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INHERITANCE BEHAVIOUR OF QUANTITATIVE TRAITS IN LINSEED (*Linum usitatissimum* L.)

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ABSTRACT

Genetic components of variances were analysed to understand the nature of inheritance of important quantitative trait in linseed using half diallel mating involving 10 parental lines their 45F1 and 45F2 progenies. Significant values for additive (D) and dominance (H1, H2) genetic components of variance were observed for most of the traits in both generations. However, non-additive dominance type of gene action was predominant. Additive gene action was observed for all the traits except days to 50% flowering and plant height in both F1 and F2 generations. In the loci ($H2 < H1$), majority of the traits showed unequal proportion of positive and negative genes with asymmetrical distribution among parental genotypes ($H2/4H1 < 0.25$). Significance of both additive and non-additive genetic variations suggested integrated breeding strategies with delayed selection for crop improvement

INTRODUCTION

Linseed also known as flax (*Linum usitatissimum* L., $2n = 2x = 30$), is an important oilseed and fibre crop grown in different geographical regions worldwide. It is presumed to be originated in South West Asia (Vavilov, 1935), and under cultivation since the beginning of civilization (Laux, 2011). The terms flax and linseed depends on their mode of utilization. Flax refers to the seed grown for fibre (linen) production, while linseed refers to oilseed flax grown for industrial and nutritional uses (Biradkar *et al*., 2016). The fibre from flax is one of the most valuable raw material in textile industries to manufacture thread/rope and packaging material (Dhirhi *et al*., 2016). Flax fibre has good lusture, high tensile strength and durability alongwith good blending capacity with wool, silk, cotton *etc*. The left over woody matters and short fibres may serve as source of wax and raw material in paper industry for making paper of quality comparable with that of currency notes (Chauhan *et al*., 2009). Flax seeds contain 26-45% oil (Diedrichsen, 2001) making it an important oilseed crop for various purposes. Due to high linolenic acid content, the flaxseed oil has been extensively used as additives in PVC plastics, anti-rust agents, laquers, varnishes and paints (El-Beltagi *et al*., 2007; Nagraj, 2009;). Edible linseed oil is the richest source of omega-3. Alpha linolenic acid is the most important Omega-3 fatty acid constitutes up to about 55-60% of total fatty acids (Bozan & Temelli, 2002).

Yield is one of the most important traits for crop improvement in linseed which is quantitative in nature and controlled by various other components. Therefore, Knowledge about the inheritance and genetic behaviour of various traits is an essential criterion for exploitation of hybrid vigour. Effective and efficient breeding program mainly depends on the genetic information underlying the trait of interest (Atnaf *et al*., 2014). The diallel cross technique developed by Hayman (1954 a,b) and Jinks, provides a method particularly in self-fertilized crops like linseed to understand about genetic information on various traits related to yield. It provides information on gene action and predict the performance of progenies in later segregating generations. Studies to generate basic genetic information of important agronomic and physiological traits had been carried out in different crop such as common bean (Atnaf *et al*., 2014) and wheat (Akram *et al*., 2008) including linseed (Shekhar *et al*., 2016, Kumar and Paul, 2015). However, identification of diverse genotypes and the knowledge of components of variance involved in the inheritance of yield and its contributing characters is of paramount importance for any breeding strategy. Thus, the present study was aimed to estimate the genetic components of variance for 10 different quantitative traits using 10 diverse parents in linseed.

MATERIALS AND METHODS

Plant material

The plant materials used in the present investigation includes 10 pure genotypes namely Neelam, Garima, Jawahar-17, Neela, EC1392, LC185, JLS-9, Heera, Mukta and GS234

selected from active germplasm stock of linseed maintained at CSIR-National Botanical Research Institute, Lucknow, India. The details of the genotypes are presented in Table 1.

These genotypes were crossed in diallel design (excluding reciprocals) and produced seeds for 45 F1 hybrids. All the F1 hybrids were raised to get F2 seeds and a fresh F1s were also made. The final experiment was conducted with 45 each F1s, F2s alongwith 10 parental genotypes.

Experimental site

The experimental field was situated between 26040´N latitude and 80045´E longitude and an altitude of 129 m above sea level. The average rainfall during the crop period (November 2014– April 2015) ranged from 3.8 mm to 21.9 mm and average day night temperature varied between 22 - 38.00C and 4.1 - 20.50C, respectively.

