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Raj Kumar Goswami
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

Rumjhum Phukan
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

Dikshita Gogoi
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

PK Barua
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

Priyabrata Sen
Department of Agricultural
Biotechnology, Assam
Agricultural University, Jorhat,
Assam, India

Sharmila Dutta Deka
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

Study of genetic variability and inheritance of foot length in Indian mustard [*Brassica juncea* L. (Czern and Coss.)] populations through NCD III

Raj Kumar Goswami, Rumjhum Phukan, Dikshita Gogoi, PK Barua, Priyabrata Sen and Sharmila Dutta Deka

Abstract
Indian mustard is one of the most important oilseed crops in the world. In India, it the second most popular oilseed crop after groundnut. Mustard is a species with genetic potential for high economic yield. Despite these positive attributes, mustard is not favoured in Assam because of its longer duration. In Assam, farmers prefer short duration oilseed varieties which are of medium to short height as the winter season is of shorter duration. It has been found that reduced foot length leads to shorter duration along with higher yield. With this idea, crosses were made between certain selected varieties to combine the high yielding capacity and shorter height to develop varieties for the short winter season of Assam. The study was conducted with the objective of assessing the genetic variation, inheritance of foot length and Correlation of foot length with yield and other yield attributes. Seventeen genotypes were grown in the *Rabi* 2015-16 consisting of 11 varieties and 6 F_2 lines. Crosses were made between selected parents to produce F_1 progeny and backcrosses were made to selected F_2 lines to produce backcross progeny which were subsequently grown in *Rabi* 2016-17. Analysis of variance revealed presence of significant amount of variation among the genotypes. In the first year all the characters exhibited high to moderate heritability for all the characters except maximum root length. In the second year all characters showed moderate to low heritability. D^2 analysis grouped 17 genotypes of the first year into 6 clusters and 15 genotypes of the second year into 4 clusters. Correlation analysis for the first year revealed that there is a significant negative correlation between foot length and all the characters except plant height, days to maturity and days to 50% flowering. Seed weight per plant was significantly correlated to all the characters except plant height, days to maturity and days to 50% flowering. In the second year, foot length was correlated only to number of primary branches per plant and stem thickness. Seed weight per plant was significantly correlated to all characters except days to 50% flowering, foot length, number of secondary branches, root length, biological yield per plant and harvest index. Analysis of variance for NCD III for two crosses namely TM 106 x TM 2 and DRMR 150-35 x TM 2 for the character foot length revealed significant difference among the parents in the first cross but not for the second cross. Narrow sense heritability for foot length was found to be 61% for the first cross and 35% for the second cross.

Keywords: *Brassica juncea,* foot length, correlation, NCD III, F_2 lines, backcross

Introduction
Brassica juncea (L.) Czern. & Coss. also known as Indian mustard, belongs to the mustard family, *Brassicaceae*. The family *Brassicaceae*, containing about 350 genera and 3500 species, is one of the ten most economically important plant families with wide range of agronomic traits (Christopher *et al*., 2005) [3]. In India, rapeseed-mustard occupied approximately 6.23 million hectares. The total production of rapeseed and mustard during 2018-19 in India was 9.41 million tonnes with a productivity of 1511 kg/ha. Mustard occupies approximately 75-80% of the total area under rapeseed-mustard in the country. Rapeseed-mustard is cultivated in Assam in about 2.87 lakh hectares with a production of 1.89 lakh tonnes and average productivity of 660 kg/ha. Assam contributes 4.82% to the total acreage and 2.46% to total production of the country (DRMR, 2020). Mustard is a species with genetic potential for high economic yield. Mustard plants are much taller than that of Toria (*Brassica rapa*). Mustard also has solid stems unlike toria and has a much higher biological yield. Despite these positive attributes, mustard is not a favoured crop in Assam because it takes much longer time to mature. In Assam, farmers prefer short duration oilseed varieties which are of medium to short height as the winter season is of shorter duration. Therefore, if varieties with shorter duration and height along with high yield capacity were developed,

Corresponding Author:
Rumjhum Phukan
Department of Plant Breeding
and Genetics, Agricultural
University, Jorhat, Assam, India

mustard can be a profitable crop in Assam condition. With this idea, crosses were made between certain selected varieties to combine the high yielding capacity and shorter height to develop varieties for the short winter season of Assam. It is believed that the yield can be increased by dispensing with the unproductive feet of the mustard plants, i.e., the portion of the main stem from the ground level to the first primary branch, which consumes a considerable proportion of the photosynthates produced by the plant, thus lowering the amount of photosynthates available for conversion to economic product *i.e.,* seed. It was proposed that selection for reduced foot length will lead to short duration and higher yield. A well performing genotype may not transmit its superiority to its next generation. Therefore, it is necessary to know and understand the inheritance patterns of a particular trait so that it can be incorporated into high performing genotypes. Therefore, the study was undertaken to evaluate selected F_2 populations and to study the inheritance of foot length and its relationship with yield and duration.

Materials and Method

The experiment was carried out in the Instructional-cum-Research (ICR) Farm, Assam Agricultural University, Jorhat, Assam. During *Rabi* 2015-16 the 17 entries comprising of 11 parents and six F_2 populations were sown in a randomized block design with three replications (Table1.1). Two F_2 populations were taken as males and were backcrossed to their respective parents in a crossing block (Table1.3). The North Carolina Design III was followed as mating design. Crosses for developing F_1 progenies were also made between selected parents (Table1.2). Fifteen Indian mustard genotypes were grown during *Rabi* 2016-17 consisting of six F_3 populations, four backcross populations, two F_1 progenies and three parents in a randomized block design with three replications (Table 1.4). In both the years, row to row spacing was maintained at 30 cm and plant to plant spacing was maintained at 15 cm. Each plot contained 4 rows measuring 4 metres in length. Observations were recorded on five random plants sampled from each plot for 15 different characters (Table 2.1 & 2.2).

