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Research Article
Genetic Analysis of Yield and Yield Attributing Traits in *Brassica napus* Using F$_2$ Progenies of Diallel Crosses

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Abstract

Background and Objective: Rapeseed (*Brassica napus* L.) is a leading oilseed crop in Bangladesh but its yield is almost lower comparing to the others rapeseed growing countries in the world. In the present study, diallel analysis in rapeseed was carried out to evaluate potential lines, hybrids and nature of gene action involved in the inheritance regarding yield and yield attributing traits. **Materials and Methods:** A total number of 21 plant materials were used in this experiment whereas six were used as parents and 15 were as F$_2$ segregating generations. The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. All data were analyzed by using one way analysis of variance (ANOVA) with the help of computer software package MSTAT-C program, followed by Duncan multiple range test. The combining ability analysis was performed using mean values according to Griffing's Model I and Method II. **Results:** Analysis of combining ability showed highly significant GCA (general combining ability) and SCA (specific combining ability) effects for the studied traits. Based on GCA, out of 15 crosses, the best general combiners were Nap-9908 for number of siliquae/plant, seed/siliqua and seed yield/plant. The higher magnitude of GCA variance was observed than that of SCA variance for all the studied characters except days to 50% flowering and number of secondary branches/plant. Similarly, based on SCA, the best combiners were Nap-9905×Nap-205 for number of primary branches and seed yield/plant, Nap-9901×Nap-205 for secondary branches, siliqua length and seeds/siliqua and Nap-9908×Nap-9901 for number of siliqua/plant could be utilize in future rapeseed breeding program. In the Vr-Wr graph, the partial dominance was observed for secondary branches/plant and seed yield/plant but except the two characters, all other characters showed over dominance. The graphical analysis also indicates wide genetic diversity among the parents. **Conclusion:** After assessing all the characters, Nap-9908 is the best general combiner and Nap-9905×Nap-205 is the best cross combiner and could be used as genetic materials for the higher rapeseed production in Bangladesh.

Key words: Diallel analysis, F$_2$ progenies, inheritance studies, rapeseed

INTRODUCTION

Rapeseed (*Brassica napus* L.) is a principal oilseed crop, which plays a vital role in the national economy of Bangladesh. But its yield production/unit area is very low compared to other rapeseed growing countries in the world due to the lack of advanced high yielding varieties. So, high yield potential genotypes can be fully exploited with its proper environment. The development of new Brassica lines with yield advancement requires information regarding the nature of combining abilities of parents and gene actions involved in expression of maturity and plant phonological traits[1,2]. Thus, the choice of assorted parents for hybridization must be based upon the combining ability of the diverse parental lines[3]. The measurement of genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the programme efficiently and effectively[4]. Heritability of any trait depends upon genetic properties of breeding material and environmental conditions in which experiments are carried out. A character which has higher range of genetic variability, high heritability and high genetic advance would be an effective tool to improve seed yield[5]. Morphological traits have been used to assess the genetic variation and relationships among populations of different oilseed species, for example, Brassica[6,7]. For the synthesis of genetically superior rapeseed variety/hybrids possessing harmonious combination of desirable parameters and increased adaptablity to a wide range of climatic conditions is prerequisite[7]. Success of any crop improvement program depends upon the presence of substantial amount of genetic variability and heritability[1].

Combining ability of the parents (GCA) and hybrids (SCA) are used to enlighten the nature of gene action concerned in the inheritance of traits[8]. Combining ability is an arithmetical technique used for analysis of diallel crosses in a universal theoretical form. This important information can give an essential implement for the rapeseed breeders in the selection of better parental combination for further improvement[7,9]. General combining ability (GCA) is used to identify the average performance of a line in hybrid combination. Specific combining ability (SCA) is used to point out those cases in which definite combinations do comparatively superior or inferior than would be expected on the basis of the mean performance of the lines involved[10]. Heritability is a mean of transmissibility of characters and as such divides the total variation into its genetic and environmental components[4,11,12]. The higher the heritability estimates the easier the selection criteria. Heritability is a proportion, its numerical value varies from 0.0-1.0.

Diallel mating is one of the methods used by rapeseed breeder to identify superior lines and their best promising hybrids through GCA and SCA effects. According to Crumpacker and Allard[13], diallel analysis could successfully unravel the major features of a genetic system and predict the outcome of selection in early generations. Griffing[14] approach of diallel analysis has been used widely for combining ability analysis. This technique elucidates the nature and magnitude of various types of gene actions involved in the expression of the studied traits. The variance for GCA includes the additive portion of the total variance, whereas for SCA includes the non additive portion of the total variance, arising largely from dominance and epistatic deviations[15,16]. Therefore, the present study was conducted with the objectives to quantify the contribution of (1) The combining ability in the reference population for yield and yield contributing characters, (2) Relationship among the different traits and their contribution to the yield and (3) Select promising genotypes considering high yielding, early maturity and shading resistance plants.

MATERIALS AND METHODS

A total number of 21 materials were used in this experiment whereas six (Nap-205, Nap-108, Nap-9901, Nap-9908, Nap-0130 and Nap-9905) were used as parents, 15 were F_2 segregating generations (Table 1) in the experimental farm at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh in the year of 2012-2013. The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The total area of the experiment was $20\,m \times 15\,m = 300\,m^2$. Each replication size was $56 \times 4\,m$ and the distance between replication to replication was 1 m. The spacing between lines was 25 cm. The seeds were placed at about 2.5-3.5 cm depth in the soil. The plots were fertilized with a general dose of urea, triple super phosphate (TSP), muriate of potash (MOP) and gypsum as sources of nitrogen, phosphorus, potassium and sulphur and were applied at 250, 175, 85 and 150 kg ha^{-1}, respectively. Intercultural operations such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. When 80% of the plants showed symptoms of maturity i.e., straw color of siliqua, leaves, stems desirable seed color in the mature siliqua, the crop was assessed to attain maturity. For studying different genetic parameters and inter-relationships among ten characters were taken into consideration. The data were recorded on 40 selected plants for each cross and ten selected plants for each parent on the following traits-plant height (cm), number of primary branches/plant, number of secondary branches/plant, days to 50% flowering, days to 80% maturity,

number of siliquae/plant, siliqua length (cm), number of seeds/siliqua, 1000 seed weight (g) and seed yield/plant (g).