Experimental design

The experiment was conducted in randomized block design with three replications. Each plot of parental genotypes and F1s had two rows while F2s had four rows of 2-meter-long with spacing of 15 cm within rows and 45 cm between rows. Non-experimental rows were also sown to check the border effect. All the recommended agricultural practices such as fertilizer dose, crop protection measures, irrigation etc. were followed to raise a healthy crop. Five plants from parental genotypes and F1s and 15 plants from F2s were randomly tagged for observations on days to 50% flowering, plant height (cm), branches/plant, capsules/plant, seeds/capsule, capsule weight/plant (g), seed weight/plant (g), husk weight/plant (g), test weight (g) and oil content (%).

Statistical analysis

Hayman's diallel approach (1954) and Mather's concept of D, H genetic components for additive and dominance variances, respectively (D used for additive variance instead of A, and H1 and H2 for dominance genetic components of variance instead of D) were used to study the genetic effects for various traits in both the generations. Mather and Jinks (1982) have also made the recent development about this technique and genetic components of variation were estimated following that method of diallel analysis (Singh and Chaudhary, 1985). In F2 populations, the formulae were modified to calculate the genetic components of variance as proposed by Verhalen and Murray (1969).

RESULTS AND DISCUSSION

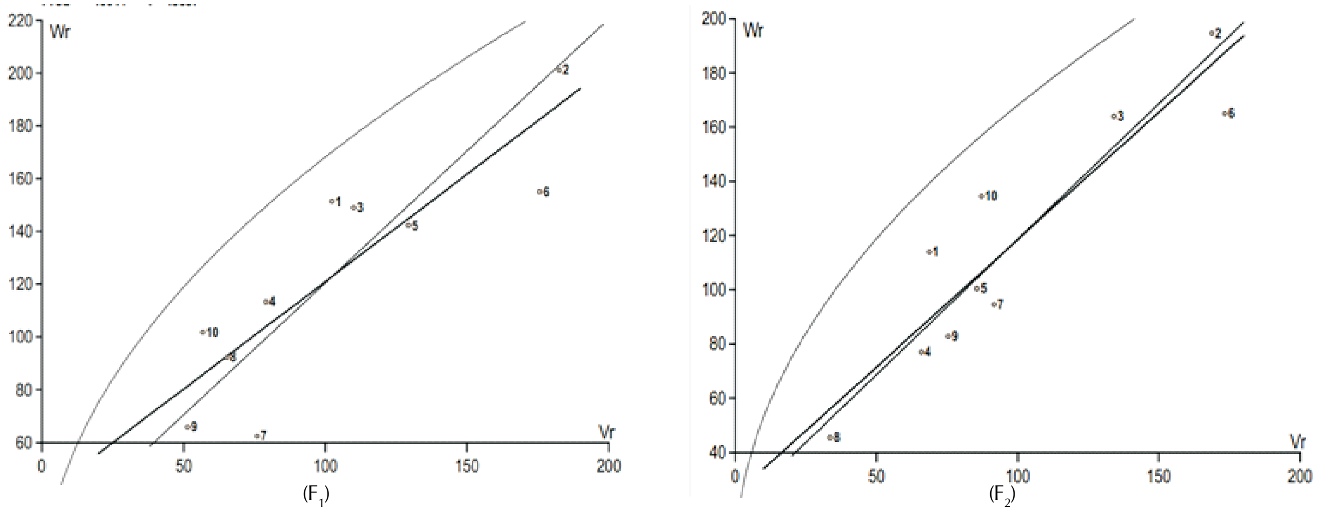
Information regarding genetic components of variations for different quantitative traits gives an opportunity for selection of genotypes during hybridization and breeding programmes. Therefore, the genetic architecture of 10 genotypes of linseed for 10 quantitative traits had been studied through Hayman's diallel analysis. Graphical analysis of the experimental data recorded was done in order to get information about allelic constitution of the parents used in the diallel cross. The trait wise result of present investigation is explained below:

Days to 50% flowering

The genetic components of variance *viz*, additive (D), dominant components (H1, H2), F and h2 were found to be significant while E value was non-significant in F1 and F2 generation (Table 2). However, the values of D was higher than H1 and H2, which indicates predominance of additive type of gene action. The average degree of dominance was less than unity confirming a low level of dominance of the loci affecting this trait. Irregular distribution of positive and negative genes was observed in both the generations due to deviation from standard value (0.25) of H2/4H1 ratio. Positive and significant value of F indicates that dominant alleles were more frequent than recessive alleles which is further supported by significant positive values of h2 and ratio of dominance and recessive genes in both the generations. The Vr-Wr graph showed over-dominance as the regression line intercepted Wr axis below the point of origin in both F1 and F2 generations (Fig 1). The distribution of parents all along the regression line below the limiting parabola shows abundance of diversity among them. However, in F1 generation genotype Mukta and JLS 9 had maximum number of dominant genes while genotype Garima had maximum number of recessive genes. The genotypes Neelum, Jawahar 17 and EC 1392 possessed equal proportion of dominant and recessive genes as occupied intermediate position along the regression line. In F2 generation, distribution of array point revealed that genotype Hira had maximum

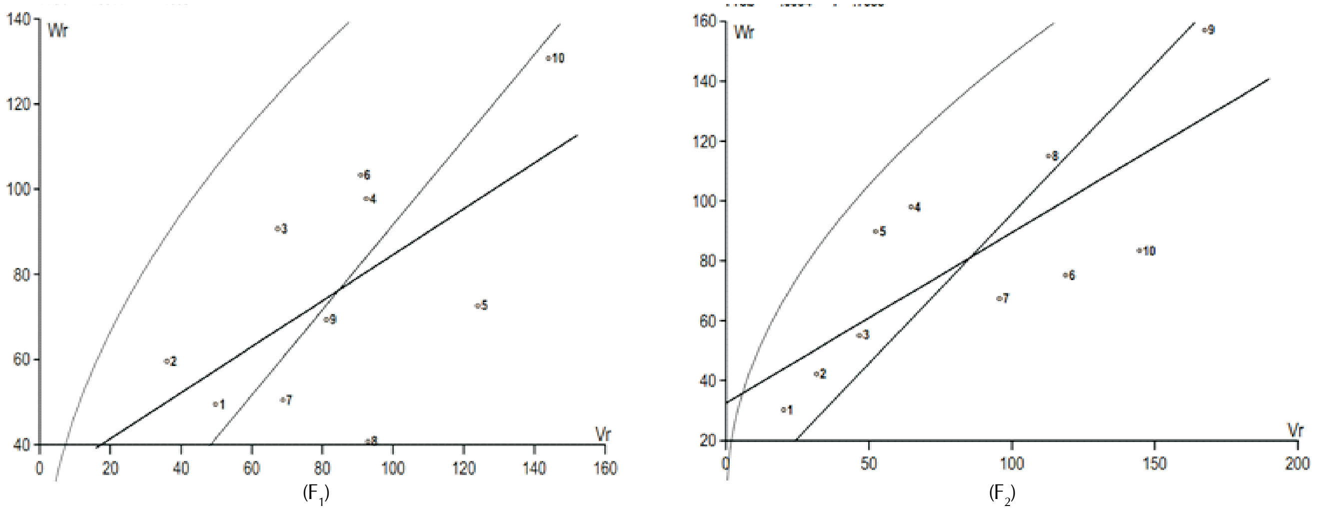
Table 1: Details of 10 linseed parental genotypes used in the present study.

S.No.	Parental Genotypes	Pedigree	Diagnostic features
1	Neelum	T-1 x NP(RR)-9	Erect type, medium height, late flowering, high seed and oil yield, blue
2	Garima	T-29 x Neelum	Erect type, medium height, moderate flowering, high seed and oil yield, blue flower, light brown seed color
3	Jawahar-17	Selection of No. 55	Semi Erect type, short height, moderate flowering, low seed and oil yield, red violet flower, dark brown seed color
4	Neela	Selection	Semi Erect type, medium height, moderate flowering, average seed and oil yield, blue flower, brown seed color
5	EC1392	-	Erect type, medium height, moderate flowering, low seed and oil yield, white flower, light brown seed color
6	LC185	NP(RR)-37 x Kangra local	Erect type, medium height, moderate late flowering, low seed and high oil yield, blue flower, yellow seed color
7	JLS-9	(RL–102 x R-7) x J23	Erect type, short height, moderate flowering, average seed and oil yield, white flower, light brown seed color
8	Hira	H 342 x NP (RR) - 9	Erect type, tall height, moderate flowering, average seed and oil yield, white flower, dark brown seed color
9	Mukta	H 342 x NP (RR) - 9	Erect type, tall height, moderate flowering, average seed and high oil yield, white flower, brown seed color
10	GS 234	-	Erect type, short height, early flowering, average seed and oil yield, white flower, dark brown seed color



