GENETIC DIVERSITY AND EVALUATION OF ADVANCED LINES FOR RESISTANCE TO DOWNY MILDEW (*Psuedoperanospora cubensis*) DISEASE IN CUCUMBER [*Cucumis sativus* (L.)]

VEENA, R.

PHK 944

DIVISION OF HORTICULTURE

UNIVERSITY OF AGRICULTURAL SCIENCES

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Affectionately Dedicated To

My Beloved Parents Brother and Friends

DIVISION OF HORTICULTURE

UNIVERSITY OF AGRICULTURAL SCIENCES

G.K.V.K., BENGALURU- 560 065.

CERTIFICATE

This is to certify that the thesis entitled **"Genetic diversity and evaluation of advanced lines for resistance to downy mildew (*Psuedoperanospora cubensis*) disease in cucumber [*Cucumis sativus*(L.)]"** submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (HORTICULTURE)** in **VEGETABLE SCIENCE** of the University of Agricultural Sciences, Bengaluru, is a bonafide record of research work done by Ms. **VEENA, R., ID No. PHK 944** during the period of his study in the University under my guidance and supervision and that no part of this thesis has been submitted for the award of any degree, diploma, associateship, fellowship or other similar titles.

Bengaluru
July, 2011

(Dr. AMRIK SINGH SIDHU)
Director,
IIHR, Bengaluru

Approved By:

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(Dr. AMRIK SINGH SIDHU)

Members: 1.....
(Dr. T. B. PUTTARAJU)

2.....
(Dr. M. PITCHAIMUTHU)

3.....
(Dr. K.V. RAVISHANKAR)

4.....
(Dr. GIRIJA GANESHAN)

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VEENA, R. 2011 Dr. AMREEK SINGH SIDHU

MAJOR ADVISOR

ABSTRACT

An investigation was taken up to assess genetic diversity, heritability, genetic advance, morphological and molecular characterization and screening for downy mildew disease resistance in advanced cucumber lines was conducted at Indian Institute of Horticultural Research (IIHR), Hessarghatta, Bangalore during 2010-2011.

To assess genetic variability and diversity 38 genotypes of diverse origin were tested for 17 quantitative morphological characters. Genotypic and phenotypic variation was high for node at first female and male flower appears and yield per plant. High heritability coupled with genetic advance over mean was recorded for node at first female flower appears and yield per plant. Fruit yield had positive and highly significant association phenotypically and genotypically with 100 seed weight, vine length, number of fruits per plant and flesh thickness. Vine length, number of fruits per plant and flesh thickness had positive and direct genotypic and phenotypic effect on fruit yield per plant.

The cucumber lines were analysed by using 13 RAPD primers those produced 103 DNA marker bands. A total of 67 polymorphic bands were obtained with a mean of 5.15 bands per primer. The cluster drawn out of the distance matrix grouped various genotypes into two major clusters as A and B, then again major cluster A is sub divided into A_1 to A_9. The highest dissimilarity percentage was between genotypes IIHR-409-2 and 595920. The genotypes Swarna Ageti, Sangeeta, Nandini, Barsati, Ajax, VR-101, VR-06-07, Local line, IIHR-405, Karur local, IIHR-407-1, IIHR0409-2 were found to be moderately resistant and *Cucumis hardwickii* showed resistance to the downy mildew.

ಸೌತೆಕಾಯಿ(*ಕುಕುಮಿಸ್ ಸಟೈವಸ್* ಎಲ್.) ಯ ಮುಂದುವರಿದ ಸಾಲುಗಳಲ್ಲಿನ ಅನುವಂಶಿಯ ವೈವಿಧ್ಯತೆ ಹಾಗೂ ಶಿಲಿಂಧ್ರ ಪ್ರತಿರೋಧಕತೆಯ ಮೌಲ್ಯ ಮಾಪನ

ವೀಣಾ, ಆರ್. ಪಿ.ಹೆಚ್.ಕೆ ೯೪೪

ಸಾರಾಂಶ

ಸೌತೆಕಾಯಿ ಬೆಳೆಯು ಕುಂಬಳ ಜಾತಿಗೆ ಸೇರಿದ ಮುಖ್ಯವಾದ ತರಕಾರಿ ಬೆಳೆಯಾಗಿದ್ದು, ಪೋಷಕಾಂಶಗಳನ್ನು ಮತ್ತು ಔಷಧೀಯ ಗುಣಗಳನ್ನು ಹೊಂದಿದೆ. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ೨೦೧೦–೨೦೧೧ ಸಾಲಿನಲ್ಲಿ ತೋಟಗಾರಿಕಾ ಸಂಶೋಧನಾ ಸಂಸ್ಥೆ (ಐ.ಐ.ಹೆಚ್.ಆರ್) ಹೆಸರಘಟ್ಟ, ಬೆಂಗಳೂರು ನಲ್ಲಿ ೩೮ ಸೌತೆಕಾಯಿ ಪ್ರಬೇಧಗಳನ್ನು ಬಳಸಿ ಅನುವಂಶಿಯ ವೈವಿಧ್ಯತೆ ಪರಸ್ಪರ ಸಂಬಂಧ ಪಾಥ ಗುಣಾಂಕ ವಿಶ್ಲೇಷಣೆ, ಅನುವಂಶಿಕ ವೈವಿಧ್ಯತೆ ಸ್ವರೂಪದಲ್ಲಿನ ಆಣ್ವಿಕ ಪಾತ್ರ ಚಿತ್ರಣ ಮತ್ತು ಶಿಲೀಂಧ್ರ ಪ್ರತಿರೋಧಕದ ಮೌಲ್ಯಮಾಪನ ನಿರ್ಣಯಿಸಲು ಕೈಗೊಳ್ಳಲಾಯಿತು.

ಈ ಅಧ್ಯಯನವು ಎಲ್ಲಾ ಗುಣ ಲಕ್ಷಣಗಳಿಗೆ ಅತ್ಯಂತ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸವನ್ನು ಬಹಿರಂಗಪಡಿಸಿದೆ. ಅತಿ ಹೆಚ್ಚು ಪಿಸಿವಿ ಮತ್ತು ಜಿಸಿವಿ ಅನುವಂಶಿಯತೆ ಮತ್ತು ಅನುವಂಶಿತ ಪ್ರಗತಿಯ ಮುಂಚಿತವನ್ನು ಮೊದಲ ಹೆಣ್ಣು ಹೂವು ಕಾಣುವ ಗಿಣ್ಣು, ಮೊದಲ ಗಂಡು ಹೂವು ಕಾಣುವ ಗಂಡು ಮತ್ತು ಪ್ರತಿ ಸಸ್ಯ ಇಳುವರಿಗಳಲ್ಲಿ ಗುರುತಿಸಿದೆ. ಪ್ರತಿ ಗಿಡದ ಇಳುವರಿಯು ಧನಾತ್ಮಕ ಮತ್ತು ಗಮನಾರ್ಹವಾಗಿ ಪರಸ್ಪರ ಸಂಬಂಧವನ್ನು ನೂರು ಬೀಜ ತೂಕ, ಬಳ್ಳಿ ಉದ್ದ, ತಿರುಳಿನ ದಪ್ಪ, ಪ್ರತಿ ಗಿಡದ ಕಾಯಿಗಳ ಸಂಖ್ಯೆಗಳಲ್ಲಿ ಹೊಂದಿದೆ. ಪಾಥ್ ಗುಣಾಂಶದ ವಿಶ್ಲೇಷಣೆಯಲ್ಲಿ ಸರಾಸರಿ ಕಾಯಿಯ ತೂಕ ಮತ್ತು ಪ್ರತಿ ಗಿಡದ ಕಾಯಿಗಳ ಸಂಖ್ಯೆಯಲ್ಲಿ ನೇರ ಹಾಗೂ ಪ್ರತ್ಯಕ್ಷ ಮತ್ತು ಇನ್ನುಳಿದ ಗುಣ ಲಕ್ಷಣಗಳಲ್ಲಿ ಪರೋಕ್ಷ ಪ್ರಭಾವ ಕಂಡು ಬಂದಿದೆ.

೩೮ ಸೌತೆಕಾಯಿ ಸಾಲುಗಳ ಆಣ್ವಿಕ ಪಾತ್ರ ಚಿತ್ರಣವನ್ನು ೧೩ RAPD ಪ್ರೈಮರ್‌ಗಳನ್ನು ಬಳಸಿ ವಿಶ್ಲೇಷಿಸಿದಾಗ ೧೦೩ ಡಿಎನ್‌ಎ ಮಾರ್ಕರ್ ಬ್ಯಾಂಡ್‌ಗಳನ್ನು ನಿರ್ಮಿಸಿತು. ಇವುಗಳ ಪೈಕಿ ೬೭ ಬಹುರೂಪಿ ಬ್ಯಾಂಡ್‌ಗಳಾಗಿದ್ದು ಒಟ್ಟು ಪ್ರತಿ ಪ್ರೈಮರ್‌ಗೆ ೫.೧೫ ತಂಡಗಳ ೧ ಸರಾಸರಿ ಜೊತೆ ಪಡೆಯಲಾಗಿತ್ತು. ಸೌತೆಕಾಯಿ ಸಾಲುಗಳನ್ನು 'ಎ' ಮತ್ತು 'ಬಿ' ಎಂಬ ಎರಡು ಪ್ರಮುಖ ಗುಂಪುಗಳಾಗಿ ವಿಂಗಡಿಸಲಾಯಿತು. 'ಎ' ಗುಂಪನ್ನು ಎ೧ – ಎ೯ ಎಂಬ ಉಪಗುಂಪುಗಳಾಗಿ ವಿಂಗಡಿಸಲಾಗಿದೆ. ಅತಿ ಹೆಚ್ಚು ಅಸದೃಶತೆಯ ಶೇಕಡವಾರು ಜೀನ್ ಮಾದರಿಗಳ IIHR-409-2 ಮತ್ತು 595920 ನಡುವ ಕಂಡು ಬಂದಿತ್ತು. ಸ್ವರ್ಣ ಆಗೇತಿ, ಸಂಗೀತ, ನಂದಿನಿ, ಬರಸಾತಿ, ಅಜಾಕ್ಸ್, ವಿ.ಆರ್–೧೦೧, ಐ.ಐ.ಹೆಚ್.ಆರ್–೪೦೫ ಸಾಲುಗಳಲ್ಲಿ ಮಧ್ಯಮ ನಿರೋಧಕತೆ ಮತ್ತು ಕುಕುಮಿಸ್ ಹಾರ್ಡವಿಕಿ ಯೆಂಬ ಬಯಲು ಮೇಡಿನ ಸಾಲು ಶಿಲಿಂಧ್ರ ಪ್ರತಿರೋಧಕತೆ ತೋರಿಸಿತು.

ಜುಲೈ, ೨೦೧೧ **ಅಮ್ರೀಕ್ ಸಿಂಗ್ ಸಿದ್ದು**

ತೋಟಗಾರಿಕೆ ವಿಭಾಗ **(ಪ್ರಧಾನ ಸಲಹೆಗಾರರು)**

ಜಿ.ಕೆ.ವಿ.ಕೆ. ಬೆಂಗಳೂರು

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Introduction

I INTRODUCTION

The family Cucurbitaceae consists of 118 genera and 825 species with worldwide distribution (Jeffrey, 1990). Cucumber [*Cucumis sativus* (L.)] is one of the popular member of this family with a chromosome number of 2n=14. It is the fourth most widely grown vegetable crop in the world (Tatlioglu, 1993) and mainly grown for its edible tender immature fruits preferred as salad ingredients, dessert fruit and also as cooked and pickled forms. The fruit of cucumber is said to have cooling effect, prevents constipation and also check jaundice and indigestion (Nandkarni, 1927). The crop is of Asian origin, the progenitor may be closely related to its wild ralative *Cucumis sativus* var. *hardwickii*, which was first found in the Himalayan foothills of Nepal. Cucumber cultivation goes back to at least 3000 years in India and 2000 years in china (Robinson and Decker-Walters, 1997). Now, it is extensively cultivated in diverse agro-climatic conditions ranging from tropical to subtropical regions of the world. However, it cannot tolerate freezing temperatures and prefers warm weather with moderate to low humidity for better growth and yield. The geography of India permits it to be grown round the year in regions ranging from plains to mid hills. In India, it is cultivated in an area of 0.23 lakh hectares with an annual production of 1.41 lakh metric tonnes, whereas very world area of 48.46 lakh hectares and the production 704.61 lakh metric tonnes (FAO, 2009).

India being the primary centre of origin, it has accumulated a wide range of variability providing good scope for improvement in yield and other character of cucumber through selection. For any effective selection programme, the information on the nature and the magnitude of variability presents in genetic stocks, heritability and genetic advance are important. Crop improvement to a large extent depends on the existing genetic variability. Considering the importance of a wide genetic

base in plant breeding, identification and characterization of available germplasm is a pre-requisite for estimation of diversity, determination of genetic relatedness, documentation and management of germplasm. This also assumes a greater relevance in the context of intellectual property rights (IPR) and trade related agreements. For this purpose, the available genetic variability has generally been assessed using morphological variation, biochemical distinctness and molecular markers. Though all the three are equally important among the molecular markers like RAPD (Random Amplified Polymorphic DNA), RFLP (Restriction Fragment Length Polymorphism), ISSR (Inter Simple Sequence Repeats), microsatellites *etc.*, provide additional advantages of complete genome coverage, environment insensitivity and developmental stage independence. Molecular markers can be used to assist in the introgression of economically important genes during population improvement and to increase the rate of gain from selection (Bonierbale *et al.*, 1994)

Higher yield and disease resistance are the most important breeding objectives in cucumber improvement programme. Yield is a polygenically governed complex character affected by a large number of various components, the multiplicative interaction of which, results in the yield changes. Hence, knowledge of correlation between yield and component characters and among component characters themselves is essential for a rational and directed improvement in yield. The correlation along with path analysis would give a better appreciation of cause and effect relationship between pairs of characters.(Rao *et al.*, 2004)

Tackling the major disease downy mildew (*Psuedoperanospora cubensis*) in cucumber is another area of improving the yield at farm level. This disease is increasingly becoming a limiting factor for successful cultivation of cucumber in various regions of the country.

Epidemics of downy mildew on the genus *Cucumis* have been observed in over 70 countries over worldwide (Patil, 1974; Cohen, 1981). It causes up to 70% yield loss when infected at vegetative growth stage and almost 100% yield loss at two leaf stage infection (Adam, 2010) Unfortunately, this problem has been a subject of neglect with respect to cultivar improvement programmes. At present, there are virtually no varieties available with considerable amount of resistance to this disease and farmers rely exclusively on application of fungicides. Such unwanted fungicide application has led to an increase in cost of cultivation along with environmental degradation. This is against the principles of sustainable farming which aims at equilibrium between human needs and the economic development within the parameters of environmental conservation to attain welfare of present generation without depriving the needs of future generations. Genetic resistance to these offers a sustainable solution. The resistant cultivars could reduce the dependence on fungicides and also be an effective component of integrated disease management strategy.

Keeping in view, the gravity of the situation, the current program was designed with the following objectives:-

1. To study the variability and association of yield and its components
2. To study the diversity pattern through morphological and molecular markers.
3. To screen the advanced lines for resistance to downy mildew disease.

Review of Literature

II REVIEW OF LITERATURE

An attempt has been made to study the genetic variability, heritability and genetic advance for yield and yield contributing characters in cucumber [*Cucumis sativus* (L.)] The relevant and available literature on different aspects studied during the course of this investigation are reviewed here briefly.

2.1.1 Genetic variability studies in cucumber

Phenotypic coefficient of variation (PCV) is the measure of total variability which is observable. It includes both genotypic and environmental variation and hence changes under different environmental conditions. Genotypic coefficient of variation (GCV) is the measure of inherent or genetic variability which remains unaltered by environmental conditions. This kind of variation is more useful to a breeder for exploitation in selection or hybridization. PCV and GCV are ration of phenotypic and genotypic standard deviations, respectively with mean and expressed in percentage (Burton, 1952).

The ratio of genotypic variance to phenotypic variance or total variance is heritability. Heritability is the heritable portion of phenotypic variance and is a good index of the transmission of characters from parent to off springs (Falconer, 1989). The heritability thus abstracted is broad sense heritability, while the ration of additive component of variance to total phenotypic variance is narrow sense heritability (Lush, 1949). If the heritability of a character is very high, selection for this character would be more effective as there is a close correspondence between genotype and phenotype (Singh, 1991). Heritable variation can be determined with greater accuracy when heritability is studied along with genetic advance (Swarup and Chughale, 1962). High heritability with high genetic gain is associated with additive gene effects (Panse,

1957). On the contrary, non additive gene effect (dominance/epistasis) is associated with characters exhibiting high heritability and low genetic advance.

Cucumber genotypes showed significant differences with regard to vegetative characters, reproductive characters, yield and yield components (Patil and Patil, 1985a; Patil and Patil, 1985b). A considerable amount of variability among the cucumber genotypes was observed for marketable and early fruit number per plot, fruit colour and overall performance (Strefeler and Wehner, 1986).

Solanki and Seth (1980) observed phenotypic coefficient of variation ranging from 10.43 for number of fruits per plant to 71.80 for plant height. Genotypic coefficient of variation was also observed to be lowest for number of fruits per plant (5.99) and highest for plant height (69.03), whereas, the environmental coefficient of variation ranged from 6.89 for days to maturity to 71.20 for fruits yield per plant.

Cucumber variety Pusa Sanyog, recorded maximum vine length (2.4 m) than the other cultivars, *cv*. White Wonder remained dwarf with less number of branches, lesser nodes on main shoot and least internodal length attributable to its inherent nature (Sandhu et al., 1972; Patil and Patil, 1985a).

Cucumber genotypes varied with regard to fruit number in a range of 2.7 fruits per plant to 46.75 fruit per plant. Fruit yield varied from 238 g per vine to 2755 g per vine. Weight of first harvested fruits varied from 14.45 to 62.50 g. Genotypes recording the highest number of fruits failed to record early and higher total yield. Least number of fruit production was attributed to fewer female flowers produced and fruit set (Patil and Patil, 1985b).

Choudhary *et al.* (1985) recorded maximum range of variation for vine length from 1.76 to 3.16 m, fruit diameter from 4.96 to 5.60 cm. Joshi *et al.* (1980) observed variability for vine length, number of branches and fruit diameter of cucumber fruit.

Saikia *et al.* (1995) recorded highest variability for yield per plant followed by node to first female flower and number of leaves per plant. The phenotypic coefficient of variation was maximum for yield per plant and minimum for days to first picking. Genotypic coefficient of variation also followed similar trend which indicated that environmental variability was not marked enough to alter five character expression.

Wide variability was reported by Hossain *et al.,* (2011) for days to seed germination, vine length harvest, petiole length and yield contributing characters namely, days to first male and female flowering, number of fruits per plant, average fruit weight, fruit length and fruit diameter. The highest GCV was recorded in yield per plant (42.75%) where number of fruits per plant (33.41%), fruit length (27.57%), number of lateral shoots (24.19%), average fruit weight (22.14%) in cucumber.

Afangideh and Uyoh (2007) reported high GCV and PCV for vine length, days to flower initiation, fruit length, mean fruit weight and total fruit yield. Yadav *et al.,* (2009) reported considerable presence of amount of genetic variability for vine length, node at first female and male flower appears, number of days to first male and female flower opening, number of fruits per plant and days to first harvest except for cavity of fruit at edible stage. The maximum PCV and GCV was observed for number of days to first female flower anthesis.

Prasad *et al.* (1993) reported that the traits expected to give positive response on the basis of such performance were number of fruits per vine, number of female flowers on primary laterals and

node number of first female flower in bottle gourd. Karuppaiah *et al.* (2002) observed high GCV for number of female flowers per plant, yield per plant, number of fruits per plant and flesh thickness in ridge gourd.

Genotypic coefficient of variation and phenotypic coefficient of variation were highest for yield per plant followed by fruit weight, fruit per plant, keeping quality of fruits and 1000-seed weight. High heritability coupled with high genetic advance was noted for fruit length, 1000-seed weight, average fruit weight and keeping quality of fruit was reported by Rakhi and Rajamony (2005).

2.1.2 Heritability and genetic advance

The heritability is a measure of efficiency of selection system in separating genotypes. Heritable variation can be determined with greater accuracy, when heritability is studied along with genetic advance (Swarup and Chaughale, 1962). High heritability with high genetic gain is associated with additive gene effects (Panse, 1957). On the contrary, nonadditive gene effect (dominance or epistasis) is associated with characters exhibiting high heritability and low genetic advance. Some available literature on various aspects of heritability and genetic advance is given in Table 1.

High heritability and low genetic advance for number of days for appearance of first female flower, number of flowers per vine and fruit length were observed, indicating non-additive gene effects (Johnson *et al.,* 1955; Choudhary *et al.,* 1985)

2.1.3 Correlation studies

Usually more than one trait is measured on progenies evaluated either for a specific trait in cyclical selection programmes or in applied breeding programmes that require a combination of traits to satisfy

Table 1: Literature on heritability and genetic advance in cucumber and other related species for yield and yield components

Crop	GA(%)	h^2	Authority
1.Days to first male flowering			
Cucumber	High	-	Prasad and Singh (1994)
Cucumber	High	Low	Saikia *et al.* (1995)
Cucumber	98.05	32.42	Abusaleha and Dutta (1990)
2. Days to first female flowering			
Cucumber	-	Lowest	Prasad and Singh (1994)
Cucumber	Low 0.32	-	Imam *et al.* (1977)
Cucumber	99.08	Low 40.98	Abusaleha and Dutta (1990)
Cucumber	Low (9%)	-	Serquen *et al.* (1997)
Cucumber	Low to moderate	-	Wehner and Cramer (1996)
Cucumber	High	Low	Saikia *et al.* (1995), Solanki and Seth (1980)
Bittergourd	High	-	Mishra *et al.* (1998)
Ridgegourd	High	Moderate	Varalakshmi *et al.* (1995)
Watermelon	-	94.85	Gopalkrishnan *et al.* (1981)
Pointed gourd	High	-	Singh *et al.* (1992)
Spongegourd	Low	Moderate	Prasad and Singh (1990)

3. Nodal position of first female flowering			
Cucumber	High	High	Prasad and Singh (1994)
Cucumber	98.57	74.68	Abusaleha and Dutta (1990)
Cucumber	High	High	Saikia *et al.* (1995)
Ridgegourd	Low	-	Varalakshmi *et al.* (1995)
Pumpkin	Low	-	Abusaleha and Dutta (1990)
4. Days to first fruit harvest			
Cucumber (early yield)	97.90%	24.70	Rastogi and Aryadeep(1990)
Cucumber (early yield)	Low to moderate	-	Wehner and Cramer (1996)
Cucumber	High	Low	Saikia *et al.* (1995)
Pickling cucumber	68	-	Smith *et al.* (1978)
Bittergourd	18.8	-	Mishra *et al.* (1998)
5. Vine length (m)			
Cucumber	High	Highest	Prasad and Singh (1994)
Cucumber	99.22	77.02	Rastogi and Aryadeep (1990)
Cucumber	91.95	59.26	Rastogi and Aryadeep (1990)
Cucumber	40	-	Serquen *et al.* (1997)
Cucumber	100	High	Saikia *et al.* (1995)
Cucumber	High	High	Choudhary *et al.* (1985), Panse (1957)
Bittergourd	56.79	-	Mishra *et al.* (1998)

Spongegourd	High	High	Prasad and Singh (1990)
Ridgegourd	High	66	Varalakshmi *et al.* (1995)
6. Number of branches per plant			
Cucumber	94.36	73.11	Abusaleha and Dutta (1990)
Cucumber	64.64	High	Rastogi and Aryadeep (1990)
Cucumber	33	-	Serquen *et al.* (1997)
Cucumber	High	High	Choudhary *et al.* (1985), Panse (1957)
Cucumber	High	Low	Solanki and Seth (1980)
Bittergourd	93.0	46.4	Rajput *et al.* (1996)
Ridgegourd	83.87	69	Varalakshmi *et al.* (1995)
Watermelon	Low	Low	Thakur and Nandpuri (1974)
7. Number of fruits/vine			
Pickling cucumber	0.32	-	El-Shawaf and Baker (1981a)
Cucumber	92.47	53.31	Abusaleha and Dutta (1990)
Cucumber	95.94	60.97	Rastogi and Aryadeep (1990)
Pickling cucumber	Moderate (17%)	-	Smith *et al.* (1978)
Cucumber	Lowest	-	Paiva (1997)
Cucumber	High	High	Saikia *et al.* (1995), Choudhary *et al.* (1985), Panse (1957)
Bittergourd	59.93	-	Mishra *et al.* (1998), Ram *et al.* (1997)
Bittergourd	Low	-	Munshi and Sirohi (1994)

Ridgegourd	86.27	92.0	Varalakshmi *et al.* (1995)
Ridgegourd	Highest	Low	Thakur and Choudhary (1965)
Spongegourd	Lowest	Lowest	Panwar *et al.* (1997)
Watermelon	High	High	Thakur and Nandpuri (1974)
Pointed gourd	High	High	Singh *et al.* (1992)
8. Total fruit yield per plant (g)			
Cucumber	96.74	Low (36.55)	Abusaleha and Dutta (1990)
Cucumber	98.50	High (116.56)	Rastogi and Aryadeep (1990)
Cucumber	Low to moderate	-	Wehner and Cramer (1996)
Cucumber	High (100%)	High (57.7%)	Saikia *et al.* (1995)
Cucumber	High	High	Solanki and Seth (1980)
Cucumber	High	-	El-hafez *et al.* (1997)
Bittergourd	91.8	63.8	Rajput *et al.* (1996)
Bittergourd	Low	-	Munshi and sirohi (1994)
Watermelon	High	High	Rajendran and Thamburaj (1994)
Ridgegourd	High (88.46%)	High (113%)	Varalakshmi *et al.* (1995)
Pointed gourd	High	High	Singh *et al.* (1992)

9. Fruit girth (cm)			
Cucumber	High	-	Prasad and Singh (1994)
Cucumber	Low (15.34%)	-	Imam *et al.* (1977)
Cucumber	89.95	35.08	Abusaleha and Dutta (1990)
Cucumber	11	-	Serquen *et al.* (1997)
Cucumber	High	Low	Saikia *et al.* (1995)
Bittergourd	High (91.2%)	Moderate (17%)	Rajput *et al.* (1996)
Bittergourd	83.68	-	Mishra *et al.* (1998)
Ridgegourd	Low (45.71%)	Low (11%)	Varalakshmi *et al.* (1995)
Pointed gourd	High	-	Singh *et al.* (1992)
10. Fruit length			
Cucumber	Highest (56%)	-	Prasad and Singh (1994)
Cucumber	High (54.51%)	-	Imam *et al.* (1997)
Cucumber	94.83	49.68	Abusaleha and Dutta (1990)
Cucumber	Least (8%)	-	Serquen *et al.* (1997)
Cucumber	High	-	Owens *et al.* (1985a)
Cucumber	High	Low	Saikia *et al.* (1995)
Cucumber	Moderately high (0.8)	-	Owens (1983, 1985b)
Cucumber	Intermediate (55%)	-	Smith *et al.* (1978)
Bittergourd	90.5	57.6	Rajput *et al.* (1996)
Bittergourd	77.45	-	Mishra *et al.* (1998)

Ridgegourd	88.19	59	Varalakshmi *et al.* (1995)
11. Flesh thickness (cm)			
Cucumber	-	Highest	Prasad and Singh (1994)
Cucumber	82	44	Abusaleha and Dutta (1990)
Cucumber	100	High	Saikia *et al.* (1995)
12. Average fruit weight (g)			
Cucumber	-	Lowest (2.61%)	Prasad and Singh (1994)
Cucumber	44.18	-	Imam *et al.* (1977)
Cucumber	99.60	96.59	Rastogi and Aryadeep (1990)
Pickling cucumber	Least (2%)	-	Smith *et al.* (1978)
Gherkin	78	-	Koch *et al.* (1991)
Cucumber	Intermediate	-	Owens *et al.* (1985b, 1983)
Cucumber	0-32	-	El-shawaf and Baker (1981)
Cucumber	Moderately high	-	Owens *et al.* (1985a)
Cucumber	High	Low	Solanki and Seth (1980), Ghaderi and Lower, (1979)
Cucumber	High	-	El-hafez *et al.* (1997)
Bittergourd	95.9	30.8	Rajput *et al.* (1996)
Bittergourd	54.71	-	Mishra *et al.* (1998)
Bittergourd	-	Highest	Srivastava and Srivastava (1976)
Ridgegourd	94.18	84	Varalakshmi *et al.* (1995)
Watermelon	High	High	Thakur and Nandapuri (1974)

growers. Although yield is usually the primary trait of interest, yield contributing traits are all corollary traits that a breeder must consider for eventual usefulness of genotypes evaluated. It is only natural, therefore that attention is given to associations among traits during selection and testing of genotypes.

