Plagiarism Report

On

Diallel Analysis and Genetic Diversity Analysis Assist in the Selection of Appropriate Parental Materials for Hybridization

Course Title: Seminar
Course code: ENS 598

SUBMITTED TO

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SALNA, GAZIPUR-1706

A SEMINAR PAPER

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ABSTRACT

This review paper was prepared to highlight the meaning of diallel analysis as well as genetic diversity analysis and their importance in selecting the appropriate parents for hybridization. The understanding of general combining ability (GCA), specific combining ability (SCA), heritability, environmental effect, gene action, degree of dominance and diverse plant group is basic requisite for plant selection in crop improvement program. Maize varieties namely CML 161, KSU 4-58 and cross CML 161 × CML 424 and CML 424 × KSU 8-33 are rewarding for plant breeding program for their better performance in GCA and SCA respectively. All characters under studied of faba bean are highly heritable except seed yield which is medium heritable. Water melon varieties CS-19-S7 (P_1), BL-14-S7 (P_2), 6372-4-S7 (P_3), and CH-8-S7 (P_4) showed location specific adaptability due to environmental effect. In case of fruit setting character, bottle gourd variety Pusa Naveen contains high frequency of dominant alleles and PBOG 13 and PBOG 22 have maximum number of recessive alleles. Crossing between cluster II (BARI Sarisha9 and SAU Sarisha1) and Cluster III (Tori 7, F6×BARI Sarisha9, BARI Sarisha9×F6, F6×Tori 7, BARI Sarisha6×BARI Sarisha9, BARI Sarisha15 and SAU Sarisha1) produced maximum number of desirable progeny as they possess maximum diversity due to their higher inter cluster distance (11.68). Thousand seed weight contributed towards higher genetic diversity for 18 mustard genotypes under studied.

Keywords: GCA, SCA, heritability, gene action, degree of dominance and environmental effect.

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CHAPTER 1

INTRODUCTION

Plant breeding is mechanism of changing the characters of plants for getting desired characteristics. It is being used to upgrade the quality of nutrition in products for benefit of the human being (Hartung & Schiemann, 2014). Plant breeding (crop improvement) is the purposeful alteration of crop species with a view to creating desired plant types that are better suitable for better yields, cultivation and disease resistant. In natural selection, plants usually seed set in favorable environment which is best suited for them and pass on the genes that made them successful in that environment. Hence plant breeding is different from natural selection (Harriman & Nwammadu, 2016). Initially early farmers selected food plants which have good desirable characteristics, and nursed these as progenitors for generation to generations, which helps in the accumulation of desirable important traits over time. Modern plant breeding is also called applied genetics, but its scientifically covers pathology, entomology, chemistry, molecular biology, cytology, systematics, physiology, and statistics (biometrics). Selection is a great technique in plant breeding which includes including of desirable characters and excluding of less desirable characters (Deppe, 2000). Classical plant breeding means crossing or hybridization of pure lines, followed by artificial selection to get plants with desirable traits of higher yield, nutrition and resistance to diseases (Bauman & Crane, 1992). Hybridization is the technique of accumulating more characters from two desirable plants species into a single offspring by process of artificial pollination. The breeding processes mainly rely upon superior genotypes selection from base population. Selection is done on the basis of phenotype but in cases where phenotypic superiority is more due to environment and less due to genotype, selection process is not very effective (Marjanovic *et al*., 2011). Therefore knowledge of genetic mechanism of crop plants involved in expression of traits is essential for the success of any breeding program. A complete diallel mating design is one that allows the parents to be crossed in all possible combinations (Pospíšilová, 2010), including selfs and reciprocals. It is required to obtain Hardy–Weinberg equilibrium in a population (Acquaah, 2012). The diallel analysis is mostly used for getting various genetic information from all mating designs (Hallauer *et al*., 2010). Sprague and Tatum (1942) introduced the diallel cross concept to plant breeding among a set of maize (Zea mays L.) inbred lines by making all possible crosses. Genetic diversity helps populations to survive in continuous changing environments. With more variation, it is more likely that some individuals in a population will

possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals.