Table 1.1: List of genotypes grown in the *Rabi* 2015-16

S.No.	Genotype	Location
1	DRMR 150-35	Dept. of PBG, AAU
2	RH – 932	Dept. of PBG, AAU
3	TM – 2	Dept. of PBG, AAU
4	SEJ – 2	Dept. of PBG, AAU
5	Pusa Bold	Dept. of PBG, AAU
6	TM 106	Dept. of PBG, AAU
7	PM – 25	Division of Genetics, IARI, New Delhi
8	PM – 26	Division of Genetics, IARI, New Delhi
9	PM – 27	Division of Genetics, IARI, New Delhi
10	PM – 28	Division of Genetics, IARI, New Delhi
11	Pusa Mahek	Dept. of PBG, AAU
12	TM 106 x TM-2 (F_2)	Dept. of PBG, AAU
13	Pusa Kranti x SEJ-2 (F_2)	Dept. of PBG, AAU
14	DRMR150-35 x TM-2 (F_2)	Dept. of PBG, AAU
15	RH-932 x TM-2 (F_2)	Dept. of PBG, AAU
16	DRMR 150-35 x Pusa Bold (F_2)	Dept. of PBG, AAU
17	GM-3 x Pusa bold (F_2)	Dept. of PBG, AAU

Table 1.2: List of F_1 crosses made during *Rabi* 2015-16

Sr. No.	Parents	F1
Cross 1	TM 106	TM 106 X TM-2
	TM-2	
Cross 2	DRMR 150-35	DRMR 150-35 X TM-2
	TM-2	

Table 1.3; List of backcross made during *Rabi* 2015-16

F_2 (Male)	Parent (Female)	Backcross
TM 106 X TM-2	TM 106	(TM 106 X TM-2) X TM 106
	TM-2	(TM 106 X TM-2) X TM-2
DRMR 150-35 X TM-2	DRMR 150-35	(DRMR 150-35 X TM 2) X DRMR 150-35
	TM-2	(DRMR 150-35 X TM-2) X TM-2

Table 1.4: List of genotypes grown in *Rabi* 2016-17

S.No.	Genotype
1	TM 106 x TM-2 (F_3)
2	Pusa Kranti x SEJ-2 (F_3)
3	DRMR150-35 x TM-2 (F_3)
4	RH-932 x TM-2 (F_3)
5	DRMR-15 x Pusa Bold (F_3)
6	GM-3 x Pusa bold (F_3)
7	(TM 106 x TM-2) X TM 106 (BC)
8	(TM 106 x TM-2) X TM-2 (BC)
9	(DRMR150-35 x TM-2) X DRMR 150-35 (BC)
10	(DRMR150-35 x TM-2) X TM-2 (BC)
11	TM 106 x TM-2 (F_1)
12	DRMR150-35 x TM-2 (F_1)
13	TM 106
14	TM-2
15	DRMR 150-35

Results and Discussion

In the study, analysis of variance revealed that in the first year, all the genotypes were found to be significantly different for the characters studied (Table 2.1). In the second year, significant differences were observed among all the genotypes for all the characters except for days to 50% flowering and number of siliquae on main shoot indicating sufficient variation among the genotypes (Table 2.2). High GCV were observed for seed yield per plant in the first year crop (Table 2.3) and for number of secondary branches per plant and foot length in the second year. High PCV was observed for seed yield per plant and biological yield per plant in the first year and for number of secondary branches per plant, seed yield per plant, foot length and biological yield per plant in the second year. Similar results were observed in Indian mustard by Akbar *et al.* (2003) [2] and Akbari and Niranjana (2015) [1]. This signified that there was scope for improvement of these characters through selection. High heritability coupled with low genetic advance was observed for days to maturity, number of primary branches per plant, number of siliqua on main shoot and stem thickness in the first year indicating the preponderance of non-additive gene action in the inheritance of these characters. Similar results were observed by Synrem *et al.* (2013) [10] and Kumar *et al.* (2013) [7]. None of the characters showed high heritability in the genotypes grown in the second year. Among the genotypes grown in the first year (Table 3.1), Pusa Bold showed the longest time for flowering (67.67 days) and the highest number of primary branches per plant (10.1 nos.). TM 106 exhibited the highest stem thickness (1.14 cm), the highest main shoot length (87.03 cm) and the

longest days to maturity (126.67 days). RH-932 was the tallest plant (213.63 cm) and had the highest thousand seed weight (4.73 g). PM-26 had the shortest foot length (32.93 cm) and DRMR 150-35 X Pusa Bold (F$_2$) exhibited the highest harvest index (26.62%). DRMR 150-35 X TM-2 (F$_2$) exhibited the highest biological yield per plant (69.72g). Pusa Kranti X SEJ-2 (F$_2$) was found to have highest means for number of primary branches (5.52). TM 106 X TM-2 (F$_2$) showed maximum root length (17.36 cm) while Pusa Mahek was the highest yielder with highest means for seed weight per plant (19.11 g) and number of siliquae on main shoot (42.57 g). TM-2 exhibited the highest means for number of seeds per siliqua (13.03). Among the genotypes grown in the second year (Table 3.2), (DRMR 150-35 X TM-2) X TM-2 (BC) was found to have the highest means for plant height (180.83 cm), main shoot length (76.13 cm), number of siliqua on main shoot (49.20) and maximum root length (24.3 cm).

(TM 106 X TM-2) X TM 106 (BC) exhibited the highest means for number of primary branches (5.23), thousand seed weight (4.67 g) and seed weight per plant (17.25 g) and the lowest mean performance for foot length (22.80 cm). TM 106 X TM-2 (F$_1$) was also found to have the highest means for number of primary branches (5.23) along with number of secondary branches (13.1) and biological yield per plant (73.24 g) and had the shortest maturity period (110.67 days). GM-3 X Pusa Bold (F$_3$) showed the longest time for days to 50% flowering (61 days) while RH 932 X TM-2 (F$_3$) exhibited the highest number of days to maturity (123 days). (TM 106 X TM-2) X TM-2 (BC) showed the highest number of seeds per siliqua (13.1), (DRMR 150-35 X TM-2) X DRMR 150-35 (BC) had highest means for stem thickness (1.33 cm), and DRMR 150-35 X TM-2 (F$_1$) had the highest harvest index (28.29%).