Correlation, measured by a correlation coefficient is important in plant breeding because it measures the degree of association, genetic or non-genetic between two or more characters. If genetic association exists, selection for one trait will cause changes in other traits called the correlated response. The cause of correlation can be genetic and/or environmental. Genetic causes may be attributed to pleiotropism and/or linkage disequilibrium. When genes are not closely linked, linkage disequilibrium is not an important cause of correlation between characters in random mated populations. In such cases the existence of genetic correlations is mostly attributable to pleiotropy (Hallauer and Miranda, 1982).

Phenotypic correlations in cucumbers have been reported by Hutchins (1940), Miller and Quisenberry (1976) and Smith *et al.* (1978). Yield per vine expressed high positive correlation with number of female flowers per vine, number of fruits per vine, fruit length and weight, both at genotypic and phenotypic levels. Path coefficient analysis revealed number of female flowers per vine, number of fruits per vine, fruit length, fruit diameter and fruit weight to be important yield contributing characters (Choudhary and Mandal, 1987).

Fruit yield per vine was positively correlated both at phenotypic and genotypic levels with node at which first female flower appeared, number of days to first female flower appearance, number of female flowers per vine, sex ratio, number of fruits per vine, average fruit weight and number of primary branches per vine. Path coefficient analysis

showed number of fruits per vine and average fruit weight to be the most important variables (Nagaprosuna and Rama Rao, 1989).

Haribabu (1985) observed fruit yield was positively correlated with fruit weight (0.62), number of fruits (0.18) and vine length (0.19). Thus, only mean fruit weight contributed more towards yield and not vine length or fruit number. Rastogi and Aryadeep (1990) also found that fruit yield recorded was positive and highly significantly associated with genotypic, phenotypic and environmental levels with fruit weight and number of fruits per plant.

Abusaleha and Dutta (1988) reported that yield was positively correlated with fruit length, fruits per vine, fruit girth, flesh thickness and days to male and female flowering, number of primary branches has direct significant effect on total fruit yield and influence the other yield contributing characters like number of female flowers per plant, fruit weight and number of fruits per plant. Number of female flowers has positive correlation with number of primary branches and number of fruits per plant. Larger vine length increased the number of male flowers per plant and produced heavier fruits.

Prudek and Wolf (1985) observed high and significant correlations (0.87-0.95) between the values of yield components in the parent and in F1 progeny. Jambhale *et al.* (1988) found total fruit weight to be positively correlated with parameters of vegetative development.

Wehner and Miller (1984) found that the best correlation with yield in the multiple harvest test was obtained when all the fruit from the plots were counted rather than those of marketable size. On the contrary, total fruit yield had a large positive correlation with marketable (0.75-1.25) and early (0.61-1.12) fruit yield (Strefeler and Wehner, 1986).

Number of nodes to first female flowering is a fair measure of both sex tendency and maturity. The lower the node number the higher the female tendency and earlier the variety (Shiefriss and Galun, 1956). Genotypic and phenotypic correlations for nodal position of first pistillate flower with lowering time and parthenocarpic yield were high (El-Shawaf and Baker, 1981b). This would help in selecting early and high yielding types.

Strefeler and Wehner (1986) observed highly significant genotypic and phenotypic correlations for the traits, total, marketable and early yield percentage of culled fruit, shape and colour of fruit, seed size and overall performance. Number of female flowers per vine, fruit length, fruit diameter and weight were positively associated with yield. Number of days for first female flower emergence was negatively associated with number of fruits per vine and yield per vine (Choudhary *et al.,* 1985). Rastogi and Aryadeep (1990) observed that number of primary branches per plant had significant effect on total fruit yield and influenced other yield contributing characters like number of female flowers per plant, fruit weight and number of fruits per plant.

Arunkumar *et al.,* (2011) 0bserved character total fruit yield per vine was showed highly significant and positive correlation with total number of fruits per vine, number of good fruits per vine, average fruit weight, fruit length, number of misshaped fruits per vine, fruit diameter, number of branches per vine, number of nodes per vine and vine length. While, it was significant and negatively correlated with days to first male flower, days to first female flower and days to first fruit harvest.

Rao *et al.,* (2004) reported yield was positively correlated with fruit weight, fruit length and flesh thickness both at genotypic and phenotypic levels. Path analysis revealed characters such as fruit weight, number of

fruits per plant, flesh thickness and node number of first female flower are having high direct effect on yield.

Ashishkumar *et al.* (2008) observed that fruit yield could be successfully improved upon by making selection for greater number of primary branches/ plant and number of fruits/plant.

2.2 Genetic Diversity studies in cucumber

2.2.1 Morphological characterization of cucumber Germplasm

Finding out the novel sources of genes for traits of interest is the ultimate use of Germplasm and the primary objective of a breeder. Characterization of cucumber germplasm for the traits such as powdery mildew (Deshpande *et al.,* 1985 and Ahmed *et al.,* 1998) and cucumber mosaic virus (Gahukar and Niriani, 1980; Acharya, 1999 and Milotay, 2003) were reported.

Knowledge on total genetic distances among genotypes is of great importance in plant breeding since it gives and insight into the amount of heterosis that could be derived upon crossing (Nandapuri *et al.* 1975). Majority of the genetic diversity studies deal with the character specific variability in most of the crop plants. Studies pertaining to total genetic distances among genotypes under consideration are rather rare and for this, cucumber is not and exception.

Prasad *et al.* (1993) studied the biological diversity in a population of 32 representative genotypes using Mahalanobis D^2 analysis was used to estimate the genetic distances among 20 cucumber genotypes (Roy and Sharma, 1996). Using eight morphological characters, genotypes were grouped into seven clusters. They reported that yield per plant, number of primary branches per plant, fruit diameter and plant height were highest contributors for D-square values. In a similar way Pandey

and Dhobal (1993) also estimated the genetic distances among thirty cucumber genotypes using multivariate D-square analysis. They classified the accessions from north eastern part of India into seven clusters based on eight morphological characters. Yield per plant, plant height, number of fruits per plant, branches per plant and fruit length contributed maximum for variation.

Mathew *et al.* (2001) studied the genetic divergence in bottle gourd using 28 accessions of bottle gourd and assessed the genetic diversity using Mahalanobis D^2 values and the accessions were grouped into eight clusters. Clustering pattern indicated that there was no association between geographical distribution of accession and genetic divergence.

Over 2000 cucumber accessions from USSR were characterized using morphological, biochemical, physiological and other evaluations such as degree of compatibility, dominance, cross pollination, homologousness in adaptive standards of reaction under stress effects and correlation dependence (Samovol *et al.,* 1987). They found that distant ancestral forms have significant potential of genetic resources of commercially valuable traits.

2.2.2 Molecular characterization of cucumber genotypes

The discovery of molecular markers has greatly enhanced the scope for detailed genetic analysis and approaches to improve crop plants. These markers act as excellent tools to study the genetic diversity, eliminate duplication in Germplasm, study genetic relationship and linkage analysis and fingerprinting leading to plant varietal protection.

The discovery of Polymerse Chain Reaction (PCR) [Mullis *et al.,* 1986; Mullis and Faloona, 1987; Amas and Pitrat, 1996; Ronning *et al.,* 1999] has led to the development of a class of dominant genetic system

named Random Amplified Polymorphic DNA (RAPD). RAPD involves PCR amplification of total genomic DNA using single random primer (usually 10 base pair long) and separating amplified fragments by agarose gel electrophoresis. In this reaction, a single species of primer binds to the genomic DNA at two different sites on opposite strands of the DNA template. If these sites are within amplifiable distance, a fragment is amplified. The presence of each amplification product identifies complete or partial strands of the DNA template. If these sites are within amplifiable distance, a fragment is amplified. The presence of each amplification product identifies complete or partial nucleotide sequence homology between the genomic DNA and the oligonuleotide primer at each end of the amplified product. On and average, each primer will direct the amplification of several discrete loci in the genome, making the assay and efficient way to screen for nucleotide sequence polymorphism between individuals (Saikia *et al.,* 1998; Welsh and McClelland, 1990; Williams *et al.,* 1990, Koller *et al.,* 1993; Zheng and Wolf, 2000).

Restriction Fragment Length Polymorphism (RFLP) involves digestion of genomic DNA with cleaving restriction endonucleases (Grodzicker *et al.,* 1974) fractionating the fragments electrophoretically and then preferentially visualising fragments containing particular homologus sequences by hybridizing them to specific DNA prove (Southern hybridization). The co-dominant nature of this marker makes it an efficient tool in fingerprinting, construction of linkage maps and differentiating heterozygotic individuals due to high level of allelic diversity. However involvement of radioactive probes and labour intensive and expensive nature makes use of RFLP less extensive (Dijkhuizen *et al.,* 1996; Zheng and Wolf, 2000; Pooleg *et al.,* 2002).

Amplified Fragment Length Polymorphism (AFLP) markers involve restriction of the DNA and ligation of oligation of oligonuleotide adapters,

selective amplification of sets of restrictions, fragments and gel analysis of the amplified fragments. AFLP is very efficient dominant marker to reveal restriction fragment polymorphisms, generate fingerprints of any DNA regardless of the origin or complexity and construct genetic marker maps (Vas *et al.,* 1995). However, the technology is intensive and involves the use of radioactive probes.

Microsatellite markers involve the amplification of tandem repeats in the genomic DNA. Highly conserved nature of these repeat sequences (1-6 base pairs) make them unique for each individual (Litt and Luty, 1989). Microsatellite markers are co-dominant in nature, PCR based, and exhibit high-level of polymorphism even between near isogenic lines. These markers are less elaborate, demanding comparatively lesser time, do not involve radioactive probes and cable of performing all the functions of RFLP, including phylogenetic studies and gene mapping.

Maintaining maximum variability even with limited number of accessions is the objective of gene banks. Identification and conservation of a representative sample, which would depict the characteristics of a group of accessions, will help to save the space and effort in gene banks. For this purpose, and algorithm to identify maximally diverse core collections was designed (Marita *et al.,* 2000). Lines representing 18.5 per cent of population based on RAPD variation were selected. Depending on the core size needed, zone around each accession were decided and no other accession within this zone were selected.

RAPD is a dominant marker, which often fails to distinguish between the lines of close genetic makeup or near isogenic lines. This condition arises when the polymorphic bands generated using random decamers is limited or nil.

Lepse (2000) studied the comparison of inbreeding and family selection on the homogenization of cucumber population using RAPD markers. Coefficient of similarity calculated from the results of RAPD analysis did not prove a high level of diversity between inbred lines and families and the dendrogram showed the segregation of genotypes during inbreeding.

Sese *et al.* (2002) studied the population structure of 15 Spanish melon accessions using 100 RAPD bands produced by 36 primers. A relatively high level of polymorphism (25.6%) was detected using RAPD markers. A high level of heterogeneity observed indicated that the Spanish melon accessions examined possessed a relatively broad genetic back ground.

Staub (2004) studied the molecular methodologies for improved genetic diversity assessment in cucumber the melon. In the study, previously mapped RAPD markers were converted to more multiplexing reactions to increase the assessment efficiency.

Material and Methods

III. MATERIAL AND METHODS

The investigation on assessment of genetic diversity in cucumber using morphological and molecular marker was undertaken during the year 2010-2011. The details of experiments, materials used and techniques adopted in the present investigation are presented in this chapter.

3.1 EXPERIMENTAL SITE

The experiment on genetic diversity using morphological markers was conducted in the Division of vegetable crops of Indian Institute of Horticultural Research (IIHR), Bangalore during *Kharif* season (2010). The soil of the experimental site comprised of red loamy soil. The assessment of molecular diversity using DNA marker Randomly Amplified Polymorphic DNA (RAPD) was carried out in the Molecular Biology Lab, Division of Plant Biotechnology, IIHR, Bangalore.

3.2 LOCATION AND CLIMATE

Bangalore is situated in eastern dry zone of Karnataka state at 13^0 58´ North latitude, 78^0 East longitudes and at an altitude of 890 meters above the mean sea level. Bangalore, which comes under zone-5 of region-3 among the agro-climatic zones of Karnataka, has benefits of both South-West and North-East monsoons. The average rainfall of this area is about 768 mm, distributed over a period of five to six months (May to October) with peaks during September. During experimental period, the meteorological observatory of the IIHR, Bangalore is presented in Appendix I.

3.3 DETAILS OF EXPERIMENT

The experimental plots were ploughed repeatedly and land was brought to a fine tilth. Raised beds were opened at a distance of 2 m

apart. True leaf stage seedlings previously raised in portrays were transplanted at a distance of 60 cm apart on the beds. Gap filling was carried out 7 days after transplanting. Earthing up was taken up as and when required during the crop growth period to support the plant stand and to provide drainage in the plot. About 25 tonnes of FYM and the recommended basal dose of fertilizers @ 30 kg of nitrogen, 50 kg of phosphorus and 80 kg of potash per hectare were incorporated into soil just before sowing as basal dose. The remaining dose of nitrogen i.e., 30 Kg was top-dressed at 30 days after transplanting. Irrigation, weed control and other cultural practices were followed as per the package of practices of UAS, Bangalore. Numbers of genotypes used for the experiment are presented in Annexure I. General view of the experimental field plot is presented in Plate 1. The details of the experiments are as follows.

3.3.1 Experiment I : Studies on genetic variability and diversity in cucumber

Genotypes : 38 (Annexure I)
Replications : Three
Design : Randomized Complete Block Design (RCBD)

3.4 Observations recorded

3.4.1 Plant characteristics

Morphological characterization of accessions with respect to the vegetative and fruit characters was done in three replications using true to type plants in each accession. Open pollinated lines showing variation from standard varietal characters were rouged out. Morphological characters were recorded following descriptors for cucumber given by NBPGR (National Bureau of Plant Genetic Resources), New Delhi. The

Plate 1: General view of experimental block

methodology adopted in recording each character with other details is as follows:-

3.4.1.1 Vine length (m)

Length of the vine was measured for five plants from base to the tip of the plant at the time of final harvest and the average was taken and expressed in meters.

3.4.1.2 Number of nodes per plant

The total number of nodes on the main vine was counted for five plants and the average was recorded during the final harvest.

3.4.1. 3 Node at first female flower appears

The node number from the cotyledonous leaves at which the first female flower appeared was recorded for five plants and the average was taken.

3.4.1.4 Node at first male flower appears

The node number from the cotyledonous leaves at which the first male flower appeared was recorded for five plants and the average was taken.

3.4.1.5 Days to first female flower opening

The number of days taken from day of sowing of seeds to the onset of first female flower on the vine was recorded for five plants and the average was taken.

3.4.1.6 Days to first male flower opening

The number of days taken from day of sowing of seeds to the onset of first male flower on the vine was recorded for five plants and the average was taken.

3.4.1.7 Days to first harvest

The number of days taken from day of sowing of seeds to the first harvest of fruits was recorded for five plants and the average was taken.

3.4.1.8 Number of fruits per plant

The total number of fruits per vine of all harvests was recorded for five plants and the average was taken.

3.4.1.9 Total yield per plant (kg)

The total weight of all marketable fruits obtained per plant was recorded for five plants and the average was expressed in kilograms.

3.4.1.10 Total yield per plot (kg)

The total weight of all the marketable fruits obtained for five plants were added up and expressed in kilograms.

3.4.1.11 Estimated total yield (t/ha)

Yield per hectare was estimated based on net plot yield and expressed in terms of tonnes.

3.4.1.12 Downy mildew incidence

The downy mildew incidence was recorded as scales from 0 to 9 with 0 for resistant plants and 9 for susceptible plants under field/lab conditions.

3.4.2 Fruit Characteristics

Fruit characters were recorded at the time of sixth picking. Five randomly selected completely developed tender fruits from each entry in each replication were used for the observations on fruit characters and mean values were worked out.

3.4.2.1 Average fruit weight (g)

The total weight of fruits divided by the total number of fruits per vine was recorded for five plants and the average was expressed in grams.

3.4.2.2 Fruit length (cm)

Fruits were cut open in the middle at vertical axis and the length of the fruit from stalk to the tip of the fruit was measured for five fruits and the average was expressed in centimetres.

3.4.2.3 Fruit Breadth (cm)

Fruits were cut open in the middle at vertical axis and the breadth of the fruit was measured horizontally at the widest point across the fruit for five fruits and the average was expressed in centimetres.

3.4.2.4 Flesh thickness (cm)

The Fruits were cut open vertically and the thickness of the edible portion without the skin was measured for five fruits and the average was expressed in centimetres.

3.4.2.5 Seed cavity length (cm)

The fruits were cut open vertically and the length of the seed cavity was measured for five fruits from stalk end to the rip of tip of the fruit excluding the flesh thickness and the average was taken and expressed in centimetres.

3.4.2.6 Seed cavity breadth (cm)

The fruits were cut open vertically and the breadth of the seed cavity was measured horizontally for five fruits at the widest point across

the fruit excluding the flesh thickness and the average was taken and expressed in centimetres.

3.4.2.7 Number of seeds per fruit

Number of seeds per fruit was recorded after harvesting of the crop when fruits are dried.

3.4.2.8 100 seed weight (g)

100 seed weight was taken by weighing the hundred random seeds and it was expressed in grams (average of 10 random plants).

3.5 STATISTICAL AND BIOMETRICAL ANALYSIS

The Statistical analysis of the quantitative data obtained during the course of investigation was done by following statistical models as under.

3.5.1 Analysis of variance

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967) using the mean values of random plants in each replication from all treatment to find out the significance of treatment effect.

3.5.1.1 Critical difference

In order to compare the means of variance entries critical difference was calculated by using the following formula.

CD = S.Ed x ' t ' value at error degrees of freedom

$$SEd = \sqrt{\frac{2 \times \text{Error MSS}}{r}}$$

r =Number of replications

t =Tabulated 't' value (at 5 percent or 1 percent probability level)

3.5.2 Estimation of genetic parameters

3.5.2.1 Genotypic, phenotypic and environmental variance

The variance due to genotype, phenotype and environment were computed as follows.

Genotypic variance (σ^2 g) = $\frac{\text{Treatment MSS} - \text{Error MSS}}{r}$

Environmental variance (σ^2 e) = Error mean sum of square

Phenotypic variance (σ^2 p) = σ^2 g + σ^2 e

Where, r is number of replications

3.5.2.2 Genotypic and phenotypic coefficient of variation

The coefficient of variation (CV) being a standardised form of variance, is useful for comparing the extent of variance between different characters with different scales (Singh and Chaudhary, 1979). Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

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

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where, $\bar{X}$ = General mean of the character

σ^2 g = Genotypic variance

σ^2 p = Phenotypic variance

The genotypic and phenotypic coefficients of variation was categorised by Siva Subramanain and Menon (1973), as follows.

0-10% = Low

11-20% = Moderate

>20% = High

3.5.2.3 Heritability

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percentages (Falconer, 1981).

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, $\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The calculated heritability was classified into three groups as suggested by Johnson *et al*, (1955).

0-30% = Low

31-60% = Moderate

>60% = High

3.5.2.4 Expected genetic advance

Genetic advance as per cent of mean for each character was worked out by adopting the following formula given by Johnson *et al*, (1955).

$$\text{Expected genetic advance (GA)} = k \times h^2 \times \sigma^2 p$$

Where, k = Selection differential (2.06) at 5 per cent selection intensity

h^2 = Heritability in broad sense

$\sigma^2 p$ = Phenotypic standard deviation

3.5.2.5 Genetic advance over mean (GAM)

Genetic advance as percentage over mean was worked as suggested by Johnson *et al*, (1955).

$$\text{Genetic advance as per cent of mean (GAM)} = \frac{GA}{\overline{x}} \times 100$$

Where, $\overline{X}$ = General mean of the character

GA = Genetic advance

The genetic advance as percent of mean was categorised by Johnson *et al*, (1955) as follows.

0-10% = Low

11-20% = Moderate

3.5.2.6 Correlation coefficients

Genotypic ($r_{g)}$ and phenotypic (r_p) coefficient of correlation were estimated as per the method suggested by AI – Jibouri et al., (1958).

$$\text{Genotypic correlation} = r_{xy(G)} = \frac{Cov_{xy(g)}}{\sqrt{V_{x(G)} \times V_{y(G)}}}$$

$$\text{Genotypic correlation} = r_{xy(p)} = \frac{Cov_{sy(p)}}{\sqrt{V_{x(P)} \times V_{y(P)}}}$$

$Cov_{xy(G)}$ - Genotypic covariance between x and y

Cov $xy_{(P)}$ – Phenotypic covariance between x and y

$V_{x(G)}$ – Genotypic variance of character x

$Vx_{(P)}$ – Phenotypic variance of character x

$V_{y(G)}$ – Genotypic variance of character y

$Vy_{(P)}$ = Phenotypic variance of character y

Significance of correlations was tested by comparing the obtained values with r values given by Olds (1938).

3.5.2.7 Path coefficient analysis

The estimates of direct and indirect effect were calculated by path coefficient analysis as suggested by Dewey and Lu (1959). The direct coefficients were calculated by solving the following the set of a P simultaneous equations by the abbreviated Doolittle technique as described by Goulden (1959).

$P_{01} + P_{02} y_{12} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{0p} y_{1p} = y_{01}$

$P_{01} y_{12} + P_{02} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{0P} y_{2P} = y_{02}$

$P_{01} y_{10} + p_{2p} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{oP} = y_{oP}$

where,

P_{01}, P_{02} ..... P_{0p} are the direct path effects of 1, 2 ..... p variables on 0 variable.

r_{12}, r_{13} ..... r_{1p}, rp (p-1) are possible correlations coefficients between various independent variables and

r_{01}, r_{02} ..... r_{0p} are the correlations of independent variables with dependent variable.

The indirect effect of i^{th} variable on j^{th} variable was worked out as (P_{oj} x r_{ij}).

Residual effect was calculated as under

$P^2_{ox} = 1-(P^2_{01} + P_{01} P_{02} r_{12} + 2_{01} P_{03} r_{13} + \ldots\ldots P^2 + 2P_{02} P_{03} r_{23} + \ldots\ldots p^2_{op})$

Residual factor = $\sqrt{p^{2ox}}$

>20% = High

3.5.3 Genetic diversity

3.5.3.1 Mahalanobis D^2 analysis

Mahalanobis's (1936) D^2 analysis was employed for assessing the genetic divergence among the test entries. The generalized distance between any two populations is given by formula.

$$D^2 = \sum \lambda ij s^{ai} s^{aj}$$

Where, D^2 = Square of generalized distance

λij = Reciprocal of the common dispersal matrix

s^{ai} = (μi 1 - μi 2)

s^{aj} = (μi 1 - μi 2)

μ = General mean

Since the formulae for computation requires inversion of higher order determinant, transformation of the original correlated un-standardised character mean (Xs) to standardise uncorrelated variable (Ys) was done to simply the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two genotypes (Rao, 1952).

3.5.3.2 Clustering of D^2 values

All the n (n-1)/2 D^2 values were clustered using Tocher's method as described by (Rao, 1952).

3.5.3.3 Average intra cluster distance

The average intra cluster distances were calculated by following the formula given by Singh and Choudhary (1977).

$$\text{Square of intra cluster distance} = \frac{\sum Di^2}{n}$$

Where, $\sum Di^2$ = The sum of distance between all possible combinations of genotype within the cluster average

n = Number of all possible combination

3.5.3.4 Average inter cluster distance

The inter cluster distances were calculated by following the formula given by Singh and Choudhary (1977).

$$\text{Square of inter cluster distance} = \frac{\sum Dj^2}{n}$$

Where, $\sum Dj^2$ = The sum of distance between all possible combinations (ninj) of the entries included in the cluster study

n = Number of all possible combination

3.5.3.5 Clustering based on principle component analysis

Quantitative data was simultaneously used in the PC analysis using morphological data. Qualitative data was used in the form of scores by adopting NBPGR descriptors. Though the genetic variation between the accessions contributing for the variation in qualitative aspects is high, comparatively larger numerical nature of quantitative data smothered qualitative characters. Accessions with higher yield were found to show a higher genetic distance from other accessions, making the qualitative observations insignificant. To give equal weightage for all characters, morphological values were transformed to 0-1 scale using the formula.

$$Vt = \frac{(V - V_{min})}{(V_{max} - V_{min})}$$

Where, V = Value of particular character of any accession

Vt = Transformed value

V_{min} = Minimum value of that character among all accessions

V_{max} = Maximum value of that character among all accessions

3.6 Assessment of genetic diversity through DNA marker using RAPD

Random amplified polymorphic DNA (RAPD) analysis has been employed to characterise and to estimate the genetic distance between 38 cucumber accessions (Annexure I).