Statistical analysis: The collected data were then analyzed statistically with the help of computer software package MSTAT-C program using the analysis of variance (one way ANOVA). The mean differences among the treatments were compared by Duncan's Multiple Range Test (DMRT) at 5% level of significant[17].

The combining ability analysis was performed using mean values following Model I and Method II of Griffing[14] method. The statistical t-student test was applied to examine the effects of general combining ability (GCA) and specific combining ability (SCA). The analysis of variance for combining ability was carried out using block mean of each entry (diallel family) as follows:

Item	df	Sum of squares	MSS	Expected MSS
GCA	P-1	S_g	Mg	$\sigma_e^2 + (P+2)\frac{1}{(P-1)}\sum g_i^2$
SCA	P(P-1)/2	S_s	Ms	$\sigma_e^2 + \frac{2}{P(P-1)}\sum_i \sum_j S_{ij}^2$
Error	(b-1)(e-1)	S_e	M_e'	σ_e^2

Where:

GCA = General combining ability

SCA = Specific combining ability

p = Number of parents

b = Number of blocks or replications

e = Number of entry (family)

Y_i = Array total of the ith parent

Y_{ii} = Mean value l of the ith parent

Y = Grand total of the ½ p(p-1) crosses and parental lines

Y_{ij} = Progeny mean values in the diallel table

S_e = Sum of square due to error

The genetic parameters such as D (additive variance), H_1 and H_2 (estimate of dominance and dominance×dominance interaction, respectively), $(H_1/D)^{1/2}$ (average degree of dominance), $H_2/4H_1$ (the proportion of genes with positive and negative effects in the parents), F (dominant to recessive alleles frequency in parents), h^2 (overall dominance effect due to heterozygous loci), dominant to recessive genes ratio in parents $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}\_F)$, E (environmental effect), broad and narrow sense heritability's were computed. Diallel analysis for the components of genetic variances and Wr-Vr graphs for all the characters were done according to Hayman[18]. To prove the additive-dominance adequate for the means of the studied parameter, the data were subjected to two tests. One test was t^2 test for the uniformity of Wr and Vr

and the other test was the analysis of regression coefficient. For the fulfillment of all assumptions of diallel analysis, the result of the t^2 for the uniformity of Wr and Vr should be constant over arrays, whereas following Mather and Jinks[19] the analysis of regression coefficient for all parameters under study should be differ significantly from zero but not from unity. Narrow-sense heritability (h^2) estimates were obtained using the following formula suggested by Verhalen and Murray[20]:

$$h^2 = \frac{0.25D}{0.25D+0.0625H1-0.125F+E}\times100$$

RESULTS AND DISCUSSION

Plant height: Plant height is the significant traits for the rapeseed breeders for the development of new *Brassica napus* lines having short stature and is less likely to lodge. So, negative combining ability effects are desirable for plant height in rapeseed. In the present study, an attempt has been made to identify the best lines and cross combinations based on combining ability for the seed trait. As illustrated the parents and cross combinations in Table 1, for parent, the lowest plant height was observed in Nap-130 (105.60 cm) and for hybrid, Nap-205×Nap-130 (95.20 cm) showed the lowest plant height followed by Nap-108×Nap-9901 (97.20 cm). Whereas the parent Nap-205 exhibited the highest plant height (118.81). The highest plant height was found in the hybrid Nap-9908×Nap-130 (124.87 cm). These hybrids were approximately 4-6 cm higher than the parents (Table 2). Out of six parental GCA, three parents showed negative GCA effect. The highest negative C_nCA effects (-3.782) was provided by Nap-108. The other parents which represented negative GCA were Nap-9901 (-1.017) and Nap-103 (-3.322). Those parents with positive and significant GCA effects were considered as good general combiner for the traits aimed to promote desirable plant height in their crosses (Table 3). The parent Nap-205 showed positive GCA effects. Chowdhury *et al.*[21] obtained dwarfness in YSK-8501 in *Brassica campestris* L. Similarly, out of 15 crosses, Nap-9908×Nap-130 (13.27) showed the highest significant positive SCA effects and Nap-205×Nap-130 (-11.28) showed the highest significant negative SCA effects for plant height and could be considered as the best combination. Thus, the cross combination Nap-9908×Nap-130 could be used for tallness of this crop (Table 4). Acharya and Swain[22] obtained dwarfness in Varuna×Pusa Bahar in *Brassica juncea*.

Table 1: Cross combinations in half diallel system of six varieties in *Brassica napus* L.

Parents	Nap-9905	Nap-108	Nap-9908	Nap-9901	Nap-205	Nap-130
Nap-9905	Nap-9905	Nap-9905×Nap-108(C1)	Nap-9905×Nap-9908(C$_2$)	Nap-9905×Nap-9901(C$_3$)	Nap-9905×Nap-205(C$_4$)	Nap-9905×Nap-130(C$_5$)
Nap-108		Nap-108	Nap-108×Nap-9908(C$_6$)	Nap-108×Nap-9901(C$_7$)	Nap-108×Nap-205(C$_8$)	Nap-108×Nap-130(C$_9$)
Nap-9908			Nap-9908	Nap-9908×Nap-9901(C$_{10}$)	Nap-9908×Nap-205(C$_{11}$)	Nap-9908×Nap-205(C$_{12}$)
Nap-9901				Nap-9901	Nap-9901×Nap-205(C$_{13}$)	Nap-9901×Nap-130(C$_{14}$)
Nap-205					Nap205	Nap-205×Nap-130(C$_{15}$)
Nap-130						Nap-130

Table 2: Mean performance for 10 different characters in 6 parents and their 15 F$_1$'s of *Brassica napus* L.

