GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS OF BC_1F_2 POPULATION IN *Brassica napus* L.

BY

SHARMIN SULTANA

REGISTRATION NO: 05-1728

A Thesis
submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka,
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE
IN

GENETICS AND PLANT BREEDING

SEMESTER: JUNE-DECEMBER, 2013

Approved by:

Prof. Dr. Firoz Mahmud
Supervisor

Prof. Dr. Naheed Zeba
Co-supervisor

Prof. Dr. Md. Sarowar Hossain
Chairman

DECEMBER, 2013

Dr. Firoz Mahmud
Professor

Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh

Phone: +8802 9144270-9, Ext. 315 (office)
Mob: +8801552432589, Fax: +88029112649
E-mail: fmahmud08@gmail.com

CERTIFICATE

This is to certify that thesis entitled, "GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS OF BC$_1$F$_2$ POPULATION IN Brassica napus L." submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE in GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out by SHARMIN SULTANA, Registration No. 05-1728 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2013
Place: Dhaka, Banaladesh

(Dr. Firoz Mahmud)
Professor
Supervisor

Dedicated to

My

Beloved Parents

ACKNOLEDGEMENTS

Up and above everything, all glory to Almighty Allah, whose blessings and exaltation flourished my thoughts and thrived by ambitions to have a cherished fruit of my modest efforts in the form of this write up from the blooming spring of blossoming knowledge. My humblest and sincerest words of respect are owned to his last prophet Hazart Muhammad Sallalah-O-Alaihe Wassalam, who is forever a torch of guidance and knowledge for the mankind.

I deem it my utmost pleasure to avail myself of this opportunity to express my heartiest gratitude and obligation to my reverend supervisor **Professor Dr. Firoz Mahmud,** *Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his personal interest, valuable suggestions, sympathetic attitude and fatherly behavior throughout the research efforts and presentation of this manuscript.*

Special thanks to my co-supervisor, **Professor Dr. Naheed Zeba** *for her kind and excellent guidance, stable supervision and incessant efforts were priceless for the completion of my research project. Her outstanding supervision made my study at Sher-e-Bangla Agricultural University memorable.*

I express my sincere respect to the Chairman, **Prof. Dr. Md. Sarowar Hossain** *and all teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for providing the facilities to conduct the experiment and for their valuable advice and sympathetic considerations in connection with the study.*

I would like to present my heartfelt thanks to my great parents, sister, and brother in law for their care, love and lifelong support.

Finally I am extremely thankful to my considerate and beloved husband **S.M. Julker Nine,** *whose uninterrupted support in various aspects of my life and studies, kept me going with grace and honor, and the courage and motivation that she gave me, made me able to complete this project.*

December, 2013
SAU, Dhaka

Sharmin Sultana

GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS OF BC_1F_2 POPULATION IN *Brassica napus* L.

BY

SHARMIN SULTANA

ABSTRACT

A field experiment was conducted at the experimental field of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh to study genetic diversity, correlation and path analysis of BC_1F_2 lines obtained through first back cross of *Brassica napus* L. during November 2011 to March 2012. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for seed yield per plant (14.67) followed by number of secondary branches per plant (11.49), number of primary branches per plant (11.41), number of siliqua per plant (9.12) and number of siliqua per plant (9.00). High heritability with low genetic advance in percent mean was observed for days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, length of siliqua and 1000 seed weight which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent mean was observed for number of primary branches per plant, number of siliqua per plant, number of seeds per siliqua and seed yield per plant indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Different multivariate analyses were performed to classify 31 genotypes. All the genotypes were grouped into five clusters. Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis gave similar results. Cluster IV was the largest cluster comprising of 8 genotypes and cluster 1 was the smallest cluster with 2 genotypes. Cluster I had the highest intra-cluster distance and cluster V had the lowest intra cluster distance. Inter cluster distance was maximum (15.405) between cluster I and III. The results revealed that genotypes chosen for hybridization from clusters with highest distance would give high heterotic and broad spectrum of variability in future segregating generations. The characters between days to 50% flowering and days to maturity, plant height and days to maturity, plant height and number of siliqua per plant, plant height and number of seeds per siliqua, number of primary branches per plant and number of secondary branches per plant, number of secondary branches per plant and number of siliqua per plant, number of siliqua per plant and yield per plant were highly positively correlated. Path coefficient analysis showed that days to maturity, plant height, number of secondary branches per plant, number of siliqua per plant, length of siliqua and number of seed per siliqua had positive indirect effect on seed yield per plant. Considering cluster distance, inter genotypic distance and other agronomic performance G6 and G8 from cluster I; G1 from cluster II; G21 and G24 from cluster III and G16 from cluster V might be considered to be better parents for future uses in hybridization program to develop high yielding varieties with early maturity.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

LIST OF ABBREVIATED TERMS

ELABORATED NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et al.*
Bangladesh Bureau of Statistics	BBS
Co-efficient of variation	CV
Days After Sowing	DAS
Degrees of freedom	d.f
Etcetera	etc.
Figure	Fig.
First Back Cross	BC_1
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genetic CO-efficient of Variation	GCV
Genotypic Variance	σ^2_g
Gram	g
Heritability in broad sense	h^2b
Journal	j.
Kilogram	Kg
Meter	m
Mean Sum of Square	MSS
Muriate of Potash	MP
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic Variance	σ^2_p
Randomized Complete Block Design	RCBD
Research	Res.
Second generation of a cross between two dissimilar homozygous parent	F_2
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	TSP

CHAPTER I

INTRODUCTION

Oilseed *Brassica* species (*B. napus*, *B. campestris* and *B. juncea*) ranks the third most important source of edible oil in the world after palm and soybean (Adnan Nasim *et al.*, 2013; Zhang and Zhou, 2006). *Brassica* is an important genus of plant kingdom consisting of over 3200 species with highly diverse morphology. The *Brassica* species can be classified into three groups, *viz*; the Cole, the rape seed and the mustard. The coles are consumed as vegetable and the other two are the valuable sources of edible oils and proteins. The mustard groups includes species like *Brassica juncea* Czern and cross, *Brassica nigra* Koch and *Brassica carinata* Barun; while the rape seed groups includes *Brassica campestris* L and *Brassica napus* L. (Yarnell, 1956). The mustard oil is not used only for edible cooking purposes but also is used in hair dressing, body massing and in different types of pickles preparation. It has also several medicinal values. Oil cake is the most important feed for livestock and is also used as organic manure. It is mainly self-pollinating crop, although on an average 7.5 to 30% out-crossing does occur under natural field conditions (Abraham, 1994; Rakow and Woods, 1987a).

In Bangladesh, *Brassica* is the most important oilseed crop. It is top of the list in respect of area and production of oil seed crops cultivated in this country. It covers about 61.2% of the total area under oil seed and 52.6% of the total oil seed production. About 246.49 thousand metric ton of local rape and mustard produced from total 623.29 thousand acre of cultivable land in the year 2010-11 (BBS, 2012). The average production of rape seed is 220000 tones in Bangladesh which is very low as compared to that of the advanced countries (FAO, 2011). The major reason for such poor yield is the use of low yielding local indigenous cultivars. The country is facing huge shortage in edible oils. Almost one fourth of the total edible oil consumed annually is imported.

From nutritional point of view fats and oils in our diets are mostly needed for calories and vitamin absorbent. It produces the highest amount of calories per unit in comparison with carbohydrate and protein diets. For human health, in a balanced diet 20-25% of calories should come from fats and oils. Although, oilseed crops play a vital role in human diet, the consumption rate of oil in our country is far below than that of balanced diet (6 g oil per day per capita against the optimum requirement of 37g per head per day) (Rahman, 1981).

The genome designations of the three elemental species of *Brassica* are "AA" for *B. campestris*, "BB" for *B. nigra* and "CC" for *B. oleracea* having the chromosome number of 10, 8 and 9 at "n" level, respectively. The tetraploid species *B. juncea* (AABB), *B. carinata* (BBCC) and *B. napus* (AACC) are amphidiploids and originated from the combinations of the three diploid elemental species (U, 1935). All these species have many cultivated varieties suited to different agro-climatic conditions. Meanwhile, about 25 mustard and rapeseed varieties have been released, among these, 15 from Bangladesh Agricultural Research Institute (BARI), 4 from Bangladesh Institute of Nuclear Agriculture (BINA), 3 from Bangladesh Agricultural University (BAU), 2 from Sher-e-Bangla Agricultural University (SAU) and 1 from Bangladesh Agricultural Development Corporation (BADC) but most of them are not popular to the farming community because of their long duration, low to moderate yield and susceptibility to severe biotic and abiotic stresses. Breeders in Bangladesh have released some improved varieties of mustard / rapeseed which require more than 110 days to mature. These varieties did not fit to the existing T. Aman-Mustard-Boro cropping pattern. Farmers are cultivating short duration Tori 7 variety though the yield of this variety is very low. This variety fits very well in the existing cropping pattern but we are deficient in short duration high yielding varieties. It is, therefore, needed to develop improved mustard and rapeseed varieties with high yield potential, shorter growth duration which could be fit into T. Aman–Mustard-Boro cropping pattern.

The F_2 materials were generated by first back crossing to develop high yielding short duration and yellow seeded materials for future release. The different promising F_2 lines were used to see variability. If these materials showed better performance in respect of yield and some yield contributing characters, individual promising materials will also be selected in future.

There is plenty of scope to increase yield per unit of area through breeding superior varieties. The production potential of rapeseed and mustard may be well exploited if the varieties can be identified with early maturity, rapid response to high fertility, large seed size and high oil content. The oil content of mustard in Bangladesh varies from 30 to 40 percent depending on the variety, climate and production condition (Rahman *et al.*, 1993).

Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1993) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations. Selection of parents based on genetic divergence has become successful in several crops (Anand and Rawat, 1984; Ashana and Pandey, 1980; De *et al.*, 1988).

Optimizing yield is one of the most important goals for most rapeseed breeders. Seed yield is a complex character that can be determined by several components reflecting positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed yield (Marjanovic-Jeromela *et al.*, 2007). Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contributions to yield variables (Ali *et al.*, 2003). Path-coefficient technique splits the correlation coefficients into direct and indirect

effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy (Sabaghnia *et al.*, 2010).

With conceiving the above scheme in mind, the present research work has been undertaken in order to fulfilling the following objectives:

Objectives

a) To analyze the genetic variation among $BC_1 F_2$,
b) To analyze the correlated offspring in genetic level,
c) Path analysis of BC_1F_2 population in which their gene expression working and
d) To identify the promising variation for variety improvement.

CHAPTER II

REVIEW OF LITERATURE

2.1 General Information of Rapeseed

Rapeseed, also known as rape, oilseed rape, rapa, rapaseed and double-low rapeseed called canola (low erucic acid and glucosinolate contents rapeseed), belongs to the species of *Brassica*, members of Cruciferae. The name rape derived from the Latin *rapum* meaning (Weiss, 1983). There are three basic species: *B. nigra, B. oleracea,* and *B. campestris*. By hybridization and chromosome doubling, the three species: *B. carinata, B. juncea,* and *B. napus* L. were synthesized. The botanical relationships among these species are illustrated by the "U triangle" (Figure 1) which was proposed by a Japanese scientist, named U, in 1935 (U, 1935).

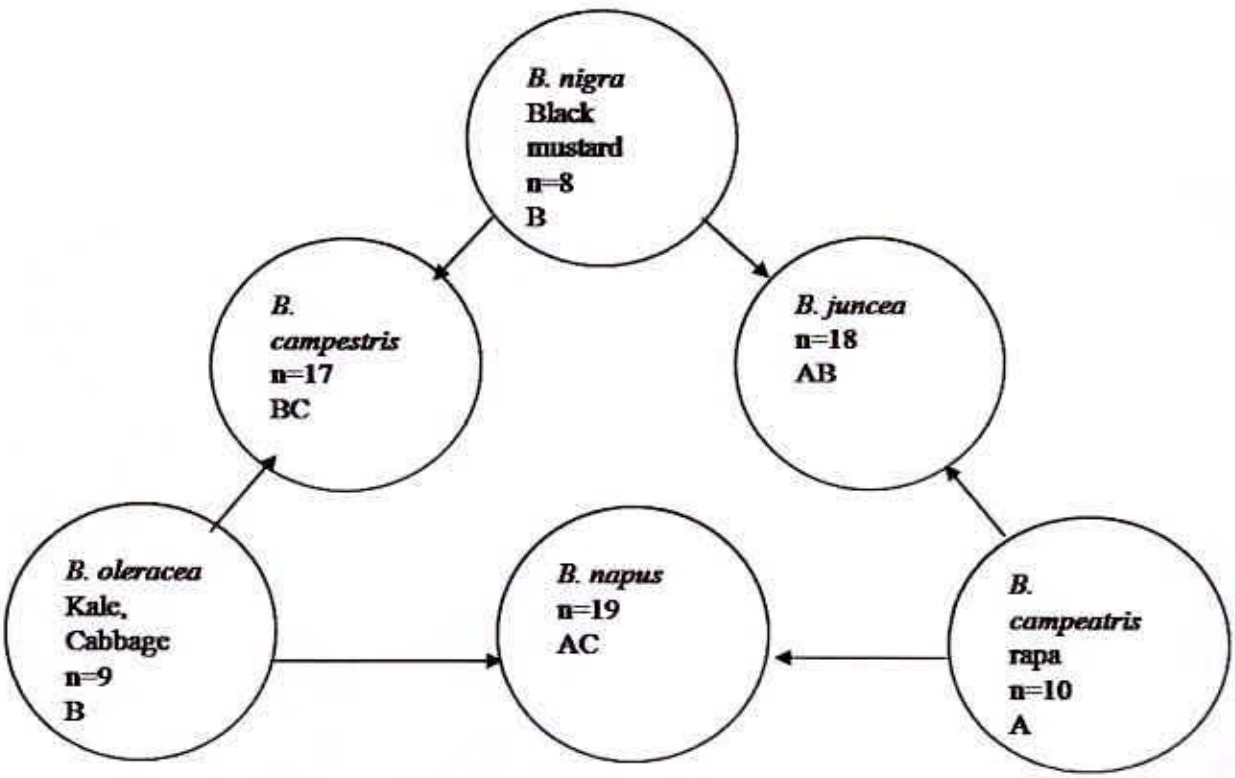


Figure 1. Relationships among important *Brassica* species shown by the triangle of U (1935).

Now *B. napus*, *B. campestris*, and *B. juncea* are the main species planted in the world. *B. juncea* has natural outcrossing rate below than 10 percent. However, some varieties may have more than 40 percent outcrossing in certain areas. *B. napus* L. has natural outcrossing rate of 10 to 30 percent in general, whereas *B. campestris* has 85 to 90 percent (Li, 1999; Rakow and Woods, 1987b). Their flower colors are bright yellow, sometimes orange yellow or pale yellow. Seed-coat colors of rapeseed are different from species. In general, they are dark-brown to black. We can find pure yellow seed in *B. campestris* and *B. juncea*, but not in *B. napus*. It was found that yellow-seeded rapeseed could have more oil and protein contents and lower fibre than brown and black rapeseed (Weiss, 1983; Liu, 1992). Yellow seed in *B. napus* L. was first found in artificially synthesized rapeseed in Sweden (Olsson, 1960).

Rapeseed can be divided according to vernalization requirements into two types including winter and spring types (Wang *et al.*, 2007). Winter varieties of *B. napus* L. are grown predominantly in most of Europe, China, and the eastern United States, whereas spring varieties predominate in Canada, northern Europe, northwest of China. *B. rapa* has a shorter growing season than *B. napus* L. and this trait makes the spring varieties of this species suitable for the more severe climates. Spring type *B. rapa* occupies approximately 50% of the Canadian rapeseed area and is also grown in northern Europe, China, and India. Winter type *B. rapa* has largely been replaced by more productive winter type *B. napus*. *B. juncea* is the leading *Brassica* oilseed in India and also produced in Canada, Europe and China (Sovero, 1993).

2.2 Variability

The representative varieties used in many different studies under certain agro ecological conditions of production have expressed different degrees of variation. Parts of these were genetic and part non-genetic. It is therefore, important to review the variabilities that have been found in different materials for some

specific characters of interest. The improvement of a crop is dependent on the magnitude of genetic variability and the extent of heritability of desirable characters of the genotypes available. A critical review of genetic variability is therefore, a prerequisite for planning and evaluation of a breeding program.

Katiyar *et al.* (2004) carried out a study on variability for the seed yield in ninety intervarietal crosses of *Brassica campestris*. Existence of significant variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations.

Tyagi *et al.* (2001) evaluated forty-five hybrids of Indian mustard obtained from crossing 10 cultivars for seed yield and yield components. Variation was highest for plant height of parents and their hybrids. The seed yield per plant exhibited the highest coefficient of variation (41.1%).

Masood *et al.* (1999) studied seven genotypes of *Brassica campestris* and standard cultivar of *Brassica napus* to calculate genetic variability. The co-efficient of variation was high for thousand seed weight, pod length and number of seeds per pod for both genotypic and phenotypic variability.

Lekh *et al.* (1998) conducted an experiment with 24 genotypes of *Brassica juncea* and 10 genotypes each of *Brassica campestris*, *Brassica carianata* and *Brassica napus* during the rabi season of 1992-93 and 1993-94. The highest genotypic co-efficient of variation was calculated for secondary branches. High genotypic and phenotypic coefficient of variation was recorded for days to 50% flowering. Shen *et al.* (2002) tested 66 F_1 hybrids of *Brassica campestris* and significant differences were found between F1s and their parents for yield per plant and seed oil content.

Labana *et al.* (1987) studied 39 strains of Ethiopian mustard and found low genetic variation. When Varshney *et al.* (1986) found high variability in plant height working with a number of strains of *B. napus, B. juncea and B. rapa* . Genotypic Co-efficient of Variation (GCV) for plant height in different genotypes of *B. juncea* was found to be 10.96 by Singh *et al.* (1987), 9.3 by Labana *et al.* (1980), 31.38 by Yadava (1973), 21.16 in brown sarson by Bhardwaj and Singh (1969), 12.32 in yellow sarson and 5.9 in toria by Tak and Patnaik (1977).

