential drought tolerance genotypes.

Different criteria for genetic parameters were assessed to predict the morpho-physiological characters under selection for the improvement of yield in wheat. And then all possible correlation coefficients between pairs of characters were estimated to evaluate the degree of association among the morpho-physiological traits including yield of 30 spring wheat genotypes grown under rainfed condition. The correlation coefficients of yield with other morpho-physiological traits were also partitioned into direct and indirect effects to find out a suitable trait that could be used for the yield improvement of spring wheat.

2. Materials and Method

2.1. Plant Materials

The experimental materials of the study consisted of thirty (30) diverse genotypes of spring wheat (*Triticum aestivum* L.) including a local check variety 'Shatabdi' (BARI Gom 21), chosen on the basis of their differences in yield and the performance of several physiological traits under rainfed conditions. The genotypes were grown in rainfed plots.

2.2. Site and Design of the Experiment

The present study was conducted at the experimental field of the Regional Wheat Research Centre (RWRC), Bangladesh Agricultural Research Institute (BARI), Rajshahi during 2010-11 cropping season. The experimental site was situated between 25.0^0 N latitude and 89.0^o E longitude with elevation of 28 m. above sea level. The soil of the experimental field was silty clay loam with a pH value of 7.1-8.5, low in organic matter and fertility level, deficient in boron but rich in iron content. The experiment was laid out in Alpha Lattice design with three replications and recommended production package of RWRC was followed to ensure a good harvest.

2.3. Soil Moisture and Field Capacity Determination

The moisture content of the experimental field soil was determined by appropriate gravimetric method. Soil sample was collected randomly from plots of all the 3 replications at 12 days interval starting from 50 days after sowing and continued up to grain filling stage. The following formula was applied to calculate soil moisture content and water at field capacity.

$$\% \text{ Soil moisture (weight basis): } \frac{\text{Weight of soil moisture}}{\text{Weight of oven dry soil}} \text{ X } 100$$

Soil moisture contents were 22%, 20.16%, 18.42% and 18.00% after 50, 62, 74 and 86 days after sowing (DAS), respectively. The water at field capacity of the experimental field soil was 38%. Rainfall of 38.4 mm was recorded at the time of crown root initiation (CRI) stage. No supplementary irrigation was provided as the experiment was conducted under rain-fed condition.

2.4. Fertilization

Recommended doses of fertilizers and manures followed by Wheat Research Centre were applied to the field. The crop was fertilized with NPKS and B @ 100, 28, 40, 20 and 2.5 kg per hectare, respectively to ensure proper growth and development. The elements N, P, K, S and B were applied in the form of Urea, Triple Super Phosphate, Muriate of Potash, Gypsum and Boric acid, respectively.

2.5. Parameters of the Experiment and Data Collection

Early ground coverage was scored visually at 21 days after sowing using 0-10 scale. Canopy temperature was measured using a handheld infrared thermometer (Mikron M90 series, Santa Clara, CA, USA). Canopy temperature was measured 2 times; before heading and grain filling stages. For determination of leaf relative water content (RWC), the leaves from the base of lamina were cut, placed in grip polythene plastic bags and transported in laboratory as quickly as possible. Fresh weights were determined within 2 hours of excision and turgid weight was taken after leaves were soaked in distilled water for 18 hours at room temperature ($20 \pm 2^{o}C$) with 60% relative humidity under low light conditions. The leaves were then taken out of water, blotted on tissue papers and turgid weight was taken. Dry weights were obtained after oven drying the turgid leaves at $70^{o}C$ for 24 hours. Relative water content (RWC) of leaf was calculated using following formula: RWC (%) = [(Fresh weight – Dry weight) / (Turgid weight–Dry weight)] × 100. Days to heading (DTH) was counted starting from sowing date to when the spikes completely came out from 50% of the plants of an individual plot. Peduncle Length was recorded in centimeter from the base of the spike to top culm node. Spikes per square meter were measured at physiological maturity. Thousand grain weight and grain yield (ton per hectare) was measured after harvesting the crop.

2.6. Analysis of Data

Descriptive statistical parameters, mean values and the coefficient of variation (CV) were determined for the traits under study. The broad-sense heritability was estimated according to the results obtained by analysis of variance as the ratio of

the total genetic variance to the total phenotypic variance. Genotypic and phenotypic correlation coefficients between different yield contributing morpho-physiological characters were estimated using the following formula as suggested by Miller *et al.* (1958); Hanson *et al.* (1956) and Johnson *et al.* (1955). The correlation coefficients of yield with other morphological traits were partitioned into direct and indirect effects by path co-efficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959). In this study, grain yield was considered as the dependent character (effect) and other morpho-physiological traits were considered as causal factors.

3. Results and Discussion

3.1. Analysis of Genetic Components of Variation for the Yield and Morpho-Physiological Traits

Analysis of variance ($P<0.01$) revealed differential expression of the selected characters and indicated the prevalence of genetic variability among the 30 spring wheat genotypes. The estimates of different genetic parameters against the morpho-physiological traits and grain yield of 30 spring wheat genotypes are presented in Table 1. Estimation of different genetic parameters is imperative to unravel the genetic basis of different traits that can contribute to crop yield. This indicated that there was some degree of environmental influence on early ground coverage and at the same time narrow range of genetic variation for this trait could be realized.

Most of the traits under study showed high estimate of broad sense heritability (h^2_b) except spikes per m^2 and indicated higher to moderate genetic advance except canopy temperature (CT) at vegetative stage. Kandic *et al*. (2009) observed that early vigor was highly significant with high heritability and genetic advance in wheat. The low and close GCV and PCV indicated narrow range of genotypic variability caused by fixed alleles and less influence of environment for the expression of the traits. This study corroborated with the studies of Rahman (2009) who reported a narrow range of variation among wheat genotypes for these traits. Higher estimate of broad sense heritability along with moderate genetic advance suggested majority were additive, hence, improvement through phenotypic selection for these traits are feasible. Reynolds *et al.* (1997) reported sensitivity of canopy temperature to environmental fluxes along with moderate heritability in bread wheat.

Canopy temperature measured by infrared thermometer to evaluate the genotypes for their ability to keep canopy cool with less impaired assimilation processes. At vegetative stage the PCV (1.645) was higher than GCV (0.786) against canopy temperature, which indicated that the environment itself had played major role for the expression of this trait. Rahman (2009) observed lower genetic advance along with moderate heritability for canopy temperature in spring wheat. Yadav *et al.* (2001) showed that relative water content (RWC) decreased significantly under soil water condition and Shamsi *et al*. (2010) reported that high relative

water content is a resistant mechanism to drought in wheat. Chaturvedi and Gupta (1995) found higher phenotypic variation than the genotypic variation and obtained higher estimates of heritability for 1000-grain weight (TGW). High heritability along with high genetic advance was found for TGW, which was also observed by some other authors (Ali *et al*., 2008). Drought imposed during later stage might additionally cause a reduction of number of grain per spike and grain weight (Gupta *et al*., 2001; Dancic *et al*., 2000). Many authors found high heritability along with high to moderate genetic advance for grain yield in wheat (Barma, 2002; Singh *et al*., 2006; Ali *et al*., 2008; Rahman, 2009). The heritability of the most important trait i.e. grain yield (GY) was rather high (over 80%) clearly indicated higher influence of genetic factors than the environment on the expression of this trait. This finding is in agreement with the findings of Kashif and Khaliq (2004) and Ul-Haq *et al.* (2008).

3.2. Analysis of Correlations between Yield and Different Morpho-Physiological Traits

The information of correlations among different plant traits can be of great use to breeders, as it points out to the traits to which selection should be directed in order to increase the yield under certain environmental conditions. Genetic correlations point to the cohesion of traits after variations due to environmental effects are eliminated and they are the basis for the indirect selection (Van Ginkel *et al*., 1998). Genotypic and phenotypic correlations between the yield and physiological traits are presented in Table 2. Significant and positive genotypic and phenotypic correlations with the yield were observed for EGC ($P < 0.01$) in this study. EGC also had strong positive association with TGW. At phenotypic level spike per m^2 was also positively but non-significantly associated with EGC. Negative correlation was found in case of canopy temperature at grain filling stage with all other traits.

Positive association of EGC with yield and TGW suggested that higher ground coverage at early stage could lead to higher biomass which might offer production of more photosynthates and finally contributed to TGW and grain yield. Kandic *et al.* (2009) also noticed a significant and positive genotypic and phenotypic correlation with the yield which was observed for EGC. Rapid early plant growth rate is an important trait because it reduces soil evaporation and increases the competitiveness of wheat plants against weeds.

Peduncle length (PdL) showed negative correlation with TGW, grain yield and spike per m^2 at both genotypic and phenotypic levels (Table 2). Gautam and Sethi (2002) observed that negative association with spikes/plant, plant height, spikelets per spike, days to maturity and heading. Naik (2000) also reported significant negative association with grain yield under drought condition for these traits. Amin *et al.* (2013) observed positive correlation of peduncle length with plant height and spike length but noticed no correlation with grain yield under terminal drought stress condition.

Table 1. Genetic components of variation for the yield and morpho-physiological traits in 30 wheat genotypes

Component	EGC (scale)	Head (days)	PdL (cm)	CT_{vg} (°C)	CT_{gf} (°C)	RWC %)	Spikes per m^2	TGW (g)	GY (kg/ ha)
Grand mean	25.78	80.06	36.50	18.89	24.03	85.95	356.94	38.53	4570.06
Range	10.0-30.0	68-83	32-42	17-22	21-27	69.61-98.84	301-434	30.7-48.5	3842-5268
MS_G	84.90	64.90	17.67	3.22	4.14	94.68	1091.50	59.48	342557.13
MS_E	5.71	0.23	0.30	0.86	0.26	4.21	518.61	0.64	10620.85
GCV	19.932	5.799	6.593	0.786	4.731	6.390	3.871	11.493	7.279
PCV	21.981	5.831	6.762	1.645	5.187	6.820	7.463	11.679	7.620
$\delta^2 g$	26.398	21.555	5.791	47.802	1.292	30.160	190.962	19.613	110645.426
$\delta^2 p$	32.107	21.788	6.091	4.695	1.553	34.365	709.571	20.252	121266.276
h^2_b	82.220	98.931	95.075	6.791	83.201	87.763	26.912	96.846	91.242
GA (10%)	37.230	11.883	13.243	6.687	8.891	12.331	4.198	23.299	14.322
F-Value	**	**	**	**	**	**	**	**	**
CV%	9.27	0.60	1.50	4.91	2.13	2.39	6.38	2.07	2.26

** indicates significant at 1% level of probability.

EGC= Early ground coverage (at 21days); PdL= Peduncle length (cm); RWC= Relative water content; CTvg= Canopy temperature at vegetative stage; CTgf= Canopy temperature at grain filling stage; TGW= 1000-grain weight; GY= Grain yield per hectare; MSG= Mean sum of squares due to genotype; MSE= Mean sum of squares due to error; GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation; δ2g= Genotypic variance; δ2p= Phenotypic variance ; h2b= Heritability in broad sense; GA= Genetic advance;

Table 2. Genotypic (r_g) and phenotypic (r_p) correlation coefficient between yield and morpho-physiological traits in 30 wheat genotypes

Character	R	PdL	CT_{gf}	RWC	Spike m^{-2}	TGW	GY
EGC	r_g	-0.345	-0.306	0.152	0.049	0.554**	0.537**
	r_p	-0.281	-0.330	0.148	0.148	0.541**	0.526**
PdL	r_g		-0.242	0.283	-0.054	-0.209	-0.059
	r_p		-0.183	0.245	-0.142	-0.175	-0.133
CTgf	r_g			-0.307	-0.002	-0.389*	-0.050
	r_p			-0.382*	-0.041	-0.385*	-0.033
RWC	r_g				0.006	-0.073	-0.091
	r_p				0.032	-0.084	-0.097
Spike m^{-2}	r_g					0.014	0.050
	r_p					0.059	0.155
TGW	r_g						0.685**
	r_p						0.689**

* and ** indicate correlation significant at 5% and 1% level (2 tailed), respectively

EGC=Early ground coverage (21 days); PdL= Peduncle length (cm); CT_{gf}= Canopy temperature at grain filling stage (^oC); RWC=Relative water content (%); TGW= 1000-grains weight (g); GY= Grain yield per hectare (kg).

Canopy temperature (CT) at grain filling stage had negative correlation with grain yield at genotypic (r_g= -0.050) and phenotypic levels (r_p= -0. 033). Significant negative correlation also observed with TGW at genotypic (-0.389) and phenotypic (-0.385) levels and with RWC at phenotypic (-0.382) level only. Number of grains spike per m^2 had non-significant negative correlation with CT at genotypic and phenotypic levels. Rahman (2009) reported strong and negative correlation of CT_{gf} with grain yield. Rahman *et al.* (1997) also observed that high yielding genotypes possessed significantly low canopy temperature and medium chlorophyll content. Balota *et al*. (2007) also observed significant correlation coefficients of CT at three developmental stages i.e. pre-heading, heading and post-anthesis with grain yield. Therefore, CT might be used as a selection criterion to improve adaptation to drought and heat. CIMMYT began CT measurements on different irrigated experiments in Northwest Mexico and it was found that phenotypic correlations of CT with grain yield were occasionally positive (Fischer *et al*., 1998). They also reported that CT has been using as a selection criterion for tolerance to drought and high temperature stress in wheat breeding program especially in early segregating generations like F_3.

Relative water content (RWC) had negative and non-significant correlation with grain yield at genotypic (r_g= -0.091) and phenotypic levels (r_p= -0.097). It was also found negative correlation with TGW at genotypic and at phenotypic levels (Table 2). Interestingly, this trait had insignificant positive association with spikes per both at genotypic and phenotypic levels. It was found that RWC decreases with concurrent increase of drought stress usually but not always in wheat under drought stress conditions; the cultivars that were resistant to drought have more RWC. Shamsi *et al*. (2010) observed positive correlation with grain yield in drought condition and also reported that with an increase in the intensity of drought stress on wheat cultivars there was a decrease in relative water content. Siegien and Leszezynska (2004) also observed significant correlation between grain yield and RWC.

Spikes per m^2 had positive correlation both at genotypic and phenotypic levels with TGW and grain yield. Several investigators found spikes per m^2 to be correlated significantly and positively with grain yield (Burio *et al.,* 2004; Munir *et al*., 2007 and Akram *et al*., 2008). Thousand grain weight (TGW) showed significant positive correlation with grain yield both at genotypic (0.685) and phenotypic (0.689) level. Guttieri *et al*. (2001) observed that grain weight per spike decreased due to drought during grain filling period. Several authors (Nayeem *et al.*, 2003; Jat *et al*., 2003; Zecevic *et al*., 2004) had reported significant and positive correlation of TGW with grain yield in wheat.

3.3. Analysis of Direct and Indirect Effects of Different Morpho-Physiological Traits on Grain Yield

The correlation coefficients usually measure the mutual association between a pair of independent variables. But when more than two variables are involved, the correlations do not give the complete information of their accurate relationships. Additionally, the path coefficient analysis is particularly useful for the study of the cause and effect relationship, because it simultaneously considers several variables in data set to obtain the coefficients. Herein, path analyses of morpho-physiological traits on grain yield are sown in Table 3.

Early ground coverage (EGC) had a positive direct effect on yield (0.273). This trait also had indirect positive effect on yield via RWC, spike per m^2 and TGW. Furthermore, it concomitantly resulted to a significant positive correlation with yield at genotypic level (Table 2). The importance of total biomass for the yield increase in wheat, especially under drought stress conditions is already established (Reynolds *et al.*, 2007b). A higher biomass production under drought stress conditions, particularly during grain filling period, would have an advantage because the translocation of assimilates from the vegetative parts of a plant to seeds contribute significantly to yield.

Peduncle length had direct positive effect on grain yield (0.149). This trait had maximum indirect negative effect on yield via EGC (-0.040) followed by CT and TGW. The effects on yield via other physiological traits were found negligible. Thus, it resulted to a negative correlation with yield at genotypic level. Almost similar findings were reported by Khan *et. al.* (2010) in wheat under drought stress condition.

Canopy temperature at grain filling stage (CT_{gf}) had direct positive (0.323) effect on yield. This trait had maximum indirect negative effect on yield via EGC (-0.089) followed by PdL (-0.078). A number of negative indirect effects on grain yield were observed for canopy temperature via yield contributing traits like, leaf area index, grains per spike, spikes per m^2 and plant height, grain weight etc. All these ultimately led to negative correlation with yield at genotypic association level (Table 3). The present findings are corroborated with the results as observed by Mohammadi *et. al.* (2014).

Relative water content (RWC) had an insignificant negative direct effect (-0.013) on grain yield which led to negative correlation co-efficient between relative water content and grain yield. Positive indirect effects on yield were observed for this trait via lower canopy temperature at grain filling stage. Similar findings were reported by Arjenak *et al*. (2012) in their study with some wheat varieties under drought stress condition.

Table 3. Direct (bold) and indirect effects of the morpho-physiological traits on grain yield in spring wheat

Traits	EGC	PdL	CT_{gf}	RWC	Spike m^{-2}	TGW	Genotypic correlation with yield
EGC	**0.273**	-0.073	-0.075	0.043	0.041	0.150	0.537**
PdL	-0.040	**0.149**	-0.036	0.036	-0.024	-0.026	-0.059
CT_{gf}	-0.089	-0.078	**0.323**	-0.111	-0.009	-0.110	-0.050
RWC	-0.002	-0.003	0.004	**-0.013**	0.000	0.001	-0.091
Spike m^{-2}	0.018	-0.019	-0.004	0.003	**0.121**	0.053	0.050
TGW	0.370	-0.119	-0.230	-0.051	0.030	**0.674**	0.685**

** indicates significant at 1% level of probability; Residual effect = 0.415

EGC= Early ground coverage (at 21 days); CT_{gf}= Canopy temperature at grain filling stage; PdL= Peduncle length; RWC= Relative water content; TGW= 1000-grain weight; GY= Grain yield per hectare.

Spikes per m^2 had direct positive effect on grain yield (0.121). This trait had a number of indirect positive effects on yield via most of the other traits studied. It has shown maximum indirect positive effect via grain weight and early ground coverage. Most of these positive indirect effects were of low in magnitude. Ultimately this trait was found associated with yield having positive correlation coefficient at genotypic level. Chaturvedi and Gupta (1995) reported positive direct effect of spikes per m^2 on yield which supported this perception.

Thousand Grain weight (TGW) showed direct positive effect on grain yield (0.674). This trait had maximum indirect positive effect on yield via early ground coverage (0.370) followed by grains per spike (0.030). Ultimately this trait had significantly positive correlation ().685) with yield at genotypic level. Ibrahim (1994) also observed direct positive effect of TGW on grain yield.

Finally, path analysis for primary yield contributing characters revealed that spikes per m^2, canopy temperature and TGW contributed considerable amount of positive direct effects on grain yield. These direct effects obviously were the principal components of their relationships with yield. Similar findings were reported by Shamsuddin and Ali (1989). According to the authors spikes per plant and TGW were correlated with yield mainly through their direct effects.

4. Conclusions

In conclusion, traits such as early ground coverage had positive correlation and had an indirect effect on grain yield. Moreover, early ground coverage, spikes per m^2 and TGW had positive correlations with grain yield. Most importantly, as early ground coverage, spikes per m^2 and TGW can be evaluated quickly as well as easily and hence, it is suggested that more emphasis should be given on the morpho-physiological (phenological and physiological) characters for selecting wheat genotypes with higher grain yield under rainfed condition.

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EFFECT OF HONEY BEE POLLINATION AND CURD SCOOPING ON SEED YIELD OF CAULIFLOWER

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Abstract

The experiment was conducted to study the effect of honey bee pollination and curd scooping on seed production of cauliflower (*Brassica oleracea* var. *botrytis* L.) cv. 'Poushali'. Eighteen combinations of treatments comprising three types of pollination viz., open pollination (natural pollination), using bees for pollination inside net (planned pollination) and plants inside net without bees (control) and six kinds of curd scooping viz., 25%, 50% and 75% of curd cutting, cross curd cutting, central curd cutting and no curd cutting (control). Honey bee (*Apis cerana* L.) was used as pollinator. Seed yield and yield attributes were significantly influenced by both factors and their combinations. Central curd cutting influenced early flowering and siliqua maturity compared to other curd cutting treatments. Planned honey bee pollination was found to inflict maximum impact on the seed production of cauliflower with an increase in seed yield of 45.46% and 23.17% higher over plants grown inside net without bees and open pollination, respectively. Central curd scooping increased 26.52% higher yield than that of no curd cutting treatment. Planned bee pollination and central curd cutting independently as well as in combination gave the maximum yield attributes of seed viz., primary and secondary flower stalks/plant, number of siliquas/plant, length of siliqua, number of seeds/siliqua,1000 seed weight, seed yield and seed germination percent of cauliflower. Planned pollination coupled with central curd cutting gave the maximum seed yield of 607.43 kg/ha in cauliflower.

Keywords: Cauliflower, curd scooping, honey bee pollination, seed production.

Introduction

Cauliflower (*Brassica oleracea* var. *botrytis* L.) is an important cole crop in the word. It is the most popular winter vegetable in Bangladesh (Rashid, 1999). The people of Bangladesh like this vegetable due to its taste, nutritional properties and versatile usability with attractive odour of the curd. It is low in fat and calories, high in vitamin C, and a good source of fiber, calcium and iron. In Bangladesh condition, the open pollinated (OP) variety of cauliflower can produce seeds and farmers themselves can produce seeds of OP variety of cauliflower. Ahmed and Hossain (1977) observed that the variety 'Poushali' produced the maximum quantity of seeds per plant and the germination percent of the seeds produced by 'Poushali' was found to be the best.

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Cauliflower is a cross pollinated crop and its pollination takes place by honey bees (Singh *et al*., 2005). Low seed yield due to inadequate pollination is often faced as a major problem of cauliflower seed production. Inadequate pollination is caused by several factors and the most important of which includes lack of adequate number and diversity of pollinators (Sushil *et al*., 2013). Pollination by insects is inevitable for cauliflower seed set, since they are generally incompatible (Sihag, 2001). Bees visit plants for its food, nectar and pollen. This floral fidelity of bees is due to their preference for nectars having sugar contents and pollens with higher nutritive values. Honey bees are best known for the honey they produce. But the principal economic role of honey bees in nature is to pollinate hundreds and thousands of flowering plants and ensure seed set in quantity and quality. Both flowering plants and honey bees are interdependent for their biology and life cycle. Flowering plants offer nectar and pollen to honey bees and honey bees reciprocate their obligation by bringing about pollination and communication of the plant species. But honey bees are still of greater importance to the farmers for the pollination service they offer and increase crop yields both qualitatively and quantitatively through pollination (Sharmah *et al*., 2015). Supplementary pollination using honey bees in hives in the seed fields of cauliflower crop ensures good seed set and thereby seed yield is greatly increased. The effectiveness of honey bees as pollinators for cauliflower seed production has been studied by different workers in open pollinated varieties (Raula, 1972; Sharma *et al.*, 1974; Adlakha and Dhaliwal, 1979: Kakar, 1981).

Cauliflower seed production is difficult because its flowering process goes through a curd formation. Morphological barriers such as curd compactness may be related with the seed production (Singh *et al.*, 2005). Curd is a pre-flower primordia which often bolts slowly and incompletely (Nieuwhof, 1969). Curd rottening, irregular and delayed flower stalk emergence and empty siliqua production are some of the common problems found to be associated with cauliflower seed production (Rahman *et al*., 1988). Again curd scooping is one of the most important technologies employed for quality seed production of cauliflower (Chowdhury, 1979; Sinohara, 1984). Curd scooping helps in earlier bolting, easy emergence of flower stalks and early flowering and thereby getting higher seed yields (Rashid and Singh, 2000). Scooping the central portion of the curd at edible stage helps in early emergence of flower stalks (Agrawal, 1994; Moniruzzaman *et al.*, 2007). In the absence of technical know-how of seed production technology, the production of quality seed in cauliflower is not up to the mark in Bangladesh. The present investigation was therefore, carried out to study the effect of honey bee pollination and curd scooping on the seed production of cauliflower.

Materials and Method

The experiment was conducted at the Horticulture Farm of Bangladesh Agricultural University (BAU) during 2002-03. The land selected for the experiment was medium high land. Dhaincha (*Sesbania rostrata*) was grown during the *kharif* season before the cauliflower cultivation. The soil of the area belongs to the Old Brahmaputra alluvial tract under AEZ- 9 of Bangladesh and was silty loam in texture (sand 13.6%, silt 71.4% and clay 16.0%). The soil pH was 6.90. Mechanical analysis of the soil of the experimental field (0-30 cm depth) was performed in the Humbldt Soil Testing Laboratory, Department of Soil Science of BAU. The treatments consisted of three types of pollination viz., P_0 = open (natural) pollination, P_b = using bees for pollination inside net (planned pollination) and C= plants inside net without bees (control) and six kinds of curd scooping viz., S_1 = 25% or ¼ portion of a curd cutting, S_2 = 50% or ½ portion of a curd cutting, S_3 =75% or ¾ portion of a curd cutting, S_4 = cross curd cutting i.e., 2mm breadth cutting on the curd just like a 'X', S_5 = central curd cutting i.e., 2 cm diameter round cutting from the central portion of the curd and S_0 = without curd cutting (control). So there were 18 treatment combinations in all. The mosquito net was used in the experiment. In case of treatment P_b, the unit plots were caged with mosquito nets along with honey bees (*Apis cerana* L.) during flowering period. Bee hives of *A. cerana* were borne to every unit plots of P_b treatment and bees were allowed to go inside the net, and thereafter the net was closed. But in case of 'C' treatment, the unit plots were caged with mosquito net where no pollinators (honey bees) were allowed. Unit plots of P_0 treatment were kept as natural open condition. The experiment was laid out in Randomized Complete Block Design with three replications.

The unit plot size was 3.0 m × 2.4 m accommodating 20 plants per plot with a spacing of 60 cm × 60 cm. The test variety was 'Poushali' which is an open pollinated (OP) variety. Forty day-old seedlings were transplanted on 25 October, 2002. The land was fertilized by well decomposed cowdung with doses 20 t/ha, and N, P, K, B and Mo with 68, 50, 110, 3 and 0.78 kg/ha. The sources of N, P, K, B and Mo were urea, TSP, MoP, borax and sodium molybdate. The whole amount of P and half of the cowdung were incorporated to the soil during final land preparation and the remaining half of cowdung and one-third of each N and K were applied to the pit while the rest of N and K were top dressed in two equal installments at 21 and 45 days after transplanting. One additional dose of N (45 kg/ha) and MoP (50 kg/ha) was applied during flowering of cauliflower. The crop after transplanting was irrigated daily by a watering can up to 6 days and then twice a week and later once a week. The crop was irrigated within 3-4 days of mulching and fertilizer application. Excess water during the rain was drained out to avoid water stagnation. The other intercultural operations and plant protection measures were taken as and when necessary. The seed crop was harvested on 2-5 April, 2003.

Data were taken on days to 50% flowering, days to siliqua maturity, number of primary and secondary flower stalks/plant, number of siliquas/plant, length of siliqua (cm), number of seeds/siliqua, 1000 seed weight, seed germination (%), seed yield/plant (g) and seed yield/ha. The data were taken randomly from 10 plants of each plot. After seed harvest, seed germination test was done in the laboratory of the Horticulture Department of BAU. Data were analyzed by using statistical package programme MSTAT-C. Mean separation was done by Least Significant Difference (LSD) test at 5% level of probability.

Results and Discussion

Effect of honey bee pollination

All the parameters differed significantly in pollination treatments (Table 1). Days to 50% flowering (75.09) and days to siliqua maturity (152.50) were found the maximum in the treatments of plants inside net without bees and open (natural) pollination, respectively. Number of primary (8.14) and secondary (71.15) flower stalks/plant, number of siliquas/plant (719.22), length of siliqua (5.62 cm), number of seeds/siliqua (11.04), 1000 seed weight (3.57g), seed germination (90.20%), seed yield/plant (18.80 g) and seed yield/ha (456.20 kg) were recorded highest when the plants were grown inside net supplying bees for pollination, and the minimum values for all the parameters except seed germination were recorded from the plants grown inside net without supplying bees for pollination. It was seen that planned pollination increased 8.97% and 32.49% higher fruit setting compared to open (natural) pollination and plants grown inside net without bees (control). Again planned pollination increased 3% and 45.45% higher seed setting than those of natural pollination and control. These corroborate the results of Sushil *et al.* (2013) who obtained 12.50% pod setting and 12.25% seed setting higher in planned pollination than those of natural pollination in broccoli. In respect of seed yield/plant, planned pollination increased 19.26% and 46.33% higher seed yield than that of natural pollination and control. The result of the highest seed yield might be due to better pollination and good fruit setting. This is in agreement with the results of Sharma *et al.* (1974) and Kakar (1981). Planned pollination gave 45.46% and 23.17% higher seed yield over control (plants inside net without bees) and natural pollination, respectively. This is in agreement with the report of Sushil *et al*. (2013).

Effect of curd scooping

All the parameters differed significantly in curd cutting treatments (Table 2). The treatment without cutting of curd (control) took the maximum days (76.63) to reach 50% flowering stage which was closely followed by 75 % cutting of curd (75.84) and the central curd cutting took the minimum days (69.88) to reach 50%

flowering stage (Table 2). Similar result was also found in case of days to siliqua maturity. Curd scooping helped in easier bolting, easy emergence of flower stalk and early flowering. This corroborates the result of Rashid and Singh (2000). Central curd cutting gave the maximum number of primary and secondary flower stalks/plant (8.17/plant and 77.74/plant), number of siliquas (735.84/plant), length of siliqua (5.83 cm), number of seeds/siliqua (12.89), 1000 seed weight (3.58 g) and seed germination (91.12%) which were followed by cross cutting of curd and their minimum values were obtained from 75% cutting of curd except 1000 seed weight and seed germination. The treatment without curd scooping gave the lowest 1000 seed weight (3.12 g) and seed germination (84.13%). The maximum seed yield (19.34 g/plant and 462.87 kg/ha) were recorded in central curd cutting treatment followed by cross cutting of curd while the minimum seed yield (8.98 g/plant and 211.96 kg/ha) was recorded from the plants with 75% curd cutting (Table 2). It was seen that 75% curd cutting gave inferior result compared to without curd cutting in terms of seed yield. Central curd scooping increased 54.16% and 26.52% higher yield than that of 75% curd cutting and control treatment, respectively. These results are in agreement with Rahman *et al*. (1988) and Moniruzzaman *et al*., 2007) who got higher values for the aforementioned parameters in the central curd cutting. The result also clearly revealed that curd scooping had positive effects on the yield and quality of cauliflower seeds. This might be due to the fact that flower stalks produced from the scooped curd were not as compact as the no scooped curd and got more space which decreased competition among the flower stalks resulting more seed yield in cauliflower.

Combined effect of honey bee pollination and curd scooping

The combination CS_0 required the maximum days to 50% flowering (77.06) and siliqua maturity (154.36), and P_bS_5 combination took the minimum days (67.55) to reach 50% flowering and siliqua maturity stages (148.20) (Table 3). Number of primary (9.76) and secondary flower stalks/plant (86.85), number of siliquas/plant (888.63), length of siliqua (6.44 cm), number of seeds/siliqua (15.60), 1000-seed weight (3.72g) and seed germination (94.44%) were found maximum from P_bS_5 combination followed by P_bS_4 combination and their minimum values were obtained from CS_3 combination. But in case of length of siliqua, 1000 seed weight and seed germination, the minimum values were recorded from CS_2 and CS_0 combinations. The combination P_bS_5 gave the maximum seed yield (25.99 g/plant and 607.43 kg/ha) which was followed by P_bS_4 combination and the combination CS_3 gave the minimum seed yield (Table 3). As all the seed yield attributes were higher in the plants grown with using bees for pollination inside net with central curd scooping (P_bS_5), those seed yield attributes combinedly resulted in the maximum seed yield in the same treatment combination.

Table 1. Effect of honey bee pollination on seed yield attributes, germination and seed yield of cauliflower

Treatments	Days to* 50% flowering	Days to* siliqua maturity	Primary flower stalks /plant (no.)	Secondary flower stalks /plant (no.)	Siliquas /plant (no.)	Length of siliqua (cm)	Seeds/ siliqua (no.)	1000 seed weight (g)	Germination of seeds (%)	Seed yield	
										g/ plant	Kg/ha
P_0	74.65	152.50	7.12	64.41	654.73	5.16	10.71	3.36	86.70	15.18	371.86
P_b	71.62	151.41	8.14	71.15	719.22	5.62	11.04	3.57	90.20	18.80	455.88
C	75.09	151.49	6.97	62.14	485.52	4.55	7.59	3.24	85.69	10.09	248.42
LSD $_{(0.05)}$	1.46	0.98	0.35	2.23	21.39	0.29	0.61	0.05	1.34	0.75	12.55
CV (%)	2.93	0.81	6.89	4.98	5.10	8.42	9.27	2.38	2.25	7.50	7.17

*From seedling transplanting

P_0 =Open pollination, P_b =Using bees for pollination inside net, C = Plants inside net without bee

Table 2. Effect of curd scooping on seed yield attributes, germination and seed yield of cauliflower

Treatments	Days to* 50% flowering	Days to* siliqua maturity	Primary flower stalks /plant (no.)	Secondary flower stalks /plant (no.)	Siliquas /plant (no.)	Length of siliqua (cm)	Seeds/ siliqua (no.)	1000 seed weight (g)	Germination of seeds (%)	Seed yield	
										g/ plant	Kg/ha
S_1	72.81	152.06	7.48	69.81	634.73	5.09	9.83	3.38	86.23	15.23	376.92
S_2	74.46	152.48	7.02	66.39	600.64	4.88	8.89	3.41	87.47	14.00	345.81
S_3	75.84	152.25	6.75	52.08	474.11	4.51	7.03	3.40	87.59	8.98	211.90
S_4	73.99	151.51	7.87	72.96	678.44	5.35	11.58	3.45	88.78	17.13	418.49
S_5	69.88	148.83	8.17	77.74	735.84	5.83	12.89	3.58	91.12	19.34	462.54
S_0	76.63	153.56	7.16	56.36	594.49	4.99	8.47	3.12	84.03	13.48	336.96
LSD $_{(0.05)}$	2.07	1.39	0.49	3.15	30.26	0.41	0.87	0.07	1.89	1.06	17.75
CV (%)	2.93	0.81	6.89	4.98	5.10	8.42	9.27	2.38	2.25	7.50	7.17

*From seedling transplanting

S_1 = 25% cutting of curd, S_2= 50% cutting of curd, S_3= 75% cutting of curd, S_4= Cross cutting of curd, S_5= Central cutting of curd, S_0=Without cutting of curd (control)

Table 3. Combined effect of honey bee pollination and curd scooping on seed yield attributes, germination and seed yield of cauliflower

Treatments	Days to* 50% flowering	Days to* siliqua maturity	Primary flower stalks /plant (no.)	Secondary flower stalks /plant (no.)	Siliquas /plant (no.)	Length of siliqua (cm)	Seeds/ siliqua (no.)	1000 seed weight (g)	Germination of seeds (%)	Seed yield	
										g/plant	Kg/ha
P_0S_1	73.48	153.27	7.34	69.05	640.87	5.00	11.17	3.34	85.29	15.75	394.08
P_0S_2	74.63	152.46	6.62	62.12	623.90	4.88	9.96	3.41	86.76	13.86	335.68
P_0S_3	76.04	153.50	6.76	55.03	691.67	4.31	7.10	3.35	88.19	9.57	214.13
P_0S_4	74.56	151.70	7.23	71.28	748.33	5.50	12.56	3.39	87.72	16.95	430.88
P_0S_5	71.68	150.36	7.65	74.84	782.86	5.87	12.81	3.56	89.50	19.12	480.78
P_0S_0	76.44	153.95	7.10	54.14	640.76	5.08	9.64	3.13	82.74	15.84	376.68
P_bS_1	71.55	151.45	8.23	75.01	746.33	5.40	10.75	3.55	88.40	18.61	462.47
P_bS_2	73.22	152.84	7.71	71.24	703.66	5.90	10.22	3.57	89.91	17.81	449.49
P_bS_3	71.34	151.60	7.11	53.55	515.25	4.88	7.60	3.62	88.99	10.57	237.63
P_bS_4	70.42	149.43	8.46	80.08	770.45	5.70	13.15	3.64	91.89	22.67	542.74
P_bS_5	67.55	148.20	9.76	86.85	888.63	6.44	15.60	3.72	94.44	25.99	606.81
P_bS_0	75.52	153.24	7.59	60.18	691.43	5.38	8.93	3.23	87.54	17.15	435.85
CS_1	73.41	151.42	6.88	65.52	515.72	4.57	7.57	3.16	84.96	11.34	274.22
CS_2	75.83	152.13	6.74	65.81	474.53	3.87	6.52	3.23	85.75	10.33	252.29
CS_3	74.15	151.66	6.38	47.65	415.82	4.34	6.39	3.26	85.56	6.79	183.99
CS_4	76.97	151.40	7.93	67.53	517.28	4.86	9.01	3.31	86.72	11.76	281.83
CS_5	70.33	153.35	7.09	71.51	536.44	5.16	9.25	3.46	89.38	12.96	300.04
CS_0	77.06	154.36	6.80	54.76	551.65	4.51	6.84	3.00	81.80	7.44	198.17
$LSD_{(0.05)}$	3.58	2.41	0.85	5.45	52.40	0.71	1.50	0.13	3.27	1.83	30.75
CV (%)	2.93	0.81	6.89	4.98	5.10	8.42	9.27	2.38	2.25	7.50	7.17

*From seedling transplanting

P_0=Open pollination, P_b=Using bees for pollination inside net, C=Plants inside net without bee,

S_1 =25% cutting of curd, S_2=50% cutting of curd, S_3 =75% cutting of curd, S_4 =Cross cutting of curd, S_5=Central cutting of curd, S_0=Without cutting of curd (control)

Conclusion

From the above study it can be concluded that honey bee pollination and curd scooping are imperative for higher seed yield and quality seed production of cauliflower. Keeping bees inside net (planned pollination) and central curd scooping could be practiced for better and quality seed production of cauliflower.