3.6.1 Plant material

Just matured leaves free from diseases, especially powdery mildew, downy mildew and viruses and developmental deformities, were collected from the research plot raised for morphological characterization studies. All leaves were collected in the same season characterization studies. All leaves were collected in the same season and plants showing morphological dissimilarities (open pollinated progenies) in a line of inbreds were not selected for collection of leaves. Leaves collected from different plants in a line of single accession were bulked. Fresh leaves were quickly brought to the laboratory in butter paper bags where they are washed with 76% ethanol to remove traces of dirt and used fresh for DNA extraction.

3.6.2.1 DNA isolation

CTAB method (maxi prep) described by Doyle and Doyle (1987) with minor modifications was followed for the isolation of genomic DNA. The protocol followed are given here under. Composition of various reagents used in this study is given in Table 2.

1. Two gram of fresh leaf tissue was ground to fine powder with liquid nitrogen using autoclaved sterile pestle and mortar and 50 mg PVP (polyvinyl pyrrolidone) was added and mixed.

Table 2: Composition of various reagents used in DNA isolation of Cucumber

1. Extraction buffer	1.86g Na EDTA (20mM) and 3.03g Tris HCL (100mM). Dissolve both these in small quantities of water, mix and adjust pH to 8.0, to this add 1.4 mM NaCl (20.45g) and 2% w/w CTAB (Cetyl Trimethyl Ammonium Bromide 5g) by heating to 60^0 C. Make up the volume to 250 ml and stored at 37^0 C. Add 0.2% of β-mercapto ethanol (0.5g) just before use.
2. TBE buffer (10X)	54g Tris base, 27.5g Boric acid, 7.44g EDTA (pH 8.0). Dissolve these in 500ml water and sterilize. Working solution 1X.
3. TE buffer	1.211g Tris HCL (10mM), 0.372g Na EDTA (1mM). Dissolve separately, mix and make up the volume to 1 litre, adjust the pH to 8.0 and sterilize.
4.Chloroformy-isoamylalcohol	24:1 v/v
5. NaCl	5M (146.1g in 500ml and sterilize)
6.Ammonium acetate	7.5M (adjust the pH 7.7 and sterilize)
7. Wash solution	76% Ethanol (v/v); chilled
8. Alcohol	95% Ethanol; stored at -20^0 C
9. Absolute alcohol	99.9% Ethanol; stored at -20^0 C
10. RNAase	10mg/ml; dissolve RNAase in 10mM Tris HCL + 15mM NaCl, pH 5.0, boil for 5 minute and cool to room temperature
11. PVPP	A pinch of required
12. Bromo phenol blue	Stock solution: 0.25% in 50% glycerol Working solution: 200µl stock + 50% glycerol
13.Ethidium bromide	10 mg/ml

2. Before thawing, contents were transferred to 50 ml centrifuge tube containing 10 ml CTAB buffer pre-hearted to 60°C and 100µl of 0, 2% β-mercapto ethanol was added.

3. Tubes were gently inverted several times and incubated for 1 hour at 60°C with intermittent gentle shaking. After the expiry of specified time period, tubes were cooled to room temperature under ordinary conditions and 10ml of chloroform-isoamyl alcohol (24:1) was added.

4. Contents were mixed gently by inverting the tubes about 25 times to form an emulsion.

5. Tubes with emulsion were spun at 5000 rpm for 15 minutes and supernatant aqueous portion was transferred to a new sterile centrifuge using cut tips. While transferring the aqueous portion, utmost care was taken to avoid even traces of debris; and to be on safer side, around 1 ml aqueous portion just above the debris was left behind to avoid proteins.

6. To aqueous portion, 2.5 ml of 5M sodium chloride (laboratory grade) was added and mixed. Again, 10ml cold absolute ethanol was added, mixed gently and refrigerated overnight at -20°C for DNA precipitation.

7. On completion of precipitation, contents were centrifuged initially for 5 minutes at 3000 rpm and subsequently at 5000 rpm for another 5 minutes at room temperature.

8. Supernatant was poured off and pellet was washed with 1 ml 76% ethanol by centrifuging at 5000 rpm for 15 minutes.

9. Washing was repeated for two more times. Supernatant was drained out and ethanol was removed by leaving the tubes

uncapped at 37°C in an incubator, without completely drying DNA.

10. The pellet was resuspended in 0.5 ml TE buffer and pooled using cut tips. RNAase was added to a final concentration of 10µg/ml and incubated at 37°C for 30 minutes. Isolated DNA was transferred to 1-5 ml eppendorff tubes, labelled.

3.6.2.2 Purification of DNA

1. The samples were diluted in 50µl TE buffer. Then 12.5µl of 7.5M Ammonium acetate was added followed by 250µl of cold ethanol. Gently mixed to precipitate DNA and kept at overnight or 1 hr at -20°C
2. Centrifuged at 12000 rpm for 20 minute at 4°C and decanted the supernatant.
3. The DNA pellet was dried at 3 7°C for 15 minute and dissolved in 50µl of TE buffer.

3.6.2.3 Casting of agarose gel

1. The 5µl of DNA sample was taken from the stock then, added 2.5µl of Bromo-phenol dye and mixed by spun at top speed for few seconds. Later this solution was used for gel electrophoresis separation.
2. 0.8% agarose solution in 1X TBE buffer for 100 ml was prepared. The agarose was heated in microwave oven to dissolve completely, and later cooled to 40°C, Ethidium bromide solution (0.5µg/ml) was added and later poured into the cast and then comb was inserted.
3. When the gel was set, the comb was removed carefully and gel was kept it in the gel electrophoresis unit.

3.6.2.4 Running the gel

1. The gel electrophoresis tray was filled with 0.5X TBE buffer. After placing the gel, DNA sample was loaded.
2. 75 volts current was applied for 1½ to 2 hours.
3. Gel was observed under UV light. A zigzag pattern of a single band indicates intact plant DNA.

3.6.3 DNA quantity and quality check

3.6.3.1 DNA quantification

DNA concentration in the sample was estimated by recording absorbance at 260 nm in UV spectrophotometer. Five µl of DNA sample was taken in a quartz cuvette and the volume was made up to 1 ml with TE buffer. Blank values were already recorded using 1 mlTE buffer. The absorbence of DNA solution was measured at 260 and 280 nm. Good DNA preparation exhibited the following spectral properties.

A_{260}/A_{280} = 1.8 to 20.

Higher and smaller ratios indicate the presence of RNA and protein, respectively.

DNA concentration is calculated using the relationship for double stranded DNA.

1 OD at 260 nm = 50 µ/ml

$$\text{Total quantity of DNA (µg/µl)} = \frac{OD_{260} \times 50 \times \text{Dilution factor}}{1000}$$

$$\text{Dilution factor} = \frac{\text{Total volume of extract}}{\text{Volume of aliquot}}$$

$$\text{In this case, } = \frac{1000\mu l}{5\mu l} = 200$$

So, quantity of DNA (µg/µl) = OD_{260} x 10

3.6.3.2 DNA quality check

Quality of isolated DNA was checked by electrophoresis on 0.8% agarose gel which was prepared by dissolving measured quantity of agarose in 1% TE buffer and volume made up with double distilled water. It was heated using microwave oven to dissolve completely, cooled at 40°C and ethidium bromide (0.5 µg/ml) was added. It was quickly poured into tray of which open ends are sealed with cello tapes and combs are inserted. When the gel got set, combs were removed and gel was kept in electrophoresis tank.

Electrophoresis tank was filled with 0.5X TBE buffer such that the gel submerges completely in buffer. Five µl of DNA solution was pipette into a micro centrifuge tube and 2.5 µl of loading dye (bromo phenol blue) was added. Samples were spun for few seconds to bring down the sample and dye to bottom. DNA solution was loaded into the wells and initially 50 V current was applied till DNA leaves the well and later increased to 70 V. Once the dye front reached 90% length of gel, electrophoresis was stopped and the gel was observed under UV. A zig zag pattern of the single intact band indicated good quality DNA.

3.6.2.6 PCR AMPLIFICATION USING RANDOM PRIMERS

Optimisation of reaction conditions should precede the actual RAPD analysis so as to get repeatable results. Following optimisation is essential:

1. Template DNA concentration
2. Taq DNA polymerase concentration
3. Mg^{2+} ion concentration
4. Primer concentration
5. Primer annealing temperature
6. Primer suitable for detection of polymorphic loci in the taxa to be analysed

All the reactions have to be set up under contamination free conditions, as PCR is very sensitive. Therefore the stock solutions are to be opened only under the laminar flow hood or on a clean table. The reaction mixes should be prepared under hood. Used only autoclaved micro-tubes, pipette tips, double distilled sterile water *etc.*,

A) REAGENTS

1. Reaction buffer (10X in 100ml):
   - a] Tris HCl 100mM
   - b] KCl 800mM
   - c] $MgCl_2.6H_20$ 20mM
   - d] TritonX 1%
   - e] Gelatin 1%

   (Adjust the pH to 9.0)

2. Primers : Stock 3µM
3. Taq DNA polymerase : Stock 3U/µl
4. Template DNA : Stock 40ng/µl
5. dNTP's : Stock 1mM (Pipette out 100µl of each dNTP & dilute to 1000 µl)
6. Bromo phenol blue : *Stock solution:* 0.25% in 50% glycerol (*Working solution:* 200µl stock + 200µl of 50 glycerol)

B) PROTOCOL

1. Switched on the thermo cycler at least 15 minute earlier to carry out the PCR.

2. Pipette out the master mix accurately using appropriate auto pipettes into sterile 0.5ml micro tubes. The reagents required for PCR as follows.

Reaction buffer 10X	02.5µl
dNTP's (1mM)	02.0µl
Taq DNA polymerase (1U/ul)	00.04µl
$MgCl_2$ (20mM)	01.00µl
Template DNA (20 ng/µl)	02.00µl
Primer (3 pM)	03.50µl
Water [25µl - (2.5 +2.0 + 1.0 + 2.0+ 3.5+ .04µl)] = 13.60µl	
Total reaction volume	**25.0µl**

3. Mixed by repeated pipetting, spun down the contents for 2 minutes at 2000 rpm.

4. Placed the tubes firmly in the wells of the thermo cycler and set the following temperature programme were optimised.

Step 1 94° C for 4 min

Step 2 94° C for 1 min

Step 3 36° C for 45 sec

Step 4 72° C for 1 min

(***Go to step 6 for 35 times)***

Step 5 72^0 C for 10 min

Step 6 **4^0** C for ever

5. At the end of the run taken out the tubes, added 2.5µl of loading dye and spun for 2-5 seconds at top speed in micro centrifuge and stored at 4°C till electrophoresis.

3.6.3 Analysis of RAPD profiles

3.6.3.1 Screening of primers

Primers were initially screened using pooled DNA (3.5 µl from each) and primers that produced maximum number of scorable bands were selected for RAPD analysis. Amplification profiles of 14 primers (Table 3) in 38 genotypes of cucumber were scored as presence (1) or absence (0) and the 0, 1 matrix generated is used for statistical analysis.

3.6.3.1 Cluster analysis and estimating genetic distance

The presence or absence of data from each study was analysed with the computer package STATISTICA. The distance matrix was developed using Squared Euclidean Distances (SED) that estimated all pair wise differences in the amplification product (Sokal and Sneath, 1973). The genetic distance was computed as,

$$\sum^{n} j = 1 \; dj^2.$$

Where, $dj = (Xik - Xjk)$

Xik = Binary code of i^{th} plant for allele 'k'

Xjk = Binary code of j^{th} plant for allele 'k'

A dendrogram was developed based on Ward's method of clustering using minimum variance algorithm (Ward, 1963).

3.6.5 Statistical analysis

The presence (1) or absence (0) of bands was manually scored for each gel profile. Binary data were subjected for cluster analysis and

Table 3: Random decamer RAPD primers used for diversity studies

Sl. No.	Primer code	Primer sequence (5' to 3')
1.	OPA 05	TGCCGAGCTG
2.	OPA 10	GTCGCCGTCA
3.	OPE 11	GGGCCACTCA
4.	OPE 15	GGAGAGACTC
5.	OPX 01	CACAGAGGGA
6.	OPX 02	AGTCACTCCC
7.	OPX 03	CTCCCTGCAA
8.	OPX 04	CCCCTCACGA
9.	OPX 06	TCCGAGAGGG
10.	OPX 07	ACGCCCAGGT
11.	OPX 09	GAAGCCAGCC
12.	OPX 10	GGACGGCGTT
13.	OPE 03	GACACGGACC

Squared Euclidean Distances (SED) were used to develop dendrogram and dissimilarity matrix.

3.6.5.1 Squared Euclidean Distances (S.E.D)

Euclidean Distance is the geometric distance in the multidimensional space computed as

$$ED(x,y) = \sqrt{\{\sum_i (xi-yi)\}^2}$$

SED are used to give greater weightage on accessions that are further apart.

$$SED\ (x,y) = \sqrt{\{\sum_i (xi-yi)\}^2}$$

xi and yi are the values of x and y accessions, which are under comparison for its character.

3.6.5.2 Percentage polymorphism

Percentage of polymorphic bands over total number of bands was calculated at five per cent level of 38 accessions *ie.*, with not less than 2.8 bands showing presence or absence in single line.

Experimental Results

IV EXPERIMENTAL RESULTS

The present investigation was carried out at Division of Vegetable Crops, IIHR, Bangalore with a view to study the extent of morphological and molecular genetic variability, correlation, path analysis and screening for downy mildew resistance in 38 genotypes of cucumber during 2010-11. The results of the experiment are presented below.

4.1 MORPHOLOGICAL STUDIES IN CUCUMBER

4.1.1 ANALYSIS OF VARIANCE

The mean sum of squares due to various sources of variance for different characters of cucumber genotypes are presented in Table 2. The results indicated highly significant variation among genotypes for all the characters *viz*. vine length, number of nodes per plant, node at which first female flower appears, at which first male flower appears, days to first female flower opening, days to first male flower opening, number of fruits per plant, fruit length, fruit breadth, flesh thickness, seed cavity length, seed cavity breadth, seeds per fruit,100 seed weight, days taken to first harvest, average fruit weight, total yield per plant, yield per plot, expected yield (t/ha).

4.1.2 GENETIC VARIABILITY

The genetic variability estimates for growth and yield characters *viz.*, Range, Mean, Phenotypic co-efficient of variation (PCV), Genotypic co-efficient of variation (GCV), broad sense heritability and Genetic advance as per cent of mean (GAM) and mean *per se* performance of 38 cucumber genotypes for each character are presented in Table-5 and 6.

Table 4: Analysis of variance for quantitative characters in cucumber genotypes.

SV	DF	Mean Sum of Squares																	
		VL	No. NPP	N@ 1st FFA	N@ 1st MFA	D 1st FFO	D 1st MFO	D 1st H	NO. Fr. PP	A Fr. W	Fr. L	Fr. B	Fl T	SCL	SCB	SNo. P Fr	100 SW	Yl. PP	Yl. PP	Yl. Pha
R	2	939.23	6.56	7.22	3.16	22.21	17.91	2.87	0.16	862.16	0.43	0.02	0.01	0.89	0.02	381.38	0.23	0.01	0.24	0.83
Tr	37	2711.92*	67.59*	18.95*	6.07*	95.66*	194.26*	103.38*	7.93*	22974.22*	64.11*	7.82*	0.54*	44.90*	4.22*	13539.78*	1.41*	1.02*	25.61*	88.48*
E	74	845.23	4.09	1.28	1.19	5.82	5.02	6.59	0.42	2731.26	2.55	0.37	0.06	2.32	0.23	225.14	0.03	0.12	3.06	10.57

* = Significant at 5 per cent level of probability

SV= Source of variance
R= Replication
Tr= Treatments
E=Error
VL= Vine length (m)
No. NPP= Number of nodes per plant
N@ 1st FFA= Node at first female flower appears
Fl T= Flesh thickness (cm)
No. Fr. PP= Number of fruits per plant
N@ 1st MFA= Node at first male flower appear
Fr. L= Fruit length (cm)
A Fr. W= Average fruit weight (g)
D 1st MFO= Days to first male flower opening
Fr. B= Fruit breadth (cm)
S No. P Fr= Number of seeds per fruit
D 1st FFO= Days to first female flower opening
SCL= Seed cavity length (cm)
SCB= Seed cavity breadth (cm)
D 1st H= Days to first harvest
100 SW= 100 seed weight (g)
Yl. PP= Yield per plant (kg)
Yl. PP= Yield per plot (kg)
Yl. Pha= Yield per hectare (t/ha)

Plate 2: Diversity in cucumber fruits

Table 5: Variability, heritability and genetic advance for growth and yield of 38 cucumber accessions

Sl. No.	Character/Source	Mean	Range	GV	PV	GCV (%)	PCV (%)	h^2 (%)	GAM (%)
1.	Vine length	1.57	1.07-2.23	622.22	1467.46	15.91	24.43	42.40	21.34
2.	Number of nodes per vine	33.23	24.71-43.27	21.16	25.25	13.84	15.12	83.82	26.11
3.	Node at first female flower appears	5.51	2.00-11.00	5.88	7.17	44.01	48.55	82.17	82.18
4.	Node at first male flower appears	3.51	1.67-6.20	1.62	2.82	36.39	47.88	57.78	56.99
5.	Days to first female flower opening	39.15	27.21-56.40	29.94	35.77	13.97	15.27	83.72	26.34
6.	Days to first male flower opening	36.47	25.23-54.60	63.08	68.10	21.77	22.62	92.63	43.17
7.	Days to first harvest	50.26	36.33-68.00	32.26	38.85	11.30	12.40	83.04	21.21
8.	Number of fruits per plant	6.35	3.90-10.25	2.50	2.92	24.93	26.92	85.78	47.57
9.	Average fruit weight (g)	278.32	65.85-540.00	6747.65	9478.92	29.51	34.98	71.18	51.29
10.	Fruit length (cm)	20.73	6.57-35.71	20.52	23.07	21.84	23.16	88.92	42.44
11.	Fruit breadth (cm)	6.44	2.25-10.71	2.48	2.86	24.47	26.24	86.91	46.99
12.	Flesh thickness (cm)	1.36	0.16-2.68	0.15	0.22	29.40	34.75	71.59	51.25
13.	Yield per plant (Kg)	1.73	0.61-3.13	0.30	0.42	31.70	37.62	71.02	55.04
14.	Yield per plot (Kg)	8.64	3.03-15.64	7.51	10.58	31.71	37.62	71.08	55.08
15.	Estimated yield (t/ha)	16.07	5.63-29.08	25.96	36.54	31.71	37.62	71.07	55.08
16.	Seed cavity length (cm)	15.24	3.97-25.58	14.19	16.51	24.72	26.66	85.97	47.22
17.	Seed cavity breadth (cm)	3.72	1.93-6.13	1.32	1.56	30.94	33.54	85.09	58.80
18.	Seed number per fruit	280.71	164.67-410.67	4438.21	4663.36	23.73	24.32	95.17	47.69
19.	100 seed weight (gm)	2.74	0.82-3.93	0.45	0.49	24.73	25.63	93.10	49.17

GV: Genotypic variance PV: Phenotypic variance GCV: Genotypic coefficient of variation

PCV: Phenotypic coefficient of variation h^2: Heritability GAM: Genetic advance over mean

Table 6: Per se performance of cucumber genotypes for various morphological characters

Sl. No.	Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	Swarna ageti	1.57	26.99	9.67	5.00	44.67	42.67	53.33	4.74	271.79	19.19	5.37	1.13	13.86	3.12	298.67	2.44	1.27	6.36	11.83
2	Punjab naveen	1.46	35.73	8.00	5.33	44.67	42.33	55.33	5.73	251.79	16.95	5.76	1.35	11.91	3.34	294.33	2.54	1.45	7.28	13.52
3	IIHR-34	1.33	29.11	8.13	6.20	45.13	42.33	54.67	3.97	229.17	17.33	4.78	0.71	11.97	3.37	410.67	3.05	0.92	4.58	8.52
4	JLG	1.95	35.07	11.00	4.93	38.29	41.53	51.67	6.57	339.70	35.71	4.23	0.89	25.58	2.45	397.00	2.33	2.20	11.00	20.44
5	Phule shubangi	1.66	28.93	9.00	5.00	43.33	34.33	52.33	7.53	282.14	18.73	5.66	1.16	13.76	3.35	300.67	2.97	2.14	10.68	19.86
6	Himangi	1.20	31.10	9.33	4.67	43.15	39.23	54.67	4.37	268.87	21.00	6.21	1.44	12.83	3.33	279.00	2.46	1.15	5.76	10.71
7	Pebkamal	1.26	36.16	9.67	5.33	39.74	41.88	51.00	6.85	234.88	18.28	5.71	1.25	12.87	3.22	224.67	3.12	1.60	7.98	14.83
8	VS 474	1.95	36.89	8.67	5.67	43.67	38.70	53.33	7.26	251.29	20.17	5.39	1.23	15.00	2.94	164.67	2.05	1.81	9.07	16.85
9	Sangeeta	1.69	43.27	4.33	5.33	33.88	38.07	45.00	7.72	318.57	22.87	5.60	1.42	16.29	2.76	220.00	3.10	2.46	12.31	22.87
10	Nandini	1.38	34.56	8.00	5.33	38.01	37.96	45.00	7.04	306.60	22.38	5.96	1.50	15.62	2.96	232.67	2.83	2.16	10.79	20.07
11	Barsati	2.05	39.12	10.00	5.00	45.33	42.69	52.33	7.16	311.40	20.37	5.72	1.37	14.63	2.99	260.00	3.43	2.25	11.24	20.89
12	SMM	1.72	39.78	4.33	2.33	33.28	37.12	46.00	6.27	208.54	26.34	9.12	1.03	19.22	7.06	372.91	2.48	1.30	6.53	12.14
13	Ajax	1.46	36.05	2.33	0.00	32.00	0.00	38.33	10.25	176.21	16.67	5.30	1.20	11.27	2.90	167.00	2.43	1.81	9.05	16.82
14	Poinsettia	1.49	37.21	5.00	2.67	39.40	36.14	45.74	6.93	183.68	23.60	8.77	1.71	17.31	5.36	245.00	2.38	1.27	6.36	11.83
15	TGB	1.52	42.45	2.00	3.00	36.00	33.00	48.67	8.73	225.35	19.79	7.90	1.98	15.98	3.94	276.67	2.44	1.97	9.83	18.28
16	I595920	1.51	35.57	5.33	2.33	38.02	35.81	49.27	5.67	276.67	18.93	7.77	1.88	12.88	4.00	227.33	2.54	1.55	7.76	14.42
17	VRC-06-08	1.35	33.64	5.50	3.30	37.58	35.17	50.77	5.30	320.00	19.66	8.28	1.86	14.03	4.57	318.00	2.20	1.67	8.35	15.51
18	VR-101	1.71	33.66	5.33	3.84	39.56	37.43	55.41	5.04	403.33	23.33	7.04	1.43	20.00	4.17	185.33	2.20	2.10	10.49	19.49
19	VR-06-07	1.90	41.12	5.93	3.33	39.67	37.96	52.71	4.00	274.33	20.67	9.05	1.46	12.37	6.13	340.10	2.33	1.14	5.70	10.59
20	IIHR-306	2.23	35.39	5.90	3.95	40.45	37.36	52.33	5.17	260.82	18.33	8.39	1.15	17.00	6.09	321.55	3.54	1.37	6.83	12.70
21	IIHR-285	1.71	34.82	7.13	4.32	41.24	38.18	53.12	3.90	193.13	20.15	7.66	1.37	17.69	4.93	347.33	2.46	1.36	6.81	12.66
22	IIHR 34-S4	1.66	36.43	5.33	2.93	40.29	37.81	51.33	7.35	209.89	20.31	8.69	1.59	18.05	5.50	209.67	1.81	1.41	7.03	13.07
23	IIHR-337	1.68	25.34	3.33	2.33	33.47	35.41	45.67	8.57	208.75	19.18	6.00	1.49	14.11	3.02	202.00	2.62	1.37	6.83	12.70

24	Pilibhat local	1.38	34.89	4.33	2.33	48.31	45.88	60.00	4.00	540.00	27.63	10.71	2.68	19.53	4.96	273.33	3.50	2.18	10.88	20.22
25	IIHR-304	1.67	35.08	3.33	5.00	34.59	33.19	46.00	7.30	340.75	22.15	5.55	1.00	16.12	3.55	355.00	3.84	2.48	12.42	23.09
26	local line1	1.38	28.52	3.33	2.00	37.06	34.12	49.00	4.90	235.80	17.63	6.06	1.36	11.82	3.34	292.33	2.65	1.14	5.70	10.59
27	IIHR-81	1.97	26.64	3.33	2.33	42.63	40.37	54.67	6.37	389.11	21.46	6.62	1.19	16.74	4.25	301.48	3.87	2.47	12.36	22.97
28	IIHR-82	1.43	26.01	3.57	2.53	39.24	37.68	50.33	5.68	447.06	24.82	6.94	1.21	19.31	4.52	213.99	3.93	2.54	12.70	23.60
29	IIHR-405	1.38	29.78	4.33	2.33	40.23	37.68	52.67	7.88	397.10	22.17	6.29	1.76	16.82	2.77	317.12	3.67	3.13	15.64	29.08
30	IIHR-36	2.24	27.52	2.33	4.00	35.30	31.90	47.00	4.05	310.00	23.48	5.11	0.81	17.42	3.49	172.55	1.64	1.26	6.28	11.67
31	Kerur local	1.72	28.92	5.00	3.00	39.69	37.60	51.00	4.32	316.83	27.01	7.25	1.30	22.44	4.66	333.33	2.87	1.38	6.89	12.81
32	IIHR-407-1	1.12	24.71	3.67	2.00	41.43	38.48	52.68	7.33	337.17	22.53	5.97	1.71	16.04	2.56	319.33	3.53	2.47	12.33	22.92
33	IIHR-384	1.28	32.79	6.00	4.00	42.79	40.57	55.33	5.98	158.15	13.85	5.62	1.11	8.28	3.40	326.92	1.64	0.94	4.71	8.76
34	Gadag local	1.71	32.71	4.67	3.00	31.85	29.00	44.67	5.23	219.49	16.81	5.19	1.07	12.07	3.05	172.34	3.05	1.15	5.72	10.63
35	IIHR-409-2	1.13	31.41	3.00	2.00	28.28	26.55	39.33	7.71	350.11	24.40	6.25	1.87	17.73	2.50	288.14	3.50	2.70	13.48	25.05
36	IIHR-177	1.41	33.26	2.47	1.67	31.79	29.88	44.67	7.22	208.80	14.85	5.32	1.68	11.49	1.95	317.00	2.85	1.50	7.50	13.93
37	IIHR-338	1.12	28.45	3.60	2.54	27.21	25.23	36.33	8.03	253.17	22.54	5.23	1.04	15.06	3.15	391.67	3.05	2.05	10.24	19.03
38	*Cucumis hardwickii*	1.05	33.49	3.30	2.33	56.40	54.60	68.00	9.16	65.85	6.57	2.25	0.16	3.97	1.93	297.00	0.82	0.61	3.03	5.63
	Mean	**1.56**	**33.23**	**5.51**	**3.51**	**39.15**	**36.47**	**50.26**	**6.35**	**278.32**	**20.73**	**6.44**	**1.36**	**15.24**	**3.72**	**280.71**	**2.74**	**1.73**	**8.64**	**16.07**
	S. Em±	**16.79**	**1.17**	**0.65**	**0.63**	**1.39**	**1.29**	**1.48**	**0.37**	**30.17**	**0.92**	**0.35**	**0.15**	**0.88**	**0.28**	**8.66**	**0.11**	**0.20**	**1.01**	**1.88**
	CD (5%)	**47.29**	**3.29**	**1.84**	**1.77**	**3.92**	**3.64**	**4.17**	**1.05**	**85.00**	**2.60**	**0.99**	**0.41**	**2.48**	**0.78**	**24.40**	**0.30**	**0.57**	**2.84**	**5.29**
	CV (%)	**18.55**	**6.08**	**20.50**	**31.11**	**6.16**	**6.14**	**5.11**	**10.15**	**18.78**	**7.71**	**9.50**	**18.52**	**9.99**	**12.95**	**5.35**	**6.73**	**20.25**	**20.23**	**20.23**

1. Vine length (m)
2. Number of nodes per plant
3. Node at first female flower appear
4. Node at first male flower appear
5. Days to first female flower opening
6. Days to first male flower opening
7. Days to first harvest
8. Number of fruits per plant
9. Average fruit weight (g)
10. Fruit length (cm)
11. Fruit breadth (cm)
12. Flesh thickness (cm)
13. Seed cavity length (cm)
14. Seed cavity breadth (cm)
15. Number of seeds per fruit
16. 100 seed weight (g)
17. Yield per plant (kg)
18. Yield per plot (kg)
19. Estimated yield (t/ha)

4.1.2.1 Vine length (m)

Maximum vine length was observed in IIHR-36 (2.24 m) followed by IIHR-306 (2.23 m) and minimum was observed in *Cucumis hardwickii* (1.05 m) with mean of 16.8 m. The Phenotypic Co-efficient of Variation (PCV) and Genotypic Co-efficient of Variation (GCV) was 24.43 and 15.91per cent respectively. The variance due to phenotype (0.15) was higher than genotypic variance (0.06). This character exhibited moderate heritability (42.40 %) coupled with lower genetic advance as per cent over the mean (21.34 %).