Plant height is an important character which is largely influenced by genotype, soil, water availability, temperature etc. But significant genetic variability was observed by many researchers like Kumar *et al.* (1996), Malik *et al.* (1995), Kumar and Singh (1994), Singh *et al.* (1991), Gupta and Labana (1989), Chauhan and Singh (1985) among different genotypes of *B. napus, B. campestries and B. juncea.*

Significant genetic variation for number of primary branches/plant was recorded by several researchers. Singh *et al.* (1989) studied this character under normal and stress conditions in 29 genotypes of *B. napus and B. rapa* and found significant variation among the genotypes. Similar result was reported earlier by Kumar and Singh (1994), Kakroo and Kumar (1991), Yin (1989), Biswas (1989), Jain *et al.* (1988), Labana *et al.* (1987), Gupta *et al.* (1987). GCV and PCV values of 14.44 and 24.43 were reported by Singh *et al.* (1987) in different strains of *B. juncea.* But, according to Tak and Patnaik (1977) these values were 33.2 and 57.1 in yellow sarson.

Usually higher the siliqua number higher is the seed yield. This trait has high variation and a considerable part of which appeared to be of environmental. Yin (1989) studied 8 cultivars of *Brassica napus* and observed high genetic variation in number of siliqua per plant. Similar results of high variation for this trait has also been observed and reported by Kumar *et al.* (1996). According to Tak and

Patnaik (1977) genotypic co–efficient of variation (GCV %) and phenotypic co-efficient of variation (PCV %) of this trait in yellow sarson were as high as 55.4% and 53.2%, respectively. The same values in Toria were 27.1% and 23.5%. Further variable result of GCV and PCV for this character 25.41 and 29.15%, respectively was observed by Singh *et al.* (1987) in *Brassica campestris*. GCV was reported to be also as 18.85% by Yadava (1973) and 97.3% by Bhardwaj and Singh (1969). These review indicated that there exists sufficient variation in number of siliqua per plants and the same is variable with variable production conditions and genetic materials as used by different authors.

In general, high number of seeds per siliqua is desirable. A good number of literatures are available on the variability of this character. Kumar *et al.* (1996) reported the presence of significant variability in the genotypes of *Brassica napus, Brassica campestris and Brassica juncea* they studied. Similar significant variability in number of seeds per siliqua in oleiferous *Brassica* materials of diverse genetic base have also been observed by Kudla (1993) and Kumar and Singh (1994). In case of genotypes of *Brassica campestris* the value of GCV was 35.85% as observed by Bhardwaj and Singh (1969). According to Tak and Patnaik (1977) values of GCV and PCV were found to be 13.1% and 18.5%, respectively in yellow sarson. While the value of the same for toria were 16.3% and 22.6%. Low values of GCV and PCV were also observed in *Brassica juncea* by Singh *et al.* (1987). According to them values were 6.46% and 9.5% for GCV and PCV, respectively. Labana *et al.* (1987) also observed GCV and PCV of 9.82% and 15.96%, respectively in genotypes of *Brassica juncea* for number of seeds per siliqua. These indicate that the genotypes of *Brassica juncea* are less variable than those of *Brassica campestris.*

Thousand seed weight is also an important trait of *Brassica* oil crops, where highest consideration is on the seed yield. This trait has been found to vary widely from genotypes to genotypes and from environment to environment including

macro and micro environments. A good number of literatures are available on the variability of this character. According to Chowdhury *et al.* (1987), Yin (1989), Labowitz (1989) and Biswas (1989) in *Brassica campestris*, Andrahennadi *et al.* (1991) in brown mustard, Kudla (1993) in sewede rape and Kumar and Singh (1994) in *Brassica juncea* reported different degrees of significant variations of thousand seed weight due to variable genotypes. In case of *Brassica campestris* (toria ecotypes), GCV and PCV, two important parameters of breeding values were found 11.8% and 18.9%, respectively (Bhardwaj and Singh, 1969). The respective values of the same were 13.1% and 16.5% in brown sarson as reported by Tak and Patnaik (1977). Labowitz (1989) studied *Brassica campestris* population for siliqua length and observed high genetic variation in this trait.

Variability in consideration of days to 50% flowering, an important yield component, is very useful in selecting materials of short, medium or long duration crop. In general, early flowering genotype mature early and late flowering genotype delayed maturity. Several workers investigated the variability in respect of days to flowering. Nanda *et al.* (1995) reported from an experiment conducted with 65 strains of *Brassica napus, B. rapa, B. juncea* and *B. carinata* found days to 50% flowering varied by genotype. Singh *et al.* (1991) studied different morphological characters of 29 genotypes of *B. napus* and *B. rapa* grown under normal and stress conditions of *Brassica* production. They found the existence of significant genetic variability for days to 50% flowering. Kumar *et al.* (1996), Kumar and Singh (1994), Andrahennadi (1991), Biswas (1989), Singh *et al.* (1987), Chauhan and Singh (1985), Thurling (1983), Thakral (1982) and many other researchers worked with different genotypes of *Brassica*. In general, according to them, significant variations were observed in the character for days to 50% flowering.

Jain *et al.* (1988) in an experiment analysis of gene effects using means of six populations of a cross Varuna X YRT-3 of Indian mustard and observed that

dominance gene action was important in the expression of days to flowering. Partial dominance was observed for this character by Kumar *et al.* (1991). It is evident from all these results that sufficient genetic variations exist for days to 50% flowering.

Days to maturity for any crop are most important criteria for assessment of variability. It is influenced by genotypes and various environmental factors. Significant genetic variation was found by several workers among different genotypes of rapeseed and mustard. Biswas (1989) found high GCV and PCV among 18 genotypes of *B. napus* while Sharma (1984) working with 46 genotypes of *B. juncea* and found low GCV and PCV values. Yadava (1973) found 7.6 GCV among 29 strains of *B. juncea,* while in yellow sarson Tak and Patnaik (1977) found this value as 4.5 and 1.8, respectively. Significant variation for days to maturity was also found by Kumar and Singh (1994), Singh *et al.* (1991), Grosse and Geisler (1988), Khera and Singh (1988), Gupta *et al.* (1987), Chauhan and Singh (1985) and many other researcher in their research work.

Yield is the most important trait for all crops in every breeding program. This is a complex trait influenced largely by a number of component characters and factors of production. A good number of research works have been conducted on this character. Significant genetic variability in genotypes belonging to toria ecotype of *Brassica campestris* was reported by Thakral (1982). Similar high variability in different genotypes of *Brassica campestris* was reported by Sharma (1994). Khera and Singh (1988) also reported significant variation in yield due to genotypes of *Brassica napus.* A high degree of variation for seed yield per plant was reported by Yin (1989) in *Brassica campestris*, Kudla (1993) in *Brassica napus* and Kumar *et al.* (1996) in *Brassica juncea.* According to Bhardwaj and Singh (1969), the value of GCV was found to be 96.99% among different strains of brown sarson (*Brassica campestris*). This value appeared to be very high for yield as because 48.76% GCV was found by Yadava (1973) among 29 strains of *Brassica juncea.*

While, Singh *et al.* (1987) observed GCV and PCV values of 44.04% and 46.9% in *Brassica juncea.* The same values were only 9.6% and 19.47% among different genotypes of *Brassica juncea* Labana *et al.* (1987). The comparative position of the genotypes of these two species indicates the presence of high variability due to difference in species and genotypes.

From the reviews above it is clear that a wide range of variability existed for different morphological characters among different genotypes of *Brassica* oil crops and it indicates the scope of utilization of these variability for further breeding programs.

2.3 Genetic Diversity

Cluster analysis showed a wide diversity of genotypes from the same geographical regions. An investigation was conducted by Malik *et al.* (1997) to determine the extent of diversity and relationships among the *B. juncea* germplasm from Pakistan using morphological characters and showed a comparatively low level of phenotypic variation amongst them and where genetically similar to the oilseed cultivars. However, the oilseed forms and vegetable cultivars were genetically distinct. They revealed that the evaluated germplasm appears to have a narrow genetic base which undergoes a high level of genetic erosion.

An investigation was carried out by Shen *et al.* (2002) to assess genetic divergence, morphological and quality attributes in 12 accessions of each of three *Brassica* species viz; *B. juncea, B. napus* and *B. carinata.* The inter species variation was higher than inter variety variability. The range of variation was highest in *B. juncea* followed by *B. napus* and *B. carinata.*

Chowdhury and Joshi (2001) studied genetic diversity among 88 entries including eighty F_4 derivatives i.e., 20 each selected from *Brassica* crosses viz., *B. juncea* × *B. napus, B. juncea* × *B. rapa var. toria, B. juncea* × *B. rapa var. yellow sarson*

and B. tournefortii × *B. juncea,* and eight parent genotypes was assessed through multivariate analysis and reported significant differences among the family groups as well as within the family were recorded for the trait that were studied. The multivariate (D^2) analysis revealed enormous diversity among inter specific cross derivatives. They also calculated genetic distances among different *Brassica* species revealed that *B. tournefortii* had maximum diversity with *B. juncea* followed by *B. napus, B. rapa* varity toria and *B. rapa* variety yellow sarson. They reported that the derivatives selected from cross of diverse parents revealed greater diversity. The clustering pattern showed that many derivatives of the cross fell into the same cluster but in many cases in spite of common ancestry many descendants of the cross spread over different clusters. They also reported that the traits namely, plant height, secondary branches/plant, days to flowering and 1000 seed weight were contributed maximum towards genetic divergence.

Islam and Islam (2000) evaluated the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were felt into four clusters. The inter cluster distances were larger than the intra cluster distances. The characters contributed maximum in divergence analysis are days to 50% flowering, plant height, branches/plant and siliqua/plant.

The clustering and ordination methods used often cannot deal explicitly with the computational consequences of large data sets with incomplete information. However, it is shown that the ordination technique of principal component analysis and the mixture maximum likelihood method of clustering can be employed to achieve such analysis. Genotypes within the cluster are having a smaller D^2 value among themselves than those from group belonging to two different clusters. On the other hand, the inter-cluster distance is the criterion used for selecting genotypes for parent for hybridization. The genotypes those in clusters with maximum inter cluster distance are genetically more divergent. Variation within the cluster is measured by inter-cluster distance.

Forty four genotypes of toria were evaluated by Mitra and Saini (1998) collected from different eco-geographical areas for yield and various components during rabi 1991-92. On the basis of D^2analysis, the 43 genotypes were grouped into seven clusters. No evidence was obtained for any correlation between genetic divergence and geographical diversity. Siliqua in the main shoot and seeds per siliqua were the major contributors to genetic divergence.

Nineteen genotypes (crosses and parents) of Indian mustard *(B. juncea)* grown at Ranchi during the winter season under rainfed conditions. Genotypes were grouped into three clusters based on D^2 analysis was studied by Mahto (1996).

Islam (1995) studied genetic divergence among 90 genotypes of groundnut using D^2 and principal components analysis and grouped the varieties into five clusters. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups.

Uddin (1994) reported from an experiment on genetic divergence among 34 genotypes of mustard were estimated using D^2 and principal component analysis. The genotypes felt into four clusters. The inter-cluster distance was larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster values were lower in all the clusters.

Nineteen genotypes of rape mustard *(B. rapa)* were studied by Jagadev *et al.* (1991) which were grown during the winter season. They studied different characters and analyzed the variance using D^2 statistic. Genotypes were grouped into five clusters. Seed weight, days to maturity and seed yield were the largest contributors to D^2 values.

Sindhu *et al.* (1989) investigated diversity in 20 strains of black gram from different agro-ecological zones of India using Mahalanobis's D^2 statistic. They observed no parallelism between geographical and genetic diversity.

Reddy *et al.* (1987) conducted a study of genetic divergence of groundnut for pod yield/plant and 12 related characters by Mahalanobis's D^2 statistics. The greatest inter cluster distance was observed between clusters I (with 10 to 11 varieties depending on years) and II (4 to 6 varieties) and between clusters I and IV.

Mahalanobis's D^2 statistic to group 83 genotypes on the basis of yield/plant and six other agronomic characters of bunch groundnut by Nadaf *et al.* (1986). They found nine clusters, which were not related to the grouping formed by geographical origin. They also observed that variation in pod yield accounted for 88% of the total variation between clusters but number of developed pods, days to 50% flowering and 1000 seed weight were important in accounting for divergence with clusters.

Shanmugam and Rangasamy (1982) observed that the characters yield per plant and pod per plant contributed considerably towards diversity in black gram. Again the same authors in 1982 assigned 45 genotypes of black gram often clusters by analyzing data on yield and nine yield components using Mahalanobis' D^2 statistic and stated that geographical diversity was not the only factor for determining genetic diversity. The clustering pattern more or less confirmed the canonical (vector) analysis. They found that yield per plant contributed most too genetic divergence.

2.4 Heritability and Genetic Advance

The variation of heritability can be estimated with greater degree of accuracy when heritability in conjunction with genetic advance as percentage of mean is studied. Johnson *et al.* (1995) suggested the necessity of estimating genetic advance along with heritability in order to draw a more reliable conclusion in a selection program. Many experiments have been conducted in the investigation of heritability and genetic advance on yield and yield components of mustard. The most relevant reviews are reviewed here.

Malik *et al.* (1995) observed very high broad sense heritability (>90%) for number of primary branches, days to 50% flowering and oil content while working with different strains of *B. napus*. They also found low heritability (<50%) for number of siliqua/plant, number of seeds/siliqua, plant height and yield. But Singh *et al.* (1991) found high heritability for all these characters. Li *et al.* (1990) also recorded similar high heritability results in studies with *B. napus*.

Varshney *et al.* (1986) found high heritability and high genetic advance for plant height when conducted an experiment of 45 genotypes of *B. napus, B. rapa* and *B. juncea* species; but high heritability and genetic advance for siliqua/plant only in B. *rapa.* Singh (1986) studied 22 genotypes of *B. napus, B. rapa and B. juncea* and reported high heritability and genetic advance in seed yield, 1000 seed weight and number of seeds/siliqua. Inheritance of seed oil content was studied by Han (1990) in seven inbreeds of *B. napus,* crossed in a diallel fashion and reported high heritability (81.16%) for this trait. However, Yadava *et al.* (1985) reported low heritability for oil content in *B. juncea.* Wan and Hu (1983) observed high heritability and genetic advance for flowering time, number of primary branches/plant and plant height. Low heritability of yield was reported by many researchers like Malik *et al.* (1995), Kumar *et al.* (1988), Yadava *et al.* (1985), Chen *et al.* (1983); but Singh (1986) reported high heritability for this character.

In a study Sharma (1984) observed high heritability for plant height, days to flowering and low heritability for days to maturity when working with 46 genotypes of *B. juncea.* He also found low genetic advance for days to maturity and high genetic advance for yield/plant. In another study of Indian mustard Singh *et al.* (1987) observed high heritability (80-95%) for oil content and yield/plant. The lowest heritability (34.9%) was recorded for number of primary branches per plant.

Labana *et al.* (1980) found that plant height and number of seeds/siliqua were highly heritability, whereas, number of primary branches and seed yield per plant were less heritable when working with 104 mutants of Indian mustard. The yield variation thus principally owed to the environmental influence, for which selection would not be much effective. The selection of the material would be more practicable for plant height and number of seed/siliqua. This confirmed the finding of Chaudhari and Prasad (1968). In the same experiment the genetic advance was highest for plant height (13.75%) followed by number of seeds/siliqua (12.43%) and seed yield/plant (9.75%). This offers scope for this improvement through selection. This is because high heritability and genetic advance together provide better indication of the amount of genetic progress that can result from selection of the best individuals.

Chandola *et al.* (1977), working with 30 varieties of *B. rapa* found high estimates of genetic advance for plant height. Paul *et al.* (1976) observed in one of experiment that a good genetic advance was expected from a selection index comprising seed yield, number of seeds/pod, number of siliqua/plant and number of primary branches per plant.

Thurling (1974) reported in the genotypes of *B. rapa* that the expected genetic advance in yield using a selection index technique based on simultaneous selection of several characters was significantly greater than that expected from selection for yield alone, and several indices including measurement of both yield components and vegetative characters were expected to promote a greater ratio of advance in yield than direct selection.

From the exceeding review it can be concluded that approximately all characters expected yield are high heritable in nature and the predictable genetic advance, being high for plant height, primary branches/plant, 1000 seed weight and yield, assortment is possible for high yield using number of characters in selection programs.

2.5 Interrelationships among the characters

Correlation coefficients among different characters are important in breeding programme. Many workers have reported their correlation among characters of *Brassica sp.* Some of this information is reviewed here.

Selection for plant height, for types where primary branches start at low heights, from ground level and number of siliqua on the main raceme can result in yield increase (Zhau and Liu, 1987).

Plant height was found to be negatively correlated with siliqua length and seeds/siliqua by Labana *et al.*, (1980). Positive correlation of plant height with seeds/siliqua, number of siliqua/plant and negative correlation with 1000 seed weight were reported by Chowdhury *et al.*, (1987). Singh *et al.* (1987) found positive correlation of plant height with number of siliqua/plant, number of primary branches/plant, number of seeds/siliqua in 179 genotypes of Indian mustard. Banerzee *et al.* (1968) also found positive association of plant height with these three characters in 8 strains of yellow sarson.

In *B. rapa* Singh *et al.*, (1987) and in *B. juncea*, Chowdhury *et al.* (1987), Lebowitz (1989) and Lodhi *et al.* (1979) reported that the siliqua length was positively correlated with both 1000 seed weight and number of seeds/siliqua. Several experiments were carried out by Chay and Thurling (1989) to study the inheritance of siliqua length among the tested lines of *B. napus*. It was observed that the siliqua length when increased there was an increase in the number of seeds/siliqua and 1000 seed weight.

1000 seed weight was positively and significantly correlated with seed yield/plant and number of siliqua/plant but negatively and significantly correlated with siliqua length and number of seeds/plant in *B. rapa* (Nasim *et al.*, 1994). Das *et al.* (1984) in F_3 population found that 1000 seeds weight had highly significant geonotypes and phenotypic correlation with seed yield in brown sarson.

