

**GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT
ANALYSIS IN CUCUMBER (*Cucumis sativus* L.)**

BY

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CERTIFICATE

This is to certify that thesis entitled, "*Genetic diversity, correlation and path co-efficient analysis in Cucumber (Cucumis sativus L.)*" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by *Sultana Afroz*, Registration No. 08-03215 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

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Dated: June, 2010
Place: Dhaka, Bangladesh

**DEDICATED
TO
MY BELOVED PARENTS**



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ABSTRACT

Twenty two genotypes of cucumber (*Cucumis sativus* L.) were studied increase line space at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during March 2010 to October 2010. The objectives of the study were to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. There was a great deal of significant variation for all the characters among the genotypes. High genotypic co-efficient of variation (GCV) was observed for yield per plant, number of male flower and number of fruits per plants whereas low genotypic co-efficient of variation (GCV) was observed for weight of fruit and breadth of fruit. In all cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in percent of mean was observed in days to first female flowering which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for yield per plant and number of fruits per plants indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Correlation studies revealed that highest significant association of yield per plant with number of female flower, number of fruit per plant followed by length of fruit at genotypic level. Path co-efficient analysis revealed maximum direct contribution towards yield per plant with leaf breadth, number of female flower followed by fruit weight. Highest intra-cluster distance was found in cluster III and lowest in cluster IV. Among four clusters, the highest inter-cluster distance was observed between cluster II and cluster III and lowest between cluster I and cluster IV. Considering all the characters the G₁₄ (Serena), G₀₇ (BD-4305), G₀₆ (BD-4256), G₁₇ (CU937F1), G₀₉ (BD-4309) were selected for future breeding programme.

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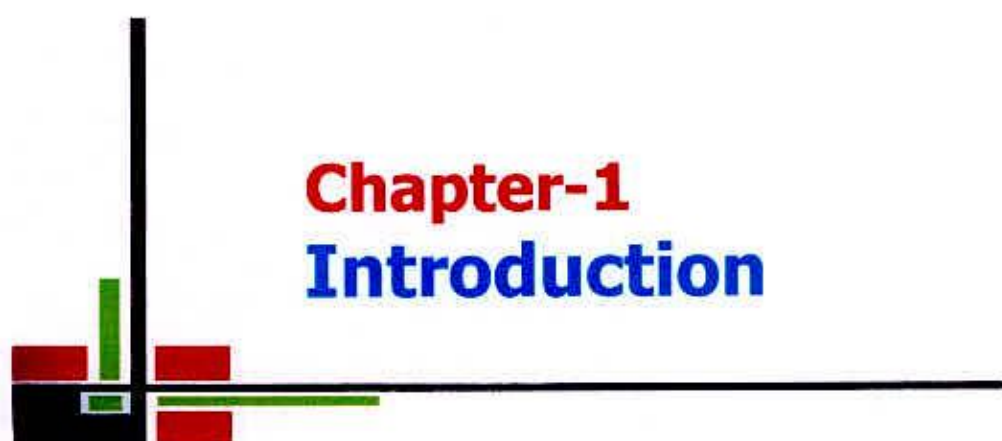
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LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
<i>et al.</i>	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
g	Gram
h^2_b	Heritability in broad sense
J.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate



Chapter-1

Introduction

CHAPTER I

INTRODUCTION

Cucumber (*Cucumis sativus* L.) locally known as Shosha, is an important home garden vegetable and widely cultivated as popular winter vegetable in Bangladesh. Cucumber belongs to the family Cucurbitaceae having chromosome number, $2n=14$, under the order cucurbitales, class magnoliopsida (Bose and Som, 1986). Cucumber is one of the cultivated annual monoecious species, which comprises 90 genera and 750 species (Sitterly, 1972). Yamaguchi (1983) reported that there are about 40 species in the genus *Cucumis*, while Nayer and More (1998) postulated that *Cucumis* genus comprises 30 species. Apparently cucumbers have originated in the foothills of the Himalayan Mountains, just north of the Bay of Bengal, the area which is now primarily occupied by Bangladesh. While there does not seem to be any wild cucumbers present in the area today, scientists have identified a small bitter fruit of the squash family, which is thought to have brought forth the cucumber.

Cucumber is a vigorous, annual, climbing vine and a lush appearance. The vine is branched and climbs by means of tendrils along the stem. Cucumbers (*Cucumis sativus* L.) are botanically categorized as berries, which are available in many different sizes shapes and colors. They range from thick, stubby little fruits (10 - 12 cm long) to Dutch greenhouse varieties (of up to 50 cm long). The most popular variety is the long smooth salad cucumber which has a smooth, dark-green skin. It's little brother, the "gherkin" is actually a cucumber that has been harvested when little and pickled in brine. The true gherkin is a different species (*Cucumis anguria*), which is primarily grown in the West Indies.

Older cook books recommend making cucumbers more digestible by salting them and discarding the water. However, it has since been discovered that the healing properties of the cucumber is contained in its juice. Deficiency diseases, such as scorbut are easily cured by cucumbers, due to its high content of Vitamin C. Eaten as part of the evening meal, cucumbers promote sleep. On hot summer days they make a very refreshing snack



and are easily taken along. Besides traces of calcium, copper and magnesium, cucumbers contain substantial amounts of potassium, iron and phosphorous, but also proteins as well as the vitamins A, B1 and C. It has 2.5 percent carbohydrate, 0.4% protein, 0.1% fat & 0.4% fiber. Cucumber prevents constipation, jaundice & indigestion.

Cucumber is one of the most popular fruit vegetables and salad crops in Bangladesh. It is grown round the year and seems to be a day neutral crop. There are about 1.02 million hectare of land under cultivation and production is about 1.61 million tons (anon, 2007) with high price potential round the year making cucumber a high value crop. The average yield works out to about 1200 to 1400kg per hectare or 80-120q/ha. Storage at temperature of 10°C and a relative humidity of 85 percent keep the fruits well for 10 to 14 days. The production of summer vegetables is about one-fourth of the winter vegetables. As a result there is an acute shortage of vegetables during the summer which leads to chronic malnutrition in Bangladesh.

There are several cultivars of cucumber which are traditionally cultivated in our country but the present production rate and the available land for its cultivation is not sufficient scope with the requirement of our increasing population. So emphasis should be given to increase its per unit production by developing high yielding varieties with quality fruits. But in our country there is no recommended variety although cucumber is cultivated throughout the year. Farmers cultivate the cucumber from their own seeds. Sometimes they fail to produce a good crop due to wrong selection of cultivars. Therefore, it is necessary to find out some superior varieties of cucumber for commercial cultivation in our country.

Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Robinson *et al.*, 1949). Crop improvement depends upon the magnitude of genetic variability and extent to which the desirable characters are heritable. The total variability can be partitioned into heritable and nonheritable

components with the help of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance. Heritable variation can be effectively studied in conjunction with genetic advance. High heritability alone is not enough to make efficient selection in segregating generation, unless the information is accompanied for substantial amount of genetic advance (Johnson *et al.*, 1955).

Hybridization is one of the major tools for achieving variability aiming at the improvement of a crop. Before hybridization genetic diversity of the existing materials or entries needs to be known. Information about genetic diversity in available germplasm is important for the optimal design of any breeding program. This helps to choose desirable parents for establishing new breeding population. Besides, better knowledge on genetic diversity could help to sustain long term selection gain (Chowdhury *et al.*, 2002).

The knowledge of association between yield and its contributing traits is of great value in planning a breeding programme. Thus determination of correlation among the characters is a matter of considerable importance in selection of correlated response. But it does not give the exact position of the relative importance of direct and indirect effects of various yield attributes. Path analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various characters on yield or any other attribute. According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the contribution of different characters towards seed yield.

Considering the availability of genetic variability, its scope of yield improvement and export potential, the present investigation was undertaken with the following objectives:

- ❖ To assess the genetic diversity among the genotypes,
- ❖ To know the association of traits with yield and its contributing traits,
- ❖ To know the yield potentiality of genotypes and
- ❖ To screen out the suitable parental groups which are likely to provide superior segregates on hybridization



Chapter-2

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Cucumber (*Cucumis sativus* L.) is an important vegetable cultivated in Bangladesh, but a few works have been done for the improvement of this crop in Bangladesh and other countries in the world. Research effort on the variability of its genetic resources, diversity on genetic and molecular level, correlation, path co-efficient analysis, heritability and genetic advance seems to be meager. However, information available in these aspects of Cucumber and some other cucurbit crops have been reviewed and presented in this section.

2.1 Variability, Heritability and Genetic Advance

Yadav *et al.* (2009) conducted an experiment of 20 cucumber genotypes to study about genetic variability, heritability and genetic advance for different characters. The study indicated existence of considerable amount of genetic variability for all the traits except cavity of fruit at edible stage. The maximum phenotypic and genotypic coefficient (PCV and GCV) was observed for number of days to first female flower anthesis. High estimates of heritability (broad sense), genotypic coefficient of variation (GCV) and genetic advance were observed for number of fruit per plant, fruit length and fruit weight.

Sharma *et al.* (2000) evaluated ten cucumber lines and testers under different environmental conditions and reported those days to first female flower, nodal position of fruits per plant, marketable yield per plant, fruit length and fruit diameter had wide range of variation.

Chen *et al.* (2002) evaluated two cultivars of cucumber for preliminary characterization of new species. From preliminary evaluation, they found that wild cultivars (*Cucumis hystrix* Chandr) were disease resistant and fruit morphology of the F₁ plants differed during the growing season.



Islam *et al.* (1993) reported wide variability in male (41-64 days) female (47-81 days) flowers anthesis in cucumber. The heritability and genetic advance for male flower were 95.55 and 36.21 for female flower were 98.36 and 50.74 respectively. He also revealed high GCV (36.93) and PVC (38.08).

Prosad and Singh (1992) found comparative narrow ranges for male and female flower appearance which ranged from 31-47 days for male and 38-55 days for female among the 31 cucumber genotypes. Prosad and Singh also found highly significant variations in cucumber ranges from 123.3-343.3g along with low heritability (33%) and genetic advance (1.76) among the 31 cucumber genotypes.

Shifriss and Galun (1956) found that the number nodes to the first pistillate flower are far measure of sex tendency in cucumber. The lower the node numbers the higher the female tendency.

In case of seed germination there was a wide range of variation. Robinson and Decker-Walkers (1997) reported that cucumber germinated from 2 days to 2 weeks. Rahman (1988) noted that in pointed gourd it took 2 to 3 weeks for sprouting and 3 months for flowering or fruiting after planting of vine or roots.

Rahman *et al.* (1991) reported that male flower were earlier than female flower in several genotypes of bottle gourd, ribbed gourd and sweet gourd. They reported significant variations for that character among the genotypes of bitter gourd, sweet gourd, ribbed gourd and bottle gourd. Significant variation for fruit length and diameter were also observed. They also reported that bitter gourd, sweet gourd, ribbed gourd and bottle gourd genotypes differed significantly for fruit breadth and weight per fruit.

Chowdhury and Sharma (2002) studied genetic variation, heritability, genetic advance and correlation for yield and yield components (vine length, number of nodes, node on which the first flower appeared, number of fruits per plant, fruit length, fruit girth and fruit weight) in 12 *Luffa acutangula* cultivars. The genetic co-efficient of variation (GCV) was higher than the phenotypic co-efficient variation (PCV) for all the characters. High values of variability, PCV, GCV and

genetic advance recorded for vine length, yield per hectare and fruit weight indicating that these characters were controlled by additive gene effects. The correlation co-efficient revealed that yield per hectare could be improved through selection for higher fruit number per plant, fruit length and girth and individual fruit weight.

Gaffar (2008) conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. Among the characters the highest GCV recorded for yield per plant (63.90) followed by top fruit perimeter (46.60) and average fruit weight (39.52). Genotypes included in cluster I were suitable for yield per plant (6.55), cluster III for having the highest mean value for inter node length (17.62), cluster V for leaf length (30.43), leaf breadth (24.65), petiole length (13.28), days to first male flower (103.28), days to first female flower (107.80) and other characters.

Hossain (1996) conducted an experiment on floral biology of ridge gourd at the experimental farm of IPSA (Institute of Post Graduate Studies). Male, female and hermaphrodite flower buds appeared 29-38 days after seeding. The male flower buds developed earlier and in lower nodes than the female and hermaphrodite ones. The first male, female/hermaphrodite flowers were produced an average in the 10th to 21st node.

Mathew and Khader (1999) conducted an experiment on genetic studies in snake gourd (*Trichosanthen anguina*) and observed the genetic variability and heritability of 12 traits in 34 snake gourd in Kerela, India and reported that the genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were almost equal for all characters. The highest GCV and PCV were recorded for mean fruit weight, seed per fruit, fruit yield per plant and fruit length. High heritability was observed for mean fruit weight, seeds per fruit, fruit length, days to first male flower and fruit yield per plant.

Abusaleha and Dutta (1990) carried out a study with 65 genetic stocks to assess the genetic variation and heritability in ridge gourd. Significant variability was

observed for all the characters at phenotypic as well as genotypic level with a very wide range of values.

Miah *et al.* (2000) studied 30 genotypes of bitter gourd and observed the highest genotypic as well as phenotypic co-efficient of variation were found for fruit length followed by days to female flowering, fruit yield per plant, fruit weight and nodes per vine.

Kumar *et al.* (2007) conducted a field experiment with twenty diverse genotypes of bottle gourd in randomized block design with three replications. Depending upon the variability, heritability and genetic advance estimates, it could be predicted that improvement by direct selection was possible in bottle gourd for traits like number of branches per vine, vine length, nodes no. of first male flower, nodes number of first female flower, length of edible fruit, number of fruit per vine, fruit weight, 100-seed weight and fruit yield per vine.

Pandit *et al.* (2005) evaluated fifteen genotypes of bottle gourd (*Lagenaria siceraria* Molina. Standl) during the autumn-winter season of 2003-04 at BCKV, West Bengal, India to study the genetic variability, heritability and potential for screening suitable genotypes for future improvement programmes. The genotypes were collected from major growing areas of South-West Bengal. There was considerable variability in all traits except fruit/plant. The moderate GCV and GA in fruit length and fruit weight indicate the probable likelihood of additive gene action. Thus, improving these characters should be effective and rewarding during selection. Promising inbreds for yield/plant were BCBG-7, 17, 19 and 33.

Rahman *et al.* (1986) studied variability, correlation and path coefficients in four lines of bottle gourd. Genotypic and phenotypic variability were high for fruit length and number of branches per plant, but very low for number of fruits per plant and length of main vine. Heritability (broad sense) and genetic advance in percentage of mean were high for fruit length, fruit diameter and fruit weight per plant.

Masud *et al.* (2006) conducted a field experiment with seven inbred lines and their twenty-one hybrids of bottle gourd. Result showed significant variation in seven characters of the twenty eight populations. Variabilities were high in all seven characters indicating the possibilities of improvement through selection. Specific combining ability variance were significant for all characters while general combining estimates were significant for days to anthesis, fruit length, fruit diameter and yield per plant which indicated the presence of dominance for all the characters but additivity is for only few characters. Parent-two showed good GCA for earliness and fruit length, Parent-five showed good GCA for fruit length only and parent-seven showed good GCA for fruit diameter and fruit yield per plant. The cross involving parent-three and parent-five, which is the best for earliness, fruit length (53.5%) and fruit yield per plant (106.8%).

Quamruzzaman *et al.* (2009) studied heterosis in bottle gourd in a set of 13 F_1 with 26 parents. Results indicated highly significant differences for all the characters among the materials studied. Heterosis was higher for yield per plant, number of fruits per plant and individual fruit weight, medium in fruit length and fruit diameter, and lower in days to 1st harvest. Hybrids (F_1) 10 x 17 and 19 x 26 manifested highest heterosis over midparent (73.1%) and better parent (61.8%), respectively, for yield per plant.

Saha *et al.* (1992) studied the variability, character association and path analysis of pumpkin and reported that phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). High genotypic variance and phenotypic variance were found for fruit length (30.34 and 31.76), fruit weight (39.55 and 41.00) and low for fruit diameter (8.87 and 10.23) among the pumpkin genotypes. They also reported high heritability estimate, for both length (91.27) and diameter (75.07) of fruits indicating effectiveness of selection based on good phenotypic performances in pumpkin.