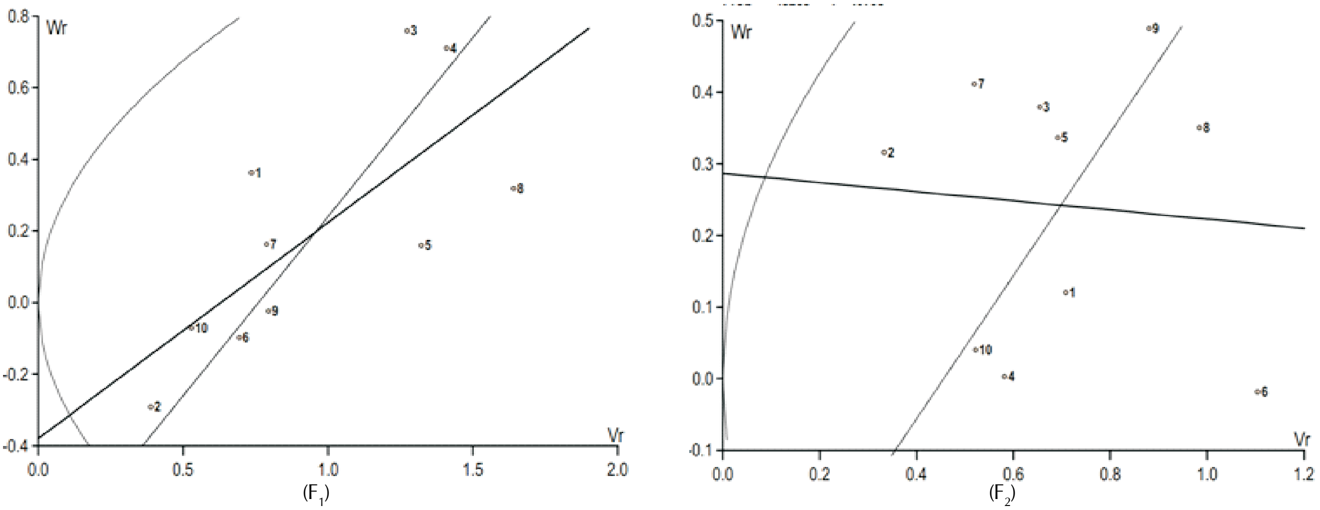
(F$_1$) (F$_2$)

Figure 1: Vr-Wr graph for days of 50% flowering in 10 parent half diallel of linseed.



(F$_1$) (F$_2$)

Figure 2: Vr-Wr graph for plant height in 10 parent half diallel of linseed.



(F$_1$) (F$_2$)

Figure 3: Vr-Wr graph for branches per plant in 10 parent half diallel of linseed.

dominant genes while maximum recessive genes were observed in Garima followed by LC 185 and Jawahar 17.

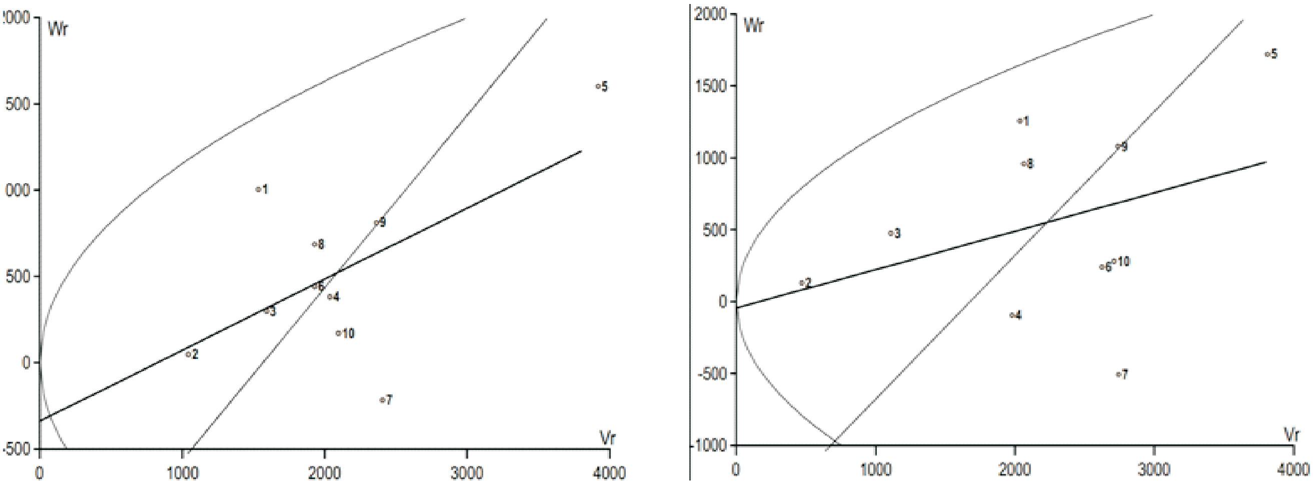
Plant height

All the genetic components of variances *i.e.* D, F, H1, H2, h2

Table 2: Estimates of genetic components of variance for 10 quantitative traits in Linseed