In artificial crosses, selection of the appropriate parents to be used is one of the main concern for plant breeders that will stimulates the expression of highest genetic variability and creation of superior recombinant genotypes. A lot of techniques are being used for the identification of promising and desirable agronomical traits genotypes for hybridization. Under selection detailed information about the genetic control of the characters is important if plant breeders want to implement their program effectively by the choice of appropriate parents and selection methodology. The use of good mating designs is important for successful plant breeding schemes. Diallel mating designs means using the same parents as females and males is important tool in plant breeding programs to get information on inheritance, such as general combining ability (GCA), specific combining ability (SCA) and heritability of qualitatively or complexly inherited traits. Heritable variation is more important for enduring genetic improvement (Singh & Ceccarelli, 1995). A precise information on nature and degree of genetic divergence would help plant breeder in selecting appropriate plant for hybridization.

Objectives

- To obtain information on inheritance such as GCA, SCA, environmental effect, degree of dominance, parental order of dominance, gene action and heritability of qualitatively or complexly inherited traits.
- To highlight the genetically diverse genotype and characters contribute to this divergence for parental selection

CHAPTER 2

MATERIALS AND METHODS

This paper is exclusively a review paper so that all of the information has been collected from the secondary sources. During the preparation of the review paper, various relevant books, journals publications etc. were studied. The related topics have been reviewed with the help of library facilities of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Bangladesh Agricultural Research Institute (BARI)), internet browsing. Valuable suggestion and information were taken from honorable major professor. After collecting all the available information, it has been presented as per the objectives of this paper.

CHAPTER 3

REVIEW OF FINDINGS

3.1. Diallel Analysis

3.1.1. Assumptions/Hypotheses of diallel cross analysis

Genetical Systems have some assumptions. Diallel cross analysis has following assumption suggested by Hayman (1954) and Obi (2013):

- Diploid segregation is normal
- There is no multiple allelism
- Absence of maternal effects
- Parents should be homozygous
- No linkage and epistasis
- Random mating between parents

3.1.2. Types of Diallel Analysis

Depending upon whether or not the parental inbreeds or the reciprocal $F_1's$ are included or both, there are four type of Diallel crossing system (Griffing, 1956).

A) Method 1 or full diallel design: Parents, one set of $F1's$ and reciprocal $F1's$ are included (all $p2$ combinations). The system gives *p2* genotypes (Griffing, 1956).

Parents	Male 1	Male 2	Male 3	Male 4
Female 1	X11	X12	X13	X14
Female 2	X21	X22	X23	X24
Female 3	X31	X32	X33	X34
Female 4	X41	X42	X43	X44

B) Method 2: Parents and one set of $F1's$ are included but reciprocal $F1's$ are not ((p+1)/2 combinations).

Parents	Male 1	Male 2	Male 3	Male 4
Female 1	X11	X12	X13	X14
Female 2		X22	X23	X24
Female 3			X33	X34
Female 4				X44

C) Method 3: One set of $F1's$ and reciprocal $F1's$ are included, but not the parents ((p−1) combinations).

Parents	Male 1	Male 2	Male 3	Male 4
Female 1		X12	X13	X14
Female 2	X21		X23	X24
Female 3	X31	X32		X34
Female 4	X41	X42	X43	

D) Method 4: One set of $F1's$ but neither parents nor reciprocal $F1's$ is included (1/2(p − 1) combinations).

Parents	Male 1	Male 2	Male 3	Male 4
Female 1		X12	X13	X14
Female 2			X23	X24
Female 3				X34
Female 4				

3.1.3. Estimation of combining ability

For the development of appropriate breeding program the knowledge about the nature and magnitude of gene action is important. Combining ability helps to know the magnitude and nature of gene action controlling quantitative traits. Unlike most other mating designs, which can only provide estimates of genetic variance components, the diallel can provide information about the combining ability of lines in addition to estimates of genetic parameters of a population. Combining ability refers to the ability of a genotype to transfer its superior performance to its cross. There are two types of combining ability viz. general combining ability and specific combining ability. In a series of hybrid combination, the average performance of a genotype is called general combining ability. The performance of a parent in a specific cross is called specific combining ability. GCA variance represents additive genetic effects, while that of SCA involves non-additive genetic effects, arising largely due to dominance and epistatic deviations. Estimates of GCA and SCA can provide valuable information about the parents used. Superior hybrids can be identified by comparing the estimated SCA effects and the trait mean for each combination. If the mean square for SCA does not significantly different from zero indicating that parents have highest GCA effect, if crossed would be rewarding in plant breeding for the production of superior

progeny. Parents that exhibit high GCA effects could be used to initiate a recurrent selection program or they could be used as a tester in a hybrid crop, such as maize.