1000 seed weight was found to be positively associated with days to 50% flowering and days to 80% maturity by Yadava *et al.* (1978) and Chowdhury *et al.* (1987) in *B. juncea* but Shivahare et al. (1975) and Singh *et al.* (1987) found negative correlation. Negative correlation of 1000 seed weight plant height, number of primary branches/plant, and number of siliqua/plant was also reported by Chowdhury *et al.* (1987) and Yadava *et al.* (1978). Positive correlation with flowering time, days to maturity and 1000 seed weight was observed by Yadava *et al.* (1978) and Singh *et al.* (1987).

Significant correlation between number of siliqua/plant and number seeds/siliqua in yellow sarson (Banerjee, 1968). But Tak (1977) in a study with *B. rapa* found negative genotypic correlation between number of siliqua/plant and number of seeds per siliqua in brown sarson and *toria* varieties. On the contrary, Das *et al.* (1984) reported that number of siliqua/plant significantly and positively correlated with number of seeds/siliqua and 1000 seed weight. Nasim *et al.* (1994) and Kumar *et al.* (1984) in *B. rapa* found positive and significant correlation between seed yield/plant and 1000 seed weight in F_2 of *B. juncea* and Chowdhury *et al.* (1987) also found similar results in the same species.

Increasing number of branches is a means of increasing yield, since the number of primary and secondary branches have a significant positive correlation with seed yield (Singh *et al.* 1969; Katiyar and Singh, 1974).

The significant partial correlation of number of secondary and tertiary racemes with seed yield indicated that branching was an important contributor to yield, independent of its association with plant size. Plants with high yields were also characterized by early maturity and early flowering (Thurling and Das, 1980).

Khulbe and Pant (1999) reported that number of siliqua/plant, siliqua length, number of seed/siliqua, 1000 seed weight were positively associated with seed yield. Kumar *et al.* (1999) studied 12 yield contributing characters in 15 genotypes

of *B. juncea*, three of *B. napus,* four of *B. rapa* and one of *B. chinensis*. For more character studied, genotypic correlation coefficients were higher in magnitude than their corresponding phonotypic coefficient. Seed yield was positively correlated with plant height, siliqua number, number of siliqua/plantand 1000 seed weight.

Yield is a highly complex and variable character and the genes for yield per seed do not exist (Grafius, 1959). Therefore, direct selection for yield is not very effective. In selection for yield, recourse has then to be made to indirect selection.

In *B. juncea* the seed yield showed significant positive association with the number of primary branches and secondary branches, plant height and days to maturity both at the genotypic and phenotypic levels (Srivastava *et al.,* 1983). The number of primary branches showed positive and significant association with the number of secondary branches, plant height and days to maturity. Plant height showed positive and significant correlation with the number of secondary branches and days to maturity.

In rape seed (*B. napus*), positive correlation between yield and yield components were generally found (Campbell and Kondra, 1978). Ramanunjan and Rai (1963), found significant positive correlations between all the yield components and yield in *B. rap acv.* yellow sarson. Similar results were reported by Zuberi and Ahmaed (1973) for *B. rapa* cv. toria and Thurling (1974) for three *B. rapa* and three *B. napus* cultivars. However, some negative associations were also found between the yield components in all studies. High yield per plant was found association with large plant size in *B. napus* (Campbell and Kondra, 1978).

Working with 65 strains of *B. juncea, B. rapa* and *B. napus,* Nanda *et al.* (1995) observed positive association between yield and siliqua filling period. Olsson (1990), found the similar result in *B. napus*. He also found positive correlation between siliqua density and yield.

Shivahare *et al.* (1975) found days to flowering were positively correlated with primary branches/plant and height. But Kumar *et al.* (1996) working with 12 genotypes of *B. juncea* found flowering time and height negatively correlated with number of primary branches/plant.

Labana *et al.* (1980) found that number of primary branches was negatively correlated with plant height and siliqua length. Number of primary branches/plant was found negatively correlated with siliqua length and 1000 seed weight, but positively with number of siliqua/plant (Singh *et al.*, 1987).

Days to maturity showed insignificant correlation with seed yield both at phenotypic and genotypic levels. Number of branches/plant and number of siliqua/plant showed significant negative correlation with number of seed/siliqua and 1000 seed weight which indicated that genotypes having high number of branches as well as siliqua reduced the number of seeds/siliqua and seed size (Malek *et al.*, 2000).

2.6 Path coefficient analysis

Partitioning the correlation coefficient into components of direct and indirect effects is necessary because correlation coefficients alone do not give a complete picture of the casual basis of association. It is established that as the number of contributing characters increased, the indirect association becomes more complex and important. Under such circumstances, path coefficient analysis is an effective tool in assigning the direct and indirect effects of different yield contributing characters.

Character association and path coefficient analysis were used to determine relationships between growth and yield parameters in 28 lines of yellow and brown sarson (*B. rapa*) by Saini and Sharma (1995). Results revealed that seed/siliqua and 1000 seed weight had direct positive effect on yield.

While working Kudla (1993), found that 1000 seed weight had positive direct effect on yield. Gupta *et al.* (1987) observed that the direct effect of primary branching and 1000 seed weight on seed yield.

Chowdhury *et al.* (1990) found days to 50% flowering and plant height contributed to plant yield indirectly. Shabana *et al.* (1990) found the highest direct effect of no. of siliqua/plant on seed yield/plant.

Working with several strains of *B. juncea* Kakroo and Kumar (1991) found that 1000 seed weight had positive direct effect but days to 50% flowering and primary branches had negative indirect effect via seeds/siliqua on seed yield. But Chauhan and Singh (1985) observed high positive direct effect of days to 50% flowering, plant height, primary branching, siliqua/plant, seeds/siliqua on yield. Kumar *et al.* (1988) observed the direct positive effect of days to 50% flowering on yield. Again, Han (1990) working with *B. napus,* observed negative direct effect of no. of siliqua/plant, siliqua length and positive direct effect of seeds/siliqua and height on yield. Kumar *et al.* (1984) observed the negative indirect effect of days to flowering via plant height and siliqua length on yield in *B. juncea*. Singh *et al.* (1978) also found negative direct effect of these traits, but Dhillon *et al.* (1990) observed the highest positive direct effect of plant height on seed yield/plant.

The results of several experiments conducted by Das and Rahman (1989) in *B. rapa,* Ghosh and Chatarzee (1988) in *B. juncea,* Mishra *et al.* (1987) in *B. rapa,* Alam *et al.* (1986) in *B. juncea,* Singh *et al.* (1985) in *B. juncea,* Chen *et al.* (1983) in *B. napus,* Srivastava *et al.* (1983) in *B. juncea* and Yadava (1982) in *B. rapa,* revealed that plant height, days to maturity, 1000 seed weight, siliqua/plant and seed/siliqua had positive direct effect and indirect effect on yield. But Varshney (1986) working with several strains of *B. rapa* found negative direct effect of plant height, siliqua/plant, seeds/siliqua and 1000 seed weight on yield.

CHAPTER III

MATERIALS AND METHODS

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period from Nov. 2011 to Mar. 2012 to study on the genotypic variability, correlation and path analysis in 31 BC_1F_2 genotypes of *Brassica napus*. The materials and methods of this experiment are presented in this chapter under the following headings –

3.1 Experimental Site

The present piece of research work was conducted in the field of Genetics and Plant Breeding Department, Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka, Bangladesh. The location of the site is 90° 33 E longitude and 23° 77' N latitude with an elevation of 8.2 meter from sea level.

3.2 Characteristics of Soil

The soil of the experimental area was loamy belonging to the Madhupur Tract under AEZ 28. The soil of the experimental plots were clay loam, land was medium high with medium fertility level. The Physical and Chemical characteristics of initial soil in the experimental field are presented in Appendix I.

3.3 Weather Condition of the Experimental Site

The geographical situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris *et. al.,* 1979). During the rabi season the rainfall generally is scant and temperature moderate with short day length. Meteorological data on rainfall, temperature, relative humidity from March 2011 to March 2012 were obtained from the Department of Meteorological centre, Dhaka-1207, Bangladesh (Appendix II).

Table 1. Sources of 31 *Brassica napus* L. genotypes

Designation	Genotypes	Sources
G1	NAP-9905xNAP-0130(NAP-9905)	SAU
G2	NAP-108xNAP-2066(NAP-108)	SAU
G3	NAP-9905xNAP-9901(NAP-9901)	SAU
G4	NAP-9906xNAP-205(NAP-205)	SAU
G5	NAP-9906xNAP-0130(NAP-9906)	SAU
G6	NAP-9905xNAP-9908(NAP-9908)	SAU
G7	NAP-9905xNAP-9908(NAP-9905)	SAU
G8	NAP-2066xNAP-0130(NAP-2066)	SAU
G9	NAP-9905xNAP-108(NAP-108)	SAU
G10	NAP-108xNAP-9908(NAP-108)	SAU
G11	NAP-2066xNAP-0130(NAP-0130)	SAU
G12	NAP-108xNAP-205(NAP-108)	SAU
G13	NAP-108xNAP-2066(NAP-2066)	SAU
G14	NAP-9906xNAP-2066(NAP-2066)	SAU
G15	NAP-9906xNAP-205(NAP-9906)	SAU
G16	NAP-9906xNAP-2066(NAP-9906)	SAU
G17	NAP-9908xNAP-0130(NAP-0130)	SAU
G18	NAP-205xNAP-0130(NAP-205)	SAU
G19	NAP-108xNAP-9908(NAP-9908)	SAU
G20	NAP-2066xNAP-205(NAP-205)	SAU
G21	NAP-9906xNAP-9901(NAP-9901)	SAU
G22	NAP-2066xNAP-205(NAP-2066)	SAU
G23	NAP-9905xNAP-9901(NAP-9905)	SAU
G24	NAP-9905xNAP-0130(NAP-0130)	SAU
G25	NAP-108xNAP-0130(NAP-0130)	SAU
G26	NAP-9901xNAP-205(NAP-9901)	SAU
G27	NAP-108xNAP-0130(NAP-108)	SAU
G28	NAP-9908xNAP-2066(NAP-9908)	SAU
G29	NAP-9908xNAP-0130(NAP-9908)	SAU
G30	NAP-9905xNAP-108(NAP-9905)	SAU
G31	NAP-205xNAP-0130(NAP-0130)	SAU

3.4 Planting materials used

Thirty one *Brassica napus* L. BC_1F_2 genotypes were used in the study. The seeds of 31 genotypes were collected from *Brassica* Breeding Project of Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, Bangladesh. Descriptions of the genotypes are given in Table 1.

3.5 Methods

The following precise methods have been followed to carry out the experiment.

3.5.1 Preparation of the Main Field

The plot selected for the experiment was opened in the first week of November 2011 with a power tiller, and was exposed to the sun for a week. After one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil for sowing of *Brassica* seeds. The experimental plot was partitioned into the unit plots in accordance with the experimental design mentioned in 3.5.3. Recommended doses of well-rotten cowdung manure and chemical fertilizers were mixed with the soil of each unit plot (Table 2).

3.5.2 Application of Manure and Fertilizers

The fertilizers N, P, K, S and B in the form of urea, TSP, MP, Gypsum and borax, respectively were applied. The entire amount of TSP, MP, Gypsum, Zinc sulphate and borax was applied during the final preparation of land. Urea was applied in two equal installments at before sowing and before flowering. The dose and method of application of fertilizer are shown in Table 2.

3.5.3 Experimental design and layout

Field lay out was done after final land preparation. The seeds of BC_1F_2 materials were laid out in a Randomized complete block design (RCBD) with three replications. The size of the unit plot was 25m×5m. A distance of 1.5 m from block to block, 30 cm from row to row and 10 cm from plant to plant was maintained. Seeds were sown in lines in the experimental plots on 11th November, 2011 by hand uniformly. The seeds were placed at about 1.5 cm depth in the soil.

Table 2. Dose and method of application of fertilizers in field

Fertilizers	Dose (kg/ha)	Application (%)	
		Basal	Before flowering
Urea	250	50	50
TSP	170	100	--
MP	85	100	--
Gypsum	150	100	--
Borax	60	100	--

Source: Krishi Projukti Hatboi, BARI, Joydebpur, Gazipur

After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seed germination started after 3 days of sowing on 14th November 2011. Treatment was distributed in the experimental unit through randomization by using the random number.

3.5.4 After Care

When the seedlings started to emerge in the beds it was always kept under careful observation. After emergence of seedlings, various intercultural operations were accomplished for better growth and development of the *Brassica* seedlings.

3.5.4.1 Irrigation

Light over-head irrigation was provided with a watering cane to the plots once immediately after germination and continued for three times for proper growth and development of the plants.

3.5.4.2 Thinning and Gap Filling

The seedling were first thinned from all of the plots at 10 Days after sowing (DAS), 2nd thinning was carried out after 17 days for maintaining proper spacing of the experimental plots.

3.5.4.3 Weeding and Mulching

Weeding and mulching were done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully after complete emergence of *Brassica* seedlings and whenever necessary. Breaking the crust of the soil, when needed was done through mulching.

3.5.4.4 Top Dressing

After basal dose, the remaining doses of urea were top-dressed in two equal installments. The fertilizers were applied on both sides of plant rows and mixed well with the soil.

3.5.5 Plant Protection

Malathion 57 EC insecticide was applied after one month of seeds sowing at 12 days interval for three times with 1 ml in 2.5 liters water for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed @ 20-g/10L water first one at the time of siliqua setting and second one after 15 days of 1st spraying to control *Alternaria* leaf spot. No remarkable disease attack was observed.

3.5.6 Harvesting

Harvesting was started from 5 February, 2012 depending upon the maturity of the plants. When 80% of the plants showed symptoms of maturity i.e.; straw colour of siliqua, leaves, stem and desirable seed colour in the matured siliqua, the crop was assessed to attain maturity. Ten plants were selected at random from each plot in each replication. The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded from these plants.

3.5.7 Collection of data

For studying different genetic parameters and inter-relationships the ten characters were taken into consideration

3.5.8 Methods of collecting data

3.5.8.1 Days to 50% flowering

Days to 50% flowering was recorded when 50% plants of a plot were at the flowering stage. Difference between the dates of sowing to the date of flowering of a plot was counted as days to 50% flowering.

3.5.8.2 Days to maturity

Number of days required from sowing to siliqua maturity of 80% plants of each entry. Maturities of the crops of 18 genotypes were recorded considering the maturity symptom such as color changing of the plant from greenish to straw colored appearance.

3.5.8.3 Plant height

The height of plants was recorded in cm as the average of 10 plants selected at random from the inner rows of each plot after harvest. The height was measured from the ground level to the tip of the growing point of the main branch

3.5.8.4 Number of primary branches/plant

The total number of branches arisen from the main stem of a plant was counted as the number of primary branches per plant.

3.5.8.5 Number of secondary branches/plant

The total number of branches arisen from the primary branches of a plant was counted as the number of secondary branches per plant.

3.5.8.6 Number of siliqua/plant

The total numbers of siliqua of the randomly selected 10 plants of a plot were recorded and then average numbers of siliqua were estimated.

3.5.8.7 Length of siliqua

Distance between the ends of the peduncle to the starting point of the beak was recorded as siliqua length and was presented in centimeter (cm).

3.5.8.8 Number of seeds/siliqua

Ten siliqua from each plant were selected randomly and number of seeds was counted and the average number of seed per siliqua was determined.

3.5.8.9 1000 seed weight

One thousand seeds were counted from randomly selected plants of each plot and then weighted in grams.

3.5.8.10 Seed yield/plant

Seed weight per plant was measured from the randomly selected plants and then average was designated as seed yield per plant.

3.5.9 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chowdhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2007 (XLSTAT) software through four techniques *viz.* Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA), etc.

The data collected as explained above was subjected to the following statistical analysis.

3.5.9.1 Mean

On the basis of individual plant observations, the mean for each character in all the genotypes was computed as follows

$$\overline{X} = \left(\sum_{i=0}^{n} Xi\right)/n$$

Where,

X = Population mean

Xi = Individual observation

n = Number of observations

3.5.9.2 Range

The minimum and maximum values on the basis of individual plant observations were used to indicate the range for a given character.

3.5.9.3 Analysis of variance (ANOVA)

The analysis of variance for different characters was carried out using the mean data in order to partition variability due to different sources by following Panse and Sukhatme (1961).

Source of Variation	d.f.	M.S.S.	Expected values of M.S.S.
Replication (r)	r-1	M_1	-
Genotypes (g)	g-1	M_2	$\sigma E_2 + r\,\sigma g^2$
Error	(r-1) (g-1)	M_3	σE_2
Total	(rg-1)	$M_1+M_2+M_3$	-

3.5.10 Estimation of variability

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952).

3.5.10.1 Estimation of genotypic and phenotypic variances: Genotypic and phenotypic variances were estimated according to the formula of Johnson *et al.* (1955).

Genotypic variance, $\delta^2 g = \frac{(MSG - MSE)}{r}$

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

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

$\delta^2 e$ = Environmental variance = Mean square of error

3.5.10.2 Estimation of Genotypic and Phenotypic Co-efficient of variation: Genotypic and phenotypic co-efficient of variation were calculated by the following formula (Burton, 1952).

Both genotypic and phenotypic coefficient of variability were computed as per the method suggested by Burton and Dewane (1953)

(a) Genotypic coefficient of variability (GCV)

$$GCV\ (\%) = \frac{\sigma g}{\overline{X}} \times 100$$

(b) Phenotypic coefficient of variability (PCV)

$$PCV\ (\%) = \frac{\sigma p}{\overline{X}} \times 100$$

Where,

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

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

3.5.10.3 Estimation of heritability: Broad sense heritability was estimated by the formula suggested by Singh and Chowdhury (1985).

$$h^2b\ (\%) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Where,

h^2b = Heritability in broad sense.