Cross combination	Plant height (cm)	Days to 50% flowering	Days to maturity	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Siliqua length (cm)	Number of seeds/siliqua	Seed yield/plant (g)	1000 seed weight (g)
Nap-9905	115.47	29	100	4.23	2.53	122.5	8.51	24.11	23.73	4.60
Nap-9901	105.82	30	99	4.43	1.93	147.23	7.72	24.69	27.23	4.42
Nap-205	118.81	34	102	4.07	1.53	94.53	8.38	26.16	19.83	4.29
Nap-108	107.14	30	98	4.91	2.63	102.57	7.41	23.09	16.62	4.21
Nap-9908	114.67	29	98	3.17	2.57	151.10	8.58	25.53	32.38	4.53
Nap-130	105.60	29	97	4.10	2.30	116.10	7.65	22.36	18.34	4.57
Nap-9905×Nap-108	117.47	30	98	3.20	3.97	173.19	8.34	26.87	35.06	4.19
Nap-9905×Nap-9908	106.08	31	98	4.78	1.80	179.94	8.87	28.13	40.27	4.35
Nap-9905×Nap-9901	114.83	30	98	4.63	3.53	117.90	8.61	25.65	19.98	4.16
Nap-9905×Nap-205	110.90	29	97	5.57	3.53	220.17	8.40	26.80	107.54	4.39
Nap-9905×Nap-130	100.79	29	97	3.67	2.57	107.80	8.02	24.15	17.21	4.54
Nap-108×Nap-9908	117.90	32	98	3.07	2.30	123.88	8.20	24.25	20.92	4.63
Nap-108×Nap-9901	97.20	30	98	5.73	3.90	170.33	7.17	25.89	24.92	4.14
Nap-108×Nap-205	105.77	33	100	5.20	3.80	198.57	7.55	21.80	29.19	4.26
Nap-108×Nap-130	106.97	30	99	2.77	2.63	164.47	8.26	21.85	21.61	4.67
Nap-9908×Nap-9901	102.37	29	97	6.07	3.90	215.97	7.89	23.67	32.45	4.44
Nap-9908×Nap-205	121.23	32	101	5.50	2.97	137.33	8.55	24.45	20.83	4.34
Nap-9908×Nap-130	124.87	31	97	4.43	3.30	195.80	7.96	23.76	29.39	4.34
Nap-9901×Nap-205	106.66	32	103	5.89	5.03	217.35	8.80	27.81	29.77	4.56
Nap-9901×Nap-130	99.47	30	99	4.08	2.88	108.21	7.74	23.25	21.80	4.58
Nap-205×Nap-130	95.20	31	108	3.70	1.74	98.94	8.25	26.79	20.27	4.18
Grand mean	109.30	309	98	4.44	2.85	150.66	8.14	24.81	29.02	4.41

Table 3: General combining ability (GCA) effects for 6 parents in 6×6 half diallel crosses of *Brassica napus* L.

Cross combination	Plant height (cm)	Days to 50% flowering	Days to maturity	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Siliqua length (cm)	Number of seeds/siliqua	Seed yield/ plant (g)	1000 seed weight (g)
Nap-9905	1.992	-0.069	-0.069	-0.094	-0.228	-1.328	0.287*	0.767	8.051	0.042
Nap-9901	-1.017	0.264	0.556*	-0.278	0.009	8.785*	-0.249	-0.458	-2.119	-0.015
Nap-205	5.626*	0.097	-0.319	0.114	0.047	-1.579	0.16	0.363	-2.45	-0.023
Nap-108	-3.782	0.056	0.264	0.644*	0.079	-2.467	-0.239	-0.154	-5.119	-0.07
Nap-9908	0.503	-0.028	-0.153	0.141	0.301	14.991*	0.218	0.629*	8.657*	-0.006
Nap-130	-3.322	-0.319	-0.278	-0.527	-0.209	-18.402	-0.177	-1.147	-7.02	0.073*
SE (gi)	1.706222	0.227976	0.249614	0.195585	0.19948	8.134155	0.102375	0.422002	4.566308	0.03091
SE (sij)	4.686014	0.62612	0.685546	0.53716	0.547857	22.33986	0.281166	1.158996	12.54103	0.084892

*p<0.05

Table 4: Specific combining ability (SCA) effects for 15 crosses in 6×6 half diallel crosses of *Brassica napus* L.

| Cross combination	Plant height (cm)	Days to 50% flowering	Days to maturity	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Siliqua length (cm)	Number of seeds/siliqua	Seed yield/ plant (g)	1000 seed weight (g)
Nap-9905×Nap-108	7.20*	0.06	0.15	-0.86	-0.33	15.07	0.16	1.75	0.11	-0.24
Nap-9905×Nap-9908	-10.84	1.23	0.36	0.32	1.30*	32.19	0.28	2.19	5.65	-0.07
Nap-9905×Nap-9901	7.33*	0.27	0.11	-0.35	-0.90	-28.97	0.43	0.22	-11.96	-0.22
Nap-9905×Nap-205	-0.89	-0.32	-0.14	1.08**	0.61	55.84*	-0.24	0.60	61.82**	-0.05
Nap-9905×Nap-130	-7.18	-0.69	-0.68	-0.15	0.16	-23.13	-0.23	-0.28	-12.84	0.02
Nap-108×Nap-9908	4.00	-0.77	0.40	-1.21	-0.60	-33.98	0.15	-0.47	-3.53	0.26**
Nap-108×Nap-9901	-7.30	-0.07	-0.18	0.93*	0.97	13.35	-0.48	1.69	3.14	-0.18
Nap-108×Nap-205	-3.02	1.02	-0.10	0.90*	0.64	24.13	-0.56	-3.18	-6.36	-0.12
Nap-108×Nap-130	2.01	0.31	0.69	-0.87	-0.02	23.42	0.55	-1.36	1.73	0.20*
Nap-9908×Nap-9901	-8.77	-0.57	-0.64	0.87	0.93	69.35**	-0.16	-1.35	11.00	0.12
Nap-9908×Nap-205	5.81	-1.15	-0.89	0.81	-0.23	-26.74	0.04	-1.35	-14.39	-0.04
Nap-9908×Nap-130	13.27**	-0.86	-0.43	0.41	0.62	65.12**	-0.16	-0.27	9.84	-0.12
Nap-9901×Nap-205	0.64	-0.44	0.52	-0.66	1.80**	54.16*	0.69*	2.53*	-2.78	0.23*
Nap-9901×Nap-130	-2.72	0.52	0.65	-0.48	0.16	-21.58	0.02	-0.27	4.92	0.17
Nap-205× Nap-130	-11.28**	1.60	0.73	-0.35	-1.20	-48.31**	0.07	2.50	-10.39**	-0.29
SEd (gi-gj) =	2.643268	0.353179	0.3867	0.30299	0.309033	12.60138	0.158599	0.653762	7.074094	0.04788
SEd (sij-sik) =	6.993431	0.934424	1.023113	0.80166	0.817625	33.34	0.419614	1.729692	18.71629	0.12669
SEd (sij-skl) =	6.474659	0.865108	0.947218	0.74219	0.756973	30.86695	0.388487	1.609384	17.32792	0.11729