Banik (2003) conducted an experiment on variability and genetic advance of 26 genotypes of snake gourd with respect of 15 quantitative yield contributing



characters and found significant difference among the characters like vine length at harvest (2.197 to 3.87 m), number of primary branches (5.23 to 11.88), days to first male flowering (41.67 to 68.67 days), days to first female flowering (48.67 to 71.33 days), node number of first male flower (6.33 to 17.67 days), fruit length (20.67 to 71.17cm), seeds per fruit (39.03 to 69.50). Banik also found that significant differences in first female flower, node number (mean value 19.28) and fruits per plant. The highest phenotypic co-efficient of variation was observed for fruiting node on main vine, fruit yield per plant, fruit length and first male flower node. The PCV was lowest for days to maturity, 100 seed weight and days to first male flower opening. The GCV along with heritability was high for the above characters. High heritability coupled with high genetic advance was noticed for fruit yield per plant (GCV and PCV 30.75 and 30.96; h^2b 98.64%), fruit length (GCV and PCV 29.92 and 30.04; h^2b 99.19%) and first female flower node number (GCV and PCV 25.87 and 26.59; h^2b 94.63%) and number of fruits per plant (GCV and PCV 19.82 and 20.59; h^2b 92.67%).

Doijode and Sulladmath (1986) found high GCV and PCV (30.2 and 36.4), high heritability (h^2b) with high genetic advance for average fruit in pumpkin. Narrow difference between GCV and PCV observed for fruit weight in bitter gourd indicating less environmental influence on this character. Significant difference was also found among bitter gourd genotypes for seeds per fruit (Mannan, 1992).

Sharma and Dhankar (1990) reported that almost similar estimates of GCV and PCV (13.54 and 14.00) for days to first female flower opening in bottle gourd. They also observed high heritability (93.47%) with considerably high genetic advance for days to flowering in bottle gourd. In watermelon days to first female flower opening ranged from 37.17 to 61.72 days and the PCV and GCV were 19.10 and 19.91, respectively (Rajendran, 1985).

Mangal *et al.* (1981) noticed that in bitter gourd significant variation for fruit length and diameter present and high heritability in bitter gourd for vine length. Mondal *et al.* (1989) studied the genetic variability of 31 watermelon genotypes and observed

a wide range of variability for days to first fruit harvest, fruit length, fruit diameter, number of fruits per plant and fruit yield per plant.

Rumaran *et al.* (1997) conducted 30 pumpkin genotypes in a field trial and reported that genotypic co-efficient of variation was smaller than phenotypic co-efficient of variation for most of the traits studied. However, GCV was high for mean fruit weight, number of fruits per plant, number of seeds per fruit, yield per plant and fruit, total soluble solids content. High heritability coupled with high genetic advance were observed for vine length, mean fruit weight, number of fruits per plant, number of seeds per fruit, fruit yield per plant and total soluble solids content of fruits. Islam (1993) reported that male flowering was earlier than female flowering in several genotypes of bottle gourd.

Varghese (1991) reported an experiment on the variability among 48 snake gourd genotypes in respect of different yield contributing characters and found significant differences among the characters. Main vine length varied from 3.035 to 7.85 m with high heritability (97.0%). In case of number of branches per vine, heritability was 91.0%. Moderate GCV and PCV in fruit length and breadth (32.15 and 32.51; 20.26 and 21.23) was also observed in snake gourd germplasms. Narrow differences between GCV and PCV in fruit weight with high heritability (h^2b) were also observed. GCV and PCV for yield per plant were 30.0 and 31.33 respectively. 100 seed weight varied from 20.0 to 41.0 g with high heritability 97.8% in snake gourd.

Kabir (2007) conducted an experiment on variability and estimation of genetic parameter, correlation, path analysis and genetic diversity of 24 accessions of pointed gourd with respect of different parameter such as days to flower, fruit length, fruit breadth, single fruit weight, pulp seed ratio, and number of fruits per plant, weight of fruit per plant and yield of fruit. The accession PG020 showed the highest performance in weight of fruits per plant, single fruit weight and yield. The highest genotypic and phenotypic co-efficients were recorded in the parameter number of fruits per plant (5415.55% and 5623.67%) and second highest was

recorded from yield of fruits ton per hectare (410.30% and 410.98%). However, days require to first flowering (49.86% and 52.41%), fruit length (7.4% and 7.42%), fruit breadth (23.56% and 26.79%), single fruit weight (172.27% and 173.28%), and weight of fruit per plant (161.87% and 162.85%) recorded moderate GCV and PCV. Correlation coefficient indicated that fruit yield per plant was highly significant and there was a positive association with weight of fruit per plant, number of fruits per plant and single fruit weight. Path analysis indicates fruit breadth, number of fruits per plant and weight of fruits per plant directly contributed to the yield of pointed gourd accessions.

Singh *et al.* (2002) conducted an experiment on 80 ridge gourd genotypes to determine variability and heritability of nineteen yield contributing characters. High PCV and GCV were observed for node number for appearance of 1st male flower, male flowers per plant, sex ratio main axis and branches, fruit per plant, fruit weight, seeds per fruit, and yield per plant. The GCV and PCV values were almost equal for most of the characters studied. The broad sense heritability estimates were high for all the characters.

Swamy *et al.* (1984) also conducted an experiment on muskmelon and reported a wide range of variability among the genotypes for number of seeds per fruit.

2.2 Correlation Co-efficient

Singh *et al.* (2002) carried out 98 hybrids of cucumber derived from crosses involving fourteen male and seven female parents and found that fruit weight, fruit girth and fruit length had high correlations with fruit yield. Genotypic correlation co-efficient were higher than phenotypic co-efficient which indicated strong association among these traits.

Li *et al.* (1997) noted that number of fruits per plant, average fruit per plant, average fruit weight, fruiting rate and leaf area of cucumber genotypes were positively correlated to yield. Days to flowering and vine length were negatively correlated.

Abusaleha and Dutta (1989) found that the yield of cucumber is positively correlated with vine length ($r = 0.35$), branches per vine ($r = 0.29$), fruits per vine ($r = 0.48$), fruit length ($r = 0.60$) and fruit girth ($r = 0.43$). Days to first male and female flowering, nodal position female flower, percentage of misshapen fruits and non-marketable yield were negatively correlated with yield.

Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlations at the genotypic and phenotypic levels between yield per plant with number of fruits and female flowers per plant, fruit length and weight.

Ananthan and Pappoah (1997) reported that fruit number per vine and seed number per fruit were positively correlated with total yield while days to first female flowering, days to first male flowering, sex ratio, fruit girth, pulp thickness and total soluble solids content were negatively correlated with total yield in cucumber.

Rajput *et al.* (1991) also found significant positive correlation between number of fruit and yield and number of branches with yield. Harvest period also influenced the yield and its degree of association with increasing vine length. The variability, heritability and scope of improvement were studied by Abusaleha and Dutta (1990) in cucumber. They found positive and significant correlation between yield and nodal position of first female flower ($r = 0.225$) in cucumber.

Rastogi *et al.* (1990) conducted an experiment with 25 diverse cucumber cultivars and found that general genotypic correlation coefficient were higher than those related to phenotypic or environmental factors. However, both genotypic and phenotypic coefficient for fruits per plant gave positive and significant association with number of primary branches, number of female flower, fruit weight and number of fruits per plant. Female flower per plant showed highly significant positive correlations with number of primary branches, fruit yield and fruit per plant. Longer vine length increased the number of male flowers and produced heavier fruits.

Ananthan and Pappoah (1997) reported that fruit number per vine and seed number per fruit were positively correlated with total yield while days to first female flowering, days to first male flowering, sex ratio, fruit girth, pulp thickness and total soluble solids content were negatively correlated with total yield in cucumber.

Badade *et al.* (2001) conducted an experiment to study the correlation of 20 bottle gourd (*Lagenaria vulgaris*) genotypes. Yield was found significantly and positively correlated with number of branch per vine, number of fruits per vine and significantly and negatively correlated with days to first male and female flower appearance and weight of deformed fruits per vine at both phenotypic and genotypic levels. Fruit length showed positive but non significant correlation with fruit yield.

Rahman *et al.* (1986) studied Variability, correlation and path coefficients in four lines of bottle gourd. Fruit weight per plant had strong positive genotypic correlation with days to first picking, length of main vine and fruit diameter and a negative correlation with fruit length.

Parhi *et al.* (1995) studied correlation and path co-efficient of thirteen genotypes of bitter gourd. Positively significant correlations of yield per plant with fruit weight, fruit length, number of seeds per fruit, vine length and days to first harvest indicated that simultaneous improvement can be made if selection is made for any one of the correlated characters.

Singh and Ram (2003) conducted an experiment on 28 musk melon genotypes to determine the correlation among fruit characters. The simple correlation among fruit traits showed that polar diameter, latitudinal diameter, flesh thickness and seed cavity size were positively correlated with fruit weight.

Shah and Kale (2002) conducted an experiment on correlation co-efficient analysis of yield components of 55 genotypes of ridge gourd. The fruit weight per vine was positively and significantly correlated with number of fruits per vine, average fruit weight, number of female flower per vine and vine length, indicating the close



association and dependency of yield these characters. The fruit length was negatively correlated with fruit diameter and fruit number per vine, while it was positively correlated with average fruit weight.

Miah *et al.* (2000) noted that fruit yield in bitter gourd showed significant positive association with average fruit weight, fruit breadth and number of nodes per vine in genotypic and phenotypic correlation with days to male flowering.

Sarker *et al.* (1999) studied correlation and path co-efficient of 16 divergence types of pointed gourd indicated that fruit weight, fruit diameter and number of primary branches per plant were positively and significantly correlated with yield per plant at genotypic and phenotypic levels.

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that positive and significant correlation of vine length, mean fruit weight, number of fruit per plant and number of seeds per fruit with fruit yield per plant.

Prasad *et al.* (1988) in a study found that phenotypic and genotypic co-efficient of variation of water melon were high for fruit per plant, average fruit weight, seed per fruit, 100 seed weight and fruit yield per plant. They also reported that fruit yield was correlated with vine length ($r = 0.47$), branches per plant ($r = 0.75$), fruit weight ($r = 0.88$), length ($r = 0.63$) and girth ($r = 0.61$).

Vijay (1987) worked with nine agronomic characters of 95 diverse musk melon stocks and found that fruits per vine and fruit weight were positively correlated with yield.

According to Singh *et al.* (1986) yield was positively and significantly correlated with fruits per plant ($r = 0.60$) and days to flowering, days to fruit set and days to ripeness were negatively correlated with all the other characters with the exception of a positive correlation between days to flowering and fruit weight in pointed gourd

Reddy and Rao (1984) observed negative and non-significant correlation between male flower pedicel length, female flower pedicel length traits ($r = 0.222$) in ribbed gourd.

2.3 Path Co-efficient

Singh *et al.* (2002) carried out 98 hybrids of cucumber derived from crosses involving fourteen male and seven female parents. Path coefficient analysis indicated that fruit weight had the highest direct effect on fruit yield.

Li *et al.* (1997) conducted an experiment on cucumber genotypes. From path analysis, they concluded that fruits per plant and average fruit weight affected the yield directly. Abusaleha and Dutta (1989) carried out an experiment on correlation and path analysis studies in cucumber. Path coefficient analysis revealed that fruits per vine and fruit length had the greatest direct effects on yield.

Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and Path co-efficient analysis revealed that the number of fruits, female flowers per plant, fruit length, fruit weight and fruit diameter were the most important characters determining yield.

Kumar *et al.* (2007) conducted an experiment to study the path coefficient of 20 bottle gourd (*Lagenaria vulgaris*) genotypes. Path analysis revealed that number of branches per vine, vine length, nodes number of first female flower and number of fruit per vine had positive direct effect on fruit yield per vine.

Rahman *et al.* (1986) studied Variability, correlation and path coefficients in four lines of bottle gourd. Path coefficient analysis revealed that fruit diameter and fruit length had high positive direct effect on fruit weight per plant. Number of fruits per plant also had considerable positive direct effect on fruit weight per plant.

Rao *et al.* (2000) conducted an experiment on the segregating population of ridge gourd for correlation and path coefficient analysis. Path analysis revealed that yield improvement could be achieved by direct selection for days to 50% flowering, girth

of fruit, fruits per plant or vine, fruit per branch and length of the vine of ridge gourd.

Miah *et al.* (2000) conducted an experiment on bitter gourd for correlation and path coefficient analysis. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield. Sarker *et al.* (1999) studied path co-efficient of 16 divergence types of pointed gourd. The path analysis revealed that fruit volume followed by fruit weight and fruit diameter had maximum positive direct effects on yield.

Sych (1990) conducted path co-efficient analysis in 150 genotypes of watermelon and found that fruit weight and number of fruits per plant had considerable direct effects on yield.

Mondal *et al.* (1989) studied path co-efficient in 31 genotypes of watermelon and observed that the number of fruits per plant and fruit diameter affected fruit yield directly. Path co-efficient analysis revealed that for increasing fruit yield selection should be based on plant having more number of fruits with larger diameter.

Kumaran *et al.* (1998) carried out an experiment on correlation and path analysis studies in pumpkin. They found that number of fruit per plant exhibited the highest direct effect on yield. High positive indirect effects were exerted by number of fruit per plant and mean fruit weight.

Parhi *et al.* (1995) studied correlation and path co-efficient of thirteen genotypes of bitter gourd. Path analysis revealed that fruit breadth, days to opening of first male and female flower, vine length and number of seeds per fruit had the maximum positive direct effect on yield in bitter gourd. The characters like fruit weight and fruit length though have significant positive correlation with yield, exhibited low direct effect. Besides direct selection for yield, indirect selection through number of seeds per fruit and fruit weight would prove worth for further improvement in yield of bitter gourd.

2.4 Genetic Diversity

Genetic diversity is one of the important tools to quantify variability in both self and cross-pollinated crops (Griffing and Lidstorm, 1954; Murty and Arunachalam, 1966; Guar *et al.* 1978).

The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse plants for a successful hybridization programme (Rao, 1952). D^2 analysis (originally outlined by Mahalanobis, 1936 and extended by Rao, 1952) is one of potential methods of estimating the degree of genetic diversity.

The wide diversity of genotypes can be shown by cluster analysis from the same geographical regions. To understand the usable variability, grouping or classification of genotypes based on suitable scale. Multivariate analysis formulated by Mahalanobis (1936) is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Studies on genetic diversity in cucumber carried out so far are presented as follows:

Prasad *et al.* (1993) evaluated 32 genotypes landraces of cucumber for 14 characters. Mahalanobis's D^2 analysis indicated considerable diversity among the genotypes that were grouped into eight clusters independently of their geographical distribution

Islam *et al.* (1993) revealed significant variation in fruit per plant of cucumber and it was varied from 4-18 fruits along with high heritability (88.14%) and genetic advanced (129.69).

Rao *et al.* (2003) found a wide significant variation in D^2 values ranges from 16.39 to 1810.2 in all the characters of 31 cucumber genotypes indicated the high diversity available in the germplasm. Based on the D^2 values, the 31 genotypes were grouped into 16 highly divergent clusters. The intra cluster divergence ranged from 30.99-85.14 and the inter cluster distance was the highest between XII and IV (1709.48) followed by XII and IX (1362.54). The germplasm that could be grouped



into a single cluster were only five i.e., in clusters CL-1, CL-2 CBL, Poona Khira, HOE-707, Sheetal, PCUC-8 and Himangi so divergent that each had to be given the status of a separate cluster.

Mathew *et al.* (1986) studied genetic distance among five botanical varieties of *Cucumis melo*. The genetic distance was calculated for nodes to first female flower, fruit weight, seeds per fruit and fruits per plant. Total D^2 was estimated according to Mahalanobis (1936). The magnitude of D^2 indicated closeness among the varieties. The character fruits per plant contributed maximum to total divergence (80%). Seeds per fruit did not contribute to the total divergence and concluded that selection of botanical varieties based on fruits per plant would be a logical step in the selection of divergence parents in crop improvement programme.

Genetic divergence using Mahalanobis D^2 statistics was studied for seven quantitative characters including yield per vine in a collection of twenty diverse cultivars of bottle gourd by Badade *et al.* (2001). The cultivars differed significantly for almost all of the characters and were grouped into 10 clusters based on the similarities of D^2 value. Considerable diversity within and between clusters was noted and it was observed for the characters viz. vine length, number of branches, fruit per vine, length and diameter of fruit and yield per vine.