General combining ability of maize hybrids is described in table 1. P_1 and P_4 showed significant differences for three characters among four characters. In case plant height, we can select P_1 and P_3 for tall plant and dwarf plant respectively. If we want to develop short duration variety then we have to select P_4 plant as it shows significant negative combining ability in case of both days to anthesis and days to silking. From table 1, P_1 and P_4 can be selected for hybridization program as they showed significantly better performance than others.

Table 1. Estimation of general combining ability of in F_1 maize hybrid plants

Parents	P_1	P_2	P_3	P_4
Plant height (cm)	14.15 **	13.62 **	-13.83**	-7.21**
Days to anthesis	3.10 **	0.51*	0.60 *	-2.90 **
Days to silking	2.85**	0.47 ^{NS}	0.06 ^{NS}	-3.57 **
Kernel weight (g)	2.39 ^{NS}	23.62*	-2.86 ^{NS}	-19.32 ^{NS}

P_1=CML 161, P_2=CML 424, P_3=KSU 8-33, P_4=KSU 4-58,

NS= Non significant,

**= Significant at 1% level significance,

*= Significant at 5% level significance

(Source: Modified from Murtadha, 2016)

Specific combining ability of F_1 maize hybrid is shown on table 2. Parents P_1, $P_2 \times P_2$ and P_3 plant can be selected for heterosis breeding as they showed significantly better performance in cross $P_1 \times P_2$ and $P_2 \times P_3$. Specific combining ability represents non additive gene action where heterosis breeding is rewarding. For the development of short duration and dwarf variety, we have to select $P_1 \times P_2$ cross as it shown significantly negative specific combining ability. If we considered yield and short duration variety we should use $P_2 \times P_3$ cross as it performs better for yield. Though P3 × P_4 cross no significant difference for maximum characters but it can be considered for better yield after $P_2 \times P_3$ cross.

Table 2. Estimation of specific combining ability of in F_1 maize hybrid plants

Parents	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_2 \times P_3$	$P_2 \times P_4$	$P_3 \times P_4$
Plant height (cm)	-14.90 **	-6.10 ^{NS}	4.81 ^{NS}	20.20**	6.34 ^{NS}	-6.50 ^{NS}
Days to anthesis	-2.98 **	-0.10 ^{NS}	0.98 ^{NS}	-1.70 **	3.53 **	-0.60 ^{NS}
Days to silking	-2.93 **	1.11 ^{NS}	0.73 ^{NS}	-2.20**	2.90**	-1.10 ^{NS}
Kernel weight (g)	45.81 *	-31.0 ^{NS}	55.99**	146.0 **	39.2 ^{NS}	66.30 **

P_1=CML 161, P_2=CML 424, P_3=KSU 8-33, P_4=KSU 4-58, NS= Non significant,

**= Significant at 1% level significance, *= Significant at 5% level significance

(Source: Modified from Murtadha, 2016)

The GCA and SCA ratio of studied characters of faba is shown in figure 1. The GCA/SCA ratio of mean squares for all studied characters in faba bean genotypes was higher than unity (1). That means it has considerable contribution towards additive effects of genes in the genetic expression. This additive effects of gene is controlling these characters. On the other hand the effect of non-additive (dominant) action is less important for the expression of these characters. Therefore, selection can be beneficial for improvement through our faba bean materials. However, it would be emphasized that GCA/SCA ratio may not always reveal the true picture of the gene action for

a particular character due to the deferential parental combining ability with each other. However such combination depends considerably upon complex interaction between genes and genotype by environment (Fikere *et al*., 2008; El-Bramawy and Osman; 2012).