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

3.5.10.4 Estimation of Genetic Advance: The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

$$GA = \frac{\delta^2 g}{\delta^2 p} \text{ . K. } \delta p$$

Where,

GA = Genetic advance

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ = Phenotypic variance

δp = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection Intensity

3.5.10.5 Estimation of Genetic Advance in percentage of mean: Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic advance (\% of mean)} = \frac{\textbf{\textit{Genetic advance (GA)}}}{\textbf{\textit{Population mean }}\overline{X}} \times 100$$

Where,

GA = Genetic advance

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

3.5.11 Inter-character correlation analysis

The correlation co-efficients were computed to determine the nature and magnitude of association of different characters with seed yield and also among yield components in each of the populations separately.

Phenotypic correlations were computed by using the formula given by Weber and Moorthy (1952).

$$r_p = \frac{COV_{p(xy)}}{\sqrt{V_{px} \times V_{py}}}$$

Where,

r_p = Phenotypic correlation

$COV_{p(xy)}$ = Phenotypic covariance between the character x and y

V_{px} = Phenotypic variance of the character x

V_{py} = Phenotypic variance of the character y

Phenotypic correlation co-efficients were compared against table 'r' values (Fisher and Yates, 1963) at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance.

Genotypic correlations were estimated according to the formula given by Al-jibori *et.al* (1958).

$$r_g = \frac{COV_{g(xy)}}{\sqrt{V_{gx} \times V_{gy}}}$$

Where,

r_g = Genotypic correlation

$COV_{g(xy)}$ = Genotypic covariance between the character x and y

V_{gx} = Genotypic variance of the character x

V_{gy} = Genotypic variance of the character y

Genotypic correlation co-efficients were compared against table 'r' values (Fisher and Yates, 1963) at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance.

3.5.12 Path co-efficient analysis

In all the environments, path coefficient analysis was carried out to know the direct and indirect effects of the yield components on seed yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1957).

3.5.13 Estimation of Diversity

3.5.13.1 Principal Component Analysis (PCA)

Principal Component Analysis (PCA), one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from sum of squares and product matrix for the characters. Therefore, Principal Component were computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity (Jager *et al.* 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.5.13.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.*, 1989).

3.5.13.3 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examine the effect of swapping two genotypes of different classes and so on.

3.5.13.4 Canonical Variate Analysis (CVA)

Using canonical vector analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the within group variations.

3.5.13.5 Computation of Average Intra-cluster Distances

When the clusters were formed, the average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotypes included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.5.13.6 Cluster Diagram

Cluster Diagram was drawn using the intra and inter cluster distance. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The present experiment was conducted to determine the breeding values in respect of genotypic effects and comparative performances of different *Brassica napus* L. BC_1F_2 materials generated through intervarietal crosses along with their parent materials. The study was carried out to find out the phenotypic and genotypic variability, co-efficient of variation, heritability, genetic advance, correlation & path analysis and genetic diversity among different genotypes to estimate the direct and indirect effect of yield contributing traits on yield. Ten characters such as plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity, number of siliqua per plant, length of siliqua, number of seeds per siliqua, thousand seed weight and seed yield per plant were studied in respect of 31 genotypes.

This chapter comprises the presentation and discussion of the findings obtained from the study. Data pertaining to 8 yield and its contributing characters were computed and statistically analyzed and the results of the present investigation are presented under the following headings:

- Genetic variability, heritability and genetic advance
- Correlation coefficient studies
- Path coefficient analysis
- Assessment of genetic diversity

4.1 Variability

The analysis of variance (ANOVA) of the data on different yield components and yield of *Brassica* are given in Table 3. The results have been presented and discussed and possible interpretations have been given. The mean values over three replications for the characters of all genotypes are presented in Table 4, genotypic, phenotypic and environmental variance and genotypic, phenotypic and environmental coefficients of variation in Table 5. Among the genotypes almost

all characters showed highly significant variation indicating wide scope of selection for these characters i.e. data revealed substantial variability and thus high possibility of improvement in most of the traits. The variability in the present study indicated the potentiality of the materials generated through intervarietal crosses for selecting out desirable segregants in BC_1F_2 generation for the development of new varieties. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations. In general environmental influences were minimal on yield and its component characters (Table 5).

4.1.1 Days to 50% flowering

From the Table 3 there were highly significant variations among the genotypes (3.374**) for days to 50% flowering. The mean value of days to 50% flowering was observed the highest (39.33 days) in G1 which was statistically similar to G2, G3, G4, G7, G9, G12, G25 and G28 but significantly differed from other genotypes. The lowest value was found in G29 (35.00 days) followed by G22, G21, G20, G30, G24 and G26 (Table 4).

Genotypic and phenotypic variance of days to 50% flowering was observed 0.90 and 1.58, respectively. Wide difference between them indicating large environmental influences on this character for their phenotypic expression and values GCV and PCV were 2.55% and 3.38%, respectively which indicated low variability present among the genotypes for this character (Table 5). Lekh *et al.* (1998) recorded the highest GCV and PCV for days to 50% flowering.

4.1.2 Days to maturity

Highly significant variation was observed among all the genotypes (2.964**) studied for this character (Table 3). The mean value of days to maturity was observed significantly the lowest in G13 (88.67 days) which was statistically similar to G16, G23, G26, G29 and G30 (Table- 4). The highest days took to mature was found in G5 (92.67 days).

Table 3. Analysis of variance of the data of 10 important characters in respect of *Brassica napus* L. (BC_1F_2) genotypes

Sources of variation	d. f	Mean sum of squares of characters									
		Days to flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Length of siliqua (cm)	Number of seeds per siliqua	1000 seed weight (g)	Seed yield/plant (g)
Replication	2	0.04	0.09	121.73	0.24	0.25	12.26	1.98	4.50	0.01	0.31
Genotype	30	3.37**	2.96**	72.37*	0.47**	0.90^{NS}	352.73**	0.92^{NS}	12.46**	0.05**	4.11**
Error	60	0.67	0.71	44.66	0.07	0.73	27.25	0.68	0.84	0.01	0.23
CV		2.21%	0.93%	6.50%	8.23%	41.32%	4.51%	11.88%	4.27%	3.44%	6.21%

*Significant at 5% level of probability, **Significant at 1% level of probability, NS= Non-significant

Table 4. Mean performance of 10 important characters in respect of *Brassica napus* L. (BC_1F_2) genotypes

Designation	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Length of siliqua (cm)	Number of seeds per siliqua	1000 seed weight (g)	Seed yield/plant (g)
G1	39.33 a	92.33 ab	109.90 ab	2.97 g-j	1.87	126.2 0 b	7.817	24.71 a	3.03 def	9.43 ab
G2	38.33 abc	91.00 a-e	109.20 ab	3.63 a-e	2.13	120.60 b-e	6.607	22.01 b-g	3.20 bcd	8.63 b-f
G3	38.33 abc	90.33 c-f	93.17 c	3.67 a-d	2.93	105.50 h-k	7.107	19.49 ij	2.93 ef	5.93 mn
G4	38.00 a-d	91.67 a-c	98.73 abc	3.47 a-g	2.17	121.40 b-e	7.153	22.32 b-f	3.00 def	8.17 c-f
G5	37.67 b-e	92.67 a	100.60 abc	3.00 g-j	1.70	103.00 jkl	7.193	22.75 b-e	3.20 bcd	7.80 f-i
G6	37.33 b-f	90.67 a-c	109.20 ab	3.60 a-e	2.77	139.10 a	7.63	24.53 a	2.97 ef	10.10 a
G7	38.67 ab	92.33 ab	105.30 abc	3.07 f-j	1.70	112.90 d-j	7.053	23.21 abc	3.13 b-e	8.20 c-f
G8	36.67 d-h	91.67 b-f	110.70 a	3.17 d-j	2.97	138.80 a	7.027	22.13 b-f	2.97 ef	9.20 b
G9	38.33 abc	92.33 ab	109.10 ab	2.93 h-k	1.60	126.60 b	7.47	23.23 abc	3.07 c-f	9.07 bc
G10	37.67 b-e	90.67 b-f	107.80 ab	3.17 d-j	1.97	127.10 b	6.6	19.97 hij	3.13 b-e	7.80 f-i
G11	37.00 c-g	91.33 a-d	105.60 abc	2.83 i-k	1.57	112.30 d-j	7.493	23.17 a-d	3.13 b-e	8.03 d-g
G12	38.67 ab	90.67 b-f	103.90 abc	3.87 ab	2.40	114.10 d-i	6.713	19.52 ij	2.93 ef	6.47 j-m
G13	36.67 d-h	88.67 g	99.77 abc	3.73 abc	2.63	110.20 f-k	6.863	21.23 e-i	3.27 abc	7.83 fgh
G14	37.33 b-f	91.33 a-d	94.20 c	3.13 e-j	2.60	114.10 d-i	7.123	20.76 f-i	3.03 def	6.97 h-k
G15	37.33 b-f	90.33 c-f	106.00 abc	3.40 b-h	1.53	101.40 kl	6.5	20.15 hij	3.00 def	6.07 k-n
G16	37.00 c-g	90.00 c-g	97.43 abc	2.90 h-k	2.07	116.20 c-g	6.593	20.07 hij	3.27 abc	8.10 d-g
G17	37.33 b-f	90.33 c-f	105.60 abc	2.70 jkl	1.37	118.80 b-f	7.04	21.35 e-h	2.93 ef	8.03 d-g
G18	37.33 b-f	90.33 c-f	105.40 abc	3.47 a-g	2.17	111.50 e-k	6.367	20.31 g-j	3.03 def	6.93 ijk
G19	36.67 d-h	90.67 b-f	109.10 ab	3.57 a-f	1.57	107.40 g-k	5.977	18.71 j	2.97 ef	5.93 lmn
G20	35.67 g-i	90.33 c-f	105.20 abc	3.30 c-i	2.17	127.10 b	7.423	22.64 b-e	3.07 c-f	8.90 bcd
G21	35.67 g-i	91.67 a-c	96.97 bc	3.80 abc	2.27	104.40 ijk	5.153	15.14 k	3.43 a	5.47 n
G22	36.33 e-i	90.33 c-f	101.40 abc	3.07 f-j	2.40	122.4 bcd	7.863	24.61 a	2.87 f	8.63 b-f
G23	36.67 d-h	89.33 e-g	98.23 abc	3.13 e-j	2.17	121.60 b-e	6.907	21.63 c-h	3.30 ab	8.53 b-f
G24	36.33 e-i	91.33 a-d	103.90 abc	2.33 l	1.67	94.40 l	7.76	24.49 a	3.00 def	6.90 jk
G25	38.33 a-c	91.00 b-e	96.50 bc	3.00 g-j	2.03	104.00 ijk	7.09	20.67 f-i	3.20 bcd	6.77 j-m
G26	35.33 hi	89.33 e-g	102.70 abc	3.97 a	3.77	126.30 b	7.19	23.46 ab	3.00 def	8.83 b-e
G27	36.33 e-i	90.33 c-f	97.70 abc	3.07 f-j	2.10	125.50 bc	7.197	22.70 b-e	3.20 def	9.13 b
G28	38.00 a-d	91.00 b-e	98.67 abc	3.30 c-i	1.77	101.90 kl	6.443	19.90 hij	3.00 def	6.60 j-m
G29	35.00 i	89.00 f-g	104.50 abc	3.20 d-j	1.47	108.90 f-k	6.963	21.42 d-h	3.07 c-f	7.23 g-j
G30	36.00 f-i	89.67 d-g	99.93 abc	2.83 ijk	1.30	114.80 d-h	7.14	22.01 b-g	3.10 b-e	7.93 efg
G31	37.33 b-f	91.33 a-d	102.60 abc	2.47 kl	1.60	109.50 f-k	6.763	20.73 f-i	2.93 ef	6.83 jkl
LSD (0.05)	1.343	1.385	10.91	0.432	NS	8.527	NS	1.504	0.171	0.278

Note: Means separated by uncommon letters in order of alphabetic preferences are significantly different from each other at p=0.05

Table 5. Estimation of statistical and genetic parameters of yield and its contributing traits of *Brassica napus* (L.) (BC_1F_2) genotypes.

Parameters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Length of siliqua (cm)	Number of seeds per siliqua	1000 seed weight (g)	Seed yield/plant (g)
Mean	37.18	90.77	102.87	3.22	2.08	115.74	6.97	21.58	3.08	7.76
Max	39.33	92.67	110.70	3.97	3.77	139.10	7.86	24.71	3.43	10.10
Min	35.00	88.67	93.17	2.33	1.30	94.40	5.15	15.14	2.87	5.47
SD	1.06	0.99	4.91	0.40	0.55	10.85	0.56	2.04	0.13	1.17
MSS	3.374**	2.964**	72.371*	0.474**	0.908^{NS}	352.734**	0.927^{NS}	12.462**	0.052**	4.117**
σ^2e	0.676	0.719	44.661	0.07	0.74	27.257	0.686	0.848	0.011	0.232
CV (%)	2.21	0.93	6.5	8.23	0.41	4.51	11.88	4.27	3.44	6.21
σ^2g	0.90	0.75	9.24	0.13	0.06	108.49	0.08	3.87	0.01	1.30
σ^2p	1.58	1.47	53.90	0.20	0.79	135.75	0.77	4.72	0.02	1.53
GCV (%)	2.55	0.95	2.95	11.41	11.49	9.00	4.06	9.12	3.80	14.67
PCV (%)	3.38	1.33	7.14	14.06	42.89	10.07	12.55	10.07	5.11	15.93
ECV (%)	2.21	0.93	6.50	8.22	41.32	4.51	11.87	4.27	3.41	6.21

**Significance at 1% level, MSS= Mean sum of square, CV (%) = Coefficient of variation, σ^2_e= Environmental variance, σ^2g= Genotypic variance, σ^2_p = Phenotypic variance, GCV (%) = Genotypic coefficients of variations, PCV (%) = Phenotypic coefficients of variations, ECV (%) = Environmental coefficients of variations.

Genotypic and phenotypic variance of days to maturity was observed 0.75 and 1.47, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of GCV and PCV were 0.95% and 1.33%, respectively which indicated that the genotypes have relatively less variation (Table 5). Higher genotypic variances indicate the better transmissibility of a character from parent to the offspring (Ushakumari *et al.*, 1991).

4.1.3 Plant height (cm)

The mean square due to genotype from the analysis of variance was found statistically significant at 5% level of probability for plant height (72.371) indicating genotypic differences present among the genotypes used under the present study (Table 3). From the mean value it was found that the tallest genotype was G8 (11.70 cm) and shortest genotype was G3 (93.17 cm) which was statistically identical to G14 (94.20 cm) (Table 4).

The phenotypic variance (53.90) was considerably higher than the genotypic variance (9.24) and PCV and GCV were 7.14% and 2.95%, respectively (Table 5). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. The highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001) in their study.

4.1.4 Number of primary branches per plant

Analysis of variance of the data for number of primary branches per plant showed statistically highly significant (0.474) differences among the genotypes (Table 3). Mean value of the maximum number of primary branches per plant was recorded in genotype G26 (3.97) which was significantly differed from other genotypes and the lowest number of primary branches per plant was recorded from G24 (2.33) (Table 4).

The phenotypic variance (0.20) was slightly higher than the genotypic variance (0.13) indicating less environmental influence in this character (Table 5) and relatively moderate genotypic co-efficient of variation (11.41%) and phenotypic co-efficient of variation (14.06%) which indicated that the genotype has moderate variability (Table 5). Chawdhury *et al.* (1987) found significant differences for number of primary branches per plant. Kuriakose and Joseph (1986), Alam *et al.* (1985) and Uddin *et al.* (1995) reported the similar results.

4.1.5 Number of secondary branches per plant

Number of secondary branches per plant did not varied significantly among the genotypes (Table 3). Considerable difference between genotypic variance (0.06) and phenotypic variance (0.79) indicated that this character was largely influenced by the environmental variation and high phenotypic coefficient of variation (42.89%) than genotypic co-efficient of variation (11.49%) indicated that environmental variation was the major determinant for this character (Table 5).

4.1.6 Number of siliqua per plant

The mean square value due to genotype from the analysis of variance was found statistically significant differences at 1% level of probability for number of siliqua per plant among the genotypes used as experimental materials under the present experiment (Table 3). From the mean value it was found that the highest number of siliqua per plant was recorded for the genotype G6 (139.10) which was statistically identical to G8 (138.80) and the lowest number of siliqua per plant was recorded from G24 (94.40).

The phenotypic variance (135.75) was higher than genotypic variance (135.75) and the phenotypic and genotypic co-efficient of variations were 10.07% and 9.00%, respectively (Table 5). The result indicated that there was a moderate variability among the genotypes. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for number of siliqua per plant were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Vankatramana *et al.* (2001).

4.1.7 Length of siliqua (cm)

There was no significant variation was recorded among the genotypes in consideration of length of siliqua (Table 3). Length of siliqua showed minimum amount of genotypic and phenotypic variance (0.08 and 0.77, respectively) with minimum difference between them indicated that they were less responsive to environmental factors for their phenotypic expression. According to Table 5, GCV and PCV of 4.06% and 12.55%, respectively for length of siliqua which indicated that insufficient genotypic variation among different genotypes. Deshmukh *et al.* (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

4.1.8 Number of seeds per siliqua

The value of the analysis of variance of the data for the number of seed per siliqua showed highly significant difference (12.462) among the genotypes of *Brassica* used in the present experiment. The mean squares value regarding to the character indicated the presence of variability among the genotypes (Table 3). Maximum number of seeds per siliqua were recorded in genotype G1 (24.71) which was statistically identical to G6 (24.53), G22 (24.61) and G28 (24.49) and the lowest number of seeds per siliqua were recorded from G21 (15.14) (Table 4).

The genotypic and phenotypic variances were 3.87 and 4.72, respectively, which indicated that there was less environmental influence for this character and genotypic coefficient of variation (9.12%) and phenotypic coefficient of variation (10.07%) indicated that there was a moderate variation among the genotypes (Table 5). The result indicated the existence of adequate variation among the population with possibility of high potential for selection. Yogendra *et al.* (2002) also reported moderate phenotypic coefficient of variation and genotypic coefficient of variation for this character.