Quamruzzaman *et al.* (2008) studied the genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*) using D^2 and principal component analysis. The genotypes were grouped into six clusters. The highest intra cluster distance was noticed for the cluster II (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) where as the lowest was observed between cluster IV and V (3.402).

Gaffar (2008) conducted an experiment with 15 sponge gourd genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during April 2007 to October 2007. The genotypes were grouped into five clusters. The highest intra cluster distance was noticed for the cluster III (0.999) and the lowest for the cluster

IV (0.439). The highest inter-cluster distance was observed between cluster IV and V (7.163) where as the lowest was observed between cluster I and IV (2.258).

Banik (2003) studied 26 genotypes of snake gourd were tested using multivariate analysis and the genotypes were grouped into seven distinct cluster. No relationship was found between genetic divergence and geographical distribution of genotypes. The highest inter genotypes distance was observed between genotypes SG 026 and SG 010 (1.897). The inter cluster distance was maximum between cluster II and IV (17.74). Main vine length, first female flower node number, nodes on main vine, fruit length and number of seeds per fruit had the highest contribution towards the divergence.

Masud *et al.* (2001) studied genetic divergence in 19 genotypes of sponge gourd (*Luffa cylindrica*) collected from local and exotic resources. The genotypes were grouped into five clusters. The genetic divergence of the genotypes did not follow their geographical distribution and was fairly at random. There was no evidence of close relationship between geographical distribution and genetic divergence as estimated by D^2 statistics. Maximum inter-cluster distance (45.9) was observed between cluster II and V and minimum (10.3) between cluster II and IV. Fruit length and diameter were significant contributors to genetic divergence.

Karuppaiah *et al.* (2005) evaluated genetic divergence in 12 genotypes of bitter gourd (*Momordica charantia*) grown in Annamalai, Tamil Nadu, India, during June-July 2001. Using Mahalanobis D^2 technique, the genotypes were grouped into clusters I (four genotypes), II (one genotype), III (three genotypes) and IV (four genotypes). Among the four clusters, cluster IV (LA-7, LA-9, LA-10 and LA-12) registered the highest mean values for vine length (6.2 m), number of male flowers per plant (79.3), number of female flowers per plant (23.2), yield per plant (5.2 kg), single fruit weight (242.2 g), fruit length (29.4 cm), number of fruits per plant (24.1), number of seeds per fruit (52.3), fruit size index (173.2), and 100-seed weight (18.6 g). Hence, it is desirable to involve LA-7, LA-9, La-10 and LA-12 of cluster IV in breeding programmes.

Khan *et al.* (2008) assessed the genetic diversity among 64 pointed gourd genotypes through multivariate analysis from an experiment conducted in Regional Agricultural Research Station, Ishurdi, Pabna during the growing season 2002-2003. The genotypes were grouped into twelve clusters. The cluster V consisted of highest number of genotypes and it was nine, the cluster VI and cluster VIII contained the lowest number of genotypes and it was two in each. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location were grouped into different clusters. The genotypes of Jessore were distributed in different clusters. The highest inter genotype distance as 366.3 observed between the genotypes P0022 and P0007 and the lowest 2.6 as observed between the genotypes P0043 and P0044. Cluster V had the highest cluster mean value for internodes length, fruit weight per plant and yield the highest inter-cluster distance was noticed between cluster III and II (45.71) and the lowest between cluster VII and VI (3.33). The highest intra cluster distance was computed for cluster III and that was lowest for the cluster II. The first five axes accounted for 77.65% of the total variation among the 13 characters describing 64 pointed gourd genotypes. Fruit weight, seeds per fruit and fruit weight per plant contributed maximum to the total divergence.

Kabir (2007) reported that genetic divergence studied 24 accessions of pointed gourd. The accessions were grouped into five clusters. The cluster I and III had the highest number of accessions (six) followed by cluster V (five), cluster II (four) & Cluster IV (three). The highest intra cluster distance was computed for cluster IV (35.80) followed by cluster I (28.12) and Cluster V (26.63). The minimum intra cluster distance was found in III (18.87).

Harshawardhan and Ram (2003) conducted an experiment on severity germplasms of musk melon lines to elucidate genetic divergence using a non-hierarchical Euclidean cluster analysis for yield and its components. The genotypes were grouped into 11 clusters irrespective of geographic and genetic diversity. Group VIII contained the largest number of 11 genotypes. The maximum genetic distance occurred between cluster II and X.

Hazra *et al.* (2003) reported that genetic divergence studied on 167 accessions of pointed gourd and grouped in eight non-overlapping clusters, with cluster IV comprising of the highest number of accessions (37 accessions) and cluster VI comprising of the lowest number of genotypes (six accessions). Inter cluster distance ranged from 1.25 in cluster I to 1.65 in cluster VII. Cluster VIII and V were the most diverse as indicated by the maximum inter cluster distance between them (6.04).

Raseed *et al.* (2002) studied the genetic divergence of 47 pumpkin genotypes collected from different parts of Bangladesh using Mahalanobis's D^2 and principal component analyses. The genotypes were grouped into seven clusters. Cluster III had the maximum (11) and cluster IV and VII had the minimum number (four) of genotypes. The characters like fruit weight yield per plant contributed maximum towards total divergence.

Sidhu and Gautam (1985) obtained higher inter cluster distance than cluster distance in watermelon and reported the low intra cluster and high inter cluster distance indicated that the population grouped were homozygous within and heterozygous between clusters.

Rashid (2000) found that no relationship between geographic distribution and genetic diversity in pumpkin. The result suggested that geographic isolation is not the only factor causing genetic diversity and this point should be considered in selecting parents for hybridization.

Varalaksmi *et al.* (1994) conducted an experiment with 48 genotypes of ridge gourd collected from different regions of India to analyze genetic divergence. Nineteen (19) quantitative characters were selected to study genetic divergence using Mahalanobis D^2 statistics and Tocher method to form cluster. The 58 genotypes were grouped into five clusters but, in general there was no association between geographical distance and genetic divergence. There was substantial variation in cluster means for whole plant sex ratio, fruit number per plant, fruit

weight and yield per plant. The inter cluster D^2 value indicated that cluster III was most divergent from the other clusters.

Principal component and grouping analyze of data on 31 plant morphological traits were used to estimate genetic divergence in 15 accessions of *Cucurbita* by Choer *et al.* (2000). It was observed that the accessions dispersed in a bidirectional space way, forming three groups, each on having two subgroups. Grouping analysis by the Ward method showed similar results to those obtained from principal component analysis. The traits that mostly contributed to genetic divergence were presence of thorns on the petiole internode number of the main vine up to the first female flower, fruit shape, fruit diameter, skin texture, predominant skin colour and number of days to the first male flower on the main vine.

Ram *et al.* (2001) performed cluster analysis in 167 pointed gourd genotypes (*Trihosanthes dioica*) collected from different ecogeographic region of India. On the basis of different yield contributing agro morphological traits, the genotypes were grouped into eight clusters which were non-overlapping. Cluster IV comprising the most number of genotypes (37 accessions) and cluster VI comprising the lowest number of genotypes (six accessions). Intra cluster distance ranged from 1.258 in cluster I and 1.655 in cluster VII. Cluster VIII and V were the most diverse as indicated by maximum inter cluster distance between them (6.049). The results indicated the potential for wide scope of varietal improvement through hybridization and selection due to the wide genetic diversity present in the accession studied.

Ramachandran *et al.*, (1981) grouped 25 bitter gourd germplasm into ten clusters based on their D^2 values. The inter-cluster distance value observed was maximum between cluster VI and VIII (8569.31) and the minimum was between cluster II and III (393.62). The co-efficient of variation estimated for different characters among the 10 clusters showed greater role for yield per plant (38.84), fruits per plant (25.68), female flowers per plant (19.82) and fruit length (19.05) in determining the inter-cluster distance. It was further observed that the character yield per plant,

fruits per plant and female flowers per plant and fruit length contributed predominantly to divergence.

Kadam and Kale (1987) observed highly significant difference between cultivars suggesting considerable divergence among 30 ridge gourd cultivars. The 30 cultivars were grouped into 20 clusters based on their D^2 values. Cluster A having two cultivars had the lowest intra-cluster D^2 values (8.22) while clusters I which has two cultivars had the highest intra-cluster value of 18.59. The highest inter-cluster distance was observed between clusters E and M (387.11) and it was minimum between cluster D and G (19.79).

Sanwal *et al.* (2008) evaluated thirty eight indigenous collections of chow-chow for eight quantitative and quality traits. On the basis of genetic divergence, relative magnitude of D^2 values thirty-eight genotypes were grouped into seven clusters. The maximum genetic divergence was observed between cluster III and VII followed by cluster II and VI. The cluster V and VI displayed lowest degree of divergence. The minimum intra-cluster distance was exhibited for cluster VI followed by cluster V. However, it was highest for cluster III. The mean values were higher in cluster I and IV for two characters i.e. fruit length and average fruit weight, while cluster II had high mean values for number of fruits/plant.

Ramos *et al.* (2000) evaluated the genetic diversity of 40 squash accessions collected from distinct areas of the Northeast region of Brazil. The data were analyzed using canonic variable and Tocher cluster analysis adopting Mahalanobis D^2 general distance. It was observed that 65% of the accessions were clustered in a group. The disperse results based on the first four canonic variables (71% of total variability) did not permit a correlation between genetic diversity and eco-geographical origin.



Chapter-3

Materials And Methods



CHAPTER III

MATERIALS AND METHODS

The investigation was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from March 2010 to October 2010 to study on the genetic variability, genetic diversity, correlation and path analysis in cucumber. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc., which are presented as follows:

3.1. Experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka during March 2010 to October 2010.

3.2 Geographical Location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004). The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain (Anon., 1988b). The experimental site was shown in the map of AEZ of Bangladesh in (Appendix I).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Meteorological information regarding temperature, relative humidity,

rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Twenty two genotypes of cucumber were used for the present research work. The purity and germination percentage were leveled as around 100 and 80, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur , Agro-G, & Lal Teer seed company. The name and origin of these genotypes are presented in (Table 1).

3.6 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. The Twenty two genotypes were distributed into the pit of each block of the prepared layout of the experiment. The genotypes of the experiment were assigned at random into pits of each replication. The distance maintained spacing pit to pit 1.5 m. The distance maintained between two blocks was 0.6 m.

3.7 Poly bag preparation and raising seedling

Due to uncertain rainfall during the period of the study, the seeds were dibbled in Poly bag for higher germination percentage and to get healthy seedlings and when the seedlings become 20 days old; those were transplanted in the main field in the pit. Seeds were sown 10th March, 2010, before sowing seeds were treated with Bavistin for 5 minutes.

Table 1. Name and origin of twenty two cucumber genotypes used in the present study

Sl. No.	Genotypes No.	BARI ACC Number	Origin
1	G ₁	BD 4207	PGRC, BARI
2	G ₂	BD 4234	PGRC, BARI
3	G ₃	BD4244	PGRC, BARI
4	G ₄	BD 4249	PGRC, BARI
5	G ₅	BD 4251	PGRC, BARI
6	G ₆	BD 4256	PGRC, BARI
7	G ₇	BD 4305	PGRC, BARI
8	G ₈	BD 4308	PGRC, BARI
9	G ₉	BD 4309	PGRC, BARI
10	G ₁₀	BD 4313	PGRC, BARI
11	G ₁₁	BD 4315	PGRC, BARI
12	G ₁₂	BD 4320	PGRC, BARI
13	G ₁₃	Chamok 34	LAL TEER
14	G ₁₄	Serena	LAL TEER
15	G ₁₅	Alavy	LAL TEER
16	G ₁₆	Sishir	LAL TEER
17	G ₁₇	CU 937 F1	LAL TEER
18	G ₁₈	Joti	AGRO-G
19	G ₁₉	Mukta	AGRO-G
20	G ₂₀	Green joint	AGRO-G
21	G ₂₁	Baromashi	AGRO-G
22	G ₂₂	Local	

Here, PGRC = Plant Genetic Resources Centre, BARI = Bangladesh Agricultural Research Institute

3.8 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the last week of February 2010. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.9 Pit preparation

After final land preparation, pits of 55 cm × 55 cm × 45 cm were prepared in each block with a spacing of 1.5 m × 0.60 m. Pits were kept open in the sun for 7 days to kill harmful insect and microorganisms. To control field cricket 5 mg Furadan was also mixed with the soils of each pit before making it ready for dibbling. Field view of experimental site is presented in Plate 1a and 1b.

3.10 Manure and fertilizers application

Total cowdung, half of TSP and one third MOP were applied in the field during final land preparation. Remaining TSP and one third MOP and whole gypsum and zinc oxide and one third of urea were applied in pit one week prior to transplantation. Remaining urea and MOP were applied as top dressing in four installments at 20, 40, 60 and 75 days after transplanting (Table 2) showing doses of manure and fertilizers used in the study.

3.11 Transplanting of seedlings

Germination of seeds was completed within 12 days and the seedlings of different accessions were planted in the pit on 29th March, 2010. In each pit two seedlings were planted and the soil around the plant was firmly pressed by hand.

3.12 Intercultural operations

The following intercultural operations were done from time to time throughout the cropping season for proper growth and development of the plants.



Plate 1a. Field view of the experimental site



Plate 1b. Field view of the experimental site

Table 2. Doses of manure and fertilizers used in the study

Sl. No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	80-120 kg/ha
3.	TSP	110-120 kg/ha
4.	MOP	80-120 kg/ha
5.	Gypsum	75 kg/ha
6.	Zinc Oxide	10 kg/ha

3.12.1 Thinning and gap filling

Only one healthy seedling was kept per pit for the proper development and avoid crowd environment. For this whatever its need thinning and gap filling was done.

3.12.2 Weeding and mulching

Several weeding and mulching were done as per requirement. At the very first stage weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

3.12.3 Irrigation and after-care

In the early stage irrigation was done twice daily by water cane. In mature stage flood irrigation was done when ever it's necessary.

3.12.4 Pesticide application

At the seedling stage red pumpkin beetle attacked tender leaves and also after the initial stage they attacked plants several times for this Malathion and Ripcord was sprayed in the field. In mature stage fruit fly caused severe damage to the fruit. For

protection from fruit fly, MSGT (Mashed Sweet Gourd Trap) and Pheromone bait was used along with ripcord, seven powders.

3.13 Harvesting

Fruits were picked on the basis of horticultural maturity, size, color and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage, frequent picking was done throughout the harvesting period. Fruits were picked with sharp knife and care was taken to avoid injury of the vine.

3.14 Data recording

Data were recorded on following parameters from the studied plants during the experiment. The details of data recording are given below on individual plant basis.

3.14.1 Plant characteristics

3.14.1.1 Leaf length (cm)

Leaf length was measured in three to five leaves in each germplasm in cm and average data was recorded.

3.14.1.2 Leaf breadth (cm)

Leaf breadth was measured in three to five leaves in each germplasm in cm and average data was recorded.

3.14.1.3 Leaf petiole length (cm)

Leaf petiole length was measured in three leaves in each germplasm in cm and average data was recorded.

3.14.1.4 Number of branches per vine

Branches per vine were counted and average data was recorded.

3.14.2 Inflorescences characteristics

3.14.2.1 Days to first male flowering

The number of days required for first male flower flowering was counted for three replication separately and average data was recorded.

3.14.2.2 Days to first female flowering

The number of days required for first female flower flowering was counted for three replications separately and average data was recorded.

3.14.3 Fruit characteristics

3.14.3.1 Number of fruits per plant

The number of fruit per plant was counted and average data was recorded

3.14.3.2 Weight of fruit (g)

Weight of three to five fruits in each germplasm during harvest for vegetable use was measured in kilogram (g).

3.14.3.3 Length of fruit (cm)

Fruit length was measured in three to five fruits in each germplasm in cm and average data was recorded during fruit harvest for vegetable use.

3.14.3.4 Breadth of fruit (cm)

Fruit diameter was measured in three to five fruits in each germplasm in cm, then the data was divided by two and average data was recorded during fruit harvest for vegetable use.

3.14.3.5 Length of fruit peduncle (cm)

Fruit peduncle length was measured in three to five fruits in each germplasm in inch and average data was recorded during fruit harvest for vegetable use.