Table 2.1: Analysis of variance for different traits in Indian mustard for year 1

Source	df	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BY	HI
Replicate	2	6.24	10.02	175.15	311.3	8.39	0.11	3.4	0.03	0.57	0.01	17.38	0.52	0.0003	155.36	3.61
Genotypes	16	56.38*	89.12**	1188.08**	186.94**	84.67**	0.74**	4.00**	0.73**	22.12**	0.75*	25.85**	1.01**	0.003*	291.74**	12.90**
Error	32	5.19	3.52	165.5	28.95	12.68	0.05	0.64	0.09	1.32	0.02	3.9	0.25	0.0002	23.42	2.16
CV		4.06	1.60	7.30	11.86	4.91	4.54	10.11	2.62	3.27	3.36	17.84	3.04	1.34	9.17	6.38

Table 2.2: Analysis of variance for different traits in Indian mustard for year 2

Source	df	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
Rep.	2	25.87	7.76	129.11	3.09	182.08	1.23	18.55	0.27	0.74	0.03	3.19	5.78	0	24.8	1.9
Genotype	14	17.58	39.71**	169.72*	252.33**	79.18*	0.94**	20.74**	1.79*	19.7	0.52**	20.88*	9.48**	0.06**	304.92**	38.07**
Error	28	14.53	4.68	63.93	21.08	34.05	0.15	4.52	0.64	12.44	0.05	7.89	3.05	0.01	36.97	3.71
CV		6.64	1.85	4.75	12.02	8.52	8.93	30.56	6.74	8.00	5.30	22.09	8.35	9.18	11.31	8.31

* Significant at P = 0.05 and ** Significant at P = 0.01
DF= Days to flowering   DM= Days to maturity   PH= Plant height   FL= Foot length   MSL= Length of main shoot
PB= No. of primary branches per plant   SB= No. of secondary branches   SPS= No. of seeds per siliqua   SMS= No. of siliqua on main shoot   TSW= Thousand seed weight
SYP= Seed yield per plot   MRL=Maximum root length   ST= Stem thickness   BYP= Biological yield per plant   HI= Harvest Index

Table 2.3: Estimates of genetic parameters for seed yield and component traits in Indian mustard for year 1

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
Mean	56.14	116.90	176.31	45.37	72.47	4.80	7.91	11.74	35.22	4.11	11.07	16.42	1.09	52.76	23.04
S.E.(m)	1.32	1.08	7.43	3.11	2.06	0.13	0.46	0.18	0.66	0.08	1.14	0.29	0.01	2.79	0.85
Range	67.67-49.67	126.67-108.67	213.63-125.29	60.74-32.93	87.03-65.43	5.52-3.67	10.10-6.63	13.03-11.03	42.57-30.73	4.73-3.20	19.11-7.63	17.36-15.34	1.14-1.00	69.72-36.09	26.62-19.68
GCV	7.36	4.57	10.47	15.99	6.76	9.97	13.37	3.92	7.48	12.05	24.44	3.06	2.80	17.92	8.21
PCV	8.40	4.84	12.76	19.91	8.36	10.96	16.77	4.71	8.16	12.51	30.26	4.31	3.11	20.14	10.40
h^2	77	89	67	65	65	83	64	69	84	93	65	50	81	79	62
GA (%)	13.27	8.88	17.7	26.47	11.26	18.7	21.96	6.7	14.11	23.91	40.67	4.48	5.21	32.87	13.35

DF= Days to flowering   DM= Days to maturity   PH= Plant height   FL= Foot length   MSL= Length of main shoot
PB= No. of primary branches per plant   SB= No. of secondary branches   SPS= No. of seeds per siliqua   SMS= No. of siliqua on main shoot   TSW= Thousand seed weight
SYP= Seed yield per plot   MRL=Maximum root length   ST= Stem thickness   BYP= Biological yield per plant   HI= Harvest Index

Table 2.4: Estimates of genetic parameters for seed yield and component traits in Indian mustard for year 2

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
Mean	57.40	117.18	168.20	38.19	68.51	4.39	6.96	11.85	44.07	4.05	12.71	20.88	1.02	53.74	23.15
S.E. (m)	2.20	1.25	4.62	2.65	3.37	0.23	1.23	0.46	2.04	0.12	1.62	1.01	0.05	3.51	1.11
Range	61.00-53.67	123.00-110.67	180.83-154.30	51.20-22.80	76.13-59.13	5.23-3.83	13.10-3.77	13.10-10.73	49.20-40.83	4.67-3.40	17.25-9.23	24.30-18.20	1.33-0.82	73.24-41.50	28.30-17.70
GCV	1.76	2.92	3.53	22.99	5.66	11.66	33.43	5.24	3.53	9.77	16.38	7.01	12.50	17.59	14.62
PCV	6.87	3.45	5.92	25.94	10.23	14.69	45.29	8.54	8.75	11.11	27.50	10.91	15.51	20.91	16.82
h^2	7	71	36	79	31	63	54	38	16	77	35	41	65	71	76
GA (%)	0.92	5.07	4.34	41.97	6.46	19.07	50.82	6.61	2.93	17.69	20.09	9.29	20.76	30.47	26.18

DF= Days to flowering   DM= Days to maturity   PH= Plant height   FL= Foot length   MSL= Length of main shoot
PB= No. of primary branches per plant   SB= No. of secondary branches   SPS= No. of seeds per siliqua   SMS= No. of siliqua on main shoot   TSW= Thousand seed weight
SYP= Seed yield per plot   MRL=Maximum root length   ST= Stem thickness   BYP= Biological yield per plant   HI= Harvest Index

Table 3.1: Mean performance of 17 genotypes (11 parents and 6 F₂populations) in Indian mustard