4.1.2.2 Number of node per vine

Highest number of nodes per vine was recorded in Sangeetha (43.27) followed by Tender Green Burbless (42.45) and lowest was recorded in IIHR-407-1 (21.37) with mean of 31.09. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 15.66 and 14.35 per cent respectively. The variance due to phenotype (25.25) was higher than genotypic variance (21.16). This character exhibited high heritability (83.82 %) coupled with low genetic advance as per cent over the mean (26.11 %).

4.1.2.3. Node at first female appears

Genotype Tender Green Burbless shows lower node (2.00) for appearance of female flower followed by Ajax (2.33) and Japanese Long Green shows higher node position (11.00) with mean of 5.51.The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 48.55 and 44.01 per cent respectively. The variance due to phenotype (7.17) was higher than genotypic variance (5.88). This character exhibited high heritability (82.17 %) coupled with very high genetic advance as per cent over the mean (82.18 %).

4.1.2.4. Node at first male appears

Genotype IIHR-177 shows lower node (1.67) for appearance of male flower followed by IIHR-409-2, IIHR-407-1 and local cucumber (2.00) and IIHR-34 shows higher node position (6.20) with mean of 3.51. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 47.88 and 36.39 per cent respectively. The variance due to phenotype (2.82) was higher than genotypic variance (1.62). This character exhibited moderate heritability (57.78 %) coupled with higher genetic advance as per cent over the mean (56.99 %).

4.1.2.5 Days to opening of first female flower

The earliness or lateness is dependent on the number of days taken for its first female flower. The genotype IIHR-338 shows earliest to open first female flower (27.21 days) followed by IIHR-409-2 (28.28 days) and the genotype *Cuucmis hardwickii* took maximum number of days (56.40 days) for female flower opening with mean of 61.68 days. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 15.27 and 13.97 per cent respectively. The variance due to phenotype (35.77) was higher than genotypic variance (29.94). This character exhibited high heritability (83.72 %) coupled with lower genetic advance as per cent over the mean (26.34 %).

4.1.2.6 Days to opening of first male flower

The earliness or lateness is dependent on the number of days taken for its first male flower. The genotype IIHR-338 shows earliest to open first male flower (25.23 days) followed by IIHR-409-2 (26.55 days) and the genotype *Cuucmis hardwickii* took maximum number of days (54.60 days) for male flower opening with mean of 36.47 days. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 22.62 and 21.77 per cent respectively. The variance due to phenotype

(68.10) was higher than genotypic variance (63.08). This character exhibited high heritability (92.63 %) coupled with moderate genetic advance as per cent over the mean (43.17 %).

4.1.2.7 Days to first harvest

The genotype IIHR-338 took minimum number of days (36.33 days) for first harvest followed by Ajax (38.33 days) and *Cucumis hardwickii* took maximum number of days (68.00 days) with the mean of 50.26 days. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 12.40 and 11.30 per cent respectively. The variance due to phenotype (38.85) was higher than genotypic variance (32.26). This character exhibited higher heritability (83.04 %) coupled with lower genetic advance as per cent over the mean (21.21 %).

4.1.2.8 Number of fruits per plant

Maximum number of fruits per plant was observed in Ajax (10.25) followed by *Cucumis hardwickii* (9.16) and minimum number of fruits per plant was observed in IIHR-285 (3.90) with the mean of 6.35. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 26.92 and 24.93 per cent respectively. The variance due to phenotype (2.92) was higher than genotypic variance (2.50). This character exhibited higher heritability (85.78 %) coupled with moderate genetic advance as per cent over the mean (47.57 %).

4.1.2.9 Average fruit weight (g)

Average fruit weight was highest in Pilibhat Local (540.00 g) followed by IIHR-82 (447.06 g) and lowest was observed *Cucumis hardwickii* (65.85 g) with the mean of 278.32. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 34.98 and 29.51 per cent respectively. The variance due to phenotype (9478.92) was higher than genotypic variance (6747.65). This character exhibited moderate

heritability (71.18 %) coupled with moderate genetic advance as per cent over the mean (51.29 %).

4.1.2.10 Fruit length (cm)

Fruit length was maximum in Japanese Long Green (35.71 cm) followed by Pilibhat Local (27.63 cm) and minimum fruit length was recorded in *Cucumis hardwickii* (6.57 cm) with mean of 20.73 cm. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 23.16 and 21.84 per cent respectively. The variance due to phenotype (23.07) was higher than genotypic variance (20.52). This character exhibited higher heritability (88.92 %) coupled with moderate genetic advance as per cent over the mean (42.44 %).

4.1.2.11 Fruit breadth (cm)

Fruit breadth was maximum in Pilibhat Local (10.71 cm) followed by SMM (9.12 cm) and minimum fruit breadth was recorded in *Cucumis hardwickii* (2.25 cm) with mean of 6.44 cm. The Phenotypic and Genotypic co-efficients of variations was 26.24 and 24.47 per cent respectively. The variance due to phenotype (2.86) was higher than genotypic variance (2.48). This character exhibited higher heritability (86.91 %) coupled with moderate genetic advance as per cent over the mean (46.99 %).

4.1.2.12 Flesh thickness (cm)

Flesh thickness was maximum in Pilibhat Local (2.68 cm) followed by Tender Green Burbless (1.98 cm) and minimum flesh thickness was recorded in *Cucumis hardwickii* (0.16 cm) with mean of 1.36 cm. The Phenotypic (PCV) and Genotypic (GCV) co-efficients of variations was 34.75 and 29.40 per cent respectively. The variance due to phenotype (0.22) was higher than genotypic variance (0.15). This character

exhibited moderate heritability (71.59 %) coupled with moderate genetic advance as per cent over the mean (51.25 %).

4.1.2.13 Yield per plant (kg)

Total yield per plant (kg) was maximum in IIHR-405 (3.13 kg) followed by IIHR-409-2 (2.70 kg) and minimum yield per plant was observed in *Cucumis hardwickii* (0.61kg) with mean of 1.73 kg. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 37.62 and 31.70 per cent respectively. The variance due to phenotype (0.42) was higher than genotypic variance (0.30). This character exhibited moderate heritability (71.02 %) coupled with high genetic advance as per cent over the mean (55.04 %).

4.1.2.14 Yield per plot (kg)

Total yield per plot (kg) was maximum in IIHR-405 (15.64 kg) followed by IIHR-409-2 (13.48 kg) and minimum yield per plot was observed in *Cucumis hardwickii* (3.03kg) with mean of 8.64 kg. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 37.62 and 31.70 per cent respectively. The variance due to phenotype (10.58) was higher than genotypic variance (7.51). This character exhibited moderate heritability (71.08 %) coupled with high genetic advance as per cent over the mean (55.08 %).

4.1.2.15 Expected yield (t/ha)

Expected yield was maximum in IIHR-405 (29.08 t/ha) followed by IIHR-409-2 (25.05 t/ha) and minimum yield per plant was observed in *Cucumis hardwickii* (5.63 t/ha) with mean of 16.07 t/ha. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 37.62 and 31.70 per cent respectively. The variance due to phenotype (36.54) was higher than genotypic variance (25.96). This character exhibited moderate

heritability (71.07 %) coupled with high genetic advance as per cent over the mean (55.08 %).

4.1.2.16 Seed cavity length (cm)

Mean seed cavity length was maximum in Japanese Long Green (25.58 cm) followed by Karur Local (22.44 cm) and minimum seed cavity length was recorded in *Cucumis hardwickii* (3.97 cm) with mean of 15.24 cm. The PCV and GCV was 26.66 and 24.72 respectively. The variance due to phenotype (16.51) was higher than genotypic variance (14.19). High heritability (85.97 %) associated with moderate genetic advance as per cent mean (47.22 %) was recorded.

4.1.2.17 Seed cavity breadth (cm)

Mean seed cavity breadth was maximum in Sweet market more (7.06 cm) followed by VR-06-07 (6.13 cm) and minimum seed cavity breadth was recorded in *Cucumis hardwickii* (1.93 cm) with mean of 3.72 cm. The PCV and GCV (33.54 and 30.94) was relatively narrow. The variance due to phenotype (1.56) was higher than genotypic variance (1.32). High heritability (85.09 %) associated with high genetic advance as per cent mean (58.80 %) was recorded for this trait.

4.1.2.18 Number of seeds per fruit

Maximum number of seeds per fruit was recorded in IIHR-34(410.67) followed by Japanese Long Green (397.00) and minimum was recorded in VS474 (164.67) with mean of 280.71. A narrow difference was noticed for PCV and GCV (24.32 and 23.73). The variance due to phenotype (4663.36) was higher than genotypic variance (4438.21). This character exhibited high heritability (95.17 %) coupled with moderate genetic advance as per cent mean (47.69 %) was recorded.

4.1.2.19 100 seed weight (g)

100 seed weight (g) was recorded maximum in IIHR-82 (3.93 g) followed by IIHR-81 (3.87 g) and minimum yield per plant was observed in *Cucumis hardwickii* (0.82 g) with mean of 2.74 g. The Phenotypic (PCV) and Genotypic (GCV) co-efficient of variations was 25.63 and 24.73 per cent respectively. The variance due to phenotype (0.49) was higher than genotypic variance (0.45). This character exhibited high heritability (93.10%) coupled with moderate genetic advance as per cent over the mean (49.17 %).

4.1.3 Association of characters

The genotypic and phenotypic correlation among 17 characters that had strong association with yield is presented in Table 7 and Table 8 respectively.

4.1.3.1 Genotypic correlation

Genotypic correlation among 17 characters was computed. The correlations are described below and presented in Table 7.

Vine length exhibited positive and significant correlation with number of nodes per vine (0.311), average fruit weight (0.375), fruit length (0.455), seed cavity length (0.595), seed cavity breadth (0.295) and yield per plant (0.320). Number of nodes per vine was positively and significantly correlated with fruit breadth (0.305) and flesh thickness (0.326).

Node at first female flower appears had positive and significant correlation with node at first male flower appears (0.798), days to first female flower opening (0.472), days to first male flower opening (0.446) and days to first harvest(0.345). However, it was negative and significantly correlated with number of fruits per vine (-0.316). Node at

Table 7: Genotypic correlation co-efficient among important quantitative character in cucumber

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.000	0.311*	0.053	0.138	-0.217	-0.093	-0.160	-0.196	0.375**	0.455**	0.201	-0.023	0.595**	0.295*	-0.170	0.206	0.320*
2		1.000	0.047	0.064	-0.091	-0.019	-0.086	0.239	-0.074	0.071	0.305*	0.326*	0.058	0.191	-0.040	-0.064	0.183
3			1.000	0.798**	0.472**	0.446**	0.345*	-0.316*	-0.022	0.135	-0.142	-0.172	0.054	-0.068	0.147	-0.079	-0.135
4				1.000	0.384**	0.542**	0.312*	-0.376*	0.032	0.086	-0.267	-0.347*	0.054	-0.112	0.117	-0.044	-0.095
5					1.000	0.753**	0.973**	-0.251	-0.025	-0.297*	-0.059	-0.185	-0.264	0.040	0.097	-0.258	-0.289*
6						1.000	0.818**	-0.387**	0.125	-0.013	0.022	-0.110	0.002	0.101	0.267	-0.118	-0.176
7							1.000	-0.345*	0.029	-0.262	-0.008	-0.130	-0.216	0.067	0.162	-0.270	-0.303*
8								1.000	-0.325*	-0.234	-0.379*	-0.60	-0.228	-0.467**	-0.198	-0.005	0.339*
9									1.000	0.686**	0.335*	0.505**	0.643**	0.076	-0.018	0.669**	0.705**
10										1.000	0.354*	0.301*	0.933**	0.257	0.153	0.354*	0.524**
11											1.000	0.696**	0.423**	0.859**	0.013	0.178	0.030
12												1.000	0.300*	0.231	-0.169	0.329*	0.399**
13													1.000	0.356*	0.087	0.359*	0.510**
14														1.000	0.136	0.004	-0.248
15															1.000	0.158	-0.029
16																1.000	0.730**
17																	1.000

Critical r value @5%-0.275 1%-0.381

1. Vine length (m)
2. Number of nodes per plant
3. Node at first female flower appear
4. Node at first male flower appear
5. Days to first female flower opening
6. Days to first male flower opening
7. Days to first harvest
8. Number of fruits per plant
9. Average fruit weight (g)
10. Fruit length (cm)
11. Fruit breadth (cm)
12. Flesh thickness (cm)
13. Seed cavity length (cm)
14. Seed cavity breadth (cm)
15. Number of seeds per fruit
16. 100 seed weight (g)
17. Yield per plant (kg)

first male flower appears exhibited positive and significant correlation with days to first female flower opening (0.384), days to first male flower opening (0.542) and days to first harvest (0.312). However it was negative and significantly correlated with number of fruits per vine (-0.376) and flesh thickness (-0.347).

Days to first female flower opening exhibited positive and significant correlation with days to first male flower opening (0.753) and days to first harvest (0.973). However it was negative and significantly correlated with number of fruit length (-0.297) and yield per plant (-0.289). Days to first male flower opening exhibited positive and significant correlation with days to first harvest (0.818). However, it was negative and significantly correlated with number of fruits per vine (-0.387). Days to first harvest was negative and significantly correlated with number of fruits per vine (-0.345) and yield per plant (-0.303).

Number of fruits per plant had positive and significant correlation with yield per plant (0.339). However, it was negative and significantly correlated with average fruit weight (-0.325), fruit breadth (-0.379) and seed cavity breadth (-0.467). Average fruit weight had positive and significant correlation with fruit length (0.686), fruit breadth (0.335), flesh thickness (0.505), seed cavity length (0.643), 100 seed weight (0.669) and yield per plant (0.705).

Fruit length had positive and significant correlation with fruit breadth (0.354), flesh thickness (0.301), seed cavity length (0.933), 100 seed weight (0.354) and yield per plant (0.524). Fruit breadth was positively and significantly correlated with flesh thickness (0.696), seed cavity length (0.423) and seed cavity breadth (0.859). Flesh thickness had a positive and significant correlation with seed cavity length (0.300), 100 seed weight (0.329) and yield per plant (0.399). Seed cavity length was positively and significantly correlated with seed cavity breadth

(0.356), 100 seed weight (0.359) and yield per plant (0.510). 100 seed weight had positive and significant correlation with yield per plant (0.730).

4.1.3.2 Phenotypic correlation

Phenotypic correlation among 17 characters was computed. The correlations are described below and presented in Table 8.

Vine length exhibited positive and significant correlation with seed cavity length (0.338).

Node at first female flower appears had positive and significant correlation with node at first male flower appears (0.722), days to first female flower opening (0.364), days to first male flower opening (0.392) and days to first harvest(0.329). Node at first male flower appears exhibited positive and significant correlation with days to first male flower opening (0.409).

Days to first female flower opening exhibited positive and significant correlation with days to first male flower opening (0.750) and days to first harvest (0.902). Days to first male flower opening exhibited positive and significant correlation with days to first harvest (0.793). However, it was negative and significantly correlated with number of fruits per vine (-0.338). Days to first harvest was negative and significantly correlated with number of fruits per vine (-0.275).

Number of fruits per vine had positive and significant correlation with yield per plant (0.369). However, it was negative and significantly correlated with fruit breadth (-0.330) and seed cavity breadth (-0.398). Average fruit weight had positive and significant correlation with fruit length (0.613), fruit breadth (0.336), flesh thickness (0.428), seed cavity length (0.587), 100 seed weight (0.563) and yield per plant (0.746).

Table 8: Phenotypic correlation co-efficient among important quantitative character in cucumber

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.000	0.271	0.040	0.117	-0.086	-0.041	-0.052	-0.043	0.174	0.257	0.107	-0.016	0.338*	0.163	-0.084	0.160	0.214
2		1.000	0.047	0.098	-0.091	-0.023	-0.085	0.249	-0.062	0.051	0.248	0.226	0.051	0.166	-0.040	-0.070	0.172
3			1.000	0.722**	0.364*	0.392**	0.329*	-0.248	-0.002	0.112	-0.126	-0.157	0.062	-0.036	0.140	-0.066	-0.089
4				1.000	0.241	0.409**	0.222	-0.230	-0.030	0.047	-0.190	-0.216	0.034	-0.075	0.101	-0.015	-0.024
5					1.000	0.750**	0.902**	-0.194	-0.006	-0.246	-0.056	-0.150	-0.218	0.025	0.096	-0.231	-0.023
6						1.000	0.793**	-0.338*	0.107	-0.013	0.009	-0.102	-0.004	0.080	0.260	-0.107	-0.133
7							1.000	-0.275*	0.036	-0.235	-0.031	-0.153	-0.190	0.066	0.157	-0.242	-0.214
8								1.000	-0.242	-0.187	-0.330*	-0.050	-0.184	-0.398**	-0.190	-0.029	0.369*
9									1.000	0.613**	0.336*	0.428**	0.587**	0.108	-0.035	0.563**	0.746**
10										1.000	0.377*	0.280*	0.918**	0.281*	0.135	0.333*	0.480**
11											1.000	0.675**	0.424**	0.818**	0.001	0.179	0.090
12												1.000	0.253	0.132	-0.165	0.283*	0.362*
13													1.000	0.369*	0.070	0.327*	0.417**
14														1.000	0.131	0.017	-0.158
15															1.000	0.172	-0.052
16																1.000	0.594**
17																	1.000

Critical r value @5%-0.275 1%-0.381

1. Vine length (m)
2. Number of nodes per plant
3. Node at first female flower appear
4. Node at first male flower appear
5. Days to first female flower opening
6. Days to first male flower opening
7. Days to first harvest
8. Number of fruits per plant
9. Average fruit weight (g)
10. Fruit length (cm)
11. Fruit breadth (cm)
12. Flesh thickness (cm)
13. Seed cavity length (cm)
14. Seed cavity breadth (cm)
15. Number of seeds per fruit
16. 100 seed weight (g)
17. Yield per plant (kg)

Fruit length had positive and significant correlation with fruit breadth (0.377), flesh thickness (0.280), seed cavity length (0.918), seed cavity breadth (0.281), 100 seed weight (0.333) and yield per plant (0.480). Fruit breadth was positively and significantly correlated with flesh thickness (0.675), seed cavity length (0.424) and seed cavity breadth (0.818).

Flesh thickness had a positive and significant correlation with 100 seed weight (0.283) and yield per plant (0.362). Seed cavity length was positively and significantly correlated with seed cavity breadth (0.369), 100 seed weight (0.327) and yield per plant (0.471). 100 seed weight had positive and significant correlation with yield per plant (0.594).

4.1.4 Path coefficient analysis

Path coefficient analysis was carried out to obtain the information on the direct and indirect contributions of different components under investigation that contribute to fruit yield per plant with 16 important characters. The genotypic and phenotypic correlations were partitioned into direct and indirect effects of components on yield and data is presented in Tables 9 and 10.

The yield per plant was considered as effect dependent on 16 independent variables, which are considered as cause. The independent characters were vine length, number of nodes per plant, node at which first female flower appears, at which first male flower appears, days to first female flower opening, days to first male flower opening, number of fruits per plant, fruit length, fruit breadth, flesh thickness, seed cavity length, seed cavity breadth, seeds per fruit, 100 seed weight, days taken to first harvest, average fruit weight.

4.1.4.1 Genotypic path analysis

Vine length had a positive direct effect (0.143) on yield per plant. It also had a positive indirect effect on average fruit weight (0.273) and seed cavity breadth (1.318) and negative indirect effect on fruit breadth (-1.279).

Direct and positive effect was exerted by number of nodes per vine (0.062) on yield per plant. It has shown high positive indirect effect through flesh thickness (1.119), seed cavity breadth (0.856) and number of fruit per plant (0.111) and negative indirect effect on fruit breadth (-1.936). Node at first female flower appears had negative direct (-0.219) effect on yield per plant. It had a high negative through days to first harvest (-0.218) and seed cavity breadth (-0.304) but also had a positive indirect through fruit breadth (0.905) and days to first female flower opening (0.329). Node at first male flower appears had a positive direct (0.117) effect on yield per plant. High indirect positive effect was seen through fruit breadth (1.697) and days to 1st female flower opening (0.267) and high negative indirect effect was seen through days to first harvest (-0.197), number of fruits per vine (-0.175), flesh thickness (-1.192) and seed cavity breadth (-0.499).

Days to first female flower opening showed a direct positive (0.696) effect on yield per plant. But it had a high positive indirect effect through fruit breadth (0.378) and negative indirect effect through days to first harvest (-0.615). Days to first male flower opening showed a direct negative (-0.014) effect on yield per plant. Very high positive indirect effect was seen through Days to first female flower opening (0.524), average fruit weight (0.091) and seed cavity breadth (0.453) but had a negative indirect effect through node at first female flower appears (-0.098), days to first harvest (-0.517), number of fruits per plant (-0.180), fruit breadth (-0.138) and flesh thickness (-0.379).