3.14.3.6 Fruit yield per plant (Kg)

Weight of edible fruits of selected plants from each accession was weighed in Kilogram (kg).

3.15.1 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.15.1.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{GMS} - \text{EMS}}{r}$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma_{ph}^2) = \sigma_g^2 + \text{EMS}$$

Where,

σ_g^2 = Genotypic variance

EMS = Error mean sum of square

3.15.1.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation } (r_{gxy}) = \frac{\sigma_{gxy}}{\sqrt{(\sigma_{gx}^2 \sigma_{gy}^2)}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ_{gx}^2 = Genotypic variance of the trait x

σ_{gy}^2 = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{\sigma_{pxy}}{\sqrt{(\sigma_{px}^2 \sigma_{py}^2)}}$$

Where,

σ_{pxy} = Phenotypic covariance between the traits x and y

σ_{px}^2 = Phenotypic variance of the trait x

σ_{py}^2 = Phenotypic variance of the trait y

3.15.1.3 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

$$\text{Genotypic co-efficient of variation (GCV \%)} = \sqrt{\frac{\sigma_g^2}{\bar{x}}} \times 100$$

Where,

σ_g^2 = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

$$\text{Phenotypic co-efficient variation (PCV)} = \sqrt{\frac{\sigma_{ph}^2}{\bar{x}}} \times 100$$

Where,

σ_{ph}^2 = Phenotypic variance

$\bar{x}$ = Population mean

3.15.1.4 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

$$h^2_b \% = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_{ph}^2 = Phenotypic variance

3.15.1.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = K \cdot h^2_b \cdot \sigma_{ph}$$

$$GA = K \cdot \frac{\sigma_g^2}{\sigma_{ph}^2} \cdot \sigma_{ph}$$

Where,

K = Selection intensity, the value which
is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_{ph}^2 = Phenotypic variance

3.15.1.6 Estimation of genetic advance in percent of mean

Genetic advance in percent of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \times 100$$

3.15.2 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.15.2.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.2.2 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 dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.15.2.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.15.2.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group 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 maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.15.2.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_i^x d_i^2 = \sum_i^x (Y_i^j - Y_i^k)^2 \quad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from $i = 1$ -----to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.15.2.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = Number of all possible combinations between the populations in cluster.

3.15.2.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the
Populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.15.2.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.15.2.9 Selection of genotypes for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

- i. Choice of cluster from which genotypes are selected for use as parent (s)
- ii. Selection of particular genotype(s) from the selected cluster(s)
- iii. Relative contribution of the characters to the total divergence
- iv. Other important characters of the genotypes performance



Chapter-4

Results And Discussion

CHAPTER IV

RESULTS AND DISCUSSION

The results obtained from the study are presented and discussed in this chapter. The data pertaining to twenty two cucumber genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

1. Genetic parameters
2. Correlation co efficient
3. Path co-efficient analysis
4. Multivariate analysis

4.1 GENETIC PARAMETERS

4.1.1 Characterization of cucumbers on the basis of yield and yield contributing characters

The analysis of variances indicated that the existence of highly significant variation among the genotypes studied (Table 3). The mean performance of genotypes are presented in Table 4. The results are discussed character wise as follows:

4.1.1.1 Leaf length (cm)

Mean sum of square for leaf length was 16.150 which was highly significant due to genotypes in cucumber (Table 3) indicating existence of considerable difference for this trait. The maximum leaf length was found 16.50 cm in BD-4249 and the minimum was recorded 7.00 cm in Sishir with mean value 11.30 cm (Table 4). Statistically BD-4249 produce longest leaf than rest of the genotypes. Li *et al.* (1997) noted that leaf area of cucumber genotypes were positively correlated to yield.

4.1.1.2 Leaf breadth (cm)

Significant mean sum of square for leaf breadth (22.260) indicated considerable difference among the genotype studied (Table 3). The maximum leaf breadth was

Table 4. Mean Performance of 22 genotypes of cucumber

Genotypes	Leaf length (cm)	Leaf breadth (cm)	Leaf petiole length (cm)	No. of branches per vine	Days to first male flowering	Days to first female flowering	No. of male flowers per plant	No. of female flowers per plant	No. of fruits per plant	Weight of fruit (g)	Length of Fruit (cm)	Breadth of Fruit (cm)	length of Fruit Peduncle (cm)	Yield per plant (kg)
BD 4207 (G1)	12.7	15.1	7.5	9	40	65	149	17	15	100.00	14.10	11.23	0.53	1.50
BD 4234 (G2)	11.5	13.2	10.2	11	61	70	153	16	12	106.67	12.60	12.23	1.57	1.29
BD4244 (G3)	13.2	16.5	6.6	14	48	65	198	13	10	108.33	14.07	12.37	1.07	1.10
BD 4249 (G4)	16.5	18.2	9.1	15	56	72	309	12	9	70.00	11.63	10.40	1.03	0.64
BD 4251(G5)	9.8	12.2	6.5	10	50	62	223	12	10	96.67	12.44	11.47	1.00	0.98
BD 4256 (G6)	11.8	13.7	7.5	8	60	80	212	13	12	96.67	15.70	15.17	0.97	1.15
BD 4305 (G7)	10.1	11.8	8.5	17	49	63	581	26	22	96.67	18.23	14.50	1.63	2.14
BD 4308 (G8)	10.7	12.3	10.5	10	59	60	252	15	13	103.33	15.33	9.57	0.97	1.35
BD 4309 (G9)	12.5	15.2	8.5	12	65	64	166	37	30	73.33	17.10	12.23	1.63	2.22
BD 4313 (G10)	13.3	17.2	12.1	13	54	70	384	17	15	83.33	12.20	12.33	1.30	1.24
BD 4315 (G11)	10.7	14.5	10.5	14	62	67	215	10	9	100.00	12.07	14.37	1.33	0.91
BD 4320 (G12)	9.2	11.5	7.2	18	46	60	251	15	12	96.67	11.03	13.13	1.40	1.15
Chamok 34 (G13)	9.5	13.4	7.0	7	62	64	115	11	8	106.67	10.87	13.50	1.30	0.85
Serena (G14)	9.0	10.0	7.0	8	32	36	152	16	13	70.00	14.40	10.23	1.20	0.92
Alavy (G15)	7.9	10.5	6.8	9	36	39	144	25	23	106.67	15.53	12.30	0.83	2.47
Sishir (G16)	7.0	8.0	5.2	13	32	65	142	25	23	90.00	15.13	10.30	0.87	2.06
CU 937 F1 (G17)	14.2	17.5	12.3	19	39	42	101	19	15	100.00	13.67	11.83	1.50	1.49
Joti (G18)	14.9	16.8	10.0	10	51	62	417	32	28	110.00	16.43	11.77	0.87	3.09
Mukta (G19)	10.7	16.0	9.5	11	38	71	538	19	16	83.33	10.70	12.40	0.97	1.32
Green joint (G20)	10.0	12.0	9.0	14	47	60	317	10	8	100.00	13.67	11.83	1.60	0.80
Baromashi (G21)	10.3	11.0	11.5	15	42	53	337	10	8	93.33	12.30	10.80	1.30	0.75
Local (G22)	13.0	15.0	12.2	13	41	47	552	14	10	93.33	15.13	13.87	1.17	0.92
Mean	11.30	13.71	8.87	12.27	48.64	60.77	268.50	17.45	14.59	94.77	13.38	12.17	1.18	1.38
Maximum	16.50	18.20	12.30	19.00	65.00	80.00	581.00	37.00	30.00	110.00	18.23	15.17	1.63	3.09
Minimum	7.00	8.00	5.20	7.00	32	36	101	10	8.00	70	10.70	9.57	0.53	0.64
% CV	8.14	11.94	7.27	11.95	3.26	3.86	8.33	10.52	10.90	14.63	15.41	12.12	19.27	12.16

found 18.20 cm in BD-4249 and the minimum was recorded 8.00 cm in Shisir with mean value 13.71 cm (Table 4). Li *et al.* (1997) noted that leaf breath of cucumber genotypes were positively correlated to yield.

4.1.1.3 Leaf petiole length (cm)

Genotype mean square for leaf petiole length was found significant (13.052) as shown in Table 3. The maximum leaf petiole length was found 12.30 cm in CU 937 F1 and the minimum was recorded 5.20 cm in Shisir with mean value 8.87 cm (Table 4). Gaffar (2008) found the similar result in sponge gourd for this trait.

4.1.1.4 Number of branches per vine

Mean sum of square for number of branches per vine was significant (32.909) due to genotypes in cucumber (Table 3) indicating existence of considerable difference for this trait. The maximum branches was found 19.00 in CU 937 F1 and the minimum was recorded 7.00 in Chamok34 with mean value 12.27 (Table 4). Abusaleha and Dutta (1989) found that the yield of cucumber is positively correlated with branches per vine ($r = 0.29$).

4.1.1.5 Days to first male flowering

Significant differences was observed among all genotypes (315.870) studied for this character (Table 3). The mean performance of days to first male flowering indicated that the maximum duration (65.00 days) to first flowering was produced by BD-4309 and that of minimum (32.00 days) by Serena and Shisir with mean value 48.64 days (Table 4). Ananthan and Pappoah (1997) reported that fruit number per vine was positively correlated with days to first male flowering.

4.1.1.6 Days to first female flowering

Days to first female flowering showed significant variation among genotype mean square (369.123). The maximum duration (80.00 days) to first flowering was produced by BD-4256 and that of minimum (36.00 days) by Serena with mean value 60.77 days (Table 4). Ananthan and Pappoah (1997) reported that fruit number per vine was positively correlated with days to first female flowering.

4.1.1.7 Number of male flowers per plant

Significant mean sum of square for number of male flower indicated considerable difference among the genotypes studied (Table 3). The maximum number of male flower was found 581 in BD-4305 and the minimum was recorded 101 in CU937F1 with mean value 268.50 (Table 4). Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlations at the genotypic and phenotypic levels between yield per plant with number of fruits and male flowers per plant.

4.1.1.8 Number of female flowers per plant

Mean sum of square for no. of female flower was significant (160.240) due to genotypes in cucumber (Table 3) indicating existence of considerable difference for this trait. The maximum number of female flowers was found 37.00 in BD-4309 and the minimum was recorded 10.00 in BD-4315, Green joint and Baromashi with mean value 17.45 (Table 4). Chadhury and Mandal (1987) conducted a study on 30 diverse cucumber genotypes and found high positive correlations at the genotypic and phenotypic levels between yield per plant with number of fruits and female flowers per plant.

4.1.1.9 Number of fruits per plant

Genotype mean sum of square for number of fruits per plant was found significant (128.188) as shown in Table 3. The maximum number of fruit per plant was found 30.00 in BD-4309 and the minimum was recorded 8.00 in Chamok34 with mean value 14.59 (Table 4).

4.1.1.10 Weight of Fruit (g)

Mean sum of square for fruit weight was significant (430.393) in cucumber (Table 3) indicating existence of considerable difference for this trait. The maximum

Table 3. Mean Sum Square from the ANOVA of 22 cucumber genotypes in respect of 14 characters

Characters	DF			MSS		
	Replication	Treatment	Error	Replication	Treatment	Error
Leaf length (cm)	2	21	42	7.475	16.150**	0.844
Leaf breadth (cm)	2	21	42	25.911	22.260**	2.678
Leaf Petiole length (cm)	2	21	42	0.732	13.052**	0.416
Number of branches per vine	2	21	42	0.864	32.909**	2.149
Days to first male flowering	2	21	42	152.318	315.870**	2.509
Days to first female flowering	2	21	42	250.409	369.123**	5.504
Number of Male flowers per plant	2	21	42	559.561	63330.561**	500.323
Number of Female flowers per plant	2	21	42	0.864	160.240**	3.372
Number of Fruits per plant	2	21	42	14.864	128.188**	2.53
Weight of fruit (g)	2	21	42	355.682	430.393*	192.19
Length of Fruit (cm)	2	21	42	6.046	13.171**	4.546
Breadth of fruit (cm)	2	21	42	3.247	6.536**	2.175
Length of fruit peduncle (cm)	2	21	42	0.055	0.270**	0.052
Yield per plant (kg)	2	21	42	0.072	1.211**	0.028

** indicates significant at 1% level of significance, MSS = Mean sum of squares due to genotypes

weight per fruit was found 110.00 g in Joti and the minimum was recorded 70.00 g in BD-4249 & Serena with mean value 94.73 g (Table 4). Saha *et al.* (1992) found similar GCV (39.55) and PCV (41.00) for the fruit weight in pumpkin. This result is in consonance with the findings of Chowdhury and Sharma (2002) in ridge gourd and Rumaran *et al.* (1997) in pumpkin.

4.1.1.11 Length of Fruit (cm)

Significant mean sum of square for fruit length (13.171) indicated considerable difference among the genotypes studied (Table 3). The maximum fruit length was found 18.23 cm in BD-4305 and the minimum was recorded 10.70 cm in Mukta with mean value 13.38 cm (Table 4). Rahman *et al.* (1986) indicated minimum difference between GCV and PCV in bottle gourd for fruit length. Sharma *et al.* (2000) evaluated ten cucumber lines and testers under different environmental conditions and reported, fruit length and fruit diameter had wide range of variation.

4.1.1.12 Breadth of Fruit (cm)

Mean sum of square fruit breadth was significant (6.536) due to genotypes in cucumber (Table 3) indicating existence of considerable variation for this trait. The maximum fruit breadth was found 15.17 cm in BD-4256 and the minimum was recorded 9.57 cm in BD-4308 with mean value 12.17 cm (Table 4). Sharma *et al.* (2000) evaluated ten cucumber lines and testers under different environmental conditions and reported, fruit length and fruit breath had wide range of variation.

4.1.1.13 Length of Fruit peduncle (cm)

Mean sum of square for fruit peduncle length was significant (0.270) due to genotypes in cucumber (Table 3) indicating existence of considerable difference for this trait. The maximum fruit peduncle length was found 1.63 cm in BD-4309 and BD-4305 and the minimum was recorded 0.53 cm in BD-4207 with mean value 1.18 cm (Table 4).

4.1.1.14 Yield per plant (kg)

Significant mean sum of square for yield per plant (1.211) indicated considerable difference among the genotypes studied (Table 3). The maximum yield per plant

was found 3.09 kg in Joti and the minimum was recorded 0.64 kg in BD-4249 with mean value 1.38 kg (Table 4). Sharma *et al.* (2000) evaluated ten cucumber lines and testers under different environmental conditions and reported marketable yield per plant, fruit length and fruit diameter had wide range of variation.

4.1.2 Variability of cucumber on the basis of yield and yield contributing characters

The genotypic and phenotypic coefficients of variations, heritability, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 5. The results are discussed character wise as follows:

4.1.2.1 Leaf length (cm)

The phenotypic variance (5.95) appeared to be higher than the genotypic variance (5.10) suggested considerable influence of environment on the expression of the genes controlling this trait (Table 5). The genotypic co-efficient of variation (20.00) and phenotypic co-efficient of variation (21.59) were close to each other. Heritability (85.81%) estimates for this trait was very high, genotypic advance (4.31) and genotypic advance in percent of mean (38.16) were found moderately high. Indicating this trait was governed by the additive gene. Gaffar (2008) found high heritability and moderate genetic advance for this trait in sponge gourd. Photograph showing variation of leaf length among different genotypes of cucumber in Plate 2.