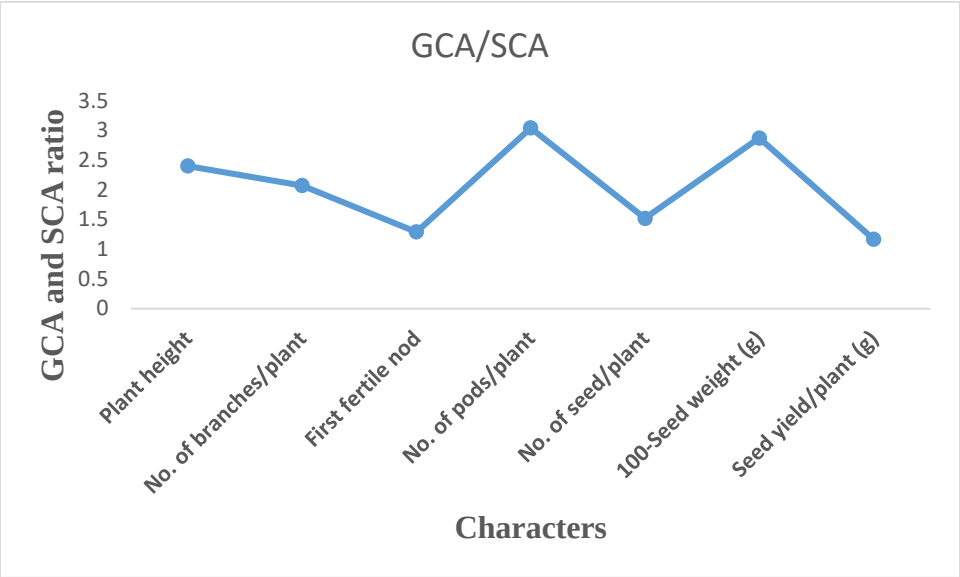

Figure 1: GCA and SCA ratio of the Characters of faba bean.

(Source: Modified Zeinab & Helal, 2014)

3.1.4. Heritability

Some genetic variation is heritable because it can be passed from parent to offspring. Some genetic variation is not strictly heritable, because it is due to dominance or epistatic interactions that are not directly passed from parent to offspring. For example, if one allele is dominant to another, the phenotype of a heterozygous parent is determined in part by the dominance interaction between the two alleles. Since a sexually-reproducing parent only passes on a single allele to its offspring, the offspring does not inherit its whole genotype from a single parent. So it does not inherit the dominance interaction, just the effect of a single allele. Heritability is due to genetic factors in the proportion of variance in a particular trait, in a particular population, as opposed to environmental influences. Heritability is the genetic variance of trait in a population which can be transferred from parents to its offspring. Heritability is the measure of transmissibility of characters from parents to offspring. The range of heritability is 0-100%. If heritability is 100%, it denotes all the variation is due to the genotype. If heritability is zero, it indicates all the variation is due to

environmental effect. There are two types of heritability viz. broad sense heritability and narrow sense heritability. Broad sense heritability is the ratio between genotypic variance to phenotypic variance and is expressed by h^2 b. The ratio between additive genetic variance and phenotypic variance is called narrow sense heritability. It is expressed by h^2 n. A grading of heritability may be given as follows-

- < 20%= low heritability
- Between 20%-50%= medium heritability
- >50% = high heritability

Heritability of studied traits of faba bean genotypes is shown on table 3. Broad sense heritability ranges from 92.45 %- 97.03% and the narrow sense heritability ranges from 23.67%-75.53%.Seed yield showed higher broad sense heritability (97.03%) but lower value for narrow sense heritability (23.67%). All the characters except seed yield are highly heritable as its narrow sense heritability is more than 50%. The heritability of seed yield is medium as its narrow sense value lies between 20%-50%.

Table 3. Estimation of heritability of studied traits of Faba bean genotypes

Character	Heritability (%)	
	Broad sense heritability	Narrow sense heritability
Plant height	95.56	70.53
No. of branches	92.45	62.00
No. of pods	93.95	76.42
No. of seed	95.75	47.90
100-Seed weight	94.87	75.53
Seed yield	97.03	23.67

(Source: Zeinab & Helal, 2014)

3.1.5. Estimation of environmental effect

Plant breeders aiming to develop variety which variation is due to genotype not for environment. If the variation is due to genotype, then the variety showed wider adaptability that means it shows constant performance in all area. If the variation is due to environment then the variety has specific adaptability that means its performance is not constant in all environment.

In table 4, environment has significant effect on the studied characters of watermelon. Also the genotype and environment interaction has significant effect on studied characters except fruit yield and no. of fruits per plant. That means the characters of these four water melon varieties namely CS-19-S7 (P_1), BL-14-S7 (P_2), 6372-4-S7 (P_3), and CH-8-S7 (P_4) is not only controlled by genotype but also by environment. So these water melon varieties showed specific adaptability instead of wider adaptability which is not desirable for good variety.

Table 4. Mean squares of combined ANOVA for yield components and fruit traits in diallel cross of four watermelon inbred lines over four environments.