Table 9: Genotypic path analysis among important quantitative character in cucumber

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	**0.143**	0.019	-0.012	0.016	-0.151	0.001	0.101	-0.091	0.273	0.027	-1.279	-0.079	0.036	1.318	-0.031	0.027
2	0.044	**0.062**	-0.010	0.008	-0.063	0.000	0.054	0.111	-0.054	0.004	-1.936	1.119	0.004	0.856	-0.007	-0.009
3	0.008	0.003	**-0.219**	0.093	0.0329	-0.006	-0.218	-0.147	-0.016	0.008	0.905	-0.590	0.003	-0.304	0.026	-0.010
4	0.020	0.004	-0.175	**0.117**	0.267	-0.008	-0.197	-0.175	0.023	0.005	1.697	-1.192	0.003	-0.499	0.021	-0.006
5	-0.031	-0.006	-0.103	0.045	**0.696**	0.010	-0.615	-0.117	-0.018	-0.018	0.378	-0.635	-0.016	0.180	0.017	-0.034
6	-0.013	-0.001	-0.098	0.063	0.524	**-0.014**	-0,517	-0.180	0.091	-0.001	-0.138	-0.379	0.000	0.453	0.048	-0.016
7	-0.023	-0.005	-0.076	0.036	0.677	-0.011	**-0.632**	-0.160	0.021	-0.016	0.053	-0.447	-0.013	0.300	0.029	-0.036
8	-0.028	0.015	0.069	-0.044	-0.175	0.005	0.218	**0.466**	-0.237	-0.014	2.410	-0.207	-0.014	-2.089	-0.036	-0.001
9	0.054	-0.005	0.005	0.004	-0.018	-0.002	-0.019	-0.151	**0.728**	0.041	-2.132	1.735	0.039	0.341	-0.003	0.088
10	0.065	0.004	-0.030	0.010	-0.207	0.000	0.165	-0.109	0.499	**0.060**	-2.252	1.034	0.057	1.151	0.028	0.047
11	0.029	0.019	0.031	-0.031	-0.041	0.000	0.005	-0.177	0.244	0.021	**-6.356**	2.391	0.026	3.843	0.002	0.024
12	-0.003	0.020	0.038	-0.041	-0.129	0.002	0.082	-0.028	0.368	0.018	-4.426	**3.434**	0.018	1.034	-0.030	0.043
13	0.085	0.004	-0.012	0.006	-0.184	0.000	0.137	-0.106	0.468	0.057	-2.690	1.030	**0.061**	1.592	0.016	0.047
14	0.042	0.012	0.015	-0.013	0.028	-0.001	-0.042	-0.217	0.055	0.016	-5.457	0.793	0.022	**4.476**	0.024	0.000
15	-0.024	-0.002	-0.032	0.014	0.068	-0.004	-0.102	-0.092	-0.013	0.009	-0.085	-0.580	0.005	0.609	**0.180**	0.021
16	0.029	-0.004	0.017	-0.005	-0.180	0.002	0.170	-0.002	0.487	0.021	-1.134	1.130	0.022	0.016	0.028	**0.132**

RESIDUAL EFFECT = 0.0332

1. Vine length (m)
2. Number of nodes per plant
3. Node at first female flower appear
4. Node at first male flower appear
5. Days to first female flower opening
6. Days to first male flower opening
7. Days to first harvest
8. Number of fruits per plant
9. Average fruit weight (g)
10. Fruit length (cm)
11. Fruit breadth (cm)
12. Flesh thickness (cm)
13. Seed cavity length (cm)
14. Seed cavity breadth (cm)
15. Number of seeds per fruit
16. 100 seed weight (g)

Direct and negative effect was exerted by days to first harvest (-0.632) on yield per plant and high positive indirect effect was seen through days to first female flower opening (0.677). Number of fruits per plant had a direct positive effect (0.466) on yield per plant. It had a high positive indirect effect through fruit breadth (2.410) and high negative indirect effect through seed cavity breadth (-2.089).

Average fruit weight showed direct positive effect (0.728) on yield. It also showed high indirect positive effect through flesh thickness (1.735) and negative through fruit breadth (-2.132). Direct and positive effect was shown by fruit length (0.060) on yield per plant. It had high indirect positive effect through days to first harvest (0.165), average fruit weight (0.499), flesh thickness (1.034), seed cavity breadth (1.151) and negative effect through days to first female flowering (-0.207), number of fruits per plant (-0.109) and fruit breadth (-2.252).

Fruit breadth showed very high negative direct effect (-6.356) with the yield per plant. It also had positive indirect effect through flesh thickness (2.391) and seed cavity breadth (3.843). Flesh thickness exerted direct positive effect (3.434) on yield per plant. It also showed indirect positive effect through seed cavity breadth (1.034) and negative effect through fruit breadth (-4.426).

Seed cavity length had a positive direct effect (0.061) on yield per plant. Very high indirect positive effect was observed through days to first harvest (0.137), average fruit weight (0.468), flesh thickness (1.030) and seed cavity breadth (1.592). Indirect negative effect was through days to first female flower opening (-0.184), number of fruits per vine (-0.106) and fruit breadth (-2.690). Direct and positive effect was exerted by seed cavity breadth (4.476) but it also had a high negative indirect effect through fruit breadth (-5.457).

It was observed that number of seeds per fruit (0.180) had a positive and direct effect on yield per plant. It also had a high indirect positive effect through seed cavity breadth (0.609) and negative effect through flesh thickness (-0.580). 100 seed weight showed direct positive effect (0.132) on yield per plant. High indirect positive effect was seen through days to first harvest (0.170), average fruit weight (0.487) and flesh thickness (1.130). It also had a negative indirect effect through days to first female flower opening (-0.180) and fruit breadth (-1.134).

4.1.4.2 Phenotypic path analysis

Vine length had a positive direct effect (0.039) on yield per plant. It also had a positive indirect effect on average fruit weight (0.140), seed cavity length (0.060) and seed cavity breadth (1.318) and negative indirect effect on fruit breadth (-1.279). Direct and positive effect was exerted by number of nodes per vine (0.086) on yield per plant. It has shown high positive indirect effect through number fruits per plant (0.130), flesh thickness (0.134), seed cavity breadth (0.109) and negative indirect effect on fruit breadth (-0.134).

Node at first female flower appears had positive direct (0.022) effect on yield per plant. It had a high negative effect through days to first harvest (-0.030), number of fruit per plant (-0.129) and seed cavity breadth (-0.024) but also had a positive indirect through fruit breadth (0.905) and node at first male flower appears (0.026). Node at first male flower appears had a positive direct (0.036) effect on yield per plant. High indirect positive effect was seen through fruit breadth (0.191) and high negative indirect effect was seen through flesh thickness (-0.128) and seed cavity breadth (-0.049).

Days to first female flower opening showed a direct positive (0.021) effect on yield per plant. But it had a high positive indirect effect through fruit length (0.033), fruit breadth (0.056) and negative indirect effect

Table 10: Phenotypic path analysis among important quantitative character in cucumber

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	**0.039**	0.023	0.001	0.004	-0.002	0.000	0.005	-0.022	0.140	-0.034	-0.108	-0.010	0.060	0.106	-0.007	0.018
2	0.010	**0.086**	0.001	0.004	-0.002	0.000	0.008	0.130	-0.050	-0.007	-0.249	0.134	0.009	0.109	-0.004	-0.008
3	0.002	0.004	**0.022**	0.026	0.008	0.000	-0.030	-0.129	-0.002	-0.015	0.127	-0.093	0.011	-0.024	0.012	-0.008
4	0.005	0.008	0.016	**0.036**	0.005	-0.001	-0.020	-0.120	0.024	-0.006	0.129	-0.128	0.006	-0.049	0.009	-0.002
5	-0.003	-0.008	0.008	0.009	**0.021**	-0.001	-0.082	-0.101	-0.005	-0.033	0.056	-0.089	-0.039	0.016	0.008	-0.026
6	-0.002	-0.002	0.009	0.015	0.016	**-0.001**	-0.072	-0.176	0.086	0.002	-0.009	-0.061	-0.001	0.052	0.023	-0.012
7	-0.002	-0.007	0.007	0.008	0.019	-0.001	**-0.091**	-0.143	0.029	0.031	0.031	-0.091	-0.034	0.043	0.014	-0.028
8	-0.002	0.022	-0.006	-0.008	-0.004	0.000	0.025	**0.520**	-0.194	0.025	0.332	-0.030	-0.033	-0.260	-0.017	-0.003
9	0.007	-0.005	0.000	0.001	0.000	0.000	-0.003	-0.126	**0.802**	-0.082	-0.338	0.254	0.105	0.071	-0.003	0.064
10	0.010	0.004	0.003	0.002	-0.005	0.000	0.021	-0.098	0.492	**-0.134**	-0.379	0.167	0.164	0.184	0.012	0.038
11	0.004	0.021	-0.003	-0.007	-0.001	0.000	0.003	-0.172	0.269	-0.050	**-1.005**	0.401	0.076	0.534	0.000	0.021
12	-0.001	0.019	-0.004	-0.008	-0.003	0.000	0.014	-0.026	0.343	-0.038	-0.679	**0.594**	0.045	0.086	-0.015	0.032
13	0.013	0.004	0.001	0.001	-0.005	0.000	0.017	-0.096	0.471	-0.123	-0.427	0.150	**0.178**	0.241	0.006	0.038
14	0.006	0.014	-0.001	-0.003	0.001	0.000	-0.006	-0.207	0.087	-0.038	-0.822	0.079	0.066	**0.653**	0.011	0.002
15	-0.003	-0.003	0.003	0.004	0.002	0.000	-0.014	-0.099	-0.028	-0.018	-0.001	-0.098	0.013	0.085	**0.088**	0.020
16	0.006	-0.006	-0.001	-0.001	-0.005	0.000	0.022	-0.015	0.451	-0.045	-0.180	0.168	0.058	0.011	0.015	**0.115**

RESIDUAL EFFECT = 0.0332

1. Vine length (m)
2. Number of nodes per plant
3. Node at first female flower appear
4. Node at first male flower appear
5. Days to first female flower opening
6. Days to first male flower opening
7. Days to first harvest
8. Number of fruits per plant
9. Average fruit weight (g)
10. Fruit length (cm)
11. Fruit breadth (cm)
12. Flesh thickness (cm)
13. Seed cavity length (cm)
14. Seed cavity breadth (cm)
15. Number of seeds per fruit
16. 100 seed weight (g)

through days to first harvest (-0.082), number of fruits per plant (-0.101), flesh thickness (-0.089), seed cavity length (-0.039) and 100 seed weight (-0.026). Days to first male flower opening showed a direct negative (-0.001) effect on yield per plant. Very high positive indirect effect was seen through node at first female flower appears (0.009), node at first male flower appears (0.015) Days to first female flower opening (0.016), average fruit weight (0.086), fruit length (0.002), seed cavity breadth (0.052) and number of seeds per fruit (0.023) but had a negative indirect effect through vine length (-0.002), number of nodes per vine (-0.002), days to first harvest (-0.072), number of fruits per plant (-0.176), fruit breadth (-0.009) and flesh thickness (-0.061).

Direct and negative effect was exerted by days to first harvest (-0.091) on yield per plant and high negative indirect effect was seen through number of fruits per vine (-0.143) and flesh thickness (-0.091). Number of fruits per plant had a direct positive effect (0.520) on yield per plant. It had a high positive indirect effect through fruit breadth (0.332) and high negative indirect effect through seed cavity breadth (-0.260). Average showed direct positive effect (0.802) on yield. It also showed high indirect positive effect through flesh thickness (1.735), seed cavity length (0.105) and negative through fruit breadth (-0.338).

Direct and negative effect was shown by fruit length (-0.134) on yield per plant. It had high indirect positive effect through average fruit weight (0.492), flesh thickness (0.167), seed cavity length (0.164), seed cavity breadth (0.184) and negative effect through fruit breadth (-0.379). Fruit breadth showed very high negative direct effect (-1.005) with the yield per plant. It also had positive indirect effect through flesh thickness (0.401) and seed cavity breadth (0.534). Flesh thickness exerted direct positive effect (0.594) on yield per plant. It also showed indirect positive effect through average fruit weight (0.343).

Seed cavity length had a positive direct effect (0.178) on yield per plant. Very high indirect positive effect was observed through average fruit weight (0.471), and seed cavity breadth (0.241). Indirect negative effect was through fruit breadth (-0.427).

Direct and positive effect was exerted by seed cavity breadth (0.653) but it also had a high negative indirect effect through fruit breadth (-0.822).

It was observed that number of seeds per fruit (0.088) had a positive and direct effect on yield per plant. It also had a high indirect negative effect through number of fruits per vine (-0.099) and flesh thickness (-0.098).

100 seed weight showed direct positive effect (0.115) on yield per plant. High indirect positive effect was seen through average fruit weight (0.451) and flesh thickness (0.168). It also had a high negative indirect effect through fruit breadth (-0.180).

4.2 Genetic Diversity

4.2.1 Morphological studies in cucumber

Divergence analysis of 38 cucumber genotypes was performed using D2 statistic in order to identify the divergence genotypes with respect to 17 quantitative morphological characters namely, vine length, number of nodes per plant, node at which first female flower appears, at which first male flower appears, days to first female flower opening, days to first male flower opening, number of fruits per plant, fruit length, fruit breadth, flesh thickness, seed cavity length, seed cavity breadth, seeds per fruit,100 seed weight, days taken to first harvest, average fruit weight and total yield per plant.

Table 11: Clustering patterns of 38 cucumber genotypes based on D^2 analysis

Cluster Number	No. Of accessions in each cluster	Accessions names
I	12	Swarna ageti, Punjab naveen, IIHR-34, Japanese Long Green, Phule shubangi, Himangi, Pebkamal, VS 474, Sangeeta, Nandini, Barsati, Sweet Market More
II	2	Poinsettia, 595920
III	2	VRC-06-08, IIHR-384
IV	2	IIHR-81, IIHR-407-1
V	2	IIHR-405, IIHR-409-2
VI	2	IIHR-177, local line
VII	2	IIHR-82, Gadag local line
VIII	2	VR-101, IIHR-34-S4
IX	2	IIHR-304, IIHR-338
X	2	IIHR-306, Kerur local
XI	2	VR-06-07. IIHR-285
XII	2	IIHR-337, Tender Green Burbless
XIII	2	Pilibhat local, IIHR-36
XIV	1	Ajax
XV	1	*Cucumis hardwickii*

Maximum D2 = 1671.099 Minimum D2 = 35.52184 Current critical D2 value = 545.1926

Table 12: Inter-cluster and intra –cluster (bold) distances among 15 clusters in cucumber based on D^2 analysis

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**211.43**	164.83	209.00	210.77	216.45	199.71	258.77	231.73	274.55	207.35	257.40	299.15	337.77	1026.34	492.41
II		**35.79**	118.90	176.26	187.15	116.99	161.76	74.91	280.19	124.10	183.11	142.14	224.14	882.82	370.59
III			**38.83**	228.02	261.44	102.06	359.05	174.17	237.92	146.26	115.25	222.48	289.05	990.14	249.02
IV				**49.06**	104.57	101.09	144.27	236.57	131.96	135.07	309.95	191.63	322.38	873.52	486.86
V					**53.83**	131.34	207.02	284.73	130.27	186.41	298.80	233.13	369.65	822.67	623.60
VI						**66.78**	203.26	176.75	131.03	123.15	222.60	129.35	284.38	795.02	329.37
VII							**83.18**	186.60	322.83	223.35	428.75	222.37	286.04	807.43	627.07
VIII								**98.00**	383.42	153.37	252.94	166.07	213.48	974.62	367.52
IX									**101.58**	210.23	24.48	273.11	452.97	891.71	578.03
X										**127.66**	170.92	209.35	265.54	1005.82	458.75
XI											**167.00**	389.33	368.75	1156.21	511.56
XII												**191.14**	314.24	820.19	347.09
XIII													**453.90**	1080.21	561.47
XIV														**0.00**	1307.43
XV															**0.00**

Table 13: Inter cluster and intra-cluster (bold) distances among 15 clusters in cucumber based on D analysis

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**14.54**	12.83	14.45	14.51	14.71	14.13	16.08	15.22	16.57	14.40	16.04	17.29	18.37	32.03	22.19
II		**5.98**	10.90	13.27	13.68	10.81	12.71	8.65	16.73	11.14	13.53	11.92	14.97	29.71	19.25
III			**6.23**	15.10	16.16	10.10	18.94	13.19	15.42	12.09	10.73	14.91	17.00	31.46	15.78
IV				**7.00**	10.22	10.05	12.01	15.38	11.48	11.62	17.60	13.84	17.95	29.55	22.06
V					**7.33**	11.46	14.38	16.87	11.41	13.65	17.28	15.26	19.22	28.68	24.97
VI						**8.17**	14.25	13.29	11.44	11.09	14.92	11.37	16.86	28.19	18.14
VII							**9.12**	13.66	17.96	14.94	20.70	14.91	16.91	28.41	25.04
VIII								**9.89**	19.58	12.38	15.90	12.88	14.61	31.21	19.17
IX									**10.07**	14.49	18.01	16.52	21.28	29.86	24.04
X										**11.29**	13.07	14.46	16.29	31.71	21.41
XI											**12.92**	19.73	19.20	34.00	22.61
XII												**13.82**	17.72	28.63	18.63
XIII													**21.30**	32.86	23.69
XIV														**0.000**	36.15
XV															**0.00**

4.2.1.1 Clustering pattern of genotypes

Mahalanobis's D^2 analysis grouped the 38 cucumber genotypes into 15 clusters on the basis of their genetic similarity so that genotypes within a cluster had smaller D^2 value among themselves than those belonging to different clusters. The composition of genotypes in different clusters are presented in Table 11. Cluster-I consists of maximum number of genotypes (twelve) followed by cluster-II to cluster XIII contains two genotypes each. The third biggest cluster was cluster XIV and XV consisting of single genotype of each.

4.2.1.2 Intra and inter cluster divergence in cucumber genotypes

The average intra (within) and inter (between) cluster D^2 analysis values are presented in Table 12 and average intra and inter cluster distances D ($D= \sqrt{D^2}$) are presented in Table 13.

Inter cluster distances of 15 clusters given in Table 13 showed that maximum genetic divergence existed between clusters XIV and XV (36.16) followed by cluster XI and XIV (34.00). The minimum genetic divergence was existed between clusters II and VIII (8.65) followed by clusters IV and VI (10.05). Intra cluster distance was maximum in cluster XIII (21.30) followed by cluster I (14.54) while, minimum in cluster XIV and XV (0.00) followed by cluster II (5.98).

4.2.1.3 Cluster means

Cluster means were calculated in all the 15 clusters for all the 17 quantitative morphological characters studied and presented in Table 14. Cluster X showed highest mean for vine length (1.98 m) followed by clusters XI and XII (1.81 m). Lowest mean for vine length was recorded by cluster XV (1.06 m).

Table 14: Cluster means for 17 quantitative parameters in cucumber based on D^2 analysis

Cluster number	Characters																
	VL	No. NPP	N@ 1st FFA	N@ 1st MFA	D 1st FFO	D 1st MFO	D 1st H	N0. Fr. PP	A Fr. W	Fr. L	Fr. B	Fl T	SCL	SCB	SNo. P Fr	100 SW	Yl. PP
I	1.60	34.73	8.34	5.01	41.10	39.90	51.22	6.27	272.90	21.61	5.79	1.21	15.30	3.41	287.94	2.73	1.75
II	1.50	36.39	5.17	2.50	38.71	35.98	47.51	6.30	230.18	21.27	8.27	1.80	15.10	4.68	236.17	2.46	1.41
III	1.32	33.22	5.75	3.65	40.19	37.87	53.05	5.64	239.08	16.76	6.95	1.49	11.16	3.99	322.46	1.92	1.31
IV	1.55	25.68	3.50	2.17	42.03	39.43	53.68	6.85	363.14	22.00	6.30	1.45	16.39	3.41	310.41	3.70	2.47
V	1.26	30.60	3.67	2.17	34.26	32.12	46.00	7.80	373.61	23.29	6.27	1.82	17.28	2.64	302.63	3.59	2.92
VI	1.40	30.89	2.90	1.84	34.43	32.00	46.84	6.06	222.30	16.24	5.69	1.52	11.66	2.65	304.67	2.75	1.32
VII	1.57	29.36	4.12	2.77	35.55	33.34	47.50	5.46	333.28	20.82	6.07	1.14	15.69	3.79	193.17	3.49	1.85
VIII	1.69	35.05	5.33	3.39	39.93	37.62	53.37	6.20	306.61	21.82	7.87	1.51	19.03	4.84	197.50	2.01	1.76
IX	1.40	31.77	3.47	3.77	30.90	29.21	41.17	7.67	296.96	22.35	5.39	1.02	15.59	3.35	373.34	3.45	2.27
X	1.98	32.16	5.45	3.48	40.07	37.48	51.67	4.75	288.83	22.67	7.82	1.23	19.72	5.38	327.44	3.21	1.38
XI	1.81	37.97	6.53	3.83	40.46	38.07	52.92	3.95	233.73	20.41	8.36	1.42	15.03	5.53	343.72	2.40	1.25
XII	1.61	33.90	2.67	2.67	34.74	34.21	47.17	8.65	217.05	19.49	6.95	1.74	15.05	3.48	239.34	2.53	1.67
XIII	1.81	31.21	3.33	3.17	41.81	38.89	53.50	4.03	425.00	25.56	7.91	1.75	18.48	4.23	222.94	2.57	1.72
XIV	1.47	36.05	2.33	0.00	32.00	0.00	38.33	10.25	176.21	16.67	5.30	1.20	11.27	2.90	167.00	2.43	1.81
XV	1.06	33.49	3.30	2.33	56.40	54.60	68.00	9.16	65.85	6.57	2.25	0.16	3.97	1.93	297.00	0.82	0.61

VL= Vine length (m)
No. NPP= Number of nodes per plant
N@ 1st FFA= Node at first female flower appears
Fl T= Flesh thickness (cm)
N0. Fr. PP= Number of fruits per plant
N@ 1st MFA= Node at first male flower appear
Fr. L= Fruit length (cm)
A Fr. W= Average fruit weight (g)
D 1st MFO= Days to first male flower opening
Fr. B= Fruit breadth (cm)
SNo. P Fr= Number of seeds per fruit
D 1st FFO= Days to first female flower opening
SCL= Seed cavity length (cm)
SCB= Seed cavity breadth (cm)
D 1st H= Days to first harvest
100 SW= 100 seed weight (g)
Yl. PP= Yield per plant (kg)

The maximum cluster mean value (37.97) for number of nodes per plant was shown by cluster XI which, closely followed by cluster II (36.39). Lowest mean for number of nodes per plant was recorded by cluster IV (25.68).

Cluster mean for node at first female flower appears was minimum in cluster XII (2.67), followed by cluster VI (2.90). Maximum mean was shown by cluster I (8.34).

The cluster VI showed lowest mean for node at first male flower appears (1.84) followed by cluster IV and V (2.17). Highest mean for node at first male flower appears was recorded by cluster I (5.01).

The minimum cluster mean value (30.90) for days to first female flower opening was shown by cluster IX which, closely followed by cluster V (34.26). Highest mean for days to first female flower opening was recorded by cluster XV (56.40).

The minimum cluster mean value (29.21) for days to first male flower opening was shown by cluster IX which, closely followed by cluster VI (32.00). Highest mean for days to first male flower opening was recorded by cluster XV (54.60).

Cluster mean for days to first harvest was minimum in cluster XIV (3.33), followed by cluster IX (41.17) maximum mean was shown by cluster V (46.00).

Cluster XIV showed highest mean for number of fruits per plant (10.25) followed by cluster XV (9.16). Lowest mean for number of fruits per plant was recorded by cluster XIII (4.03). For, average fruit weight cluster mean was maximum in cluster XIII (425.00 g), followed by cluster V (373.61 g) and minimum in cluster XV (65.85 g). The maximum cluster mean value (25.56 cm) for fruit length was shown by cluster XIII which,

closely followed cluster IV (23.29 cm). The minimum cluster mean for fruit length was found in cluster XV (6.57 cm) while, cluster XI (8.36 cm) shown highest mean for fruit breadth which, closely followed by cluster II (8.27 cm) and lowest in cluster XV (2.25 cm).

Cluster V showed highest mean for flesh thickness (1.82 cm) followed by cluster II (1.80 cm). Lowest mean for flesh thickness was recorded by cluster XV (0.16 cm).

The maximum cluster mean value (19.72 cm) for seed cavity length was shown by cluster X, closely followed by cluster VIII (19.03 cm). The minimum cluster mean value (3.97 cm) was found in cluster XV while, cluster XI (5.53 cm) was shown highest mean for seed cavity breadth which, closely followed by cluster X (5.38 cm) and lowest in cluster XV (1.93 cm).

The number of seeds per fruit highest for cluster IX (373.34) closely followed by cluster XI (343.72) and least number in cluster XIV (167.00). The 100 seed weight was found maximum in cluster IV (3.70 g) followed by cluster V (3.59 g) and minimum was recorded in cluster XV (0.82 g).

Cluster means for yield per plant was maximum (2.92 kg) in cluster V which is closely followed by cluster IV (2.47 kg). The minimum mean value for yield per plant was found in cluster XV (0.61 kg).

4.2.1.4 Contribution of different characters towards genetic divergence

The relative ranking of different characters and their contribution towards total genetic divergence is given in Table 15. It is evident from the that, yield per plant (40.97 %) contributed maximum to the total divergence followed by 100 seed weight (22.48 %) and number of seeds

HIERARCHICAL CLUSTER ANALYSIS (Ward's Method)

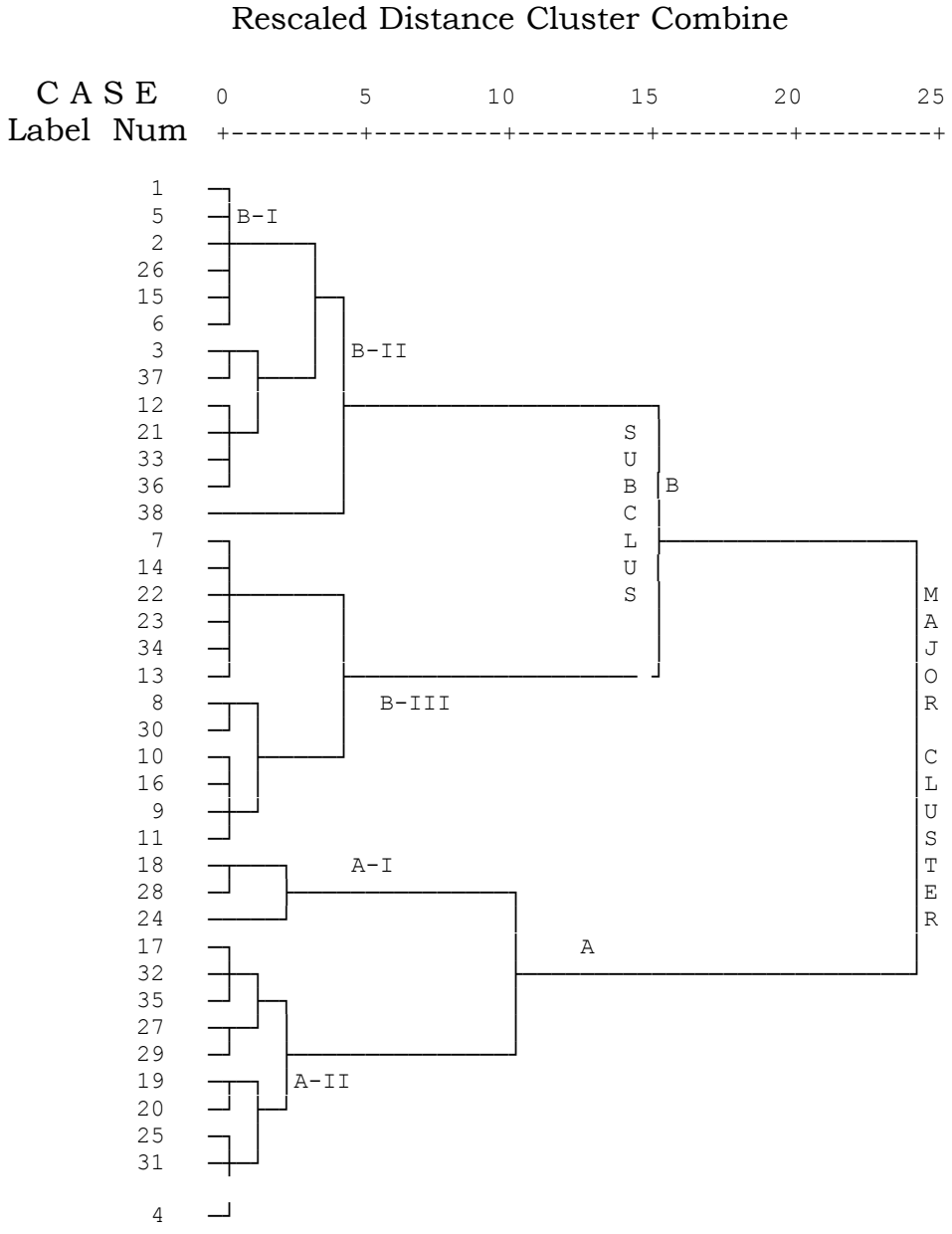

Figure 1: Dendrogram showing the genetic diversity among 38 Cucumber accessions using 17 quantitative morphological characters. Legend, 1 to 38 accessions (*ref. Apendix* I)

per fruit (13.52 %) and they were potential traits which could be recognized as parameters, where as vine length (0.00 %), node at first male flower appears (0.14 %) and seed cavity breadth (0.14 %) showed lower contribution to the total divergence.