4.1.2.2 Leaf breadth (cm)

The genotypic variance and phenotypic variance were 6.53 and 9.21, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 18.64 and 22.13, respectively. Heritability (70.91%) estimates for this trait was high, genotypic advance (4.43) was low and genotypic

Table 5 Genetic parameters of 14 vegetative and yield contributing characters of twenty two cucumber genotypes

Parameters	σ^2_g	σ^2_p	σ^2_e	GCV	PCV	ECV	h^2_b	GA (5%)	GA in % of mean (5%)
Leaf length (cm)	5.10	5.95	0.84	20.00	21.59	8.13	85.81	4.31	38.16
Leaf breadth (cm)	6.53	9.21	2.68	18.64	22.13	11.94	70.91	4.43	32.33
Leaf Petiole length (cm)	4.21	4.63	0.42	23.13	24.25	7.27	91.01	4.03	45.46
Number of branches per vine	10.25	12.40	2.15	26.09	28.69	11.94	82.67	6.00	48.87
Days to first male flowering	104.45	106.96	2.51	21.01	21.26	3.26	97.65	20.81	42.78
Days to first female flowering	121.21	126.71	5.50	18.12	18.52	3.86	95.66	22.18	36.50
Number of male flowers per plant	20943.41	21443.74	500.32	53.89	54.53	8.33	97.67	294.62	109.72
Number of female flowers per plant	52.29	55.66	3.37	41.43	42.74	10.52	93.94	14.44	82.71
Number of fruits per plant	41.89	44.42	2.53	44.36	45.68	10.90	94.30	12.95	88.73
Weight of fruit (g)	79.40	271.59	192.19	9.40	17.39	14.63	29.24	9.93	10.47
Length of fruit (cm)	2.88	7.42	4.546	12.26	19.69	15.41	38.74	2.17	15.72
Breadth of fruit (cm)	1.45	3.63	2.175	9.90	15.65	12.11	40.06	1.57	12.91
Length of fruit peduncle (cm)	0.07	0.12	0.05	22.79	29.85	19.28	58.29	0.42	35.84
Yield per plant (kg)	0.39	0.42	0.03	45.54	47.13	12.13	93.37	1.25	90.64

Here, σ^2_e = Environmental variance, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV= Environmental coefficient of variation, h^2_b = Heritability, GA = Genetic advance.

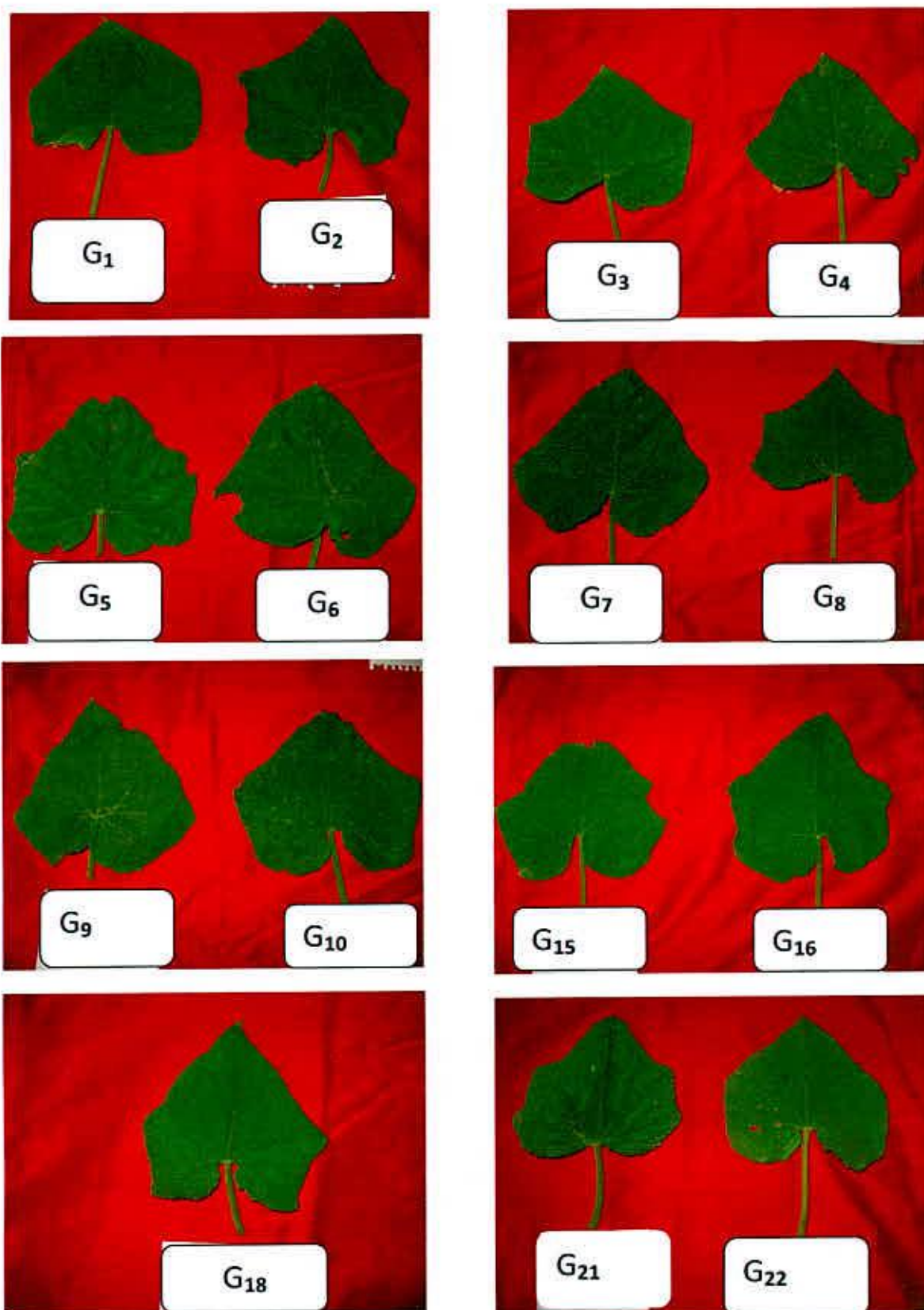


Plate 2. Showing variation in leaf among different cucumber genotypes (G₁-G₂₂)

advance in percent of mean (32.33) was found moderately high, indicated that this character was governed by non-additive gene. Gaffar (2008) found the similar GCV (20.95%) and PCV (23.31%) in sponge gourd. Photograph showing variation of leaf breadth among different genotypes of cucumber in Plate 2.

4.1.2.3 Leaf petiole length (cm)

The genotypic variance and phenotypic variance were 4.21 and 4.63 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling leaf petiole length. The genotypic co-efficient of variation (23.13) and phenotypic co-efficient of variation (24.25) were close to each other. Heritability (91.01%) estimates for this trait was high, genotypic advance (4.03) and genotypic advance in percent of mean (45.46) was found moderately high, indicated that the character was controlled by additive gene. Gaffar (2008) found the similar result in sponge gourd for this trait.

4.1.2.4 Number of branches per vine

The genotypic variance (10.25) and phenotypic variance (12.40) for this trait were low. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 26.09 and 28.69, respectively. Heritability (82.67%) estimates for this trait was high, genotypic advance (6.00) and genotypic advance in percent of mean (48.87) were found moderately high, indicated that the trait is governed by additive gene effects. Varghese (1991) noticed high heritability (90.1%) in snake gourd. Variation in twig among different cucumber genotype is presented in the plate 3.



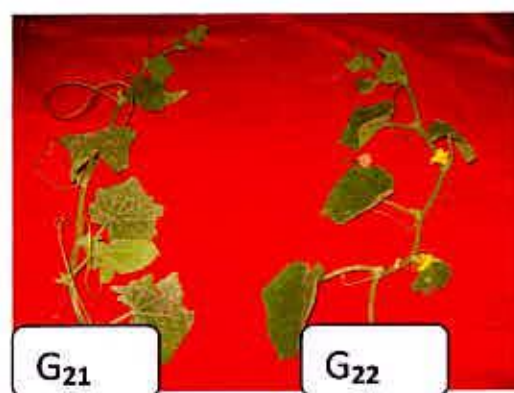
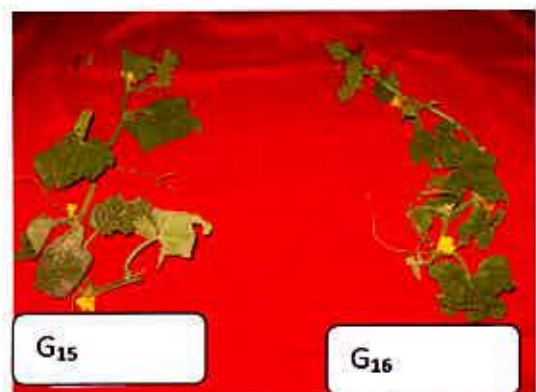
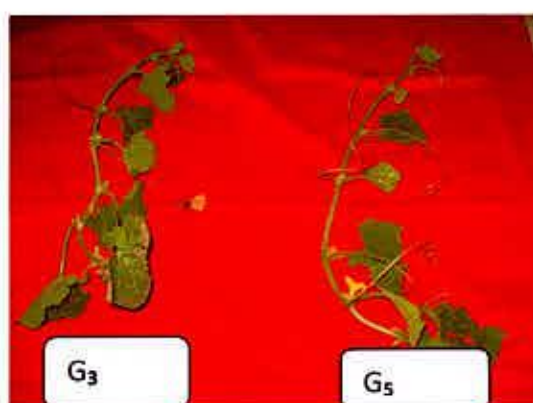


Plate 3. Showing variation in twig among different genotypes (G₁-G₂₂)

4.1.2.5 Days to first male flowering

Highest genotypic and phenotypic variance was observed 104.45 and 106.96 respectively for days to first male flowering with large environmental influence and difference between the genotypic co-efficient of variation (21.01) and phenotypic co-efficient of variation (21.26) indicating existence of less variation among the genotypes. Heritability for this trait was estimated very high (97.65%) and genetic advance (20.81) and genetic advance in percent of mean (42.78) were found high, indicated that the possibility of predominance of additive gene effect. Singh *et al.* (2002) also found phenotypic co-efficient of variation higher than genotypic co-efficient of variation in respect to days to first male flower opening in cucumber. Variation in male and female flowers among different cucumber genotype is presented in the plate 4a and 4b.

4.1.2.6 Days to first female flowering

The genotypic variance and phenotypic variance for this trait were 121.21 and 126.71, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (18.12) and phenotypic co-efficient of variation (18.52) were close to each other (Table 3). Heritability for this trait was estimated very high (95.66%) and genetic advance (22.18) and genetic advance in percent of mean (36.50) were found high, revealed that the character is governed by additive gene. Miah *et al.* (2000) and Yadav *et al.* (2009) estimated high GCV and PCV for days to first female flowering. Kadam and Kale (1987) also found high heritability with genetic advance in case of days to flowering.

4.1.2.7 Number of male flowers per plant

The genotypic variance (20943.41) and phenotypic variances (21443.74) were close to each other. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the

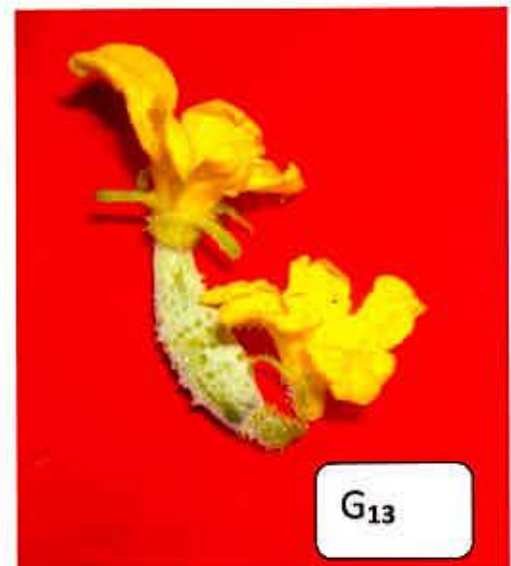
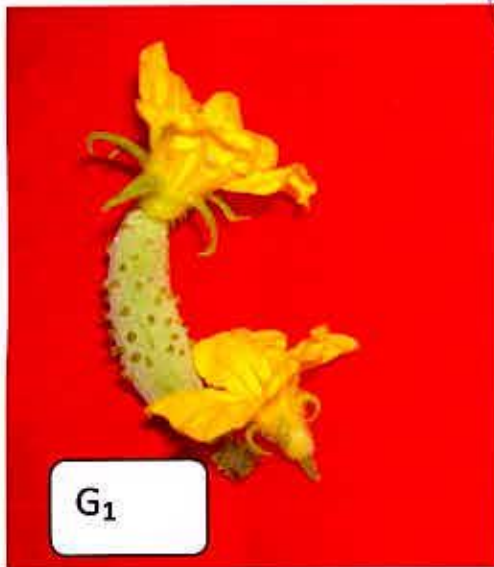


Plate 4a. Showing phenotypic variation in male and female flower among different genotypes of cucumber



Plate 4b. Showing phenotypic variation in male and female flower among different genotypes of cucumber

expression of the genes controlling this character. The genotypic co-efficient of variation was 53.89 and phenotypic co-efficient of variation was 54.53. Heritability (97.67%) estimates for this trait was very high, genotypic advance (294.62) was moderately high and genotypic advance in percent of mean (109.72) was found high, indicated that the trait was governed by additive gene. Singh *et al.* (2002) also estimated high GCV and PCV for male flowers per plant in ridge gourd.

4.1.2.8 Number of female flowers plant

The differences in magnitudes in between genotypic (52.29) and phenotypic (55.66) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 41.43 and 42.74, respectively. Heritability (93.94%) estimates for this trait was high, genotypic advance (14.44) was moderately high and genotypic advance in percent of mean (82.71) was found high, revealed that the trait was controlled by additive gene.

4.1.2.9 Number of fruits per plant

The genotypic variance (41.89) and phenotypic variance (44.42) for this trait were moderate. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 44.36 and 45.68, respectively which indicated presence of considerable variability among the genotypes. Heritability (94.30%) estimates for this trait was high, genetic advance (12.95) was found low and genetic advance in percent of mean (88.73) was found moderately high, indicated that the character was controlled by additive gene.

4.1.2.10 Weight of fruit (g)

The differences in magnitudes in between genotypic (79.40) and phenotypic (271.59) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 9.40 and 17.39, respectively for fruit weight which indicating that significant variation exists among different genotypes.

Heritability (29.24%) estimates for this trait was high together with considerable high genetic advance (9.93) and genetic advance in percent of mean (10.47) indicated that selection for this character would be effective. Saha *et al.* (1992) found similar GCV (39.55) and PCV (41.00) for the fruit weight in pumpkin. This result is in consonance with the findings of Chowdhury and Sharma (2002) in ridge gourd and Rumarán *et al.* (1997) pumpkin.

4.1.2.11 Length of fruit (cm)

The genotypic variance and phenotypic variance were 2.88 and 7.42 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation (12.26) and phenotypic co-efficient of variation (19.69) were close to each other. Heritability (38.74%) estimates for this trait high, genotypic advance (2.17) and genotypic advance in percent of mean (15.72) were found moderately high, indicated that the trait was governed by additive gene and selection for this character would be effective. Rahman *et al.* (1986) indicated minimum difference between GCV and PCV in bottle gourd for fruit length. Mathew and Khader (1999) also reported high heritability for fruit length in snake gourd. Photograph showing variation of fruit length among some genotypes of cucumber in Plate 5a and 5b.

4.1.2.12 Breadth of fruit (cm)

The genotypic variance and phenotypic variance were 1.45 and 3.63 respectively. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 9.90 and 15.65 respectively. Heritability (40.06%) estimates for this trait was high along with moderately high genetic advance (1.57) and genetic advance in percent of mean (12.91) indicated that this character was controlled by additive gene effects. Rahman *et al.* (1986) indicated minimum difference between GCV and PCV in bottle gourd for fruit breadth. This result is in consonance with the finding of Saha *et al.* (1992) in pumpkin.