**p<0.01, *p<0.05
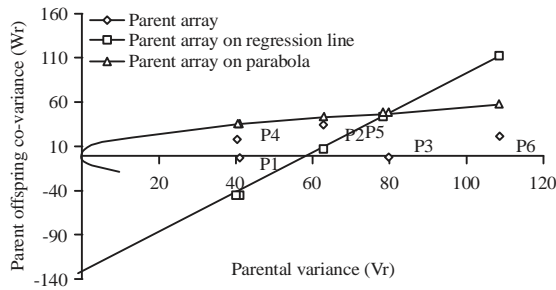
Fig. 1: Vr-Wr graph for plant height in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 1). The distribution of array points indicated two parents Nap-9901 (p_4) and Nap-9905 (p_1) contained most dominant alleles as they fell closer to the point of origin. The parents Nap-108 (p_2) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. Whereas, rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Both additive and dominant component were significant, but due to higher magnitude dominant gene effects the latter appeared to have more control of the character. Inequality of H_1 (359.059) and H_2 (797.434) showed the unequal frequency of both positive and negative alleles. Negative F value (-61.146) indicated that the recessive alleles were predominantly in excess in its inheritance (Table 5), the estimate was however non-significant. Farshadfar *et al.*[23] also reported both additive and dominant gene action in *B. napus*. The dominance effect (a^2) was negative and non-significant. Over dominance was found for plant height. The value of $H_2/4H_1$ indicates asymmetrical distribution of positive and negative alleles. The environmental component E effect (29.847) was also significant playing a role in the expression of this trait. The analysis gave narrow sense heritability (h^2n) estimate of 12.96%. Rao and Gulati[24] also reported high broad sense heritability and low narrow sense heritability for the stated trait in *B. juncea*.

Days to 50% flowering: Early flowering is one of the important traits in majority of the crop plants as it offers adequate time for grain development and can result in early maturity. In case of days to 50% flowering, it ranged from 28-33 days for parent. However, the parent Nap-9905, Nap-9908 and Nap-130 (29 days) flowered within the lowest time but the parent Nap-205 (34 days) took the highest duration. On the other hand, the hybrid combination

Table 5: Components of variation and genetic parameters for ten characters in a 6x6 F_2 half diallel crosses of *Brassica napus* L.

| Items	Plant height (cm)	Days to 50% flowering	Days to maturity	Number of primary branches/plant	Number of secondary branches/plant	Number of siliquae/plant	Siliqua length (cm)	Number of seeds/siliqua	Seed yield/ plant (g)	1000 seed weight (g)
D	3.149**	0.149**	-0.289	-0.031	-0.169	-120.635	0.155**	0.420**	-168.28**	0.033**
F	-61.146	1.507**	-0.746	0.673**	0.492**	130.610**	-0.065	1.324**	-403.89**	0.123**
H_1	359.059**	2.051**	2.147**	0.674**	-0.532	2628.69**	2.657**	13.428**	148.854**	0.215**
H_2	797.434**	9.500**	3.307**	9.817**	12.394**	6786.61**	1.764**	42.191**	4968.88**	0.527**
h^2	-53.087	0.171**	1.286**	5.138**	11.981**	167.214**	1.704**	8.207**	-1.48	-1.057
E	29.847**	0.492**	0.619	0.359**	0.371**	650.630**	0.099**	1.656**	204.067	0.009**
¼ [(H₁/D)]½	5.339	1.857	0	0	0.888	0	2.068	2.828	0	1.272
$H_2/4H_1$	0.555	1.158	0.385	3.643	-5.829	2.548	0.166	0.785	8.345	0.012
h^2/H_2	0.06657	0.01801	0.38881	0.52336	0.9666	0.00624	0.96632	0.19452	0.0003	0.98068
h^2n	0.1296	0.0792	0.0935	0.025	0.1797	0.039	0.1242	0.0431	0.1896	0.528

**p<0.01
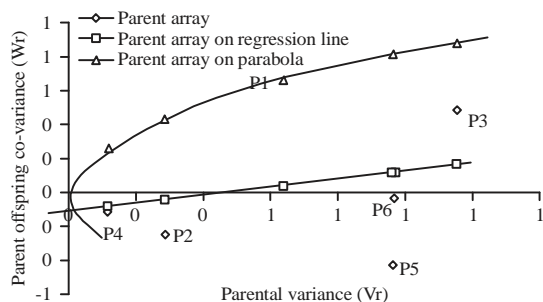
Fig. 2: Vr-Wr graph for days to flowering in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130
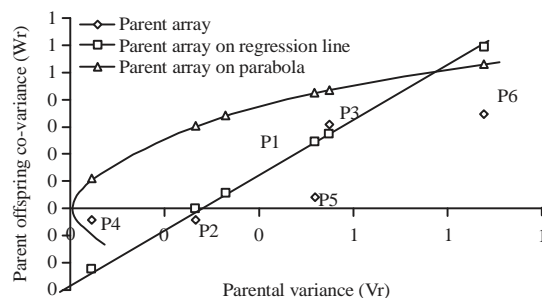

Fig. 3: Vr-Wr graph for days to maturity in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130

Nap-9905×Nap-130 (29 days) produced 50% flowers within shortest possible time (Table 2). A significant positive GCA effect is useful for shorter growth duration. Out of six parents, three parents were exhibited insignificant and positive GCA effect. Other three parents showed insignificant and negative GCA values. None parent could be used to improve this character (Table 3). Chowdhury *et al.*[21] found earliness in Din-2 in *Brassia napus* L. The highest positive SCA value was exhibited by Nap-205×Nap-130 (1.60) followed by Nap-9905×Nap-9908 (1.23) for days to 50% flowering but it was non-significant (Table 4). On the other hand, the highest negative SCA value was provided by Nap-9908×Nap-205 (-1.15) but it was also insignificant. Singh *et al.*[25] obtained earliness on YSK-8501×SS-2 in *Brassica campestris*.