Genotype	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
Pusa Mahek	52.00	122.33	190.47	41.07	81.77	5.33	6.87	11.70	42.57	4.67	19.11	15.35	1.06	67.83	24.00
Pusa Bold	67.67	122.00	171.00	35.50	69.11	5.10	10.10	11.67	40.73	4.40	11.25	16.93	1.12	52.87	22.55
DRMR 15035	56.00	113.33	166.77	45.43	68.90	4.10	7.10	11.53	35.67	3.53	8.46	16.29	1.07	36.09	21.98
TM 106	58.67	126.67	193.63	40.57	87.03	4.67	6.70	11.53	32.70	4.60	12.62	16.50	1.14	43.03	20.90
TM-2	54.00	112.00	175.57	47.70	67.93	4.73	7.77	13.03	35.40	3.93	7.63	17.05	1.10	53.82	23.27
SEJ-2	57.67	110.67	175.57	47.97	71.00	4.77	7.23	k11.90	35.20	4.47	12.58	16.35	1.10	43.83	20.21
RH-932	53.00	123.00	213.63	57.37	69.40	5.13	9.57	11.63	34.63	4.73	10.52	17.05	1.09	42.78	20.62
PM-25	59.00	113.67	168.60	35.19	73.73	4.43	6.77	11.43	35.03	3.73	12.39	16.85	1.06	42.24	19.68
PM-26	50.67	121.67	158.40	32.93	65.43	4.40	7.13	12.00	30.73	3.60	8.17	15.80	1.09	50.01	24.11
PM-27	49.67	116.33	154.63	45.20	68.20	3.67	6.63	12.73	33.40	3.60	7.75	16.55	1.09	46.60	20.73
PM-28	58.33	111.00	164.87	37.60	71.33	4.43	8.73	11.03	34.50	3.87	9.11	15.87	1.00	50.42	23.53
Pusa Kranti X SEJ-2 (F2)	55.33	113.00	184.89	46.05	72.45	5.52	9.25	11.67	33.80	4.40	10.97	16.53	1.09	53.59	25.57
GM-3 X Pusa Bold (F2)	60.67	119.67	183.47	48.59	70.54	4.79	8.54	11.55	34.69	4.67	15.35	16.72	1.10	64.42	23.38
RH-932 X TM-2 (F2)	51.67	120.33	125.29	56.22	71.00	5.27	8.48	11.67	34.85	3.73	9.81	16.10	1.09	59.25	25.49
DRMR 150-35 X TM-2 (F2)	56.33	108.67	189.19	49.35	75.40	5.42	9.27	11.17	34.90	3.20	9.79	15.34	1.08	69.72	24.21
TM106 X TM-2 (F2)	56.33	112.00	186.40	43.75	75.85	4.80	6.70	11.75	35.07	3.93	10.11	17.36	1.09	55.90	24.85
DRMR 150-35 X Pusa Bold (F2)	57.33	121.00	194.90	60.74	72.99	5.10	7.69	11.49	34.87	4.73	12.53	16.45	1.13	64.51	26.62

DF= Days to flowering DM= Days to maturity PH= Plant height FL= Foot length MSL= Length of main shoot
PB= No. of primary branches per plant SB= No. of secondary branches SPS= No. of seeds per siliqua SMS= No. of siliqua on main shoot TSW= Thousand seed weight
SYP= Seed yield per plot MRL=Maximum root length ST= Stem thickness BYP= Biological yield per plant HI= Harvest Index

Table 3.2: Mean performance of 15 genotypes (6 F₃, 4 backcrosses, 2 F₁ and 3 parents) in Indian mustard

Genotype	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
Pusa Kranti X SEJ-2 (F3)	57.00	119.67	173.77	51.20	64.67	3.83	4.47	11.90	40.83	4.20	15.49	21.47	0.96	45.52	22.33
GM-3 X Pusa Bold (F3)	61.00	121.67	173.83	41.63	66.93	4.00	5.27	11.47	44.13	3.67	11.69	21.67	1.05	52.73	21.96
RH-932 X TM-2 (F3)	54.00	123.00	175.50	44.40	66.20	3.90	5.20	11.13	44.27	3.40	10.09	19.53	0.91	50.95	20.16
DRMR 150-35 X TM-2 (F3)	57.67	112.00	169.67	49.23	69.27	4.10	5.10	11.07	42.73	3.47	10.99	21.77	0.98	50.83	22.24
TM 106 X TM-2 (F3)	56.00	114.33	169.23	36.40	68.60	4.57	6.37	11.63	41.93	3.93	10.55	20.20	0.98	51.69	25.51
DRMR150-35 X Pusa Bold (F3)	61.00	120.33	168.77	45.63	59.13	3.90	4.73	10.97	43.13	4.47	9.23	19.57	0.83	41.97	17.70
(TM 106 X TM-2) X TM-106 (BC)	58.67	119.33	162.63	22.80	73.67	5.23	9.10	12.00	42.73	4.67	17.25	22.17	1.11	60.13	26.24
(TM 106 X TM-2) X TM-2 (BC)	61.00	121.00	163.37	28.10	70.40	5.20	9.67	13.10	45.17	4.13	12.78	21.77	1.17	65.84	26.99
(DRMR 150-35 X TM-2) X DRMR150-35 (BC)	57.00	116.33	170.27	31.83	74.30	4.43	8.97	13.00	47.70	3.93	14.00	23.60	1.33	53.29	20.29
(DRMR 150-35 X TM-2) X TM-2 (BC)	54.33	117.33	180.83	32.40	76.13	5.20	9.77	11.60	49.20	4.07	15.04	24.30	1.12	53.95	27.00
DRMR 150-35 X TM-2 (F1)	56.33	114.67	154.30	34.40	65.67	4.13	7.53	12.27	41.43	4.53	14.40	18.67	1.06	72.58	28.30
TM 106 X TM-2 (F1)	59.00	110.67	163.60	23.33	75.13	5.23	13.10	13.00	48.00	4.53	16.86	19.27	1.11	73.24	28.09
TM 106	57.67	117.33	177.57	43.83	71.83	4.30	6.07	10.73	43.60	4.40	11.67	21.57	1.06	46.81	18.67
TM-2	53.67	116.00	157.37	39.67	60.67	3.90	5.23	12.47	41.20	3.87	9.38	18.20	0.86	45.08	19.88
DRMR-150-35	56.67	114.00	162.30	47.97	65.03	3.87	3.77	11.43	45.00	3.53	11.23	19.53	0.82	41.50	21.92

DF= Days to flowering DM= Days to maturity PH= Plant height FL= Foot length MSL= Length of main shoot
PB= No. of primary branches per plant SB= No. of secondary branches SPS= No. of seeds per siliqua SMS= No. of siliqua on main shoot TSW= Thousand seed weight
SYP= Seed yield per plot MRL=Maximum root length ST= Stem thickness BYP= Biological yield per plant HI= Harvest Index