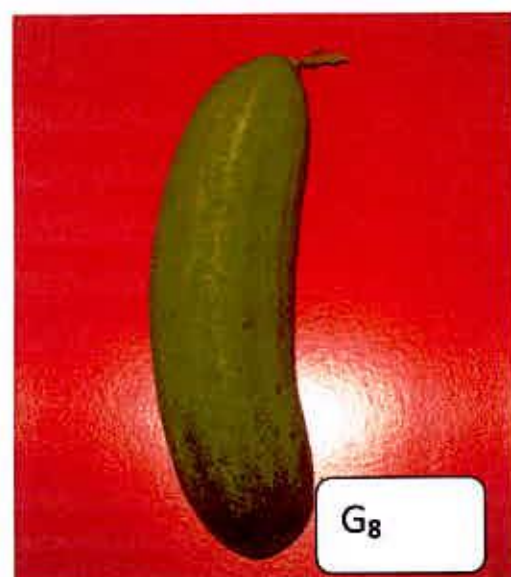
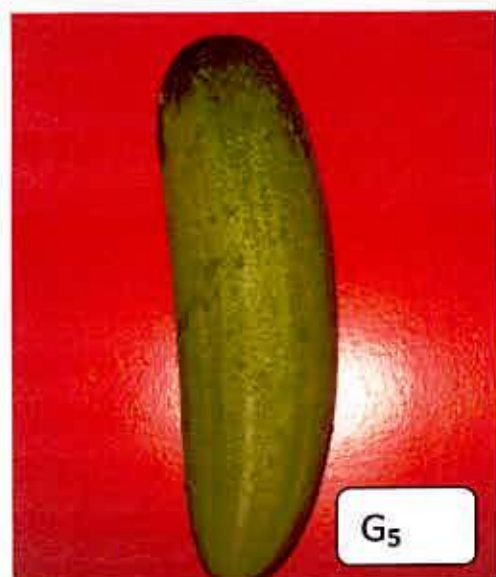


Plate 5a. Showing phenotypic variation in fruits among different genotypes of cucumber

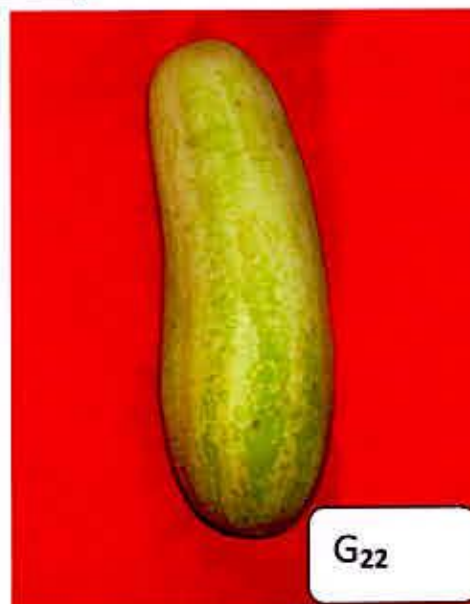
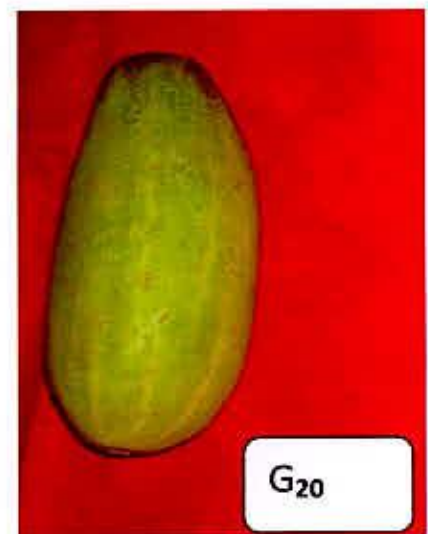
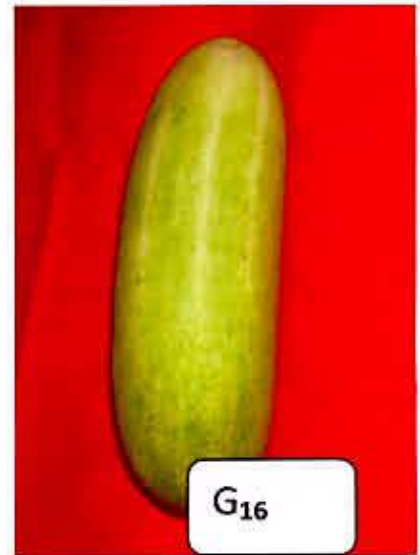


Plate 5b. Showing phenotypic variation in fruits among different genotypes of cucumber

4.1.2.13 Length of fruit peduncle (cm)

The genotypic variance (0.07) and phenotypic variances (0.12) were close to each other. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation was 22.79 and phenotypic co-efficient of variation was 29.85. Heritability (58.29%) estimates for this trait was moderately high, genotypic advance (0.42) and genotypic advance in percent of mean (35.84) were found moderately high, indicated that this trait was controlled by additive gene. Gaffar (2008) reported almost similar estimates of GCV and PCV (28.47% and 28.52%) and heritability was high (1.00%) with moderate genetic advance (6.59) for peduncle length in sponge gourd.

4.1.2.14 Yield per plant (kg)

The differences in magnitudes in between genotypic (0.39) and phenotypic (0.42) variances was relatively high for this trait indicating large environmental influence on these characters. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 45.54 and 47.13, respectively for yield per plant which indicating that significant variation exists among different genotypes. The heritability value (93.37%) as well as genetic advance (1.25) and genetic advance in percent of mean (90.64) were observed very high. The very high heritability with moderate genetic advance provided opportunity for selecting high valued genotypes for breeding programme.

4.2. CORRELATION CO-EFFICIENT

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the

association by genetic and non genetic factors. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al.* 1973). Results of genotypic and phenotypic correlation co-efficient of nine yield and its contributing traits of cucumber were estimated with yield and shown in Table 6 which discussed character wise as follows:

4.2.1 Leaf length (cm)

Leaf length showed significant and highly positive correlation with leaf breadth at both genotypic and phenotypic level (Table 6) revealed that if the leaf length was increased, then leaf breadth also increased. Leaf length also showed positive correlation with number of branch, number of male flower, number of female flower at both genotypic and phenotypic level. But this character produced insignificant and negative correlation at both genotypic and phenotypic level with yield per plant, number of fruits per plant and weight of fruit. Li *et al.* (1997) also found similar result in cucumber for this trait.

4.2.2 Leaf breadth (cm)

Leaf breadth also showed insignificant positive correlation with number of branches per vine, number of male flowers, number of female flowers, breadth of fruit at both genotypic and phenotypic level (table 6) indicated that if the leaf breadth was increased, then number of branch, male flower, female flower, breadth of fruit also increased. On the other hand this character produced insignificant negative correlation with yield at genotypic level indicated that the association among these traits was largely influenced by environmental factors. Li *et al.* (1997) also found similar result in cucumber for this trait.

Table 6. Genotypic and phenotypic correlation of nine characters with yield of twenty two cucumber genotypes

		Leaf breadth (cm)	Number of branches per vine	Number of male flowers per plant	Number of female flowers per plant	Number of fruits per plant	Weight of fruit (g)	Length of fruit (cm)	Breadth of fruit (cm)	Yield per plant (kg)
Leaf length (cm)	r_g	0.936**	0.203	0.224	0.061	-0.010	-0.172	0.038	-0.038	-0.021
	r_p	0.884**	0.216	0.187	0.017	-0.007	-0.066	-0.039	0.076	-0.005
Leaf breadth (cm)	r_g		0.185	0.229	0.030	-0.028	-0.162	-0.185	0.117	-0.060
	r_p		0.145	0.186	0.013	-0.016	0.031	-0.175	0.240	0.001
Number of branches per vine	r_g			0.265	-0.039	-0.069	-0.059	-0.074	0.109	-0.088
	r_p			0.245	-0.012	-0.066	-0.085	-0.091	0.059	-0.098
Number of male flowers per plant	r_g				0.064	0.057	-0.195	0.145	0.329	0.058
	r_p				0.092	0.063	-0.077	0.094	0.206	0.061
Number of female flowers per plant	r_g					0.999**	-0.164	0.871**	-0.038	0.938**
	r_p					0.958**	-0.077	0.436*	-0.043	0.861**
Number of fruits per plant	r_g						-0.128	0.851**	-0.054	0.960**
	r_p						-0.044	0.474*	-0.033	0.901**
Weight of fruit (g)	r_g							0.074	0.435*	0.194
	r_p							0.041	0.298	0.223
Length of Fruit (cm)	r_g								0.127	0.824**
	r_p								0.035	0.499*
Breadth of fruit (cm)	r_g									0.075
	r_p									0.016

** indicates significant at 0.01 level of significance and * indicates significant at 0.05 level of significance

4.2.3 Number of branches per vine

This character showed insignificant and positive correlation with male flower and breadth of fruit at both genotypic and phenotypic level (Table 6) indicating that any increase in the number of branches per vine should bring about increase in male flower and breadth of fruit. This character also showed insignificant and negative correlation with female flower, number of fruits per plants, weight of fruit, length of fruit. Yield negatively correlated with number of branches per vine.

4.2.4 Number of male flowers per plant

The character number of male flower showed insignificant positive correlation with yield per plant at both genotypic and phenotypic level (Table 6) which revealed that if the number of male flower was increased and then yield per plant was also increased. Insignificant but positive correlation was observed with number of fruit per plant, length of fruit, fruit breadth and number of female flower at both genotypic and phenotypic level. But this character produced negative correlation with weight of fruit at both genotypic and phenotypic level indicated that if the numbers of male flower are increased, then fruit weight is decreased. This finding also supported Chadhury and Mandal (1987) findings in cucumber.

4.2.5 Number of female flowers per plant

Number of female flowers showed highly significant and positive correlation with yield per plant, number of fruit per plant, length of fruit and at both genotypic and phenotypic level (Table 6) which revealed that if the number of female flower was increased and then yield per plant, number of fruit per plant, length of fruit also increased. But insignificant and negative correlation of this character with weight of fruit, fruit breadth at both genotypic and phenotypic level indicated that the association among these traits is largely influenced by environmental factors. This result is in consonance with the finding of Shah and Kale (2002) in ridge gourd. This finding also supported Chadhury and Mandal (1987) findings in cucumber.

4.2.6 Number of fruits per plant

Number of fruits per plant showed highly significant and positively correlated with length of fruit and yield of fruit per plant at both genotypic and phenotypic level (Table 6) indicating that any increase in number of fruit per plant should bring an enhanced in length of fruit and the yield. The character number of fruit per plant showed insignificant and negative correlation with fruit weight, breadth of fruit. Kumar *et al.* (2007), Badade *et al.* (2001) also reported that yield was significantly and positively correlated with number of fruit per plant in bottle gourd. The finding also supported Narayan *et al.* (1996) finding in bottle gourd for this trait.

4.2.7 Weight of fruit (g)

The trait, fruit weight showed significant and positive correlation with fruit breadth at genotypic level (Table 6) indicated that if the fruit weight is increased, then the fruit breadth and yield are also increased. The character also showed positive but insignificant correlation with fruit length and yield at both genotypic and phenotypic level. Rumarani *et al.* (1997) also reported in respect to average fruit weight in ridge gourd and pumpkin respectively. Narayan *et al.* (1996) also found similar result in bottle gourd for this trait.

4.2.8 Length of fruit (cm)

Positive and highly significant correlation of fruit length was found with fruit yield per plant at both genotypic and phenotypic level (Table 6) indicated that if the fruit length is increased, then fruit yield also increased. But insignificant and positive correlation of this character with fruit breadth was observed at both genotypic and phenotypic level indicated that if the fruit length is increased, then fruit breadth is increased. The finding also supported Badade *et al.* (2001) findings for fruit length in bottle gourd. Kumar *et al.* (2007) also found significant correlation for this trait in bottle gourd.

4.2.9 Breadth of Fruit (cm)

Yield per plant showed positively correlated with fruit breadth at both genotypic and phenotypic level (Table 6) revealed that any increased in the trait should bring about an enhancement in the yield. The finding also supported Rahman *et*



al. (1986) finding for this trait in bottle gourd. Miah *et al.* (2000) also found similar result for this trait in bitter gourd.

4.3 PATH CO-EFFICIENT ANALYSIS

Partitioning of genotypic correlation of different genotype, yield and its contributing traits in cucumber are shown in Table 7 and discussed character wise as follows:

4.3.1 Leaf length (cm)

Leaf length showed negatively direct effect (-0.612) on yield (Table 7). This character, however, showed positive indirect effect through leaf breadth (0.574), number of male flower (0.030); number of female flower (0.043), length of fruit (0.010), and breadth of fruit (0.010). The negative indirect effect via number of branch (-0.002), fruits per plant (-0.001), weight of fruit (-0.074) which were contributed to result insignificant negative genotypic correlation with yield per plant (-0.0207). Li *et al.* (1997) also found similar result in cucumber for this trait.

4.3.2 Leaf breadth (cm)

Leaf breadth showed a positive direct effect (0.614) on yield (Table 7). This character, however, showed also positive indirect effect through number of male flower (0.031), female flower (0.021). The negative indirect effects were also observed via leaf length (-0.573) followed by number of branch(-0.001),fruits per plant(-0.002) which were contributed to result insignificant negative genotypic correlation with yield per plant (-0.0597). Li *et al.* (1997) also found similar result in cucumber for this trait.

4.3.3 Number of branches per vine

Number of branches per vine showed the negative direct effect (-0.008) on yield (Table 7). This character also showed positive genotypic correlation with leaf breadth (0.114) and number of male flower(0.036).This character also showed negative and insignificant genotypic correlation with yield per plant (-0.0883) due to moderately high indirect effect through leaf length (-0.124), number of female flower (-0.028) was observed on yield.

Table 7. Path analysis of nine yield contributing characters of twenty two cucumber genotypes

	Leaf length (cm)	Leaf breadth (cm)	Number of branches per vine	Number of male flowers per plant	Number of female flowers per plant	Number of fruits per Plants	Weight of fruit (g)	Length of fruit (cm)	Breadth of fruit (cm)	Genotypic correlation with yield
Leaf length (cm)	-0.612	0.574	-0.002	0.030	0.043	-0.001	-0.074	0.010	0.010	-0.0207
Leaf breadth (cm)	-0.573	0.614	-0.001	0.031	0.021	-0.002	-0.070	-0.050	-0.030	-0.0597
Number of branches per vine	-0.124	0.114	-0.008	0.036	-0.028	-0.005	-0.025	-0.020	-0.028	-0.0883
Number of male flowers per plant	-0.137	0.141	-0.002	0.136	0.045	0.004	-0.084	0.039	-0.084	0.0577
Number of female flowers per plant	-0.037	0.018	0.000	0.009	0.698	0.078	-0.071	0.233	0.010	0.9383**
Number of fruits per Plant	0.006	-0.017	0.001	0.008	0.697	0.078	-0.055	0.228	0.014	0.9600**
Weight of fruit (g)	0.105	-0.099	0.000	-0.026	-0.114	-0.010	0.430	0.020	-0.111	0.1941
Length of Fruit (cm)	-0.024	-0.114	0.001	0.020	0.607	0.067	0.032	0.268	-0.032	0.8244**
Breadth of fruit (cm)	0.023	0.072	-0.001	0.045	-0.026	-0.004	0.187	0.034	-0.255	0.0745

Residual effect , R= 0.02

** indicates significant at 0.01 level of significance and * indicates significant at 0.05 level of significance

4.3.4 Number of male flowers per plant

Number of male flowers per plant showed a positive direct effect (0.136) on yield (Table 7). This character, however, showed also positive indirect effect through leaf breadth (0.141), length of fruit (0.039), number of fruit per plant (0.004), and fruit breadth (0.002). The negative indirect effects were also observed via leaf length (-0.137), number of branch (-0.002), fruit weight (-0.084), breadth of fruit (-0.084) which were contributed to result insignificant positive genotypic correlation with yield per plant (0.0577). This finding also supported Chadhury and Mandal (1987) findings in cucumber.

4.3.5 Number of female flowers per plant

Number of female flower produced a positive direct effect (0.698) on yield (Table 7). The character, however, showed also some positive indirect effect through number of fruit per plant (0.078), and fruit breadth (0.010), length of fruit (0.233), male flower (0.009) and leaf breadth (0.018). The negative indirect effects were also observed via leaf length (-0.037), weight of fruit (-0.071) which were contributed to result significant positive genotypic correlation with yield per plant (0.9383). This finding also supported Chadhury and Mandal (1987) findings in cucumber. Figure 1 showing Path diagram of yield and its contributing traits in twenty two genotypes of cucumber.

4.3.6 Number of fruits per plant

Number of fruit per plant had the highest positive direct effect on yield (0.078) (Table 7). The character produced positive indirect effect via leaf length (0.006), number of branch (0.001), male flower (0.008), female flower (0.697), fruit breadth (0.014) and fruit length (0.228). But the negative indirect effect via leaf breadth (-0.017), weight of fruit (-0.055) were also observed. The balanced total association is positive and highly significant with yield per plant (0.9600). So direct selection based on this traits would be effective to increase the yield of this crop. The finding supported Narayan *et al.* (1996) findings in bottle gourd for this trail.