Source of variance	Degrees of freedom	Fruit yield	No. of Fruits/ plant	Vine length	Days to first female flower	Days to Maturity	Fruit weight
Environments (E)	3	441.08**	6.42**	38.19**	579.05**	2162.11 **	53.20**
Replication	12	15.99	0.45	0.18	2.76	8.00	1.44
Genotypes (G)	15	46.15**	0.82*	1.34**	31.51**	113.10**	11.31**
G × E	45	15.55	0.45	0.29**	8.91**	37.23**	1.78*

**= Significant at 1% level significance, *= Significant at 5% level significance

(Source: Modified from Bahari *et al.*, 2012)

3.1.6 Estimation of gene action and degree of dominance

For the selection of appropriate plant and breeding program for crop improvement through hybridization largely depends the knowledge of gene action. The expression of genes in a genetic population is known as gene action. The genetic material used in the experiment usually control the gene action. Generally additive dominance and epistasis type gene action found in F_2 or advanced generation of a cross between two pure lines. Homozygous line showed additive gene action. But in segregating population both additive and non-additive types of gene action occurred. Self-pollinated crops showed additive gene action. In contrary cross pollinated non additive gene action as it associated with heterozygosity. The characters are controlled by few gene are known as oligogenic or qualitative characters which are governed by non-additive gene action. Polygenic or quantitative characters are usually controlled by many gene governed by both additive and non-

additive type of gene action. Additive gene action is very important for selection as it is the only genetic variance which responds to selection. The presence of significant amount of dominant and epistasis variance is important for commercial exploitation of heterosis. Both additive and non-additive gene actions are important for varietal adaptability, because adaptability is associated with heterogeneity and heterozygosity. The higher stability of hybrid is due to non-additive gene action and in varietal blends of self-pollinated species, it is due to additive gene action.

Parental order of dominance, gene action and degree of dominance can be estimated by Hayman's Graphical approach (Vr-Wr graph). In Vr-Wr graph there are two lines, one is parabola line and another is regression line. The average level of dominance can be detected by the nature and magnitude of 'a' (the intercept of Y- axis) which indicates the point on Wr xis (Y axis in Vr-Wr graph) where the regression line intersect the Wr axis in relation to the origin '0'. So when

- a= 0, i.e. regression line passing through the origin means complete dominance
- a>0, i.e. regression line passes above the origin means partial dominance
- a<0, i.e regression line passes below the origin means over dominance.
- When regression line touches the limiting parabola indicates no dominance

When all the parents remain below the regression line indicates duplicate gene action. When all the parents remain both up and below the regression line indicates complementary gene action. Parents falling nearby the origin supposed to have maximum dominant allele and parents away from origin supposed to contain recessive allele. Parents occupying the intermediate position have equal frequency of both dominant and recessive allele.

In figure 2, regression line passes below the origin it indicates days to first flowering is over dominance character. Parents 8 namely Pusa Naveen remains near to origin that means it has maximum number of dominant allele. On the other hand parents 1 (PBOG 13) and 2(PBOG 22) remain away from origin indicating that they have maximum number of recessive allele. The other remaining parents have both dominant and recessive allele due to their intermediate position. Parents are remaining up and below the regression line denotes complemantary gene action.

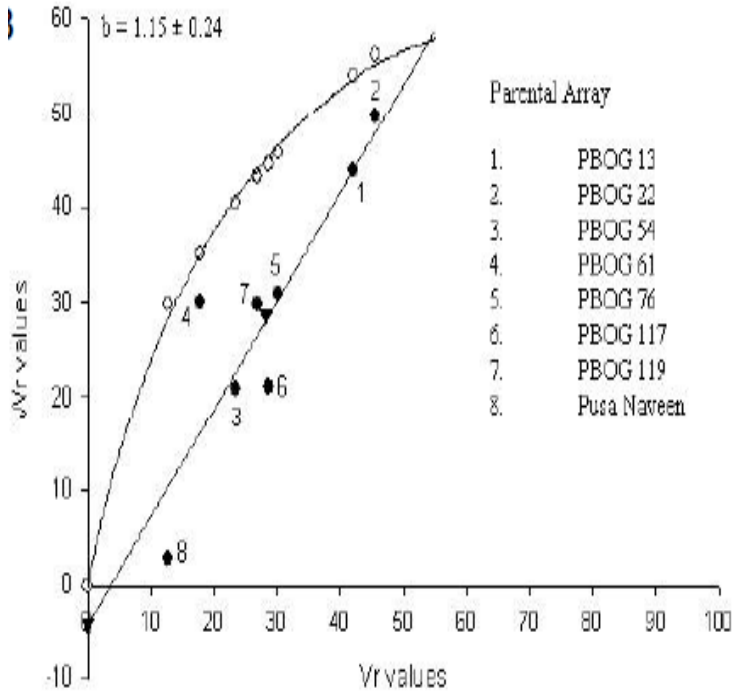

Figure 2: Vr-Wr graph for days to first fruit harvest.