The regression line intersected below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 2). The distribution of array points indicated two parents Nap-9901 (p_4) and Nap-108 (p_2) contained most dominant alleles as they fell closer to the point of origin. The parents Nap-9905 (p_1) fallen at the middle portion, means they contained equal frequencies of dominant and recessive alleles. Whereas, rest of the parents fallen far from the origin indicated that they possess maximum frequency of recessive alleles. Dominance component was significant and H_1 was greater in magnitude than additive component, indicating greater role of dominance component in the inheritance. Positive value of F revealed that the dominant alleles were predominantly in excess in its inheritance (Table 5) but then the estimate was significant H_2 value differed from H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. The results of dominants effect (h^2) were positive and significant. Over dominance was found for days to 50% flowering. The analysis gives narrow sense heritability was 7.9% (Table 5). Vaghela *et al.*[26] and Nasim *et al.*[27] reported predominant role of non-additive genetic effects in inheritance of days to 50% flowering.

Days to 80% maturity: Most of the rapeseed breeding programs primarily focused on development of new lines with early maturity as it escape genotypes form environmental stresses. Considering earliness, the parent Nap-130 (97 days) showed the lowest duration for maturation but the parent Nap-205 (102 days) had taken the highest duration. On the other hand, the hybrid combination Nap-9905×Nap-130, Nap-9908×Nap-9901, Nap-9908×Nap-130 (97 days) matured with the lowest growth duration which was required same days for maturity (Table 2). The parent Nap-9901 (0.556) provided the highest positive GCA effects for days to maturity hence the parent were desirable general combiners to promote the earliness in *Brassica rapa* L. (Table 3). Four parent Nap-9905 (-0.069), Nap-205 (-0.319), Nap-9908 (-0.153) and Nap-130 (-0.278) showed insignificant and negative GCA effects. The highest positive SCA value was exhibited by Nap-205×Nap-130 (0.73) followed by Nap-108×Nap-130 (0.69) for days to maturity but it was insignificant (Table 4). Shehzad *et al.*[3] reported highly significant GCA and SCA effects in Brassica napus. On the other hand the highest negative SCA value was provided by Nap-9908×Nap-205 (0.89) but it was also insignificant. Acharya and Swain[22] found early maturity in JC 26×Jai Kisan in *Brassica juncea*.

The regression line intersected above the point of origin suggesting partial dominance gene action for controlling the trait (Fig. 3). The parents Nap-9901 (p_4) and Nap-108 (p_2) contained maximum dominant alleles as they fell very closer to the point of origin. The parent Nap-130 (p_6) fell far from the origin and thus it contained maximum frequency of recessive alleles. Ishaq and Raziuddin[8] observed partial dominance in *Brassica napus*. Trivedi and Mukherjee[28] found over dominance in *Brassica juncea*. The components H_1 and H_2 are significant but D is not significant for days to maturity (Table 5). This indicates the importance of dominance effect of genes in the days to maturity. The magnitude of H_1 was much higher than D, suggesting the preponderance of dominance
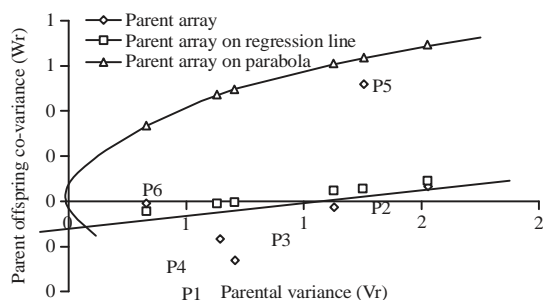
Fig. 4: Vr-Wr graph for primary branches/plant in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130

type of gene action for this trait. Dominance effect (h^2) was found positive and significant. The $[¼ (H_1/D)_4]^{½}$ value was zero that means complete dominance for the character. The analysis gives narrow sense heritability as 9.3% (Table 5). The gene action in current study is in conformity with Vaghela *et al.*[26] and Nasim *et al.*[6], who reported predominant role of non-additive genetic effects in inheritance of days to maturity.

Number of primary branches/plant: More numbers of healthier primary branches/plant with more number of pods are the major yield contributing traits therefore, positive combining ability effects are desirable for number of branches in *Brassica napus*. In this parameter, the value ranged from 2.77-6.07 in all the parents and the hybrids. As parent, Nap-108 (4.91) showed the highest value while as hybrid, the highest value was in the combination of Nap-9908×Nap-9901 (6.07) which was higher than parents (Table 2). There was only one parent viz. Nap-108 (0.644) provided significant and positive GCA effects out of six parents which indicated that this parent was good general combiners for promising primary branches. So, such parent was considered as good to use in the breeding programme for more primary branches (Table 3). Other parents showed insignificant positive and negative effects. Ishaq and Raziuddin[8] obtained more primary branches on the genotype AUP-14 in *Brassica Napus* L. Singh *et al.*[25] observed maximum number of primary branches on YSP-842 in *Brassica campestris* L. The cross combination Nap-9905×Nap-205 (1.08) was found to be the best to improve this crop with more number of primary branches as it showed the highest significant and positive SCA effects for this trait (Table 4). Gupta *et al.*[10] and Fayyaz *et al.*[1] reported highly significant GCA and SCA effects in rapeseed.

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance

gene action for controlling the trait (Fig. 4). The parent Nap-130 (p_6) and Nap-9901 (p_4) fell close to the origin means they contained maximum frequencies of dominant alleles. The parent Nap-9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The other parents fallen far from the origin and thus it contained maximum frequency of recessive alleles. The components H_1 and H_2 are significant but D is not significant and the magnitude of H_1 was much higher than D, suggesting the preponderance of dominance type of gene action for this trait. Positive value of F revealed that the dominant alleles were predominantly in excess in its inheritance (Table 5) and the estimate was significant. Dominance effect (a^2) were positive and significant. Marinkovic *et al.*[11] also reported higher and significant H component and non-significant value of D component for primary branches. Low narrow sense heritability (0.025) and high (0.52336) broad sense heritability (Table 5) was observed for primary branches/plant showed higher contribution of dominance genetic variation to this trait as compared to additive genetic variation. Rao and Gulati[24] reported low to medium narrow sense heritability for primary branches/plant. Singh *et al.*[12] reported similar results of high broad sense heritability in *B. compestris*.