In the first year, diversity analysis revealed that 17 genotypes were grouped into six cluster (Table 4.1). Cluster I was the largest cluster with 12 genotypes while other 5 clusters were mono-genotypic clusters. Cluster I exhibited the highest mean for number of seeds per siliqua (11.83) (Table 4.2). Cluster II had the highest means for thousand seed weight (4.73g), and harvest index (26.62%). Cluster III showed the highest means for plant height (213.63 cm), number of secondary branches (9.57), and maximum root length (17.05 cm). Cluster IV had the highest means for days to flowering (58.67 days), days to maturity (126.67 days), main shoot length (87.03 cm) and stem thickness (1.14 cm) and the lowest mean for foot length (40.57 cm). Cluster V showed the highest means for number of primary branches per plant (5.42) and biological yield per plant (69.72 g) while cluster VI had the highest means for number of siliquae on main shoot (42.57) and seed yield per plant (19.11g).Highest inter cluster distances were observed between cluster III and cluster V in the first year (Table 4.3). In the second year, the genotypes were divided into four clusters among which cluster I had 6 genotypes while cluster III and IV had 4 genotypes each and cluster II had a single genotype (Table 4.4). Cluster II showed the highest means for plant height (180.83 cm), main shoot length (76.13 cm), number of primary branches per plant (5.2), number of siliqua on main shoot, maximum root length and stem thickness (Table 4.5). Cluster III had the highest means for days to 50% flowering, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight, seed yield per plant, biological yield per plant and harvest index and the lowest mean for foot length among all the clusters. The mean for foot length in Cluster III was the lowest compared to the clusters in both the years indicating that recombination had occurred among the segregating genotypes and crosses. Cluster IV had the highest mean for days to maturity. Highest inter cluster distances were observed between cluster I and cluster III in the second year (Table 4.6). In both the years, thousand seed weight was the highest contributor to the genetic diversity (41.18%, 26.67%)

Table 4.1: Grouping of varieties into clusters for year 1

Cluster	Number of genotypes	Genotypes
I	12	DRMR 150-35, PM-25, PM-26, PM-27, PM-28, RH-932XTM-2 (F$_2$), TM106 X TM-2 (F$_2$), SEJ-2, TM-2, Pusa Kranti X SEJ-2 (F$_2$), Pusa Bold, GM-3 X Pusa Bold (F$_2$)
II	1	DRMR 150-35 x Pusa bold (F$_2$)
III	1	RH-932
IV	1	TM106
V	1	DRMR150-35 X TM-2 (F$_2$)
VI	1	Pusa Mahek

Table 4.2: Cluster means for year 1

Cluster	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
I	56.42	115.47	167.95	43.51	70.46	4.67	7.87	11.83	34.92	3.99	10.3	16.53	1.08	50.75	22.95
II	57.33	121	194.9	60.74	72.99	5.1	7.69	11.49	34.87	4.73	12.53	16.45	1.13	64.51	26.62
III	53	123	213.63	57.37	69.4	5.13	9.57	11.63	34.63	4.73	10.52	17.05	1.09	42.78	20.62
IV	58.67	126.67	193.63	40.57	87.03	4.67	6.7	11.53	32.7	4.6	12.62	16.5	1.14	43.03	20.9
V	56.33	108.67	189.19	49.35	75.4	5.42	9.27	11.17	34.9	3.2	9.79	15.34	1.08	69.72	24.21
VI	52	122.33	190.47	41.07	81.77	5.33	6.87	11.7	42.57	4.67	19.11	15.35	1.06	67.83	24
Contribution (%)	3.68	8.82	0.74	0	0.74	5.88	0.74	8.82	8.09	41.18	1.47	0.74	4.41	8.82	5.88

Table 4.3: Cluster distances for year 1

Cluster	I	II	III	IV	V	VI
I	43.66	70.72	84.57	85.57	85.62	89.94
II		0	34.1	42.26	151.6	103.25
III			0	36.5	215.5	119.85
IV				0	210.97	87.81
V					0	119.36
VI						0

Table 4.4: Grouping of varieties for year 2

Cluster	Number of genotypes	Genotypes
I	6	DRMR 150-35 X TM-2 (F$_3$), DRMR 150-35, TM-2, TM106XTM-2 (F$_3$), RH-932XTM-2(F$_3$), GM-3XPusa bold(F$_3$)
II	1	(DRMR 150-35 X TM -2) X TM-2 (BC)
III	4	DRMR 150-35 X TM-2 (F$_1$), TM106 X TM-2 (F$_1$), (TM106 X TM-2)X TM-2 (BC), (TM106 X TM-2)XTM106 (BC)
IV	4	DRMR 150-35 X Pusa Bold (F$_3$), TM 106, (DRMR 150-35 X TM-2) X DRMR 150-35 (BC), Pusa kranti X SEJ-2 (F$_3$)

Table 4.5: Cluster means for year 2

Cluster	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
I	56.5	116.83	167.98	43.22	66.12	4.06	5.16	11.53	43.21	3.64	10.66	20.15	0.93	48.8	21.94
II	54.33	117.33	180.83	32.4	76.13	5.2	9.77	11.6	49.2	4.07	15.04	24.3	1.12	53.95	27
III	58.75	116.42	160.98	27.16	71.22	4.95	9.85	12.59	44.33	4.47	15.32	20.47	1.11	67.95	27.4
IV	58.17	118.42	172.59	43.13	67.48	4.12	6.06	11.65	43.82	4.25	12.6	21.55	1.05	46.9	19.75
Contribution (%)	0	6.67	0	11.43	0	0.95	0.95	0	0.95	26.67	0.95	2.86	12.38	20	16.19

Table 4.6: Cluster distances for year 2

Cluster	I	II	III	IV
I	12.4	21.98	38.52	20.27
II		0	18.29	19.36
III			14.94	35.71
IV				16.09

Correlation of foot length with seed yield and other yield attributing characters was observed at both genotypic and phenotypic levels and it was found that among the genotypes in the first year, foot length was significantly negatively correlated to all characters except days to 50% flowering, days to maturity and maximum root length at phenotypic level and days to 50% flowering, days to maturity and maximum root length and positively correlated to plant height at genotypic level (Table 5.1). Similar results were also reported by Yadava *et al.* (2011) [11]. In the second year, foot length

exhibited significant and positive genotypic correlation only with number of primary branches per plant, stem thickness and harvest index (Table 5.2). The difference in pattern of correlation of the character foot length in both the years can be accounted for the fact that the genetic make-up of the populations used in the study in respective years was completely different. The first year comprised of cultivated varieties and F$_2$ populations of those varieties as parents. However, in the second year, the studied population consisted of F$_3$ populations, backcrosses (BC$_1$ and BC$_2$), F$_1$ populations and three parental lines. The perusal of the correlation values between the individual generations of populations given in (Table 5.3, 5.4, 5.5 & 5.6) revealed that certain characters showed both positive and negative correlation with seed yield or foot length in different generations. Maximum root length was found to be positively correlated to foot length in the parental, F$_3$ and backcross generations but exhibited negative

correlation with foot length in the F$_2$ generation. Such changes in correlation have been observed for several characters. Changes in correlation between same characters in F$_2$ and F$_3$ generations may be due to sampling size while changes in correlation between parents and F$_2$ generation can be attributed to recombination and segregation of genes. Differences in correlation between the same character in the backcross generation as compared to other generations can be attributed to further recombination and pleiotropy. In the first year, the phenotypic correlation of the traits *viz.*, length of main shoot, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, thousand seed weight, maximum root length, stem thickness, biological yield per plant and harvest index with seed yield per plant is less than genotypic correlation, In the second year, the phenotypic correlation of the traits *viz.*, plant height, length of main shoot, number of primary branches per plant, number of siliquae on main shoot, thousand seed weight, and biological yield per plant with seed yield per plant is less than genotypic correlation. Lower value of phenotypic correlation than genotypic correlations may indicate the presence of strong coupling phase linkage (Sharma, 1988) [9].