(Source: Dubey & Ram, 2005)

3.1.7. Advantages of Diallel analysis

- Diallel cross evaluates several single crosses in terms of genetic component variance.
- Aids in the selection of suitable parents for hybridization.
- Helps in appropriate breeding procedure selection.
- Provide information on both additive and dominant gene effect.
- Provides information on GCA, SCA and heritability

3.1.8. Disadvantages of Diallel analysis

- It can test limited number of plants at a time.
- All assumptions are seldom full filled.
- Analysis is little bit of complicated as same parent used as both male and female parent (Isik, 2009).

3.2. Genetic Diversity Analysis

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. Plant can adopt to changing environment due to genetic diversity. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals. Not only geographical separation but also the genetic barriers to crossability causes genetic diversity. Genetic diversity helps to identify the genetically divergent parent in plant breeding to obtain the desirable recombination in the segregating generations because hybrids between lines of diverse group generally show a great heterosis than those are remain in closely related strains (Singh, 1983). A precise information on nature and degree of genetic divergence would plant breeder in selecting appropriate plant for hybridization.

Eighteen genotypes were used for genetic diversity analysis. Here the name and source of these 18 genotypes were given in table 5.

Table 5. Sources of 18 *Brassica rapa* genotypes

Designation	Genotypes	Source
G1	BARI Sarisha6	BARI
G2	SS-75	BARI
G3	F6	SAU
G4	Tori 7	BARI
G5	BARI Sarisha9	BARI
G6	F6×BARI Sarisha9	SAU
G7	BARI Sarisha9×F6	SAU
G8	Tori 7×BARI Sarisha6	SAU
G9	BARI Sarisha6×Tori-7	SAU
G10	Tori 7×F6	SAU
G11	F6×Tori 7	SAU
G12	Tori 7×SS 75	SAU
G13	SS 75×Tori 7	SAU
G14	BARI Sarisha9×BARI Sarisha6	SAU
G15	BARI Sarisha6×BARI Sarisha9	SAU
G16	BARI Sarisha15	BARI
G17	Real Tori7	Farmer's field
G18	SAU Sarisha1	SAU

(Source: Jahan *et al*., 2013)

In figure 3, eighteen genotype of brassica are divided in four group based on their principal component scores. Group I contains 3 genotypes, group II contains 2 genotypes, Group III contains 6 genotypes and group IV contains 7 genotypes. Cluster II and Cluster IV showed higher genetic distance. Selection of parents from these two cluster will produced diverse progeny which is very important for selection in plant breeding program.

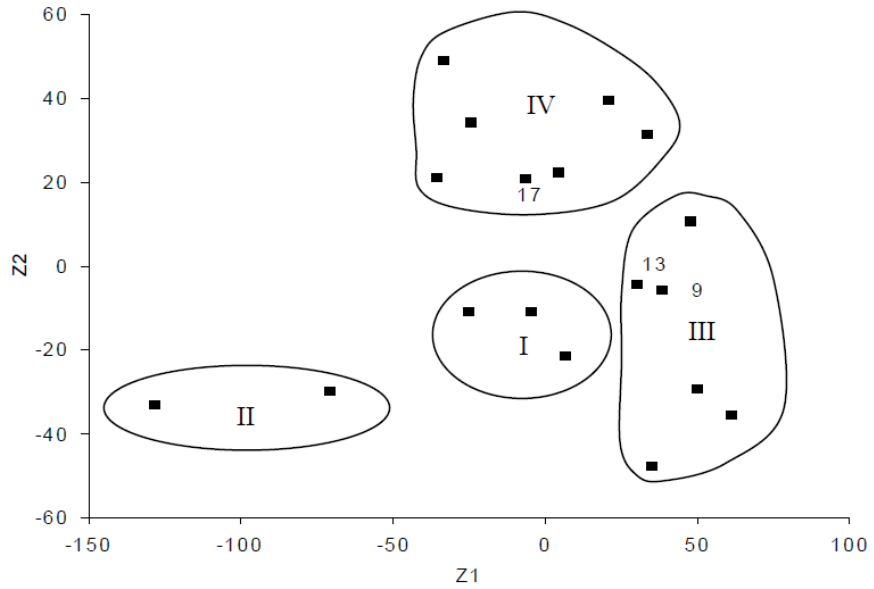

Figure 3: Scatter distribution of 18 brassica genotype based on principal component scores superimposed with clustering.