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VARIABILITY AND PATH CO-EFFICIENT FOR YIELD AND YIELD COMPONENTS IN RICE

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Abstract

Twenty five rice varieties were evaluated for their variability with regard to yield and yield components. Estimates of heritability and genetic advance as per cent mean were also obtained for the above traits. In addition, studies on character associations and path co-efficients were also undertaken. The results revealed high variability, heritability and genetic advance as per cent mean for productive tillers per plant, number of tillers per plant, number of grains per panicle and number of filled grains per panicle, while days to maturity was recorded with high heritability coupled with low genetic advance as per cent of mean. Further, yield was observed to be positively associated with number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle. Among these, number of tillers per plant, productive tillers per plant and number of filled grains per panicle were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through productive tillers per plant indicating importance of the trait as selection criteria in crop yield improvement programmes.

Keywords: Correlation, grain yield, heritability, path analysis, rice, variability, yield components.

Introduction

Rice (*Oryza sativa* L.) is the world's most staple food for more than half the world's population. Crop yield improvement is of prime importance to meet its rising demand owing to constant increase in population. In this context, assessment of variability in the crop for grain yield and yield attributes is the essential for successful exploitation and improvement of yield through breeding. Further, grain yield depends on various component characters and knowledge of correlations among yield component traits and yield is of great importance in selection of elite genotypes for breeding programmes. Path analysis also helps in determining the direct and indirect causes of association and formulation of effective breeding strategies for development of better genotypes. In this direction, the present investigation was undertaken to assess the magnitude of variability and character associations, in addition to direct and indirect effects among yield and yield component characters in 25 different rice varieties.

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Materials and Method

Experimental materials for the present investigation comprised of 25 rice varieties obtained from different rice research stations of the erstwhile Andhra Pradesh state of India, namely, Bapatla, Jagtial, Nandyal, Nellore, Rajendranagar, Ragolu and Rudrur of Acharya N. G. Ranga Agricultural University. These were sown during *kharif* 2013 in a randomized block design with three replications. Thirty day-old seedlings of each variety were transplanted in four-row plots of 4.0 m length, at a spacing of 20 cm between rows and 15 cm between plants within the row. All recommended practices were followed to raise a healthy crop and observations were recorded for grain yield and yield component characters. The observations on plant height, number of tillers per plant, productive tillers per plant, panicle length, number of grains per panicle, number of ill-filled grains per panicle, number of filled grains per panicle, test weight, harvest index and grain yield per plant were recorded from five randomly selected plants for each entry in each replication. However, observations on days to 50 per cent flowering and days to maturity were recorded on plot basis. Data thus obtained were subjected to standard statistical procedures proposed by Panse and Sukhatme (1961). The variability parameters, namely, genotypic and phenotypic co-efficient of variation were calculated as per the formulae proposed by Burton and Devane (1952) and categorized as per the procedure suggested by Sivasubramanian and Madhavamenon (1973). Estimates of heritability in broad sense [$h^2_{(b)}$] and genetic advance were calculated by the formulae given by Lush (1940) and Johnson *et al.* (1955), respectively. Categorization was done as per the procedure outlined by Johnson *et al*. (1955). Further, genotypic and phenotypic correlation coefficients were calculated using the method detailed by Johnson *et al.* (1955), while the direct and indirect contribution of different yield component characters on grain yield per plant was estimated by path co-efficient analysis suggested by Wright (1921).

Results and Discussion

Analysis of variance (ANOVA) for yield and yield component characters studied is presented in Table 1. The results revealed highly significant mean squares due to varieties for all traits, indicating the existence of sufficient variation among the varieties for yield and yield component characters studied in the present investigation, and a scope for effective selection.

Information on mean, range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability, genetic advance and genetic advance as per cent mean for yield and yield component traits are furnished in Table 2. A perusal of these results revealed maximum range of variability for number of grains per panicle followed by number of filled grains per panicle. Higher phenotypic variance and co-efficient of variation were in

general recorded for all the traits studied in the present investigation, compared to genotypic variance and co-efficient of variation, indicating the influence of environment. Similar findings were reported earlier by Mamta Singh *et al.* (2007). However, the high (>20%) phenotypic variance (days to 50 per cent flowering, days to maturity, plant height, number of grains per panicle, number of filled grains per panicle and harvest index) and co-efficient of variation (number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle) observed in the present investigation was noticed to be essentially associated with high genotypic variance and co-efficient of variation of the particular trait, indicating the minimal influence of environment and presence of high genetic variability for these traits in the experimental material. Hence, selection on the basis of phenotype can also be effective for improvement of these traits. Similar results were reported earlier by Babu *et al.* (2012). Further, the high (>20%) estimates of genotypic and phenotypic co-efficient of variation recorded for productive tillers per plant, number of tillers per plant, number of grains per panicle and number of filled grains per panicle in the present study are in conformity with the findings of Bekele *et al.* (2013) for productive tillers per plant; Prasad *et al.* (2013) for number of tillers per plant; Deepa Sankar *et al.* (2006) for grains per panicle and Srinivas *et al.* (2004) for filled grains per panicle. However, moderate (10-20%) genotypic and phenotypic variance estimates were recorded in the present study for 1000 seed weight, while grain yield per plant, number of ill-filled grains per panicle and harvest index had recorded moderate (10-20%) estimates of genotypic and phenotypic co-efficient of variation. These results are in conformity with the findings of Das *et al.* (2005) for grain yield per plant and Dhanwani *et al.* (2013) for harvest index. In contrast, low (<10%) estimates of genotypic and phenotypic variance and co-efficient of variation were observed in the present study for number of tillers, followed by productive tillers per plant, panicle length, number of ill-filled grains per panicle and grain yield per plant, while days to 50 per cent flowering, days to maturity, plant height and panicle length had low (<10%) genotypic and phenotypic coefficient of variation, indicating low variability for these characters in the present experimental material and therefore little scope for improvement of these traits. Similar findings were reported earlier by Adilakshmi and Girijarani (2012) for days to 50 per cent flowering; Satish *et al.* (2003) for plant height and Idris *et al.* (2013) for days to maturity.

High (>60%) estimates of heritability were recorded for all characters studied in the present investigation (Table 2). Maximum heritability was recorded for number of filled grains per panicle, followed by number of grains per panicle, productive tillers per plant, days to maturity, number of tillers per plant, harvest index, 1000 seed weight, days to 50 per cent flowering, number of ill-filled

grains per panicle, panicle length, grain yield per plant and plant height. These results are in conformity with the reports of Idris *et al.* (2013) for number of filled grains per panicle, days to maturity, 1000 seed weight, panicle length and plant height; Bisne *et al.* (2009) for productive tillers per plant; Singh *et al.* (2012) for number of grains per panicle; Idris *et al.* (2013) for harvest index; Dhanwani *et al.* (2013) for days to 50 per cent flowering; Babu *et al.* (2012) for number of ill-filled grains per panicle and Kundu *et al.* (2008) for grain yield per plant.

A perusal of the results on genetic advance revealed high (>20%) values for number of grains per panicle and number of filled grains per panicle. The estimates of genetic advance as per cent mean was also high (>20%) for productive tillers per plant, followed by number of tillers per plant, number of grains per panicle, number of filled grains per panicle, 1000 seed weight, grain yield per plant, number of ill-filled grains per panicle and harvest index. These results are in conformity with the findings of Parvathi *et al.* (2011) for productive tillers per plant and number of tillers per plant; Idris *et al.* (2013) for number of grains per panicle; Babu *et al.* (2012) and Dhanwani *et al.* (2013) for number of filled grains per panicle and number of ill-filled grains per panicle; Dhanwani *et al.* (2013) for 1000 seed weight and grain yield per plant and Mamta singh *et al.* (2007) for harvest index. In contrast, moderate (10-20%) estimates of genetic advance were noticed in the present study for days to 50 per cent flowering, days to maturity and plant height. Moderate (10-20%) genetic advance as per cent mean were also recorded for panicle length, days to 50 per cent flowering and plant height. Similar results were reported by Parvathi *et al.* (2011) for panicle length and days to 50 per cent flowering and Babu *et al.* (2012) for plant height. Further, low (<10%) estimates of genetic advance were recorded in the present investigation for number of tillers per plant, productive tillers per plant, panicle length, number of ill-filled grains per panicle, 1000 seed weight, harvest index and grain yield per plant. Low (<10%) estimates of genetic advance as per cent mean were also noticed for days to maturity in the present investigation. These results are in conformity with the findings of Seyoum *et al.* (2012).

High heritability coupled with high genetic advance as per cent mean was recorded for all the characters under study, except days to 50 per cent flowering, days to maturity, plant height and panicle length indicating that the high heritability observed is due to additive gene effects and selection may be effective for these characters. Similar observations were reported by Bekele *et al.* (2013) for tillers per plant; productive tillers per plant and harvest index; Idris *et al.* (2013) for number of grains per panicle; Dhanwani *et al.* (2013) for number of filled grains per panicle and number of ill-filled grains per panicle and

Table 1. Analysis of variance (ANOVA) for yield and yield components in rice

Source of variation	Degrees of freedom	Days to 50 per cent flowering	Days to maturity	Plant height	Number of tillers per plant	Productive tillers per plant	Panicle length	Number of grains per panicle	Number of ill-filled grains per panicle	Number of filled grains per panicle	1000 Seed weight	Harvest index	Grain yield/ plant
Replications	2	0.89	0.81	17.32	0.26	0.48	0.39	13.59	1.06	11.73	0.12	1.79	1.31
Varieties	24	120.06**	117.72**	137.71**	14.79**	13.94**	15.32**	5894.99**	19.52**	4802.74**	34.77**	65.73**	20.98**
Error	48	2.05	1.22	10.84	0.17	0.13	0.69	20.40	0.89	9.63	0.54	0.95	1.16

*, ** Significant at 0.05 and 0.01 levels, respectively.

Table 2. Estimates of variability and genetic parameters for yield and yield components in rice

Character	Mean	Range		Variance		Co efficient of variation (%)		Heritability in broad sense (h^2_b)	Genetic advance (%)	Genetic Advance as per cent of mean
		Minimum	Maximum	Genotypic (Vg)	Phenotypic (Vp)	Genotypic (GCV)	Phenotypic (PCV)			
Days to 50 per cent flowering	104.71	89.67	129.33	39.34	41.39	5.99	6.14	95.05	12.60	12.03
Days to maturity	136.08	117.67	158.33	38.83	40.05	4.58	4.65	96.95	12.64	9.29
Plant height (cm)	109.27	87.13	124.53	42.29	53.13	5.95	6.67	79.60	11.95	10.94
Number of tillers/plant	9.34	7.40	11.43	4.87	5.04	23.64	24.04	96.63	4.47	47.86
Productive tillers/plant	8.83	6.87	11.27	4.60	4.73	24.30	24.64	97.25	4.36	49.36
Panicle length (cm)	24.74	20.53	29.30	4.88	5.57	8.93	9.54	87.60	4.26	17.21
Number of grains/panicle	214.08	161.00	293.14	1958.20	1978.60	20.67	20.78	98.97	90.69	42.36
Number of ill-filled grains/panicle	19.80	9.80	37.87	6.21	7.10	12.59	13.46	87.46	4.80	24.25
Number of filled grains/panicle	194.28	151.20	262.27	1597.70	1607.33	20.57	20.64	99.40	82.09	42.26
1000 Seed weight (g)	17.08	11.69	25.22	11.41	11.95	19.78	20.24	95.48	6.80	39.81
Harvest index (%)	41.99	32.86	48.96	21.59	22.54	11.07	11.31	95.79	9.37	22.31
Grain yield/plant (g)	19.85	17.63	23.59	6.61	7.77	12.95	14.04	85.06	4.88	24.60

Adilakshmi and Girijarani (2012) for 1000 seed weight. On the contrary, high heritability coupled with moderate genetic advance as per cent mean was observed for plant height and panicle length indicating the role of both additive and non-additive gene effects for control of the characters. The results are in conformity with the reports of Seyoum *et al.* (2012) for plant height. However, for days to maturity, high heritability coupled with low genetic advance as per cent of mean was noticed in the present investigation, which was similar to the findings of Singh *et al.* (2012).

Burton and Devane (1952) had reported that information on genetic variation along with heritability and genetic advance estimates gave a better idea about the efficiency of selection. In the present study, high GCV and PCV coupled with high heritability and high genetic advance as per cent mean were observed for productive tillers per plant followed by number of tillers per plant, number of grains per panicle and number of filled grains per panicle, indicating the pre-ponderance of additive gene action and scope for their improvement through selection. Similar results were reported earlier by Selvaraj *et al.* (2011) for productive tillers per plant.

Yield is a complex character and is the end product of multiplicative interaction between various yield components (Grafius, 1956). Information on the nature and extent of association among yield and yield component characters is therefore essential for systematic crop improvement. Further, the study of genetic correlations also gives an idea about the extent to which the characters are under the control of genes and this kind of analysis could help the breeder to design his selection for effective crop improvement. Correlations (phenotypic and genotypic) of yield and yield component characters in the present investigation are presented in Table 3. A perusal of these results, in general, revealed phenotypic and genotypic correlations of similar direction and significance. However, genotypic correlations had recorded a higher magnitude, compared to phenotypic correlations, indicating the masking effect of environment (Johnson *et al.*, 1955). Further, grain yield per plant was observed to be positively and significantly associated with number of tillers per plant, productive tillers per plant, number of grains per panicle and number of filled grains per panicle indicating an increase in grain yield with an increase in these characters. Therefore, priority should be given to these traits, while making selection for yield improvement. The findings are in agreement with the reports of Manikyaminnie *et al.* (2013) for productive tillers per plant and number of grains per panicle; Sudharani *et al.* (2013) for number of filled grains per panicle and Idris *et al.* (2013) for number of tillers per plant. On contrary, non-significant association was noticed for grain yield with days to 50 per cent flowering, days to maturity, plant height, panicle length, number of ill-filled grains per panicle, 1000 seed weight and harvest index. The findings are in consonance with the

reports of Yadav *et al.* (2010) for days to 50 per cent flowering, plant height, panicle length; and Panwar and Mashiat Ali (2007) for number of ill-filled grains per panicle.

Studies on inter-character associations for yield components revealed significant and positive association of days to 50 per cent flowering with days to maturity; plant height with panicle length; number of tillers with productive tillers per plant, number of grains per panicle, and number of filled grains per panicle; productive tillers with number of grains per panicle and number of filled grains per panicle; number of grains per panicle with number of ill-filled and filled grains per panicle, indicating a scope for simultaneous improvement of these traits through selection. The results are in agreement with the reports of Singh *et al.* (2012) for days to 50 per cent flowering with days to maturity, and number of tillers with number of grains per panicle; Manikyminnie *et al.* (2013) for plant height with panicle length, and productive tillers with number of grains per panicle; and Bekele *et al.* (2013) for number of tillers with productive tillers per plant; Sudharani *et al.* (2013) for number of tillers with number of filled grains per panicle; Gopikannan and Ganesh (2013) for productive tillers per plant with number of filled grains per panicle; and Vanisree *et al.* (2013) for number of grains per panicle with number of filled grains per panicle. However, significant and negative inter-character associations were observed for number of grains per panicle with 1000 seed weight; number of filled grains per panicle with 1000 seed weight; and number of ill-filled grains per panicle with 1000 seed weight probably due to competition for a common possibility, such as nutrient supply. The results are in conformity with the reports of Panwar and Mashiat Ali (2007).

Path co-efficient analysis provides an effective means of finding out the direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation and also measures the relative importance of each causal factor. Hence, the study of direct and indirect effects of yield components on grain yield per plant from genotypic correlation was undertaken in the present investigation and the results obtained are presented in Table 4. The results revealed high residual effect, indicating that variables studied in the present investigation explained only 48 per cent of the variability in yield and therefore, other attributes besides the characters studied are contributing for grain yield per plant. The results also revealed maximum direct effect of productive tillers per plant followed by number of filled grains per panicle and number of tillers per plant on grain yield per plant. High positive direct effect of productive tillers per plant (Manikyaminnie *et al.* 2013); number of filled grains per panicle and tillers per plant (Parvathi *et al.* 2011) on grain yield were also reported earlier. These traits had also exhibited highly significant and strong positive association with grain yield per plant. High direct effects of these traits therefore, appeared to be the main factor for their strong association

Table 3. Phenotypic (r_p) and Genotypic (r_g) correlation co-efficients for yield and yield components in rice

Character	r	Days to maturity	Plant height	Number of tillers/ plant	Productive tillers/ plant	Panicle length	Number of grains/ panicle	Number of ill-filled grains/ panicle	Number of filled grain/ panicle	1000 Seed weight	Harvest index	Grain yield/ Plant
Days to 50 per cent flowering	rp	0.7560**	0.2262	-0.4007**	-0.3480	0.3261	-0.1209	-0.3656	-0.0603	0.3749	-0.4107*	-0.1960
	rg	0.7701**	0.2322	-0.4506**	-0.3908*	0.3391	-0.1372	-0.4255*	-0.0699	0.3800	-0.4579*	-0.2707
Days to maturity	rp		0.0328	-0.3030	-0.2547	0.1608	-0.2691	-0.4731*	-0.2027	0.2503	-0.5274**	-0.2639
	rg		0.0359	-0.3347**	-0.2852	0.1677	-0.2999	-0.5459**	-0.2294	0.2524	-0.5894**	-0.3047
Plant height	rp			-0.1121	-0.0931	0.7275**	0.2129	0.1012	0.2155	0.2724	-0.1448	0.2768
	rg			-0.1426	-0.1270	0.7696**	0.2102	0.1115	0.2147	0.2855	-0.1661	0.3297
No. of tillers/plant	rp				0.9878**	0.0451	0.4469*	0.3420	0.4262*	-0.1904	0.2446	0.5964**
	rg				0.9951**	0.0248	0.4951**	0.3834*	0.4817*	-0.2240	0.2493	0.7426**
Productive tillers/ plant	rp					0.0728	0.4675*	0.3491	0.4476*	-0.1913	0.2086	0.6097**
	rg					0.0577	0.5318**	0.4018*	0.5195**	-0.2254	0.2175	0.7549**
Panicle length	rp						0.1140	0.1040	0.1053	0.0450	-0.2739	0.0796
	rg						0.0653	0.1039	0.0529	0.0501	-0.3181	0.0737
Number of grains/ panicle	rp							0.6001**	0.9869**	-0.4000*	0.1908	0.6107**
	rg							0.6913**	0.9896**	-0.4024*	0.1992	0.8538**
Number of ill-filled grains/panicle	rp								0.4633*	-0.3852*	0.2866	0.3021
	rg								0.5802**	-0.4112*	0.4037*	0.3363
Number of filled grains/panicle	rp									-0.3890*	0.1536	0.5996**
	rg									-0.4236*	0.1442	0.8059**
1000 Seed weight	rp										0.0795	0.3098
	rg										0.0821	0.3331
Harvest index	rp											0.2770
	rg											0.2929

*, ** Significant at 5% and 1% levels, respectively

Table 4. Path co-efficients for yield and yield components in rice

Character	Days to 50 per cent flowering	Days to maturity	Plant height	Number of tillers/ plant	Productive tillers/ plant	Panicle length	Number of grains/ panicle	Number of ill-filled grains/ panicle	Number of filled grains/ panicle	1000 Seed weight	Harvest index	Grain yield/ plant
Days to 50 per cent flowering	0.4652	-0.1935	0.1652	-0.9641	0.3840	-0.3614	0.3324	-0.7780	-0.1065	0.4206	0.3653	-0.2707
Days to maturity	0.4353	-0.2513	0.0256	-0.7161	0.7267	-0.1787	0.2802	-1.1265	-0.2494	0.2793	0.4702	-0.3047
Plant height	0.2312	-0.0090	0.4115	-0.3050	0.2248	-0.8203	-0.5092	0.2301	0.3272	0.3159	0.2325	0.3297
Number of tillers/plant	-0.2547	0.0841	-0.1014	0.6397	-0.4776	-0.0264	-0.1996	0.7911	0.7340	-0.2479	-0.1989	0.7426**
Productive tillers/plant	-0.2209	0.1870	-0.0904	1.1293	0.8824	-0.0615	-2.2887	0.8491	0.7916	-0.2495	-0.1735	0.7549**
Panicle length	0.1916	-0.0421	-0.1476	0.0530	0.3567	-0.3658	-0.1581	0.2038	0.0806	0.0554	-0.1538	0.0737
Number of grains/ panicle	-0.0775	0.0704	0.1495	0.0193	0.5225	-0.0696	-1.4230	0.4266	1.5079	-0.1134	-0.1589	0.8538**
Number of ill- filled grains/panicle	-0.2405	0.2372	0.1793	0.8203	-0.3747	-0.1107	-0.4751	0.0636	0.8841	-0.3250	-0.3221	0.3363
Number of filled grains/panicle	-0.0395	0.0576	0.1528	1.0307	-0.5104	-0.0564	-1.7978	1.1972	0.9238	-0.0372	-0.1150	0.8059**
1000 Seed weight	0.2148	-0.0634	0.2431	-0.4793	0.2815	-0.0534	0.2482	-0.5485	-0.0512	0.6067	-0.0655	0.3331
Harvest index	-0.2588	0.1481	-0.1182	0.0361	0.8330	0.3090	-0.4827	0.3137	0.2197	0.0908	-0.7978	0.2929

*, ** Significant at 5% and 1% levels, respectively Residual effect = 0.5292 Diagonal and Bold values = Direct effects;
Off-Diagonal values = Indirect effects

with grain yield per plant. Hence, these traits should be considered as important selection criteria in all rice improvement programmes and direct selection for these traits is recommended for yield improvement. The results are in conformity with the findings of Meena Kumari *et al.* (2011).

Days to 50 per cent flowering, plant height and 1000 seed weight also had high positive direct effects on grain yield per plant. The results are in consonance with the findings of Seyoum *et al.* (2012) for days to 50 per cent flowering and Adilakshmi and Girijarani (2012) for plant height and 1000 seed weight. However, its association with grain yield per plant was noticed be non-significant in the present investigation indicating the need for adoption of restricted simultaneous selection model to nullify the undesirable indirect effects and make use of the direct effect (Singh and Kakar, 1977).

High negative direct effects on grain yield per plant was recorded by number of grains per panicle. However its association with grain yield per plant was observed to be highly significant and positive indicating a major role of indirect effects, namely, number of filled grains per panicle, productive tillers per plant and number of ill-filled grains per panicle and hence, a need for simultaneous consideration of these traits in selection programmes along with number of grains per panicle. In addition, days to maturity, panicle length and harvest index also had high negative direct effects on grain yield per plant. The results are in agreement with the reports of Madhavilatha *et al.* (2005). Association of these traits with grain yield per plant was however, non-significant indicating the indirect effects of these traits on grain yield per plant through other characters. High indirect effects of these traits were noticed mostly through productive tillers per plant indicating importance of the trait as selection criteria. The findings are in conformity with the reports of Manikyaminnie *et al.* (2013).

A perusal of the results thus emphasized the need for selection based on productive tillers per plant, number of filled grains per panicle and number of tillers per plant for improvement of grain yield in rice.

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GENETIC DIVERSITY OF MUSKMELON USING MULTIVARIATE TECHNIQUE

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Abstract

An experiment was conducted at the experimental farm of Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI), Gazipur in 2011 to estimate genetic diversity through multivariate technique. Based on multivariate analysis and application of covariance matrix for non-hierarchical clustering, 64 genotypes of muskmelon were grouped into six clusters to indicate the existence of considerable diversity among the genotypes. The cluster IV was consisted of single genotypes (BD2303). The highest number of genotypes possessed in Cluster I. The first principal axis largely accounted for the variation among the genotypes which alone contributed 25.65% of the variations. The highest inter genotypic distance (2.878) was observed between the genotypes BD2303 and BD2313 followed by the genotypes BD2303 and BD2314 (2.808).The highest intra cluster distance was computed for cluster III (0.839) followed by cluster I (0.751). Cluster VI showed the least intra cluster distance which indicated that the genotypes in this cluster were more or less homogeneous. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different clusters. Cluster mean pointed out the heavier fruit in cluster IV (2533.3g). The size of this cluster was also far different from all other clusters. Similarly, the highest total fruit weight per plant was found in cluster IV (13.5 kg) which was also far different from other clusters. So it revealed that genotypes of this cluster could be used for developing high yielding variety. Cluster VI showed the highest brix reading (5.6%). Therefore, the genotypes of this cluster could be used for the development of sweet muskmelon variety. Hybridization between the genotypes of cluster IV and those of cluster VI could develop high yielding sweet muskmelon variety(s).

Keywords: Genetic diversity, *Cucumis melo*, Cluster and Multivariate analysis.

Introduction

Nature of out crossing in muskmelon is always generating genetic diversityin this crop (Saxena, 2005 and Hancock, 2012). Moreover, genetic diversity is essential for a plant breeding programme. A new variety as per farmer's demand can be developed from an assembled diverse genetic stock of any crop.

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So success of any breeding program depends much on the genetic diversity available and the judicious selection of parents. The importance of genetically diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been reported by several workers (Baenziger *et al*., 2006 and Stuthman *et al.*, 2007). The importance of genetic diversity in any crop improvement programme has been stressed both in self and cross pollinated crops (Flowers, 2004).

Genetic resources are, in the sense, the building blocks and also fundamental not only to a crop improvement program, but also for the very survival of the species in time and space (Swaminathan, 1983). Moreover, evaluation of genetic diversity is important to know the source of genes for particular trait within the available germplasm (Tomoka, 1991). Multivariate analysis by means of Mahalanobis' D^2 statistics is a useful tool in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Murty and Arunachalam, 1966; Das and Gupta, 1984). From the plant breeding point of view the degree of genetic diversity between two parents is an index for determining the hybridity over parents or nature of the segregants in the follow-up generation. D^2 statistics can help in selecting desirable parents for achieving desired goal by the breeder. Though information on genetic divergence is available in most of the crops, such information in muskmelon is very rare (Kalloo *et al*., 1982). Considering the above facts, the present investigation was undertaken to assess the genetic diversity among the collected germplasm and to identify the diverse parents for use in further genetic study.

Materials and Method

The experiment was conducted at the experimental farm of Plant Genetic Resources Centre (PGRC), Bangladesh Agricultural Research Institute (BARI), Gazipur in 2011. The data on quantitative parameter of muskmelon was recorded and used to estimate genetic diversity through multivariate technique. The quantitative parameters were as follows:

a. Fruit length (cm)
b. Fruit width (cm)
c. Fruit girth (cm)
d. Flesh thickness(cm)
e. Cavity diameter (cm)
f. Fruit size (g)
g. Number of fruits per plant
h. Number of seeds per fruit
i. 100 seed weight (g)
j. Seed yield per plant (g)
k. Total fruit weight (kg)
l. Brix %

Analysis of data

Mean data for each character was subjected to multivariate analysis techniques *viz*. Principal component analysis (PCA), Principal coordinate analysis (PCO), Canonical vector analysis (CVA) and Cluster analysis (CLSA) using GENSTAT 5.13 software.

Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first component and succeeding components with latent roots greater than unity (Jeger *et al*., 1983). The latent roots are called "Eigen values". The first component has the property of accounting for maximum variance. The PCA displays most of the original variability in a smaller number of dimensions, since it finds linear combinations of a set of variate that maximize the variation contained within them. Contributions of the different characters towards divergence are discussed from the latent vectors of the two principal components.

Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of p it gives the minimum distances between each pair of the N points using similarity matrix (Digby *et al.*,1989). Inter-distances between genotypes were studied by PCO.

Canonical variate analysis (CVA)

CVA complementary to D^2-statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively are derived. Canonical variate analysis finds linear combination of original variability that maximizes the ratio of between groups to within groups variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformations sequentially maximize the ratio of among groups to within group variations.

Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using nonhierarchical classification. In Genstat, the algorithm is used to search for optimal values of the chosen criterion. The optimal values of the criteria followed by some initial

classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. No further transfer can be found to improve the criterion. The algorithm switches to second stages that examine the effect swapping two genotypes of different classes, and so on.

Computation of average Intra-cluster distance

Computation of Average Intra-Cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

Cluster diagram

It was drawn using the values between and within cluster distances, which presents a momentary idea of the pattern of diversity among the genotypes included in a cluster.

Computation of average inter - cluster distances

The procedure for calculating inter-cluster distance between cluster II and I, between cluster III and I, between cluster IV and I, between cluster V and I, between cluster VI and I and between cluster II and III and so on. The clusters were taken one by one and their distances from other clusters were calculated.

Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization programme. The genotypes grouped together are less divergent among themselves than different clusters. Clusters separated by the largest statistical distance (D^2), express the maximum divergence among the genotypes included into these different clusters.

Results and Discussion

Principal component analysis

Eigen values of twelve principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 1. The result revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 25.25% of the variations. While the first six Eigen values for the principal component axes of genotypes accounted for 85.38% of the total variation among

12 characters describing 64 genotypes while the former three accounted for 56.6%. Henane *et al*. (2013) reported that the first three axes explained 89.86% of the observed phenotypic diversity and the first principal component explained 54.5% of the total variance.

Table 1. Eigen values and percentage of variation for corresponding 12 component characters in muskmelon genotypes

Principle of component axis	Eigen values	Percentage of total values accounted	Cumulative percentage
Fruit length (cm)	3.078	25.65	25.65
Fruit width (cm)	1.8974	15.81	41.46
Fruit girth (cm)	1.8165	15.14	56.6
Flesh thickness(cm)	1.4319	11.93	68.53
Cavity diameter (cm)	1.1044	9.2	77.73
Fruit size (g)	0.9175	7.65	85.38
No. of fruits / plant	0.7087	5.91	91.29
No. of seeds / fruit	0.633	5.27	96.56
100 seed weight (g)	0.4	3.33	99.89
Seed yield / plant (g)	0.0098	0.08	99.97
Total fruit weight/plant (kg)	0.0027	0.02	99.99
Brix %	0	0	99.99

Construction of scatter diagram

Based on these values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1Z_2) using component scores 1 as X axis and component scores 2 as Y axis was constructed which has been presented in Fig.1. The positions of the genotypes in the scatter diagram were apparently distributed into 6 groups which indicated the existence of considerable diversity among the genotypes. Significant genetic diversity in muskmelon was also investigated by Escribano and Lazaro (2009); Nasrabadi *et al.* (2012) and Trimech *et al.* (2013) using different morphological characters.

Principal coordinate analysis(PCO)

PCO was done to get inter genotypic distances. The highest inter genotypic distance (2.878) was observed between the genotypes BD2303 and BD2313 followed by the genotypesBD2303 and BD2314 (2.808).The lowest distance (0.249) was observed between genotypes BD2288 and BD2310 followed by BD2259 and BD2309 (0.252).The intra cluster distance wascalculated from inter genotypic distance as suggested by Singh and Chaudhary (1985).The magnitude

of the intracluster distances were not always proportional to the number of genotypes in the cluster. Zhang *et al*. (2012) studied on principal of coordinateanalysis in Mediterranean region and south Asian region and found that fruit length and fruit girth dominated in PC_1 and PC_2, respectively.

The study revealed that the cluster I composed of the largest number of genotypes 20 (Table 2), but intra cluster distance was not necessarily the highest. Statistical distances were representing the index of genetic diversity among the cluster. The highest intra-cluster distance was computed for cluster III (0.839) which consisted of 11 genotypes followed by cluster I (0.751) having 20 genotypes (Table 3). The intra distance of cluster IV is 0.00 since the cluster consisted of only one genotype (BD 2303). Cluster VI showed the least intra cluster distance indicating that the genotypes in this cluster were more or less homogeneous (Fig.2). Henane *et al*. (2013) observed ahigh degree of polymorphism in muskmelon for almost all of qualitative characters. Moreover, cluster analysis and distribution of populations of PCO separated the varieties in different groups with a divergence variety from the other varieties.

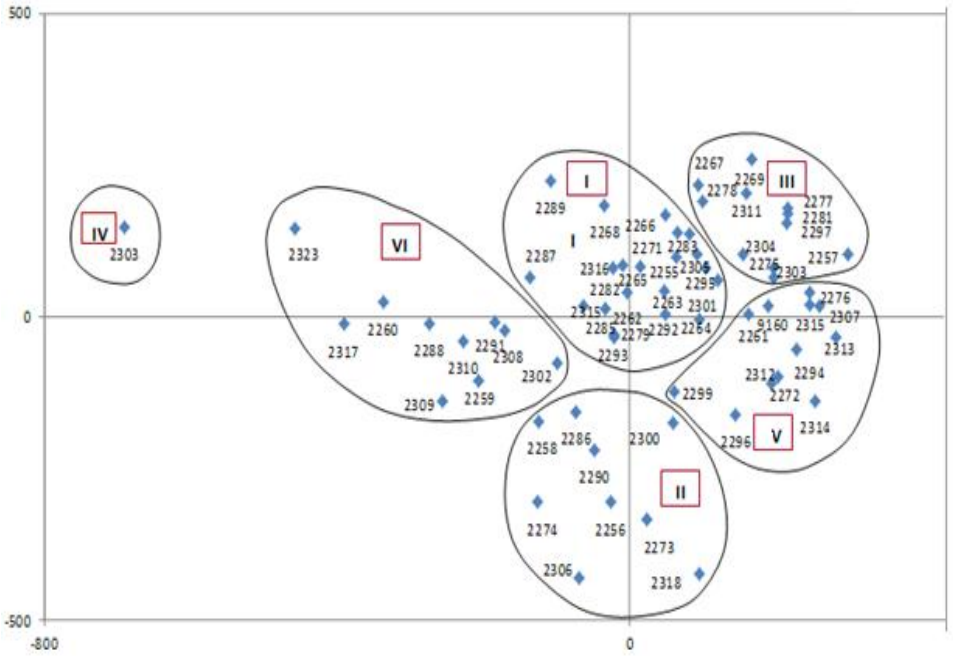

Fig. 1. Scatter diagram of 64 muskmelon genotypes based on their principal component scores super imposed with clustering.

Table 2. Distribution of 64 genotype in different clusters

Cluster	Genotypes	Number of genotypes
I	BD-2255, BD-2262, BD-2263, BD-2264, BD-2265, BD-2266, BD-2268, BD-2271, BD-2279, BD-2282, BD-2283, BD-2285, BD-2289, BD-2292, BD-2293, BD-2295, BD-2301, BD-2305, BD-2315, BD-2316	20
II	BD-2256, BD-2258, BD-2273, BD-2274, BD-2286, BD-2290, BD-2300,BD-2306, BD-2318	9
III	BD-2257,BD-2267,BD-2269,BD-2275,BD-2277,BD-2278,BD-2281,BD-2297,BD-2298,BD-2304,BD-2311	11
IV	BD-2303	1
V	BD-2261, BD-2272, BD-2276, BD-2280, BD-2294, BD-2296, BD-2299,BD-2307, BD-2312, BD-2313, BD-2314, BD-9160	12
VI	BD-2259, BD-2260, BD-2287, BD-2288, BD-2291, BD-2302, BD-2308, BD-2309, BD-2310, BD-2317, BD-2323	11
	Total genotypes	64

Canonical variate analysis

The CVA was performed to obtain the inter cluster distances (Mahalanobis' D^2 Values) The values of inter-cluster distance (D^2) are presented in Table 3. Statistical distances represented the index of genetic diversity among the clusters. The inter cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different clusters (Table 4).The inter-cluster distance (Fig. 2) was maximum between clusters III and IV (30.111) followed by clusters IV and V, while the minimum distance was found between clusters I and V (2.934) followed by cluster I and III (3.272). The maximum value of inter-cluster distance indicated that the genotype belonging to this cluster were far diverged. The minimum cluster distance suggesting a close relationship between the genotypes of clusters. These relationships were also reflected in the scatter diagram.

Table 3. Intra and inter cluster distances of 64 muskmelon genotypes

I	**0.751**					
II	5.271	**0.636**				
III	3.272	7.261	**0.839**			
IV	27.852	26.81	**30.111**	**0.00**		
V	2.934	5.196	3.106	30.107	**0.730**	
VI	4.449	4.555	6.964	23.917	6.384	**0.630**
	I	**II**	**III**	**IV**	**V**	**VI**

The genotypes of distant clusters could be used in hybridization programme for obtaining a wide range of variation among the segregate. Similar reports were also made by Uddin *et al.* (1994) and Swain and Dikshit (1997). Wen Xing *et al.* (1994) reported the beneficial effect of crossing carried out between genotypes having genetic distance (D^2) greater than 12.5. Thus it could be suggested that crosses should be made between genotypes belonging to the distant cluster for higher heterotic response.