Number of secondary branches/plant: For the number of secondary branches/plant, the parent Nap-108 (2.63) showed the highest value. Similarly, in the hybrid, the highest value of number of secondary branches/plant was provided by the combination Nap-108×Nap-9901 and Nap-9908×Nap-9901 (3.90) which were almost double than the average value of the parents (Table 2). The highest significant and positive value for this character was revealed by Nap-9908 (1.30). Thus, Nap-9901×Nap-205 (1.80) and Nap-9905×Nap-9908 (1.30) were the best cross combinations to improve plants with more number of secondary branches and Nap-205×Nap-130 (-1.20) was the best combinations to obtain plants with minimum secondary branches (Table 4). Chowdhury *et al.*[21] found maximum secondary branches in Sampad× Din-2. Acharya and Swain[22] obtained more secondary branches in BM 20-12-3×JC 26 in *Brassica juncea*. For number of secondary branches/plant, four parents were exhibited insignificant and negative effect. Other two parents showed insignificant and positive GCA values. None parent could be used to improve this character.

The regression line intersected the Wr axis below the point of origin indicating the existence of partial dominance gene action for controlling the trait (Fig. 5). The parent Nap-130 (p_6) and Nap-108 (p_2) fell closer to the point of origin
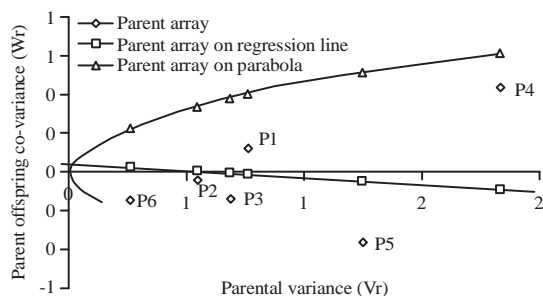
Fig. 5: Vr-Wr graph for secondary branches/plant in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130
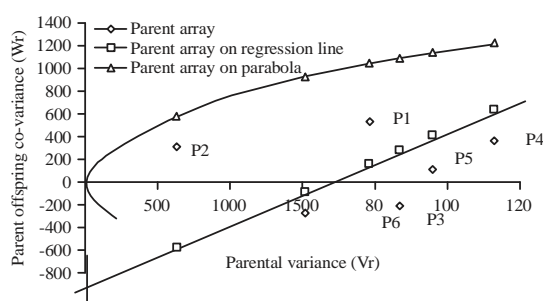

Fig. 6: Vr-Wr graph for number of siliquae/plant in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130

suggesting they contained maximum number of dominant alleles. The parent Nap-9908 (p_3) and Nap-9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parent Nap-9901 (p_4) and Nap-205 (p_5) fell far from the origin indicating the presence of maximum frequency of recessive alleles. Chaghakaboodi *et al.*[5] obtained partial dominance in *Brassica napus.* Result suggested that only additive component played role in the expression of the trait. Significant and positive indicates that the dominant alleles were predominantly in excess in its inheritance and significant. Dominance effect was significant. The narrow sense heritability was 17.9% (Table 5). Rahman *et al.*[29], obtained a result which is agreed the present study.

Number of siliquae/plant: Number of siliquae/plant was varied from 94.53-151.10 where the parent Nap-205 produced the lowest (94.53) and Nap-9908 produced the highest (151.10) number of siliquae/plant considering the hybrid performance, it was ranged from 98.94-220.17. In the hybrid combinations, Nap-9905×Nap-205 provided the highest (220.17) number which was much higher than its parent

(Table 2). The parent Nap-9908 exhibited the highest (14.991) significant GCA effects for this character. This parent was selected as the best general combiner and desirable to use in hybridization program to improve the number of siliquae/plant in *Brassica napus* L. (Table 3). On the other hand, next significant and positive GCA value was provided by Nap-9901 (8.785). The other parent showed insignificant and negative GCA effects. Chowdhury *et al.*[21] found the highest number of siliquae in Din-2 *Brassica rapa.* Among the cross combinations, Nap-9908×Nap-9901 (69.35) showed the highest significant and positive SCA effects followed by Nap-9908×Nap-130 (65.12), Nap-9905×Nap-205 (55.84) and Nap-9901×Nap-205 (54.19). On the other hand, Nap-205×Nap-130 (-48.31) showed the significant but negative SCA effects (Table 4). So, Nap-9908×Nap-9901 was the best combination for this trait. Singh and Murty[30] observed more siliquae/plant in YSP-842×SS-3 in *Brassica rapa.* Acharya and Swain[22] obtained highest siliquae/plant in Pusa Bahar×JC 26 in *Brassica juncea.*

The regression line intersected the Wr axis below the point of origin indicating the existence of over dominance gene action for controlling the trait (Fig. 6). The parent Nap-108 (p_2) contained maximum number of dominant alleles as it fell closer to the point of origin. The parents Nap-130 (p_6) and Nap-9905 (p_1) fallen at the middle portion means they contained equal frequencies of dominant and recessive alleles. The parent Nap-9908 (p_3), Nap-205 (p_5) and Nap-9901 (p_4) fell far from the origin indicating the presence of maximum frequency of recessive alleles. Trivedi and Mukherjee[28] obtained over dominance in *Brassica juncea.* Results suggested that only additive component played roe in the expression of the trait. Significant and positive F value revealed that the dominant alleles were predominantly in excess in its inheritance overall difference between parent and cross were substantiated by significant h^2 value. The $H_2/4H_1$ value is not equal to unity that positive and negative values were asymmetrically distributed. The narrow sense heritability was 3.9% (Table 5). Khan and Khan[31] reported narrow sense heritability for pods/plant in *B. napus.*