(Source: Jahan *et al*., 2013)

After comparing D^2 values, 18 genotypes were grouped into four clusters. Cluster IV had maximum number of (7) genotypes followed by III, I and II which had 6, 3, and 2 genotypes, respectively (Table 6).These results confirmed the clustering pattern of the genotypes obtained through principal component analysis.

Table 6. Distribution of 18 genotypes of *Brassica rapa* in four clusters

Clusters	No. of genotype	Name of Genotype
I	3	G2, G8, G14
II	2	G5, G18
III	6	G1, G3, G9, G10, G12, G13
IV	7	G4, G6, G7, G11, G15, G16, G17

(Source: Jahan *et al*., 2013.

The highest inter-cluster distance was recorded between clusters II and III (11.697), followed by between cluster II and IV (9.812), I and II (8.721), III and IV (6.770) (Table 7). The lowest inter-cluster distance was found between cluster I and III (3.619), followed by I and IV (3.941). The

maximum inter-cluster distance was obtained between the clusters II and III (11.697) maintaining more distance than other clusters. Genotypes from these two clusters if involved in hybridization may produce a wide spectrum of segregating population.

Table 7. Average inter cluster distance (D^2) and Intra cluster distance (bold) for 18 *Brassica rapa* genotypes

Cluster	I	II	III	IV
I	**0.630**			
II	8.721	**1.057**		
III	3.619	11.697	**0.631**	
IV	3.941	9.812	6.770	**0.739**

(Source: Jahan *et al*., 2013)

Cluster means for ten characters are presented in Table 8. Primary branches per plant had the highest mean (5.99) in cluster 1. Days to flowering, siliqua length, seeds per pod, and 1000-seed weight had the highest means (37.83, 4.53, 18.22 and 3.00, respectively), while primary branches per plant and secondary branches per plant had the lowest means (4.40 and 3.17, respectively). Plant height, secondary branches per plant, siliquae per plant and yield per plant had the highest means (109.63, 7.51, 236.72, and 7.16, respectively), while siliqua length and seeds per pod had the lowest means (3.70 and 15.71, respectively). Considering duration and yield, crosses involving cluster II and cluster III may exhibit high heterosis for yield. Crosses between the genotypes belonging cluster II with cluster IV and genotypes in cluster I with cluster II might produce high heterosis for yield as well as for earliness. Also the crosses between genotypes from cluster II with cluster I and IV might produce high level of segregating population. So the genotypes belonging to cluster I and cluster II, cluster II and cluster IV and cluster III and cluster IV have been selected for future hybridization program.

Table 8 Cluster means for 10 characters of 18 *Brassica rapa* genotypes.

Characters	I	II	III	IV
Plant height	105.64	94.75	109.63	94.91
No. of primary branches/plant	5.99	4.40	5.97	5.56
No. of secondary branches/plant	5.84	3.17	7.51	6.49
Days to 50% flowering	35.56	37.83	33.56	32.33
Days to maturity	95.33	90.83	91.67	92.81
Siliquae/plant	186.86	106.43	236.72	174.83
Siliqua length	3.86	4.53	3.70	3.84
Seeds/pod	17.18	18.22	15.71	17.22
1000-seed wt.	2.89	3.00	2.89	2.87
Yield/plant	6.26	4.78	7.16	6.43

(Source: Jahan *et al*., 2013)

Average height of four cluster shown in figure 4. Cluster III showed maximum height (109.63 cm) followed by cluster I (104.64 cm). Minimum height was found from Cluster II and IV which are 94.75 cm and 94.91 cm respectively. If we want to develop dwarf variety then plant should be selected from cluster II and cluster IV.

Figure 4: Average plant height of four cluster.

(Source: Modified from Jahan *et al*., 2013)

Average yield performance /plant of four cluster shown in figure 5. Cluster III showed maximum yield per plant which is 7.16 kg followed by cluster IV which is 6.43 kg. The minimum yield was found from cluster 2 (4.78 kg).For better yield performance we should select parent from cluster III and cluster IV.