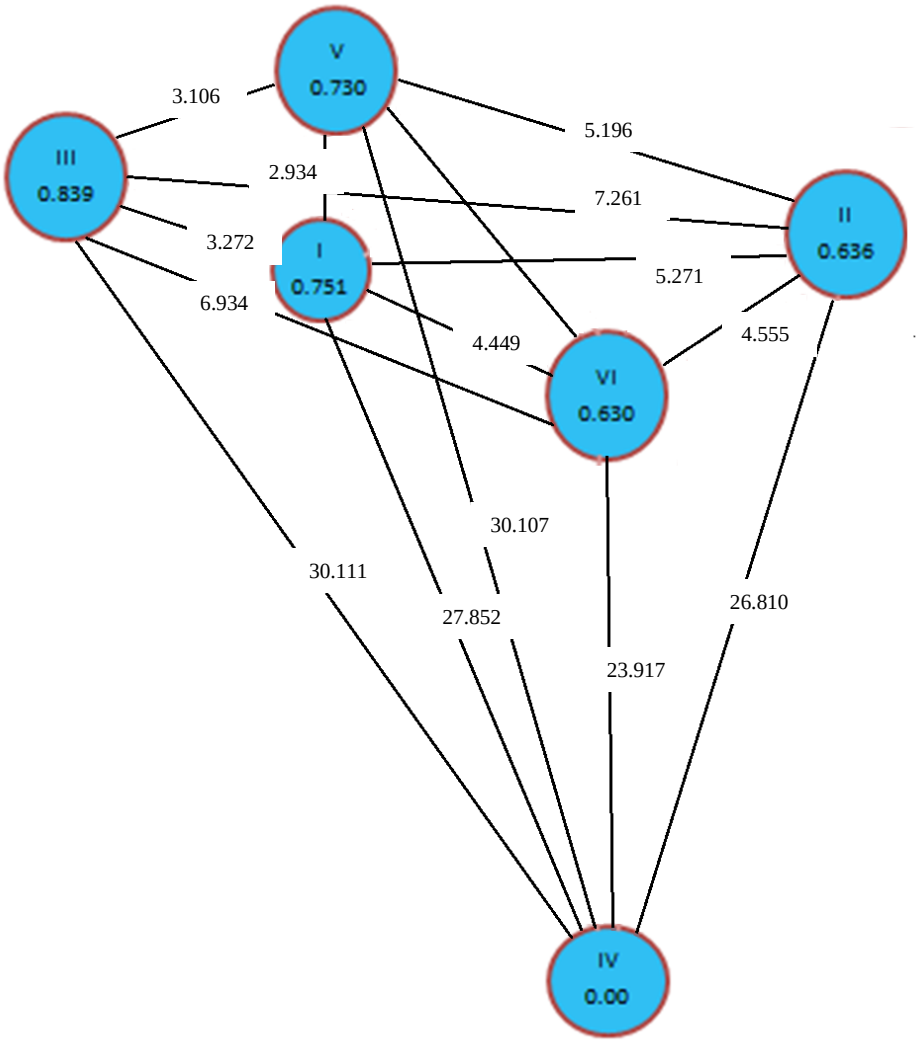

Fig. 2. Diagram showing the inter cluster distance and intra-cluster (inside the circle) distances of 64 muskmelon genotypes.

The highest inter cluster distance between III and IV (30.111) suggesting that crossing between the desirable genotypes of the two clusters for getting greater heterotic effect. Moreover, the heterosis could also be exploited by crossing between genotypes with moderate diversity like I and IV, II and IV, IV and V and IV and VI (Fig.2). Szamosi *et al*. (2010) found heterosis by crossing between the genotypes with higher inter cluster distance.

Non- hierarchical clustering

With the application of covariance matrix for non-hierarchical clustering, the 64 genotypes were grouped into six different clusters. These results confirmed the clustering pattern of the genotypes according to their principal component analysis.

The cluster composition with different genotypes including their collection site is presented in Table 4. On the basis of D^2 analysis, the 64 genotypes were grouped into six clusters. The distribution pattern indicated that the maximum number of genotypes (20) included in cluster I followed by cluster V (12). Cluster III and VI had same (11) number of genotypes. The lowest number of genotypes was found in Cluster II. Diversity is generally associated with geographical diversity but genetic diversity is not directly related with geographic distribution (Luan *et al*, 2008 and Szamosi *et al.,* 2010).

The clustering pattern of the genotypes under this study revealed that the genotypes originating from the same country did not form a single cluster. Even, the local genotypes collected from the same district did not form the same cluster which indicated that the geographic diversity is not always related to the genetic diversity and it might be due to the continuous exchange of germplasm among the researcher and grower. Therefore, it may be concluded that the selection of cultivars for hybridization should be based on genetic diversity instead of geographic diversity.

Table 4. Distribution and place of collection of 64 genotypes of muskmelon in different cluster

Cluster	Total no.	Genotype no.	Source of collection
I	20	BD2255	Kushtia
		BD2262	Kushtia
		BD2263	Kushtia
		BD2264	Kushtia
		BD2265	Kushtia
		BD2266	Munshigonj
		BD2268	Kushtia
		BD2271	Kushtia
		BD2279	Faridpur

Table 4. Cont'd

Cluster	Total no.	Genotype no.	Source of collection
		BD2282	Faridpur
		BD2283	Chittagong
		BD2285	Jamalpur
		BD2289	Mymensingh
		BD2292	Tangail
		BD2293	Tangail
		BD2295	Tangail
		BD2301	Comilla
		BD2305	Sirajgonj
		BD2315	Munshigonj
		BD2316	Sirajgonj
II	9	BD2256	Kushtia
		BD2258	Munshigonj
		BD2273	Kushtia
		BD2274	Kushtia
		BD2286	Jamalpur
		BD2290	Tangail
		BD2300	Comilla
		BD2306	Sirajgonj
		BD2318	Sirajgonj
III	11	BD2257	Kushtia
		BD2267	Kushtia
		BD2269	Kushtia
		BD2275	Kushtia
		BD2277	Faridpur
		BD2278	Faridpur
		BD2281	Faridpur
		BD2297	Tangail
		BD2298	Comilla
		BD2304	Sirajgonj
		BD2311	Sirajgonj
IV	1	BD2303	Sirajgonj
V	12	BD2261	Kushtia
		BD2272	Kushtia
		BD2276	Faridpur
		BD2280	Faridpur
		BD2294	Tangail
		BD2296	Tangail
		BD2299	Comilla

Table 4. Cont'd

Cluster	Total no.	Genotype no.	Source of collection
		BD2307	Sirajgonj
		BD2312	Sirajgonj
		BD2313	Sirajgonj
		BD2314	Sirajgonj
		BD9160	Pabna
		BD2259	Kushtia
		BD2260	Kushtia
		BD2287	Mymensingh
		BD2288	Mymensingh
		BD2291	Tangail
VI	11	BD2302	Sirajgonj
		BD2308	Sirajgonj
		BD2309	Sirajgonj
		BD2310	Sirajgonj
		BD2317	Sirajgonj
		BD2323	Kushtia

Result of different multivariate techniques have been superimposed in Fig.1. The clustering pattern obtained with the apparent grouping pattern performed by non-hierarchical clustering.

Cluster means for 12 characters in muskmelon

Cluster means for twelve characters are presented in Table 5. Fruit length had the highest mean value in cluster VI (16.8 cm) followed by cluster IV (16.4 cm) and II (16.2 cm). The genotypes of cluster V (15.1 cm) produced the shortest fruit length. The highest fruit width was produced by the genotypes under the cluster IV (8.3 cm) followed by cluster II (7.8 cm), I (7.5 cm) and VI (7.3 cm). The lowest mean values of this trait were shown by cluster III (6.9 cm). Maximum fruit girth was found in Cluster IV (26.2 cm). Similar girth was found in Cluster II and VI (25.5cm) and cluster III and V (23.8 cm) which had minimum girth among the clusters. Flesh thickness of muskmelon fruit was more or less equal (1.5 cm) in all clusters except cluster VI (1.6 cm) which has been marked as thicker groups compared to others. Cavity diameter was found highest in cluster IV (5.2 cm) and that the lowest cavity diameter was in Cluster III and VI (4.0 cm). The heaviest fruit was found in cluster IV (2533.3 g). This cluster was composed of only one genotype (BD2303). Therefore, it may be revealed that genotype of this cluster could be used for developing high yielding variety of while the small size fruit was found in cluster V (372.5 g). Maximum number of fruits per plant (5.9) was found in cluster I and II. The highest number of seeds per fruit was found in cluster II (688) and that of the lowest number was in cluster III (249.5). Hundred seed weight was found maximum in cluster IV (2.1g)

which was followed by cluster III and VI (1.9 g). The cluster II showed the highest seed yield (74.7 g) per plant and the cluster III showed the lowest seed yield (25.6g). The highest total fruit weight per plant was found in cluster IV (13.5 kg) which was far different from other clusters. The lowest total fruit weight was found in cluster III and V. Sweetness of fruit is indicated by brix %. Cluster VI showed the highest brix % (5.6). Hence, the genotypes of this cluster could be used for sweetened variety development. The lowest brix % (5.0) was found in cluster IV: however it was less sweet.

Table 5. Cluster mean values for different characters of muskmelon genotypes

Characters	I	II	III	IV	V	VI
Fruit length (cm)	15.8	16.2	15.6	16.4	15.1	16.8
Fruit width (cm)	7.5	7.8	6.9	8.3	7.1	7.3
Fruit girth (cm)	24.7	25.5	23.8	26.2	23.8	25.5
Flesh thickness (cm)	1.5	1.5	1.5	1.5	1.5	1.6
Cavity diameter (cm)	4.4	4.7	4	5.2	4.1	4
Fruit size (g)	557.3	606.3	399.1	2533.3	372.5	828.2
Number of fruits / plant	5.9	5.9	5.4	5.3	5.6	5.6
Number of seeds / fruit	334.4	688	249.5	297.3	456.8	429.7
100 seed weight (g)	1.6	1.8	1.9	2.1	1.7	1.9
Seed yield / plant (g)	31.8	74.7	25.6	33.7	43	44.3
Total fruit weight / plant (kg)	3.3	3.6	2.1	13.5	2.1	4.6
Brix %	5.3	5.1	5.3	5	5.5	5.6

Finally, based on multivariate analysis and application of covariance matrix for non-hierarchical clustering, 64 genotypes of muskmelon were grouped into six clusters indicating the existence of considerable diversity among the genotypes. Principal coordinate (PCA) analysis showed the highest inter genotypic distance (2.878) between the genotypes BD2303 and BD2313,while the lowest distance (0.249) was observed between genotypes BD2288 and BD2310. The most diverse genotypes were found in cluster III while the least diverse genotypes were found in Cluster VI. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different clusters. In addition, the inter-cluster distance was maximum between cluster III and IV (30.111) and the minimum distance was found between cluster I and V (2.934). Furthermore, mean values of various cluster pointed out the heavier fruit in cluster IV (2533.3g). So genotypes of this cluster could be used for developing high yielding variety. Sweetness of fruit is indicated by brix reading. Cluster VI showed the highest brix reading. Hence, the genotypes of this cluster could be used for sweetened variety development of muskmelon.

Hybridization between the genotypes of cluster IV and those of cluster VI could develop high yielding sweet muskmelon variety(s).

Conclusion

Genetic diversity of the muskmelon was assessed using multivariate technique. A considerable range of genetic diversity was found in the genotypes. The cluster analysis grouped the genotypes into six divergent clusters. The highest genotypes possessed in Cluster I. The Principal component analysis revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 25.65% of the variations. The maximum fruit weight per plant was found in cluster IV and the genotypes of this cluster could be used for developing high yielding variety. TSS indicates the sweetness of fruits. The genotype BD2312 (8^0brix) was found as the sweetest muskmelon among the tested genotypes.

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DEVELOPMENT OF INTEGRATED PEST MANAGEMENT APPROACHES AGAINST *Helicoverpa armigera* (Hubner) IN TOMATO

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K. BEGUM[4] AND D. SARKER[5]

Abstract

Five IPM packages viz. T_1=Pheromone trap @ 70 traps ha^{-1} + Neem seed kernel extract @ 50 g L^{-1} of water; T_2=Pheromone trap + HaNPV @ 0.4 ml L^{-1} of water and *Bt* @ 2.0 g L^{-1} of water; T_3=Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*; T_4=Pheromone trap + *Trichogramma chillnis* @ 50,000 ha^{-1} and *Bracon hebetor* @ 1200 ha^{-1}; T_5=Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor* were evaluated against *H. armigera* in tomato. The lowest fruit infestation by number (12.55%) was attained from T_5 followed by T_2 (15.49%). Significantly the lowest fruit infestation by weight was found in treatment T_2 (10.60%) followed by T_5 (11.73%). The highest yield was obtained from T_5 (29.74 t ha^{-1}) followed by T_2 (26.77 t ha^{-1}). The highest marginal benefit cost ratio was achieved from T_2 (3.41) followed by T_5 (3.35). Hence, considering benefit cost ratio, T_2 and T_5 packages may be the effective tools for managing *H. armigera* in tomato.

Keywords: IPM, pheromone trap, HaNPV, *Bt*, neem, *Helicoverpa armigera*, tomato.

Introduction

Tomato fruitworm, *Helicoverpa armigera* (Hubner) (Lepidoptera: Noctuidae) is one of the most serious insect pests of tomato. It is widely distributed in Asia, Africa, Australia and the Mediterranean Europe (Mehrvar, 2009, Chari *et al*., 1990). The four chief characteristics i.e., polyphagy, high mobility, high fecundity, and facultative diapauses of *H. armigera* help attaining the status of a major pest (Fitt, 1989). Being polyphagous, this pest feeds on more than 500 plant species, including economically important crops such as cotton, maize, sorghum, chickpea, pigeon pea, sunflower, vegetables and fruits. It was reported that infestation range of *H. armigera* on tomato was up to 46.85 per cent at Jessore, Bangladesh (Alam *et al*., 2007). *Helicoverpa* species preferably feeding on buds, flowers and fruits. Zalucki *et al*. (1986) reported that the voracious larvae of *H. armigera* prefers to move from one fruit to another, often without consuming it completely and the lower number of large larvae may cause extensive damage of crops. An indiscriminate application of pesticides, during

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1980s and 1990s was responsible for severe outbreaks of *H. armigera* (Ahmad *et al*., 1997).

Now a days, Integrated Pest Management (IPM) is being used to find ecologically sound and environmentally safe ways of pest control. Botanical pesticides are now emerging as a valuable component of IPM strategies on all crops due to their efficacy to pests and safety to natural enemies (Srinivasa *et al.*, 1999). The use of neem seed kernel extract has given the most satisfactory control of *Helicoverpa* in pulse crops (Schmutterer, 1990). Sachan and Lal (1990) reported that extracts from neem and custard apple kernels were effective against *H. armigera* both in the laboratory and field conditions. Neem seed kernel extract and neem rind extract provided maximum protection to chickpea due to their antifeedant properties against *H. armigera* (Dubey *et al.*, 1991). A large number of parasitoids and predators have been recorded on *Helicoverpa* spp. and altogether 77 parasitoids have been reported in India. Seven species of Trichogrammatids have been recorded as egg parasitoids (Yadav *et al.*, 1981). Divakar and Pawar (1987) reported that release of *Trichogramma chilonis* Ishii, *Trichogramma brasiliensis* Parkins, *Trichogramma pretiosum* Riley caused 92.4 per cent reduction in *H. armigera* in tomato. *Bracon hebetor* is a common gregarious ecto-larval parasitoid. Female *Bracon* at first inject venom and thus paralyze insect larvae. A female *Bracon* can paralyze 500-1000 larvae and the paralyzed larvae cannot survive. Some of the microbial were effective for the control of *H. armigera* which included bacteria, *B. thuringiensis* (Chari *et al.*, 1995), nuclear polyhedrosis virus (Yearian *et al.*, 1986; Chand *et al.*, 1999). Two pathogens, Nucleopolyhedrosis viruses (NPV) and the bacterium *Bacillus thuringiensis* (commonly called *Bt*) are available commercially to control *Helicoverpa* larvae. *Bt* is available as a selective spray that only kills moth larvae. Sex pheromones are powerful chemical attractants which have aroused great interest because of their potential as pest control agents. Malik and Ali (2002) reported pheromone traps as a good tool to monitor and control lepidopterous pests. Knight (1995) found pheromone traps more economical than other controlling techniques. Hence, a study was envisaged to combat the *H. armigera* with an objective to develop sustainable and eco-friendly management option(s) against *H. armigera* in tomato.

Materials and Method

The experiment was conducted in the experimental field of the Entomology Division, BARI, Gazipur during *rabi* 2009-10. The tomato variety BARI Tomato 2 seeds were collected from Olericulture Division, Horticulture Research Center (HRC), BARI, Gazipur. Tomato seeds were sown in beds (3m × 1m) 5 cm apart in rows for raising seedlings.

Experimental design and raising of crops

The experiment was laid out in randomized complete block design (RCBD) with three replications. The unit plot size was 3.6m × 3m with a distance of 100 cm between the plots and 150 cm between the blocks. In unit plots, row to row distance was 60 cm and plant to plant was 40 cm. One month old healthy seedlings of equal height were selected for transplanting in the experimental plots. Standard agronomic practices such as watering, gap filling, application of fertilizer, weeding, propping were followed during the study period (Rashid and Singh, 2000)

Treatments and application

Five IPM packages were tested against *H. armigera*. In addition, one untreated control treatment was included for comparison. The package treatments were: T_1= Pheromone trap @ 70 traps ha^{-1} + Neem seed kernel extract @ 50 g L^{-1} of water at 10 days interval; T_2= Pheromone trap + alternate spraying of HaNPV (Heli-Cide 100 LE $1x10^9$ POB ml^{-1}) spraying @ 0.4 ml L^{-1} of water at 10 days interval and *Bt* (*Bacillus thuringiensis* Halt 5% WP) @ 2.0g L^{-1} of water at 10 days interval; T_3= Pheromone trap + Neem seed kernel extract + HaNPV and *Bt* (alternate spraying); T_4= Pheromone trap + *T. chilonis* (50,000 ha^{-1}) at 7 days interval and *B. hebetor* (@ 1200 ha^{-1}) at 7 days interval; T_5= Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor* and T_6= Untreated control. Among the treatments there were three dispersed replications at a distance of 200 m for the package of T_4, T_5 and control. The rest of the packages were set up at the distance of 1.5m row to row and 1.0 m plot to plot.

Installation of pheromone trap: For all packages pheromone traps were set up at a distance of 12 m at 40 days after transplanting and continued up to last harvest. Soapy water of 3-4 cm height is maintained inside trap throughout the season. The pheromone lure is hung through the center of the lid inside the trap in such a way that it is 2 to 3 cm above the surface of the soapy water.

Release of bio-control agents: When tomato plant started flower initiation weekly release of egg parasitoids, *T. chilonis* (@ 50,000 ha^{-1}) and larval parasitoid *Bracon hebetor* (@ 1200 adults ha^{-1}) were ensured and continued seven times.

Preparation of neem seed extract and application: Neem seeds were collected from the farmer's home of ChapaiNababgonj, Rajshahi. Collected seeds were air dried and then seeds with kernel were grinding into coarsely milled product by grinder. Two hundred fifty g grinded neem seed were added to 5 l of water, mixed well and left it to soak for 12 hours. Finally, it was filtered through moslin cloth. The filtered product was then ready for spraying. Neem seed kernel

extract was first sprayed just before flower initiation stage and then 2nd, 3rd sprays were done at 10 days intervals.

Microbial application: *Bt* and HaNPV were first sprayed just before flower initiation stage and then 2nd, 3rd 4th and 5th sprays were done at 10 days intervals with the help of Knapsac sprayer.

Percent fruit infestations by number at in-situ condition: In this case the data recording were started just after first fruit set. All fruits of six plants per plot were considered for data recording. Data on percent fruit infestation by number were recorded at 7 days interval.

Per cent fruit infestation by number: At harvest, the total fruits were sorted into healthy and infested ones for each treatment. On the basis of the number of total fruits and infested fruits the percent fruit infestation was calculated.

Per cent fruit infestation by weight: Accordingly, the weight of infested (bored) and weight total fruits were recorded and the per cent fruit infestation by weight was determined

Marginal benefit cost ratio: The marginal benefit cost ratio was calculated on the basis of prevailing market prices of tomato, sex pheromone, botanicals, microbials, bio-control agents and their spraying cost. Marginal benefit cost ratio of different treatments was also determined following Ali *et al*. (1996) was calculated as follows:

$$\% \text{ Marginal BCR} = \frac{\text{Benefit on control}}{\text{Cost of treatment}}$$

Statistical Analysis

Data were analyzed statistically using MSTAT-C (1991) to find out the variation among the treatments by F-test. Treatment means were compared by DMRT.

Results and Discussion

Infestation status of *H. armigera* (In-situ condition)

The percent fruit infestation by number due to various packages ranged from 0 to 34.56% (Fig. 1). The trend of infestation increased over time. The lowest fruit infestation was found in package T_5 (Pheromone trap + Neem seed kernel extract + *T.chilonis* and *B. hebetor*) (11.07%) followed by package T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) (11.66%), package T_2 (Pheromone trap + HaNPV and *Bt* (13.67%), Pheromone trap + *T. chilonis* and *B. hebetor*) (13.85%) and package T_1 (Pheromone trap + Neem seed kernel extract) (15.27 %). However, the highest fruit infestation was in the control plots (18.03%) (Fig. 1).

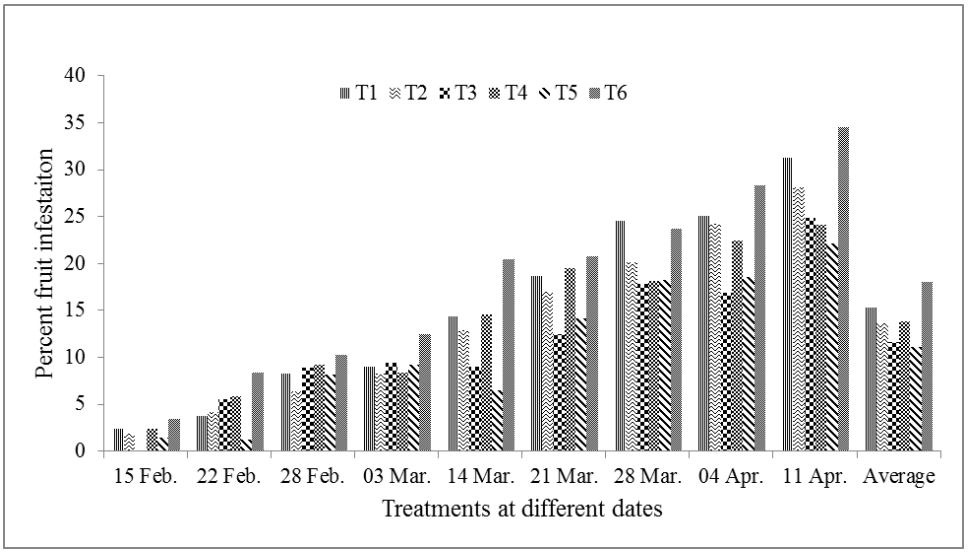

Fig. 1. Effect of IPM approaches on *H. armigera* (in-situ condition) during 2009-2010 Rabi season.

T_1= Pheromone trap + Neem seed kernel extract, T_2= Pheromone trap + HaNPV and *Bt*, T_3= Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*, T_4= Pheromone trap + *T. chilonis* and *B. hebetor*, T_5= Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor*, T_6= Untreated control

Per cent infestation by number of infested fruits

The treatment effect on fruit infestation was the lowest (12.55%) in package T_5 (Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor*) treated plot which was statistically similar with package T_2 (Pheromone trap + HaNPV and *Bt*) (15.49%), T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) (15.89%) and T_1 (Pheromone trap + Neem seed kernel extract) (17.43%). while, the highest infestation (24.15%) was observed in control plot which was statistically identical with package T_4 (Pheromone trap + *T. chilonis* + *B. hebetor*) (18.23%) treated plot. Percent infestation reduction over control was the highest in treatment package T_5 (48.03%) followed by T_2 (35.86%), T_3 (34.20%), T_1 (27.83%) and T_4 (24.51) (Table 1).

Per cent infestation by weight of infested fruits

The lowest fruit infestation based on weight (22.29%) was found in package T_2 (Pheromone trap + HaNPV and *Bt*) treated fruits which was statistically similar to package T_5 (Pheromone trap + Neem seed kernel extract + *T.chilonis* and *B. hebetor*) (11.73%) and T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) while the highest fruit infestation (18.24%) was observed in control plot

which was statistically similar with package T_1 (Pheromone trap + Neem seed kernel extract (14.88%) and T_4 (Pheromone trap + Neem seed kernel extract + *T. chilonis* + *B. hebetor*) (16.08%) (Table 1). Percent infestation reduction over control was highest in package T_2 (41.86%) followed by T_5 (35.69%), T_3 (29.06%), T_1 (18.42%) and T_4 (11.84%) (Table 1).

Table 1. Effect of different IPM packages on *H. armigera* during 2009-2010 Rabi seasons

Treatment	% Fruit infestation (number)	% Infestation reduction over control	% Fruit infestation (weight)	% Infestation reduction over control	Yield (t ha^{-1})	% Yield increase over control
T_1	17.43 bc (3.97)	27.83	14.88 ab (3.58)	18.42	23.04 cd	20.00
T_2	15.49 c (3.50)	35.86	10.60 c (2.98)	41.86	26.77ab	39.43
T_3	15.89 c (3.69)	34.20	12.94 bc (3.26)	29.06	24.66 bc	28.44
T_4	18.23 ab (4.33)	24.51	16.08 ab (3.80)	11.84	20.54 de	6.98
T_5	12.55 c (3.54)	48.03	11.73 bc (3.43)	35.69	29.74 a	54.90
T_6	24.15 a (4.65)	-	18.24 a (3.83)	-	19.20 e	_
CV (%)	6.62		7.96		3.40	

In a column, means followed by same letter(s) are statistically similar at 5% level by DMRT. Figure within parentheses are the transformed values based on SQRT transformation

T_1= Pheromone trap + Neem seed kernel extract, T_2= Pheromone trap + HaNPV and *Bt*, T_3= Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*, T_4= Pheromone trap + *Trichogramma chillnis* and *Bracon hebetor*, T_5= Pheromone trap + Neem seed kernel extract + *Trichogramma chilonis* and *Bracon hebetor*, T_6= Untreated control.

Yield

The highest yield (29.74 t ha^{-1}) was obtained from the plot treated with package T_5 (Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor*) which was statistically similar to that of package T_2 (Pheromone trap + HaNPV and *Bt*) (26.77 t ha^{-1}) treated fruits. No significant difference was observed between package T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) (24.66 t ha^{-1}) and T_1 (Pheromone trap + Neem seed kernel extract)

(23.04 t ha^{-1}). However, the lowest yield was obtained from control plots (19.20 t ha^{-1}) (Table 1). The highest yield increased over control was observed in package T_5 (54.90%) followed by T_2 (39.43%). T_3 (28.44%), T_1 (20.00%) and T_4 (6.98%). While, the lowest yield (12.09t/ha) was obtained from untreated control (Table 1).

Income and marginal benefit cost ratio

Income and marginal benefit cost ratio are presented in Table 2. The highest net income (Tk.79,656.00 ha^{-1}) was calculated from package T_5 (Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor*) treated plot followed by T_2 (Pheromone trap + HaNPV and *Bt*) (Tk 58,549.00 ha^{-1}), T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) (Tk. 22,295.00 ha^{-1}) and T_1 (Pheromone trap + Neem seed kernel extract) (Tk. 19,654.00 ha^{-1}) treated plots. (Table 2).

Table 2. Effect of IPM package application on net income and marginal benefit cost ratio in tomato during 2009-2010 Rabi season

Treatments	Yield (t ha^{-1})	Additional yield over control (t ha^{-1})	Additional income over control (Tk ha^{-1})	Cost of treatment application (Tk ha^{-1})	Net income (Tk ha^{-1})	Marginal benefit cost ratio (MBCR)
T_1	23.04	3.84	38,400.00	18,754.00	19,654.00	1.04
T_2	26.77	7.57	75,700.00	17,151.00	58,549.00	3.41
T_3	24.66	5.46	54,600.00	32,305.00	22,295.00	0.69
T_4	20.54	1.34	13,400.00	8,590.00	4,810.00	0.56
T_5	29.74	10.34	103,400.00	23,744	79,656.00	3.35
T_6	19.20	-				

T_1= Pheromone trap + Neem seed kernel extract; T_2= Pheromone trap + HaNPV and *Bt*; T_3= Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*; T_4= Pheromone trap + *T. chilonis* and *B. hebeto*; T_5 = Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor* ; T_6= Control.

From the marginal benefit cost analysis of IPM packages T_2 (Pheromone trap + HaNPV and *Bt)* treated plots showed the highest monetary benefit. For each taka spent, T_2 package gave on an average the profit of Tk. 3.41 as against Tk. 3.35, Tk. 1.41, Tk.0.69 and Tk. 0.56 calculated from T_5 (Pheromone trap + Neem seed kernel extract + *T. chilonis* and *B. hebetor*), T_1 (Pheromone trap + Neem seed kernel extract), T_3 (Pheromone trap + Neem seed kernel extract + HaNPV and *Bt*) and T_4 (Pheromone trap + *T. chillnis* and *B. hebetor*) treated plots, rrespectively (Table 2).

The present results are in partial agreement with Alam *et al.* (2011) who carried out an experiment at the farmers' field of Danakata and Malkadagga, Boda, Panchagarh during the year of 2010-11 for evaluating IPM package against fruits borers of late winter tomato. They showed that the lowest fruit infestation by number (5.47%) and weight (5.33%) was obtained from the IPM plots at both places whereas the highest fruit infestation by number (23.83%) and by weight (22.83%) was in non IPM plots. Comparatively higher yield was obtained from IPM plots (19.97 t ha^{-1}in Danakata and 18.02 t ha^{-1} in Malkadanga) than non IPM plots (13.63 t ha^{-1}in Danakata and 12.13 t ha^{-1} in Malkadanga) at both places. Alam *et al.* (2012) conducted another field experiment at the farmers' field of Tunirhat, Panchagarh during 2011-2012 for evaluating IPM package (weekly release of egg parasitoid *Trichogramma evanescens*, larval parasitoid *Bracon hebetor* and use of pheromone trap) against fruits borers of late winter tomato. They observed that IPM package resulting 74.5% reduction of fruit infestation over non-IPM package (spraying of Proclaim 5SG @ 1g l^{-1}). Comparatively higher yield was also obtained from IPM plots (39.90 t ha^{-1}) than non-IPM plots (30.48 t $ha^{-1)}$. The finding of the present study also partially supported by Gopalkrishnan and Ashokan (1998) and they reported that application of five rounds of *Ha*NPV @ 250 LE ha^{-1} at weekly intervals effectively controlled the fruit borer incidence. Reddy and Manjunatha (2000) reported combinations of nimbecidine 2% + NPV at 250 larval equivalents (LE) ha^{-1} and dipel 8 l + NPV @250 LE ha^{-1}were the most effective treatments *against H. armigera.* The integrated pest management components (*T. chilonis*, *C. carnea*, NPV, nimbecidine, dipel and synthetic chemicals) were imposed at different intervals on the basis of pheromone trap threshold level (7 moths/trap per night) on a consolidated block of 40 ha cotton (MCU-1) fields at two locations, Shankarabanda and Korlagundi. The results demonstrated a significant superiority of the IPM strategy in terms of both cost versus benefit and environmental safety over that used in the farmer's fields where only conventional control methods were followed. The main reason for the higher efficacy of IPM approaches on insect pest suppression probably due to the integration of different IPM options in a package under the study. Hence, considering efficacy and profitability, it is concluded that T_2 and T_5 packages may be the best options for efficient management of *H. armigera.*

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EFFECT OF STORAGE DURATION ON THE STORED PUPAE OF PARASITOID *Bracon hebetor* (Say) AND ITS IMPACT ON PARASITOID QUALITY

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M. R. U. MIAH[4] AND M. I. H. MIAN[5]

Abstract

The ecto-endo larval parasitoid, *Bracon hebetor* (Say) is an important bio-control agent. Effective storage methods for *B. hebetor* are essential for raising its success as a commercial bio-control agent against lepidopteran pests. The study was undertaken to determine the effect of storage duration on the pupae of *Bracon hebetor* in terms of pupal survival, adult emergence, percent parasitism, female and male longevity, female fecundity and sex ratio. Three to four days old pupae were stored for 0, 1, 2, 3, 4, 5, 6, 7 and 8 weeks at 4 ± 1°C. The ranges of time for adult emergence from stored pupae, production of total adult, survivability of pupae, parasitism of host larvae by the parasitoid, longevity of adult female and male and fecundity were 63.0 -7.5 days, 6.8-43.8/50 host larvae, 13.0-99.5%, 0.0 -97.5%, 0.00-20.75 days, 0.00-17.25 days and 0.00-73.00/50 female, respectively. The time of adult emergence and mortality of pupae increased but total number of adult emergence, survivability of pupae, longevity of adult female and male decreased gradually with the progress of storage period of *B. hebetor* pupae. The prevalence of male was always higher than that of female. Therefore, short-term storage of *B. hebetor* pupae could be stored for up to 4 weeks without disturbing the functioning of the parasitoid. It is important for sustaining and accumulating large numbers of parasitoids in mass rearing programs and subsequent use of field application.

Keywords: Cold storage, pupae, *Bracon hebetor*; biological control.

Introduction

The ecto-endo larval parasitoid, *Bracon hebetor* (Hymenoptera: Braconidae) is deemed as an important bio-control agent of different lepidopteran pests invading warehouse and field (Uwais *et al*., 2006; Imam *et al*., 2007; Garba and Gaoh, 2008). It is broadly used in studies of host parasitoid relations and biological control due to its high propagative rate, short cohort time and extensive range of host species (Asfaq *et al*., 2011).

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The mass production of *B. hebetor* is restricted by the accessibility of host larvae. Moreover, host larvae parasitized by *B. hebetor* may be oversupplied and rejected when demand for parasitoids is low. As a result, finding effective storage methods for *B. hebetor* is necessary for increasing its success as a commercial biocontrol agent against lepidopteran pests. One of the major difficulties to the use of biological control agent as insect natural enemies is the breakdown to obtain adequate numbers required for release (Coudron *et al*., 2007). As a result, the enhancement of storage methods for biocontrol agents is very important for efficient mass production of the parasitoid (Tezze and Botto, 2004; Greenberg *et al*., 1996; Leopold, 1998). Cold storage is regarded as an important tool for storage of mass reared biocontrol agents (Chen *et al*., 2011). For escalating the shelf-life of natural enemies and to make available a stable and enough number of parasitoids for biological control programs low temperature storage is an important technique. Storage at low temperature also permits coordinated field releases of natural enemies during the crucial stages of pest occurrences (Venkatesan *et al*., 2000; Colinet and Boivin, 2011).

Adults and pupae have been accounted to be the most cold-hardy stages of *B. hebetor* (Franqui Rivera, 1995; Carrillo *et al*., 2005). Very few studies have been done with cold storage on the performance of *B. hebetor*, and this study has focused on the adult stage (Al-Tememi and Ashfaq, 2005). Storage of *B. hebetor* pupae at 6^0C for 3 weeks resulted in an 82.7% decrease in adult emergence (Al-Tememi and Ashfaq, 2005). According to Chen *et al.* (2011) more than 30 days of storage decreases parental parasitism but had no effect on parasitism of the F_1 generation. Parental durability and fecundity reduced after more than 20 days of storage. The present study was undertaken to determine the effect of storage duration of pupae of *B. hebetor* at 4±1 ^{o}C on some biological parameters of adults and their progeny.

Materials and Method

Collection of host insect wax moth (*Galleria mellonella*)

The target host used in the study was *Galleria mellonella* (L.) (Lepidoptera: Pyralidae). It was originally collected from infested bee-hive and maintained on artificial diet in IPM laboratory, Entomology Division, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh. The dark bee wax was sterilized by boiling and put in 1000 ml glass jars. One hundred larvae of wax moth were kept in the glass jar. The adults of *G. mallonella* coming out from the wax in the jar were allowed to mate and egg laying. After egg hatching, the 1st and 2nd instar larvae of wax moth were released in jars containing artificial diet. The diet was prepared by mixing wheat flour, maize crush, milk, sugar, animal fat, wax and yeast and autoclaved at 120 ^{o}C under 1.0 Kg cm^{-2} pressure for 70 minutes. Full grown final instar larvae were collected after 18 to 20 days and used as host for

rearing of *B. hebetor*. The ambient temperature of the rearing room was 26.0 ± 2°C, relative humidity 70 ± 5 % and 12L: 12D photoperiod.

Collection of *Bracon hebetor*

Bracon hebetor was obtained from IPM laboratory, Entomology Division, BARI, Gazipur. It is used for many years for the biocontrol of lepidopteran pest and maintained on honey and last instar larvae of *G. mellonella*. Adult parasitoids were introduced into plastic jars (1000 ml) containing last instar larvae of *G. mellonella* and a cotton ball soaked with honey. Mouth of the jar was covered with black cloth. Environmental conditions of the rearing were the same as used for rearing the host *G. mellonella*. To obtain newly emerged parasitoids, 3 females and 2 males of *B. hebetor* adults were released into a plastic jar containing 10 *G. mellonella* final instars larvae and the whole container was covered with black cloth and kept for 3-4 days. To assess the parasitic activity of the *B. hebetor* in low temperature, 3 to 4 days old parasitoid pupae were isolated from the laboratory culture and placed in plastic jars. Before placing of pupae, the jars were sterilized in an electric oven. Each jar received 50 parasitoid pupae. The jars were stored in a refrigerator at 4±1°C and 60-70% RH for 1, 2, 3, 4, 5, 6, 7 and 8 weeks. Four jars (replications) were used for each treatment (storage period). Another four jars containing pupae of the parasitoid were stored at room temperature, which served as a control.