4.2.1.5 Characterization of cucumber genotypes using cluster analysis of the quantitative morphological characters

Dendrogram showing the genetic relatedness of 38 cucumber accessions based on the cluster analysis of 17 morphological characters are presented in Fig. 1. A dendrogram was constructed by Ward's method (Ward, 1963) using new version SPSS 16.0 window software. Based on the analysis, 38 cucumber accessions have been formed to 12 clusters which are further grouped into two major clusters as A and B showing rescaled genetic distance of 25 units and which further divided into sub clusters as A into A-I and A-II, where as B into B-I and B-II showing rescaled genetic distance of near to 6 units.

The sub cluster B-I forms three groups were consisting of six genotypes *viz.*, Swarna Ageti, Phule shubangi, Punjab Naveen, Local Line, Tender Green Burbless and Himangi shows close similarities (at near 4.0 units distance) with another group consisting of six genotypes *viz.*, IIHR-34, IIHR-338, Sweet market more, IIHR-285, IIHR-38 and IIHR-177. Both the groups showed close similarity (at near 5.0 units distance) with other group consisting of only one genotype *Cucumis hardwickii.* The sub cluster B-II also forms two groups consisting of six genotypes *viz.*, Peb kamal, Poinsettia, IIHR-34-S4, IIHR-337, Gadag local and Ajax shows very close similarities (at near 5.0 units distance) with another group consisting of six genotypes *viz.*, VS-474, IIHR-36, Nandini, 595920, Sangeetha and Barsathi.

Table 15: Relative contribution of each character to total divergence in cucumber accessions

Sl. No.	Characters	No. of first rank	% Contribution
1.	Vine length (m)	0	0.00
2.	No. of nodes per vine	20	2.85
3.	Node @ 1st female flower appears	13	1.85
4.	Node @ 1st male flower appears	1	0.14
5.	Days to 1st female flower opening	16	2.28
6.	Days to 1st male flower opening	16	2.28
7.	Days to 1st harvest	11	1.57
8.	No. of fruit per vine	11	1.57
9.	Average fruit weight (g)	2	0.29
10.	Fruit length (cm)	29	4.13
11.	Fruit breadth (cm)	25	3.56
12.	Flesh thickness (cm)	11	1.57
13.	Seed cavity length (cm.)	6	0.86
14.	Seed cavity breadth (cm.)	1	0.14
15.	Seed number per fruit	95	13.52
16.	100 Seed weight (gm)	158	22.48
17.	Yield per vine (kg)	288	40.97
	Total	**703**	**100**

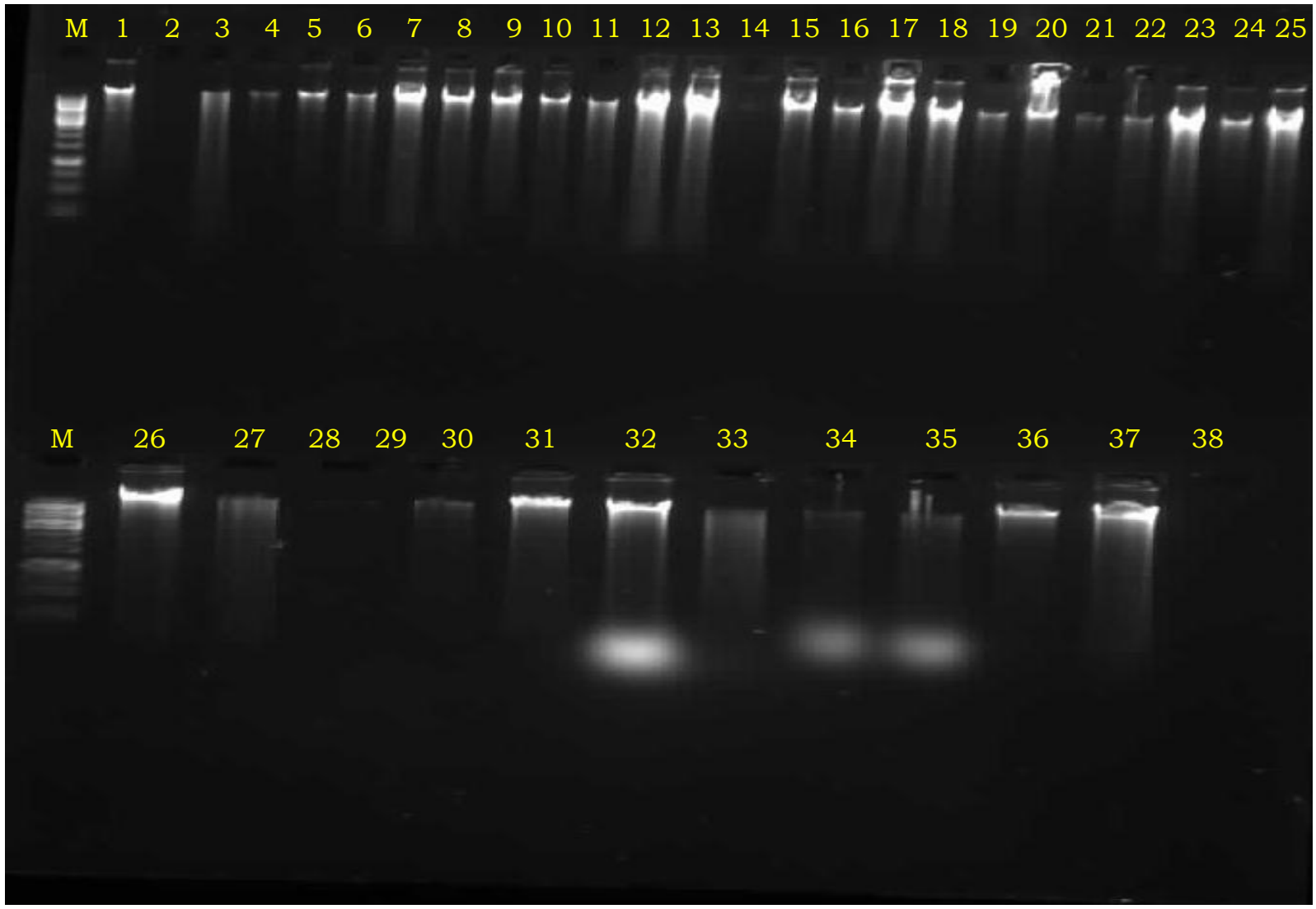

Plate 3: Genomic DNA of 38 cucumber genotypes

The sub cluster A-I is further divided into two groups were consisting of two genotypes *viz.*, VR-101 and IIHR-82 very close similarities (at near to 2.0 unit distance) with another group consisting of only one genotype Pilibhat Local. The sub cluster A-II is further divided into four groups consisting of three genotypes *viz.*, VRC-06-08, IIHR-407-1 and IIHR-409-2, second group consisting of two genotype IIHR-81 and IIHR-405, third group consisting of two genotypes VR-06-07 and IIHR-306 very close similarities (at near 3.0 unit distance) with other group consisting of three genotypes IIHR-304, Karur local and Japanese Long Green.

4.2.2 Molecular studies in cucumber

4.2.2.1 Isolation of genomic DNA and its quantification

Genomic DNA was isolated from the 38 cucumber accessions using "Maxi-prep" method as described in materials and methods from fresh young leaves. The extraction method yielded good quality and quantity DNA. The amount of DNA present was determined by UV-Vis spectrophotometer at an emission spectrum of 260 nm. The quantity of DNA samples varied to with mean of and A260/A280 ratio of DNA ranged from 1.70 to 2.42 with mean of 1.81 (Table 16). Further the quality and quantity of isolated DNA samples were tested and found good enough by 0.8 % Agarose gel electrophoresis to carry out the PCR amplification (Plate 3).

4.2.2.2 Characterisation using RAPD markers

The RAPD analysis of 38 cucumber genotypes was done using 14 arbitrary decamer primers (Operon Technologies, USA) adopting the procedure of Williams *et al.*, (1990). From the initial screening 14 RAPD primers were selected for dendrogram construction using cluster analysis. RAPD gel profiles amplified by the primers OPE-3, OPE-11,

Table 16: Genomic DNA quality and quantity of cucumber Genotypes

Sl. No.	Accession Number	OD260/OD280 Ratio	Concentration ng/µl
1.	Swarna Ageti	1.95	900
2.	Punjab Naveen	1.78	930
3.	IIHR-34	1.77	4180
4.	Japanese Long Green	1.97	2090
5.	Phule shubangi	1.95	860
6.	Himangi	1.71	550
7.	Pebkamal	1.70	2010
8.	VS 474	1.82	1210
9.	Sangeeta	1.75	3370
10.	Nandini	1.87	2760
11.	Barsati	1.83	2630
12.	Sweet Market More	1.98	1030
13.	Ajax	1.84	2910
14.	Poinsettia	1.76	1020
15.	Tender Green Burbless	1.83	1190
16.	I595920	2.01	2500
17.	VRC-06-08	1.78	3110
18.	VR-101	1.82	2740
19.	VR-06-07	1.91	2700
20.	IIHR-306	1.91	920
21.	IIHR-285	1.76	630
22.	IIHR 34-S4	1.96	1630
23.	IIHR-337	2.42	510
24.	Pilibhat local	1.86	1162
25.	IIHR-304	1.92	1020
26.	local line1	1.77	2570
27.	IIHR-81	1.98	3220
28.	IIHR-82	1.84	2720
29.	IIHR-405	1.86	1710
30.	IIHR-36	1.83	3770
31.	Kerur local	1.85	3850
32.	IIHR-407-1	1.79	2690
33.	IIHR-384	1.89	3210
34.	Gadag local	1.76	1710
35.	IIHR-409-2	1.80	1010
36.	IIHR-177	1.83	4010
37.	IIHR-338	1.73	2010
38.	*Cucumis hardwickii*	1.92	2469
	Mean	**1.81**	**2038.74**

OPE15, OPA-05, OPA-10, OPA-13, OPX-01,OPX-02, OPX-03, OPX-04, OPX-06, 0PX-07, OPX-09, OPX-10 are shown in the Plates 4-8. All the tried 13 primers gave good amplification with polymorphisms and they were generated a total of 103 RAPD bands (Table-13), most of which were polymorphic across the accessions (65.05%). The number of bands resolved per amplification was primer dependent and varied from 4 (OPX-7) to 15 (OPX-1) with an average of 7.92 bands per primer. The size range of amplification products also differed with selected primers as well as the genotypes and ranged from 250bp to 1500bp.

The RAPD profiles obtained by using various primers varied from one another. This may be difference in primer sequence are change in PCR conditions. The different primers were capable of developing different banding patterns. Out of 13 primers tested, the primer OPA-05 gave maximum number (6 of total bands of which 05 bands showed 83.33% polymorphisms followed by OPX-10 (83.3%) and OPX-02 (83.33%). The primers viz., OPX-07 showed very least polymorphisms of 33.33% followed by primer OPX-01 (42.85%).

4.2.2.3 Cluster analysis of 38 cucumber genotypes using RAPD markers

RAPD bands were manually scored from the gel profiles (Plate 4.1 to 4.14) by assigning the values '1' for the presence and '0' for the absence such a binary data generated from all the profiles were used for statistical analysis. Dissimilarity matrix was computed using Squared Euclidean Distance (SED) to estimate pair wise differences in the amplification product for all varieties (Sokal and Sneath, 1973). The pooled RAPD data were utilised for cluster analysis and principle component analysis (PCA) using the statistical programme called STATISTICA for the 38 cucumber genotypes.

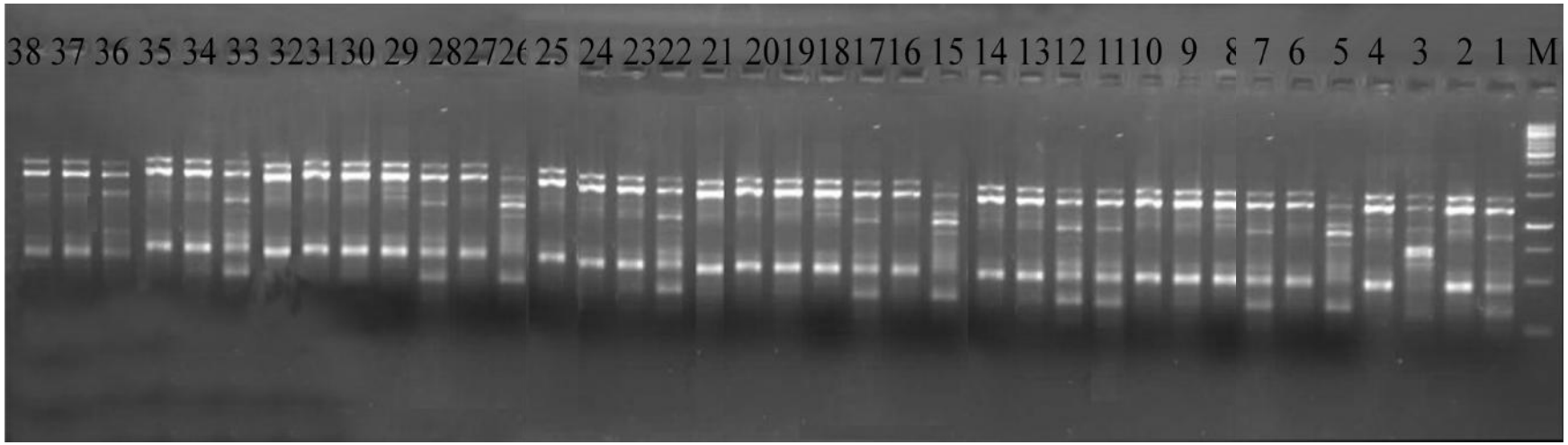

Plate 4.1: RAPD profiles of 38 cucumber genotypes using primer OPA-5 (Lane M- 1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

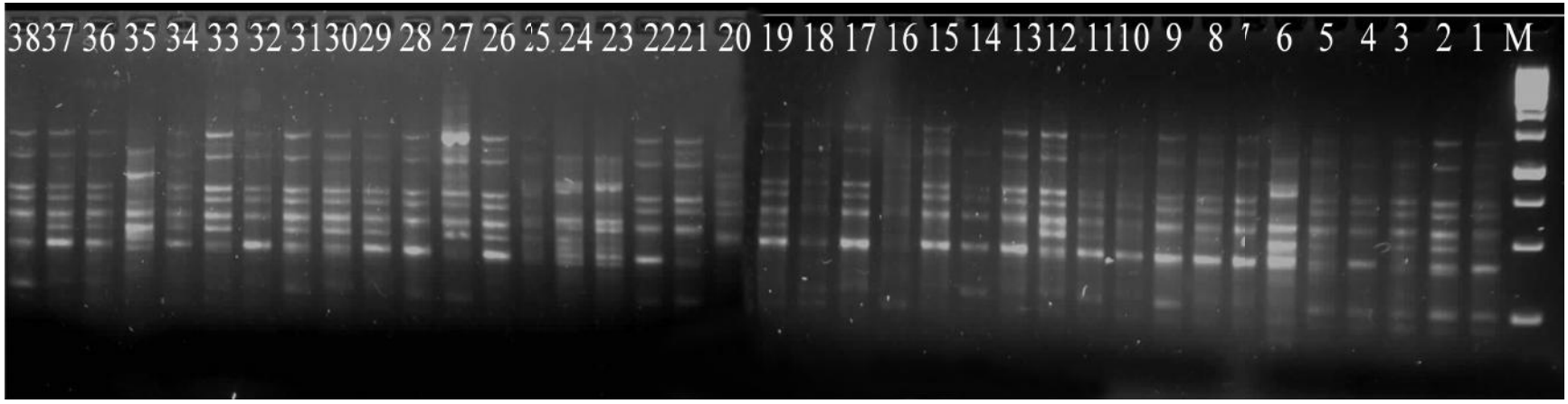

Plate 4.2: 2 RAPD profiles of 38 cucumber genotypes using primer OPX-1(Lane M- 1 kb DNA ladder, Lane 1-38represent the genotypes same order as listed in Annexure-I)

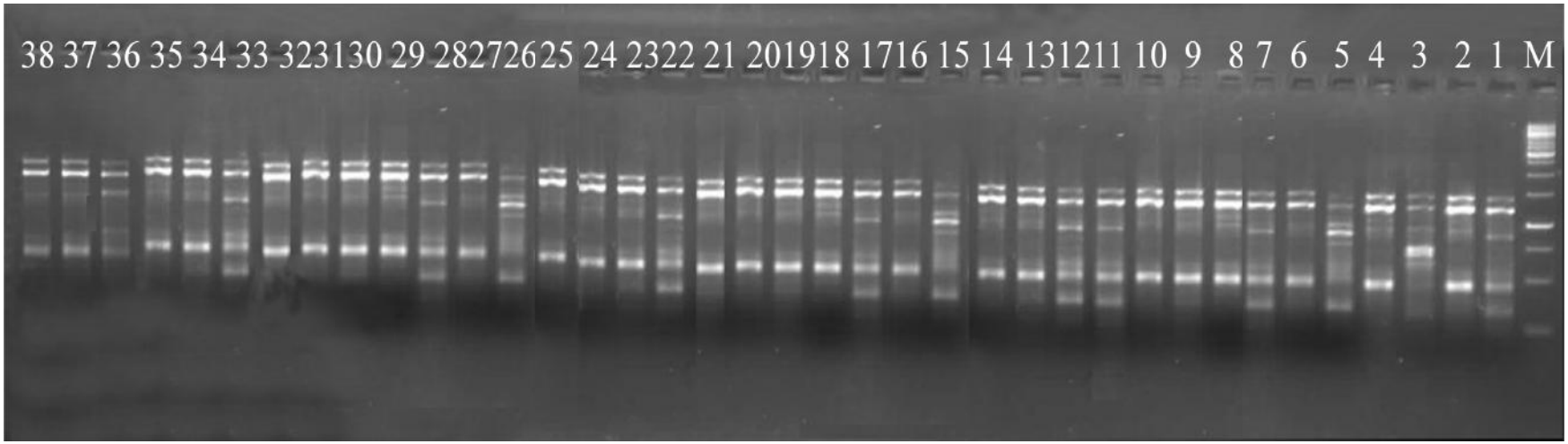

Plate 4.3: RAPD profiles of 38 cucumber genotypes using primer OPX-2 Lane M- 1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

Plate 4.4: RAPD profiles of 38 cucumber genotypes using primer OPX-3 Lane M-1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

Plate 4.5: RAPD profiles of 38 cucumber genotypes using primer OPX-4 Lane M-1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

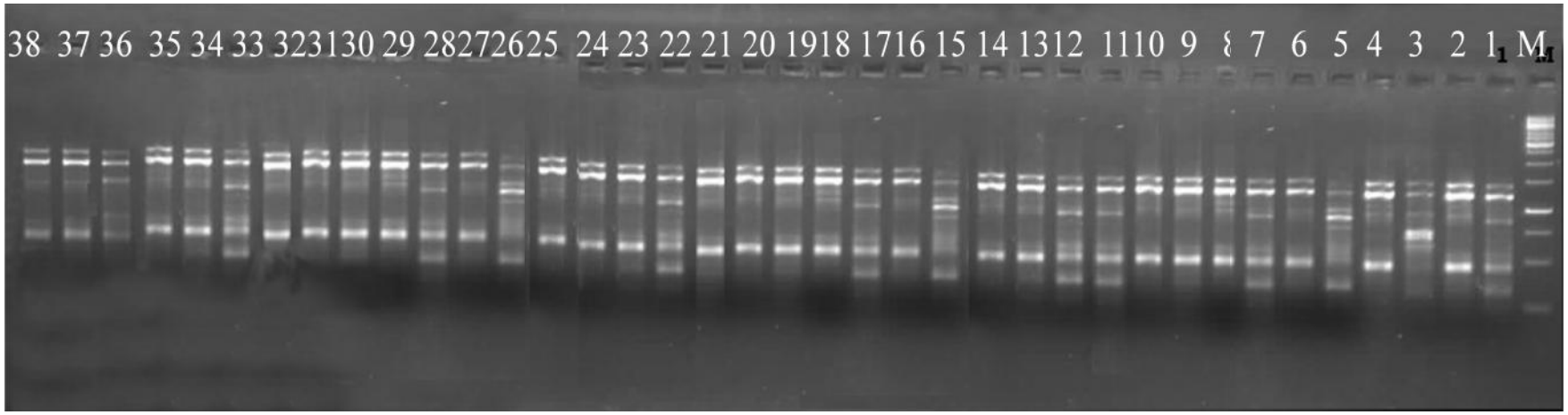

Plate 4.6: RAPD profiles of 38 cucumber genotypes using primer OPX-5 Lane M-1 kb DNA ladder, Lane, 1-38 represent the genotypes same order as listed in Annexure-I)

Plate 4.7: RAPD profiles of 38 cucumber genotypes using primer OPE-15 (Lane M- 1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

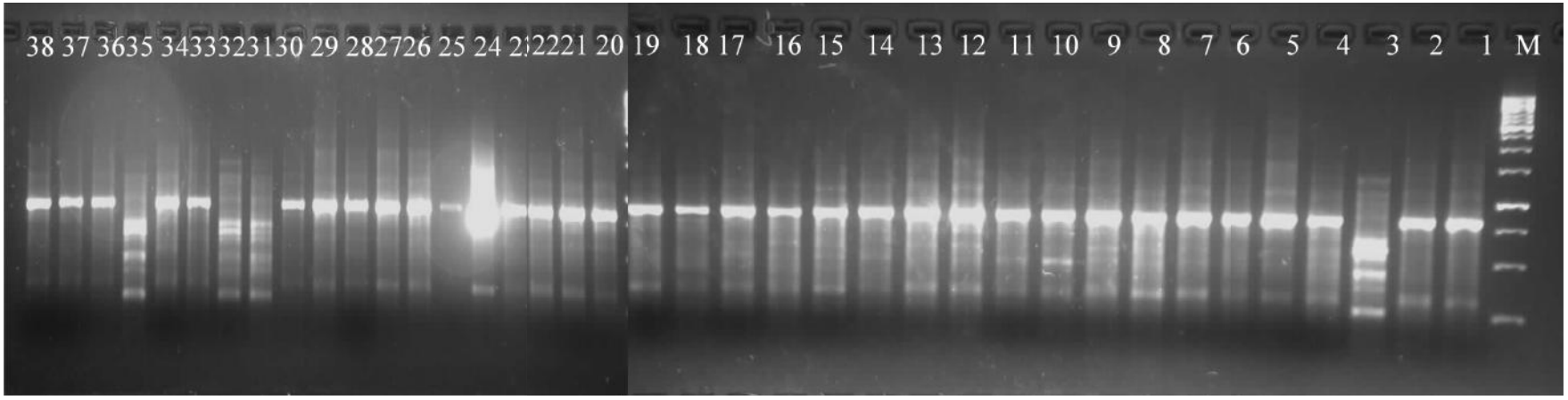

Plate 4.8: RAPD profiles of 38 cucumber genotypes using primer OPX-9 (Lane M- 1 kb DNA ladder, Lane 1- 38 represent the genotypes same order as listed in Annexure-I)

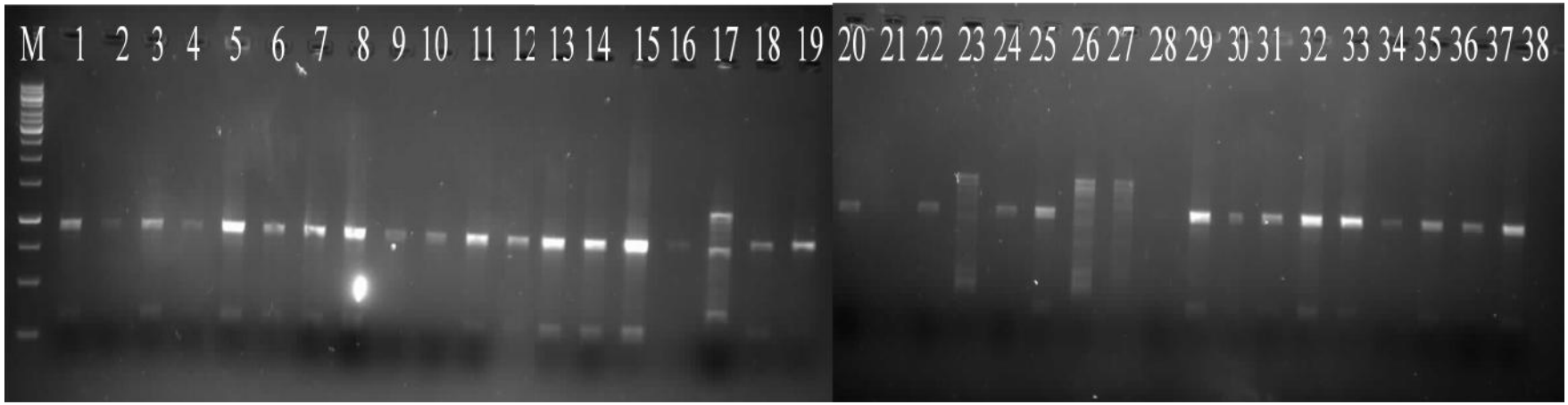

Plate 4.9: RAPD profiles of 38 cucumber genotypes using primer OPX-7 Lane M-1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