Siliqua length: Positive combining ability effects for siliquae length are desirable and longer siliquae are likely to host more seeds. Siliqua length of parent was ranged from 7.41-8.58. The parent Nap-9908 produced the longest (8.58 cm) siliqua while the parent Nap-108 produced the shortest (7.41 cm) siliqua. On the other hand, the values varied from 7.17-8.87 cm from hybrids. In this regard, the hybrid combination Nap-9905×Nap-9908 (8.87 cm) exhibited the highest length
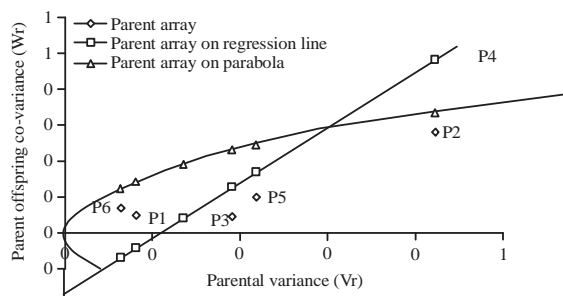
Fig. 7: Vr-Wr graph for length of siliqua in *Brassica napus*,
P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901,
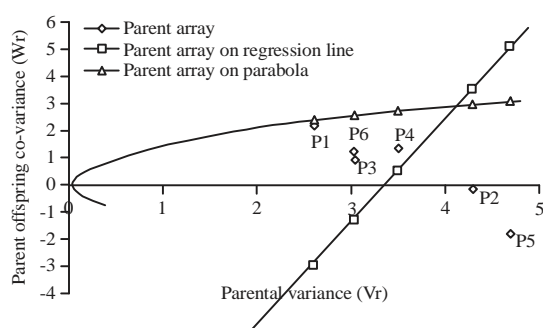P5: Nap-205, P6: Nap-130

Fig. 8: Vr-Wr graph for seeds/siliquae in *Brassica napus*,
P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901,
P5: Nap-205, P6: Nap-130

of siliqua and that was higher than that of its' either parent (Table 2). Out of six parents, Nap-9908 (0.629) showed significant and positive GCA effects which was selected as the best general combiner to use in breeding program (Table 3). Other parent showed insignificant positive and negative GCA effect. Among the cross combinations, Nap-9901×Nap-205 (0.69) showed the significant and positive SCA effects. On the other side, the remaining combinations showed insignificant positive or negative SCA effects for the trait (Table 5). Hence, the cross combination Nap-9901×Nap-205 was the best for siliqua length. Acharya and Swain[22] observed maximum siliqua length in BM 20-12-3×Pusa Bahar in *Brassica juncea*.

The regression line intersected the Wr axis above the point of origin suggesting partial dominance gene action for controlling the trait (Fig. 7). The parent Nap-130 (p_6) and Nap-9905 (p_1) contained maximum dominant alleles as it fell closer to the point of origin. The parents Nap-9908 (p_3) and Nap-205 (p_5) fallen at the nearly middle portion means they contained nearly equal frequencies of dominant and recessive alleles. The parent Nap-108 (p_2) and Nap-9901 (p_4) fell far from the origin and thus it contained maximum frequency of recessive alleles. Ali *et al.*[9] found over dominance

in *Brassica napus*. Both additive and dominance components were significant for the trait. But dominance component was preponderant. Negative value of F suggested that the presence of recessive alleles but the estimate was non-significant. The result of dominance effect (h^2) was positive and significant over dominance was found for this trait. The $H_2/4H_1$ was asymmetrical distribution of positive and negative alleles in the parent. The narrow sense heritability was 12.42% (Table 5). These results are corroborated with the findings of Nasim *et al.*[27].

Seeds/siliqua: As genotypic mean square was highly significant, so diallel analysis was carried out seeds/siliqua. Seed/siliqua also varied from 22.36-25.53 and from 21.80-28.13 in hybrids. The hybrid Nap-9905×Nap-9908 (28.13) produced an excellent number of seeds/siliqua which was higher than any one parent in this programme (Table 2). Out of six parents, only Nap-9908 was exhibited significant and positive GCA effect (0.629). So the parent would be considered as general combiner for the character and could be used for hybrid production with more seeds/siliqua development in breeding programme. Rest of the parent provided insignificant GCA effects. Among the cross combinations, Nap-9901×Nap-205 (2.53) exhibited the highest significant and positive SCA value. The other cross combinations showed either insignificant or negative SCA effects. Hence, Nap-9901×Nap-205 was the best cross combination to increase the number of seeds/siliqua (Table 4). Singh *et al.*[25] obtained more seeds/siliqua in YSP-842×YSK-8501 in *Brassica campestris*. Acharya and Swain[22] observed maximum number of seeds/siliqua in BM 20-12-3×Pusa Bahar in *Brassica juncea*.

The regression line intersected the Wr axis above the point of origin suggesting over dominance gene action for controlling the trait (Fig. 8). The parent Nap-9905 (p_1) contained maximum dominant alleles as it fell closer to the point of origin. The parents Nap-205 (p_5) fallen far from the origin indicating the presence of maximum frequency of recessive alleles in this parent. Ishaq and Raziuddin[8] observed over dominance in *Brassica napus*, Ali *et al.*[16] found over dominance in *Brassica napus.* For seed/siliqua most of the genetic parameters (D, H_1, H_2) were significant (Table 5). Both additive and dominant effects of genes were important for the character expression. But H_1 was greater than D indicating greater role of dominance component in the inheritance of the trail. Positive and significant F value revealed that the dominant alleles were predominantly in excess in its inheritance. Dominance effect was significant. Positive and negative alleles were more or less asymmetrically distributed
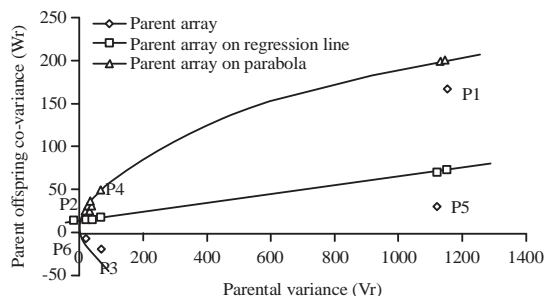
Fig. 9: Vr-Wr graph for seed yield/plant in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap-130

as $H_2/4H_1$ value was not exactly 0.25. The narrow sense heritability was 4.3% (Table 5). Khan and Khan[31] also reported low narrow sense heritability for this trait in *B. napus*.