Effect of cold storage on *Bracon hebetor* parental generation

At the end of each storage period, the pupae were moved to a chamber having ambient temperature of 26±2 °C and RH 70±5%. Data on pupal survivability (adults emerged per parasitized pupae), time of adult emergence (days between the end of cold storage of the pupae until emergence of adult parasitoid) and sex ratio (adult females per total individuals) were recorded. The effects of storage time in low temperature storage on parasitism, longevity and fecundity of the parental generation were noted. To examine the capability and performance of a female *B. hebetor* after low temperature storage, a female and a male were taken where emerged from each cold storage period. Both male and were placed in a plastic jar (1000 ml) having corrugated sheet containing 10 released larvae of *G. mellonella* and a cotton ball dipped in honey. The mouth of the jars was covered with black cloth and the whole container was covered with black cloth. The wax moth larvae and *B. hebetor* were placed on a rack for 8-10 days for parasitization, egg laying, pupation and adult emergence of *B. hebetor*. Data were expressed as % parasitism, fecundity and total adult progeny and sex ratio for each storage duration. Each treatment was replicated four times using completely randomized Design. There was also a control treatment maintaining room temperature 26±2 °C and 70±5% RH.

Statistical analysis

Data were analyzed using SPSS 16 software and presented in mean ± SE. Mean time of developmental, parasitism, longevity of adult, sex ratio, and daily and lifetime fecundity of the parasitoid were evaluated using one-way Analysis of Variance (ANOVA). Differences among the means were evaluated using Turkey's Honestly significant differences test. Before performing ANOVA, % parasitism, survival and mortality were transformed using arcsine transformation.

Results and Discussion

Effect of cold storage on *B. hebetor* parental generation

The minimum time of 5.3 days was required for adult's emergence from pupae under control. The time increased to 6.3-7.5 days when the pupae were stored in a refrigerator for 1 to 8 weeks. The increase in emergence time was significant over control when the pupae were stored for 2-8 weeks. The differences in adult emergence time from pupae stored for 2-8 weeks were not significant (Fig. 1).

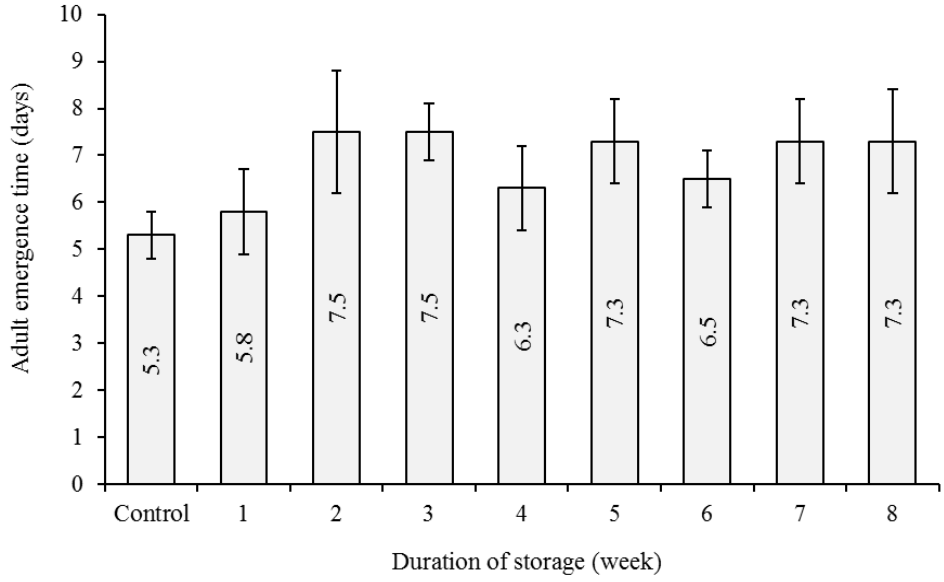

Fig. 1. Adult emergence time (days) of *Bracon hebetor* from pupae stored at 4°C in a refrigerator for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean.

Significantly the highest number of adult (49.8) was emerged in control. Adult emergence decreased 43.8 - 6.8 50^{-1} pupae when the pupae were stored for 1-8 weeks. The lowest number of adults emergence was recorded from pupae stored for 8 weeks (Fig. 2).

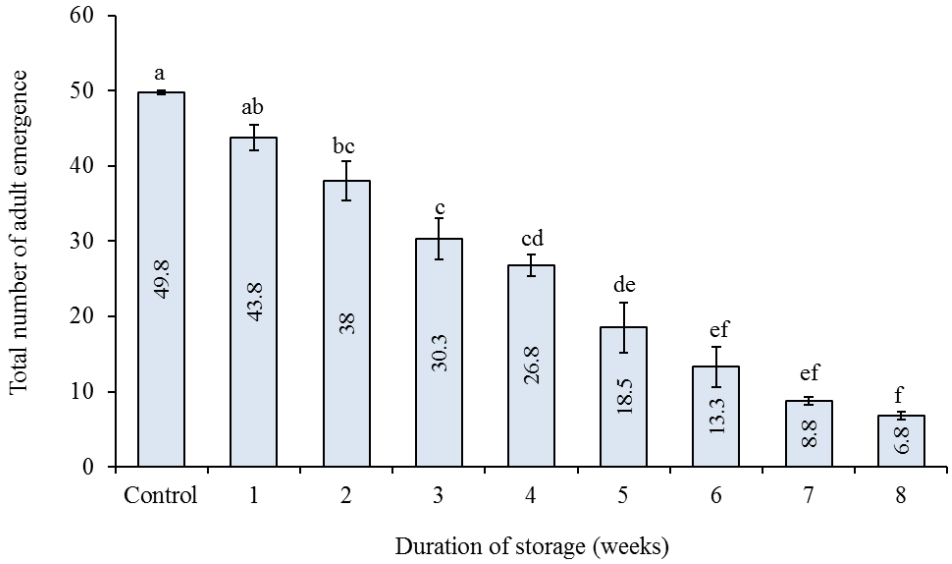

Fig. 2. Total number of adult emergence from pupae of *Bracon hebetor* stored at 4°C in a refrigerator for 1 to 8 weeks. Vertical line in the bar denotes the standerd error of mean. Bars indicating the same letter are not significantly different by Tukey's HSD test.

Significantly the highest percentage of survival (99.5%) of *B. hebetor* pupae was recorded in control. The survival rates were significant differences. The lowest survival rate (13.0%) was recorded after 8 weeks of storage (Fig. 3).

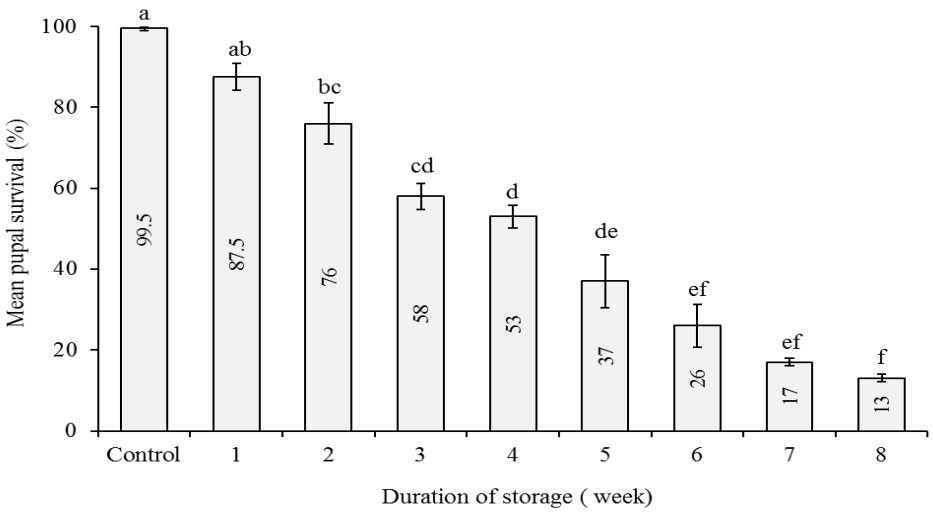

Fig. 3. Mean survival percentage of *Bracon hebetor* pupae stored at 4°C for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean. Bars followed by the same letter are not significantly different by Tukey's HSD test.

Parasitism efficacy of *Bracon hebetor* after 1-8 weeks of storage

Percentage parasitism in 1 and 2 weeks were 97.5, 97.5 and 95.0%, which were statistically similar but significantly higher compared to other period of storage. After 2 weeks, the parasitism decreased gradually. The lowest parasitism was found after 6 weeks, which was statistically similar to 5 weeks of storage (Fig. 4). The pupae of *B. hebetor* stored for more than 6 weeks failed to parasitize the host larvae (Fig. 4).

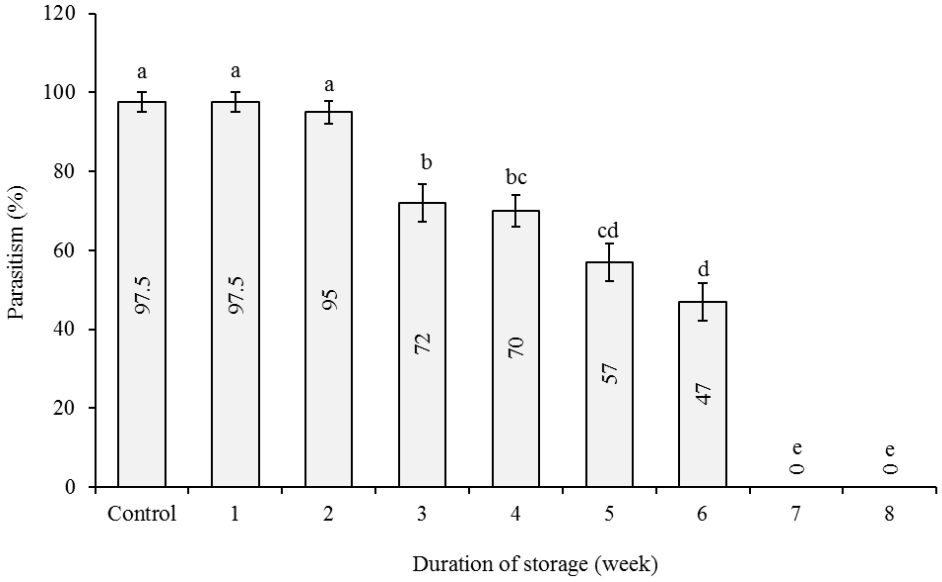

Fig. 4. Percentage of parasitized host (*G. mellonella*) larvae per female of *Bracon hebetor* emerged from pupae stored at 4°C for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean. Bars indicating the same letter are not significantly different by Tukey's HSD test.

The highest longevity of parent female was recorded from control, which was statistically similar to the females emerged from pupae stored for 1 and 2 weeks. The lowest longevity was found after 6 weeks of storage. The maximum survivability was found in parent male emerged from pupae stored at room temperature (control) followed by pupae stored at 4°C for 1, 2, 3 and 4 weeks (Fig. 5). The lowest longevity of F_1 male was recorded from pupae stored for 6 weeks followed by 5 weeks of storage (Fig. 6). Both F_1 female and male were recorded when the pupae were stored for 7 weeks or longer duration because no parasitism occurred. It is evident that the longevity of parents was generally lower than that of their F_1offspring in both the cases of male and female.

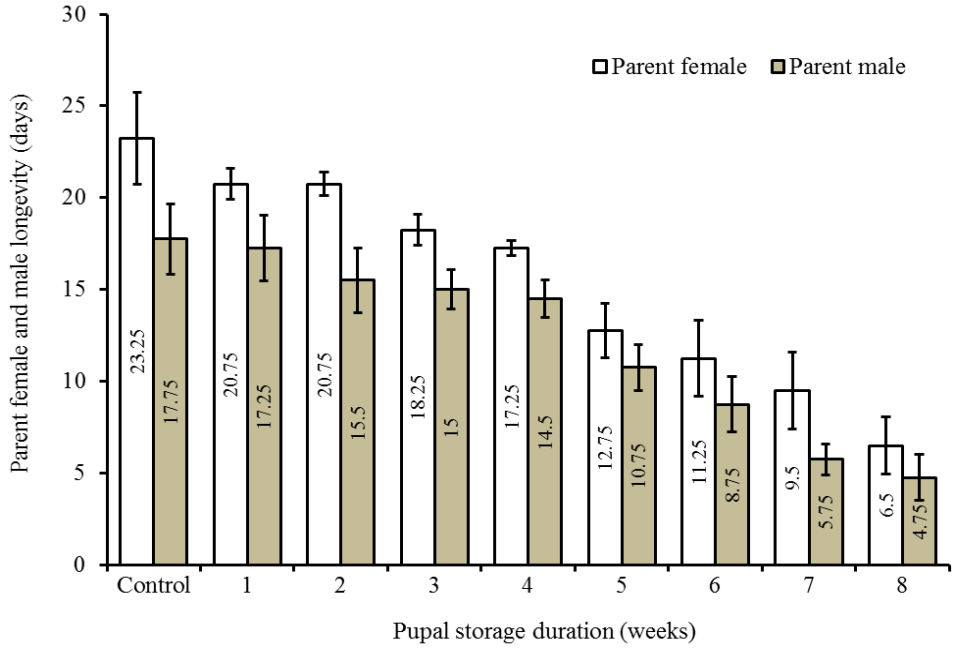

Fig. 5. Longevity of female and male parents emerged from pupae of *Bracon hebetor* tored at 4°C for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean.

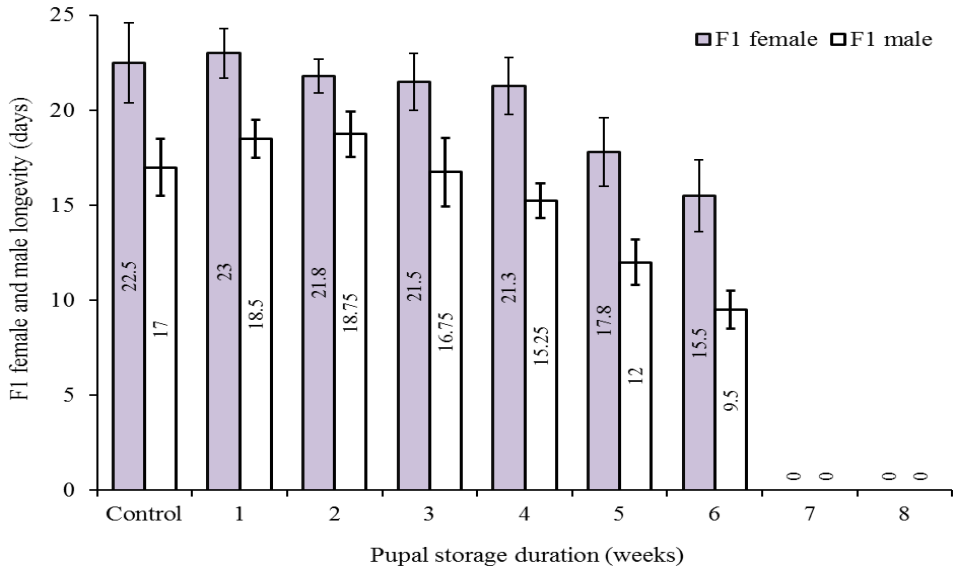

Fig. 6. Longevity of F_1 female and male parents emerged from pupae of *Bracon hebetor* at 4°C for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean.

Fecundity of parents

The highest fecundity (76.3 adults female^{-1}) was recorded from pupae stored under room conditions, which was not significantly different from that of parents emerged from pupae stored for 1 week at 4^{o}C. The fecundity of parents emerged from pupae stored at 4^{o}C for 2, 3 and 4 weeks was different. The lowest fecundity was observed after 6 week of storage (8.5 adults female $^{-1}$) followed by the storage duration of 5 weeks (Fig. 7).

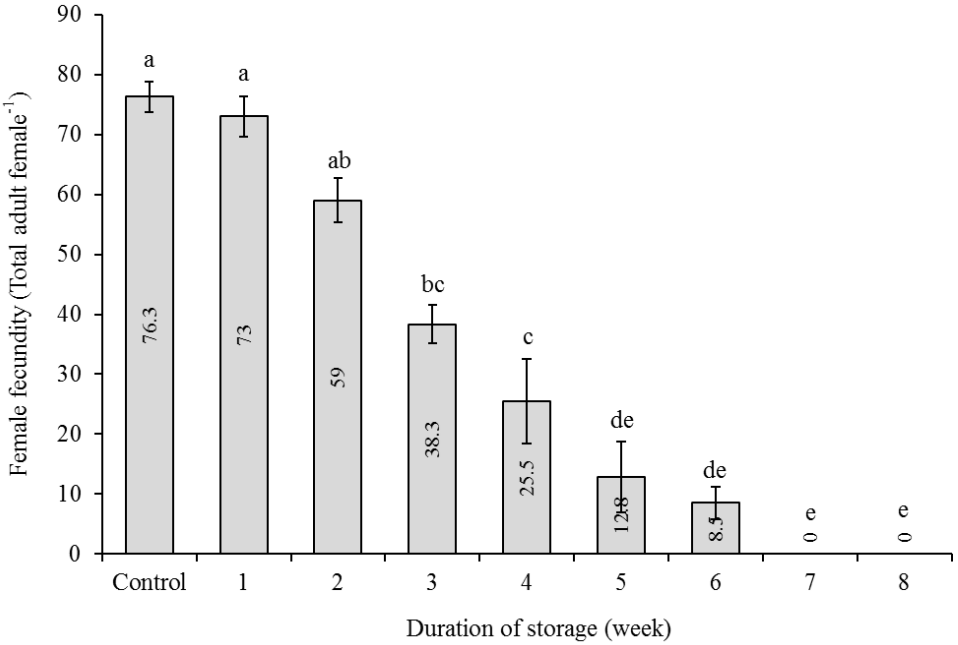

Fig. 7. Fecundity (total adult female $^{-1}$) of *Bracon hebetor* parents emerged from pupae stored at 4^{o}C for 1-8 weeks. Vertical line in the bar denotes the standerd error of mean. Bars indicating the same letter are not significantly different by Tukey's HSD test.

Sex ratio of parent and F_1 progeny

The percentages of female and male emerged from pupae stored under control and at 4ºC for 1-8 weeks ranged 26.97 – 40.43% with a mean of 40.44% and 51.40 – 59.57% with a mean of 59.57%, respectively. After each storage duration in refrigerator as well as under control, the prevalence of male was higher than that of female (Fig. 8). Like parent female and male sex ratio (%), the prevalence of male was higher compared to F1 female. The percentage of F_1 female ranged 26.97 – 46.36% with a mean of 40.98% and that of male ranged 51.71 – 63.61% with mean 43.96% (Fig. 9).

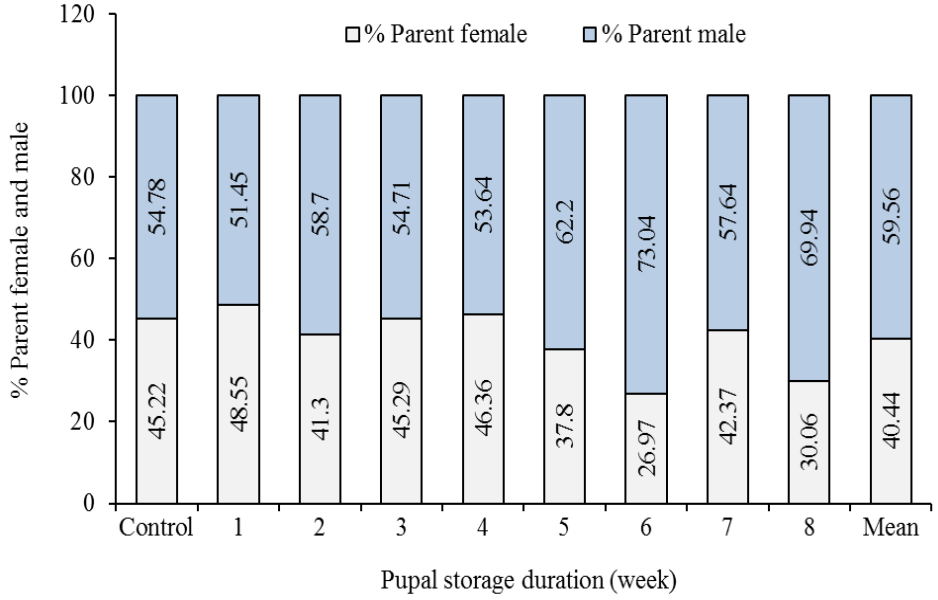

Fig. 8. Percentage of parent adult female and male emerged from pupae of *Bracon hebetor* stored at 4°C for 1-8 weeks.

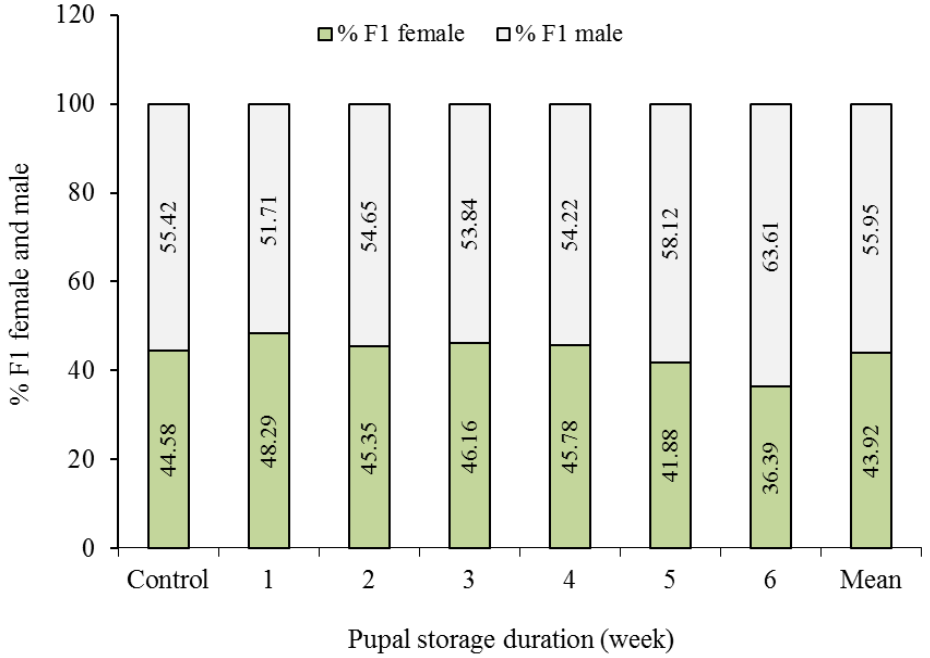

Fig. 9. Percentage of F_1 female and male of *Bracon hebetor* emerged from pupae stored under room conditions and at 4°C for 1 to 6 weeks.

Due to storage of *B. hebetor* pupae in a refrigerator at 4ºC for 1- 8 weeks, the time of adult emergence and mortality of pupae increased but total number of adult emergence, survivability of pupae, longevity of adult female and male decreased gradually with the progress of storage period of *B. hebetor* pupae of the parasitoid. The prevalence of male is always higher compared to female. Similar findings have been reported by many other investigators (Al-Ramahi and Ali, 1983; Ahmed *et al.*, 1985). Adult emergence time is vital to realize the time needed for adult coming out after removing pupae from cool storage, particularly in order to synchronize adult emergence of parasitoid and availability of mature larvae of the pest in the field. Cold temperature prevented the embryonic growth of *Trichogramma nerudai* pupae (Tezze and Botto, 2004). In addition, in the existing observation the adult emergence time for cold stored pupae was 1 day higher than in the control group. This dissimilarity might be due to putting off in returning back to standard metabolic conditions at exposure after being cold stored for longer period. It is a correct statement that organisms placed at low, above zero temperatures have seasonal restructuring of metabolism as a way of cold-hardiness (Danks, 1978).

Mortality denotes the overall result of extended cold exposure. Moreover to cool damage, parasitoids stored as undeveloped may not have adequate energy to complete their growth and/or to come forward. In some solitary species, dissection of non-emerged parasitoids after cold storage has shown that mortality occurred mainly after metamorphosis in pharate adults (Colinet *et al*., 2006; Colinet and Hance, 2009). There have been reported that the completely developed adults dying during the exclusion process (Levie *et al*., 2005; Luczynski *et al*., 2007). The procedure of coming out is energy-consuming as it needs strong muscle convulsion (Yocum *et al*., 1994) and chilling is known to induce muscular nonfunctions (Kelty *et al*., 1996). Emergence of pharate adults fail after cold storage due to lack of energy along with muscular perturbation. In another species, mortality withstands generally during pupation (Chen and Leopold, 2007).

Longevity of parents and their F_1 offspring declined with increase in cold storage period. Because living organisms have limited resources which are spent on growth, reproduction, and maintenance (Green and Rothstein, 1991), a possible explanation for the decline in longevity may be that increasingly larger amounts of resources are depleted by maintenance during longer periods of cold storage at 4^{o}C thereby resulting in reduced performance and survival (Salt, 1961). In addition, accumulation of toxic metabolites also causes death or reduced fitness after prolonged exposures to cold (Storey and Storey, 1988).

Fecundity of parents declined with increase in cold storage period. Decline in fecundity with increase in cold storage period is probably due to the aforementioned reasons. The reproductive organs are particularly vulnerable to

low temperature effects (Denlinger and Lee, 1998). In *Euchalcidia caryobori* (Hanna), low temperature may either cause retardation of egg maturation or, in its extremes, malformation of reproductive organs in both sexes (Hanna, 1935). Numerous observations have been made on the reduction of parasitoid fecundity after cold storage. Like most of the traits affected by cold storage, the fecundity cost is generally proportional to both the temperature and the duration of exposure (Venkatesan *et al*., 2000; Al-Tememi and Ashfaq, 2005).

Our present results demonstrated that the low temperature storage of the maternal age group did not seem to impact F_1 generation characters when cold storage periods were shorter than 35 days. This probably might be due to action of cold storage for the maternal generation only. The procedure for overtaking maternal effects of chilling injury to the F_1 generation is unidentified. One possible explanation is the property of eggs laid by females stored for a long time may decline. An alternative grounds for reduced fitness of the F_1 progeny might have been due to maternal aging (Hercus and Hoffmann, 2000; Opit and Throne, 2007).

Effect of low temperatures recurrently deform insect sex ratios (Denlinger and Lee, 1998). Hymenopteran parasitoids typically have a haplodiploid sex-determination system, as their females are able to decide the sex of their generation by regulating fertilization (Flanders, 1956). Deformation of sex ratio may appear from diverse origins. First alteration of the ratio of fertilized eggs oviposited (i.e. primary sex ratio) may be monitored following alteration of the female reproductive approach or the incapability of males to mate or inability to produce viable sperm after a cold treatment (Lacoume *et al*., 2007). Sex ratio deformations can also result from a discrepancy of mortality between sexes when undeveloped stages are exposed to cold (i.e., secondary sex ratio). The results of the present study are similar to the findings of other studies (Ashfaq *et al*., 2011; Shawkit *et al*., 2000). They found that the ratio of adult-emergence from the cold-stored pupae of this parasitoid decreased with the increase of storage period. Findings denoted that the sex ratio of *B. hebetor* was 1:1.3 (F:M) (Al-Ramahi and Ali, 1983). Another study indicated that female: male sex ratio was 1:3.9 (Ahmed *et al.*, 1985). Male biased sex ratio was obtained in the present which explained that the male eggs hatched before than the female eggs, and the male larvae would have a better survivability due to sufficient food (Benson, 1973).

Our findings reveal that *B. hebetor* can be stored up to 4 weeks without affecting the performance of the parasitoid. However, short-term storage of *B. hebetor* pupae can be used for regulating and gathering huge numbers of parasitoids in mass production programs.

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EVALUATION OF INBRED LINES OF BABY CORN THROUGH LINE × TESTER METHOD

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Abstract

Seven lines of baby corn were crossed with 3 testers in a Line × Tester (L × T) mating design and the resulting 21 crosses along with parents and standard check 'Baby Star' were evaluated to develop high yielding baby corn hybrids during *rabi*, 2014-15. Variance due to sca was larger than gca variance for all the characters indicating the preponderance of non additive gene action in the expression of various traits. Among the parents, BCP/S_4-29, BCP/S_4-31 and tester VS/S_3-1 and VS/S_3-26 were found as good general combiners for baby corn yield and important yield contributing characters. Considering baby corn yield, number of cobs/plant and other performances, the crosses BCP/S_4-2×VS/S_3-1, BCP/S_4-5×VS/S_3-8, BCP/S_4-10×VS/S_3-8, BCP/S_4-22×VS/S_3-26 and BCP/S_4-29×VS/S_3-1 were selected as promising baby corn hybrids.

Keywords: Baby Corn, inbred lines, SCA, GCA and line × tester method.

Introduction

Maize is unique among the cereals on account of its amenability to diverse uses and it has huge potential in the present era of crop diversification. Baby corn is a young finger like unfertilized cob of maize harvested between two days before silking and three days after silking, depending upon the developmental conditions of the plant and the ear shoot size, denominated cob (Bar-Zur and Saadi, 1990). It is a new product that can be consumed fresh or in cans. It adds a special, gourmet touch to many dishes and salads. Its miniature size is appealing, as is the taste, color and crunch. Most people like to steam baby corn for 5 minutes or until tender before using in other dishes.

Another important feature of baby corn is safe vegetable to eat as it is almost free from residual effects of pesticides as the young cob is wrapped with husk and well protected from insect and diseases and its nutritional value is comparable to cauliflower, cabbage, tomato, eggplant and cucumber. Its by-products, such as tassel, young husk, silk and green stalk provide good cattle feed. These trends underline the value of baby corn as a cash crop for intensive agro-ecosystems in South Asia where small farmers grow three or more crops in highly diverse cropping systems (Sharma, 2009). Farmers can grow four to five crops a year and

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thus it can generate employment among the rural poor of all ages. Major baby corn markets are U.K., U.S.A., Malaysia, Taiwan, Japan and Australia. The majority of the industrialized baby-corn products are imported from Thailand (Pereira Filho *et al.*, 1998).

Despite manifold uses of baby corn, very little information on breeding strategies followed for improvement in baby corn (Chauhan and Mohan, 2010). It is a fact that selection of parents on the basis of their mean performance does not necessarily lead to desired results (Rai and Asati, 2011). Therefore, devising a sound breeding strategy to improve the yield of this crop is of paramount importance. Early ripening, low height, flowering uniformity and prolificity are considered the most important traits for the production of baby corn (Thakur *et al.*, 2000). In addition, agronomic practices such as population densities, nitrogen fertilization and detasseling can increase baby corn yield considerably. Farmers can also grow under either high population density, for baby corn only, or lower population density where the first ear is picked for baby corn and the second ear is left intact for further development as sweet or field corn. Information regarding general and specific combining ability and gene action in a breeding material is a prerequisite to launch effective corn breeding. The success of a hybridization program primarily depends upon the judicious choice of parents for producing the hybrids with high yield. Combining ability analysis is an important tool in the choice of suitable parent together with the information regarding nature and magnitude of gene effects controlling quantitative traits (Basbag *et al.*, 2007). The present investigation was accomplished to get **i**nformation regarding general and specific combining ability and gene action in the heritance of different yield contributing traits of baby corn.

Materials and Method

Seven S_4 lines of baby corn variety 'BCP271' were used as female lines and three S_3 lines of baby corn hybrid 'Victory Super' were used as tester to produce 21 baby corn hybrids in 2013-14. The resulted 21 F_1's along with their parents and one check variety 'Baby Star' were evaluated in a Randomized Block Design with two replications during *rabi* 2014-2015 at Bangladesh Agricultural Research Institute, Joydebpur, Gazipur. Unit plot size was single row 4m long maintaining spacing 60 cm from row to row and 20 cm from plant to plant. All the recommended cultural practices were followed to raise a healthy crop per hill. Data were recorded on 10 randomly selected plants in each replication with respect of plant height (cm), upper ear height (cm), lower ear height (cm), days to first cob picking, days to second cob picking, days to third cob picking, days to fourth cob picking, ear length (cm), ear diameter (cm), harvest duration, number of cobs/plant, fodder yield/plant, baby corn yield with husk/plant (g) and baby corn yield/plant (g). Mean values were subjected to statistical analysis as per model suggested by Kempthorne (1957) and procedure of Singh and Chaudhary (1985).

Results and Discussion

Analysis of variance for combining ability was carried out for yield and yield contributing characters and the mean sum of squares are presented in Table 1. The analysis of variance revealed that genotypes exhibited highly significant differences among themselves for all the traits studied. The crosses exhibited significant differences, indicating varying performance of cross combinations. When the effects of crosses partitioned into lines, testers and line × tester effects, the interaction effects (line × testers) were found to be significant for all the traits under study indicating that hybrids differed significantly in their *sca* effects. Except ear length, all the traits showed significant variations among lines and mean sum of squares due to tester were larger than due to lines, indicating greater diversity among testers for lower ear height, harvest duration, number of cobs/plant, cob yield with husk per plant, baby corn yield per plant, ear length and ear diameter. The parents exhibited significant differences for all the traits indicating greater diversity in the parental lines. The parents vs. crosses which indicates average heterosis, was also significant for all traits, thus considerable amount of average heterosis was reflected in hybrids. Highly significant differences were observed for line x tester interaction for all traits which implies the role of dominance and non-additive effects in all traits. Therefore, both additive and non-additive effects were responsible for controlling these traits. Tucak *et al*. (2012) and Atif *et al.* (2012) observed highly significant differences for testers, lines and line x tester interaction. The ratio of σ^2gca to σ^2sca was less than one for all of the characters (Table 1) which indicates the predominant role of non-additive type of gene action in the inheritance of those characters. Similar findings were also reported by Ceyhan *et al.* (2008), Kanagarasu *et al.* (2010) and Motamedi *et al.* (2014).

The proportional contribution of lines was higher for plant height, upper ear height, lower ear height, days to first cob picking, days to second cob picking, days to third cob picking, days to fourth cob picking, harvest duration and cob yield with husk per plant, indicating their predominant maternal influence (Table 2). Testers showed less influence to be contributed for all the traits except ear length. The relative contribution of line × tester interaction was more important for fodder yield per plant, number of cobs/plant, cob yield without husk per plant, ear length and ear diameter. Motamedi *et al.,* (2014) found less influence of testers for kernel yield. The higher contribution of interactions of the line × tester than lines and testers, indicating higher estimates of variances due to non-additive genetic effects and the importance of specific combining ability. Shams *et al.,* (2010) observed higher estimates of SCA variance due to line × tester interaction in corn for different characters.

Table 1. Mean squares and estimates of variance for grain yield and yield contributing characters in baby corn

Source	df	Plant height	Upper ear height	Lower ear height	1st cob picking	2nd cob picking	3rd cob picking	4th cob picking	Ear length	Ear diameter	Harvest duration	No. of cobs/ plant	Fodder yield/ plant	Baby corn yield with husk/ plant	Baby corn yield/ plant
Replication	1	0.14	0.15	1.03	0.02	0.06	0.06	0.06	0.19	0.02	0.79	0.02	32.66	2.94	1.11
Geno-type	30	2123.6**	450.6**	108.6**	46.9**	47.4**	711.7**	5777.1**	1.3**	0.02**	40.5**	0.6**	34520.4**	4281.4**	104.15**
Cross	20	245.9**	100.7**	64.9**	14.6**	15.8**	31.5**	5269.0**	0.2**	0.02**	31.2**	0.4**	4376.0**	3048.2**	66.40**
Line©	6	590.8**	268.5**	135.3**	32.8**	33.2**	66.3**	7640.4**	0.1	0.02**	39.8**	0.5**	5318.5**	5174.7**	70.43**
Tester©	2	272.3**	24.7**	161.8**	3.2**	10.7**	2.5**	7495.1**	0.3*	0.03**	79.5**	0.7**	4248.5**	7496.7**	186.98**
L X T ©	12	69.1**	29.4**	13.5**	7.4**	7.9**	18.9**	3712.3**	0.3**	0.01*	18.7**	0.2**	3926.0**	1243.5**	44.29**
Parent	9	908.9**	70.5**	28.2**	15.7**	12.0**	2285**	0	1.1**	0.01**	21.8**	0.5**	5413.2**	3749.0**	20.62**
Cross vs Par	1	50610**	10869**	1706**	975**	998**	149**	67931**	23.7**	0.07**	394**	4.7**	899373**	33737**	1610**
Error	30	2.51	1.31	0.7	0.22	0.13	0.06	0.03	0.09	0.01	0.49	0.05	490.22	89.87	1.89
Estimation of component of variances															
σ^2g (Line)		86.96	39.84	20.29	4.22	4.22	7.91	654.67	-0.03	0.001	3.51	0.05	232.08	655.19	4.36
σ^2g(Tester)		14.52	-0.34	10.59	-0.31	0.2	-1.17	270.2	0.01	0.001	4.34	0.03	23.04	446.66	10.19
σ^2gca		6.91	2.78	2.01	0.28	0.31	0.49	60.81	-0.01	0.001	0.48	0.01	17.58	70.49	0.86
σ^2sca		33.33	14.11	6.48	3.61	3.88	9.42	1856.17	0.1	0.004	9.3	0.15	1802.45	578.27	21.09
σ^2gca/ σ^2sca		0.21	0.2	0.31	0.08	0.08	0.05	0.03	-0.02	0.05	0.05	0.04	0.01	0.12	0.04

* Significant at 5% percent level; ** Significant at 1% percent level.