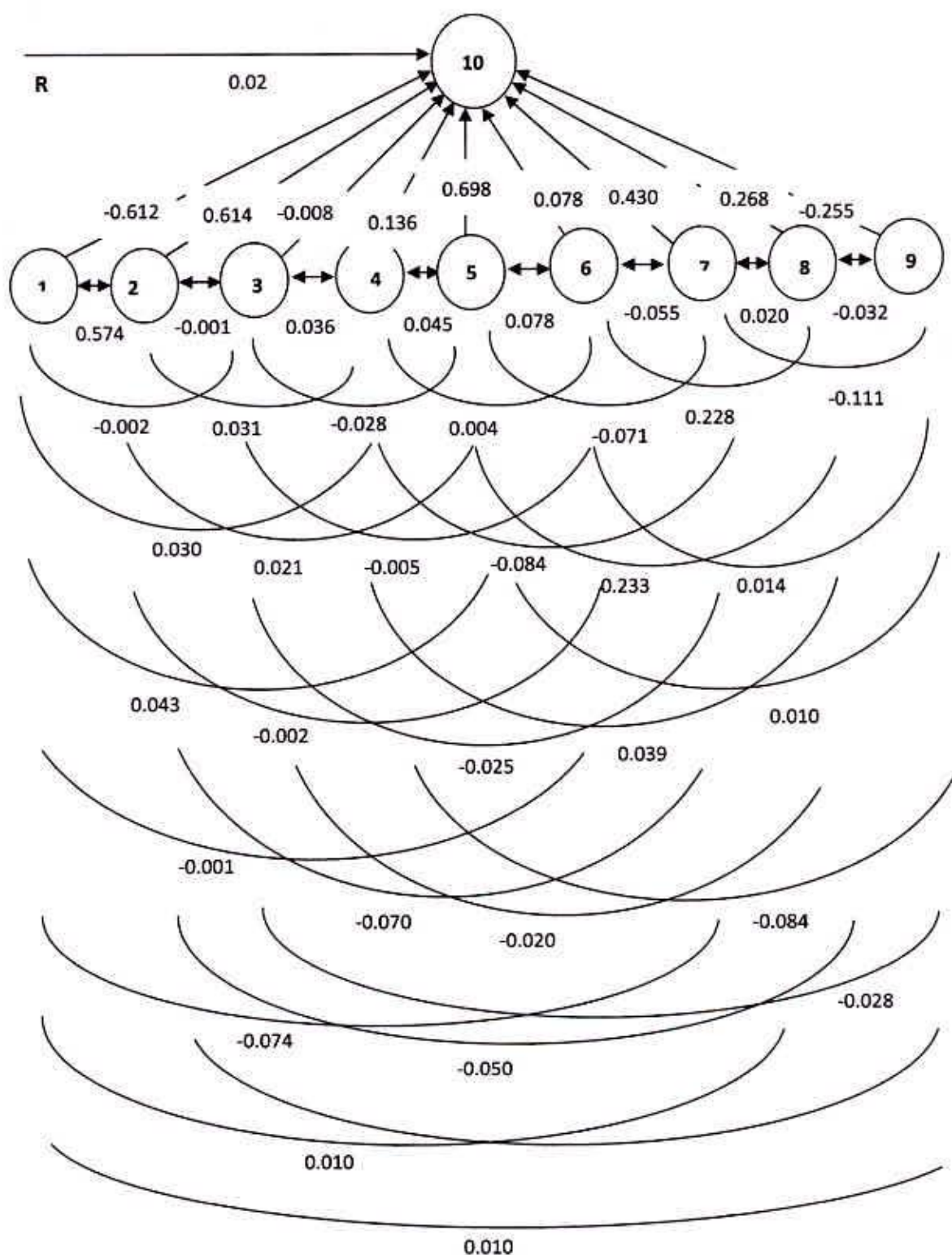


Fig. 1. Path diagram of nine yield and yield contributing characters of twenty two cucumber genotypes

1= Leaf length (cm), 2= Leaf breadth (cm), 3= No. of branch, 4=Male flower, 5= Female flower, 6= Fruits/plant, 7=Weight of fruit, 8= Length of Fruit, 9= Breadth of fruit and 10=yield/plant.
R= residual effects.

4.3.7 Weight of fruit (g)

Weight per fruit had the positive direct effect (0.430) on yield (Table 7). This character also showed positive effect indirect effect through number of leaf length (0.105), number of branch (0.000), and fruit length (0.020). But negative indirect effect through leaf breadth (-0.099), fruit per plant (-0.1010), fruit breadth (-0.111), fruit peduncle length (-0.005), male flower (-0.026) and number of female flower (-0.114) were also found. However, all these effects contributed to result insignificant positive genotypic correlation with yield per plant (0.1941). Significant genotypic correlation between fruit weight and yield further strengthened their reliability in the process of selection for higher yield. The result is in consonance with the finding of Kumaran *et al.* (1998) in pumpkim for this trait. The result is in also agreement with those of Rahman *et al.* (1986) and Narayan *et al.* (1996) finding for this trait in bottle gourd.

4.3.8 Length of fruit (cm)

Fruit length showed positively direct effect (0.268) on yield (Table 7). This character, however, showed positive indirect effect through number of branch (0.001), male flower (0.020), fruit weight (0.032), number of fruit per plant (0.067) and number of female flower (0.607). The negative indirect effects were also observed via leaf length (-0.024) and leaf breadth (-0.114), breadth of fruit (-0.032) which were togetherly contributed to result significant positive genotypic correlation with yield per plant (0.8244). Miah *et al.* (2000) also found similar result in bitter gourd.

4.3.9 Breadth of fruit (cm)

Fruit breadth showed negatively direct effect (-0.255) on yield (Table 7). This character, however, showed positive indirect effect through leaf length (0.072), leaf breadth (0.072), fruit weight (0.187), fruit length (0.034), and male flower (0.045). The negative indirect effects were also found number of branch (-0.001), fruit per plant (-0.004) and number of female flower (-0.026) which were contributed to result insignificant positive genotypic correlation with yield per plant (0.745). The result is in also agreement with those of Rahman *et al.* (1986) in

bottle gourd and Parhi *et al.* (1995) in bitter gourd. Chadhury and Mandal (1987) and Mondal *et al.* (1989) also found similar result for fruit breadth in cucumber and water melon, respectively.

4.4 MULTIVARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with twenty-two genotypes of cucumber. First three Eigen values for three principal coordination axes of genotypes accounted for 77.65% variation (Table 8). A two dimensional scattered diagram (Fig. 2) was developed on the basis of the principal component score; Z_1 and Z_2 score (Appendices IV).

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G7 and G13 (2.333) followed by G13 and G18 (2.309) and the lowest distance was observed (0.359) between genotypes G20 and G21 followed by the distance (0.556) between genotypes G3 and G5 (Table 9). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 22 genotypes of cucumber. The highest intra-cluster distance was recorded in cluster III (1.284) containing eight genotypes BD-4207, BD-4234, BD-4309, chamok34, Serena, Alavy, Sishir, CU937F1. The lowest intra-cluster distance was observed in cluster IV (0.707) having six genotype viz. BD-4244 and BD-4251, BD-4256, BD-4308, BD-4315, BD-4320. It favored to decide that intra-group diversity was the highest in cluster III and the lowest in cluster IV. Cluster I having five genotypes viz. BD-4249, BD-4313, Jotti, Green joint, Baromash and had an intra-cluster distance 1.201. Cluster II having three genotypes viz. BD-4305, Mukta, Local and had an intra-cluster distance 1.036.

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among twenty two genotypes of cucumber and grouped them into four clusters. Gaffar

Table 8. Eigen values and percent contribution of 14 yield contributing characters of twenty two cucumber genotypes

Parameters	Eigen values	Percentage of total variation accounted for individual characters	Percentage of cumulative variation
Leaf length (cm)	7.126	36.33	36.33
Leaf breadth (cm)	6.092	31.06	67.39
Leaf Petiole length (cm)	2.011	10.26	77.65
Number of branches per vine	1.508	7.69	85.34
Days to first male flowering	0.965	4.92	90.26
Days to first female flowering	0.639	3.26	93.52
Number of male flowers per plant	0.493	2.51	96.03
Number of female flowers per plant	0.288	1.47	97.50
Number of fruits per plant	0.256	1.31	98.81
Weight of fruit (gm)	0.123	0.62	99.43
Length of fruit (cm)	0.07	0.35	99.78
Breadth of fruit (cm)	0.024	0.13	99.91
Length of peduncle (cm)	0.016	0.08	99.99
Yield per plant (kg)	0.003	0.01	100.00

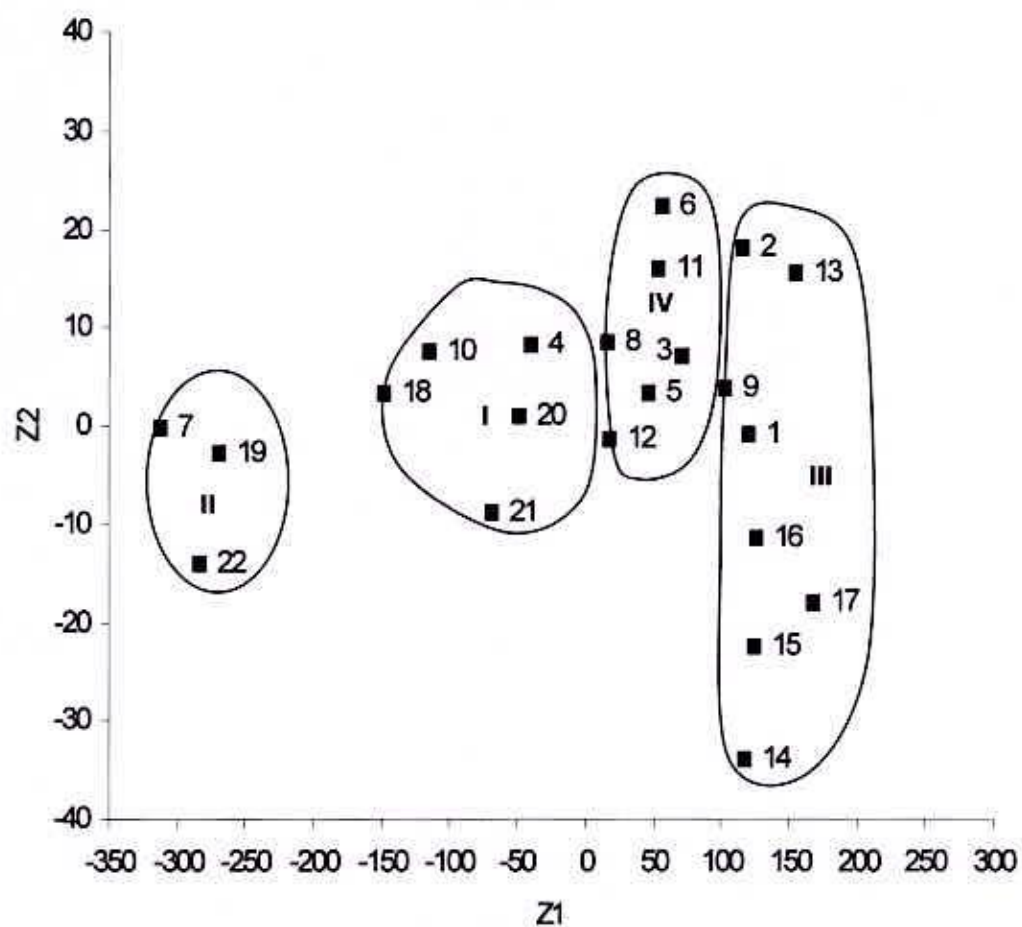


Fig. 2. Scattered diagram of twenty two cucumber genotypes superimpose cluster

(2008) reported similar number of clustering in 15 sponge gourd genotypes. Quamruzzaman *et al.* (2008) reported four clusters, Badade *et al.* (2001) ten clusters in bottle gourd. The clustering pattern obtained coincided with this apparent grouping pattern performed by PCA. So the result obtained through PCA were confirmed by non-hierarchical clustering.

Table 10 represents the clusters occupied by 22 genotypes of cucumber. It explains that cluster III contained the highest number of genotypes eight, cluster IV constitute by six genotypes, cluster I constitute by five genotypes and cluster II constitute by three genotypes. Cluster III was composed of BD-4207, BD-4234, BD-4309, Chamok34, Serena, Alavy, Sishir and CU937F1. The genotypes of cluster III are collected from Plant Genetic Resource Centre, BARI, Gazipur. Cluster mean for 14 traits are presented in (Table 11). From the (table 11), it was observed that the mean value of cluster III ranked first for female flower (20.75), fruit per plant (17.38), yield per plant (1.60). Cluster IV was formed by six genotype viz. BD-4244 and BD-4251, BD-4256, BD-4308, BD-4315, BD-4320. They were collected from Plant Genetic Resource Centre, BARI, Gazipur. Among 14 characters cluster IV produced the maximum cluster mean for the days to first male flowering (54.17), first female flowering (65.67), weight of fruit (100.28g). Among 14 characters cluster II produced the maximum cluster mean for the five characters viz. number of branches per vine (13.67), length of fruit (14.69 cm), number of male flower (557.0), breadth of fruit (13.59 cm) and length of peduncle (1.26 cm). Similarly, cluster I ranked first for leaf breadth (15.04), leaf length (13.00), petiole length (10.34).

4.4.4 Canonical variate analysis

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D² values. Statistical distances represent the index of genetic diversity among the clusters. The highest inter-cluster distance was observed (Table 12 or Figure 3) between cluster II and cluster III (27.666) followed by between cluster II and

Table 9. Ten highest and ten lowest inter genotypic distance among the Twenty two cucumber genotypes

Sl. No.	Genotypic combination	Distances
A. 10 highest inter genotypic distance		
1	Chamok 34 - BD 4305 (G13-G7)	2.333
2	Joti - Chamok 34 (G18-G13)	2.309
3	Baromashi - BD 4309 (G21-G9)	2.139
4	Local – Sishir (G22-G16)	2.105
5	Alavy - BD 4249 (G15-G4)	2.055
6	Green joint - BD 4309 (G20-G9)	2.044
7	Local - BD 4313 (G22-G10)	2.042
8	Sishir - BD 4249 (G16-G4)	2.028
9	CU 937 F1 - BD 4305 (G17-G7)	1.997
10	Baromashi – Joti (G21-G18)	1.995
B. 10 lowest inter genotypic distance		
1	Baromashi - Green joint (G21-G20)	0.359
2	BD 4251 - BD4244 (G5-G3)	0.556
3	BD 4256 - BD 4251 (G6-G5)	0.591
4	Green joint - BD 4315 (G20-G11)	0.602
5	Mukta - BD 4313 (G19-G10)	0.635
6	BD 4315 - BD4244 (G11-G3)	0.656
7	BD 4308 - BD 4251 (G8-G5)	0.657
8	BD 4308 - BD 4234 (G8-G2)	0.673
9	Green joint - BD 4251 (G20-G5)	0.680
10	BD 4308 - BD 4256 (G8-G6)	0.691

Table 10. Distribution of twenty two cucumber genotypes in four clusters

Cluster	Numbers of genotypes	Genotype number	Accession number
1	5	4, 10, 18, 20, 21	BD 4249, BD 4313, Joti, Green joint, Baromashi
2	3	7, 19, 22	BD 4305, Mukta, Local
3	8	1, 2, 9, 13, 14, 15, 16, 17	BD 4207, BD 4234, BD 4309, Chamok 34, Serena, Alavy, Sishir, CU 937 F1
4	6	3, 5, 6, 8, 11, 12	BD 4244, BD 4251, BD 4256, BD 4308, BD 4315, BD 4320

Table 11. Cluster mean of 14 characters of twenty two cucumber genotypes

Parameters	Cluster			
	I	II	III	IV
Leaf length (cm)	13.00	11.27	10.54	10.90
Leaf breadth (cm)	15.04	14.27	12.86	13.45
Leaf Petiole length (cm)	10.34	10.07	8.06	8.13
Number of branches per vine	13.40	13.67	11.00	12.33
Days to first male flowering	50.00	42.67	45.88	54.17
Days to first female flowering	63.40	60.33	55.63	65.67
Number of male flowers per plant	352.80	557.00	140.21	225.17
Number of female flowers per plant	16.20	19.67	20.75	13.00
Number of fruits per plant	13.60	16.00	17.38	11.00
Weight of fruit (gm)	91.33	91.11	94.17	100.28
Length of fruit (cm)	13.25	14.69	14.18	13.44
Breadth of fruit (cm)	11.43	13.59	11.73	12.68
Length of peduncle (cm)	1.22	1.26	1.18	1.12
Yield per plant (kg)	1.30	1.46	1.60	1.10

Table 12. Average intra- and inter-cluster distances of twenty two cucumber genotypes

cluster	Cluster			
	I	II	III	IV
1	1.201			
2	13.514	1.036		
3	14.158	27.666	1.284	
4	6.865	20.099	8.241	0.707

cluster IV (20.099) and between cluster I and cluster III (14.158). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program. However, the highest inter-cluster distance was observed between clusters II and III indicated the genotypes in these clusters were far diverged than those of other clusters. Similarly, the lowest inter-cluster distance was observed between the cluster I and cluster IV (6.865).