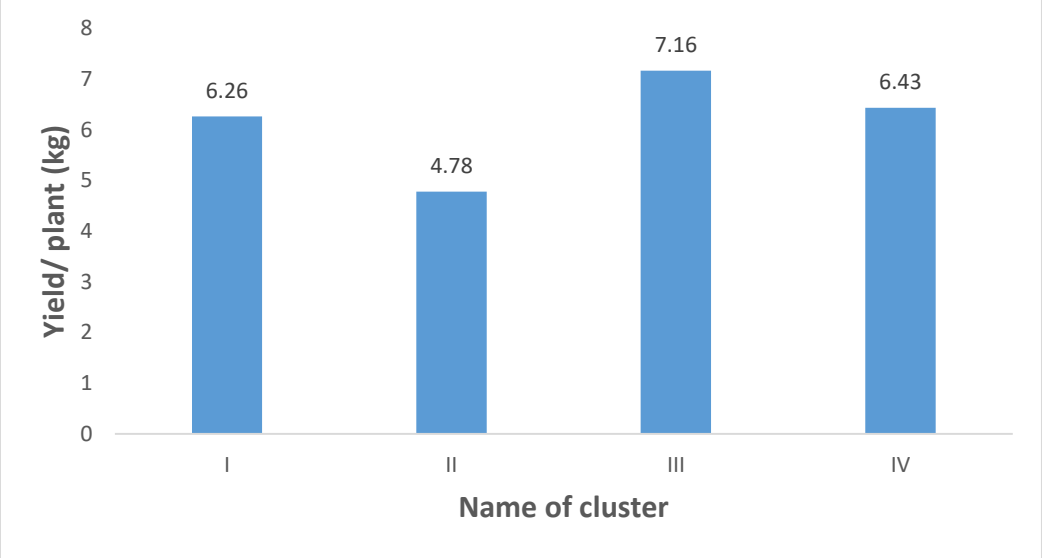

Figure 5: Average yield/plant performance of four cluster.

(Source: Modified from Jahan *et al*., 2013)

Contribution of characters towards divergence of the genotypes is presented in Table 9. The vector-I (Z1) obtained from PCA, the important characters responsible for genetic divergence in the first axis of the differentiation were 1000-seed wt (3.2986), no. of primary branches/plant (1.2725), no. of secondary branches/plant (0.2329) and days to 50% flowering (0.0216). In vector-II (Z2), no. of primary branches/plant (0.4983), seeds/pod (0.4577), days to 50% flowering (0.2696), days to maturity (0.0868), siliquae/plant (0.0013) and no. secondary branches/plant (0.0004) were important, but plant height, days to maturity, siliquae/plant, siliqua length, seeds/pod, yield/plant played only a minor role in the first axis of differentiation. The role of number of primary branches/plant, number of secondary branches/plant and days to 50% flowering in both the vectors were important components for genetic divergence in these materials.

Table 9. Latent Vectors for 10 characters of 18 *Brassica rapa* genotypes

Characters	Vector I	Vector I
Plant height	-0.0410	-0.1276
No.of primary branches/plant	1.2725	0.4983
No.of secondary branches/plant	0.2329	0.0004
Days to 50% flowering	0.0216	0.2696
Days to maturity	-0.3396	0.0868
Siliquae/plant	-0.0893	0.0013
Siliqua length	-0.1884	-1.9633
seed/pod	-0.2035	0.4577
1000-seed wt	3.2986	-0.0089
Yield/plant	-0.6378	-0.6309

(Source: Jahan *et al*., 2013)

CHAPTER 4

CONCLUSIONS

- For general combining ability, maize variety CML 161 and KSU 4-58 can be selected for plant breeding. For specific combining ability, selection of CML 161 × CML 424 and CML 424 × KSU 8-33 is rewarding for heterosis breeding. All the characters of Faba bean are highly heritable except the seed yield.
- Environment affects the yield of water melon indicating these water melon varieties CS-19-S7 (P_1), BL-14-S7 (P_2), 6372-4-S7 (P_3), and CH-8-S7 (P_4) showed specific adaptability.
- Bottle gourd variety Pusa Navven has dominant genes and PBOG 13 & PBOG 22 has recessive genes for fruit setting.
- Highest number of desired progeny obtained from the crossing between cluster II (BARI Sarisha9 and SAU Sarisha1) and Cluster III (Tori 7, F6×BARI Sarisha9, BARI Sarisha9×F6, F6×Tori 7, BARI Sarisha6×BARI Sarisha9, BARI Sarisha15 and SAU Sarisha1) as they have higher genetic diversity due to their maximum inter cluster distance (11.68).
- Thousand seed weight contributes more towards genetic divergence followed by no. of primary branch per plant and days to 50 % flowering for 18 mustard genotypes.

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