Table 2. Proportional contribution (%) of lines, testers and their interactions to total variance in baby corn

Source	Plant height	Upper ear height	Lower ear height	1st cob picking	2nd cob picking	3rd Cob picking	4th Cob picking	Ear length	Ear diameter	Harvest duration	No. of cobs/ plant	Fodder yield/ plant	Baby corn yield with husk/ plant	Baby corn yield/ plant
Due to Lines	72.07	80	62.52	67.27	63.04	63.15	43.5	12	40.73	38.35	41.01	36.46	50.93	31.82
Due to Testers	11.07	2.45	24.93	2.17	6.81	0.82	14.22	15.72	16.35	25.52	17.42	9.71	24.59	28.16
Due to Line x Tester	16.85	17.55	12.55	30.56	30.14	36.03	42.27	72.28	42.92	36.14	41.57	53.83	24.48	40.02

General combining ability (GCA) effects

The GCA effects of the parents are presented in Table 3. Lines BCP/S_4-29 and BCP/S_4-31 exhibited positively significant GCA effects for baby corn yield. As BCP/S_4-31 had desirable GCA effects for plant height, upper ear height, lower ear height, number of cobs/plant, baby corn yield, it was the best general combiner. However, testers VS/S_3-1 showed desirable GCA effects for days to first picking, days to second picking, cob yield with husk per plant, baby corn yield. So these parents could be used extensively in hybrid breeding program to improve baby corn yield and its quality.

Dhasarathan *et al.* (2015) and Rodrigues and da Silva (2002) also observed and verified significant positive number of baby corns per plant, baby corn length, baby corn weight and baby corn yield per plot. None of the parents showed significant positive GCA effects for ear length, which is supported by Rodrigues and da Silva (2002) and opposed by Dhasarathan *et al*. (2015).

Specific combining ability (SCA) effects

High positive estimates of SCA in absolute values indicate that hybrid performance was relatively superior or inferior to parent lines general combining ability, showing the importance of non-additive interactions resulting from the complementation degree among parent lines in relation to frequency of alleles in loci with some dominance, while low estimates of specific combining ability in absolute value indicated that hybrids behave as expected in relation to general combining ability of parent lines (Dhasarathan *et al*., 2015). In the selection of parent lines used to produce hybrids, the effect of a specific combining ability analyzed in an isolated way had a limiting value. Thus, other parameters should be considered such as the average of hybrids and general combining ability of the respective parent lines (Oliveira *et al*., 1998). Therefore, superior hybrid combinations, which are important for breeding, are involved with at least one parental line which has the most favorable effects of general combining ability (Cruz and Regazzi, 1997).

The highly desirable negative significant SCA effects of plant height, upper ear height, lower ear height, 1st and 2nd cob picking and harvest duration were observed in BCP/S_4-31×VS/S_3-26, BCP/S_4-14×VS/S_3-1, BCP/S_4-22×VS/S_3-1, BCP/S_4-2×VS/S_3-8 and BCP/S_4-14×VS/S_3-26, respectively. However, hybrids BCP/S_4-22×VS/S_3-26, BCP/S_4-2×VS/S_3-1 and BCP/S_4-29×VS/S_3-1 showed the highest positive significant SCA effects for number of cobs/plant, fodder yield, baby corn yield with husk per plant. Six crosses viz. BCP/S_4-2×VS/S_3-1, BCP/S_4-5×VS/S_3-8, BCP/S_4-10×VS/S_3-8, BCP/S_4-10×VS/S_3-26, BCP/S_4-22×VS/S_3-26 and BCP/S_4-29×VS/S_3-1 exhibited significant positive SCA effects for baby corn yield of which BCP/S_4-29×VS/S_3-1 was the highest. These results were in agreement with the findings of Dhasarathan *et al.* (2015) who also got significant positive SCA effects for some of the characters of baby corn.

Table 3. General combining ability (GCA) effects and mean of parents for different characters in baby corn.

Parents	Plant height		Upper ear height		Lower ear height		1st cob picking (days)		2nd cob picking (days)		3rd Cob picking (days)		4th Cob picking (days)	
	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean
Lines :														
1. BCP/ S_4-2	10.4**	119	5.9**	56	7.1**	25	-4.2**	97	-4.2**	100	-5.02**	108	-	0
2. BCP/ S_4-5	10.2**	109	11.9**	55	3.6**	24	-1.3**	98	-1.4**	102	-3.02**	107	-	0
3. BCP/ S_4-10	6.6**	98	-5.4**	48	-3.7**	22	-0.8**	100	0.3	104	1.5**	108	-	0
4. BCP/ S_4-14	-6.3**	116	-4.7**	55	1.1**	25	2.3**	102	1.6**	105	2.2**	108	-	0
5. BCP/ S_4-22	-12.8**	85	-4.4**	41	1.9**	21	0.5*	105	0.1	106	0.8**	108	-	0
6. BCP/ S_4-29	3.1**	86	0.8	57	-5.0**	25	1.0**	103	0.3	105	-1.2**	109	-	0
7. BCP/ S_4-31	-11.1**	130	-4.4**	63	-5.2**	34	2.5**	102	3.3**	106	4.8**	108	-	0
SE (gi)	0.64		0.45		0.3		0.3		0.2		0.1			
SE (gi-gj)	0.89		0.64		0.5		0.3		0.2		0.2			
Testers :														
1. VS/S_3-1	0.4	150	0.9**	58	3.9**	29	-0.3*	98	-0.6**	102	0	108	-	0
2. VS/S_3-8	4.2**	138	0.6	54	-1.6**	26	0.2	98	-0.4**	104	0.4**	107	-	0
3. VS/S_3-26	-4.6**	117	-1.5**	56	-2.3**	30	0.5**	97	1.0**	99	-0.4**	0	-	0
SE (gi)	0.42		0.29		0.21		0.12		0.12		0.08			
SE (gi-gj)	0.59		0.42		0.29		0.18		0.17		0.12			

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

Table 3. Cont'd.

Parents	Baby cobs ear length		Baby cobs ear diameter		Baby cobs harvest duration		Fodder yield/plant (g)		Baby corn yield (g)				No. of baby cobs/plant	
									With husk/plant		Yield/ plant			
	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean
Lines :														
1. BCP/S_4-2	0.2	7.9	-0.07*	1	-1.5**	11	3.6	311	-17.1**	200	-3.3**	28	-0.4**	3
2. BCP/S_4-5	-0.1	7.1	-0.1**	0.8	2.6**	9	-2.2	336	-15.5**	150	-0.3	19	0.3**	3
3. BCP/S_4-10	-0.8	7.6	0.03	0.9	3.1**	13	-34.4**	263	53.7**	250	0.9	22	0.3**	4
4. BCP/S_4-14	0.1	6.6	0.01	0.8	-2.4**	6	-20.7*	320	-10.6*	132	-2.0**	17	-0.2**	3
5. BCP/S_4-22	0.1	6.1	0.01	0.8	-1.9**	4	0.8	308	-33.7**	198	-3.5**	22	-0.4**	3
6. BCP/S_4-29	-0.4	6.1	0.1**	0.9	-2.4**	8	60.3**	385	22.5**	212	1.8**	21	-0.02	3
7. BCP/S_4-31	0.1	7.4	0.04	0.8	2.4**	6	-7.4	356	0.8	148	6.3**	20	0.3**	3
SE (gi)	0.13	-	0.02	-	0.2	-	7.35	-	3.81	-	0.59	-	0.06	-
SE (gi-gj)	0.19	-	0.04	-	0.2	-	10.3	-	5.40	-	0.84	-	0.09	-
Testers :														
1. VS/S_3-1	0.1	6.8	0.1*	0.8	2.7**	10	8.7	334	25.0**	156	2.9**	21	0.2**	3
2. VS/S_3-8	-0.3	7.3	-0.1*	0.8	-1.6**	9	-20.0**	432	-21.0**	203	-4.1**	22	-0.3**	3
3. VS/S_3-26	0.2	5.5	0.01	0.7	-1.1**	2	11.4*	261	-4	109	1.2**	17	0.1*	2
SE (gi)	0.09	-	0.02	-	0.11	-	4.79	-	2.49	-	0.39	-	0.04	-
SE (gi-gj)	0.12	-	0.02	-	0.16	-	6.77	-	3.52	-	0.55	-	0.06	-

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

Table 4. Specific combining ability (SCA) and mean of the crosses for grain yield and yield contributing characters in baby corn

Crosses	Plant height		Upper ear height		Lower ear height		1st cob picking (days)		2nd cob picking (days)		3rd Cob picking(days)		4th Cob picking(days)	
	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean
1. BCP/S_4-2×VS/S_3-1	-2.9*	184	0.1	90	1.4*	50	0.3	87	0.6	90	0	95	49.4**	106
2. BCP/S_4-2×VS/S_3-8	-6.2**	184	-0.6	89	1.9**	45	-2.8**	84	-2.1**	88	-2.4**	93	-10.0**	0
3. BCP/S_4-2×VS/S_3-26	9.1**	191	0.5	88	-3.3**	39	2.4**	90	1.5**	93	2.4**	97	-39.4**	0
4. BCP/S_4-5×VS/S_3-1	-0.3	186	5.1**	101	1.4*	46	0.5	90	1.8**	94	0.9**	98	-19.6**	107
5. BCP/S_4-5×VS/S_3-8	1.5	192	-0.6	95	-2.1**	37	0.4	90	-0.5	92	1.1**	99	25.5**	106
6. BCP/S_4-5×VS/S_3-26	-1.2	180	-4.5**	89	0.6	39	-0.9*	90	-1.3**	93	-2.0**	95	-5.9**	104
7. BCP/S_4-10×VS/S_3-1	-1.1	182	1.4	80	0.7	38	-0.5	90	-1.4**	93	-3.0**	99	-20.6**	107
8. BCP/S_4-10×VS/S_3-8	0.2	187	0.7	79	-0.7	31	1.4**	92	0.4	95	2.6**	105	25.0**	107
9. BCP/S_4-10×VS/S_3-26	0.9	179	-2.1*	74	-0.02	31	-0.9*	90	1.0**	97	0.4	102	-4.4**	107
10.BCP/S_4-14×VS/S_3-1	0.7	171	-4.7**	74	-2.1**	40	-1.2**	92	-1.7**	94	-0.7**	102	50.7**	108
11.BCP/S_4-14×VS/S_3-8	0.1	174	0.1	79	1.4*	38	1.2**	95	2.0**	98	2.9**	106	-10.6**	0
12.BCP/S_4-14×VS/S_3-26	-0.7	164	4.7**	81	0.6	37	0	94	-0.3	97	-2.2**	100	-40.1**	0
13.BCP/S_4-22×VS/S_3-1	0.2	164	-4.6**	75	-3.4**	40	1.6**	93	1.3**	95	2.6**	104	-55.6**	0
14.BCP/S_4-22×VS/S_3-8	1.5	169	0.7	80	-0.4	37	-1.9**	90	-1.5**	93	-1.7**	100	-1**	0
15.BCP/S_4-22×VS/S_3-26	-1.7	157	3.8**	81	3.8**	41	0.2	93	0.2	96	-0.9**	100	65.6**	106
16.BCP/S_4-29×VS/S_3-1	-0.6	179	-0.2	84	-1.4*	35	0.6	93	0.6	95	-2.4**	97	14.0**	106
17.BCP/S_4-29×VS/S_3-8	-4.8**	178	-1.9*	82	0.1	31	-1.4**	91	-1.6**	93	-2.7**	97	-45.3**	0
18.BCP/S_4-29×VS/S_3-26	5.4**	180	2.2*	84	1.3*	31	0.8*	94	1.0**	97	5.1**	104	31.3**	107
19.BCP/ S_4-31×VS/ S_3-1	4.1**	169	2.9**	82	3.3**	39	-1.4**	92	-1.4**	96	2.6**	108	-18.3**	112
20.BCP/S_4-31×VS/ S_3-8	7.8**	177	1.7*	81	-0.2	30	3.1**	97	3.4**	101	0.3	106	25.4**	110
21.BCP/S_4-31×VS/S_3-26	-11.9**	148	-4.6**	72	-3.0**	27	-1.7**	93	-2.0**	97	-2.9**	102	-7.1**	107
SE (Sij)	1.1		0.78		0.56		0.34		0.31		0.22		0.15	
SE (Sij-Skl)	1.55		1.11		0.79		0.48		0.44		0.31		0.21	

* Significant at 5 percent level; ** Significant at 1 percent level.

Table 4. Cont'd.

Crosses	Ear length		Ear diameter		Harvest duration		Fodder yield/plant		Baby corn yield (g)				No. of baby cobs/plant	
									With husk/plant		Yield/ plant			
	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean
1. BCP/S_4-2×VS/S_3-1	0.1	8.5	0.05	0.9	4.3**	18	11.7	612	30.2**	264	5.4**	37	0.5**	4
2. BCP/S_4-2×VS/S_3-8	0.1	8.2	-0.01	0.8	-0.9**	9	41.4**	613	-17.1*	171	-1.8	23	0	3
3. BCP/S_4-2×VS/S_3-26	0.1	8.5	-0.04	0.8	-3.4**	7	-53.1**	550	-13	191	-3.6**	26	-0.4**	3
4. BCP/S_4-5×VS/S_3-1	-0.3	7.7	0.07	0.9	-1.9**	17	27.1*	622	-3.1	231	-1.7	33	-0.2	4
5. BCP/S_4-5×VS/S_3-8	0.8	7.9	0.01	0.8	1.9**	16	-27.8*	538	16.2*	206	2.9**	30	0.3*	4
6. BCP/S_4-5×VS/S_3-26	0.3	8.5	-0.07	0.7	0	14	0.7	598	-12.2	194	-1.9	31	-0.1	4
7. BCP/S_4-10×VS/S_3-1	-0.3	7.8	-0.06	0.9	-1.9**	17	-23.3	539	-26.6**	278	-6.8**	29	-0.2	4
8. BCP/S_4-10×VS/S_3-8	0.2	8.1	-0.06	0.8	0.4	15	-4.1	530	4.5	263	4.2**	33	0.3*	4
9. BCP/S_4-10×VS/S_3-26	0.1	8.4	0.11*	1	1.4**	17	27.4*	593	22.1**	297	2.6*	37	-0.1	4
10.BCP/S_4-14×VS/S_3-1	-0.3	8	-0.08	0.9	2.1**	16	-58.9**	517	7.7	248	1.1	34	0.3**	4
11.BCP/S_4-14×VS/S_3-8	-0.3	7.9	0.05	0.9	1.9**	11	10.2	558	6.1	201	-0.4	25	-0.2*	3
12.BCP/S_4-14×VS/S_3-26	0.3	8.7	0.03	0.9	-4.0**	6	48.7**	628	-13.8*	197	-0.7	30	-0.1	3
13.BCP/S_4-22×VS/S_3-1	0.2	8.4	-0.03	0.9	-3.4**	11	-34.9*	563	-28.2**	189	-4.4**	27	-0.5**	3
14.BCP/S_4-22×VS/S_3-8	0.4	8.5	0.05	0.9	0.4	10	47.2**	616	27.2**	199	1.6	26	-0.1	3
15.BCP/S_4-22×VS/S_3-26	-0.6*	7.8	-0.02	0.9	2.9**	13	-12.3	588	1	189	2.8*	32	0.6**	4
16.BCP/S_4-29×VS/S_3-1	0.6*	8.7	0.10*	1.1	-0.4	13	19.6	677	33.5**	307	6.9**	43	0.2	4
17.BCP/S_4-29×VS/S_3-8	-0.4	7.5	-0.06	0.9	-3.0**	6	-24.3	604	-29.3**	198	-7.4**	22	-0.4**	3
18.BCP/S_4-29×VS/S_3-26	-0.3	7.9	-0.04	0.9	3.4**	13	4.7	665	-4.2	240	0.5	35	0.2*	4
19.BCP/ S_4-31×VS/ S_3-1	-0.7	8.1	-0.06	0.9	1.3**	20	58.7**	648	-12.5	239	-1.1	40	-0.2	4
20.BCP/S_4-31×VS/ S_3-8	-0.1	7.9	0.02	0.9	-0.9**	13	-42.6**	518	-7.6	198	0.9	35	0.3*	4
21.BCP/S_4-31×VS/S_3-26	0.2	8.5	0.04	1	-0.4	14	-16.1	576	20.0**	242	0.3	40	-0.1	4
SE (Sij)	0.23		0.05		0.3		12.67		6.59		1.03		0.11	
SE (Sij-Skl)	0.33		0.06		0.42		17.92		9.33		1.45		0.15	

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

Conclusion

The lines BCP/S_4-29 and BCP/S_4-31 were the best among the parents and VS/S_3-1 among the 3 testers as it showed desirable mean and GCA effects for most of yield and its contributing traits. Therefore, these parents could be used extensively in hybrid breeding program with a view to increasing baby corn yield with quality. Furthermore, based on mean and SCA effects of baby corn yield and number of cobs/plant 4 hybrids viz. BCP/S_4-2×VS/S_3-1, BCP/S_4-5×VS/S_3-8 , BCP/S_4-10×VS/S_3-8 and BCP/S_4-22×VS/S_3-26 were proved to be the best to increase the baby corn yield. For varietal improvement, these crosses could also be utilized for exploiting promising recombinants and it could be useful towards enhancing babycorn yield.

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EFFECT OF FOLIAR APPLICATION OF ZINC ON YIELD OF WHEAT GROWN BY AVOIDING IRRIGATION AT DIFFERENT GROWTH STAGES

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Abstract

A field experiment was carried out at micronutrient experimental field of Soil Science Division, BARI, Joydebpur, Gazipur to study the effect of foliar application of zinc on yield of wheat (BARI gom-25) grown by skipping irrigation at different growth stages of the crop. The experiment was designed in a split plot design on sixteen treatments comprising four irrigation treatments (regular irrigation, skipped irrigation at crown root initiation, skipped irrigation at booting stage and skipped irrigation at grain filling stages of wheat growth) and four foliar application of zinc (0.0%, 0.02%, 0.04% and 0.06% of zinc). Zinc Sulphate Monohydrate ($ZnSO_4$. H_2O) was used as a source of Zn. The interaction effect of irrigation and foliar application of zinc significantly influenced the yield and yield components of wheat. The highest yield (5.59 t ha^{-1}) was recorded in normal irrigation which was identical with skipping irrigation at flowering and heading stage with 0.06% foliar application of zinc. Skipping irrigation at crown root initiation stage had the most negative effect on growth and yield. Skipping irrigation at flowering and heading stage of wheat with 0.04% foliar application of zinc gave the identical yield in regular irrigation with 0.04% and 0.06% foliar application of zinc. Thus, foliar application of zinc played a major role on yield and yield components of wheat at later stages of growth. The response of foliar application of Zn was positive and quadrate in nature. The optimum dose was appeared as 0.04% foliar application of zinc for grain yield of wheat in the study area of Joydebpur, Gazipur (AEZ-28).

Keywords: Foliar, Zinc, Irrigation, Wheat and Yield.

Introduction

Wheat is an important cereal crop and serves as a staple food in many countries of the world. Most of the wheat-growing areas in the world suffer from low water supply and irregular distribution of rainfall during the growing season (Bagci *et al.*, 2007). Drought stress is also a serious abiotic stress factor limiting crop production in Bangladesh. However, the stress response depends upon the intensity, rate and duration of exposure and the stage of crop growth (Wajid *et al.*, 2004). Depending on the time, amount and distribution of the precipitation,

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drought stress results in substantial yield losses and in combination with Zn deficiency the decreases in yield becomes more severe (Ekiz *et al.,* 1998). When considering a water regime for a crop, it is wise to understand the sensitive growth stages for water and the water requirement of the crop. In order to achieve maximum yield and, maintaining adequate soil moisture condition during moisture-sensitive stages of growth so irrigation water may be saved if soil water could be depleted to a greater extent during certain growth stages without affecting yield (Thalooth *et al.,* 2006).

As well documented by plant physiologists, zinc exerts a great influence on basic plant life processes, such as (i) nitrogen metabolism – uptake of nitrogen and protein quality; (ii) photosynthesis – chlorophyll synthesis, carbon anhydrase activity; (iii) resistance to abiotic and biotic stresses – protection against oxidative damage (Cakmak, 2008). Zinc is known to have an important role either as a metal component of enzymes or as a functional, structural or regulatory cofactor of a large number of enzymes (Grotz and Guerinot, 2006). Zinc also plays an important role in the production of biomass (Kaya and Higgs, 2002; Cakmak, 2008). Furthermore, zinc may be required for chlorophyll synthesis, pollen function and fertilization (Kaya and Higgs, 2002; Pandey *et al.,* 2006). Low solubility of Zn in soils rather than low total amount of Zn is the major reason for the widespread occurrence of Zn deficiency problem crop plants (Cakmak, 2008).

Zinc nutritional status of plants may affect the drought sensitivity of plants in different ways. Zinc is involved in detoxification of Reactive Oxygen Species (ROS) and it is also important for reducing the production of free radicals by superoxide radical producing enzymes (Cakmak *et al.,* 1989; Cakmak, 2000). An adequate Zn nutrition has also protective effects on photoxidative damage catalyzed by ROS in chloroplasts (Cakmak, 2000, Wang and Jin, 2005). Drought stress represents an oxidative stress and kills plants by inducing production of ROS, especially during photosynthesis (Selote *et al.,* 2004, Goodman and Newton, 2005). It is, therefore, likely that drought stress-related production of ROS and sensitivity of plants to photoxidative damage in chloroplasts are additionally accentuated when plants would simultaneously suffer from Zn-deficiency stress.

Foliar-applied nutrients have limited direct use for enhancement of stress resistance mechanisms in field crops. Among the micronutrients, Zn and Fe nutrition can affect the susceptibility of plants to drought stress (Sultana *et al.,* 2001; Khan *et al.,* 2003; Cakmak, 2008). Foliar application of zinc greatly affects plant growth and crop production. It is, therefore, important to study the efficiency of foliar application of zinc on yield of wheat under water stressed condition at different growth stages of the crop. The present study was, therefore, undertaken a) to know the effect of foliar application of zinc on yield of wheat

grown by skipping irrigation and b) to find out the optimum foliar dose of Zn application for sustainable yield of wheat.

Materials and Method

A field experiment was carried out in the micronutrient experimental field of Soil Science Division, Bangladesh Agricultural Research Institute located at 23º59′26″ N and 90º24′52″ E., Grey Terrace Soil of Joydebpur, Gazipur (AEZ-28) on 27 November, 2013 with a view to studying the effect of foliar application of zinc on yield of wheat grown by skipping irrigation. The experiment was laid out in a split plot design with three replications. Irrigation was assigned in a main plot and foliar application in the subplot. Wheat (*Triticum aestivum* var. BARI Gom 25) was used in the experiment.

There were sixteen treatment combinations comprising of four irrigation treatments *i.e.*, T_1: regular irrigation: irrigation at crown root initiation stage, booting stage and grain filling stage, T_2: skipping one irrigation at crown root initiation stage, T_3: skipping one irrigation at booting stage, T_4: skipping one irrigation at grain filling stage and four levels of foliar spray of zinc i.e., Zn_0: control, Zn_1: 0.02%, Zn_2: 0.04% and Zn_3: 0.06% foliar application of Zn. Irrigation water was applied to the field condition in each plot as per treatment. Foliar application of zinc was done during the skipping irrigation at respective days. Zinc Sulphate Monohydrate ($ZnSO_4$. H_2O) was used as sources of Zn. Urea, triple supper phosphate, muriate of potash, gypsum and boric acid were used as sources of N, P, K, S and B, respectively. Fertilizers were applied based on BARC Fertilizer Recommendation Guide-2012. All PKSB and half of N were applied at the final land preparation and the remaining half of N was applied before booting stage. Initial properties of the soil samples of experimental field are presented in Table 1. Weather data during the crop growth period was presented in Fig.1. Wheat seeds were sown directly on 27 November, 2013 and the crops were harvested on 21 March, 2014 at full maturity. Ten plants from each plot were sampled randomly for collection of different plant characters and yield attributes. Data on yield and yield contributing characters such as plant height (cm), spike length (cm), grain spike^{-1}, 100 grain wt, yield (t ha^{-1}) were recorded. Plants of 1 m^2 area from each plot were selected for data collection. Data on yield and yield contributing parameters were recorded and statistically analyzed with the help of statistical package MSTAT-C and mean separation was tested by Duncan's Multiple Range Test (DMRT) at 5% level of probability.

Determination of Zn content in wheat grain

One gram of each sample was weighed into 50 ml beaker, followed by the addition of 10 ml mixture of analytical grade acids HNO_3: $HClO_4$ in the ratio 5:1, and left overnight for complete contact of material. Next day, the digestion was

performed at a temperature of about 190 ºC for 1.5 h. After cooling, the samples were transferred into 100 ml volumetric flask and solution was made up to a final volume raised up to the mark with distilled water. The metal concentrations were determined by atomic absorption spectrometry using a Zeenit model 700 Atomic Absorption Spectrophotometer (AAS). Analysis of each sample was carried out three times to obtain representative results and the data reported in µg g^{-1} (on a dry matter basis).

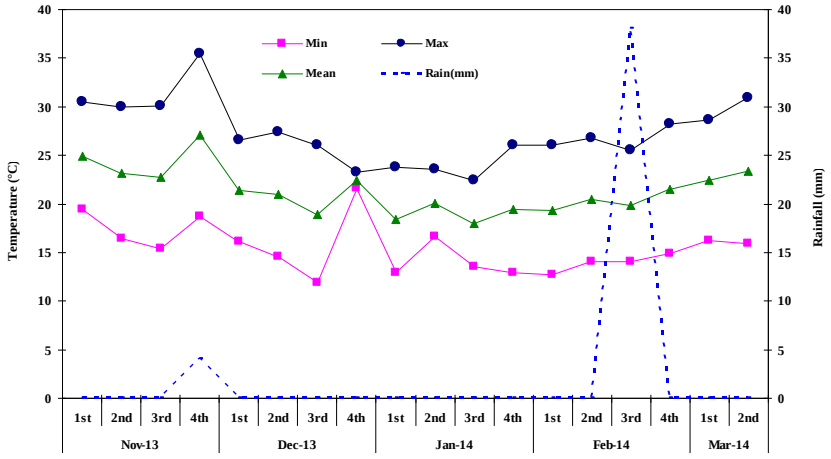

Fig. 1. Rainfall, minimum, maximum and mean temperature during growing period.

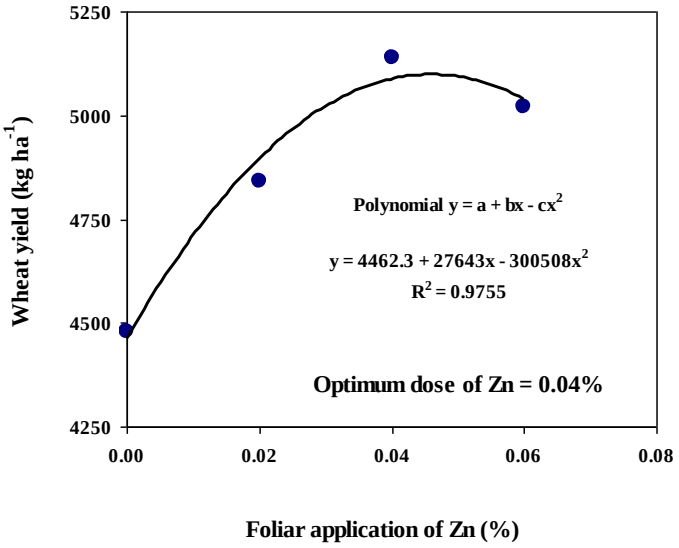

Fig. 2. Response of wheat to foliar application of Zn.

Results and Discussion

Effect of irrigation

The effect of irrigation on the grain yield and yield components of wheat has been shown in Table 3. The highest grain yield (5.29 t ha^{-1}) was obtained with regular irrigation (T_1), which was identical with skipping irrigation at heading and flowering stage (T_4). The lowest yield (4.33 t ha^{-1}) was obtained from skipping irrigation at crown root initiation stage (T_2), which was significantly lower than other treatments. This finding revealed that crown root initiation was the most critical stage for irrigation and its omission at this stage reduced the grain yield of 33 to 42% which was supported by Cheema *et al.* (1973). Crown root initiation (CRI) stage is the most critical stage for irrigation in wheat because any shortage of moisture at this stage results in less tillering and great reduction in yield. Bajwa *et al.* (1993) reported that number of tillers improved with irrigation at crown root stage and better grain yield was recorded with irrigation at crown root and booting stage.

Effect of foliar application of zinc

Foliar application of zinc played a significant role in the yield and yield components of wheat (Table 2). Yield components were influenced significantly due to foliar application of Zn. The grain yield of wheat increased significantly due to added zinc up to 0.04%. Kaya and Higgs (2002) and Cakmak (2008) reported that zinc plays an important role in the production of biomass. Firstly, Zn is involved in detoxification of Reactive Oxygen Species (ROS) and in this respect may play a protective role in preventing photoxidative damage catalyzed by ROS in chloroplasts (Cakmak, 2000; Cakmak and Römheld, 1997; Ducic and Polle, 2005). Secondly, this micronutrient might greatly contribute to drought-stress tolerance by protection against oxidative damage of membranes (Cakmak, 2000; Cakmak and Römheld, 1997; Ducic and Polle, 2005).The highest yield (5.14 t ha^{-1}) was found with 0.04% foliar application of Zn which was higher than the rest of the doses. There was no significant difference between 0.02% and 0.06% foliar application of Zn.

Interaction effects of irrigation and foliar application of zinc

The interaction effect between irrigation and foliar application of zinc on the yield and yield components of wheat was significant (Table 3). The highest grain yield (5.59 t ha^{-1}) was recorded in regular irrigation (T_1) with 0.04% foliar application of zinc which was statistically with T_4 treatment (skipping irrigation at grain filling stage). Skipping irrigation at crown root initiation (CRI) stage of growth caused the reduction in all yield components and grain yield of wheat. This might be due to reduced crown root development which decreased the grain

Table 1. Initial properties of the soil samples of experimental field

Soil Properties	Texture	pH	OM (%)	Ca	Mg	K	Total N %	P	S	B	Cu	Fe	Zn
				meq $100g^{-1}$				µg g^{-1}					
Result	Sandy clay loam	6.50	1.06	10.2	1.49	0.67	0.03	22	11	0.50	1.6	120	0.96
Critical level	-	-	-	2.0	0.80	0.20	-	14	14	0.20	1.0	10	2.0

ASI method.

Table 2. Main effect of irrigation and foliar application of Zn on yield and yield components of wheat in 2014

Treatment	Plant height (cm)	spike length (cm)	No of grain $spike^{-1}$	100 grains wt. (g)	Grain wt. m^{-2} (g)	Grain yield (t ha^{-1})
Irrigation mean						
T_1 = Regular irrigation	80.8ab	10.8a	50.4a	5.78a	529a	5.29a
T_2 = Skipping irrigation at CRI stage	78.3bc	10.3a	45.4b	4.98b	433c	4.33c
T_3 = Skipping irrigation at booting stage	77.79c	10.6a	47.4ab	5.16b	464b	4.64b
T_4 = Skipping irrigation at grain filling stage	82.0a	10.5a	50.1a	5.56a	520a	5.20a
Foliar application						
Zn_0 =Control	79.0a	10.1c	45.9b	5.21b	447c	4.47c
Zn_1 = 0.02% Zn	79.9a	10.4bc	47.6bc	5.24ab	484b	4.84b
Zn_2 = 0.04% Zn	80.4a	11.0a	50.2a	5.63a	514a	5.14a
Zn_3 = 0.06% Zn	79.5a	10.7ab	49.5ab	5.48ab	502ab	5.02ab

Values in a column followed by a common letter are not significantly different at $P < 0.05$ by DMRT.

Table 3. Interaction effect of irrigation and foliar application of Zn on yield and yield components of wheat

Treatment combination		Plant height (cm)	Spike length (cm)	No of grain spike^{-1}	100 grains wt. (g)	Grain wt. m^{-2} (g)	Grain yield (t ha^{-1})
Irrigation	Foliar application						
T_1 = Regular irrigation	Zn_0 = Control	78.1abcd	10.6abc	48.3ab	5.68abc	491bcde	4.91bcde
	Zn_1 = 0.02% Zn	79.1abcd	10.5abc	52.6ab	5.42abc	539abc	5.39abc
	Zn_2 = 0.04% Zn	84.3a	11.2ab	53.6ab	6.13a	559a	5.59a
	Zn_3 = 0.06% Zn	81.8abcd	10.8abc	47.0ab	5.92ab	527abc	5.27abc
T_2 = Skipping irrigation at CRI stage	Zn_0 = Control	77.9abcd	10.0abc	42.0b	4.50d	396h	3.96h
	Zn_1 = 0.02% Zn	82.7abc	10.1abcd	45.0ab	4.93cd	430fgh	4.30fgh
	Zn_2 = 0.04% Zn	75.6d	10.4abc	48.0ab	5.49 abc	463defg	4.63defg
	Zn_3 = 0.06% Zn	77.0cd	10.6abc	46.6ab	5.00cd	445efgh	4.45efgh
T_3 = Skipping irrigation at booting stage	Zn_0 = Control	78.8abcd	9.8c	46.3ab	4.93cd	418gh	4.18gh
	Zn_1 = 0.02% Zn	76.8cd	10.7abc	44.0ab	5.17bcd	454efg	4.54efg
	Zn_2 = 0.04% Zn	83.3abcd	11.3a	49.47ab	5.18bcd	498bcde	4.98bcde
	Zn_3 = 0.06% Zn	77.2bcd	10.7abc	50.0ab	5.35abcd	488cde	4.88cde
T_4 = Skipping irrigation at grain filling stage	Zn_0 = Control	81.3abcd	9.86bc	47.0ab	5.41abc	484cdef	4.84cdef
	Zn_1 = 0.02% Zn	80.9abcd	10.2abc	49.0ab	5.45abc	513abcd	5.13abcd
	Zn_2 = 0.04% Zn	83.6ab	11.1abc	50ab	5.73abc	535abc	5.35abc
	Zn_3 = 0.06% Zn	82.2abc	10.7abc	54.4a	5.64abc	548ab	5.48ab
CV (%)		4.74	5.63	9.77	3.36	8.28	8.28

Values in a column followed by a common letter are not significantly different at $P < 0.05$ by DMRT.

CRI = Crown Root Initiation.

yield significantly. This result is in agreement with Thalooth *et al.* (2006) who reported that missing one irrigation at any stages of growth significantly reduced yield and yield components as well as photosynthetic pigments content as compared with regular irrigation. Skipping irrigation at flowering and heading stage with 0.04% foliar application of zinc gave the identical yield in regular irrigation (crown root initiation, booting stage, flowering and heading stage) with 0.04% and 0.06% foliar application of zinc. Timing of foliar Zn application is an important factor determining the effectiveness of the foliar applied Zn fertilizers in increasing grain Zn concentration. It is expected that large increases in loading of Zn into grain can be achieved when foliar Zn fertilizers are applied to plants at a late growth stage. Ozturk *et al.* (2006) studied changes in grain concentration of Zn in wheat during the reproductive stage and found that the highest concentration of Zn in grain occurs during the milk stage of the grain development. Results showed a high potential of Zn fertilizer strategy for rapid improvement of grain Zn concentrations, especially in the case of late foliar Zn application. Khan *et al.* (2010) reported that foliar application of zinc at reproductive growth stage increased grain and straw yield significantly in wheat. Foliar application of crop nutrients at latter stages will ensure better crop nutrition at anthesis and grain filling stage which in turn may result in increased grain weight. These results are in agreement with those of Soylu *et al*. (2005) who reported significant variations for 1000 grains weight for foliar application of boron. Similarly Kenbaev and Sade (2002) and Hosseini (2006) reported improvement in yield components for application of zinc. Moreover, zinc by its participation in the action of superoxide dismutase (SOD) enzyme, may contribute to drought stress tolerance (Bagci *et al.,* 2007).

Zn content and uptake by wheat grain

The concentration of Zn in wheat grain ranged from 46.5 to 63.0 ppm (Table 4). Skipping irrigation at grain filling stage treatment (T_4) under foliar applied different zinc concentrations showed significantly higher content of Zn in grain compared to other irrigation treatment with different size concentrations that were foliar sprayed. Consequently the uptake of Zn was higher in T_4 treatment compared to other treatments under different size concentrations which were foliar sprayed.

Economic performance:

The economic performance of different treatments is presented in Table 5. The highest gross return, gross margin and BCR (TK. 87713 ha^{-1}, Tk. 69257 ha^{-1} and 4.75, respectively) was recorded in T_4 Zn_3 concentration. The lowest gross return, gross margin and BCR (TK. 63360 ha^{-1}, Tk. 45044 ha^{-1} and 3.46, respectively) was found in T_2 Zn_0 combination.