Seed yield/plant: Genotypic mean square was highly significant therefore, diallel analysis was carried out. Seed yield/plant of the genotype varied from 16.62-32.38 g in parents and from 17.21-107.54 g hybrids. The highest seed yield of the parent was found in Nap-9908 (32.38 g) whereas, the lowest in Nap-108 (16.62 g). Similarly, the highest seed yield was also observed in the hybrid Nap-9905×Nap-205 (107.54 g) which was almost 3 times highest than both its parent (Table 2). A significant and positive GCA effect was observed in Nap-9908 (8.657). This parent might be selected as promising general combiner for high yield. On the other hand, Nap-9901 (-2.119), Nap-205 (-2.450), Nap-108 (-5.119) and Nap-130 (-7.020) showed insignificant and negative GCA effect and were not fit for increasing seed yield (Table 3) which indicates that the parents were not good for improving seed yield/plant. Chowdhury *et al.*[21] found highest seed yield/plant in *Brassica rapa* L. In the cross combination, Nap-9905×Nap-205 (61.82) exhibited the highest significant and positive SCA effects for seed yield/plant. The other cross combinations Nap-205×Nap-130 (-10.39) showed the significant and negative SCA effects. (Table 4). Singh *et al.*[25] observed more seed yield/plant in YSP-842×YSK-8501 in *Brassica campestris*. Acharya and Swaim[22] found maximum seed yield/plant in Pusa Bold× Pusa Bahar in *Brassica juncea*.

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 9). The parents Nap-108 (p2), Nap-9908 (p3), Nap-9901 (p4) and Nap-130 (p6) fell closer to the point of origin indicating that it contained maximum dominant alleles. The parent Nap-9905 (p1) and Nap-205 (p5) fell far from the origin indicated that they possess maximum

frequency of recessive alleles. Iqbal *et al.*[7] obtained over dominance in *Brassica rapa*. Farshadfar *et al.*[23] also reported the effectiveness of over dominance for seed yield/plant in *B. napus*. Dominance component was significant and H_1 was greater in magnitude than additive component, indicating greater role of dominance component in the inheritance. Significant and negative F value indicated that the recessive alleles were predominantly in excess in its inheritance (Table 5). Dominance effect was negative and significant. The $H_2/4H_1$ value indicates that there was asymmetrical distribution of positive and negative alleles in the parents. The narrow sense heritability was 18.96% (Table 5). Rahman *et al.*[29] also reported higher number of dominant genes for seed weight/plant trait in toria. h^2 value (1822.47) and environmental component E effect value (24.62) were significant showing their role in the expression of seed weight/plant. Ali *et al.*[16] also agreed with the similar result of the present study.

Thousand seed weight: Positive combining ability effects for 1000 seed weight is desirable, heavier the seed higher will be the yield. It was varied with some extent i.e., from 4.21-4.60 g in parent and from 4.14-4.67 g in hybrids. However, the heaviest seeds were produced by the parent Nap-9905 (4.60) and also by the hybrid combination Nap-108×Nap-130 (4.670. The hybrids produced the highest weighted seeds which was higher than it's both parents (Table 2). Most of the parent showed insignificant positive and negative GCA effect except Nap-130 (0.073). Nap-130 line showed significant and positive GCA effect and could be considered as the best general combiner for this trait. Chowdhury *et al.*[21] found highest seed weight in Dhali in *Brassica rapa* L. In the cross combination, Nap-108×Nap-9908 (0.26) exhibited the highest significant and positive SCA effects followed by Nap-108×Nap-130 (0.20) and Nap-9901×Nap-205 (0.23). The remaining combinations showed insignificant effects for the trait. Acharya and Swain[22] observed high 1000-seed weight in BM 20-12-3×Pusa Bahar in *Brassica juncea*. Rameeh[4] reported significant maternal effect for 1000-seed weight in *B. napus*.

The regression line intersected the Wr axis below the point of origin suggesting over dominance gene action for controlling the trait (Fig. 10). The distribution of array points indicated that two parents Nap-9908 (p3) and Nap-205 (p5) contained most dominant alleles as they fell closer to the point of origin. Nap-205 (p6) and Nap-9901 (p4) fallen at the middle portion suggesting they contained equal frequencies of dominant and recessive alleles. The parents Nap-9905 (p1) and Nap-108 (p2) fell far from the origin indicated that they possess maximum frequency of recessive alleles. Ishaq and
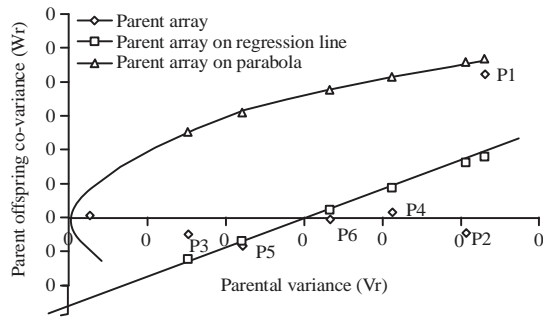
Fig. 10: Vr-Wr graph for thousand seed weight in *Brassica napus*, P1: Nap-9905, P2: Nap-108, P3: Nap-9908, P4: Nap-9901, P5: Nap-205, P6: Nap

Raziuddin[8] found partial dominance in *Brassica napus*, Trivedi and Mukherjee[28] observed over dominance in *Brassica juncea*. For thousand seed weight most of the genetic parameters (D, H_1, H_2) were significant (Table 5). Both additive and dominant effects of genes were important for the character expression. But H_1 was greater than D indicating greater role of dominance component in the inheritance of the trait. Positive F value revealed that the dominant alleles were predominantly in excess in its inheritance. Negative and non-significant result was found for dominance effect. Over dominance was found for thousand seed weight. The $H_2/4H_1$ value indicates positive and negative alleles were more or less asymmetrically distributed. The narrow sense heritability was 52.8% (Table 5). The results agree with Rahman *et al.*[29] in turnip rape. Khan and Khan[31] also reported low narrow sense heritability for 1000 seed weight.

CONCLUSION

Analysis of combining ability revealed that Nap-9908 was the best general combiner for number of siliquae/plant, seed/siliqua and seed yield/plant. In cross combinations in SCA, the best combiners were Nap-9905×Nap-205 for number of primary branches, Nap-9908×Nap-9901 for number of siliqua/plant, Nap-9901×Nap-205 for seeds/siliqua, Nap-108×Nap-9908 for thousand seed weight and Nap-9905×Nap-205 for seed yield/plant and could be utilize in rapeseed breeding programs. The Vr-Wr graph indicated over dominance for plant height, days to flowering, primary branches/plant, siliquae/plant, seeds/siliqua, siliqua length and thousand seed weight while partial dominance was observed for secondary branches and seed yield/plant. Therefore, selection in later segregating generations could be fruitful to develop early maturing lines with modified plant architecture in *Brassica napus*.

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