4.1.9 1000 Seed weight (g)

The mean square of genotypes from the analysis of variance was found statistically significant at 1% level of probability for 1000 seed weight indicating genotypic differences among the genotypes used under the present experiment

(Table 3). From the mean value it was found that the highest 1000 seed weight was recorded from the genotype G21 (3.43 g) which was statistically similar to G23 (3.30 g), G13 (3.27 g) and G16 (3.27 g), and significantly the lowest 1000 seed weight was recorded from G22 (2.87 g) (Table 4).

The genotypic (0.01) and phenotypic (0.02) variances were so close to each other indicating there was less environmental variation (Table 5). The GCV and PCV were 3.80% and 5.11%, respectively. The result indicated the existence of inherent variability among the population with possibility of high potential for selection.

4.1.10 Seed yield per plant (g)

In the present study, the genotypic mean square for seed yield per plant was found significant (4.117) at 1% level (Table 3). The seed yield per plant was recorded highest in G6 (10.10 g), which was statistically similar to G1 (9.43 g) and the lowest seed yield per plant (5.47 g) from G21 (Table 4). Shen *et al.* (2002) observed significant differences between F_{1s} and their parents for yield per plant. Katiyar *et al.* (2004) found significant variation among parents and crosses indicated the presence of adequate genetic variance which reflected in differential performance of intervarietal cross combinations of *Brassica campestris*.

Seed yield per plant showed low values of genotypic (1.30) and phenotypic (1.53) variance with little differences indicating that there was less environmental impact for this character and moderate GCV (14.67%) and PCV (15.93%) indicating that the genotypes were considerably variable for this character (Table 5). Bhardwaj and Singh (1996) reported GCV of seed yield per plant was 96.99% in *B. campestris* and Singh (1987) reported values 44.04% and 46.90% of GCV and PCV, respectively for *B. juncea*.

4.2 Heritability and Genetic Advance

Findings of the heritability, genetic advance and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 6.

4.2.1 Days to 50% Flowering

Days of 50% flowering showed high heritability (57.09%) with low genetic advance (1.48%) and genetic advance in percentage of mean (3.97) revealed that the character was governed by non-additive genes and heterosis breeding might not be useful and also indicated that the character was highly influenced by the environmental effects (Table 6).

4.2.2 Days to Maturity

The magnitude of heritability in broad sense (h^2b) of this character was high (51.00%) and low genetic advance (1.27%) and low genetic advance in percentage of mean (1.40) (Table 6). These findings indicative of non-additive gene action. The high heritability was exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. Similar findings were reported by Alam *et al.* (1985) and Hossain (1988).

4.2.3 Plant Height

Plant height showed very high heritability (65.80%) together but low genetic advance (2.59%) and genetic advance in percentage of mean (2.52) which indicated that most likely the heritability was due to non-additive gene effects (Table 6) and selection may not be effective which was also earlier reported by Singh and Singh (1999).

4.2.4 Number of Primary Branches/Plant

Number of primary branches/plant showed high heritability (65.80%) coupled with low genetic advance (0.61%) and genetic advance in percentage of mean (19.06). These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

Table 6. Heritability, Genetic advance and Genetic advance in percent of means for yield and yield contributing characters of 31 genotypes of *Brassica napus* L.

Parameters	Heritability h^2b (%)	Genetic advance GA (5%)	Genetic advance in percent (GAPM)
Days to 50% flowering	57.09	1.48	3.97
Days to maturity	51	1.27	1.4
Plant height (cm)	17.14	2.59	2.52
Number of primary branches/plant	65.8	0.61	19.06
Number of secondary branches/plant	7.18	0.13	6.34
Number of siliqua/plant	79.92	19.18	16.57
Length of siliqua (cm)	10.48	0.19	2.71
Number of seeds per siliqua	82.03	3.67	17.01
1000 seed weight (g)	55.41	0.18	5.83
Seed yield/plant (g)	84.81	2.16	27.83

4.2.5 Number of Secondary Branches per Plant

This character showed very low heritability (7.18%) coupled with very low genetic advance (0.13%) and low genetic advance in percentage of mean (6.34) (Table 6). These findings revealed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection may not be rewarding which was also earlier reported by Kumar *et al.* (1998)

4.2.6 Number of Siliqua per Plant

Number of siliqua per plant showed very high heritability (79.92%) coupled with moderate genetic advance (19.18%) and very high genetic advance in percentage of mean (16.57) (Table 6). As this trait possessed high genetic advance, it had high potential for effective selection for further genetic improvement of this trait.

4.2.7 Length of Siliqua (cm)

Length of siliqua showed low heritability (10.48%) with very low genetic advance (0.19%) and genetic advance in percentage of mean (2.71) (Table 6). These findings exposed the action of non-additive gene effect on the expression of this character as well as narrow scope of improvement through selection.

4.2.8 Number of Seeds per Siliqua

The magnitude of heritability in broad sense (h^2b) of this trait was very high (82.03%) and low genetic advance (3.67%) and moderate genetic advance in percentage of mean (17.01) (Table 6). These results indicated non-additive genes involvements in the expression of the character and this with moderate scope of improvement by direct selection.

4.2.9 1000 Seed Weight (g)

High heritability (55.41%) associated with very low genetic advance (0.18%) and genetic advance in percentage of mean (5.83) (Table 6) was calculated in respect of 1000 seed weight of *Brassica* genotypes. These findings exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection.

4.2.10 Seed yield per plant (g)

Very high heritability (84.81%) coupled with low genetic advance (2.16%) and moderate genetic advance in percentage of mean (27.83) was recorded in respect of yield per plant (Table 6). These findings revealed that it was indicative of non-additive gene action. The high heritability was exhibited due to favorable influence of environment rather than genotypes and there was moderate scope of improvement through this character.

4.3 Correlation Coefficient

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, simultaneously affects a number of other correlation traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. Genotypic and phenotypic correlation coefficients between pairs of characters of present study in *Brssica napus* are presented in Table 7. In general, the genotypic correlation co-efficient for each character pair was higher than the respective phenotypic correlation co-efficients. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al.,* 1973).

The results are discussed under the following heads:

4.3.1 Days to 50% flowering

Days to 50% flowering were positively and highly significantly correlated with days to maturity and Significant negatively associated with number of secondary branches per plant.

Table 7. Genotypic (r_g) and phenotypic (r_p) correlation among yield and its contributing traits of *Brassica napus* L. (BC_1F_2) genotypes

Parameters		DM	PH	NPBPP	NSBPP	NSPP	LS	NSPS	TSW	SYPP
DFF	r_g	0.49**	0.22^{ns}	-0.05^{ns}	-0.31*	-0.05^{ns}	0.12^{ns}	0.04^{ns}	-0.21^{ns}	-0.02^{ns}
	r_p	0.65**	0.07^{ns}	-0.02^{ns}	-0.08^{ns}	0.03^{ns}	0.12^{ns}	0.07^{ns}	-0.09^{ns}	0.02^{ns}
DM	r_g		0.44^{**}	-0.33*	-0.66**	-0.04^{ns}	0.03^{ns}	0.15^{ns}	-0.07^{ns}	0.04^{ns}
	r_p		0.11^{ns}	-0.24^{ns}	-0.10^{ns}	0.02^{ns}	0.15^{ns}	0.11^{ns}	-0.03^{ns}	0.05^{ns}
PH	r_g			-0.16^{ns}	-0.97**	0.62**	-0.35*	0.49**	-0.75**	0.50**
	r_p			0.03^{ns}	0.07^{ns}	0.34*	0.28^{ns}	0.29^{ns}	-0.06^{ns}	0.37*
NPBPP	r_g				0.98**	0.15^{ns}	-0.85**	-0.41*	0.09^{ns}	-0.17^{ns}
	r_p				0.43**	0.12^{ns}	-0.27^{ns}	-0.33*	0.06^{ns}	-0.10^{ns}
NSBPP	r_g					0.91**	-0.51**	-0.06^{ns}	-0.21^{ns}	0.38*
	r_p					0.27^{ns}	0.17^{ns}	0.09^{ns}	-0.03^{ns}	0.19^{ns}
NSPP	r_g						0.62**	0.45**	-0.22^{ns}	0.85**
	r_p						0.27^{ns}	0.41*	-0.04^{ns}	0.81**
LS	r_g							0.99**	-0.92**	0.94**
	r_p							0.67**	-0.13^{ns}	0.46**
NSPS	r_g								-0.36*	0.82**
	r_p								-0.25^{ns}	0.71**
TSW	r_g									-0.10^{ns}
	r_p									0.10^{ns}

Where, DFF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBPP= Number of primary branches per plant, NSBPP= Number of secondary branches per plant, LS= Length of siliqua (cm), NSPS= Number of seeds per siliqua, TSW= 1000 seed weight (g), SYPP= Seed yield per plant (g). *Significance at 5% level, ** Significant at 1% level, ns= Non significant, r_g= Genotypic correlation coefficient and r_p= Phenotypic correlation coefficient

4.3.2. Days to maturity

Days to maturity were highly significant positively associated with plant height both at genotypic and phenotypic level but negatively and non-significantly associated with other characters (Table 7).

4.3.3 Plant height (cm)

Plant height found positive highly significant relationships with number of siliqua per plant and number of seeds per siliqua and seed yield per plant at genotypic and phenotypic level indicated that the traits were governed by same gene by pleotropic effect and simultaneous improvement would be effective. The character reflected negative association with number of primary branches per plant, number of secondary branches per plant, length of silqua and 1000 seed weight both at genotypic and phenotypic level (Table 7).

4.3.4 Number of primary branches per plant

Number of primary branches per plant was highly significantly and positively correlated with number of secondary branches per plant both at genotypic and phenotypic level at 1% per cent level of significance (Table 7). While, it had significantly negative correlation with length of siliqua but non significant correlation with number of seeds per siliqua and seed yield per plant. This trait was positively associated with number of secondary branches per plant but found non-significant association. Degenhart and Kondra (1984), as well as Gillani *et al.* (1993) estimated strong negative correlation between plant height and seed yield.

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant was found positively and highly significantly correlated with number of siliqua per plant and positive significant with seed yield per plant at genotypic level (Table 7). Association of this trait with number of seeds per siliqua and thousand seed weight per siliqua was found negative and non-significant except length of siliqua, where it was found negatively significant association. Similar results were obtained by Guo *et al.* (1987), Kis *et al.* (2006) and Ana *et al.* (2008) who analyzed correlation between number of lateral branches and seed yield per plant, they found strong correlation between them.

4.3.6 Number of siliqua per plant

Number of siliqua per plant was positively and highly significantly correlated with length of siliqua, number of seeds per siliqua and seed yield per plant both at genotypic and phenotypic level except association with length of siliqua where it was found positive but non-significant association at phenotypic level (Table 7). Guo *et al.* (1987), Behl *et al.* (1989), Ozer *et al.* (1999) and Ana *et al.* (2008) reached to the quite similar results of strong correlation between the number of siliqua per plant and seed yield per plant.

4.3.7 Length of siliqua (cm)

Length of siliqua had highly significant and positive correlation with number of seeds per siliqua and seed yield per plant both at genotypic and phenotypic level (Table 7). There was negatively significant at genotypic and negatively non-significant association at phenotypic level was observed with 1000 seed weight. But Khan *et al.* (2000) observed dissimilar results, he found strong positive association between length of siliqua and 1000 seed weight.

4.3.8 Number of seeds per sliqua

Number of seeds per siliqua was highly significant and positive correlation with seed yield both at genotypic and phenotypic level (Table 7). But negative significant correlation was observed with 1000 seed weight at genotypic level and negative non-significant association at phenotypic level. Quite dissimilar result was observed by Khan *et al.* (2000).

4.3.9 1000 Seed weight (g)

1000 seed weight showed negative non-significant association with seed yield per plant at genotypic and positive non-significant association at phenotypic level (Table 7). Similar result of such negative non-significant association with seed yield was observed by Khan *et al.* (2000).

4.4 Path analysis

The genotypic correlation co-efficients of different characters with seed yield were subjected to path co-efficient analysis for estimating the direct and indirect effects of component traits with seed yield which is considered as dependent variable for the analysis. The direct and indirect effects of various traits are given in Table 8.

4.4.1 Days to 50% flowering

A positive direct effect was observed for days to 50% flowering on seed yield per plant (0.149) (Table 8). The indirect effect via days to maturity (-0.043), secondary branches per plant (-0.087), number of siliqua per plant (-0.028), length of siliqua (-0.034) and 1000 seed weight (-0.011) were found to be negative. The indirect effect via plant height (0.001), number of primary branches (0.025) and number of seeds per siliqua (0.032) were contributed to result totally significant positive genotypic correlation with seed yield per plant.

4.4.2 Days to maturity

Days to maturity had negative direct effect on seed yield per plant (-0.087) (Table 8). Days to maturity showed negative indirect effect through number of secondary branch per plant (-0.187), number of siliqua per plant (-0.025), length of siliqua (-0.007) and 1000 seed weight per plant (-0.011). Positive indirect effect through days to 50% flowering (0.074), plant height (0.002), number of primary branches per plant (0.171), number of seeds per siliqua (0.107) and seed yield per plant (0.036).

4.4.3 Plant height (cm)

Plant height showed positive direct effect on seed yield per plant (0.004) (Table 8). Plant height showed positive indirect effect through days to 50% flowering (0.033), number of primary branches per plant (0.084), number of siliqua per plant (0.351), siliqua length, number of seeds per siliqua (0.352) and seeds yield per plant (0.499). The negative indirect effect of this character was found on days to maturity (-0.038), number of secondary branches per plant and 1000 seed weight (-0.114).

Table 8. Partitioning of genotypic correlation with grain yield into direct (bold) and indirect effect of yield contributing traits in *Brassica napus* L. (BC_1F_2) genotypes

Parameters	DFF	DM	PH	NPB	NSB	NSP	SL	NSS	TGW	YLD
DFF	**0.149**	-0.043	0.001	0.025	-0.087	-0.028	-0.034	0.032	-0.031	-0.016
DM	0.074	**-0.087**	0.002	0.171	-0.187	-0.025	-0.007	0.107	-0.011	0.036
PH	0.033	-0.038	**0.004**	0.084	-0.274	0.351	0.101	0.352	-0.114	0.499
NPB	-0.007	0.029	-0.001	**-0.513**	0.276	0.085	0.243	-0.292	0.014	-0.165
NSB	-0.046	0.058	-0.004	-0.502	**0.282**	0.518	0.146	-0.041	-0.032	0.378
NSP	-0.007	0.004	0.002	-0.077	0.257	**0.569**	-0.178	0.319	-0.033	0.855
SL	0.017	-0.002	-0.001	0.434	-0.143	0.353	**-0.287**	0.709	-0.140	0.940
NSS	0.007	-0.013	0.002	0.209	-0.016	0.253	-0.284	**0.716**	-0.056	0.818
TGW	-0.031	0.006	-0.003	-0.046	-0.060	-0.122	0.264	-0.261	**0.152**	-0.101

Residual Effect^2= 0.0258096

Where, DFF= Days to 50% flowering, DM= Days to maturity, PH= Plant height (cm), NPBPP= Number of primary branch per plant, NSBPP= Number of secondary branch per plant, LS= Length of siliqua (cm), NSPS= Number of seeds per siliqua, TSW= 1000 seed weight (g), SYPP= Seed yield per plant (g).

4.4.4 Number of primary branches per plant

Number of primary branches per plant showed negative direct effect on seed yield per plant (-0.513) (Table 8). This character, however, showed positive indirect effect through days to maturity (0.029), number of secondary branches (0.276), number of siliqua per plant (0.085), length of siliqua (0.243) and 1000 seed weight (0.014) and negative indirect effect on days to 50% flowering (-0.007), plant height (-0.001) and number of seeds per siliqua. Khan *et al.* (2000) found indirect positive effect on 1000 seed weight but negative effect on seed yield per plant.

4.4.5 Number of secondary branches per plant

Number of secondary branches per plant showed positively direct effect on seed yield per plant (0.282) (Table 8). The indirect effect via days to maturity (0.058), number of siliqua per plant (0.518), length of siliqua (0.146) and seed yield per plant (0.378) were found positive. The negative indirect effect were observed through days to 50% flowering (-0.046), plant height (-0.004), number of primary branches per plant (-0.502), number of seeds per siliqua (-0.041) and 1000 seed weight (-0.032). Similar result was reported by Khan *et al.* (2000) and Belete (2011), they found indirect positive effect on seed yield per plot for this character.

4.4.6. Number of siliqua per plant

Positive direct effect was noted by number of pods per plant on seed yield per plant (0.569) (Table 8). The indirect effect via days to 50% flowering (-0.007), number of primary branch per plant (-0.077), length of siliqua (-0.178) and 1000 seed weight (-0.033) were observed negative. The positive indirect effect of number of siliqua per plant via days to maturity (0.004), plant height (0.002), number of secondary branches per plant (0.257), number of seeds per siliqua (0.319) and seed yield per plant (0.855) were found. Positive effect of number of siliqua on yield per plant was observed by Ana *et al.* (2008).

4.4.7 Length of siliqua (cm)

Negative direct (-0.287) effect of length of siliqua was observed. Days to 50% flowering (0.017), number of primary branch (0.434), number of secondary branch (0.353), number of seeds per siliqua (0.709) and seed yield per plant (0.940) were found positive and days to maturity (-0.002), plant height (-0.001), number of secondary branch (-0.143) and 1000 seed weight were found negative. Positive indirect effect of length of siliqua on number of branches, number siliqua per plant, number of seeds per siliqua and negative effect on seed yield per plant was observed by Rameeh (2011).

4.4.8 Number of seeds per siliqua

Number of seeds per siliqua (0.716) showed positive direct effect on seed yield. Positive indirect effects were observed in days to 50% flowering (0.007), plant height (0.002), number of primary branch (0.209), number of siliqua per plant (0.253) and seed yield per plant (0.818). Days to maturity (-0.013), number of secondary branch (-0.016), length of siliqua (-0.284) and 1000 seed weight (-0.056) were found negative as indirect effect. Positive direct effect and positive indirect effect of seeds per siliqua on number of siliqua per plant and seed yield per plant was observed by Rameeh (2011).