Table 4. Zn concentration and uptake of wheat grain in different treatment

Treatment combination		Grain yield	Zn concentration	Zn concentration	Zn uptake by grain
Irrigation	Foliar application	(kg ha^{-1})	(ppm)	(%)	(kg ha^{-1})
T_1 = Regular irrigation	Zn_0 = Control	4921	46.5	0.0047	0.229
	Zn_1 = 0.02% Zn	5397	46.5	0.0047	0.251
	Zn_2 = 0.04% Zn	5588	48.8	0.0049	0.273
	Zn_3 = 0.06% Zn	5275	50.3	0.0050	0.265
T_2 = Skipping irrigation at CRI stage	Zn_0 = Control	3960	51.8	0.0052	0.205
	Zn_1 = 0.02% Zn	4300	54.8	0.0055	0.236
	Zn_2 = 0.04% Zn	4633	55.2	0.0055	0.256
	Zn_3 = 0.06% Zn	4449	60.8	0.0061	0.271
T_3 = Skipping irrigation at booting stage	Zn_0 = Control	4189	56.8	0.0057	0.238
	Zn_1 = 0.02% Zn	4544	57.3	0.0057	0.261
	Zn_2 = 0.04% Zn	4987	61.2	0.0061	0.305
	Zn_3 = 0.06% Zn	4881	61.0	0.0061	0.298
T_4 = Skipping irrigation at grain filling stage	Zn_0 = Control	4849	56.3	0.0056	0.273
	Zn_1 = 0.02% Zn	5129	56.7	0.0057	0.291
	Zn_2 = 0.04% Zn	5350	59.3	0.0059	0.317
	Zn_3 = 0.06% Zn	5482	63.0	0.0063	0.345

CRI = Critical Root Initiation

Table 5. Economic performance of wheat production was influenced by irrigation and application of Zinc.

Treatment combination		Grain yield (kg ha^{-1})	Variable cost (Tk ha^{-1})	Gross return (Tk ha^{-1})	Gross margin (Tk ha^{-1})	BCR on variable cost (Tk ha^{-1})
Irrigation	Foliar application					
T_1 = Regular irrigation	Zn_0 = Control	4921	19190	78737	59547	4.10
	Zn_1 = 0.02% Zn	5397	19237	86356	67119	4.49
	Zn_2 = 0.04% Zn	5588	19283	89409	70125	4.64
	Zn_3 = 0.06% Zn	5275	19330	84394	65064	4.37
T_2 = Skipping irrigation at CRI stage	Zn_0 = Control	3960	18316	63360	45044	3.46
	Zn_1 = 0.02% Zn	4300	18363	68800	50437	3.75
	Zn_2 = 0.04% Zn	4633	18409	74133	55724	4.03
	Zn_3 = 0.06% Zn	4449	18456	71185	52729	3.86
T_3 = Skipping irrigation at booting stage	Zn_0 = Control	4189	18316	67022	48706	3.66
	Zn_1 = 0.02% Zn	4544	18363	72710	54347	3.96
	Zn_2 = 0.04% Zn	4987	18409	79788	61379	4.33
	Zn_3 = 0.06% Zn	4881	18456	78091	59635	4.23
T_4 = Skipping irrigation at grain filling stage	Zn_0 = Control	4849	18316	77584	59268	4.24
	Zn_1 = 0.02% Zn	5129	18363	82061	63698	4.47
	Zn_2 = 0.04% Zn	5350	18409	85600	67190	4.65
	Zn_3 = 0.06% Zn	5482	18456	87713	69257	4.75

[§] Variable cost considered only fertilizer and irrigation cost.
Input prices (Tk kg^{-1}): Urea: 16; TSP: 25; MOP: 15; Gypsum: 15; Zinc sulphate: 140; Boric acid: 240. Single irrigation cost 874 Tk.
Out put price (Tk kg^{-1}): Wheat grain: 16.

Response function

A quadratic relationship was observed between grain yield of wheat and foliar application of zinc (Fig. 2). From the regression equation, the optimum dose of foliar application of zinc appeared as 0.046%. So foliar application of 0.04% Zn may be considered as the best suitable dose for grain yield of wheat.

Conclusion

It can be concluded that wheat plants grown by skipping irrigation with foliar application of zinc counteracted the adverse effect of water deficit on the yield, especially at later stages of growth and helped the plants grow successfully under these unfavorable conditions. According to the results of the experiment, using 0.04% zinc as foliar application increased grain yield compared to all other treatments.

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INHERITANCE MECHANISM OF YIELD AND YIELD COMPONENTS IN TOMATO

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Abstract

A set of 9x9 half diallel cross comprising of promising genotypes was studied to analyze the inheritance pattern of yield components in tomato. Hayman's analysis of variance (ANOVA) indicated importance of both additive and non-additive genetic components for all the thirteen yield contributing characters. The ANOVA showed unidirectional dominance, asymmetrical gene distribution and residual dominance effects for all the characters studied. Five out of the thirteen characters viz., number of flowers/cluster, individual fruit weight, fruit breadth, number of locules and number of seeds/fruit followed the simple additive-dominance genetic model. The rest of the characters showed non-allelic gene interaction or epistasis. P_6 had most of the dominant genes for both number of flowers/cluster and number of locules, while P_3 contained most dominant genes for individual fruit weight and P_5 possessed that for both fruit breadth and number of seeds/fruit. The estimates of components of variance demonstrated involvement of both additive and dominant components in the inheritance of all those five characters. The distribution of dominant and recessive genes was equal in the parents for only fruit breadth. There was drastic influence of environment on these characters following simple additive-dominance genetic model except fruit breadth.

Keywords: Tomato, inheritence, additive and non-additive genetic components, epistasis.

Introduction

Tomato (S*olanum lycopersicum* L.) is one of the most important vegetables of Bangladesh. It is rich in a plethora of natural antioxidants and bioactive compounds. The regular ingestion of an adequate amount of fresh tomatoes or processed tomato products has been inversely correlated with the development of widespread human diseases (Erdman *et al.,* 2009 and Prakash *et al.,* 2014) and with an increase in plasma lipid peroxidation levels (Balestrieri *et al.,* 2004).This protective effect has been mainly attributed to the carotenoid constituents of the fruits, particularly lycopene and β-carotene which act as antioxidants in detoxifying free radicals (Erdman *et al.,* 2009). In Bangladesh, national average yield is 10.0 t/ha (Annon. 2014), which is very low compared to other tomato growing countries. So yield of tomato is to be increased several

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folds in a unit area. It is reported that hybrid variety of tomato resulted in increased yield of 20 to 50%. Apart from high yield, the hybrids may have some other specific advantages of earliness, higher number of fruits per plant, fruit size, improved quality, uniformity, higher adaptation capability to adverse conditions etc. It was further mentioned that exploitation of hybrid vigor in tomato is economical because each fruit contains larger number of seeds as compared to other vegetables and per unit area seed requirement is also very little. At present, farmers are very interested to grow hybrid variety for avoiding disease problem and to get early harvest (short duration), good quality fruit along with better yield. But there is lacking of good hybrid varieties, though different seed companies are advertising different advantages to attract farmers. Most of the hybrid tomato varieties cultivated in Bangladesh are imported. BARI has so far developed nine hybrid tomato varieties (four varieties already obsolete). Therefore, more hybrid varieties need to be developed and seeds of those tomato varieties can be produced locally and marketed at lower price compared to imported varieties.

The improvement program of tomato can be enhanced to considerable extent if some basic information relevant to the pattern and genetic variability is made available to the plant breeders. The inheritance pattern and combining ability studies are the basic themes to derive such information which can be used as guidelines in planning tomato breeding program for achieving short and long term objectives.

Gene action refers to the mode of expression of genes in a breeding population. Mode of gene action provide guidelines in the selection of parents for utilization in hybridization program as well as choice of breeding procedures for genetic improvement of various quantitative traits of interest. Its main attributes include genetic components of variance which comprises the magnitude of combining ability variances and their relative effects. On the basis of genetic variance, gene action is being described in three different forms i.e., additive gene action, dominant gene action and epistatic gene action, respectively. The later two are collectively termed as non-additive gene action. Different factors affect the mode of gene action which includes type of genetic material utilized, mode of pollination, pattern of inheritance, sample size, sampling methods, existence of linkages and methods of derivation on gene action. Therefore, it was tried to define the inheritance pattern of some yield contributing characters of tomato which would be helpful for further breeding program.

Materials and Method

The experiment was carried out at the experimental field of Olericulture Division of HRC, BARI during winter season of 2013-14. Nine genotypes of tomato viz., P_1 (TLB-182), P_2 (BARI Tomato 15), P_3 (BARI Tomato 2), P_4 (GWT-038), P_5

(BARI Tomato 14), P_6 (GWT 034), P_7 (GWT 070), P_8 (TLB-182PE) and P_9 (SL(CNG) 010) with different characters were crossed in diallel fashion excluding reciprocals. The seeds of these tomato lines were sown in the seedbed on October 16, 2013. Thirty days old seedlings were transplanted in the main plot on November 15, 2013. The crop was fertilized with cow dung 10 t, urea 550 kg, TSP 450 kg and MOP 250 kg per ha, respectively. Half cow dung, entire TSP and half of MOP were applied during land preparation. The remaining half of the cow dung was applied during pit preparation. The rest of MOP and entire urea were applied at three equal installments at 15, 30 and 45 days after transplanting. Gap filling, plant protection, irrigation and other intercultural operations were done as and when necessary.

Measured characters and data collection: Data on thirteen yield and yield attributing parameters (given below) were recorded from 20 inner plants of each plot escaping border plants following AVRDC guideline:

Data on days to 50% flowering (DF), number of flowers/cluster (F/C), number of flower clusters/plant (C/P), days to first harvest (DFH), number of fruits/plant (F/P), individual fruit weight (IFW), harvest duration (HD), plant height (PH), fruit length (FL), fruit breath (FB), number of locules (NL), number of seeds/fruit (S/F) and fruit yield/plant (FY/P).

Design and statistical analysis: The experiment was laid out in randomized complete block design (RCBD) with 3 replications. The size of unit plot was 4.8 m × 1m, and the plant spacing was 60 cm x 40 cm. Each unit plot contained 2 rows of plants (24 plants/ plot). The recorded quantitative data were analyzed statistically for analysis of variance and Vr-Wr graph following Hayman (1954a) and Hayman (1954b). Components of genetic parameters were calculated following numerical approach of Jinks and Hayman (1953) based on Mather's notation (Mather and Jinks, 1982).

Results and Discussion

Preliminary ANOVA : From the preliminary ANOVA (Table 1) it was observed that all the thirteen characters showed highly significant mean sum of squares due to genotypes, which indicated significant differences among genotypes and we would proceed forward with all those characters.

Morley Jones ANOVA : Additive (a) and dominance (b) components of all the studied traits showed significant to highly significant mean sum of squares (Table 2), which proved the importance of both additive and dominance genetic components for the inheritance of those traits and the authenticity of further Vr-Wr graph analysis.

Table 1. Preliminary analysis of variance (Mean Sum of square) for different yield contributing traits in 9 parent diallel cross of tomato

Item	DF	F/C	C/P	DFH	F/P	1FW	HD	PHLH	FL	FB	NL	S/F	FY/P
Replication	2.23	0.01	0.03	0.58	1.26	0.71	3.27	0.74	0.0003	0.0001	0.02	3.26	0.01
Genotype	15.6**	1.1**	12.2**	181.1**	652.3**	845.3**	39.4**	7598.8**	0.6**	2.69**	4.35**	1587.5**	1.7**
P (Parent)	9.8**	1.0**	9.2**	34.9**	360.6**	2609.3**	64.9**	4734.**	0.6**	3.83**	4.07**	1662.8**	0.7**
F_1	9.6**	0.9**	12.8**	13.5**	732.4**	336.9**	13.8**	8468.1**	0.5**	2.49**	4.54**	1580.9**	2.0**
P vs. F_1	273**	6.9**	13.8**	7216**	183.9**	4525.3**	732.7**	92.4**	0.3**	0.64**	0.03*	1217.2**	1.6**
Error	1.31	0.007	0.05	0.47	0.59	0.43	0.95	0.92	0.0003	0.0001	0.01	1.29	0.002

*p<0.05; **p<0.01, DF = Days to 50% flowering, F/C = Flowers/Cluster (no.), C/P= Flower cluster/plant, DFH = Days to first harvest, F/P= Fruits/plant (no.), IFW= Individual fruit weight, HD= Harvest duration, PHLH= Plant height at last harvest, FL= Fruit length, FB= Fruit breadth, NL= No. of locales, SIF= Sub/fruit (no.), FY/P= Fruit yield/plant.

Table 2. Hayman analysis of variance (MS) following Morley Jones modification for different yield contributing traits of tomato

	df	DF	F/C	C/P	DFH	F/P	1FW	HD	PHLH	FL	FB	NL	S/F	FY/P
a	8	77.7**	5.3**	31.4**	116.6**	10635**	9606.9**	191.6**	154534**	3.0**	46.9**	78.9**	30234**	24.1**
b	36	274.4**	22.6**	297.9**	2964**	7484**	6890.6**	575.6**	55714**	11.9**	21.7**	37.8**	11538**	25.5**
b_1	1	101.1**	2.5**	5.1**	2672.6**	68.1**	1676.0**	271.3**	34.2**	0.1**	0.24**	0.01**	450**	0.6**
b_2	8	19.6**	3.8**	38.3**	52.7**	1140**	2666.6**	72.4**	14004**	2.3**	0.94**	6.0**	3342**	7.1**
b_3	27	153.6**	16.2**	254.5**	238.6**	6276**	2547.9**	231.8**	41675**	9.5**	20.6**	31.7**	7744**	17.8**
Error	88	0.44	0.002	0.02	0.16	0.20	0.14	0.34	0.30	0.0001	0.00003	0.003	0.44	0.001

*p<0.05; **p<0.01, DF = Days to 50% flowering, F/C = Flowers/Cluster (no.), C/P= Flower cluster/plant, DFH = Days to first harvest, F/P= Fruits/plant (no.), IFW= Individual fruit weight, HD= Harvest duration, PHLH= Plant height at last harvest, FL= Fruit length, FB= Fruit breadth, NL= No. of locales, SIF= Sub/fruit (no.), FY/P= Fruit yield/plant.

Unidirectional dominance and significant differences between mean of hybrids and mid parental value (significant b_1) were observed for days to 50% flowering, number of flowers/cluster, number of flower clusters/plant, days to first harvest, number of fruits/plant, individual fruit weight, harvest duration, plant height at last harvest, fruit length, fruit breath number of locules, number of seeds/fruit and fruit weight/plant. Highly significant b_1 component for number of flowers/cluster, fruit width, days to first fruit ripening, plant hight was found by Gul (2011). Again, asymmetrical gene distribution (significant b_2) was obtained for all the traits examined. Finally, the significant residual dominance effects (b_3) which is specific to individual crosses, was found for all the studied traits. Gul (2011) also observed significant b_2 and b_3 for all the characters he had studied.

Vr-Wr graph: From the Vr-Wr related statistical analysis, it was observed that only five traits out of thirteen traits, fulfilled the assumptions related to the simple additive-dominance genetic model, while the others exhibited epistasis or non allelic gene interaction (Table 3). Therefore, the Vr-Wr graph and Hayman's numerical approach had been subjected for number of flowers/cluster, individual fruit weight, fruit breadth, number of locules and number of seeds/fruit only. Bhutani and Kalloo (1991) found similar result for number of locules, while Ahmed *et al.* (2010), observed for fruit breath and number of seeds/plant. In contrast to the result fully adequate additive dominance model were found by Gul (2011) for plant height and number of fruits per plant.

Tabele 3. Statistics related to Vr-Wr analysis for different yield contributing traits in a 9-parent diallel cross of tomato

Characters	a	b	SE (b)	b=1	b=0	t^2	Significance of t^2
Days to 50% flowering	-0.69	0.36	0.20	*	ns	2.25	ns
Number of flowers/cluster	-0.16	0.53	0.21	ns	*	0.85	ns
Number of flower clusters/ plant	-0.06	0.03	0.29	*	ns	0.53	ns
Days to first harvest	-21.82	0.58	0.07	**	**	19.14	**
Number of fruits/plant	25.79	0.28	0.06	**	**	58.34	**
Individual Fruit weight	67.51	0.93	0.10	ns	**	0.07	ns
Harvest duration	3.06	0.12	0.02	**	**	860.02	**
Plant height at last harvest	-34.98	0.63	0.11	**	**	6.08	*
Fruit length	0.06	-.23	.28	**	ns	0.52	ns
Fruit breath	0.12	0.79	0.22	ns	**	0.00	ns
Number of locules	-0.13	0.81	0.22	ns	**	0.00	ns
Number of seeds/fruit	54.98	0.57	0.23	ns	*	0.39	ns
Fruit yield/plant	0.02	0.05	0.05	**	ns	118.02	**

* $p < 0.05$; ** $p < 0.01$.

Partial dominance in the inheritance was observed for individual fruit weight, fruit breath and number of seeds/fruit as their regression line intercepted Wr-axis above the origin with the 'a' value of 67.51, 0.12 and 54.98, respectively. On the contrary, number of flowers/cluster and number of locules showed over dominance as regression lines intercepted Wr-axis below the origin with the negative value of 'a' -0.16 and -0.13, respectively. These results are in agreement with the findings of Bhatt *et al*. (2001) who also reported non–additive gene action for the trait. However, Pratta *et al*. (2003) reported prevalence of additive gene action for the genetic determination for number of flowers/cluster.

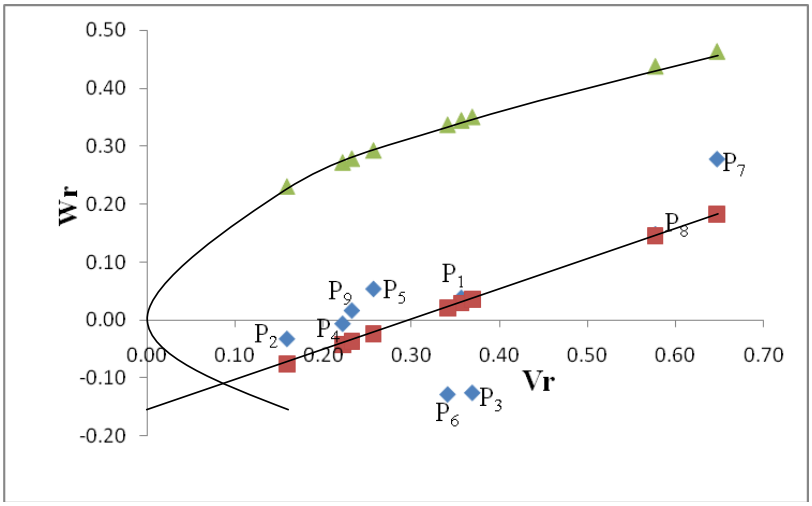

Fig. 1. Vr-Wr graph for number of flowers/cluster.

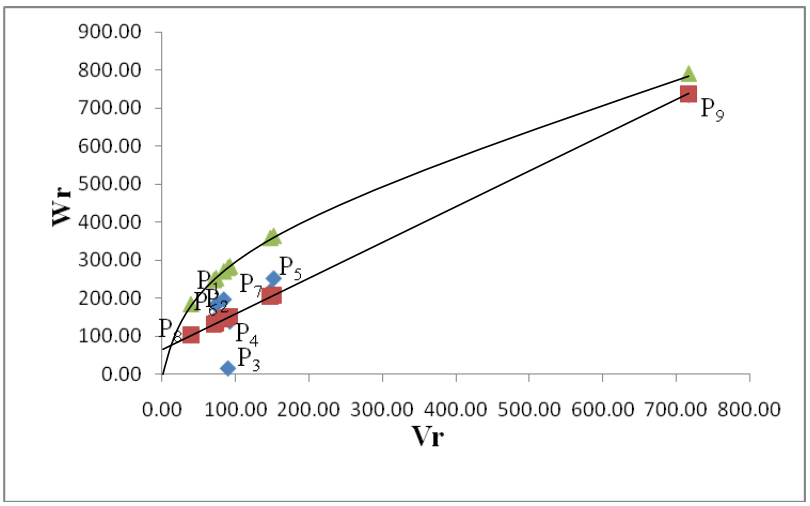

Fig. 2. Vr-Wr graph for individual fruit weight.

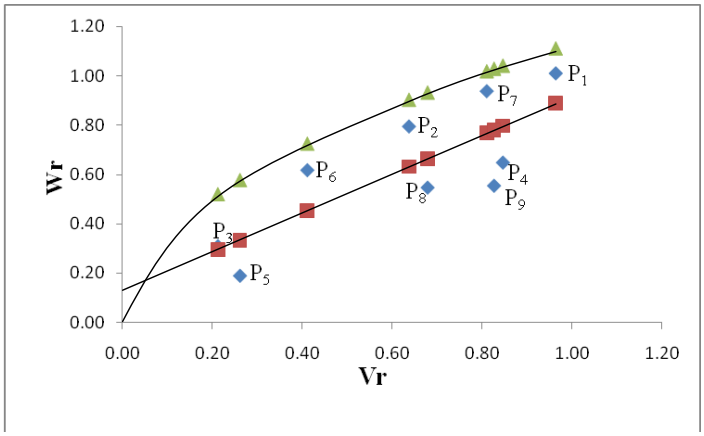

Fig. 3. Vr-Wr graph for fruit breath.

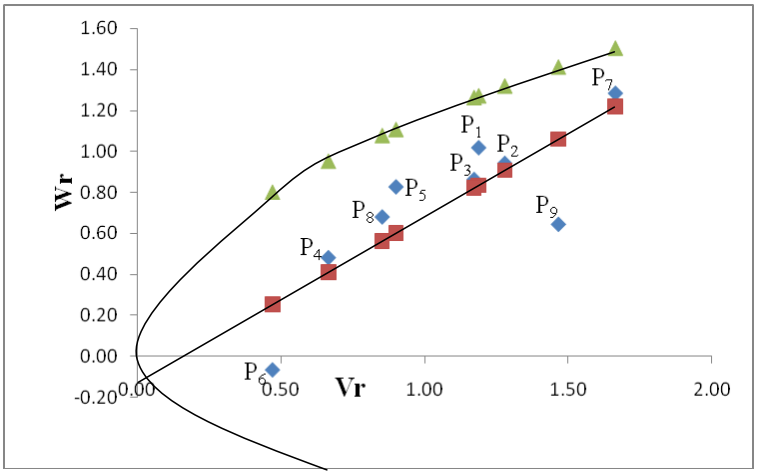

Fig. 4. Vr-Wr graph for number of locules.

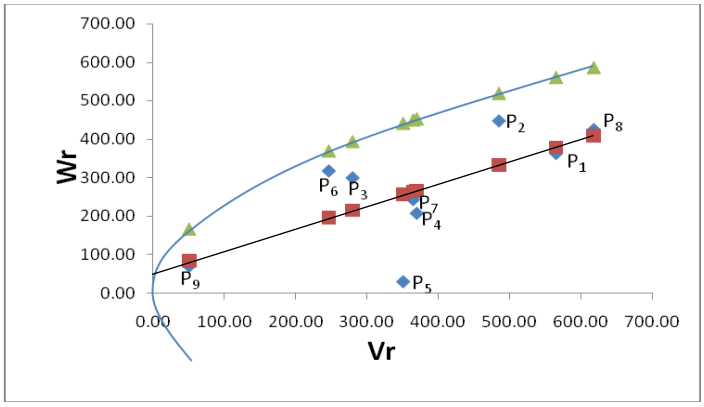

Fig. 5. Vr-Wr graph for number of seeds/fruit.

Most of the recessive genes for both number of flowers/cluster (Fig.1) and number of locules (Fig.4) belonged to P_7, while most dominant genes were possessed to P_6. P_5 contained most of the dominant genes and P_1 had most of the recessive genes for fruit breath (Fig.3). P_3 had most of the dominant genes for individual fruit weight (Fig.2), while P_9 had most of the recessive genes. In case of number of seeds/fruit (Fig.5) most of the recessive genes were possessed by P_2 and most of the dominant genes by P_5.

Components of variance : From the table 4, it was observed that additive (D) and dominance variance (H_1 and H_2) were highly significant for all the five characters - number of flowers/cluster, individual fruit weight, fruit breath, number of locules and number of seeds/fruit. The significant results instigated the importance of both additive and non-additive genetic variance in the inheritance of these five characters. Dominant component (H_1) was more predominant than additive component (D) except for individual fruit weight, where additive component was predominant.

Near equality of the two components H_1 and H_2 for fruit breadth indicated symmetry of dominant and recessive alleles distribution in parents, while the other four characters showed the unbalance distribution of dominant and recessive alleles. This finding was further strengthened by the value and sign of F. The significant positive value of F for number of flowers/cluster, individual fruit weight and number of seeds/fruit suggested the more frequency of dominant alleles than recessive alleles, while negative value for number of locules indicated the prevalence of recessive alleles in parents. However, fruit breath had balance distribution of both the dominant and recessive alleles. Ameri *et al.* (2009) also found equal frequencies for positive and negative alleles in the parents for fruit breath, but unlikely they got balance distribution for fruit length too. The results were confirmed by the ratio $\{(4DH_1)^{1/2}+F\}/\{(4DH_1)^{1/2}-F\}$. The ratio with higher value than unity indicated the asymmetric distribution and equal or near equal value to unity indicated the symmetric distribution of dominant and recessive alleles in parents.

The proportion of dominant genes with positive and negative effects is determined by $H_2/4H_1$ ratio, from which it was observed that except fruit breadth all the characters had dominant genes with irregular distribution (as the ratio deviated from 0.25) of increasing and decreasing effects in parents. The mean degree of dominance can be detected by $\{(H_1/ D)^{1/2}\}$. The unit value for fruit breadth indicated the equal proportion of dominance and recessive alleles in parents. Higher value than unity for number of flowers/cluster, number of locules and number of seeds/fruit indicating the abundance of dominant alleles and deficit of recessive alleles, while individual fruit weight had the reverse alleles distribution as its value was less than unity.

Table 4. Components of variance and genetic parameters for some yield components in an 9-parent diallel cross of tomato

Components	No. of flowers/cluster	Individual fruit wt.	Fruit breadth	No. of locules	No. of seeds/fruit
D	0.33** ±0.0004	869.63** ±0.178	1.28** ±0.0005	1.35** ±0.0007	553.85** ±0.3972
F	0.56** ±0.0009	861.95** ±0.415	0.06** ±0.0012	-0.25** ±0.0016	38.75** ±0.9267
H_1	1.63** ±0.0008	641.66** ±0.393	1.30** ±0.0012	2.68** ±0.0016	964.79** ±0.8768
H_2	1.25** ±0.0007	382.52** ±0.338	1.21** ±0.001	2.09** ±0.0013	640.16** ±0.7537
h^2	1.01** ±0.0005	662.08** ±0.226	0.09** ±0.0007	0.003* ±0.0009	177.92** ±0.5049
E	0.002** ±0.0001	0.15* ±0.0563	0.00003 ±0.0002	0.003** ±0.0002	0.44** ±0.1256
$(H_1/ D)^{1/2}$	2.22	0.86	1.01	1.41	1.32
$H_2/4H_1$	0.19	0.15	0.23	0.19	0.17
$\{(4DH_1)^{1/2}+F\}$ $/\{(4DH_1)^{1/2}-F\}$	2.23	3.73	1.05	0.88	1.05
r_{xy}	-0.52	0.91**	-0.30	0.17	-0.32
r^2	0.27	0.83	0.09	0.03	0.10
h^2/ H_2	0.81	1.73	0.08	0.001	0.28

The significant E value for all the characters except fruit breadth instigated the drastic influence of environment on these traits. The correlation coefficient (r) between parental measurement (Yr) and parental order of dominance (Wr + Vr) was positive and significant for individual fruit weight indicating that the parents had dominant alleles with negative effects. Again, negative correlation coefficient for number of flowers per cluster, fruit breadth and number of seeds per fruit revealed recessive alleles to have positive effects. The completely dominant or recessive parents prediction were not possible as r^2 was not less than unity for all the five traits. Number of blocks of dominant genes was estimated from h^2/ H_2 ratios, which was the highest for individual fruit weight (1.73) and lowest for number of locules.

Based on these information it may be concluded that the importance of both additive and non-additive genetic parameters suggests the use of integrated breeding strategies for tomato improvement. The use of hybrid breeding accompanied with recurrent selection may provide ample opportunities for novel recombination and accumulation of genes of interest.

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EFFECT OF FERTILIZER ON CORIANDER SEED PRODUCTION

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Abstract

A field experiment on coriander (*Coriandrum sativum* L.) was carried out during *rabi* seasons of 2011-12 and 2012-13 in Low Ganges River Flood Plain Soil under AEZ-12 at Farming System Research and Development Site, Hatgobindapur, Faridpur to find out optimum and economic doses of fertilizers for coriander (var. BARI Dhania 1) for sustainable higher yield and to update balanced fertilizer recommendation for target yield. The experiment was laid out in a randomized complete block design with 8 treatments viz. T_1=$N_{118}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kgha^{-1}, T_2= $N_{147}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}, T_3= $N_{147}P_{59}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}, T_4= $N_{147}P_{47}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kgha^{-1}, T_5= $N_{118}P_{59}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kgha^{-1}, T_6= $N_{147}P_{59}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kgha^{-1}, T_7= $N_{88}P_{35}K_{19}S_8Zn_{1.6}B_{0.6}$ Kgha^{-1} and T_8= Native nutrient (Control). The highest seed yield (1373 kg ha^{-1}) was obtained from the treatment T_3 which was statistically similar with T_1, T_2, T_3, T_4, T_5 and T_6 treatments. The soil test based treatment T_1 produced 1311 kg yield ha^{-1} and yield difference of ther added fertilizer treatment with T_1 was only 5%. The fertilizer added treatments didn't exert the significant difference with soil based treatment (T_1) on yield and yield contributing characters. However, T_1 treatment appeared to be the best suited combination because of its higher gross margin Tk 41,769 ha^{-1}, capability in reducing nutrient cost Tk 13106 ha^{-1} and the highest marginal rate of return (MRR) (108%) whereas treatment T_3 covered 21% MRR and the highest nutrient cost among the treatments and hence treatment, $N_{118}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1} (100% NPKSZnB from STB dose) may be recommended for coriander seed production in the study area.

Introduction

Coriander (*Coriandrum sativum* L.) is one of the important spices in Bangladesh. Seeds of the crops are used as spice, while its tender green leaves are used as culinary herbs. In Bangladesh, the average area of coriander is around 0.33 lakh hectares of land and production 0.38 lakh metric tons in 2013-14 (DAE, 2015). Faridpur district stands first in terms of area (2573 ha) and production (2433 tons) among other districts of Bangladesh. Bangladesh imported coriander seed about 93 tons expending 3000 US dollar in 2006 and 190 tons in 2008-09 (Anon., 2011). The average yield (825 kg ha^{-1}) of coriander is low whereas the research yield is 1.5 tha^{-1} (SAARC Ag. centre, 2006). One of the most important reasons for low yield is the application of imbalanced and improper fertilization. Fertilizer is the vital input that plays a significant role in exploring the highest

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yielding capacity of any crop. The requirement of fertilizer for any crop varies with the cultivars and soil types in agro-ecological zones (Mitra *et al.,* 1990). An adequate supply of plant nutrients is required in order to ensure proper development and potential yield for a particular crop. Judicious application of fertilizer has positive impact on growth and yield of crop. In order to obtain satisfactory results the nutrients should be applied in optimum dose. It was reported that the application of macronutrients (NPKS) markedly increased yield of coriander seed (Anon., 2008). Among different major plant nutrients, nitrogen is required in large amounts by plants because it is a constituent of macromolecules such as protein, encourages cell elongation and vegetative growth. The coriander absorbs most of phosphorous in early growth stages and increases seed yield (Gosh *et al,* 1986). Potassium is responsible for chlorophyll formation which plays an important part in the strength of cells and encourages flower and fruit formation. Tripathi *et al.*, (2009) reported that the seed yield increases with the application of sulphur and potassium. In Bangladesh, soil nutrient is diminishing day by day due to intensive cropping and the soil C and N status in Bangladesh has decreased considerably (Ali *et al.,* 1997). A judicial application of fertilizer must be followed for reducing soil nutrient. Research information regarding the suitable dose of NPKSZnB for the satisfactory production of coriander in Bangladesh is very meagre although some fertilizer based research has accomplished by scientists of BARI. Considering the above facts, the present study was undertaken to assess the appropriate combination of N, P, K, S, Zn and B for obtaining satisfactory yield of coriander seed in AEZ-12 and also to evaluate the economic return of coriander.

Materials and Method

The study was conducted at Farming System Research and Development Site, Hatgobindapur, Sadar Faridpur during *rabi* season of 2011-12 and 2012-13. Soil samples were collected from the experimental fields from a depth of 0-15 cm prior to application of fertilizers in both the years. Results of soil analysis are presented in Table 1. The soil of experimental field was clay to clay loam and slightly alkaline in nature. The average soil nutrient level of N and P was very low, K and S was medium and Zn & B was low (Table 1).

The experiment was set up in a randomized complete block design with six dispersed replications. The recommended fertilizer dose for coriander was computed on average data of soil test base (STB) value for high yield goal.There were eight treatments *viz.*, T_1 = 100% NPKSZnB (STB), T_2 = T_1+ 25% N, T_3 = T_1+ 25% NP, T_4 = T_1+ 25% NK, T_5 = T_1+ 25% PK, T_6 = T_1+ 25% NPK, T_7 = 75% of $T_1$and T_8 = Native nutrient (Control). The treatments with full amounts of nutrients were shown in below:

T_1=$N_{118}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_2= $N_{147}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_3= $N_{147}P_{59}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_4= $N_{147}P_{47}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_5= $N_{118}P_{59}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_6= $N_{147}P_{59}K_{32}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}

T_7= $N_{88}P_{35}K_{19}S_8Zn_{1.6}B_{0.6}$ Kg ha^{-1}

T_8= Native nutrient (Control)

Table 1. Initial properties of the soil samples (average of two years)

	Texture	pH	OM (%)	Total N (%)	Available P (µg/g soil)	K (meq/ 100g soil)	S (µg/g soil)	Zn (µg/g soil)	B (µg/g soil)
Average	Clay, Clay loam		1.32	0.073	6.06	0.25	16.66	0.90	0.21
Interpretation			L	VL	VL	M	M	L	L
Range		7.7-8.2	0.58-1.98	0.03-0.11	1.80-13.00	0.20-0.39	4.1-34.0	0.11-1.33	0.15-0.26
Interpre-tation		Slightly Alkaline	Very Low to Medium	Very Low to Low	Very Low to Low	Medium to High	Very Low to High	Very Low to Mediu m	Very Low to Low
Critical limit				0.12	10	0.12	10	0.6	0.2

The unit plot size was 5m X 4m. The variety was BARI Dhania 1and seeds were collected from Spices Research Centre, BARI, Faridpur. Coriander seeds were sown in 4 November to 5 December, 2011 and 30 November to 7 December, 2012 providing spacing of row to row 30 cm and seed to seed 15 cm. Half of nitrogen and whole amount of phosphorus, potassium, sulphur, zinc and boron were applied as basal in the form of urea, TSP, MoP, gypsum, zinc sulphate monohydrate and boric acid, respectively. The remaining nitrogen was top dressed at 30 days after sowing (DAS) of seeds followed by irrigation. Weeding cum thinning was done at 25 and 50 DAS. Mulching was done after irrigation. Sevin powder was sprayed around the plot at initial stage to protect the seeds against ant. Malathion @ 1.5 ml/L was sprayed against aphid. The spray was done at an interval of 15 days up to 45 days. Harvesting was done when the seeds reached at right stage of maturity. The harvesting was done from 1 to 19 March, 2012 and 18 to 23 March, 2013. Data on yield and yield attributes along with other parameters were collected and subjected to statistical analysis by Least Significant Test (LSD) test. Partial budget and marginal analysis of undominated fertilizer responses on coriander were done following the method suggested by Elias and Karim (1984).

Results and Discussion

The result obtained from two years was almost similar in yield and yield attributes and therefore pooled analysis was done.

Plant population

The effect of applied fertilizer on plant population m^{-2} of coriander was non-significant (Table 2). However, plant population m^{-2} varied from 79 to 88. The highest number of plants m^{-2} (88) was observed in T_4 (T_1+ 25%NK) treatment followed by 100% STB (T_1) and the lowest (79) in control (T_8) but this variation was statistically non-significant.

Table 2. Effect of different fertilizer dose on yield and yield contributing characters of coriander (Pooled data of 2011-2012 and 2012-2013)

Treatment	Plants m^{-2} (no.)	Plant height (cm)	Seeds $plant^{-1}$ (no.)	1000 seed weight (g)	Seed yield (Kg ha^{-1})	Straw yield (Kg ha^{-1})
T_1- 100% NPKSZnB (STB)	86	73.94	215	4.95	1311	1613
T_2 = T_1+ 25% N	85	73.44	215	5.06	1342	1795
T_3 = T_1+ 25% NP	84	74.44	229	5.10	1373	1877
T_4 = T_1+ 25% NK	88	73.45	216	5.06	1261	1820
T_5 = T_1+ 25% PK	81	72.80	223	4.96	1263	1932
T_6 = T_1+ 25% NPK	84	74.25	222	4.93	1312	1866
T_7 = 75% of T_1	84	69.80	191	4.96	1137	1719
T_8 = Native nutrient	79	54.55	111	5.15	728	929
CV(%)	12.77	8.63	10.93	6.99	11.84	11.38
LSD ($_{0.05}$)	NS	6	40	NS	143	275

STB = Soil test base; NS = Not significant.

Plant height

Application of fertilizer significantly influenced the plant height of coriander. But there was no significant variation among the treatments in respect of plant height of coriander (Table 2). However, the plant height among the added fertilizer treatments varied from 69.80 – 73.44 cm, where all the treatments showed similar except T_8 treatment which produced the shortest plant height. The above results showed that fertilizer virtually had no significant effect on the plant height of coriander plant but Oliveira *et al.* (2003) evaluated that N fertilizer plays an important role to increase plant height.