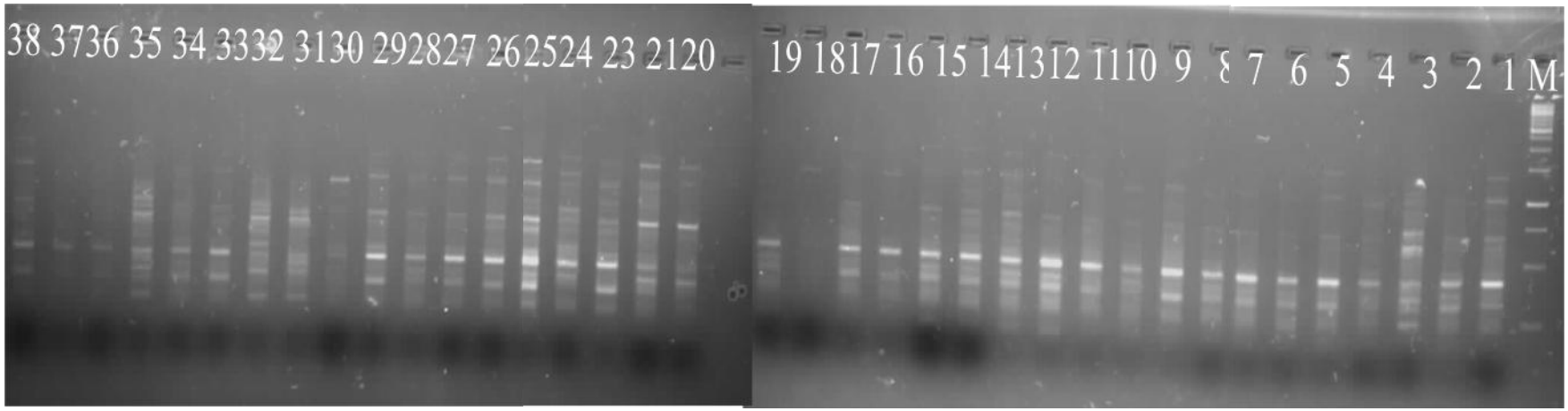

Plate 4.10: RAPD profiles of 38 cucumber genotypes using primer OPE-11 (Lane M- 1 kb DNA ladder, Lane 1-38 represent the genotypes same order as listed in Annexure-I)

Table 17: Polymorphism in 38 cucumber genotypes generated by 13 RAPD primers

Sl. No.	Primer	No. Of bands produced	No. of polymorphic bands	Percentage of polymorphism (%)
1.	OPA 05	6	5	83.33
2.	OPA 10	8	6	75.00
3.	OPA 13	6	5	83.33
4.	OPE 11	8	5	62.55
5.	OPE 15	9	7	77.77
6.	OPX 01	14	6	42.85
7.	OPX 02	6	5	83.33
8.	OPX 03	9	6	66.66
9.	OPX 04	12	8	66.66
10.	OPX 06	9	3	50.00
11.	OPX 07	5	2	33.33
12.	OPX 09	5	4	80.00
13.	OPX 10	6	5	83.33
Mean		**7.92**	**5.15**	**68.31**
Total		**103**	**67**	**65.04**

Table 18: Distance matrix (Squared Euclidean Distance) for 38 cucumber genotypes using RAPD data

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38
1	0	35	27	33	27	32	36	39	31	40	30	30	37	33	30	34	38	35	33	36	32	32	41	36	33	41	39	36	36	33	34	37	34	28	34	35	34	35
2		0	28	16	28	29	35	40	32	33	39	33	44	40	41	35	41	34	38	31	27	27	40	35	38	48	48	33	45	32	39	38	35	29	33	34	39	32
3			0	26	16	29	33	34	34	41	39	37	42	34	37	39	41	36	36	27	29	27	30	33	34	40	40	39	41	40	43	44	41	39	35	40	33	28
4				0	26	29	31	38	30	37	39	29	38	36	39	37	43	38	40	35	27	23	40	33	30	40	46	33	45	32	39	48	39	35	37	38	41	36
5					0	27	25	28	30	37	35	31	34	32	27	33	33	32	34	31	29	31	30	37	38	42	42	45	41	44	45	46	37	37	37	36	35	36
6						0	18	17	25	28	30	24	37	29	32	36	38	33	29	36	26	24	37	32	31	41	43	36	52	39	42	43	44	38	36	35	38	41
7							0	15	25	30	28	28	35	39	32	40	34	29	33	34	30	30	35	36	33	43	41	42	46	39	44	47	44	42	38	37	44	45
8								0	24	31	27	31	36	36	31	39	35	36	30	37	33	33	40	39	36	42	42	45	55	44	49	50	53	43	43	36	45	46
9									0	23	25	29	34	32	29	29	31	32	34	37	27	25	38	31	32	40	40	33	41	28	39	40	39	37	29	34	37	42
10										0	26	32	45	35	38	32	32	35	39	42	28	28	39	36	39	47	45	34	48	35	38	41	38	32	34	33	38	45
11											0	18	33	29	28	30	30	27	31	38	38	38	39	40	37	47	45	42	44	37	42	41	42	36	38	43	42	45
12												0	23	19	22	24	32	25	27	34	32	28	39	34	33	45	43	36	44	35	36	45	44	38	40	37	38	41
13													0	24	27	25	35	32	30	41	35	33	36	33	36	40	38	37	41	38	39	46	47	51	43	38	39	48
14														0	21	21	31	26	24	37	33	27	38	33	30	38	36	33	43	36	39	46	39	41	39	36	39	40
15															0	22	26	31	25	32	30	32	35	36	31	33	29	38	40	37	40	43	44	40	40	37	42	41
16																0	28	27	29	34	28	28	39	28	35	39	43	28	44	35	38	47	48	40	34	31	38	41
17																	0	25	27	42	38	42	33	46	45	41	39	40	48	45	44	47	44	44	40	41	44	45
18																		0	20	27	31	31	36	35	28	38	40	31	35	34	39	40	39	37	33	32	39	38
19																			0	29	33	33	36	41	30	36	36	39	47	40	47	44	49	43	41	38	41	38
20																				0	24	26	41	30	27	39	41	36	38	37	40	45	40	34	32	31	34	33
21																					0	12	31	18	17	27	35	26	36	23	38	47	42	36	32	31	40	41
22																						0	33	14	13	29	33	24	36	21	34	45	36	34	28	27	34	35
23																							0	35	38	24	28	43	39	44	45	48	49	47	37	46	43	42
24																								0	21	33	33	18	38	25	34	45	44	40	34	31	36	41
25																									0	22	30	25	35	20	35	40	41	35	37	32	39	40
26																										0	22	35	35	36	43	48	49	47	43	44	45	44
27																											0	33	37	38	43	46	47	53	45	48	49	52
28																												0	34	17	26	35	38	30	32	27	34	37
29																													0	25	30	31	28	30	30	33	42	43
30																														0	21	34	33	25	29	28	35	38
31																															0	33	34	32	34	29	32	45
32																																0	25	23	33	34	33	38
33																																	0	24	30	33	36	37
34																																		0	24	23	28	23
35																																			0	21	28	29
36																																				0	23	30
37																																					0	19
38																																						0

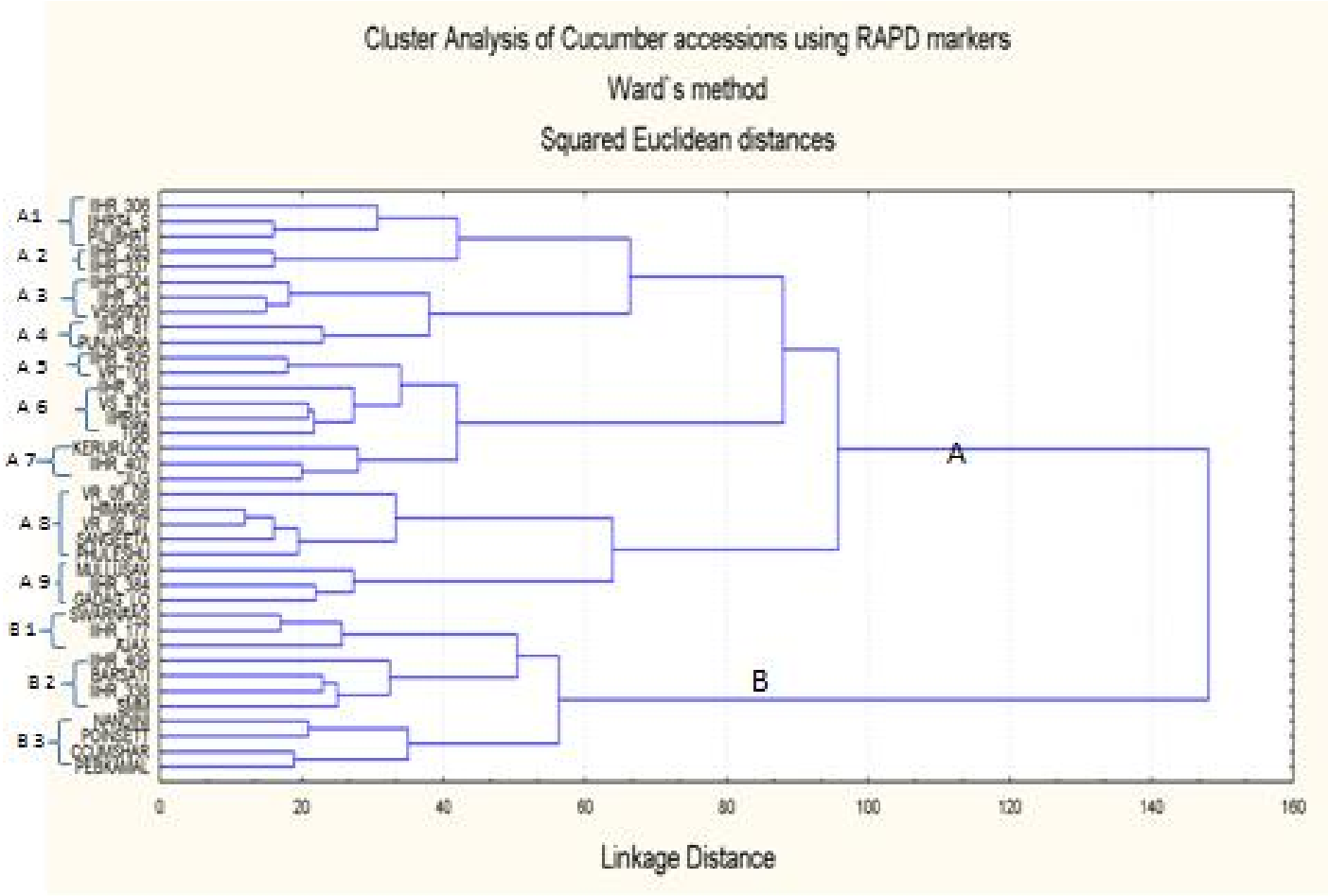

Figure 2: Dendrogram showing the genetic diversity among 38 cucumber accessions using cluster analysis of RAPD data.

The genetic dissimilarity value in the distance matrix ranged from 0 to 55 (Table 18), suggesting a narrow genetic base within the cucumber genotypes. The highest genetic distance of 55 was observed between 595920 & IIHR-409 followed by 595920 & Sweet market more (53), IIHR-304 & IIHR-409 (52), IIHR-36 & IIHR-338 (51) and 595920 & Barsati (50). Similarly the lowest genetic distance 12 was observed between Himangi & VR-0607 followed by VR-0607 & Sangeeta (13), VR-0607 & Phule Shubangi (14), IIHR-34 & 595920 (15), and IIHR-285 & IIHR-337 and IIHR-34-S & Pillibhat local (16).

4.2.2.5 Dendrogram analysis

A dendrogram was constructed by Ward's method of clustering using minimum variance algorigthm (Ward, 1963). Cluster analysis based on a total of 103 bands with 67 polymorphic bands in 38 cucumber genotypes using 13 primers is presented in Fig 2.

It is clearly evident from the dendrogram (Fig 2) that, all the 38 cucumber accessions are grouped into 2 major clusters A and B. The total dissimilarity value across all the accession was 148 units. Cluster A differed from cluster B with 56 units. Cluster A comprises of total of 27 genotypes whereas cluster B comprises total of 11 genotypes. Further cluster A subdivided into 6 sub clusters namely A_1 to A_9. A phylogenetic tree constructed on the basis of dissimilarity of 41 units between the genotypes made it possible to classify 38 cucumber genotypes into a total of distinct clusters. Subcluster A_1 consisted of 3 genotypes namely IIHR-306, IIHR-34-S4, Pilibhat Local. Sublcuster A_2 comprised of 2 genotypes namely IIHR-285, IIHR-337. Subcluster A_3 involved 3 genotypes namely IIHR-304, IIHR-34, 595920. Subcluster A_4 includes 2 genotypes namely IIHR-81 and Punjab Naveen. Subcluster A_5 consists of 2 genotypes namely IIHR-405, VR-101. Subcluster A_6 includes 4 genotypes namely IIHR-36, VS-474, IIHR-82 and Tender Green Burbless. Subcluster A_7

Table 19: Comparative resistance of different cucumber genotypes to downy mildew incidence

Sl. No	Genotypes	Downy mildew incidence (%)	Scoring
1.	Swarna Ageti	23.42	2
2.	Punjab Naveen	33.70	3
3.	IIHR-34	41.32	3
4.	Japanese Long Green	18.03	2
5.	Phule shubangi	72.34	4
6.	Himangi	38.42	3
7.	Pebkamal	34.36	3
8.	VS 474	27.31	3
9.	Sangeeta	12.68	2
10.	Nandini	11.35	2
11.	Barsati	14.27	2
12.	Sweet Market More	24.39	2
13.	Ajax	11.12	2
14.	Poinsettia	37.18	3
15.	Tender Green Burbless	68.13	4
16.	I595920	47.29	3
17.	VRC-06-08	64.26	4
18.	VR-101	18.63	2
19.	VR-06-07	16.20	2
20.	IIHR-306	52.47	4
21.	IIHR-285	42.39	3
22.	IIHR 34-S4	66.72	4
23.	IIHR-337	73.27	4
24.	Pilibhat local	59.13	4
25.	IIHR-304	31.05	3
26.	local line1	11.34	2
27.	IIHR-81	28.15	3
28.	IIHR-82	29.53	3
29.	IIHR-405	13.82	2
30.	IIHR-36	46.34	3
31.	Kerur local	21.67	2
32.	IIHR-407-1	14.98	2
33.	IIHR-384	72.67	4
34.	Gadag local	44.23	3
35.	IIHR-409-2	16.72	2
36.	IIHR-177	37.84	3
37.	IIHR-338	71.36	4
38.	*Cucumis hardwickii*	6.21	1
	Mean	37.53	

Table 20: Grouping of cucumber genotypes into different categories on the basis of per cent downy midew infestation

Sl No.	Per cent downy mildew Infestation	Reaction Category	Number of genotypes	Genotypes
1	0-10	Resistant	1	*Cucumis hardwickii*
2	11-25	Moderately Resistant	14	Swarna Ageti, Japanese Long Green, Sangeeta, Nandini, Barsati, Sweet Market More, Ajax, VR-101, VR-06-07, Local line, IIHR-405, Karur local, IIHR-407-1, IIHR0409-2
3	26-50	Moderately Susceptible	7	Punjab Naveen, IIHR-34, Himangi, Peb Kamal, VS-474, Poinsettia, 595920, IIHR-285, IIHR-304, IIHR-81, IIHR-82, IIHR-36, Gadag Local, IIHR-177
4	51-75	Susceptible	6	Phule Shubangi, Tender Green Burbless, VRC-06-08, IIHR-306, IIHR-34-S4, IIHR-337, Pilibhat Local, IIHR-384, IIHR-338
5	>75	Highly Susceptible	1	Mullu Savate (check)

consists of 3 genotypes Kerrur local, IIHR-407 and Japanese Long Green. A_8 consists of 5 genotypes VR-06-08, Himangi, VR-06-07, Sangeeta and Phule Shubangi. A_9 comprised of 3 genotypes Local Line, IIHR-384 and Gadag Local. The dissimilarity between $A_1$and A_2 subcluster was 32 units similarly A_3 and A_4 was 38 and A_5 and A_6 was 30 and A_7 and A_8 was 32 and A_9 was 28.

Cluster B was subdivided into 3 groups B_1, B_2 and B_3. Subcluster B_1 consisted of 3 genotypes namely Swarna Ageti, IIHR-177 and Ajax. Subcluster B_2 involved 4 genotypes namely IIHR-409-1, Barsati, IIHR-338 and Sweet market more. Subcluster B_3 involved 4 genotypes namely Nandini, Poinsettia, *Cucumis hardwickii* and Pebkamal. The dissimilarity between B_1 and B_2 was 30 units and B_3 was 32 units.

4.3 Screening for resistance to downy mildew

The reaction of different genotypes to downy mildew incidence after artificial inoculation is presented in Table 19.

The disease intensity recorded per cent leaf area infected ranged from 6.21 to 73.27. The lowest intensity (6.21%) in genotype *Cucumis hardwickii* and highest (73.27%) in genotype IIHR-337, the mean disease severity was 37.53%.

Based on per cent leaf area infested scoring was done and genotypes were grouped into five categories (Table 20). Out of 38 genotypes 6 were susceptible, 7 were moderately susceptible, 14 were moderately resistant and only one genotype shown resistance and none of them were immune to this disease.

Discussion

V DISCUSSION

The magnitude of heritable variability is the most important component in any breeding material as it has a close relation on response to selection. Therefore, occurrence of adequate genetic variability is an essential pre requisite for all crop improvement programmes. The knowledge of the amount of variability and heritability helps the crop breeder for improvement in any crop by choosing suitable breeding technique. The source material for genetical improvement would be identified by studying the amount of variability available in the gene pool (or) germplasm. Accordingly 38 accessions of cucumber germplasm were evaluated for their genetic potential in respect of yield and yield attributes and also downy mildew disease resistance so as to identify source material to enhance productivity.

Molecular markers are widely used for estimation of genetic diversity and are reported to be more precise than the morphological methods (Gupta and Varshney, 2000). Fingerprinting the accessions using the molecular markers and especially microsatellites can establish the genetic identity and will be helpful in case of litigation (Gupta *et al.*, 1996). Since India is the centre of origin of cucumber, an immeasurable value of genetic diversity is well recognised and this necessitates the conservation of variability in cucumber.

The objective of any breeding programme will mostly be oriented towards the improvement of the yield. Since the yield is dependent upon different growth and yield characters, to study growth and yield characters and genetic potential of yield must be probed through the study of its component characters by employing useful biometrical tools. Some of these parameters include genotypic (GCV) and phenotypic (PCV) co-efficients of variation, heritability, genetic advance overmean

Genotypic and phenotypic correlations help, to base selection procedure to a required balance when two opposite desirable characters affecting the principle characters which are being selected. It also helps to improve different characters simultaneously (Falconer, 1981).

5.1 Genetic Variability and association studies

5.1.1 Variability studies

The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits. Genetic variability in the breeding material is important for the improvement of a crop plant. Such information helps in locating suitable parental lines for a breeding programme. Thus, in order to make selection and improvement programs effective, it is essential to study and partition the total variability existing in a germplasm into genetic, phenotypic and environmental variability. Thus enables the breeder to adopt a suitable breeding programme.

For any genetic improvement programme in crop plants, the aim would be evolving genotypes that are more efficient and show substantial increase over the existing types in respect of yield and other economic characters. The degree of improvement depends upon the beneficial and utilizable variability.

The Non-Euclidean cluster analysis revealed a medium diversity among 38 cucumber accessions comprising the advanced breeding lines collected from different parts of India and abroad, established varieties and hybrids from private seed companies. A mere phenotypic measure would not be reliable under fluctuating environments and meagre knowledge of existence of variability for different characters may not reveal that which particular character is showing the highest degree of

variability. This problem could be solved through genetic estimates such as phenotypic and genotypic co-efficient of variability.

High phenotypic variance was recorded for number of nodes per vine, days to first female flower opening, days to first male flower opening, days to first harvest, average fruit weight, fruit length, yield per hectare and number of seeds per fruit. But, phenotypic variance is not very reliable, since it includes both genetic and environmental effects. Thus, it is essential to split total variance into genetic and non-genetic components. Almost all the characters except vine length showed more genotypic variance than environmental variance. This indicated that genetic component in total variation is more and environmental influence is less in case of these traits. Thus, selection scheme planned based on these characters will have high selection response. Higher values of all three variations for characters like number of nodes per vine, days to first female flower opening, days to first male flower opening, days to first harvest, average fruit weight and number of seeds per fruit indicates the presence of significant variation for these characters in the genotypes under study. Similar results were obtained by Smith *et al.* (1978), Abusaleha and Dutta (1990), Saikia *et al.* (1995) and Imam *et al.* (1997).

The phenotypic and genotypic co-efficient of variation ranged from 12.40 to 11.30 for days to first fruit harvest and 48.55 to 44.01 for the node at first female flower appears. Higher magnitude of phenotypic and genotypic co-efficient of variation has been noticed for node at first female flower appears,(48.55 and 44.01), node at first male flower appears (47.88 and 36.39), average fruit weight (34.98 and 29.51), flesh thickness (34.75 and 28.40), yield per plant (37.62 and 31.70) and seed cavity breadth (33.54 and 30.94). This indicates that the genotype varied more widely with respect to these characters due to genetic basis and hence permits selection as means of rapid improvement in the traits.

This finding is in accordance with the findings of Solanki and Seth (1980), Abusaleha and Dutta (1990) Arunkumar *et al.* (2011) and Hanchinamani (2006).

The estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were quite closer to each other for most of the traits like number of nodes per vine, days to first female flower opening, days to first male flower opening, days to first harvest, number of fruits per vine, fruit length, fruit breadth, seed cavity length, number of seeds per fruit and 100 seed weight. This reveals that influence of the environment for these characters is negligible and the role of the genotypic performance for the full expression of the phenotype. The similar results are correlated with Rastogi and Aryadeep (1990), Abusaleha and Dutta (1990), Prasad and Singh (1994), Arunkumar *et al.* (2011) and Hanchinamani (2006)

In general according to the present investigation on variability, the selection for fruit yield in cucumber should be based on the most variable characters namely *viz.*, vine length, node at first female flower appears, node at first male flower appears, average fruit weight, flesh thickness and yield per plant.

5.1.2 Heritability and genetic advance

The estimation of genetic coefficient of variation indicates the amount of genetic variation present for different desirable traits while the heritability gives an insight into the proportion of variation which is inherent. The heritability estimates gives an idea about the proportion of observed variability, which is attributed to genetic difference. Heritability in broad sense may play greater role about information of relative value of selection in the material on the hand, but Jhonson *et a*l., 1955 had

shown that heritability and genetic advance should be jointly considered for reliable conclusion.

Heritability estimates were high for characters like number of nodes per vine (83.43), node at first female flower appears (82.17), days to first female flower opening (83.72), days to first male flower opening (92.63), days to first harvest (83.04), number of fruits per plant (85.78), fruit length (88.92), fruit breadth (86.91), seed cavity length (85.97), seed cavity breadth (85.09), number of seeds per fruit (95.17) and 100 seed weight (93.10). From the heritability estimates it is clear that these characters are less influenced by the environmental factors and controlled by additive gene effect. Similarly, high heritability for the above traits were reported by Smith *et al.*, 1978, Rasthogi and Aryadeep 1990, Arunkumar *et al.* (2011) and Reshmi (2006).

Average fruit weight (71.18), flesh thickness (71.59), Yield per plant (71.02), yield per plot (71.08) and yield per hectare (71.07) were recorded moderate heritability. Similar reports were obtained by Abusaleha and Dutta 1990, Prasad and Singh 1994, Arunkumar *et al.*, (2011) and Hanchinamani (2006).

In the present study high genetic advance over mean coupled with high heritability was observed in characters like node at first female flower appears and seed cavity breadth. However, the estimates were moderate for days to first male flower opening, number of fruits per plant, average fruit weight, fruit length, fruit breadth, flesh thickness, yield per plant, seed cavity length, number of seeds per fruit and 100 seed weight. Therefore, the higher heritability coupled with moderate to high genetic advance values observed for these traits in the present findings suggest the existing variability among the genotypes with respect to the traits is mainly due to additive type of genes (Panse 1957).

Higher heritability estimates were accompanied by lower genetic advance over the mean for days to first female flower opening and days to first harvest. This suggests that selection may not be useful for the improvement of this trait because of the narrow range of phenotypic variation among the genotypes in respect of this character. In agreement with these results, Smith et al., (1978) and El-shawaf and Baker (1991) reported low genetic advance in cucumber.

5.1.3 Character association in cucumber

5.1.3.1 Correlation studies

Plant characters do not exist in isolation but a complex association exists among them. These characters are often correlated with each other either due to pleiotropy or due to genetic linkage (Harland, 1939). The relationship between phenotypic, genotypic and environmental correlations as entwined by Falconer 1989 emphasising that for the characters having high heritability, the environmental correlations are generally expected to be lower than genotypic correlations. Since the phenotypic correlation includes a part of environmental correlation responding to the heritable portion of variation in two characters, it is therefore expected that for highly heritable characters genotypic correlation would be higher than phenotypic correlations when the correlation are in same direction. Further, Falconer (1981) stated that phenotypic correlations can exceed genotypic correlation only if the heritability of the two characters were low and environmental correlations were high. Hence an important stratergy designed to break the barriers of yield. In other words high positive correlations between twp traits makes simultaneous improvement in two or more attributes, where as negative association indicates the compromise between desirable characters.