4.4.9 1000 seed weight (g)

A positive direct effect was recorded in 1000 seed weight (0.152) (Table 8). The negative indirect effect via days to 50% flowering (-0.031), plant height (-0.003), number of primary branch (-0.046), number of secondary branch per plant (-0.060), number of siliqua per plant (-0.122), number of seeds per siliqua (-0.261) and seed yield per plant (-0.101) were found. The indirect effect via days to maturity (0.006) and length of siliqua (0.264) were found positive. Similar result of negative indirect of 1000 seed weight on seed yield per plant was reported by Khan *et al.* (2000)

4.5. Diversity

The result of the genetic diversity of *Brassica* genotypes are presented in Table 8 to 13 and Figure 1 to 3.

4.5.1 Principle Component Analysis (PCA)

The principle component analysis produce Eigen values of principle component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 62.91% (Table 9).

The first two principal axes accounted for 49.13% of the total variation among the ten characters describing 31 genotypes. On the basis of principal axes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented in Figure 2. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 3).

4.5.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter genotypic distances obtained from Principal Coordinate Analysis showed that the highest distance (0.864) was observed between the genotypes G6 and G21 followed by G1 and G21 (0.834), G14 and G26 (0.797), G21 and G26 (0.789), G26 and G30 (0.789), G9 and G21 (0.786), G19 and G26 (0.784), G15 and G26 (0.778), G17 and

Table 9. Eigen values and percentage of variation for corresponding 10 component characters in 31 *Brassica napus* L. ($BC_1 F_2$) genotypes.

Component	Eigen values	% of total variation accounted for	Cumulative %
I	3.05	30.54	30.54
II	1.86	18.59	49.13
III	1.38	13.78	62.91
IV	1.09	10.86	73.78
V	0.82	8.21	81.99
VI	0.74	7.37	89.36
VII	0.45	4.47	93.83
VIII	0.29	2.86	96.69
IX	0.27	2.66	99.35
X	0.06	0.65	100.00

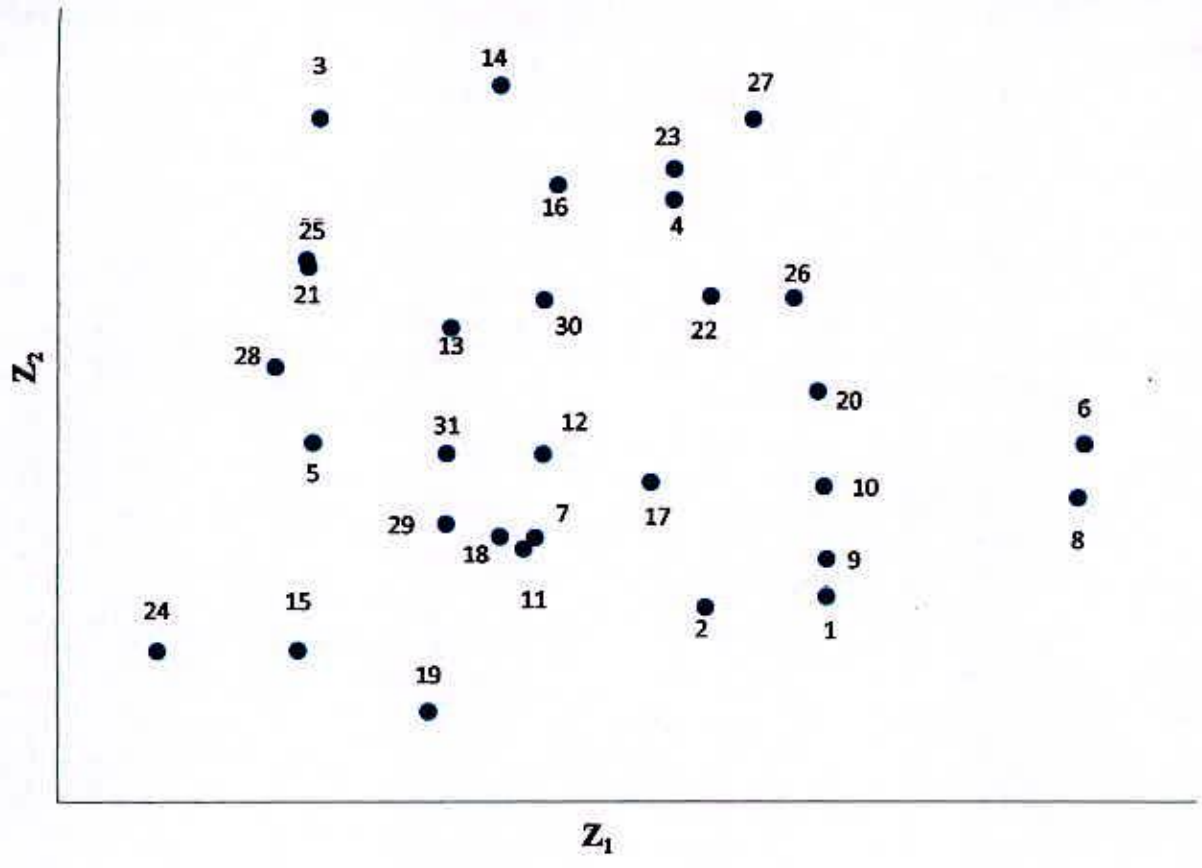


Figure 2: Scatter distribution of 31 *Brassica napus* L. BC_1F_2 genotypes based on their principal component scores

G26 (0.774) and G26 and G31 (0.767). The lowest distance was observed between the genotypes G1 and G9 (0.131) followed by G5 and G11 (0.130), G4 and G23 (0.129), G15 and G19 (0.128), G16 and G23 (0.124), G5 and G7 (0.119), G20 and G27 (0.107), G7 and G11 (0.106), G17 and G30 (0.102) and G23 and G27 (0.098) (Table 9). By using these distances from distance matrix intra-cluster distances were calculated (Table 12). The highest intra-cluster distance was found in cluster IV (0.785) composed of eight genotypes followed by cluster III (0.648) with seven genotypes. The lowest intra-cluster distance was found in cluster V (0.039) composed of seven genotypes. These result revealed that the genotypes in cluster IV were distantly related; on the other hand the genotypes in cluster V were closely related.

4.5.3 Non-Hierarchical Clustering

Using co-variance matrix with the application of non-hierarchical clustering, the 31 genotypes were grouped into five clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Golakiya and Makne (1991) while assessing genetic diversity of 23 groundnut genotypes and grouped them into six clusters. Reddy and Reddy (1987) reported on 48 genotypes of which were grouped into 11 clusters. On the other hand Baydar and Bayraktar (1994) reported 35 genotypes which were divided into 6 clusters of different genetic divergences. Badignnavar *et al.* (2002), Joel and Mylsamy (1998), Islam *et al.* (1995) were found the same results Compositions of different clusters with their corresponding genotypes in each cluster are presented in Table 13.

Cluster IV had maximum number of genotypes (8) followed by II, III and V contain seven genotypes each and lowest number of genotypes were in cluster I (2) (Table 10). From the clustering mean values (Table 11), it was observed that the mean value of cluster I ranked first for plant height (109.97 cm), number of primary branch (3.38), number of secondary branch (2.87), number of siliqua per

plant (138.95), length of siliqua (7.33 cm), number of seeds per siliqua (23.33) and seed yield per plant (9.65).

Cluster II was composed of seven genotypes namely G1, G2, G9, G10, G17, G20 and G20 (Table 10). Cluster II had the highest cluster mean for days to 50% flowering (37.43) (Table11).

Cluster III constituted of seven genotypes namely G3, G5, G15, G21, G24, G25 and G28 (Table 10). This group possessed genotypes with the highest cluster mean for 1000 seed weight (3.11) (Table 11).

Cluster IV had the maximum number of (8) genotypes namely G7, G11, G12, G13, G18, G19, G29 and G31 (Table 10). This group does not have highest cluster mean for any of the characters (Table 11).

4.6 Canonical Variate Analysis (CVA)

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 13 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.* (1987) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in mustard. Results indicated that the highest inter-cluster distance was observed between clusters I and III (15.405), followed by between cluster I and IV (11.366), I and V (11.250), II and III (9.421) (Table 13). The lowest inter-cluster distance was observed between cluster III and IV (4.043), followed by IV and V (4.391) and I and II (5.995). However, the maximum inter-cluster distance was observed between the clusters I and III (15.405) maintaining more distance than other clusters. Genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population.

Table 10. Ten highest and ten lowest inter genotypic distance among 31 *Brassica napus* L. (BC_1F_2) genotypes

Sl. No.	Genotype combinations	Distances
10 highest inter genotypic distances		
01.	G6-G21	0.864
02.	G1-G21	0.834
03.	G14-G26	0.797
04.	G21-G26	0.789
05.	G26-G30	0.789
06.	G9-G21	0.786
07.	G19-G26	0.784
08.	G15-G26	0.778
09.	G17-G26	0.774
10.	G26-G31	0.767
10 lowest inter genotypic distances		
01.	G1-G9	0.131
02.	G5-G11	0.130
03.	G4-G23	0.129
04.	G15-G19	0.128
05.	G16-G23	0.124
06.	G5-G7	0.119
07.	G20-G27	0.107
08.	G7-G11	0.106
09.	G17-G30	0.102
10.	G23-G27	0.098

Table 11. Distribution of 31 genotypes of *Brassica napus* L. (BC_1F_2) genotypes.

Cluster	Number of genotypes	Name of genotypes
I	2	G6, G8
II	7	G1 , G2, G9, G10, G17, G20, G26
III	7	G3, G5, G15, G21, G24, G25, G28
IV	8	G7, G11, G12, G13, G18, G19, G29, G31
V	7	G4, G14, G16, G22, G23, G27, G30

Table 12. Cluster mean for 10 characters of 31 genotypes *Brassica napus* L . (BC_1F_2) genotypes

Characters	Cluster				
	I	II	III	IV	IV
Days to 50% flowering	37.00	37.43	37.38	37.17	36.81
Days to maturity	91.17	90.90	91.19	90.54	90.38
Plant height (cm)	109.97	107.07	99.40	104.54	98.24
Number of primary branches/plant	3.38	3.24	3.21	3.28	3.09
Number of secondary branches/plant	2.87	2.12	1.99	1.89	2.11
Number of siliquae/plant	138.95	124.68	102.10	110.86	119.42
Length of siliqua (cm)	7.33	7.16	6.75	6.77	7.14
Number of seeds per siliqua	23.33	22.48	20.37	21.04	22.01
1000 seed weight (g)	2.97	3.06	3.11	3.06	3.11
Seed yield/plant (g)	9.65	8.67	6.50	7.18	8.21

Table 13. Average intra and inter cluster distances (D^2) of 31 *Brassica napus* L. (BC_1F_2) genotypes

	I	II	III	IV	V
I	**1.139**				
II	5.995	**0.424**			
III	15.405	9.421	**0.648**		
IV	11.366	5.378	4.043	**0.785**	
V	11.250	6.014	6.720	4.391	**0.039**

Similar reports were also made by Singh *et al.*, (1996). Zhang *et al.*, (1987) reported that the greater genetic distances implying higher heterosis than those with similar genetic distances. The intra-cluster distance varied from 0.039-0.785. Result of different multivariate analysis were superimposed in Figure 3 from which it might be concluded from the above results that different multivariate techniques supplemented and confined one another.

A two-dimensional scatter diagram was constructed using component I in X-axis and component II in Y-axis, reflecting in the relative position (Figure 2). As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster III was more diverse from the genotypes of cluster I. It is assumed that the maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level production. In the present study the maximum distance existed between clusters I and cluster III (Figure 3). Mian and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis. Keeping this in view, it appears that the crosses between the genotypes belonging cluster I with cluster IV and genotypes in cluster I with cluster V might produce high heterosis for yield as well as for earliness. Also the crosses between genotypes from cluster II with cluster III might produce high level of segregating population. So the genotypes belonging to cluster I and cluster IV, cluster I and cluster V and cluster II and cluster III have been selected for future hybridization program.

4.7 Contribution of Characters towards Divergence of the Genotypes

Contribution of characters towards divergence of the genotypes is presented in table 13. The vector-I (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of the differentiation were days to 50% flowering (0.100), number of primary branches per plant (1.905), number of seeds per siliqua (1.326) and 1000 seed weight (5.324). In vector-II (Z_2), days to

maturity (0.456), plant height (0.612), number of secondary branches per plant (2.632), length of siliqua (5.071) and seed yield per pant (3.678) were important but plant height, number of secondary branches per plant, number of siliqua per plant, length of siliqua and seed yield per plant played only a minor role in the first axis of differentiation. The role of days to maturity and number of primary branch in both the vectors were important components for genetic divergence in these materials.

4.8 Comparison of Different Multivariate Techniques

The clustering pattern of D^2 analysis through non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 (principle component score I) and Z_2 (principle component score II) vectors of the principle component analysis. The D^2 and principle component analysis were found to be alternative methods in giving the information regarding the contribution of characters towards divergence in mustard.

4.9 Selection of Parents for Future Hybridization

A higher heterosis could be produced from the crosses between genetically distant parents. Selection of genetically diverse parents with specific objectives is an important step for hybridization program. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G6 for higher seed yield per plant and for seeds per siliqua, G8 for the highest plant height and number of siliqua per plant from cluster I; G1 for the highest number of seeds per siliqua and seed yield per plant from cluster II; G21 for the highest 1000 seed weight; G24 for higher number of siliqua per plant from cluster III; G16 for the highest number of seeds per siliqua from cluster V were found promising. Therefore considering group distance and other agronomic performance genotypes G1, G6, G8, G16, G21, G24 and inter genotypic crosses between G6 and G21; G1 and G21; G14 and G26; G21 and G26 may be suggested for future hybridization program to develop high yielding varieties with early maturity.

Table 14: Latent vectors for 10 principal component characters of 31 *Brassica napus* L. ($BC_1 F_2$) genotypes

Characters	Vector 1	Vector 2
Days to 50% flowering	0.100	-0.137
Days to maturity	0.221	0.456
Plant height (cm)	-0.374	0.612
Number of primary branches/plant	1.905	0.587
Number of secondary branches/plant	-1.819	2.632
Number of siliquae/plant	-0.127	-0.438
Length of siliqua (cm)	-1.069	5.071
Number of seeds per siliqua	1.326	-2.649
1000 seed weight (g)	5.324	-3.434
Seed yield/plant (g)	-2.547	3.678

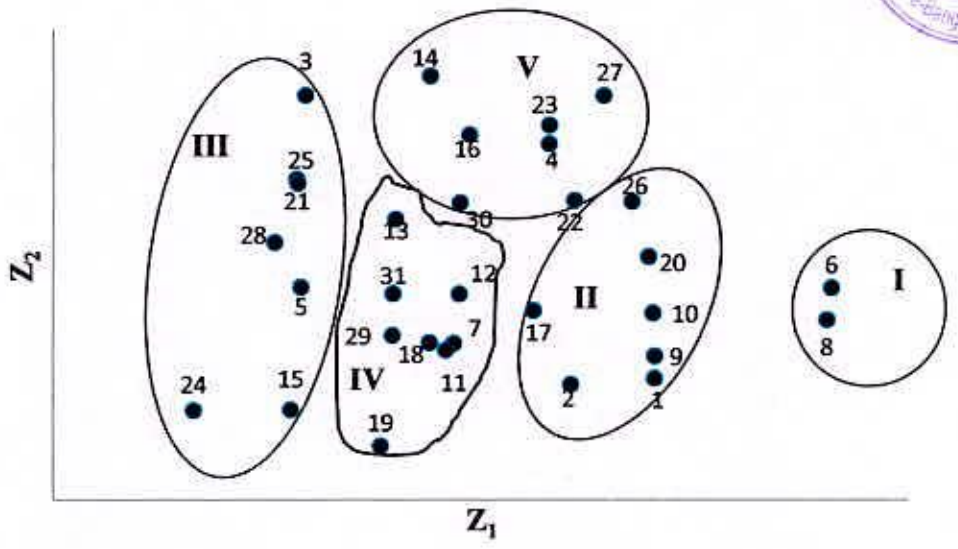


Figure 3: Scatter distribution of 31 *Brassica napus* L. genotypes based on their principle component scores superimposed with clustering

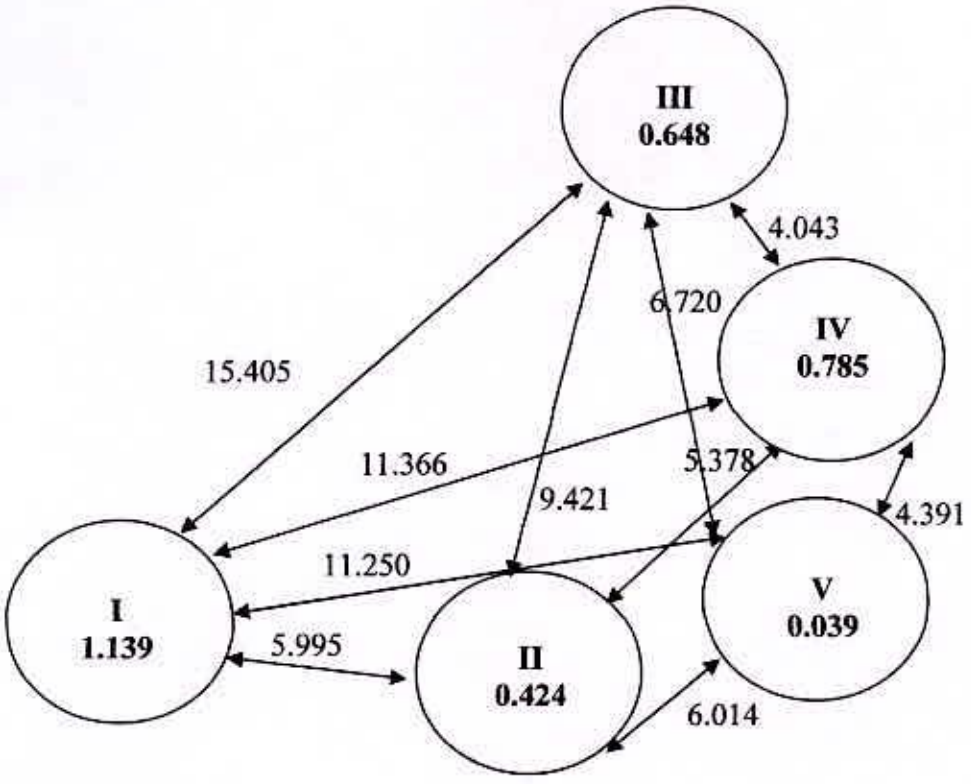


Fig. 4: Diagram showing intra and inter cluster distances of 31 *Brassica napus* L. (BC_1F_2) genotypes

CHAPTER IV

SUMMARY AND CONCLUSION

Inter-genotypic variability, correlation and path analysis were studied in 31 *Brassica napus* L. BC_1F_2 lines obtained through inter varietal crosses of *Brassica napus* L. at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2011 to March 2012. Seeds were sown in the field in Randomized Complete Block Design (RCBD) with three replications. Data on Plant height (cm), number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity, number of Siliqua per plant, 1000 seed weight (g), number of seeds per siliqua, Siliqua length (cm), seed yield per plant (g) were recorded. There were highly significant variations among the different genotypes for almost all the characters studied.