Seeds $plant^{-1}$

The effect of different nutrient combinations was significant on the number of seeds $plant^{-1}$ (Table 2). Fertilizer application increased seeds $plant^{-1}$ from 111 to

229. Maximum seeds plant^{-1} (229) was observed in T_3 (T_1+25%NP) treatment and it was identical with rest of the treatments except T_8 treatment. The lowest number of seeds plant^{-1} was obtained from control treatment. The present results are close to the findings of Channabasavanna *et al.* (2002) who reported that application of 60 kg N ha^{-1} + 60 kg P ha^{-1} produced the maximum number of seeds plant^{-1}.

Thousand seed weight

There was no significant effect of fertilizer among the treatments in terms of 1000 seed weight of coriander (Table 2). However, the 1000 seed weight among the fertilizer treatments varied from 4.93 to 5.15 g.

Seed Yield

Seed yield ha^{-1} was significantly influenced by the application of different fertilizer treatments (Table 2). Fertilizer application increased seed yield from 728 to 1373 kg ha^{-1}. The maximum seed yield (1373 kg ha^{-1}) was obtained from the treatment T_3 due to higher number of seeds plant^{-1} (229) and thousand seed weight (5.10 g). The experimental soil was deficient in different nutrients. So the application of different nutrients to the soil resulted in the higher uptake by plants which ultimately helped increase production of assimilates that causes higher seeds plant^{-1} and seed size. Response on the yield of coriander to higher doses of fertilizers was observed. Seed yield of coriander was higher when 100% fertilizer dose was used but yield decreased when 25% less fertilizer applied. On the other hand, variation in seed yield was found in different combinations of fertilizer treatments (from T_3 to T_6) although it was statistically similar. The maximum yield was observed in T_3 treatment where N and P combination was used. The treatment of T_4 (combination of NK) and T_5 (combination of PK) showed the lower seed yield. Gosh *et al.* (1986) also reported that yield was greatly influenced by interaction of N and P at 60 and 40 kg ha^{-1}. Channabasavanna (2002) reported that application of K_2O did not show any beneficial effect on seed yield of coriander. The treatment T_6 (T_1+25%NPK) also showed the lower yield than treatment T_3 due to excess use of K perhaps which created nutrient imbalance in the soil (soil inherently belongs to medium to high amount of K (Table 1). The lowest yield (728 Kg ha^{-1}) was obtained from native nutrient (T_8) where no fertilizer was used.

Stover yield

The straw yield ha^{-1} varied significantly with different fertilizer treatments (Table 2). The treatment T_5 produced the maximum straw yield (1932 kg ha^{-1}), which was statistically similar with all fertilizer added treatments except T_1 (1613 kg ha^{-1}). The lowest straw yield (929 kg ha^{-1}) was obtained from control treatment (T_8).

Economic performance

Gross return was calculated from the price of coriander. Costs that vary were calculated from the cost involved for fertilizer nutrients used for the experimental treatments. The partial budget analysis of fertilizer showed that the highest gross return (Tk. 57922 ha^{-1}) and gross margin (Tk. 42244 ha^{-1}) was accounted for T_3 treatment because of higher yield though higher cost was involved (Table 3). The dominance analysis of various treatments showed that treatments T_4,T_5 and T_6 were cost dominated due to obtain lower net return against increase of investment (Table 4). Marginal increase in gross margin, marginal increase in cost and marginal rate or return (MRR) of cost undominated treatments were shown in Table 5. The highest MRR (108%) was obtained from T_1 (Soil test based treatment, 100% NPKSZn) followed by T_7 (75% of T_1) treatment. Higher doses of fertilizer treated plots in T_2 and T_3 provided the highest gross margin but showed lower MRR among the cost undominated treatments and hence, they may not be economic. However, application of only chemical fertilizers at the rate of soil test based treatment (T_1) was appeared at the most suitable treatment for coriander cultivation due to its yield performance (1311 t ha^{-1}), satisfactory gross margin (Tk 41769 ha^{-1}) and higher marginal rate of return (108%). On the contrary, the second highest MRR (79%) was received from the treatment T_7 reduced nutrient cost 33% than T_1 treatment which could be suitable for the poor resource farmers.

Table 3. Cost and return analysis of coriander production as influenced by different fertilizer doses (Pooled data of 2011-2012 and 2012-2013)

Treatment	Gross return (Tk. ha^{-1})	Nutrient cost (Tk. ha^{-1})	Gross margin (Tk. ha^{-1})
T_1=100% NPKSZnB (STB)	54875	13106	41769
T_2 = T_1+ 25% N	56355	14386	41969
T_3 = T_1+ 25% NP	57922	15678	42244
T_4 = T_1+ 25% NK	53169	13301	39868
T_5 = T_1+ 25% PK	53434	14594	38840
T_6 = T_1+ 25% NPK	55269	**15874**	39395
T_7 = 75% of T_1	48069	9830	38239
T_8 = Native nutrient	30525	-	30525

Price of input (Tk. kg^{-1}):

Urea: Tk. 20.00, TSP: Tk. 22.00, MoP: Tk. 15.00, Gypsum: Tk 8.00, Boric acid: Tk. 160.00,

Zinc sulphate monohydrate Tk 160.00

Labor Cost (Tk. $labor^{-1}$): 300.00

No. of labor required for 1 ha fertilizer application (2 times): 3 (2 labor needed for basal application and remaining 1 for top dressing in 1 ha.)

Price of output (Tk. kg^{-1}): Seed: Tk. 40.00 and Straw: Tk. 1.50 (average of years)

Table 4. Dominance analysis of various treatments applied in coriander (Pooled data of 2011-2012 and 2012-2013)

Treatments	Gross margin (Tk. ha^{-1})	Nutrient cost (Tk. ha^{-1})	Inference
$T_3 = T_1$+ 25% NP	42244	15678	CUD
$T_2 = T_1$+ 25% N	41969	14386	CUD
T_1- 100% NPKSZnB (STB)	41769	13106	CUD
$T_4 = T_1$+ 25% NK	39868	13301	CD
$T_6 = T_1$+ 25% NPK	39395	**15874**	CD
$T_5 = T_1$+ 25% PK	38840	14594	CD
T_7 = 75% of T_1	38239	9830	CUD
T_8 = Native nutrient	30525	0.00	CUD

CUD: Cost undominated and CD: Cost dominated

Table 5. Marginal analysis of cost undominated treatments applied in coriander at FSRD site, Faridpur (Pooled data of 2011-2012 and 2012-2013)

Cost undominated treatments	Gross margin (Tk ha^{-1})	Nutrient cost (Tk ha^{-1})	Marginal increase in gross margin (Tk ha^{-1})	Marginal increase in variable cost of fertilizer as nutrient (Tk ha^{-1})	Marginal rate of return (%)
T_1= 100% NPKSZn (STB)	41769	13106	3530	3276	108
$T_2 = T_1$+ 25% N	41969	14386	200	1280	16
$T_3 = T_1$+ 25% NP	42244	15678	275	1292	21
T_7 = 75% of T_1	38239	9830	7714	9830	79
T_8 = Native nutrient	30525	0	30525	--	--

Conclusion

Two years study revealed that a package of 100% soil test based dose of chemical fertilizer ($N_{118}P_{47}K_{26}S_{10}Zn_{2.2}B_{0.8}$ Kg ha^{-1}) may be recommended for the cultivation of coriander in low Ganges river flood plain soil for higher yield with economic profitability.

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DEVELOPMENT OF MOUZA LEVEL DATABASES OF POTATO IN MUNSHIGONG, BOGRA & RANGPUR DISTRICT

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Abstract

A study was conducted to build the mouza and union level databases of potato during 2011-12 using both primary and secondary data. Primary data were collected from potato growers of unions of three upazilas, namely Vober Char, (Gazaria, Munshigonj), Atmul, (Shibganj, Bogra) and Mittipur (Pirganj, Rangpur), respectively. Mouza, union, upazila and district level digitized maps of Bangladesh were used in the program. GIS, GPS, MIS, Modem and mobile phone technologies were used. Databases of different parameters such as area, production, yield, and varietal information etc. of potato were obtained. Mouza have been used as the smallest unit of land use management for agriculture because it has administrative boundary and social identity. Average yield of potato was 17.45 t/ha in the study areas during 2011-12. Out of total potato areas 69.06% was cultivated by HYVs and the rest 30.94% by local varieties. Out of 46 HYVs released by BARI, 11 varieties were cultivated in the study areas during the same period. Databases and maps developed by data collection from root level (Farmer's field, mouza, block and union etc.) may help to identify variety wise area coverage of potato.

Keywords: Potato, Cultivation, Variety, Mouza, HYV and Database.

Introduction

Bangladesh is a small country with 160 million people. Its population is increasing rapidly but cultivated land is decreasing sharply. So the food production need to be increased to meet the increased demand. As such research on foods and its cultivation technique is very important in our country. Bhuiyan *et al.* (2002) studied on food requirements projection. They found that food requirement would increase from 20.96 million tons from 10.71 million ha cultivable area in 2002 to 27.81 million ton from 10.17 million ha cultivable area in 2025. The population has doubled in the last 30 years despite a decline in the annual population growth rate from 2.26 in 1961 to 1.47 in 2004 (BBS, 2005). Potato is a staple food in the developed countries and which accounts for 37% of the total production in the world (FAO and CIP, 1995). Considering the trend of population growth and consequently the increased demand for food in the country and dwindling cultivable land area, the potato is likely to play a vital role in the future. Potato is a popular and important vegetable in Bangladesh. For the

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whole year, it is used as the main vegetable. Potato production in Bangladesh in the fiscal year (FY) 2012-2013, hit a new record of 8.603 million tons surpassing the record of 8.38 million tonnes in FY'11. The production witnessed a negative growth in FY'12 when it plunged to 8.205 million tons- a 2.08 per cent fall compared to that of FY'11. The Government statistics provider, Bangladesh Bureau of Statistics (BBS, 2013) in its latest release, said potato the most consumed vegetable item of the country was cultivated on 444 million hectares of land in FY'13. The acreage had increased by 14,000 hectares compared to that of FY'12 which also helped achieve a higher output. Potato was produced on 4.6 million hectares in FY'11.This scenario shows that Bangladesh has to produce additional 0.274 million tons of food annually to maintain pace with the rate of population growth. The increased demand for food would have to meet with less land and water due to increasing population pressure on ever shrinking and degrading land and water resources.

Potato is an important food that may reduce the increasing demand of foods in the country. Akhter *et, al.* (2001) conducted a survey on potato production in some selected areas of Bangladesh. This study showed that potato production is highly profitable and it could be provide cash money to farmers. In terms of profitability, potato production was more attractive than any other winter vegetables. Per unit yield and gross return of potato were found higher than other competitive crops. It is cultivating in all the areas of the country and Union is consisting of some Mouzas in the biggest area where potato is cultivating.

Each centimeter of land should be used properly and methodically. Union is a big place for a densely populated small country like Bangladesh. So it should be divided into small parts as possible for proper and scientific use of agricultural land. Mouza should be used as the smallest unit of land use management for agriculture because it has administrative boundary and social identity. In future, for image data analysis and social identity, it will be useful; because, it is globally representable by longitude, latitude and altitude. Database is also suitable for crop zoning and crop suitability.

Bangladesh Agricultural Research Institute (BARI) is the largest multi-crop research institute. It conducts research activities on 202 crops. Scanty information of these crops and crop related factors are in the farmers' fields. Therefore, documentation of information of all crop related factors is essential. Per head cultivable land in Bangladesh is about 12 decimals only (Rashid, 2001). Considering the above factors, the present study on "Development of mouza level databases of potato" was selected with the specific objectives:

(1) To build mouza databases of potato at selected unions

(2) To determine variety wise area coverage of potato in mouza, union, upazila and district.

Materials and Method

A study was conducted on mouza level databases and maps of potato in 2011-12. All mouzas of three unions, namely Vober Char (Gazaria, Munshiganj), Atmul (Shibganj, Bogra) and Mittipur (Pirganj, Rangpur) were selected for the study. There were 43 mouzas in three unions, among them 9 mouzas in Vober Char, 22 mouzas in Atmul and 12 mouzas in Mittipur union of Munishiganj, Bogra and Rangpur districts, respectively (DAE, 2012). Among 43 mouza maps, 22 were digitized and 21 were collected. This root level digital databases and maps will be useful for crop zoning, crop suitability, and to compare with image data analytical result. It will be possible to use each unit of land for proper and scientific management in this way. These sites were selected purposively. Simple random sample procedure were followed for data collection and complete enumeration of different varieties of potato were taken for whole population. Data were collected from primary and secondary sources.

Primary data collection

1. Potato data were collected from all potato growers of different mouzas, blocks according to the prescribed schedule by Sub Assistant Agriculture Officers (SAAO) during 2011-12.
2. The database structure was filled up by UAO/SAAO with the help of researcher.
3. To cross check the information, farmers were interviewed by the researcher from different locations.
4. At the time of data collection, GPS and mobile phone were used.

Secondary data collection

Secondary sources were NGOs and GOs such as Soil Resources Development Institute (SRDI), Bangladesh Bureau of Statistics (BBS) and Department of Agricultural Extension (DAE) as well as international organization like Food and Agricultural Organization (FAO). Software package program such as Excel, SPSS and MS word were used in the study in addition to Arc View (GIS) program.

Results and Discussion

There were 89 blocks under 36 unions in the upazilas Gazaria, Shibganj and Pirganj of Munshiganj, Bogra and Rangpur districts, respectively (Table 1). Production related different agricultural information of potato under these upazilas were noted below:

Table 1. Blocks, unions and cultivable lands of different upazilas of Munshiganj, Bogra and Rangpur districts, respectively during 2011-12

Upazila	Gazaria (Munshiganj)	Shibganj (Bogra)	Pirganj (Rangpur)	Total
Block	24	30	35	89
Union	08	12	16	36
Cultivable land (ha)	7456	25690	33334	66480

Source: Field Survey, 2012 & DAE (2012).

Data were recorded from the potato growers of the target upazilas regarding cultivable land, area under potato cultivation, production, as well as yield of the crop (Table 2). Databases of cultivable land, area, production and yield of potato during 2011-12 were prepared according to district, upazila and union.

Table 2. Union wise area(ha), production(t) and yield(t/ha) of potato and cultivable land at Gazaria, Munshiganj during 2011-12

Union	Cultivable land (ha)	Area (ha)	Production (t)	Yield (t/ha)
Hossendi	970	155	4650	30.00
Baluakandi	809	76	2270	29.87
Tangar char	692	259	7246	27.98
Vaber char	724	190	5320	28.00
Boushia	1180	250	7885	31.54
Goagachia	1035	265	7595	28.66
Emampur	1265	720	22220	30.86
Gozaria	781	220	6600	30.00
Total	7456	2135	63786	29.88
Average	932	266.875	7973.25	-
Std	214.89	193.73	6049.16	1.30
Min	692	76	2270	27.98
Max	1265	720	22220	31.54
Cv%	23.06	72.59	75.87	4.35

Source: Field survey, 2012 & DAE (2012); Std. = Standard deviation.

There were 24 blocks under eight unions at Gazaria upazila, Munshiganj. Information on area, production and yield of potato were mentioned in the

Table 2. Total cultivable land of Gazaria upzila was 7456 ha. Area production and yield of potato at Gazaria upzila were 2135 ha, 63786 t and 29.88 t/ha, respectively. Yields were 27.43 and 29.49 t/ha during the period 2009-10 and 2010-11, respectively. Weather was suitable for potato production (Uddin *et al.*, 2010).

There were 43 mouzas under three unions in the upazilas Gazaria, Shibganj and Pirganj of Munshiganj, Bogra and Rangpur districts, respectively (Table 3). Production related different agricultural information of potato under these unions were noted in the following pages.

Table 3. Mouzas, unions and areas of different unions of Munshiganj, Bogra and Rangpur districts, respectively during 2011-12

Union	Vober Char (Gazaria, (Munshiganj)	Atmul (Shibganj, Bogra)	Mittipur (Pirganj, Rangpur)	Total
No. of Mouza	9	22	12	43
Mouza area (ha)	869	3174	2746	6789
Potato area (ha)	190	2200	600	2990

Source: Field survey , 2012.

Data were recorded from the potato growers of the target mouzas regarding mouza area, potato cultivated area, production etc. (Table 3). Database of different information of potato during 2011-12 were prepared for mouza union, upazila and district.

Table 4. Mouza wise potato growing areas (ha) at Vober Char union, Gazariaupazila, Munshiganj, 2011-12.

Mouza Name	Mouza Code	Mouza Area (ha)	Potato area (ha)	Production (t)	Yield (t/ha)
Anarpur	43	11	5	142.5	28.5
Umedarkandi	44	71	0	0	0
ChhotaAlipur	45	114	10	300	30
Bhitikandi	46	82	2	58	29
Satkahania	47	39	3	84.6	28.2
Bhaberchar	48	32	10	295	29.5
Lakshmipura	49	115	0	0	0
Pkhiarpar	50	69	40	1140	28.5
Srinagar	51	336	120	3300	27.5
Total		869	190	5320.1	28.00

There were nine mouzas at Vober Char union in Gazariaupazila, Munshiganj. Information on area, production and yield of potato were mentioned in the Table 4. Potato cultivated area, production and yield were 190 ha, 5320.1 t and 28.00 t/ha, respectively during 2011-12.

In each mouza of Vober Char union, database of potato area, production and yield is accessible. This database can be upgraded and fields may be added according to need.

Table 5. Union wise area, production and yield of potato and cultivated land at Shibganj, Bogra during 2011-12

Union	Cultivable land (ha)	Area (ha)	Production (t)	Yield (t/ha)	HYVs (t/ha)	LVs (t/ha)
Burigong	1820	1655	22698	13.71	16.00	10.71
Bihar	1920	1335	19475	14.59	16.91	12.24
Deulee	2208	1020	17565	17.22	17.50	16.44
Shibganj	2674	1450	20650	14.24	17.21	11.88
Sayedpur	2170	950	14354.5	15.11	17.14	11.00
Mosihata	1100	725	10536	14.53	16.40	11.19
Mazdanhata	2653	1210	18130	14.98	19.84	11.68
Mokamtala	2150	1150	20100	17.48	17.37	18.00
Kichok	2340	2270	33700	14.85	16.00	10.00
Pirob	1900	1900	24700	13.00	16.00	11.50
Raynagor	2120	1045	17772.5	17.01	17.16	15.60
Atmul	2635	2200	31193.75	14.18	16.09	9.90
Total	25690	16910	250874.75	15.08	16.97	12.51
Average	2140.83	1409.17	20906.23	-	-	-
Std	439.98	499.53	6529.93	1.43	1.07	2.66
Min	1100.00	725.00	10536.00	13.00	16.00	9.90
Max	2674.00	2270.00	33700.00	17.48	19.84	18.00
Cv%	20.55	35.45	31.23	9.46	6.33	21.24

Source: Field survey, 2012; Std. = Standard deviation.

Table 5 indicates that there were 30 blocks under 12 unions in Shibganj upazila, Bogra. Total cultivable land at Shibgonj, Bogra was 25690ha. Area, production and yield of potato were 16910 ha, 250874.75t and 15.08 t/ha, respectively.

Yield of HYV potato was 16.97 t/ha in 2011-12 (Table 5) but it was 16.61 and 18.30 t/ha in 2009-10 and 2010-11 respectively. Yield of local varieties of potato

was 12.51 t/ha during 2011-12 but it was 10.35 and 12.54 t/h in 2009-10 and 2010-11, respectively (Anon., 2011).

Table 6. Mouza wise potato growing areas (ha) at Atmul union, Shibganjupazila, Bogra, 2011-12

Mouza Name	Mouza Code No	Mouza Area (ha)	Potato area (ha)	Production (t)	Yield (t/ha)
Saduria	113	90	65	891.15	13.71
Putkhur	114	121	80	1167.20	14.59
Phenigram	115	263	195	2839.20	14.56
ChakKani	116	80	65	925.60	14.24
Katgara	117	159	107	1616.77	15.11
Dabur	118	60	45	653.85	14.53
Chandanpur	119	37	30	449.40	14.98
Ramkandi	120	91	70	1085.00	15.50
Barabelgharia	121	113	85	1262.25	14.85
Paramandahpur	122	44	30	435.90	14.53
Saidpur	123	47	35	510.65	14.59
Badaldighi	124	82	70	992.60	14.18
Betgari	125	90	70	959.70	13.71
Jagadish	126	79	70	996.80	14.24
ChhotaBelgharia	127	101	75	975.00	13.00
Gorna	128	95	70	1050.00	15.00
Teail	129	101	70	992.60	14.18
Atmul	130	473	305	4880.00	16.00
Atahar	131	128	80	1139.20	14.24
Dopara	132	141	80	1040.00	13.00
Nadura	133	277	175	2537.50	14.50
Kurahar	134	502	328	3793.63	11.57
Total	-	3174	2200	31194.00	-

There were 22 mouzas at Atmul union in Shibganjupazila, Bogra. Information on area, production and yield of potato were mentioned in the Table 6. There were 2200 ha potato area and production was 31194 t during 2011-12.

Table 7. Union wise area, production and yield of potato and cultivable land (ha) at Pirganj, Rangpur during 2011-12

Union	Cultivable land (ha)	Area (ha)	Production (t)	Yield (t/ha)	HYVs (t/ha)	LV (t/ha)
Chaitrakal	40	58	930	17.50	25.00	15.00
Bhendabari	1886	55	1054	18.97	21.50	13.50
Bara dargah	2258	53	1071	20.14	25.00	11.00
Rosolpur	900	40	693	17.33	25.00	9.65
Kumedpur	1033	80	1090	13.63	17.00	8.00
Modankhali	2169	210	4250	19.86	22.50	15.00
Tukuria	1913	160	3075	19.27	22.00	15.20
Bara Alampur	2939	270	4155	15.34	18.50	12.00
Raipur	2100	155	2110	13.61	18.00	10.00
Pirganj	2883	180	3727	19.30	22.75	14.00
Shanerhat	2147	135	2690	19.84	20.00	13.50
Panchgachha	1800	35	600	17.25	17.50	15.00
Mithapur	2161	600	9695	16.82	17.00	14.00
Ramnathpur	2905	1350	19710	14.49	14.60	12.30
Chatra	3219	275	4745	17.25	17.30	13.00
Kabilpur	2981	180	3470	18.25	21.30	10.00
Total	33334	3836	63065			
Average	1960.81	225.65	3709.71	16.44	20.46	12.44
Std	840.90	321.18	4707.43	2.13	3.43	2.38
Min	40	35	600	13.61	14.60	8.00
Max	3219	1350	19710	20.14	26.00	15.20
CV (%)	42.89	142.34	126.90	12.97	16.79	19.11

Source: Field survey, 2012; Std = Standard deviation; HYV = High Yielding Varieties; LV = Local Varieties.

Union wise information of Pirganj upazila of Rangpur district was presented in (Table 7). Total cultivable land at Pirganj was 33334 ha. Out of which potato cultivated area and production were 3836ha and 63065 t, respectively during 2011-12. Average yield of HYV potato was 20.46 during 2011-12, which was higher than previous years. Average yield of local varieties potato was 12.44 t/ha during 2011-12 but 11.50 t/ha and 12.42 t/ha during 2009-10 and 2010-11, respectively. Weather was favorable for potato production during the period.

Table 8. Mouza wise potato growing areas (ha) at Mittipur union, Pirganjupazila, Rangpur2011-12

Mouza name	Mouza Code No	Mouza area (ha)	Potato area (ha)	Production (t)	Yield (t/ha)
Kutubpur Gobra	142	133	19	319.2	16.8
Bhagioar	143	99	23	325.68	14.16
Fatepur Nandaram	144	66	5	84.1	16.82
Sadra Kutubpur	145	191	28	546	19.5
Shampur	146	47	17	286.11	16.83
Kasimpur	147	307	86	1376	16
Mittipur	148	310	122	2136.74	14.17
Akobpur	149	483	30	450	15
Akobpur Para	150	124	20	336	16.8
Durapur Mittipur	151	390	200	3088	15.44
Rosanpur	152	358	35	495.6	14.16
Hasonpur	153	238	15	252.45	16.83
Total	-	2746	600	9695.88	16.16

Table 9. Area, production and yield of potato at Gazaria, Shibganj and Pirganjupazilas of Bangladesh, during 2011-12

Upazilas	Potato area (ha)	Production (t)	Yield (t/ha)	Price (Tk/kg)	Cost of Production (Tk/kg)	Benefit/ Profit (Tk/kg)	BCR
Gazaria (Munshiganj)	2135	63786	29.88	10.01	7.00	3.01	1.43
Shibganj (Bogra)	16910	250875	16.97(HYV)	10.53	7.21	3.32	1.46
			12.51 (LV)	12.00	7.53	4.47	1.60
			15.08 (com)	-	-	-	
Pirganj (Rangpur)	3836	63065	20.46(HYV)	10.91	7.56	3.35	1.44
			2.44(LV)	13.85	8.50	5.53	1.62
			16.44(com)				
Total	22881	377726	-				
Average		-	22.44 (HYV)	10.48 (HYV)	7.25 (HYV)	3.23	1.45
			12.47 (LV)	12.92 (LV)	8.01 (LV)		
			17.45 (com)	11.70 (com)	7.63 (com)		

Source: Field survey, 2012; HYV = High yielding variety; LV = Local variety.

There were 12 mouzas at Mittipur union, in Pirganj upazila, Rangpur. Information on area, production and yield of potato were mentioned in Table 8.

Area, production and yield of potato were 600 ha, 9695.88 t and 16.16 t/ha, respectively during 2011-12.

Total cultivated area of potato in the study areas was 22881 ha and the maximum (16910 ha) at Shibganj (Table 9). Total production was 377726 t, the maximum production was 250875 t at Shibganj and the minimum 63065t at Pirganj. Average yield of potato was 17.45 t/ha for these upazilas. It was observed that yields of the local varieties at Shibganj and Pirganj were 12.51 and 12.44 t/ha, respectively .The highest yield was obtained by HYVs at Gazaria (29.88 t/h).Those were reasonably high yielders. On the other hand, Shibganj and Pirganj had low yields for HYVs.

Table 10. Variety wise area coverage of HYVs of potato at upazilas during, 2011-12

Variety	Gazaria (ha)	Shibganj (ha)	Pirganj (ha)	Total	Percentage (HYVs)
Diamant	1543 (72.27)	1439.6 (12.22)	81.5 (4.32)	3064	19.39
Cardinal	67 (3.14)	3554 (30.17)	842 (44.64)	4463	28.25
Granola	77 (3.61)	4840 (41.09)	261 (13.84)	5178	32.77
Binella	29 (1.360	-	-	29	0.18
Patrones	195 (9.13)	60 (0.51)	185 (9.81)	440	2.78
KufriSinduri	-	-	507 (26.81)	507	3.21
Multa	54 (2.53)	8.4 (0.07)	-	62.4	0.39
Ailsha	86 (4.03)	-	-	86	0.54
Elvira	-	888 (7.54)	4 (0.21)	892	5.65
Ladiro	-	-	4 (0.21)	4	0.03
Asterix	-	990 (8.40)	1.5 (0.08)	991.5	6.27
Others	84 (3.93)	-		84	0.53
Total (HYVs)	2135 (100)	11780 (100)	1886 (100)	15801	100.00

Source: Field survey, 2012. * Value in bracket indicates Percentage

Table 11. Area coverage of local varieties of potato at three upazilas during 2011- 12.

Variety	Gazaria (ha)	Shibganj (ha)	Pirganj (ha)	Total	Percen tage (LV)
Pakri	-	2620 (51.07)	331.5 (17.00)	2951.5	41.69
Talpakri	-	607 (11.83)	-	607	8.57
Lalpakri		1080 (21.05)	348 (17.85)	1428	20.17
Indurkani	-	-	1067.5 (54.74)	1067.5	15.08
Sadapakri	-	20 (0.39)	75 (3.85)	95	1.34
Shilpakri	-	178 (3.47)	-	178	2.51
Surjimukhi	-	315 (6.14)	-	315	4.45
Shilbilati	-	100 (1.95)	16 (0.82)	116	1.64
Hagrai	-	10 (0.19)	-	10	0.14
Sadadeshi		-	62 (3.18)	62	0.88
Others		200 (3.90)	50 (2.56)	250	3.53
Total		5130 (100)	1950 (100)	7080	100.00

Source: Field survey, 2012. * Value in bracket indicates percentage.

Table 12. Area coverage (ha) by potato varieties in three upazilas during 2011-12

Variety	Gazaria	Shibganj	Pirganj	Total
Total (HYV)	2135 (100)	11780 (69.66)	1886 (49.17)	15801 (69.06)
Total (LV)	-	5130 (30.34)	1950 (50.83)	7080 (30.94)
Grand Total	2135 (100)	16910 (100)	3836 (100)	22881 (100)

Source: Field survey, 2012; Value in bracket indicates percentage.

Adoption status and area coverage by the HYVs and the LVs of potato in the study areas are given in Table 10. Table 12 showed that out of 22881 ha, maximum (15801 ha) area was cultivated by HYVs and the rest (7080 ha) by the local varieties. Among 15801 ha HYVs potato, 2135 ha (100%) was cultivated by HYVs at Gazaria. However, 11780 ha (69.66%) and 1886 ha (49.17%) were cultivated by HYVs at Shibganj and Pirganj, respectively and the rest by the local varieties. At Gazaria, out of 2135 ha of HYV potato (Table 9) 1543 ha (72.27%), 195 ha (9.13%) and 86 ha (4.03%) were cultivated by Diamant, Patrones and Ailsha, respectively. At Shibganj, out of 11780 ha (69.66%) HYV potato 4840 ha (41.09%) and 3554 ha (30.17%) were cultivated by Granola and Cardinal, respectively and the rest (28.74%) by other HYVs. At Pirganj, among1886 ha (49.17%) HYVs potato, 1610 ha (85.36%) was cultivated by Cardinal, KufriSinduri and Granola and the rest (14.64%) by others (Table 10).

The results in Table 12 indicated that at Shibganj, out of 16910 ha (100%) potato area, 5130 ha (30.34%) was cultivated by the local varieties. Among the local varieties, 2620 ha (51.07%), 1080 ha (21.05%) and 607 ha (11.83%) were cultivated by Pakri, Lalpakri and Talpakri, respectively and the rest by other locals (Table 11). For Pirganj (Rangpur), out of 1950 ha (100%) local varieties, 1067.5 ha (54.74%), 348 ha (17.85%), 331.5ha (17.00%) were cultivated by Indurkani, Lalpakri and pakri, respectively and the rest by others.

Conclusion

Database of different parameters such as area, production, yield, and varietal information etc. of potato were obtained. Mouza, union, upazila, and district database of potato were developed. Mouza should be used as the smallest unit of agriculture in the root level because it has administrative boundary and social identity in comparison to union which is a big place. Average yield of potato was 17.45 t/ha in the study areas during 2011-12. Out of total potato areas, 69.06% was cultivated by HYVs and the rest 30.94% by local varieties. Out of 46 HYVs released by BARI, 11 varieties were cultivated in the study areas in the same period. Maximum area (80.41%) of HYVs potato was covered by three varieties Diamant, Cardinal and Granola. It is a system development program for data collection, variety wise area coverage determination in mouza, union, upazila production of digital databases and maps of potato as well as for other crops.

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STUDY ON COMBINING ABILITY AND HETEROSIS FOR EARLINESS AND SHORT STATURED PLANT IN MAIZE

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Abstract

An experiment was carried out in 6x6 diallel crosses for combining ability analysis for grain yield, maturity and growth parameters in maize. Analysis of variance for combining ability showed that mean square value due to GCA & SCA were highly significant for all characters except SCA in days to tasseling and days to maturity indicated that all but two traits were governed by both additive and non-additive gene action. Variances due to GCA were much higher in magnitude than SCA indicated additive gene effects were much more important for all characters except cob length, thousand grain weight and ear height. The Parent P_5 was the best general combiner for yield and most of the yield contributing characters. The Parent P_1 & P_2 were best general combiner for both dwarf and earliness. The crosses showing significant SCA effects for yield involving average x average, average x low and low x low general combining parents. The crosses P_3xP_6 & P_4xP_5 showed either significantly or numerically higher heterosis than checks BHM-5, BHM-7 & BHM-9 for yield.

Keywords: Maize, GCA, SCA and heterosis.

Introduction

Maize is one of the important cereal crops in our country. The maize area and production is increasing gradually and the crop is being popular among the farmers. It is well established that hybrid maize has more yield potential than composite or synthetic varieties. Due to yield advantages and other agronomic characters growers are very much interested to cultivate hybrid maize. But maximum seeds of the hybrid maize varieties are imported from foreign countries. The imported hybrid maize is very costly and farmers are not getting seed timely. For this reason, Plant breeding division of BARI is trying to fulfill this constrain. The nature and magnitude of gene action is an important factor in developing an effective breeding program. Combining ability analysis is useful to assess the potential inbred lines and also helps in identifying the nature of gene action involved in various quantitative characters. This information is helpful to plant breeders for formulating hybrid breeding program. Therefore, the present

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investigation with 6x6 diallel cross was undertaken for isolating superior inbred lines and better combining parents for suitable hybrids.

Materials and Method

The experiment was conducted at RARS, Jamalpur during *rabi* 2012-13. Six inbred lines of maize were mated in a diallel fashion excluding the reciprocals. The resulting 15 F_1s were grown in alpha lattice design with three replications. Each plot consisted of two rows of 5m long. The spacing between row to row was 60cm and plant to plant was 20cm. One plant per hill was maintained. Fertilizers were applied @ 250, 120,120 40, 5 and 1 kg/ha of N, P_2O_5, K_2O, S, Zn and Boron, respectively.

Irrigation and other intercultural operations were done as and when necessary. Ten randomly selected plants from each plot were used for recording data of plant and ear height. Other data were collected by considering all the plants in a plot. Grain yield kg/plot was converted into grain yield t/ha. General combining ability (GCA) and specific combining ability (SCA) were estimated by following Griffing's method II, model IV. Percent heterosis was calculated by the formula as heterosis (%) =[(F_1-CV)/CV] X100. Where, F_1 and CV represented the mean performance of hybrid and standard check variety. The estimated heterosis was tested according to Singh and Singh (1994).

Results and Discussion

1. Analysis of variance

Analysis of variance for combining ability showed that mean square values due to GCA & SCA were highly significant for all characters except SCA in days to tasseling and days to maturity (Tables 1a and 1b). It indicated that all but above mentioned two traits were governed by both additive and non-additive gene action. Similar findings in maize were reported by Aguiar *et al.* (2004), Bhatnagar *et al.* (2004) and Abdel-Moneam *et al.* (2009). The additive gene action played a major role in controlling the character days to tasseling and days to maturity because of non-significant SCA of these characters. Kadir (2010) also observed non-significant SCA variance for some characters in maize.Variances due to GCA were much higher in magnitude than SCA indicated additive gene effect were much more important for all characters except cob length, thousand grain weight and ear height. This indicated predominance of additive gene action for all the characters except cob length, thousand grain weight and ear height seemed to be controlled by non additive gene action. Vacaro *et al.* (2002) and Uddin *et al.* (2006) also reported that mean sum of square for GCA effects was greater than that for SCA effects for some characters which indicating the predominance of additive effects.

Table 1a. Mean squares due to general and specific combining ability on yield and yield components of maize.

Sources	d.f	Yield (t/ha)	Cob length	Cob girth	No. of rows/ ear	No. of grains/ row	TGW (g)
Rep	2	0.28	0.01	0.17	0.07	5.43	21.51
Crosses	14	6.69**	7.08**	6.71**	14.67**	34.44**	3479.19**
GCA	5	7.79**	5.58**	13.19**	34.43**	60.04**	3355.07**
SCA	9	6.08**	7.92**	3.11**	3.70**	20.22**	3548.15**
Error	28	0.37	0.35	0.26	0.22	1.09	74.62
GCA/SCA	0.56	1.28	0.71	4.24	9.31	2.97	0.95

** indicate significant at 1% level; TGW = Thousand grain weight.

Table 1b. Mean squares due to general and specific combining ability on maturity and growth parameters of maize

Sources	d.f	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Ear height (cm)
Rep	2	1.76	2.96	28.80	16.80	31.67
Crosses	14	9.09**	8.12**	18.61*	852.29**	233.14**
GCA	5	14.39**	12.29**	31.37*	713.30**	118.77**
SCA	9	6.14ns	5.80**	11.52ns	929.50**	296.69**
Error	28	3.21	0.91	7.97	21.59	22.17
GCA/SCA	0.56	2.34	2.12	2.72	2.16	0.40

*,** indicate significant at 5% and 1% level, respectively, ns= non-significant.

Table 2a. Mean performance of crosses for yield and yield components

Cross	Yield (t/ha)	Cob length	Cob girth	No. of rows/ ear	No. of grains/ row	TGW (g)
P_1XP_2	9.27	14.84	13.86	11.13	27.70	323.53
P_1XP_3	10.17	16.88	14.54	13.17	29.07	341.29
P_1XP_4	8.74	13.85	14.13	14.85	26.68	285.08
P_1XP_5	11.08	14.73	16.57	16.81	31.81	302.42
P_1XP_6	7.46	13.79	13.92	14.06	26.10	275.76
P_2XP_3	6.46	11.69	10.74	9.81	19.78	272.06
P_2XP_4	9.01	15.51	13.97	13.88	25.42	314.39
P_2XP_5	9.94	15.94	14.69	14.32	29.73	279.14
P_2XP_6	10.34	16.56	14.25	14.02	25.21	333.78
P_3XP_4	10.78	16.95	14.27	13.85	28.45	330.83
P_3XP_5	11.07	16.70	14.55	17.31	28.51	317.39
P_3XP_6	11.53	16.41	15.32	14.14	28.45	404.51
P_4XP_5	11.55	16.29	17.15	17.46	29.54	292.31
P_4XP_6	8.92	15.10	16.13	17.31	25.31	289.77
P_5XP_6	10.83	17.37	15.76	15.89	34.73	299.33
BHM5 (check1)	10.68	16.05	14.37	14.33	29.33	322.00
BHM7(check2)	11.38	16.23	15.20	16.57	30.29	316.00
BHM9(check3)	11.21	15.83	14.71	15.30	27.25	331.00
Mean	10.02	15.60	14.67	14.68	27.96	312.81

2. Mean performance of crosses for different characters

Eight crosses showed higher yield than overall mean (Table 2a). Two crosses namely P_3xP_6 & P_4xP_5 produced higher yield than overall mean and also higher yield than all check varieties. All tested crosses were few days earlier than all checks for days to tasseling, silking & maturity (Table 2b). Short stature plants were also observed for all crosses than all the three check varieties. So all the tested crosses were early & dwarf in stature compare to the checks.