In the present study genotypic correlations among characters were higher than phenotypic correlations indicating high heritable nature of characters. Yield per plant showed a positive and significant correlation at both genotypic and phenotypic level with number of fruits per plant, average fruit weight, fruit length, flesh thickness, seed cavity length and 100 seed weight. Yield per plant had positive and significant correlation with vine length. A negative and significant genotypic correlation of yield per plant with days to first female flower opening and days to first harvest is desirable correlation since earliness is associated with high yield. From the positive correlations it is very clear that, the fruit characteristics are the most important characters deciding the high yield. Linear relationship between fruit characters and yield per plant suggest that selection method of crop improvement should be by operating pressure over fruit characteristics. Similar results have been reported for number of fruits per plant and fruit length by Choudhary and Mandal (1987), Abusaleha and Dutta (1988) and Arunkumar *et al.*, (2011) and Hanchinamani (2006). Average fruit weight got a positive correlation with yield which is in conformity with present results and previously reported by Choudhary and Mandal (1987), Prasad and Singh (1994) and Reshmi (2006). Seed cavity length reported a positive correlation with yield per plant. Similar kind of positive correlation was reported by Choudhary and Mandal (1987), Abusaleha and Dutta (1988).

5.1.3.2 PATH CO-EFFICIENT ANALYSIS

The association of correlation between two characters is not a simple relationship but is a rather a product of the interaction of direct and indirect relationship. The direct association becomes more complex as more and more variables are considered in the correlations. Path coefficient analysis separates the direct and indirect effects through other variables and measures the relative importance of the casual factors involved. This was developed and discussed by Wright (1921) as a tool of

genetic analysis, the utility of which in plant selection was demonstrated by Dewey and Lu (1959).

In the present study path analysis was performed for total yield per plant. Both genotypic and phenotypic path were worked out, but genotypic path should be considered with more weight age as phenotypic path will have greater influence of environmental factors genotypic path was considered with greater weight age.

Vine length recorded positive direct effect on yield per plant. Its positive effect also enhanced by number of nodes per vine, node at first male flower appears, days to first harvest, average fruit weight and seed cavity breadth and the indirect negative effects of node at first female flower appears, days to first female flower opening, number of fruits per plant and fruit breadth. This observation is in agreement with the findings of Prasad and Singh (1992).

Number of nodes per plant showed a positive direct effect on yield per plant. Positive direct effect has been enhanced by node at first male flower appears, number of fruits per plant, flesh thickness and seed cavity breadth was cancelled by the indirect negative effects of node at first female flower appears, days to first female flower opening, average fruit weight, fruit breadth and 100 seed weight. The results obtained in the agreement with the previous reports of Choudhary and Mandal (1987) and Abusaleha and Dutta (1988), Prasad and Singh (1992), Arunkumar *et al.*, (2011) and Dhiman and Chander Prakash (2005)

Though the node at first female flowering recorded a negative direct effect on yield per plant, high levels of indirect positive effects through node at first male flowering, days to first female flower opening, fruit breadth, seed cavity length and seed number per fruit resulted in a final positive correlation between node at first female flower appears and yield

per plant. This observation is in agreement with the results of Choudhary and Mandal (1987).

Node at first male flower appears had a positive direct effect on yield per plant, which is enhanced by days to first female flower opening, average fruit weight and fruit breadth. While its direct positive effect was reduced by indirect negative effects through node at first female flower appears, days to first harvest, number of fruits per plant, flesh thickness and seed cavity breadth. Similar reports were obtained by Dhiman and Chander Prakash (2005) and Rao *et al.*,(2004).

Direct and positive effect on yield per plant was observed for days to first female flower opening. Its high direct effect is further enhanced by indirect positive effects of node at first male flower appears, fruit breadth, seed cavity breadth and number of seeds per fruit while positive direct effect is reduced by indirect negative effects through vine length, node at first female flower appear, number of fruits per plant, fruit breadth and flesh thickness. Similar findings were obtained by Rao *et al.*, (2004).

Yield per plant had a direct negative effect through days to first male flower opening but high levels of indirect positive effect through node at first female flower appears, days to first female flower opening, average fruit weight, seed cavity breadth and number of seeds per fruit finally contributed to the positive effect. These results were found to be with similar results obtained by Arunkumar *et al.*, (2011).

Days to first harvest recorded a high positive direct effect on yield per plant in the present study. Its high positive direct effect is also enhanced by the positive indirect effects through node at first male flower appears, days to first female flower opening, average fruit weight, fruit breadth and number of seeds per fruit. It also had indirect negative effect through vine length, number of nodes per vine, number of fruits per

plant and fruit length. These results were found to be in similar with findings of Arun kumar *et al.*, (2011), Rao *et al.*, (2004).

Number of fruits per plant had high significant direct positive effect on yield per plant. Though its direct effect was reduced by negative indirect effects through vine length, node at first female flower appears, average fruit weight, fruit length and seed cavity breadth, indirect positive effects of number of nodes per vine, node at first female flower appears, days to first male flower opening and fruit breadth contributed for final high positive value. The results quite obvious since higher number of fruits will definitely contribute to high yield per plant. This is in agreement with the findings of Arun kumar *et al.*, (2011), Rao *et al.*, (2004) and Prasad and Singh (1992).

Average fruit weight also showed a high positive significance on yield per plant. The positive direct effect was enhanced by positive indirect effects through number of nodes per vine, node at first female flower appears, fruit length, flesh thickness, seed cavity breadth and 100 seed weight. This result was in agreement with the results obtained by Arun kumar *et al.*, (2011), Rao *et al.*, (2004) and Prasad and Singh (1992).

Fruit length also had positive direct effect on yield per plant. This is achieved by the positive effects through vine length, number of nodes per plant, node at first male flower appears, days to first harvest, average fruit weight, flesh thickness and seed cavity breadth. The results of work done by Dhiman and Chander Prakash (2005), Arun kumar *et al.*, (2011) are in conformity with these observations.

Though fruit breadth had negative direct effect on yield per plant, characters such as vine length, number of nodes per vine, days to first

harvest, average fruit weight, flesh thickness and seed cavity breadth reduced the negative direct effect on yield.

Flesh thickness also reported positive direct effect on yield per plant. Its positive direct effect is enhanced through number of nodes per vine, node at first female flower appears, node at first male flower appears, days to first female flower opening, days to first harvest, average fruit weight and 100 seed weight and it also had a negative indirect effect through vine length, number of fruits per plant, fruit breadth and number of seeds per fruit. Similarly Hanchinamani (2006), Arun Kumar *et al.*, (2011) also observed that yield improvement can be achieved by selection for flesh thickness.

Seed cavity length and seed cavity breadth also reported a positive direct effect on yield per plant. Direct effect on yield per plant was enhanced through positive indirect effect by vine length, number of nodes per vine, average fruit weight, flesh thickness and 100 seed weight.

Number of seeds per fruit and 100 seed weight had a positive direct effect on yield per plant. It was also enhanced through positive indirect of node at first male flower appears, fruit length, seed cavity length and seed cavity breadth.

5.2 Morphological characterization of cucumber germplasm

5.2.1 Genetic diversity using cluster analysis

The genetic diversity between 38 cucumber accessions were studied using non-heirachial Euclidean cluster analysis. In the present study, 38 cucumber accessions were clustered into fifteen clusters based on the morphological similarity. Maximum contribution to the clustering

was from yield per plant, days to first harvest followed by the node at first female flower appears and average fruit weight.

Cluster I had twelve lines which consists of four hybrids (Sangeetha, Nandini,VS-474 Barsati) developed from private company exhibiting a less genetic dissimilarity between varieties, five cultivated varieties (Swarna Ageti, Punjab Naveen, Phule Shubangi, Himangi, Pebkamal), one exotic collection (Sweet Market More from USA), one introduced variety (Japanese Long Greeen) and one advanced line(IIHR-34). Similarly, Cluster II consists of only two breeding lines which both exotic (Poinsettia from USA) and indigeneous (595920). Cluster III consists of two genotypes of which one is the advanced line (IIHR-384) and other is VR-06-08. Cluster IV had two green fruited breeding lines of which one is advanced line (IIHR-81 and IIHR-407-1) other one IIHR-81 is from private seed company. Cluster V consists of two advanced lines (IIHR-405 and IIHR-409-2) with high yield and green coloured fruit. Cluster VI had two lines of which one is advanced line (IIHR-177) and other is the local variety(local line) collected from Bangalore local region. Cluster VII consists of two breeding lines of which one is local line (Gadag local) collected from Gadag region and another one is private company hybrid (IIHR-82) both had long duration for first fruit harvest. Cluster VIII had two breeding accessions of which one is advanced line (IIHR-34-S4) and other is VR-101 with moderate resistance to downy mildew.

Cluster IX consists of two breeding lines both are advanced lines (IIHR-304 and IIHR-338) collected from CHES, Ranchi. Cluster X had two lines of which one is advanced line (IIHR-306)collected from CHES, Ranchi and other one is local line collected from Karoor region, both had almost on par yield trait. Cluster XI included two genotypes one is VRC-06-07 and other one is advanced line (IIHR-285) collected from

Holenarsipura region with almost similar number of nodes per vine. One of the exotic cultivar (Tender Green Burbless) collected from USA and another advanced line (IIHR-337) collected from CHES, Ranchi were grouped together as XII cluster. Similarly XIII cluster also consisted of two breeding lines of which both are local line (IIHR-36) collected from Ottapalm, Kerala region and another one is collected from Pilibhat region (Pilibhat Local). The gynoecious line Ajax and *Cucumis hardwickii* grouped into two separate clusters XIV and XV respectively indicating the distinctness between the species. Similarly Prasad *et al.*, (1993) studied the biological diversity in 32 genotypes using D-square values and found that they are grouped into eight clusters with appreciable genetic divergence in the population.

Roy and Sharma (1996) in their results pointed out that many characters were used for clustering but with high numerical value such as yield per plant, number of fruits per plant and number of nodes gave good results. Similar types of reports were obtained by Mathew *et al.*, (2001).

5.2.2 Characterization of cucumber genotypes using cluster analysis of the quantitative morphological characters.

In the present study, genetic distances between 38 cucumber accessions were estimated through cluster analysis of 17 morpholgical quantitative characters. Based on the analysis, 38 cucumber accessions have been formed to 12 clusters which were further grouped into two major clusters A and B showing rescaled genetic distance of 25 units and which further divided into sub clusters A as A-I and A-II, where as B into B-I and B-II shoeing the rescaled genetic distance of near to 6 units. Dendrogram based on phenotypic marker data successfully distinguished all 38 cucumber genotypes from one another.

Cluster A and B consisted of wide diversity of genotypes which are mainly collected from India. Cluster B-I consisted of wide diversity of genotypes which mainly collected from India except one collected from USA. All are green fruited type except one genotype which is white fruit type (Himangi). Cluster B-II consisted of all the advanced lines except one collected from USA. Cluster B-III consisted of single genotype which is belongs to wild species. Cluster B-IV comprised of different genotypes of which one is gynoecious line, another one is local line and another one is introduced variety from USA. Cluster B-V consists of three private company hybrids and rest of others are advanced lines. Cluster A-I includes three genotypes in which all the three were moderately resistant to downy mildew. Cluster A-II consisted of different genotypes in most of them are having higher yield.

From these observations, it is clear that the methodology is effective to characterize the exotic and indigenous accessions with no differentiation in quantitative characters. So far no reports in which quantitative data were used for morphological characterization are available and also these accessions were not used in study. Apart from quantitative and qualitative characters can also be included for morphological characterization.

5.2.3 Characterization of cucumber accessions using RAPD markers

Randomly Amplified Polymorphic DNA markers are used to estimate the genetic distance between 38 cucumber accessions. A total of 13 RAPD markers were employed in the analysis of molecular variation. The ability of the RAPD markers in distinguishing different species of cucumber were previously reported by Staub *et al.*, (2001). Apart from RAPD, DNA markers such as RFLP and AFLP were efficient in distinguishing different species of cucumber.

It is clear from the results that RAPD analysis was efficient to prove the genetic distances between cucumber accessions at the genomic level. It is evident from the tree diagram that the green fruited varieties Swarna Ageti, Sweet Market More, Ajax and others clustered together. While the white fruited type Himangi (pure white), Sangeetha (70% white) are clustered together. The cultivars having similar fruit shape like *Cucumis hardwickii* are clustered together. Mas *et al.*, (2001) in their AFLP analysis reported that the two accessions from a single cluster are genetically very close and those falls separately will show a wider genetic base. Usefulness of RAPD markers for screening cucumber accessions for major disease such as powdery mildew and anthracnose is already reported by Sese *et al.*, (2002).

5.2.4 Comparison study of morphological and molecular characterization of cucumber accessions

An effort has made to compare the morphological clustering pattern with molecular clustering. The dendrogram was constructed among 38 cucumber genotypes using 12 morphological quantitative characters by using SPSS 16.0 windows software and molecular dendrogram among the 38 cucumber genotypes were constructed with help of 13 random decamer primers by using STATISTICA software.

It was found from the dendrogram that, most of the genotypes do not follow the clustering based on their geographic based origin. The number of clusters formed from the morphological characters is less compared to the molecular analysis. The present investigation confirms that, the clustering pattern based on the molecular analysis is more accurate than the clustering based on the morphological characters. The main reason for this is, the morphological markers are mainly influenced by the environmental effect but the molecular markers are free from such influences.

The present study shows similar results for few genotypes, the accession number Peb Kamal and Poinsettia were closely grouped to each other from both the analysis. The similar results are also holds good with IIHR-36 & IIHR-04 VS-474 and VR-101 & IIHR-82. The accession like IIHR-405 and IIHR-407-1 were originated from the same species called *Cucumis sativus* var.*sativus* grouped into same clusters in morphological analysis but it was not followed in case of molecular analysis. The genotypes namely Sweet Market More, Tender Green Burbless and Poinsettia collected from the USA were grouped into different cluster in both morphological and molecular clustering pattern.

From these observations, it is clear that the morphological clustering methodology is effective to characterize the accessions with no difference in morphological and molecular characterizations. So far no reports in which quantitative data were used for morphological characterization.

5.3 DOWNY MILDEW INCIDENCE

Downy mildew caused by *Pseudoperonospora cubensis* is an important disease causing severe damage in Cucumber. However, works on screening the cucumber genotypes against this disease are limited .Thus, it is necessary to screen different cucumber genotypes against the disease under different agro-climatic conditions. In the present study 38 cucumber genotypes were screened for resistance to downy mildew incidence (Fig. 6). None of the genotypes were free from this disease incidence. The frequency of downy mildew in the 20 genotypes is shown in Fig. 8.

It was observed that 18.42 per cent of genotypes were moderately susceptible and none of genotypes fall under high susceptible group, 15.78 per cent were susceptible, 36 per cent of the genotypes (14 out of

38 genotypes) were moderately resistant and only one genotype was found to be resistant. None of the genotype was fall under immune group. Based on disease resistance and yield IIHR-407-1, IIHR-409-2 and IIHR-405 were most promising, but none of the genotypes were found most promising line for disease resistance. Similar studies have been reported by Reddy *et al.* (1995) and Thakur *et al.* (1996) in bitter gourd, Pan *et al.* (1996) in musk melon, Jamadar and Desai (1999) and Thammaiah *et al.* (1999), Kagadi *et al.* (2000) in ridge gourd.

Summary

VI SUMMARY

The present research work on "Genetic diversity and evaluation of advanced lines for resistance to Downy mildew (*Psuedoperanospora cubensis*) in Cucumber [*Cucumis sativus* (L.)]" was conducted at Indian Institute of Horticultural Research (IIHR), Hessarghatta, Bangalore during 2010-2011 to study the genetic diversity, heritability, genetic advance, morphological and molecular characterization and screening for downy mildew disease resistance. The findings of the research work are summarized here under.

The cucumber collections of diverse origin were tested for range of variability for 17 quantitative morphological characters. The analysis of variance due to treatments (genotypes) was significant (at P= 0.05) for all the characters studied. Means of genotypes varied greatly for several traits indicating the higher magnitude of variability in the germplasm. Environmental influence was evident on the expression of characters. The genotypic and phenotypic coefficients of variations were high (> 20%) for characters *viz.*, vine length, number of nodes per vine, days to first female flower opening, days to first male flower opening, days to first harvest, average fruit weight and number of seeds per fruit. This indicated broad genetic base, less environmental influence and these traits are under the control of additive genes. High value (30-50%) values of GCV and PCV were observed for the characters *viz.*, node at first female flower appears, node at first male flower appears, yield per plant, yield per plot and expected yield. Moderate (20-30%) values of GCV and PCV were observed for the characters *viz.*, days to first male flower opening, number of fruits per plant, average fruit weight, fruit length, fruit breadth, flesh thickness, seed cavity length and breadth, number of seeds per fruit and 100 seed weight. Lower magnitude (< 20%) of GCV and PCV were observed for the characters like vine length, number of

nodes per vine, days to first female flower opening and days to first harvest indicates the predominance of non-additive gene action, which can be exploited through hybridization or heterosis breeding. High heritability (> 60%) coupled with high GAM (> 20%) were observed for all the characters, except for the trait like vine length were observed high heritability with low GAM indicating low variability for this trait.

100 seed weight had maximum positive correlation with yield per plant in the present study. Similarly vine length, number of fruits per plant, average fruit weight, fruit length, flesh thickness and seed cavity length had significant positive correlation with the yield per plant but, days to first female flower opening and days to first harvest had significant negative correlation with the yield per plant. Vine length, number of nodes per vine, node at first male flower appears, days to first female flower opening, number of fruits per plant, average fruit weight, fruit length, flesh thickness, seed cavity length, seed cavity breadth, number of seeds per fruit and 100 seed weight had positive direct effects on yield per plant. While node at first female appears, days to first male flower opening, days to first harvest and fruit breadth had negative direct effects on yield per plant. With the high level of positive significant correlation, direct positive effects, high GCV and GA, selection for high yield should be based on number of fruits per plant and average fruit weight.

Morphological characterization using 17 quantitative morphological characters following non- heirchial Euclidean cluster analysis resulted in fifteen clusters. In this, 38 cucumber accessions were clustered into fifteen clusters based on their morphological similarity. Maximum contribution for clustering was from yield per plant followed by days to first harvest followed by the node at first female flower appears and average fruit weight. Minimum diversity within the

cluster and Maximum diversity between the clusters were noticed. Highest inter-cluster distance was observed between cluster XIV and XV (36.16) and the considerable magnitude of intra-cluster distance in cluster XIII (21.30), followed by cluster XII (13.82), indicated that there is good scope for future breeding programme. It is observed that yield per plant, 100 seed weight, number of seed per fruit, fruit length and number of nodes per vine had contributed predominantly towards divergence. Hence selection of parents differing in these traits may be useful for the utilization of divergent material for heterosis breeding programme.

The genetic distances between 38 cucumber accessions were estimated through cluster analysis of 17 morphological quantitative characters using software SPSS window 16.0. Based on the analysis, 38 cucumber accessions have been distributed to 12 clusters which are further grouped into two major clusters A and B showing highest genetic distance. However, the clusters did not associated with geographic origins of cucumber genotypes. From this study it is clear that the methodology is effective to characterise the exotic and indigenous accessions with no differentiation in quantitative characters. So far there is no report in which qualitative data were used foe morphological characterization.

The present investigation was carried out to study the molecular analysis of genetic diversity in cucumber genotypes collected from the different parts of India and abroad using DNA markers (RAPD). The RAPD analysis of 38 cucumber genotypes was done using 13 arbitrary decamer primers which generated a total of 103 RAPD bands, most of which were polymorphic across accessions. Out of 13 primers tested OPX-10, OPA-05 showed highest polymorphism percentage (83.33). The pooled binary data derived from profiles of 38 genotypes was used to

develop distance matrix displaying the pair wise genetic distance between the genotypes. The cluster drawn out of the distance matrix, gave grouping of various genotypes into two major clusters as A and B, then again major cluster A is sub divided into A_1 to A_9. However, most of the clusters did not associated with the geographic origin of cucumber genotype. The genetic dissimilarities values ranged from 0 to 55 suggesting moderate genetic variation within cucumber genotypes. The highest dissimilarity percentage was between genotypes IIHR-409-2 and 595920 and these genotypes would be useful for increasing high yield and quality of cucumber crop.

The genotypes Swarna Ageti, Japanese Long Green, Sangeeta, Nandini, Barsati, Sweet Market More, Ajax, VR-101, VR-06-07, Local line, IIHR-405, Karur local, IIHR-407-1, IIHR0409-2 were found to be moderately resistant and *Cucumis hardwickii* showed resistance to the downy mildew. These genotypes can be used as sources of resistance to develop downy mildew resistant cultivars.

Future line of work

- Total genetic variation in selected cucumber genotypes was high. Thus helps to direct selection can be exercised for improvement of characters *viz.*, number of fruits per plant, fruit length and average fruit weight

- Yield parameters like vine length, average fruit weight, days to first harvest, node at female flower are predominantly controlled by non-additive gene action and hence higher yield be exploited through heterosis breeding or through recurrent selection for SCA

- RAPD markers revealed that, the maximum diversity expressed between the genotypes IIHR-409-2 & 595920 (52%), IIHR-36 &

IIHR-338 (51%) followed by 595920 & Barsati(50) may be exploited by effective crossing between these genotypes to obtain desirable segregates for further selection of superior lines.

- Exploiting the genetic distance from molecular marker data helps to identifying genotypes for mapping populations and also to identify molecular markers linked to desirable traits (resistance to downy mildew) for marker assisted selection (MAS).

- Potential of the other molecular markers that amplify relatively less conserved regions of cucumber genomes such as ISSR, SSR and SCAR should also be investigated to enhance the cucumber breeding programmes.

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**Original not seen*

Appendix

APPENDIX-I

Meteorological data from April 2010 to March 2011, IIHR, Bangalore-89

Month	Temperature(°C)		Relative Humidity (%)		U.S.W.B. Class 'A' Pan- Evaporation (mm)	Mean wind speed (km/h)	Rainfall (mm)
	Maximum	Minimum	07.30 hrs	14.00 hrs			
Apr-10	34.9	19.5	77.6	60.5	6.9	5.5	75.0
May-10	32.0	20.4	70.2	52.2	5.2	2.7	74.9
Jun-10	29.4	19.8	69.5	53.7	4.9	7.6	7.4
July-10	28.4	19.3	72.2	55.7	4.5	11.4	30.4
Aug-10	29.2	19.8	74.6	57.0	4.4	6.6	26.4
Sep-10	28.2	19.9	79.2	61.8	3.6	5.6	205.2
Oct-10	28.2	18.2	65.7	53.6	3.5	4.8	16.2
Nov-10	29.2	18.1	73.8	56.9	2.7	5.2	34.8
Dec-10	27.0	16.0	69.9	51.0	2.8	5.3	9.0
Jan-11	27.0	14.8	64.0	42.6	3.7	4.9	-
Feb-11	31.2	13.8	56.5	37.8	5.0	4.9	-
Mar-11	33.8	16.0	60.7	36.4	7.0	4.9	24.0

Annexure

ANNEXURE- I

List of genotypes used for experiments

Sl. No.	**Genotypes**	Donar's Name	Taxonomic name	Source of collection
1	Swarna Ageti	CHES, Ranchi	*Cucumis Sativus*	Ranchi, India
2	Punjab Naveen	NA	*Cucumis Sativus*	NA
3	IIHR-34	NA	*Cucumis Sativus*	Poona collection
4	Japanese Long Green	NA	*Cucumis Sativus*	NA
5	Phule shubangi	NA	*Cucumis Sativus*	NA
6	Himangi	NA	*Cucumis Sativus*	NA
7	Pebkamal	NA	*Cucumis Sativus*	NA
8	VS 474	NA	*Cucumis Sativus*	NA
9	Sangeeta	U.S. Agri seeds	*Cucumis Sativus*	NA
10	Nandini	U.S. Agri seeds	*Cucumis Sativus*	U.S. Agri seeds
11	Barsati		*Cucumis Sativus*	
12	Sweet Market More	Haris Moran Seed Company, USA	*Cucumis Sativus*	Haris Moran Seed Company, USA
13	Ajax	Nunhemps pvt. Hybrids	*Cucumis Sativus var. sativus*	Nunhemps pvt. Hybrids
14	Poinsettia	Haris Moran Seed Company, USA	*Cucumis Sativus*	Haris Moran Seed Company, USA
15	Tender Green Burbless	Haris Moran Seed Company, USA	*Cucumis Sativus*	Haris Moran Seed Company, USA
16	I595920	NA	*Cucumis Sativus*	NA
17	VRC-06-08	NA	*Cucumis Sativus*	NA
18	VR-101	NA	*Cucumis Sativus*	NA

Sl. No.	**Genotypes**	Donar's Name	Taxonomic name	Source of collection
19	VR-06-07	NA	*Cucumis Sativus*	NA
20	IIHR-306	CHES, Ranchi	*Cucumis Sativus*	Ranchi, India
21	IIHR-285	Holenarsipura local	*Cucumis Sativus*	Holenarsipura, Hassan dist.
22	IIHR-34-S4	NA	*Cucumis Sativus*	NA
23	IIHR-337	CHES, Ranchi	*Cucumis Sativus*	Ranchi, India
24	Pilibhat local	NA	*Cucumis Sativus*	NA
25	IIHR-304	NA	*Cucumis Sativus*	Karoor, TN
26	local line 1	Bangalore local line	*Cucumis Sativus*	Bangalore
27	IIHR-81	Prakash Agarwal	*Cucumis Sativus*	Prakash Agarwal company, Lucknow
28	IIHR-82	Kaushal beej company, Faizabad	*Cucumis Sativus*	Kaushal beej company, Faizabad
29	IIHR-405	NA	*Cucumis Sativus*	NA
30	IIHR-36	Ottapalam collection	*Cucumis Sativus*	Ottapallam, Kerala
31	Kerur local	Karoor local line	*Cucumis Sativus*	Karoor, TN
32	IIHR-407-1	NA	*Cucumis Sativus*	NA
33	IIHR-384	NA	*Cucumis Sativus*	NA
34	Gadag local	Gadag local	*Cucumis Sativus*	Gadag Dist.
35	IIHR-409-2	NA	*Cucumis Sativus*	NA
36	IIHR-177	NA	*Cucumis Sativus*	NA
37	IIHR-338	CHES, Ranchi	*Cucumis Sativus*	Ranchi, India
38	*Cucumis hardwickii*	NA	*Cucumis hardwickii*	NA