Table 5.1: Correlation for first year

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
DF		0.61**	-0.39*	-0.22	0.62**	0.45**	0.53**	-0.18	0.2	0.01	0.28	0.28	0.37*	0.73**	0.17
DM	0.07		0.48**	0.16	-0.35	-0.14	-0.33*	-0.29	-0.33*	-0.06	-0.22	0.29	-0.03	-0.24	-0.36*
PH	0.04	0.27		0.47**	0.2	-0.04	-0.27	-0.79**	0.26 *	-0.35*	-0.22	0.97 **	0.09	-0.51**	-0.44**
FL	-0.16	0.09	0.16		-0.85**	-0.89**	-0.85**	-0.78**	-0.63**	-0.60 **	-0.76 **	-0.21	-0.70**	-0.89**	-0.74**
MSL	-0.14	-0.16	0.38*	-0.49**		0.73**	0.92 **	0.59**	0.73 **	0.24	0.64 **	0.91 **	0.73 **	0.78**	0.74 **
PB	0.13	-0.15	0.02	-0.72**	0.54**		0.87 **	0.65 **	0.84**	0.57 **	0.91 **	0.52 **	0.79 **	0.71 **	0.86 **
SB	0.04	-0.18	0.01	-0.79**	0.66**	0.79**		0.83 **	0.80 **	0.61 **	0.89 **	0.32*	0.83 **	0.89 **	0.89 **
SPS	0.17	-0.11	-0.32 *	-0.63**	0.11	0.34*	0.54**		0.31*	0.38*	0.70 **	-0.04	0.61 **	0.86 **	0.70 **
SMS	0.02	0.01	0.40*	-0.38*	0.48**	0.43**	0.59**	0.28		-0.09	0.29	0.71 **	0.77 **	0.47**	0.44**
TSW	0.07	-0.05	-0.17	-0.44**	0.19	0.33*	0.40*	0.18	-0.01		0.72 **	0.04	0.37*	0.49 **	0.40*
SYP	0.08	-0.12	0.05	-0.50**	0.45**	0.40*	0.57**	0.34*	0.37*	0.45**		0.51 **	0.73 **	0.81 **	0.92 **
MRL	0.11	0.12	0.36*	-0.17	0.45**	0.37*	0.25	0.05	0.41**	-0.07	0.31*		0.75 **	-0.03	0.14
ST	0.18	-0.04	0.15	-0.66**	0.58**	0.48**	0.64**	0.57**	0.44**	0.21	0.52**	0.58**		0.69 **	0.45 **
BYP	0.03	-0.24	-0.30 *	-0.58**	0.27	0.55**	0.57**	0.40*	0.14	0.41**	0.45**	-0.03	0.44**		0.90**
HI	-0.01	-0.26	-0.22	-0.59**	0.32*	0.51**	0.44**	0.34*	0.1	0.3	0.43**	0.04	0.35*	0.71**	

Genotypic correlation above diagonal

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering   DM= Days to maturity   PH= Plant height   FL= Foot length   MSL= Length of main shoot
PB= No. of primary branches per plant   SB= No. of secondary branches   SPS= No. of seeds per siliqua   SMS= No. of siliqua on main shoot   TSW= Thousand seed weight
SYP= Seed yield per plot   MRL=Maximum root length   ST= Stem thickness   BYP= Biological yield per plant   HI= Harvest Index

Table 5.2: Correlation for year 2

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
DF		0.01	0.25	-0.24	0.14	0.15	0.42**	-0.45**	0.35 *	0.32*	0.26	0.35*	0.22	0.01	-0.13
DM	0		0.15	0.04	0.28	0.13	0.01	-0.02	0.12	0.58**	0.43 **	0.03	0.50 **	0.01	-0.03
PH	0.13	0.13		0.27	0.46**	0.42**	0.18	-0.25	0.17	0.64**	0.48 **	0.29	0.29	0.15	-0.06
FL	-0.28	0.04	0.15		-0.11	0.44**	0.29	0.05	-0.12	0.29	0.03	0.13	0.38 *	0.3	0.36*
MSL	0.09	0.25	0.34*	-0.04		0.35*	-0.36*	-0.46**	0.28	0.36*	0.73 **	-0.25	0.13	0.22	-0.04
PB	0.17	0.11	0.28	0.28	0.23		0.59 **	-0.41**	0.40 *	0.42**	0.50 **	-0.16	0.19	0.67**	0.62**
SB	0.33*	-0.02	0.1	0.17	-0.21	0.56**		-0.37*	0.21	0.16	-0.09	0.14	0.01	0.31*	0.3
SPS	-0.39*	-0.02	-0.15	-0.01	-0.23	-0.26	-0.24		-0.09	-0.1	-0.34*	0.45**	0.31*	-0.14	-0.14
SMS	0.29	0.11	0.11	-0.05	0.16	0.33*	0.14	-0.08		0.31*	0.64**	-0.17	-0.1	0.34*	0.03
TSW	0.27	0.51**	0.49**	0.23	0.28	0.37*	0.14	-0.07	0.32 *		0.73**	0.33*	0.43**	0.1	-0.01
SYP	0.2	0.30*	0.30*	-0.02	0.41**	0.32*	-0.1	-0.32*	0.48**	0.58**		-0.21	0.1	0.45**	0
MRL	0.26	0.04	0.08	0.09	-0.14	-0.17	-0.12	0.22	-0.03	0.23	-0.19		0.45**	-0.48**	-0.32*
ST	0.16	0.45**	0.17	0.29	0.09	0.2	-0.01	0.27	-0.1	0.35*	0.01	0.32*		0.08	0.11
BYP	-0.05	0.04	0.06	0.26	0.17	0.52**	0.2	-0.16	0.30 *	0.11	0.36*	-0.28	0.05		0.75**
HI	-0.12	0.01	-0.09	0.23	0.03	0.39*	0.17	-0.18	0.06	0.02	0.06	-0.2	0.01	0.70**	