The highest mean value was observed for number of siliqua per plant (115.74). This character also exhibited the highest range of variation (94.40-139.10) indicated that all the genotypes showed wide range of variation in respect of this character. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. However, these differences were in case of days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, length of siliqua indiicating greater influence on environment for the expression of these characters. Among these characters number of primary branches per plant, number of siliqua per plant, number of seeds per siliqua, 1000 seed weight and seed yield per plant showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters. All these characters showed low to moderate phenotypic and genotypic co-efficient of variation except days to maturity. Among the characters the highest genotypic co-efficient of variation was recorded in seed yield per plant (14.67) followed by number of secondary branches per plant (11.49), number of primary branches/plant (11.41), number of siliqua per plant (9.12), number of siliqua per plant (9.00) in order of merit.

Heritability in broad sense was low to high for all the characters studied and it ranged from 7.18% to 84.81 % which indicated that selection based on phenotypic expression of any character for breeding could be effective. The genetic advance was low to moderate for almost all the characters. Thus, the genotypes which performed well in various characters were due to genetic reasons and have a possibility for improvement through selection in the subsequent generations.

The characters between days to maturity and days to 50% flowering, plant height and days to maturity, plant height and number of seeds per plant, plant height and number of seeds per siliqua, number of primary branch and number secondary branch per plant, number of secondary branch per plant and number siliqua per plant, number of siliqua per plant and yield per plant were highly positively correlated. Path coefficient analysis showed that days to maturity, plant height, number of secondary branch per plant, number of siliqua per plant, length of siliqua and number of seed per siliqua had positive indirect effect on seed yield per plant.

Multivariate analysis was performed through Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis using GENSTAT 513 and STATA software program. As per PCA, D^2 and cluster analysis, the genotypes grouped into five clusters. Five clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Inter genotypic distances obtained from Principal Coordinate Analysis showed that the highest distance (0.864) was observed between the genotypes G6 and G21 and the lowest distance was observed between the genotypes G23 and G27 (0.098). The highest intra-cluster distance was found in cluster I (1.139) which composed of 2 genotypes and the lowest in cluster V (0.039). The highest inter-cluster distance was observed between cluster I and cluster III (15.405) followed by cluster I and cluster IV (11.366) and cluster I and V (11.250). The lowest inter-cluster distance observed between cluster III and IV (4.043) followed by cluster IV and cluster V (4.391). Genotypes included in cluster I and II were important for seed yield per

plant, highest plant height and number of seeds per siliqua; cluster III for highest number of siliqua per plant and cluster IV were found promising for highest seeds per siliqua.

Considering cluster distance, inter genotypic distance and other agronomic performance G6 and G8 from cluster I; G1 from cluster II; G21 and G24 from cluster III and G16 from cluster V may be considered to be better parents for future uses in hybridization program to develop high yielding varieties with early maturity.

REFERENCES

Abraham V. (1994) Rate of out-crossing in Indian mustard, *Brassica juncea*. *Cruciferae Newsl.* **16**:69-70.

Adnan Nasim, Farhatullah, Sidra Iqbal, Sikandar Shah, Syed Muhammad Azam. (2013). Genetic Variability and Correlation Studies for Morpho-physiological Traits in *Brassica Napus* L. *Pak. J. Bot.* **45**(4):1229-1234.

Al-jibouri H.A., Miller P.A., Robinson H.F. (1958) Genotypic and environmental variances and covariancea in upland cotton cross of inter specific origin. *Agron. J.* **50:** 633-636.

Alam M.S., Rahman A.R.M.S., Khair A.B.M.A. (1985) Genetic variability and character association in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Agric.* **10**: 9-16.

Ali N., Javidfar F., Elmira J.Y., Mirza M.Y. (2003) Relationship among yield components and selection criteria for yield improvement in winter rapeseed (B. napus L.). *Pak J Bot.* **35**:167-174.

Allard R.W. (1960) Principles of Plant Breeding. John Willey and Sons. Inc. New York:**36.**

Ana M., Radovan M., Anto M., Zvonimir Z., Sonja I., Mirjana J. (2008) Correlation and Path Analysis of Quantitative Traits in Winter Rapeseed (*Brassica napus* L.). *Agriculturae Conspectus Scientificus.* **73**:13-18.

Anand I.J., Rawat D.S. (1984) Genetic diversity, combining ability and heterosis in brown mustard. *Indian J. Genet. Pl. Breed.* **44** (2):226-234.

Andrahennadi C.P., Weerasena L.A., Aberyratne M.D.R.S. (1991) Evaluation of brown mustard germplasm in Srilanka. *Cruciferae Newsl.* **14-15**:62-63.

Ashana A.N., Pandey V.K. (1980) Genetic divergence in linseed. *Indian J. Genet. Pl. Breed.* **40**:247-250.

Azad M.A.K., Hamid M.A. (2000) Genetic variability, character association and path analysis in groundnut (*Arachis hypogaea* L.). *Thai J. Agric. Sci.* **33**:153-157.

Badignnavar A.K., Kale D.M., Murty G.S.S. (2002) Genetic variability and diversity in groundnut genotypes. *Pl. Breed.* **121**: 348-353.

Banerzee H.T., Bhattacharjee H., Das M. (1968) A note on the relationship between growth and yield of yellow sarson var. Prain. *Indian j. Agron.* **13**:203-204.

Baydar H., Bayraktar N. (1994) Correlation and path coefficientanalysis among quantitative characters on Virginia type peanut(*Arachis hypogaea* L.) cultivars Ankara Universities Ziraat Fakiiltesi Yilligi. **44:** 59-64.

BBS. (2012) Monthly Statistical Bulletin of the Bangladesh Bureau of Statistics (August). Administration and MIS Wing, Bangladesh Secretariat, Dhaka.

Behl R.K., Chaudhary B.D., Singh R.P., Yadava T.P. (1989) Oil yield determinants in Brassica juncea under dryland conditions. In: Vorträge für Pfl anzenzüchtung 15. XII EUCARPIA Congress. Göttingen. Germany:**11-14.**

Belete Y.S. (2011) Genetic variablity, correlation and path analysis studies in Ethiopian mustard (*Brassica carinata* A. Brun) genotypes. *Int. J. Pl. Breed. and Genet.* **5**:328-338.

Bhardwaj R.P., Singh R.R. (1969) Morphological and genetic variability in brown sarson (*B. campestris* var. Brown sarson). *Madras Agric. J.* **56**: 28-31.

Biswas K.P. (1989) Performance evaluation of 18 genotypes of oleriferous Brassica. Proceeding of the 14th Annual Bangladesh Sci., Conf.

Burton G.W. (1952) Quantitative inheritance in grass pea. Proc. 6th Grassl. Cong. **1**:277-283.

Campbell D.C., Kondra Z.P. (1978) Relationship among growth patterns, yield components and yield of rape seed. *Canadian. J. Pl. Sci.* **58**:87-93.

Chandola R.F., Dixit P.K., Sharina K.N., Saxena D.K. (1977) Variability in B. juncea under three environments. *Indian J. Agric. Sci.* **47**:680-683.

Chauhan J., Singh P. (1985) Association of some morphological determinates with seed yield in Toria (*B. campestris* L. var. Toria). . Thesis Abstract, XII: 42-43.

Chen C., Hau K.K., Liu C.P., Lin M.S. (1983) Selection criteria for yield improvement in rape. Journal of the Agricultural association of China. **124**:63-73.

Chey P., Thurling N. (1989) Identification of genes controlling siliqua length in spring rapeseed and their utilization for yield improvement. *Pl. Breed.* **103**:54-62.

Chowdhury B.R., Joshi P. (2001) Genetic diversity in advanced derivatives of Brassica interspecific hybrids. Kluwer Academic Publishers of the Netherlands. **121:**1-7.

Chowdhury L.B., Prasad B. (1968) Genetic variation and heritability of quantitative characters in Indian mustard. *Indian J. Agric. Sci.* **38**: 820-825.

Chowdhury B.D., Thakural S.K., Singh D.P., Singh P. (1987) Genetics of yield and its components in Indian mustard. *Narenda Deva J. Agric. Res.* **3**:37-43.

Chowdhury P.K., Singh P., Kumar A. (1990) Association and interdependence of morphophysiological characters under moisture stress in *Brassica Beitrage Zar Tropichen Landurishaft.* **18**:43-47.

Comstock K., Robinson P.R. (1952) Estimation of genetic advance. *Indian J. Hill.* **6** :171-174.

Das M.L., Rahman A. (1989) Correlated response and path analysis in mustards (*Brassica campestris* L.). *Bangladesh J. Agril. Res.* **7**:37-41.

Das M.L., Rahman A. (1994) Evaluation of mutants of rape seed for earliness, seed yield and response to change environments in M_2 generation. *Bangladesh J. Nuclear Agric.* **10**:75-80.

De R.N., Seethara R., Sinha M.K., Banarjee S.P. (1988) Genetic divergence in rice. *Indian J. Genet. Pl. Breed.* **48**:189-194.

Degenhart D.F., Kondra Z.P. (1984) Relationships between seed yield and growth characters, yield components and seed quality of summer-type oilseed rape (*Brassica napus L.*). *Euphytica.* **33**:885-889.

Deshmukh S.N., Basu M.S., Reddi P.S. (1986) Genetic variability, character association and path coefficient of quantitative traits in Virginia bunch varieties of groundnut. *Indian J. Agric.* **56**:816-821.

Dewey D.R., H. L.K. (1957) Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51**: 515-518.

Dhillon S.S., Labana K.S., Ahuja K.L. (1990) Association analysis in Indian mustard. *J. Res.* **27**:385-388.

Digby P., Galway N., Lane P. (1989) GENSTAT 5.0, A second course. Oxford science publications, Oxford:103-108.

Edris K.M., Islam A.T.M.T., Chowdhury M.S., Haque A.K.M.M. (1979) Detailed Soil Survey of Bangladesh Agricultural University Farm, Mymensingh. Dept. Soil Survey, Govt. People's Republic of Bangladesh:118

FAO. (2011) Production Year Book, Food and Agricultural Organization of United Nations, Rome, Italy. **57:**115-133.

Fischer R.A., Yates F. (1963) Statistical Tables for Biological, Agricultural and Medical Research. Oliver and Boyd, Edinburg.

Ghosh R.K., Chaterjee B.N. (1988) Path analysis of important growth functions of Indian mustard. *J. Agron. and Crop Sci.* **160:**112-118.

Gilani M.M., Hussain B., Aziz K. (1993) Estimation of correlation and genetc variability in various turnip rape types (*Brassica campestris* L. var. sarson). *J. Agric. Res.* **31**(3):267-271.

Golakiya P.R., Makne V.G. (1991) Genetic diversity in Spanish bunch groundnut. *J. Maharastra Agric. Univ.* **16**: 337-339.

Grafius J.E. (1959) Heterosis in barley. *Agron. J.* **51**:515-518.

Grosse C., Geisler G. (1988) Variability in the physiological yield characteristics and assortment of water rape cultivars yield components. Milteilungen der pflangen baurissenschaften. **1**:67-69.

Guo J.C., Guo X.X., Liu R.H. (1987) A study of correlations between yield components in mutants of *Brassica napus* L. *Oil Crops of China.* **2**:23-25.

Gupta M.L., Labana K.S., Badwal S.S. (1987) Correlation and path coefficient of metric traits contributing towards oil yield in Indian mustard Proceedings of the 7th International Rapeseed Congress. Poland:pp. 11-14.

Gupta S.K., Labana K.S. (1989) Triple test cross analysis for some physio morphological traits in oil seed rape. *Indian J. Genet.Pl. Breed.* **49**: 365-367.

Han J.X. (1990) Genetic analysis on oil content in rapeseed (*Brassica napus* L.). *China Oilseed Crops.* **2**:1-6.

Hossain, K. G. (1988). Genetic variability and character association in groundunt. M. Sc. (Ag) Thesis. Department of Genetics and plant Breeding Bangladesh Agricultural University, Mymensingh.

Islam M.S., Rasul M.G. (1998) Genetic parameters, correlation and path coefficient analysis in groundnut (*Arachis hypogaea* L.) *Bangladesh J. Sci. Ind. Res.* **33**:250-252.

Islam M.S., Islam M.O. (2000) Genetic diversity in rapeseed and mustard (*Brassica* sp.). *Bangladesh J. Pl. Breed. Genet.* **13**: 25-30.

Jagadev P.N., Samal K.M., Lekha L. (1991) Genetic Divergence in rape mustard *Indian J. Genet. Pl. Breed.* **13**:25-30.

Jain A.K., Tiwari A.S., Kushwah V.S. (1988) Genetics of quantitative traits in Indian mustard. *Indian J. Genet. Pl. Breed.* **48:** 117-119.

Joel A.J., Mylsamy V. (1998) Genetic divergence in groundnut. *Madras Agric. J.* **85:** 134-135.

Johnson H.W., Robinson H.F., Comstock R.E. (1955) Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**:314-318.

Kakroo P., Kumar S. (1991) Genetic determination of seed yield through its components in Indian mustard Thesis Abstract, XVII-I:82.

Katiyar A.P., Singh B. (1974) Inter-relationship among yield and its components in Indian mustard. *Indian J. Agric. Sci.* **44**.

Katiyar R.K., Chamola R., Singh H.B., Tickoo S. (2004) Heterosis and combining ability analysis for seed yield in yellow sarson (*Brassica campestris*). *Brassica.* **6:** 23-28.

Khan A., Rahim M., Khan A., Khan M.I., Riaz S. (2000) Correlation and path analysis coefficient analysis for yield contributing parameters in *Brassica napus*. *Pakistan J. Agric. Res.* **16:**127-130.

Khera M.K., Singh P. (1988) Sensitivity and performance of some Brassica napus genotypes in stress and non-stress environments. *Crop Improvements.* **15**: 209 - 211.

Khulbe R.K., Pant D.P. (1999) Correlation and path coefficient analysis of yield and its componenets in Indian mustard. *Crop Res. Hisar*. **17**:209-211.

Kis D., Maric S., Juric T., Antunovic M., Guberac V. (2006) Performance of diff erent eruca acid type oil seed rape cultivars in a Croatian agro-environment. Cereal Research Communications. **34**(1):437-440.

Kudla M. (1993) Comparative analysis of winter swede rape genotypes. Biuletyn Instytutu Hodowli Roslin. **190:**99-107.

Kumar C.H.M.V., Arunchalam V., Rao P.S.K. (1996) Ideotype and relationship between morphological characters and yield in Indian mustard (B. juncea). *Indian J. Agric. Sci.* **66:** 14-17.

Kumar C.H.M.V., Arunchalam V., Rao P.S.K. (1996) Ideotype and relationship between morphological characters and yield in Indian mustard (*B. juncea*). *Indian J. Agric. Sci*. **66:** 14-17.

Kumar N., Bisht J.K., Joshi M.C. (1988) Correlation and discriminant function analysis in Indian mustard. *Indian J. Agric. Sci.* **58**:51-52.

Kumar P., Yadava T.P., Yadav A.K. (1984) Association of seed yield and its component traits in the F_2 generation of Indian mustard. *Indian J. Agric. Sci.* **54**:604-607.

Kumar P., Yadava T.P., K. Y.A. (1991) Association of seed yield and its component traits in the F2 generation of Indian mustard. *Indian J. Agric. Sci.* **54** 604-607.

Kumar R., Ghosh J., Sah J.N. (1998) Variability and correlation studies in mutant cultures of groundnut. *J. Appl. Biol.* **8**: 20-23.

Kumar S., Sangwan R.S., Yadava I.S. (1999) Path coefficient analysis in *Brassica* species under rainfed conditions. *Cruciferae Newsl.* **24**:59-60.

Kumar V., Singh D. (1994) Genetics of yield and its components in Indian mustard (*B. juncea* L. Czern & Coss). *Crop Res.* **7**:243-246.

Kumar V., Singh D. (1994) Genetics of yield and its components in Indian mustard (*B. juncea* L. Czern & Coss). *Crop Res.* 7:243-246.

Kuriakose K.P., Joseph C.A. (1986) Path analysis and selection index in groundnut. *Agric. Res. J. Kerala.* **24**:111-117.

Labana K.S., Chaurasia B.D., Singh B. (1980) Genetic variability and inter-character associations in the mutants of Indian mustard. *Indian J. Agric. Sci.* **50:** 803-806.

Labana K.S., Ahuja K.L., Banga S.S. (1987) Evaluation of some ethiopian mustard (*B. carinata*) genotypes under Indian conditions. In 7th International rapeseed congress, poznan, Poland:115.

Labana K.S., Ahuja K.L., Banga S.S. (1987) Evaluation of some ethiopian mustard (*B. carinata*) genotypes under Indian conditions. In 7th International rapeseed congress, poznan, Poland:115.

Lebowitz R.J. (1989) Image analysis measurements and repeatability estimates of siliqua morphological traits in *B. campestries. Euphytica* **43:** 113-116.