Table 2b. Mean performance of crosses for the characters of maturity and growth parameters

Cross	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Ear height (cm)
P_1XP_2	88.33	92.67	140.00	177.33	102.67
P_1XP_3	88.00	92.00	143.00	198.67	115.33
P_1XP_4	87.33	92.00	143.67	185.00	102.00
P_1XP_5	86.33	91.33	144.33	190.67	107.67
P_1XP_6	88.00	93.00	148.33	143.33	95.67
P_2XP_3	90.00	97.00	140.67	166.00	82.33
P_2XP_4	88.33	93.67	140.00	177.33	96.67
P_2XP_5	85.33	89.67	142.67	191.33	103.33
P_2XP_6	89.67	93.67	146.33	200.00	111.67
P_3XP_4	88.67	92.67	140.00	194.67	112.33
P_3XP_5	92.00	92.67	145.00	198.67	107.00
P_3XP_6	91.33	94.67	145.33	196.67	105.00
P_4XP_5	88.67	92.67	145.33	186.33	101.33
P_4XP_6	89.67	94.33	143.67	166.33	89.33
P_5XP_6	87.67	92.67	143.67	207.67	107.67
BHM5(check1)	96.33	99.67	147.33	214.00	125.00
BHM7(check2)	93.67	97.67	146.67	225.00	150.00
BHM9(check3)	96.33	100.00	149.67	241.33	144.67
Mean	89.76	94.00	144.09	192.24	108.70

3. General combining ability (GCA) effects

The GCA effects of the parents for different characters are presented in Tables 3a and 3b. A wide range of variability for GCA effects were observed among the parents for different traits. The GCA effects are important indicators of the values of inbreds in hybrid combinations. The parents P_5 showed highly significant positive GCA effect for grain yield. In addition to grain yield, P_5 had

highly significant positive GCA for cob length, cob girth, number of grain rows/ear, number of grains/row. The Parent P_4 was good general combiner for cob girth and number of grain rows/ear. The Parent P_6 was found good general combiner for cob length, cob girth, no. of grain rows/ear and thousand grain weight. So, parent P_4, P_5 and P_6 could be used to develop high yielding maize hybrids. Alam *et al*. (2008) and Amiruzzaman (2010) also observed similar phenomenon in maize.

Table 3a. General combining ability effects for yield and yield components in 6x6 diallel cross

Parent	Yield (t/ha)	Cob length (cm)	Cob girth (cm)	No. of grain rows/ear	No.of grains/row	TGW (g)
P_1	-0.58*	-0.86**	-0.07	-0.66**	0.63	-6.44*
P_2	-1.01**	-0.75**	-1.44**	-2.38**	-2.75**	-7.74*
P_3	0.24	0.27	-0.97**	-1.10**	-1.14**	28.05**
P_4	-0.01	0.04	0.59**	1.17**	-0.86*	-10.37**
P_5	1.36**	0.87**	1.36**	2.28**	3.87**	-15.82**
P_6	0.01	0.42*	0.52*	0.69**	0.24	12.32**
SE(gi)	0.16	0.16	0.13	0.13	0.28	2.28
$LSD_{(0.05)}$	0.41	0.41	0.34	0.32	0.72	5.86
$LSD_{(0.01)}$	0.65	0.65	0.54	0.50	1.13	9.19

*,** indicate significant at 5% and 1% levels, respectively, TGW= Thousand grain weight.

Table 3b. General combining ability effects for maturity and growth parameters in 6x6 diallel cross.

Parent	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Ear height (cm)
P_1	-1.28*	-0.97*	0.50	-7.92**	2.50
P_2	-0.36	0.44	-1.92*	-3.67*	-4.17*
P_3	1.72*	1.03**	-0.83	7.00**	2.17
P_4	-0.11	0.11	-1.17	-4.25*	-2.92
P_5	-0.78	-1.47**	0.92	12.00**	3.42*
P_6	0.81	0.86	2.5	-3.17*	-1.00
SE(gi)	0.47	0.25	0.50	1.22	1.24
$LSD_{(0.05)}$	1.21	0.64	1.29	3.14	3.19
$LSD_{(0.01)}$	1.90	1.00	2.01	4.92	4.50

*,** indicate significant at 5% and 1% levels, respectively.

For maturity and growth parameters significant negative GCA effect is desirable for dwarf and earliness in plant. The parent P_1 had significant negative GCA effect was seen for days to tasseling, days to silking and plant height.The parent P_2 had significant negative GCA effect for days to maturity, plant height and ear height. So, the parent P_1 & P_2 could be used to develop early maturing dwarf hybrid. Das and Islam (1994), Hussain *et al.* (2003) and Banik (2006) also found some inbred lines with short plant type in their studies.

4. Specific combining ability effects

The specific combing ability effects for different characters are presented in Table 4a and 4b. For yield and yield components, significant positive SCA effect is desirable. Four crosses (P_1x P_2, P_2x P_6, P_3 x P_4 and P_3 x P_6) exhibited significant positive SCA effect for grain yield involving average x average, average x low and low x low general combining parents . The cross P_3xP_6 involved average x average general combiner, exhibited the second highest significant positive SCA effects along with the second highest mean value for yield. Amiruzzaman *et al.* (2013) and Ahmed (2013) also reported significant SCA effects in some of the crosses involving the parents of average x average , average x low and low x low general combiners for grain yield in maize. The highest yielding hybrid (P_4 x P_5) could not show significant SCA value. These results showed that high general combining parent (P_5) could not show high SCA effects in hybrid combinations . Similar findings were also reported by lvy and Hawlader (2000) in maize. On the contrary, Paul and Duara (1991) reported that parents with high GCA always produce hybrids with high estimates of SCA. The cross P_1xP_6, P_2xP_3, and P_4xP_6 showed significant negative SCA effects along with their low/average GCA value for grain yield. Hoque *et al*. (2008) and Amiruzzaman *et al*. (2013) also observed similar results in some of crosses in their study in the same crop. These four crosses also showed significant SCA effects in some yield components. Significant positive SCA effects were observed in five crosses (P_1x P_2, P_1x P_3, P_1x P_5 , P_3 x P_6 and P_4x P_5) for cob girth, five crosses (P_1x P_5, P_2x P_4, P_2x P_6, P_3 x P_5 and P_4 x P_6) for number of grain rows/ear, six crosses (P_1x P_2, P_1x P_3, P_2 x P_4 ,P_3 x P_4 ,P_3 x P_6 and P_5 x P_6) for number of grains/row and six crosses (P_1x P_2, P_1x P_3, P_1x P_5 , P_2 x P_4,P_2x P_6, and P_3 x P_6) for thousand grain weight involving high, average and low general combining parents. Uddin *et al*. (2006) and Ahmed *et al*. (2008) also observed significant positive SCA effects for some crosses for the mentioned characters.

For maturity and growth parameters, significant negative SCA effect is desirable for dwarfness and earliness in plant. Significant negative SCA effect was observed in one cross (P_2x P_5)for days to tasseling, three crosses (P_1x P_3, P_2x P_5 and P_3 x P_4) in days to silking and two crosses (P_1x P_2 and P_5 x P_6) for days to maturity indicating earliness in flowering. These crosses involved high x average,

high x low, average x average and average x low general combining parents which is in accordance with Uddin *et al*. (2006) and Ahmed (2013). Significant negative SCA effect was observed in five crosses (P_1x P_6, P_2x P_3, P_3x P_5 , P_4x P_5 and P_4 x P_6) for plant height indicating dwarfness of the hybrids involved high x high, high x low, average x average and low x low general combining parents. Significant and negative SCA effect was observed in 3 crosses (P_1x P_6, P_2x P_3 and P_4x P_6) for ear height indicating lower ear placement involved average x average and average x low general combining parents. Ahmed (2013) also observed significant and negative SCA effects involved high x high, high x average, high x low and low x low general combining parents in his study for plant and ear height.

Table- 4a. Specific combining ability (SCA) effects for different characters in 6x6 diallel cross for yield and yield contributing characters

Crosses	Yield (t/ha)	Cob length	Cob girth (cm)	No. of grain rows/ ear	No. of grains/ row	TGW (g)
P_1xP_2	1.05**	0.95	0.71*	-0.36	2.05**	26.95**
P_1xP_3	0.70	1.96	0.92**	0.40	1.81**	8.91*
P_1xP_4	-0.47	-0.84	-1.05**	-0.20	-0.86	-8.88*
P_1xP_5	0.49	-0.79	0.62*	0.66*	-0.46	13.91**
P_1xP_6	-1.77**	-1.28	-1.19**	-0.50*	-2.54**	-40.89**
P_2xP_3	-2.58**	-3.34	-1.50**	-1.25**	-4.10**	-59.03**
P_2xP_4	0.22	0.71	0.16	0.56*	1.26*	21.73**
P_2xP_5	-0.22	0.31	0.12	-0.12	0.84	-8.07
P_2xP_6	1.53**	1.38	0.51	1.17**	-0.05	18.42**
P_3xP_4	0.74*	1.13	-0.02	-0.76**	2.69**	2.37
P_3xP_5	-0.33	0.05	-0.50	1.59**	-1.99**	-5.62
P_3xP_6	1.47**	0.21	1.10**	0.01	1.58**	53.36**
P_4xP_5	0.40	-0.13	0.54*	-0.52*	-1.24*	7.72
P_4xP_6	-0.89**	-0.87	0.36	0.92**	-1.84**	-22.95**
P_5xP_6	-0.34	0.56	-0.78**	-1.61**	2.85**	-7.95
SE(ij)	0.27	0.26	0.23	0.21	0.47	3.86
$LSD_{(0.05)}$	0.71	0.60	0.52	0.48	1.06	8.73
$LSD_{(0.01)}$	0.82	0.86	0.75	0.69	1.53	12.54

*,** indicate significant at 5% and 1% level, respectively; TGW = Thousand grain weight.

Table 4b. Specific combining ability (SCA) effects for different characters in 6x6 diallel cross for maturity and growth parameters

Crosses	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Ear height (cm)
P_1xP_2	1.35	0.22	-2.05*	3.58	1.67
P_1xP_3	-1.07	-1.03*	-0.13	14.25**	8.00**
P_1xP_4	0.10	-0.12	0.87	11.83**	-0.25
P_1xP_5	-0.23	0.80	-0.55	1.25	-0.92
P_1xP_6	-0.15	0.13	1.87	-30.92**	-8.50**
P_2xP_3	0.02	2.55**	-0.05	-22.67**	-18.33**
P_2xP_4	0.18	0.13	-0.38	-0.08	1.08
P_2xP_5	-2.15*	-2.28**	0.20	-2.33	1.42
P_2xP_6	0.60	-0.62	2.28*	21.50**	14.17**
P_3xP_4	-1.57	-1.45**	-1.47	6.58*	10.42**
P_3xP_5	2.43*	0.13	1.45	-5.67*	-1.25
P_3xP_6	0.18	-0.20	0.20	7.50**	1.17
P_4xP_5	0.93	1.05*	2.12*	-6.75*	-1.83
P_4xP_6	0.35	0.38	-1.13	-11.58**	-9.42**
P_5xP_6	-0.98	0.30	-3.22**	13.50**	2.58
SE(ij)	0.80	0.43	0.85	2.08	2.11
$LSD_{(0.05)}$	1.81	0.97	1.92	4.70	4.77
$LSD_{(0.01)}$	2.60	1.40	2.76	6.76	6.86

*,** indicate significant at 5% and 1% level, respectively.

5. Heterosis

The estimates of standard heterosis for different characters of 15 single cross maize hybrids is presented in the Tables 5a and 5b. The magnitude of heterosis varied widely among crosses for different characters from cross to cross for the same character.

For grain yield, only two crosses viz. P_3xP_6 and P_4xP_5 showed significant positive heterosis 7.93% and 8.18% respectively over check BHM 5.These two crosses also produced numerically higher yield than other two check variety BHM 7 & BHM 9. Rest of the characters were compared with the highest yielding check BHM 7 to calculate heterosis. The cross P_3XP_6 showed significant positive heterosis (28.01%) for thousand grain weight also. The cross P_4XP_5 showed significant positive heterosis (12.85%) for cob girth also. Significant positive heterosis was observed in one cross (P_5XP_6) for cob length, 3 crosses (P_1XP_5,

P_4XP_5, P_4XP_6) for cob girth, one cross (P_5XP_6) for number of grains/row and 2 crosses (P_1XP_3, P_3XP_6) for thousand grain weight (TGW). Amiruzzaman *et al*. (2013) found highest 9.71 % heterosis for grain yield than check variety in maize. Appreciable percentage of heterosis for grain yield in maize was also reported by Roy *et al*.(1998) and Uddin *et al*. (2006).

Table 5a. Percent heterosis over BHM-7 for yield and yield contributing characters

Crosses	Yield (t/ha) Over 3 check variety			Cob length (cm)	Cob girth (cm)	No. of grain rows/ ear	No. of grains/ row	TGW (g)
	BHM 5	BHM 7	BHM 9					
P_1xP_2	-13.17**	-18.51**	-17.28**	-8.54**	-8.84**	-32.83**	-8.54*	2.38
P_1xP_3	-4.81	-10.66**	-9.31*	3.98	-4.32	-20.50**	-4.04	8.00*
P_1xP_4	-18.16**	-23.20**	-22.03**	-14.66**	-7.02*	-10.40**	-11.93**	-9.78**
P_1xP_5	3.71	-2.67	-1.19	-9.22**	8.99**	1.47	5.01	-4.30
P_1xP_6	-30.15**	-34.45**	-33.45**	-15.05**	-8.42**	-15.13**	-13.83**	-12.73**
P_2xP_3	-39.54**	-43.26**	-42.40**	-27.95**	-29.32**	-40.80**	-34.69**	-13.91**
P_2xP_4	-15.67**	-20.86**	-19.66**	-4.44	-8.11**	-16.21**	-16.07**	-0.51
P_2xP_5	-6.96	-12.68**	-11.36**	-1.79	-3.36	-13.58**	-1.85	-11.66**
P_2xP_6	-3.18	-9.14*	-7.76*	2.05	-6.25*	-15.41**	-16.76**	5.63
P_3xP_4	0.91	-5.30	-3.87	4.46	-6.14*	-16.42**	-6.06	4.69
P_3xP_5	3.65	-2.72	-1.25	2.92	-4.25	4.47	-5.88	0.44
P_3xP_6	7.93*	1.29	2.82	1.13	0.77	-14.69**	-6.07	28.01**
P_4xP_5	8.18*	1.52	3.06	0.39	12.85**	5.39	-2.47	-7.50*
P_4xP_6	-16.51**	-21.65**	-20.46**	-6.94*	6.14*	4.47	-16.43**	-8.30**
P_5xP_6	1.37	-4.86	-3.42	7.00*	3.68	-4.08	14.66**	-5.28
Mean	-8.16	-13.81	-12.50	-4.44	3.57	-12.28	-8.33	-1.66
Std error	3.61	3.39	3.44	2.44	2.54	3.45	2.89	2.78
Minimum	-39.54	-43.26	-42.4	-27.95	-29.32	-40.80	-34.69	-13.91
Maximum	8.18	1.52	3.06	7.00	12.85	5.39	14.66	28.01
CD(0.05)	7.74	7.27	7.37	5.24	5.45	7.39	6.19	5.97
CD(0.01)	10.75	10.09	10.24	7.28	7.56	10.26	8.60	8.28

*,** indicate significant at 5% and 1% levels, respectively; TGW = Thousand grain weight.

Significant and negative heterosis was observed for maximum crosses in case of maturity and growth parameters which is desirable for a breeder. Out of 15 crosses all crosses showed significant negative heterosis for days to tasseling wih a range of -8.90% to -1.78%. Fourteen crosses showed significant negative heterosis for days to silking and maturity with the range of -8.19% to -0.69% and -4.55% to -0.23%, respectively. Roy *et al.* (1998) and Uddin *et al*. (2006) also observed significant and negative heterosis in some crosses for days to tasseling

and silking in their studies. All the crosses showed significant negative heterosis for plant height (-36.30 to 7.70) and ear height (- 45.11 to -23.11) indicating dwarfness of the hybrids. Hoque *et al.* (2008) and Kadir (2010) also observed significant and negative heterosis in some crosses for plant height and ear height in their studies.

Table 5b.Percent heterosis over BHM-7 for maturity and growth parameters.

Cross combination	Days to tasseling	Days to silking	Days to maturity	Plant height (cm)	Ear height (cm)
P_1xP_2	-5.70**	-5.12**	-2.50**	-21.19**	-31.56**
P_1xP_3	-6.05**	-5.81**	-2.50**	-11.70**	-23.11**
P_1xP_4	-6.76**	-5.81**	-2.05**	-17.78**	-32.00**
P_1xP_5	-7.83**	-6.49**	-1.59**	-15.26**	-28.22**
P_1xP_6	-6.05**	-4.78**	-o.46	-36.30**	-36.22**
P_2xP_3	-3.92**	-0.69	-4.09**	-26.22**	-45.11**
P_2xP_4	-5.70**	-4.10**	-4.55**	-21.19**	-35.56**
P_2xP_5	-8.90**	-8.19**	-2.73**	-14.96**	-31.11**
P_2xP_6	-4.27**	-4.10**	-0.23	-11.11**	-25.56**
P_3xP_4	-5.34**	-5.12**	-4.55**	-13.48**	-25.11**
P_3xP_5	-1.78**	-5.12**	-1.14**	-11.70**	-28.67**
P_3xP_6	-2.49**	-3.07**	-0.91*	-12.59**	-30.00**
P_4xP_5	-5.34**	-5.12**	-0.91*	-17.19**	-32.44**
P_4xP_6	-4.27**	-3.42**	-2.05**	-26.07**	-40.44**
P_5xP_6	-6.41**	-5.12**	-2.05**	-7.70**	-28.22**
Mean	-5.39	-4.80	-2.24	-18.30	-31.56
Std error	0.48	0.44	0.37	1.90	1.52
Minimum	-8.90	-8.19	-4.55	-36.30	-45.11
Maximum	-.78	-0.69	-0.23	-7.70	-23.11
CD(0.05)	1.03	0.93	0.80	4.27	3.25
CD(0.01)	1.42	1.29	1.12	5.93	4.52

*,** indicate significant at 5% and 1% level, respectively.

Conclusion

From the study, it may be concluded that the parents P_5 & P_6 were good combiner for yield and the parents P_1 & P_2 were good combiner for both dwarf and earliness. The two hybrids (P_3 x P_6 & P_4 x P_5) showed good performance for yield and other desirable characters. However, for confirmation, these two hybrids would be further evaluated in wider agro-ecological zones of Bangladesh.

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SCREENING OF MUNGBEAN (*Vigna radiata* L. Wilczek) GENOTYPES UNDER NUTRIENT STRESS IN SOIL

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M. M. BAZZAZ[4] AND M. S. A. KHAN[5]

Abstract

A pot experiment was conducted at the Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur during *kharif* season of 2010 to investigate the genetic divergence of some mungbean genotypes under nutrient stress condition using Mahalanobis' statistic (D^2) and principal component analysis. Analysis of variance showed significant difference for all the characters. Results of multivariate analysis revealed that 200 mungbean genotypes formed five clusters at nutrient stress condition where cluster II had the maximum genotypes (83) followed by cluster I (65), cluster III (30), cluster IV (9) and then cluster V (13). The highest intra-cluster distance was observed between cluster IV containing lowest 9 genotype and cluster V containing 13 genotypes. The highest inter-cluster distance was observed between cluster IV and III and lowest was observed between cluster V and Cluster I. Cluster III had the highest cluster mean for total dry matter, root dry mass, pods per plant, seeds per pod, 1000 seed weight and seed yield. Considering cluster distance and other agronomic performance the genotypes IPSA 1, IPSA 12, IPSA 5 and others genotypes from cluster III may be considered for better performance under nutrient stress condition.

Keywords: Mungbean, Nutrient stress, Cluster analysis, Seed yield.

Introduction

Mungbean (*Vigna radiata* L.) Wilczek) is an important grain legume grown in the tropical and subtropical regions of the world. It is one of the important sources of protein for both man and domestic animals. Another important feature of mungbean is its ability to fix atmospheric nitrogen in symbiosis with nodule forming rhizobium bacteria. Nutrient stress soil was defined soil contains nutrient below the critical level (FRG, 2005).

Mungbean is a short duration crop and very effective for intensive cropping system. Mungbean can be easily fitted in mungbean – T. aus – T. aman (southern region), mungbean - aman -wheat (north western region) and mungbean - aus -

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aman - potato (northern region) cropping systems without considering the fertility status of the soil (Haque *et el.*, 2001). One of the reasons of ignoring soil fertility in mungbean cultivation is its ability to fixation of atmospheric nitrogen (Hardarson and Danso, 1993). However, amount of nitrogen fixed by microbial association varies over different soil types and environmental factors, which might not be sufficient for proper growth and yield formation of mungbean. Most of the researchers evaluated mungbean genotype in optimum soil condition but they ignored low nutrient environments for evaluation of mungbean (Anjum *et al.*, 2006; Akbari *et al.*, 2008; Malik *et al.*, 2002). There exists ample scope to evaluated mungbean genotypes that have inherent capability for producing higher yield under nutrient poor conditions.

The seed yield of mungbean however, remains extremely low in Bangladesh compared with the yield potential (Hossain *et al*., 2009). One of the major limitations of mungbean productivity is soil fertility as many soils of the country are inherently poor in plant nutrients. This is specially true for char areas where sand particles dominate in soil texture. Under the limitation of soil fertility seed yield of mungbean may be increased either by genetic improvement or by identifying genotypes that are efficient in nutrient accumulation in plants. Therefore, the present study was undertaken with a view to identifying potential ones by screening a large number of mungbean genotypes under nutrient stress soil.

Materials and Method

A pot experiment was carried out at Bangbandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur during the kharif season (August – November) of 2010. The soil used in this experiment belonged to Collected to charland area. Four samples were collected from bulk volume to determine physical and chemical properties of soil. Textural classes of the soil sample were determined by hydrometer method. Organic carbon of the soil sample was determined by wet digestion method to estimate organic matter. Total nitrogen was determined by Kjeldahl method and available phosphorus was determined by percloric digestion method and other nutrient elements were measured as per respective method. Physical and chemical properties of soil are presented in Table 1.

The experimental pots were filled with 12 kg of soil. No fertilizer was used in the pots to maintain soil as nutrient stress environment. A total of 200 mungbean genotypes were collected from Department of Agronomy, BSMRAU and seeds sown on 31 August, 2010. The experiment was laid out in complete randomized design with four replications. Initially four plants were grown up to measure the physiological characters. One pot was considered as one replication and finally one plant was considered. All agronomic practices like weeding, irrigation and

mulching were done as and when necessary. Insect pest was controlled by spraying admire @ 0.5 ml litre^{-1} of water during the entire growth period of the crop. The crop was harvested at full maturity. Harvesting was done for pod picking by hand twice one on 31 October and another on 13 November in 2010. In Last harvest dry matter partitioning was measured. Data on plant height, growth, nodule number, yield and yield components of mungbean genotypes were recorded. Plant height was considered as the height from ground level to the longest leaf of the plant. For dry matter determination shoots and roots were oven dried at 70^0 C to constant weight and the dry weights were taken. Yield and yield contributing characters viz. number of pods per plant, seeds per pod and 1000 seeds weight and seed yield per plant were recorded.

Table 1. Physical and chemical properties of the experimental soil before sowing

Soil properties	Present value	Critical limit
Sand (%)	62.23	-
Silt (%)	21.77	-
Clay (%)	16.00	-
Soil pH	6.90	-
Textural class	Sandy loam	-
Rhizobium/g soil	4.55×10^8	-
Total N (%)	0.05	0.10
Available P (ppm)	0.16	8.0 0
Exchangeable K (meq/100g soil)	0.85	0.08
Available S (ppm)	7.00	8.00
Available B (ppm)	0.15	0.16
Available Zn (ppm)	0.25	0.50
Exchangeable Ca (meq/100g soil)	14.83	2.00
Exchangeable Mg (meq/100g soil)	1.76	0.50
CEC meg/100g soil	6.904	3-7.5
Organic matter (%)	0.536	-

Tocher's method was followed to determine the group constellation. Canonical variate analysis was performed as per Rao (1964) to confirm the results of cluster D^2 analysis. Mean data for each character was subjected to both univariate and multivariate analysis. Univariate analysis of the individual characters (analysis of variance) was done by computer using MSTAT-C program. Genetic diversity of 200 mungbean genotypes at nutrient stress was analyzed using GENSTAT 5.13 soft were program.

Results and Discussion

The mungbean genotypes showed significant variation for all the morphological characters. Eigen values of 8 principal components are presented in Table 2. These results revealed that first axes accounted for 56.27% of the total variation among the genotypes which 8 of these eigen values accounted for 100%. The first two axes of eight Eigen values above the unity accounted for 78.34% of the total variation. These findings are in agreement with Azam (2012).

Table 2. Eigen values and percentage of variation for corresponding 8 component characters in 200 mungbean genotypes

Sl. No.	Principal component axis	Eigen values	Percentage of total variation	Cumulative percentage of variation
1	Plant height (cm)	6.0723	56.27	56.27
2	Total dry matter (g plant^{-1})	1.0231	22.07	78.34
3	Root dry matter (g plant^{-1})	0.7021	9.07	87.41
4	Nodule number plant^{-1}	0.6107	5.07	92.48
5	pods plant^{-1}	0.4261	4.21	96.69
6	Seeds pod^{-1}	0.231	2.07	98.76
7	1000 seeds weight (g)	0.0724	0.90	99.74
8	Seed yield (g plant^{-1})	0.0021	0.26	100.00

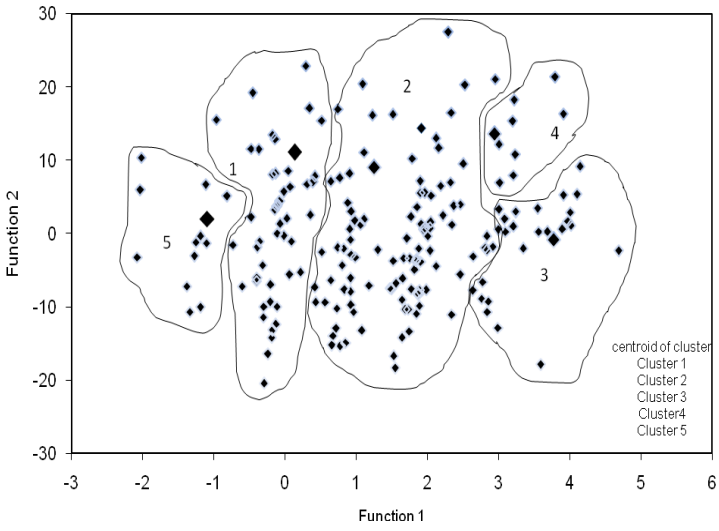

Fig. 1. Scatter distribution of 200 mungbean genotypes based on their principal component scores superimposed with clusters.

Based on the principal component I and II obtained from the principal component analysis a two dimensional scatter diagram (Z_1 –Z_2) was constructed using component score I {Z_1(Function 1)} as X axis and II {Z_2 (Function 2)} as Y axis (Fig. 1). The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that considerable diversity exists among the genotypes.

The inter genotypic distance were used in computation of intra-cluster distances from distance matrix of PCO according to Singh and Choudhari (2001). The intra-cluster distances were not always proportional to the number of the genotypes in the cluster (Table 3). In present study the cluster II composed of the largest number (83) of genotypes but their intra-cluster distances were not the highest. The statistical distances represent the index of genetic diversity among the clusters (Biswas *et al.*, 2014). The intra-cluster distances ranged from 0.000 to 26.630. Intra-cluster distances in all clusters were more or less low which indicated that genotypes within the same cluster were closely related. These findings are in conformity with the findings of Datta and Mukherjee (2004), Singh *et al.* (2005), Marker and Krupaker (2009). Cluster analysis has been used to study the adaptation of genotype to environment by simplifying the pattern responses and by dividing genotypes and environments into more homogeneous categories (Crossa, 1990; Piepho, 1998). It may be said that cluster and scattered distribution mainly classify and group a large number of germplasm into a number of homogenous group.

Table 3. Average inter-cluster and intra cluster (bold) distance (D^2) of 200 mungbean genotypes obtained by canonical variate analysis

Cluster	I	II	III	IV	V
I	**14.490**				
II	13.506	**18.759**			
III	26.06	26.072	**26.110**		
IV	60.514	46.715	57.676	**26.630**	
V	12.23	20.12	23.24	17.36	**0.00**

Canonical variate analysis was done to compute the inter-cluster Mahalanobis D^2 values. The intra and inter-cluster distance (D^2) are presented in Table 3. Results indicate that the highest inter-cluster distances between cluster I and IV (60.514) followed by III and IV (57.676). The higher inter-cluster distances between these clusters indicated to the wide spectrum of variability in the population. However, the highest intra-cluster distance was observed between clusters IV and I which indicated that the genotypes in these clusters were more diverged than those of the others. The clusters V and I (12.23) suggest that a close relationship exist among the genotypes within the clusters.

The application of non hierarchical clustering using 200 mungbean genotypes were grouped into five different clusters. Cluster II had maximum 83 number of genotypes (Table 4). The clustering pattern of the genotypes under this study revealed that genotypes of the same clustered are not collected from the same district or country. These results are in agreement with the findings of Sharma *et al.* (1998), Goel *et al.* (2005) and Sharma and Pawar (2007).

Table 4. Distribution of 200 mungbean genotypes into different clusters,

Cluster	Total no. of genotypes in the clusters	Genotypes included in different clusters
I	65	IPSA 7, IPSA, 10, IPSA 14, IPSA 16, IPSA 19, IPSA 24, CO-24, ACC12810002, ACC12810008, ACC12810009, ACC12860017, ACC12890032, ACC12890043, ACC12890044, ACC12890053, ACC12890054, ACC12890055, ACC12890078, ACC12890083, ACC12890085, ACC12890087, ACC12910105, ACC12910110, ACC12910111, ACC12910112, V01372AG, V01539AG, V01547AG, V01551AG, V01586AG, V01613AG, V01693BG, V01697BG, V01902BG, V01973AG, V01991AG, V01998BG, V01999BG, V01643AG, V01656BG, V01659BG, V0 660BG, V01663AG, V01665AG, V01668AG, GK1, GK2, GK3, GK5, GK6, GK8, GK9, GK12, GK13, GK15, GK30, GK36, GK37, GK48, GK49, GK50, GK61, IPK1040-94, PDM-54, Dinajpur local
II	83	IPSA 2, IPSA 3, IPSA 8, IPSA 13, IPSA 18, ACC12810004, ACC12810006, ACC12810010, ACC12840014, ACC12870021, ACC12880028, ACC12890056, ACC12890071, ACC12890080, ACC12900102, ACC12910106, V01372BG, V01371AG, V01396AG, V01549AG, V01575AG, V0 1577AG, V0 1597BG, V01598BG, V01621BG, V01639BG, V0 1699BG, V01782AG, V01900AG, V01959BG, , V01995BG, V02008AG, V02103AG, V02096AG, V02097AG, V01689BG, V01642BG, V01657BG, V01658BG, V01661BG, V01662BG, V01668BG, V0 1669AG, V01674BG, V01689AG, V02000AG, V02006AG, V02007BG, V02073AG, GK 4, GK 7, GK 10, GK 14, GK 16, GK 17, GK 18, GK 20, , GK 28, GK 29, GK 32, GK 33, GK 34, GK 38, GK 39, GK 40, GK 42, GK 43, GK 46, GK 47, GK 51, GK 52, GK 53, GK 55, GK 56, GK 57, GK 58, GK 59, GK 60, , GK 64, IPK2558-97, SML-134, ML-267, ML-613, BUmug 2, Barisal local, BARI Mung-6
III	30	IPSA 1, IPSA 4, IPSA 5, IPSA 6, IPSA 9, IPSA 11, IPSA 12, IPSA15, IPSA 20, IPSA21, IPSA 22, ACC12810001, ACC12870020, ACC12880023, ACC12880024, ACC12890073, ACC12890079, ACC12890081, ACC12890098, ACC12890102, V0 1396BG, V01548AG,

Table 4. Cont'd.

Cluster	Total no. of genotypes in the clusters	Genotypes included in different clusters
		V01654AG, GK 11, GK 35, GK 65, PDM-11, SML-12, NM-94, Sonamung
IV	9	V01983BG, V01986BG, V01994BG GK16, GK21, GK22, GK24 GK 27, Bina mung-5
V	13	IPSA23, ACC12880027, ACC12890084, V01995AG V01982AG, GK17, GK18, GK20 GK23, GK63, IPK103894, PUSA9092, BUmug 4

Composition of different clusters with their corresponding genotypes and collection site included in each cluster are presented in Table 4. Results of the different multivariate techniques were superimposed with the clusters. The clustering pattern obtained was coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results obtained through PCA were established by non-hierarchical clustering

An attempt was made to characterize the individual genotypes in respect of their mean values for different characters with a view to getting the idea weather the genotype having similar characteristics could be disseminates. The intra-cluster mean values for all the 8 characters along with the making of the highest and lowest for each of the cluster are presented in Table 5. The data revealed that different clusters exhibited different mean values for almost all the characters. Plant height had the highest intra cluster means in cluster I followed by Cluster V. The lowest intra cluster means for this trait was observed in cluster IV. The highest total dry matter, root dry mass, nodule number, pods per plant, seed per pod, 1000 seed weight and seed yield was found in cluster III followed by cluster II and the lowest mean value (29.35) was observed for 1000 seed weight in cluster IV.

Canonical variate analysis is an alternative multivariate method that can be used to classify individual genotypes or environments of pre known classes into two or more alternative categories on the basis of a set of measurements (Tabachnick and Fidell, 1989; Afifi and Clark, 1996). Canonical variate analysis revealed that in canonical vector I, the major axes of differentiation, plant height, pods per plant and total dry matter were the important characters responsible for the genetic divergence (Table 6). In vector II, plant height, total dry matter, nodule number and pods per plant had the important role (positive) in both the vectors. Contribution of characters towards the divergence obtained from canonical variate analysis is presented in Table 5. In this methods vector was calculated to represent the varieties in the graphical form (Rao, 1964). The absolute magnitude of the coefficients in the first two canonical vectors also reflects to a great extent,

the importance of the characters for primary and secondary differentiation. The character which gives high absolute magnitude for vector II, is considered to be responsible for secondary differentiations. Likewise, the characters which give higher absolute magnitude for vector I is considered to be responsible for primary differentiation. If the same characters give equal magnitude for both the vectors then the character is considered responsible for primary as well as secondary differentiation.

Table 5. Cluster means of eight discriminating variables mungbean genotypes

Characters	Cluster				
	I	II	III	IV	V
Plant height (cm)	59.65H	52.49	57.68	52.25L	59.35
Total dry matter (g plant^{-1})	12.28	13..21	15.91H	9.56L	10.24
Root dry mass (g plant^{-1})	1.15	1.11	1.54H	1.05L	1.16
Nodule number plant^{-1}	17.03	17.30	20.39H	13.0L	14.00
Pods per plant	14.73	19.92	25.19H	13.01L	14.25
Seeds per pod	9.39	9.15	10.45H	10.22	8.41L
1000 seeds weight(g)	30.59	30.65	30.77H	29.35L	30.37
Seed yield (g plant^{-1})	4.89	5.07	9.58H	3.89L	4.11

Table 6. Latent vectors associated with the first two components for eight characters of mungbean

SL No.	Characters	Vector I	Vector II
1.	Plant height (cm)	0.02612	0.90117
2.	Total dry matter per plant	0.00840	-0.00157
3.	Root dry matter per plant	-0.00012	0.00928
4.	Nodule number per plant	-0.01827	0.06667
5.	Pods per plant	0.01822	0.37847
6.	Seeds per pod	-0.00257	0.03077
7.	1000 seeds weight (g)	-0.00237	-0.00250
8.	Seed yield (g plant^{-1})	0.01242	-0.14027

In vector I (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were total dry matter (0.0084) and pods per plant (0.0182). In vector II (Z_2), the second axis of differentiation, root dry matter, nodule number and seeds per pod were important because all these character had positive value. Plant height and pods per plant had positive values in both the vectors, which indicated that they were the important component characters having higher contribution to the genetic divergence among the mungbean genotypes and tolerant to nutrient stress condition studied.

Conclusion

The results indicated that the plant height and the number of pods per plant had maximum contribution to the genetic divergence among the genotypes. Considering the cluster distance, cluster mean and other agronomic performances the genotypes IPSA 1, IPSA 5, IPSA 12 and other genotypes from cluster III might be considered as better for nutrient stress soil.

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