Genotypic correlation above diagonal

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering   DM= Days to maturity   PH= Plant height   FL= Foot length   MSL= Length of main shoot
PB= No. of primary branches per plant   SB= No. of secondary branches   SPS= No. of seeds per siliqua   SMS= No. of siliqua on main shoot   TSW= Thousand seed weight
SYP= Seed yield per plot   MRL=Maximum root length   ST= Stem thickness   BYP= Biological yield per plant   HI= Harvest Index

Table 5.3: Correlation among parents grown in 1st year

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
DF															
DM	0.00														
PH	0.00	0.52**													
FL	-0.35*	-0.09	0.58**												
MSL	0.13	0.47**	0.48**	-0.11											
PB	0.31*	0.42**	0.72**	0.14	0.34*										
SB	0.51**	0.13	0.30*	0.16	-0.34*	0.48**									
SPS	-0.46**	-0.14	-0.22	0.30*	-0.36*	-0.24	-0.23								
SMS	0.36*	0.10	0.23	-0.03	0.24	0.62**	0.30*	-0.14							
TSW	0.24	0.53**	0.85**	0.36*	0.56**	0.84**	0.35*	-0.22	0.46**						
SYP	0.12	0.36*	0.48**	-0.09	0.73**	0.66**	-0.15	-0.37*	0.66**	0.68**					
MRL	0.34*	-0.06	0.20	0.39*	-0.27	-0.01	0.38*	0.31*	-0.14	0.06	-0.41**				
ST	0.17	0.51**	0.26	0.18	0.13	0.17	0.00	0.42**	-0.08	0.34*	-0.04	0.49**			
BYP	-0.12	0.22	0.07	-0.25	0.21	0.53**	0.08	0.18	0.62**	0.31*	0.52**	-0.47**	-0.17		
HI	-0.15	0.10	-0.20	-0.37*	-0.12	0.22	0.15	0.06	0.25	-0.12	0.00	-0.58**	-0.26	0.69**	

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering DM= Days to maturity PH= Plant height FL= Foot length MSL= Length of main shoot
PB= No. of primary branches per plant SB= No. of secondary branches SPS= No. of seeds per siliqua SMS= No. of siliqua on main shoot TSW= Thousand seed weight
SYP= Seed yield per plot MRL=Maximum root length ST= Stem thickness BYP= Biological yield per plant HI= Harvest Index

Table 5.4: Correlation among F₂s grown in year 1

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
DF															
DM	0.05														
PH	0.74**	-0.39*													
FL	-0.22	0.70**	-0.29												
MSL	-0.03	-0.79**	0.49**	-0.37*											
PB	-0.56**	-0.34*	-0.16	0.13	0.03										
SB	-0.10	-0.19	-0.12	-0.01	-0.34*	0.74**									
SPS	-0.24	0.34*	-0.34*	-0.21	-0.28	-0.35*	-0.50**								
SMS	0.05	0.10	-0.10	0.27	0.35*	-0.56**	-0.59**	-0.21							
TSW	0.52**	0.65**	0.31*	0.21	-0.53**	-0.38*	-0.22	0.42**	-0.34*						
SYP	0.82**	0.55**	0.33*	0.10	-0.58**	-0.54**	0.00	0.02	-0.10	0.78**					
MRL	0.28	0.21	0.18	-0.35*	-0.01	-0.70**	-0.74**	0.82**	-0.01	0.58**	0.30*				
ST	0.38*	0.71**	0.28	0.70**	-0.27	-0.36*	-0.39*	0.04	0.19	0.74**	0.56**	0.25			
BYP	0.38*	0.01	0.22	0.39*	0.08	-0.02	0.26	-0.89**	0.50**	-0.24	0.24	-0.66**	0.21		
HI	-0.50**	0.30*	-0.09	0.60**	0.03	0.35*	-0.23	0.24	-0.14	0.24	-0.33*	0.05	0.49**	-0.32*	

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering DM= Days to maturity PH= Plant height FL= Foot length MSL= Length of main shoot
PB= No. of primary branches per plant SB= No. of secondary branches SPS= No. of seeds per siliqua SMS= No. of siliqua on main shoot TSW= Thousand seed weight
SYP= Seed yield per plot MRL=Maximum root length ST= Stem thickness BYP= Biological yield per plant HI= Harvest Index

Table 5.5: Correlation between F₃s grown in Year 2

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP	HI
DF															
DM	0.10														
PH	-0.34*	0.70**													
FL	0.05	0.03	0.18												
MSL	-0.47**	-0.53**	0.14	-0.25											
PB	-0.22	-0.65**	-0.53**	-0.75**	0.56**										
SB	-0.31*	-0.40*	-0.28	-0.89**	0.58**	0.94**									
SPS	-0.18	0.00	0.29	-0.07	0.27	0.20	0.12								
SMS	0.16	0.46**	0.30*	-0.29	-0.02	-0.20	0.09	-0.66**							
TSW	0.46**	0.12	-0.43**	0.10	-0.77**	-0.12	-0.31*	0.21	-0.52**						
SYP	-0.09	0.04	0.42**	0.50**	0.15	-0.28	-0.41**	0.82**	-0.66**	0.16					
MRL	0.28	-0.36*	0.10	0.37*	0.50**	-0.05	-0.19	0.40*	-0.28	-0.24	0.64**				
ST	0.04	-0.23	0.27	-0.25	0.78**	0.34*	0.37*	0.52**	-0.01	-0.50**	0.40*	0.76**			
BYP	-0.34*	-0.21	0.30	-0.49**	0.90**	0.49**	0.65**	0.13	0.36*	-0.85**	-0.08	0.32*	0.79**		
HI	-0.38*	-0.57**	-0.07	-0.42**	0.80**	0.77**	0.69**	0.67**	-0.46**	-0.27	0.35	0.42**	0.72**	0.64**	

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering DM= Days to maturity PH= Plant height FL= Foot length MSL= Length of main shoot
PB= No. of primary branches per plant SB= No. of secondary branches SPS= No. of seeds per siliqua SMS= No. of siliqua on main shoot TSW= Thousand seed weight
SYP= Seed yield per plot MRL=Maximum root length ST= Stem thickness BYP= Biological yield per plant HI= Harvest Index