Moderate or intermediate distance was found between cluster I and cluster II (13.514). On the other, the highest intra-cluster distance was found in cluster III (1.284) followed by cluster I (1.201). The lowest intra-cluster distance was observed between in cluster IV (0.707). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity existed among the genotype of different groups . Quamrzzaman *et al.* (2008) obtained longer inter-cluster distances than the intra-cluster distances in a multivariate analysis.

Result of different multivariate analysis were superimposed in Figure 3 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

As per scatter diagram the genotypes were apparently distributed into four clusters. It was also revealed that the genotypes of cluster II were more diverse from the genotypes of cluster III. Islam *et al.* (2004) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding, the objective is not only high heterosis but also to achieved high-level production. In the present study the maximum distance existence between cluster II and cluster III. But considering the yield and duration crosses involving cluster II and III may be exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis.

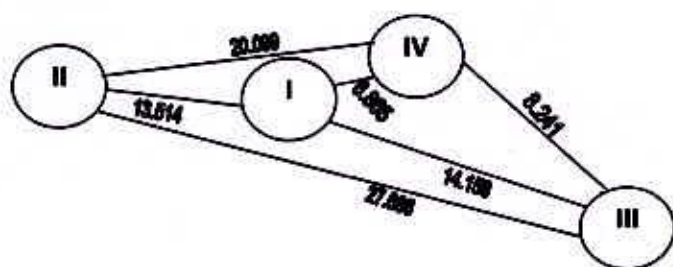


Fig. 3. Diagram showing intra and inter-cluster distances of twenty two genotypes of cucumber



4.4.5 Contribution of characters towards divergence of the genotypes

The values of Vector I and Vector II are presented in Table 13. Vector I obtained from PCA expressed that leaf length (0.7280), petiole length (0.2612), number of female flower (0.1314), fruits per plant (0.0237), fruit breadth (0.0111) fruit peduncle length (1.4305) and yield per plant (1.5726) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to first male flowering (0.1786), number of branches per vine (0.4075), leaf breadth (0.3672), number of male flower (0.0010), fruit weight (0.000), fruit length (0.3315) showed their important role toward genetic divergence. Negative values in both vectors for days to first female flowering had lower contribution towards the divergence.

4.4.6 Selection of genotypes as parent for future hybridization programme

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.*, 1962; Ramanujam *et al.*, 1974; Ghaderi *et al.*, 1984).

Considering the magnitude of cluster mean and agronomic performance the genotype G₁₄ (Serena) for minimum days of first male and female flowering from cluster III; G₀₇ (BD-4305) for maximum fruit weight from II; G₀₉ (BD-4309) for maximum number of fruit per plant and G₁₇ (CU937F1) for maximum number of branches per vine from cluster III were found promising and G₀₆ (BD-4256) for maximum number of fruit breadth from cluster IV. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G₁₄ (Serena) and G₀₇ (BD-4305), G₁₄ (Serena) and G₀₉ (BD-4309) ; G₁₄ (Serena) and G₀₆ (BD-4256) ; G₀₇ (BD-4305) and G₁₇ (CU937F1), G₀₇ (BD-4305) and G₀₉ (BD-4309); G₀₇ (BD-4305) and G₀₆ (BD-4256) may be suggested for future hybridization program.

Table 13. Latent vectors for 14 principal component characters of twenty two cucumber genotypes

Parameters	Vector 1	Vector 2
Leaf length (cm)	0.7280	-0.6726
Leaf breadth (cm)	-0.7558	0.3672
Leaf Petiole length (cm)	0.2612	-0.2306
Number of branches per vine	-0.2692	0.4075
Days to first male flowering	-0.0117	0.1786
Days to first female flowering	-0.0017	-0.0418
Number of male flowers per plant	-0.0636	0.0010
Number of female flowers per plant	0.1314	-0.1367
Number of fruits per plant	0.0237	-0.0033
Weight of fruit (g)	-0.0027	0.0000
Length of fruit (cm)	-0.4437	0.3315
Breadth of fruit (cm)	0.0111	-0.0082
Length of peduncle (cm)	1.4305	-4.8643
Yield per plant (kg)	1.5726	-0.2049



Chapter-5

Summary And Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The present experiment was carried out in the Farm of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh to evaluate the field performance, variability, character association and genetic divergence of twenty two cucumber genotypes using morphological characters.

The field experiment was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant differences were found among the accessions in respect of different characters studied. The maximum value in respect of days to first male flowering (65.00 days) was observed in G₀₉ (BD-4309) and minimum days (32 days) to first male flowering was recorded in G₁₄ (Serena) and G₁₆ (Sishir). Genotype number G₀₆ (BD-4256) recorded the maximum value (80 days) days to first female flowering and lowest days to first female flowering (36 days) was recorded in G₁₄ (Serena). In respect of number of branches per vine, genotype number G₁₇ (CU937F1) recorded the highest value (19) and genotype number G₁₃ (Chamok34) counted the lowest value (7). Genotype number G₄ (BD-4249) was the highest leaf length (16.50 cm) and genotype number G₁₆ (Sishir) was the lowest leaf length (7.00 cm). In case of leaf breadth, the highest value (18.20 cm) was recorded in G₀₄ (BD-4249) and the lowest value was (8.00 cm) recorded in G₁₆ (Sishir). In respect of leaf petiole length, highest value (12.30 cm) was observed in G₁₇ (CU937F1) and the genotype number G₁₆ (Sishir) had the smallest petiole length of (5.20 cm). In case of number of male flower per plant, the highest value (581) was observed in G₇ (BD-4305) and the lowest value (101) was observed in G₁₇ (CU937F1). In case of number of female flowers per plant, the highest value (37) was observed in G₉ (BD-4309) and the lowest value (10) was observed in G₁₁ (BD-4315). Genotype number G₉ (BD-4309) was the highest number of fruit per plant (30) and genotype no. G₁₃ (Chamok34) was the lowest number of fruits per plant (8). In respect of fruit

length, longest fruit (18.23 cm) was observed in G₇ (BD-4305) and the genotype number G₁₉ (Mukta) had the smallest length of (10.70 cm). In case of fruit diameter, the highest value (15.17 cm) was observed in G₆ (BD-4256) and the lowest value (9.57cm) was observed in G₈ (BD-4308). In respect of fruit peduncle length, longest peduncle length (1.63cm) was observed in G₉ (BD-4309) and the genotype no. G₁ (BD-4207) had the smallest length of (0.53 cm). In case of average weight per fruit, the highest value (110g) was observed in G₁₈ (Joti) and the lowest value (70 g) was observed in G₁₄ (Serena) and G₄ (4249). The highest average yield per plant (3.09 kg) was in G₁₈ (Joti) and the lowest yield per plant (0.64 kg) was recorded in G₄ (BD-4249).

The phenotypic variance was higher than the corresponding genotypic variance in all the characters, indicating greater influence of environment on the expression of these characters. The maximum differences between phenotypic and genotypic coefficient of variation were 17.39% and 9.40%, respectively which indicated that the weight of fruit per plant mostly depended on environmental effect. The highest estimated heritability among fourteen yield contributing characters 97.67%, 97.65% and 95.66% was in male flowers per plant, days to first male flowering and days to first female flowering. The lowest heritability was 29.24% in weight of fruit.

The maximum genetic advance was observed in respect of number of male flowers per plant (294.62) and followed by maximum value was 22.18 in respect of genetic advance for days to first female flowering among fourteen characters of cucumber genotypes. The maximum genetic advance in percent of mean (GAMP) was obtained for number of male flowers per plant (109.72%) and the lowest was for weight of fruit (10.47%).

Multivariate analysis was carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat 5.13 software programme. The first three principal characters with Eigen values were contributed 77.65% variation toward divergence. As per as PCA, D² and cluster analysis using the genotypes were grouped into four different

clusters. Cluster I, II, III and IV comprised five, three, eight and six genotypes, respectively.

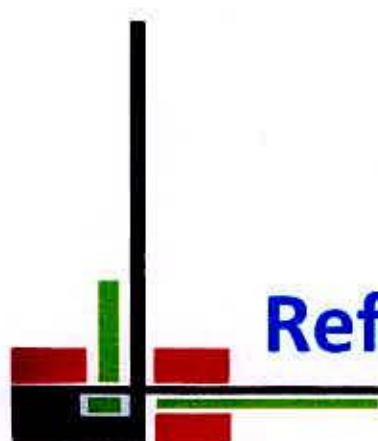
The maximum inter-cluster distance was observed between cluster II and III (27.666) followed by the distance between clusters II and IV (20.099), I and III (14.158), I and II (13.514). The lowest inter-cluster distance was observed between cluster I and IV (6.865) followed by III and IV (8.241).

The highest intra-cluster distance was identified in cluster III (1.284) and the lowest intra-cluster distance was observed in cluster IV (0.707). Genotypes included in cluster IV were suitable for fruit diameter (15.17) and cluster III were suitable for no. of fruit per plant (30.00). Cluster III and VI had the highest mean for days to first male flowering (65 days) and days to first female flowering (80 days), respectively.

Findings of the present study indicated significant variation among the genotypes for all the character studied. Considering diversity pattern and other field performances, the genotypes G_{14} (Serena) from cluster III; G_{07} (BD-4305) from cluster II; G_{09} (BD-4309) and G_{17} (CU937F1) from cluster III and G_{06} (BD-4256) from cluster IV could be best choice as suitable parents for efficient hybridization programme. The inter genotypic crosses between G_{14} (Serena) and G_{07} (BD-4305), G_{14} (Serena) and G_{06} (BD-4256), G_{14} (Serena) and G_{09} (BD-4309); G_{07} (BD-4305) and G_{17} (CU937F1), G_{07} (BD-4305) and G_{06} (BD-4256); G_{07} (BD-4305) and G_{09} (BD-4309) might be suitable choice for future hybridization programme.

The result of the present study revealed that a wide variability exists among the collected cucumber genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of cucumber. From the findings of the present study, the following conclusions could be drawn:

- i. Wide range of genetic diversity existed among the cucumber genotypes. That variability could be used for future breeding programme of cucumber in Bangladesh.
- ii. Selection procedure would be applied for desired characters such as days to first male flower, first female flower and increase number of branches per vine, fruit length, fruit breadth, number of fruits per plant to develop high yielding varieties.
- iii. Further collection of cucumber germplasm would be continued for getting more variability and desired traits in cucumber.



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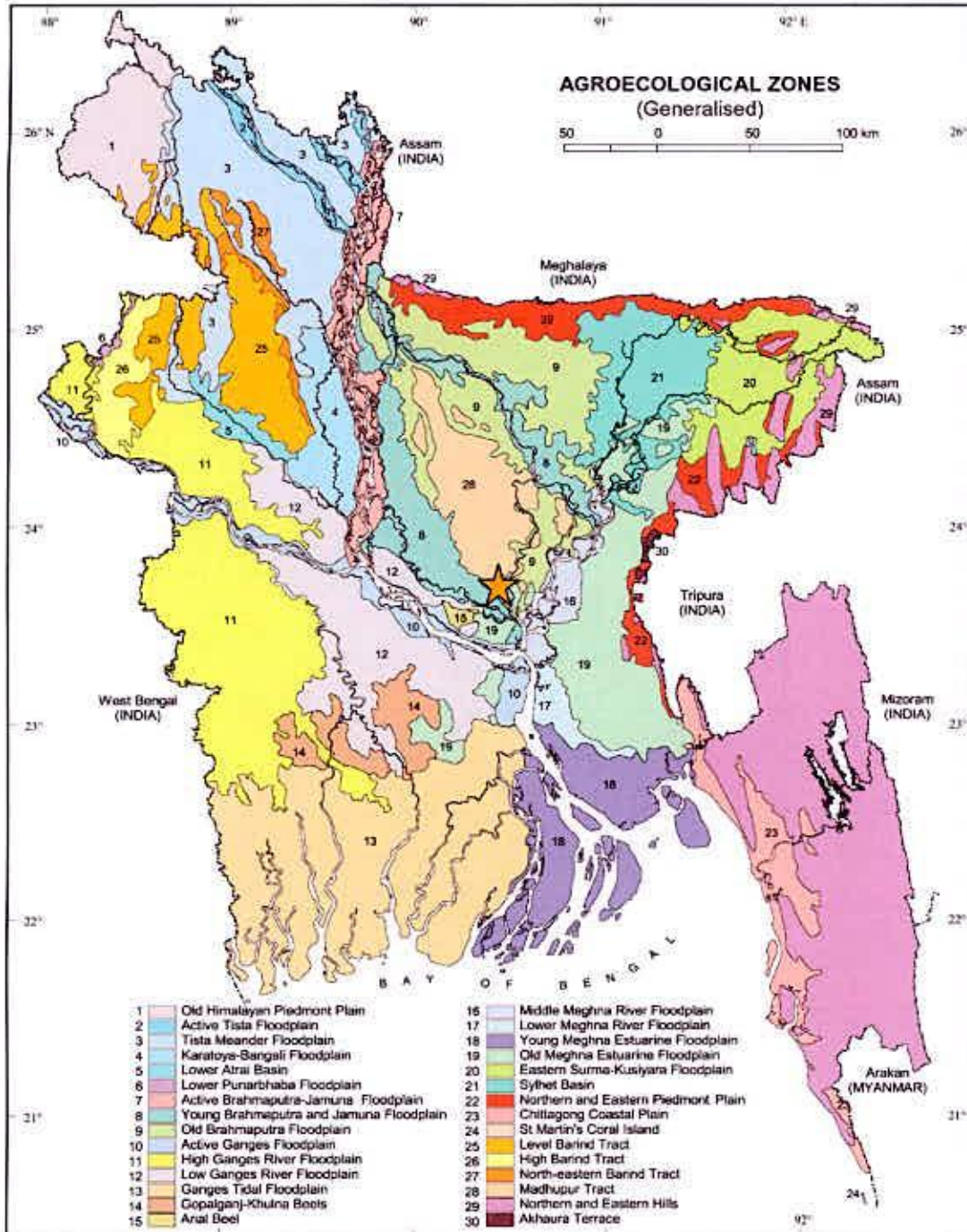
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APPENDICES

Appendix I. Map showing the experimental site under study



★ The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from March, 2010 to September, 2010

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
March, 2010	34.6	16.5	67	45	7.3
April, 2010	35.8	20.3	65	88	8.3
May, 2010	34.7	25.9	70	185	7.8
June, 2010	32.4	25.5	81	628	3.2
July, 2010	31.4	25.7	84	753	4.1
August, 2010	32.4	26.4	80	505	3.6
September, 2010	32.4	25.3	76	203	6.5

Source: Bangladesh Metrological Department (Climate division), Dhaka-1212.

Agargaon,



Appendix III. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day,1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1 : 2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Dhaka

Appendix IV. Principal component score of twenty two genotypes of cucumber

SL NO.	Z1	Z2
G 1	119.50	-1.03
G 2	115.64	17.90
G 3	70.65	7.12
G 4	-40.81	8.29
G 5	45.63	3.24
G 6	56.46	22.30
G 7	-312.47	-0.13
G 8	16.73	8.47
G 9	102.22	3.82
G 10	-115.67	7.47
G 11	53.62	15.87
G 12	17.57	-1.51
G 13	153.78	15.48
G 14	116.49	-34.01
G 15	124.82	-22.56
G 16	126.33	-11.35
G 17	167.62	-17.96
G 18	-148.37	3.20
G 19	-269.71	-2.71
G 20	-48.34	0.97
G 21	-68.38	-8.85
G 22	-283.33	-14.03

38 938
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