Lekh R., Hari S., Singh V.P., Raj L., Singh H. (1998) Variability studies in rapeseed and mustard. *Ann. Agril. Res.* **19**:87-88.

Li D.R. (1999) Heterosis and Hybrid Seed Production in Agronomic Crops (pp. 217-260). New York - London - Oxford: Food Products Press.

Lodhi G.P., Singh R.K., Sharma S.C. (1979) Correlated response in brown sarson. *Indian j. Genet.* **39**:373-377.

Mahto N.R. (1996) Diversity in Indian mustard. *Indian j. Agron.* **45**:95-98.

Malek M.A., Das M.I., Rahman A. (2000) Genetic variablity, character assiciation and path analysis in rape seed. *Bangladesh J. Agril. Sci.* **27**:25-29.

Malik V., Singh H., Singh D. (1995) Gene action of seed yield and other desirable characters in rapeseed. *Annal. Biol (Ludhiana).* **11**:94-97.

Marjanovic-Jeromela A., Marjanovic R., Mijic A., Zdunic Z., Ivanovska S., Jankulovska M. (2007) Correlation and path analysis of quantitative traits in winter rapeseed (*B. napus* L.). *Agri. Conspectus Scientificus.* **73**:13-18.

Masood T., Gilani M.M., Khan F.A. (1999) Path analysis of the major yield and quality characters in Brassica campestris. . *JAPS. J. Animal Pl. Sci.* **9**:69-72.

Mishra L.K., Yadav R.K. (1992) Genetic variability and correlation studies in summer groundnut. *Adv. Pl. Sci.* **5**: 106-110.

Mishra R.M., Kouth G.K., Bilaiya S.K. (1987) D^2 and metrograph analysis in soybean. *J. Oilseed Res.* **4**:103-107.

Mitra S.K., Saini S.A. (1998) D2 and metroglyph analysis in mustard. *Indian J. Genet. Pl. Breed.* **50:** 120-125.

Nadaf H.L., Habib A.F., Goud J.V. (1986) Analysis of Genetic Divergence in bunch groundnut. *J. Oilseeds Res.* **3**:37-45.

Nanda R., Bhargava S.C., Tomar D.P.S. (1995) Rate and duration of siliqua and seed filling and their relation to seed yield in Brassica species. *Indian J. Agric. Sci.* **64**: 227-232.

Nandpuri B.S., Singh S., Lal T. (1973) Studies on the genetic variability and correlation of some economic characters in tomato. *J. Res.* **10**:316-321.

Nasim M., Rahman L., Quddus M.A., Shah-E-Alam M. (1994) Correlation and path analysis in *Brassica campestris* L. *Bangladesh J. Agril. Sci.* **21**:15-23.

Olsson G. (1960) Species crosses within the genus Brassica. II. Artificial B. napus L. *Hereditas.* **46**:351-396.

Olsson G. (1990) Species crosses within the genus Brassica. II. Artificial B. napus L. *Hereditas.* **46**:351-396.

Ozer H., Oral E., Dogru U. (1999) Relationship between yield and yield components on currently improved spring rapeseed cultivars. *Turkish. J. Agric. Fores.* **23:**603-607.

Panse V.G. (1957) Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet Pl. Breed.* **17**:318-328.

Paul N.K., Joarder O.I., Eunus A.M. (1976) Genotypic and phenotypic variability and correlation studies in *B. juncea* L. . *Zeitschriflfur pflazenzuchtun.* **77:** 145-154.

Rahman L. (1981) Oilseed research and development activities at the BAU. Proc. of the workshop on oil crop improvement, BARI, Oilseed Research Project. Ed. by Khaleque, M.A., A.B.M, Abdul Khair, Md. Ali Akber and Md. Moszammal Haque:25.

Rahman L., Quddus M.A., Rahman M.A. (1993) Recent advances in advances in oilseeds breeding in Bangladesh. Advances in Crop Science Proc. of the 1st Biennial conference of the Crop Science Society of Bangladesh held during 18-20 January 1992.

Rakow G., Woods D.L. (1987a) Outcrossing in rape and mustard under Saskatchewan prairies conditions. *Canadian. J. Pl. Sci.* **67**:147-151.

Rakow G., Woods D.L. (1987b) Outcrossing in rape and mustard under Saskatchewan prairie conditions. *Canadian. J. Pl. Sci.* **67**:147-151.

Ramanijan S., Rai B. (1963) Analysis of yield components in *Brassica campestris* var. yellow sarson. *Indian J. Genet.* **23:**312-319.

Rameeh V. (2011) Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components. *J. Oilseed Brassica* **2**:56-60.

Reddy V.R.G., Singh B.N., Rai B. (1987) Analysis of genetic divergence in spreading varieties of groundnut. *Crop Improv.* **14** :149-152.

Sabaghnia N., Dehghani H., Alizadeh B., Mohghaddam M. (2010) Interrelationships between seed yield and 20 related traits of 49 canola (B. napus L.)genotypes in non-stressed and water-stressed environments. *Spanish J. Agri. Res.* **8**:356-370.

Saini H.C., Sharma R.P. (1995) Model plant architecture through association and path coefficient analysis in Indian colza. *Indian J. Agric. Res.* **29**:109-115.

Shabana R., Shrief S.A., Geisler G. (1990) Correlation and path analysis for some new release spring rapeseed cultivars grown under different competitive systems. *J. Agron. and Crop Sci.* **65**:138-143.

Shanmugam A.S., Rangasamy S.R.S. (1982) Multivariate Analysis of genetic divergence in black gram. *Madras Agric. J.* **69** :701-706.

Sharma S.K. (1984) Variation and correlation studies in Indian mustard (*B. juncea*). Thesis Abstract **10**: 146-147.

Shen J.X., Fu T.D., Yang G.S. (2002) Heterosis of double low self incompatability in oil seed rape (*Brassica rapa* L.). *Agril. Sci. China.* 7:732-737.

Shivahare M.D., Singh A.B., Chauhan Y.S., Singh P. (1975) Path coefficient analysis of yield component in Indian mustard. *Indian J. Agric. Sci.* **45**:422-425.

Shrivastava P.P., Salara B.S., Gowda M.V.C. (1983) Variability and correlation studies in groundnut (*Arachis hypogea*). *Crop Improv.* **25**:122-123.

Shrivastava P.P., Singh P., Dixit R.K. (1987) Combining ability analysis of yield and developmental traits in Indian canola (*Brassica campestris* L. var. yellow sarson prain). *Farm Sci. J.* **2**:170-174.

Sindhu J.S., Ahamed S., Singh M.B., Singh K.P. (1989) Multivariate Analysis in black gram. *Legume Res.* **12**:35-37.

Singh A., Yadava T.P., Asawa B.M., Gupta V.P. (1978) Note on path coefficient analysis in Indian mustard. *Indian J. Agric. Sci.* **48**:622-623.

Singh B.D. (1993) Plant Breeding in Biometrical Techniques. Plant Breeding. Kaylani Publishers 100-125.

Singh D.P., Singh D., Singh S.P., Singh A.B., Mishra S.N. (1969) Relationship among some important agronomic characters in Indian mustard. *Indian J. Agric. Sci.* **39**.

Singh H. (1986) Genetic variability, heritability and drought Indices analysis in Brassica species. *J. Oilseed Res.* **3:** 170-177.

Singh H., Yadav A.K., Yadava T.P. (1989) Morphophysiological attributes in relation to seed yield in Indian mustard. *Haryana Agric. Univ. J. Res.* **15** 295-299.

Singh P., Khera M.K., Gupta V.P. (1991) Variability and correlation studies for oil and seed yield in gobhi sarson. *Crop Improv.* **18**:99-102.

Singh P.K., Chaudhary B.D. (1985) Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India:318.

Singh R.P., Singh D.P., Chaudhury B.D. (1987) Morphological variation in Indian mustard. *Annal. Biol.* **3:** 26-31.

Singh S.B., Singh J.P. (1999) Correlation analysis of growth and yield components in groundnut. *J. Maharastra Agric. Univ.* **17:** 224-226.

Sovero M. (1993) Rapeseed, a new oilseed crop for the United States. In J. Janick and J. E. Simson (eds), New Crops, New York: Wiley:302-307.

Tak G.M., Patnaik M.C. (1977) Genetic variation and heritability on the 3 forms of *B. campestris. Indian J. Agric. Res.* **11**: 89-93.

Tak G.M., Patnaik M.C. (1977) Genetic variation and heritability on the 3 forms of B. campestris. *Indian J. Agric. Res.* **11**: 89-93.

Thakral N.K. (1982) To study the association of some morphophysiological attributes with yield of toria. Thesis Abstract. **8:** 66-67.

Thurling N. (1974) An evaluation of an index method of selection for high yield in turnip rape, *B. campestris* L. spp. *Euphytica.* **23**: 321-331.

Thurling N. (1983) Variation in pod length in spring rape (B. napus) and its relationship to yield. In proceedings, Australian Plant Breeding conference, Adelaide, South Australia:14-18.

Thurling N., Das L.D.V. (1980) The relationship between pre-anthesis development and seed yield of spring rape (*Brassica napus* L.). *Australian. J. Agric. Res.* **31**:25-36.

Tyagi M.K., Chauhan J.S., Kumar P.R., Singh K.H. (2001) Estimation of heterosis in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. *Annal. Agri. Bio. Res.* **6**:193-200.

U. (1935) Genome analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization. *Japan. J. Bot.* 7:389-452.

Uddin M.J. (1994) Genetic divergence in mustard. *Bangladesh J. Pl. Breed. Genet.* 7:23-27.

Uddin M.J., Chowdhury M.A.Z., Sultan M.K., Mitro B.N. (1995) Genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.). *Bangladesh J. Sci. Ind. Res.* **30:** 235-241.

UN. (1935) Genome analysis in Brassica with special reference to the experimental formation of B. napus and peculiar mode of fertilization. *Japan. J. Bot.* 7:389-452.

Ushakumari R.M., Subramanian M., Subramaniam. (1991) Studies on coefficient of variation and heritable components of some quantitative characters of Brinjal. *Indian J. Hort.* **48**:75-78.

Varshney S.K., Rai B., Singh B. (1986) Component analysis of harvest index in Brassica oilseeds. *Indian J. Agric. Res.* **20** :129-134.

Venkatramana P., Sheriff R.A., Janakiraman N. (2001) Assessment of groundnut germplasm and isolation of elite genotypes for improvement. *J. Soils Crops.* **11**: 156-160.

Wan Y.L., Hu G.C. (1983) Studies on heritability, genetic correlations and genetic advances of the major characters in rape. *Chinese oil crops*. **1**:1-7.

Wang J.S., Wang X.F., Zhang Y.F., Zhang Z., Tian J.H., Li D.R. (2007) Study on heterosis among subspecies or varieties in B. campestris L. In Proceedings the 12th International Rapeseed Congress (Vol. I, pp108-110). Wuhan, China: Science Press USA Inc.

Weber, Moorthy B.R. (1952) Heritability and variability of oil content and agronomic charecterstics in the F_2 generation of soybean crosses. *Agron. J.* **44:** 202-209.

Weiss E.A. (1983) Oilseed Crops. Longman Inc. New York:660.

Wright S. (1921) Correlation and causation. *Indian J. Agric Res.* **20** 557-587.

Yadava T.P. (1973) Variability and correlation studies in B. juncea (L.). *Madras Agric. J.* **60**:1508-1511.

Yadava T.P., Yadav A.K., Singh H. (1978) A concept of plant Ideotype in Indian mustard (*B. juncea* L. Czern and Coss). 5th International Rapeseed Conf. :7.

Yadava T.P., Kumar P., Thakral S.K. (1982) Association of pod yield with some characters in groundnut. *Haryana Agric. Univ. J. Res.* **14**:75-88.

Yadava T.P., Parkash K., Thakral N.K., Yadav A.K. (1985) Genetic divergence, its relationship with heterosis and character association among seed yield and its components traits in Indian mustard. *J. Oilseed Res.* **2**:163-173.

Yarnell S.H. (1956) Cytogenetics of Vegetable crops II. *Crucifers Bot. Rev.* **22** (2):61-66.

Yin J.C. (1989) Analysis on Ecological, Physiological and Production characteristics of high quality rapeseed cultivars. *Acta Agriculture Shanghai* **5:** 25-32.

Yogendra P., Verma A.K., Haider Z.A., Mahto J., Prasad Y., Mahto J. (2002) Variability studies in Spanish bunch groundnut. *J. Res.* **14:** 91-93.

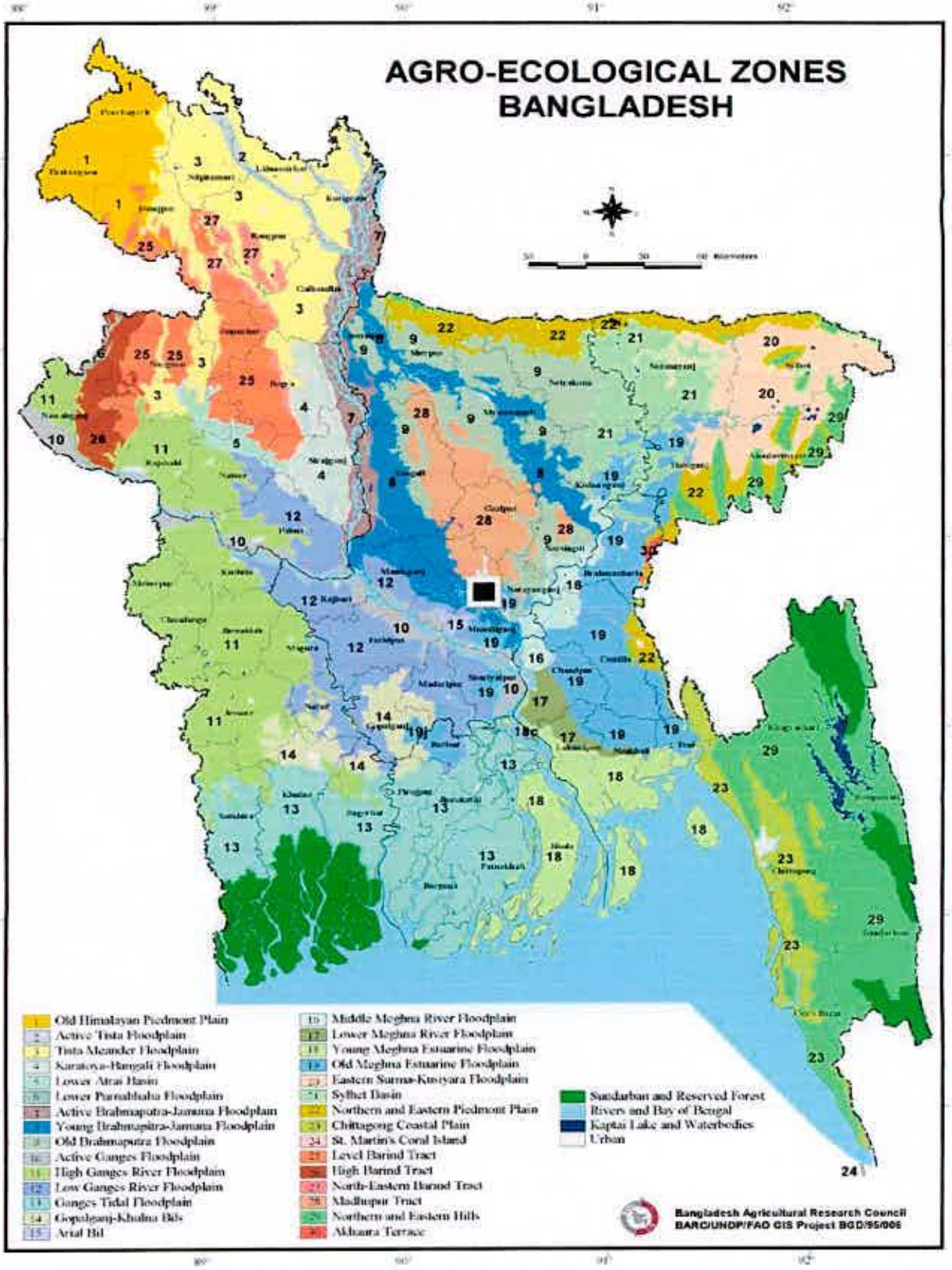
Zhang G., Zhou W. (2006) Genetic analyses of agronomic and seed quality traits of synthetic oilseed B. napus produced from inter specific hybridization of *B. campestris* and *B. olearacea*. *J. Genet.* **85**(1):45-51.

Zhau Y.M., Liu H.L. (1987) Canonical correlation analysis between characters in *B. napus*. *Cruciferae Newsl.* **12**:42-43.

Zuberi M.I., Ahmed S.V. (1973) Genetic study on yield and some of its components in *Brassica campestris* var. toria. *Crop Sci.* **13**:13-15.

APPENDICES

Appendix I. Map showing the experimental site under the study



Appendix II: Monthly average record of air temperature, rainfall, relative humidity, soil temperature and sunshine of the experimental site during the period from March, 2011 to March, 2012.

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (Total)	Sunshine (hrs.)
	Maximum	Minimum			
March, 2011	37.6	17.5	70	51	7.5
April, 2011	36.5	21.5	71	86	8.2
May, 2011	38.0	22.3	88	211	7.8
June, 2011	34.7	21.7	83	580	4.5
July, 2011	35.0	25.2	89	623	2.6
August, 2011	35.7	22.3	82	278	5.0
September, 2011	33.4	24.2	78	145	5.4
October, 2011	34.6	20.2	72	162	6.0
November, 2011	31.5	15.8	67	32	8.0
December, 2011	28.9	12.9	65	0	4.5
January, 2012	27.7	10.1	62	0	3.5
February, 2012	32.6	17.7	68	0	8.6
March, 2012	35.7	21.4	71	74	8.4

Appendix III: Physical characteristics and chemical composition of soil of the experimental plot.

Soil characteristics	Analytical results
Agroecological Zone	Madhupur Tract
P^H	6.00-6.64
Organic matter	0.88
Total N (%)	0.46
Available phosphorous	22 ppm
Exchangeable K	0.41 meq/100 g soil

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