Table 5.6: Correlation between Backcross progenies grown in Year 2

	DF	DM	PH	FL	MSL	PB	SB	SPS	SMS	TSW	SYP	MRL	ST	BYP
DF														
DM	0.83**													
PH	-0.92**	-0.68**												
FL	-0.60**	-0.63**	0.79**											
MSL	-0.97**	-0.83**	0.80**	0.41**										
PB	0.18	0.69**	-0.10	-0.49**	-0.18									
SB	-0.10	0.37*	0.42**	0.30*	-0.09	0.65**								
SPS	0.67**	0.23	-0.54**	0.09	-0.73**	-0.53**	-0.27							
SMS	-0.75**	-0.69**	0.91**	0.98**	0.57**	-0.38*	0.36*	-0.13						
TSW	0.32*	0.48**	-0.55**	-0.95**	-0.12	0.59**	-0.24	-0.40*	-0.85**					
SYP	-0.29	-0.13	-0.05	-0.59**	0.49**	0.30*	-0.37*	-0.73**	-0.42**	0.80**				
MRL	-0.96**	-0.89**	0.94**	0.78**	0.89**	-0.37*	0.09	-0.46**	0.88**	-0.56**	0.04			
ST	0.02	-0.51**	-0.04	0.47**	-0.05	-0.97**	-0.57**	0.72**	0.32*	-0.63**	-0.49**	0.20		
BYP	0.90**	0.99**	-0.75**	-0.60**	-0.91**	0.57**	0.29	0.38*	-0.69**	0.40*	-0.23	-0.92**	-0.36*	
HI	0.16	0.68**	-0.02	-0.37*	-0.19	0.99**	0.76**	-0.49**	-0.27	0.46**	0.18	-0.32*	-0.94**	0.56**

* Significant at P=0.05; ** Significant at P=0.01

DF= Days to flowering	DM= Days to maturity	PH= Plant height	FL= Foot length	MSL= Length of main shoot
PB= No. of primary branches per plant	SB= No. of secondary branches	SPS= No. of seeds per siliqua	SMS= No. of siliqua on main shoot	TSW= Thousand seed weight
SYP= Seed yield per plot	MRL=Maximum root length	ST= Stem thickness	BYP= Biological yield per plant	HI= Harvest Index

The inheritance of the foot length was studied under the North Carolina Design III analysis method of Comstock and Robinson (1952) for the two crosses TM 106 X TM-2 and DRMR 150-35 X TM-2. Analysis of variance revealed significant differences between the parents for the cross TM 106 X TM-2 while no significant differences were observed between the parents for the cross DRMR 150-35 X TM-2 (Table 6.1 &6.3). This fact is supported by the observation that the two parents for the cross TM 106 X TM-2 belong to different clusters as seen in the cluster analysis indicating presence of genetic diversity between the two parents while the two parents for the cross DRMR 150-35 X TM-2 belong to the same cluster indicating lack of such diversity between them.

Evaluation of components of variance revealed that the narrow sense heritability for the character of foot length was high for the cross TM 106 X TM-2 while it was low for DRMR 150-35 X TM-2 (Table 6.2 &6.4). This is because the dominance component of variance for the cross DRMR 150-35 X TM-2 was much higher than the dominance component for the cross TM 106 X TM-2. Thus, the results indicate that different magnitudes of components of variance for different crosses for the same character. The probable cause for the higher values of dominance component of variance for the cross DRMR 150-35 X TM-2 could be due to linkage phase or due to epistasis or both. High frequency of coupling phase (*AB/ab*) causes an upward bias in the estimates of additive and dominance variances (Hallauer and Miranda, 1981) [6]. An excess of repulsion phase linkage (*Ab/ab*) leads to upward bias in dominance variance and downward bias in additive variance. Gardner and Lonnquist (1959) [5] have reported estimates of testing effects of linkage and found that they were an important bias in the estimates of additive and dominance components of variance. The ratio of additive genetic variance/ dominance genetic variance is more than one for the cross TM106 X TM-2 which indicates that foot length is governed by additive gene action and is fixable. However, the ratio of additive genetic variance/ dominance genetic variance is less than one for the cross DRMR 150-35

X TM-2 which indicates that foot length is governed by dominance gene action and hence the selection of superior plants should be postponed to later generation (Nadaranjan *et al*. 2016) [8].

Table 6.1: Anova for NCD III for foot length for TM 106 X TM-2

Source of Variation	df	MS	F
REP	2	34.45	0.95
GEN	59	189.7	5.28*
Parents	1	1264.05	34.77*
Males	29	203.04	5.58*
Males x Parents	29	139.33	3.83*
Error	118	36.36	
Total	179		

Table 6.2: Components of variance for foot length for cross TM106 X TM-2

Component	Value
σ^2_m	27.78
σ^2_{mp}	34.32
σ^2_A	111.12
σ^2_D	34.32
σ^2_P	181.8
σ_P	13.48
h^2NS	0.61
GA (5%)	16.98

Table 6.3: Anova for NCD III for foot length cross DRMR 150-35 X TM-2

Source of Variation	DF	MS	F
REP	2	225.58	3.35
GEN	59	323.09	4.80*
Parents	1	14.45	0.21
Males	29	219.55	3.26*
Males x Parents	29	437.28	6.50*
Error	118	67.32	
Total	179		

Table 6.4. Components of variance for foot length for cross DRMR 150-35 X TM-2

Component	Value
σ^2_m	25.37
σ^2_{mp}	123.32
σ^2_A	101.49
σ^2_D	123.32
σ^2_P	292.13
σ_P	17.1
h^2NS	0.35
GA (5%)	12.23

Conclusion

Based on analysis of variance and mean performance it can be concluded that, lower foot length can be selected for increasing the seed yield of the genotype. The backcross (TM 106 X TM-2) X TM 106 is one promising line which shows low foot length along with high seed yield per plant. Based on diversity analysis, parents belonging to different clusters can be chosen as parents for developing crosses with better performance for traits and for recovering transgressive sergeants and better recombinants. From North Carolina Design III analysis for foot length, it can be concluded that foot length is governed by genes which are influenced by epistasis and linkage phase effects. Since the effects of linkages, if any, are dissipated by backcrossing in NCD III, therefore the estimates of components of variance are more precise in NCD III.

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