		D	F	H_1	H_2	h^2	E	$H_1/D^{1/2}$	$H_2/4H_1$	$4DH_1^{1/2}+F/4DH_1-F^{1/2}$	h^2/H_2	r
Days of 50%	F_1	281.96**	70.83**	198.43**	165.17**	15.67**	0.83	0.83	0.2	1.35	0.09	0.87
flowering	F_2	284.42**	189.23**	816.15**	703.43**	109.61**	1.37	0.85	0.21	2.3	0.15	0.92
Plant height	F_1	215.43**	127.76**	237.72**	135.46**	66.02**	6.20**	1.05	0.14	1.78	0.48	0.6
	F_2	215.47**	216.76**	886.73**	650.10**	-8.45**	6.16**	1.01	0.18	2.96	-0.01	0.76
Branches/plant	F_1	0.72	0.72	3.41**	2.72	3.70**	0.19	2.17	0.19	1.6	1.35	0.73
	F_2	0.77	1.27	9.44**	8.10**	11.17**	0.13	1.74	0.21	2.78	1.38	-0.08
Capsules/	F_1	1302.58**	534.64**	7520.16**	6280.44**	12300.25**	26.79**	2.4	0.2	1.18	1.95	0.59
Plant	F_2	1309.85**	838.27**	31955.58**	26063.72**	34254.63**	19.52**	2.47	0.2	1.29	1.31	0.36
Seeds/	F_1	0.94	1.39	5.80**	4.74**	8.78**	0.06	2.47	0.2	1.85	1.85	0
Capsules	F_2	0.91	3.53**	24.41**	17.37**	11.20**	0.09	2.58	0.17	6.9	0.64	-0.17
Capsule	F_1	8.07**	12.45**	62.84**	50.35**	132.44**	0.22	2.79	0.2	1.76	2.63	0.19
Weight	F_2	8.02**	25.45**	293.48**	229.29**	386.90**	0.27	3.02	0.19	3.2	1.68	-0.08
Seed weight	F_1	4.13**	5.33**	41.13**	35.19**	93.58**	0.21	3.15	0.21	1.51	2.65	0.43
	F_2	4.13**	10.43**	210.12**	166.60**	287.63**	0.22	3.56	0.19	2.09	1.72	0.08
Husk weight	F_1	1.07	2.06	4.28**	2.8	3.29**	0.2	1.99	0.16	2.84	1.17	0.4
	F_2	1.02	4.47**	18.58**	12.79**	6.97**	0.26	2.13	0.17	-78.24	0.54	-0.03
Test weight	F_1	2.53*	3.00**	5.21**	3.49**	0.32	0.06	1.43	0.16	2.4	0.09	0.47
	F_2	2.47*	5.60**	19.37**	12.96**	2.35*	0.12	1.4	0.16	9.57	0.18	0.64
Oil content	F_1	2.47*	0.78	29.13**	26.39**	1.87	0.24	3.43	0.22	1.09	0.07	0.59
	F_2	2.41*	9.23**	190.25**	166.43**	20.87**	0.3	4.43	0.21	2.51	0.12	0.15

*, ** significance at 5% &1% respectively, D = variations due to additive effect; F = the mean of 'Fr' over the arrays, Fr is the covariance of additives and non-additive effects in single array; H_1 = components of variation due to the dominance effect of the genes ; H_2 = calculations to predict the proportion of positive and negative genes in the parents; h^2 = the dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses); E = the expected environmental components of variation ; $H_1/D)^{1/2}$ = the mean degree of dominance ; $H_2/4H1$ = the proportion of genes with positive and negative effects in the parents ; $4DH_1^{1/2}+F/4DH_1-F^{1/2}$ = the proportion of dominant and recessive genes in the parents ; h^2/H_2 = the number of groups of genes which control the character and exhibit dominance



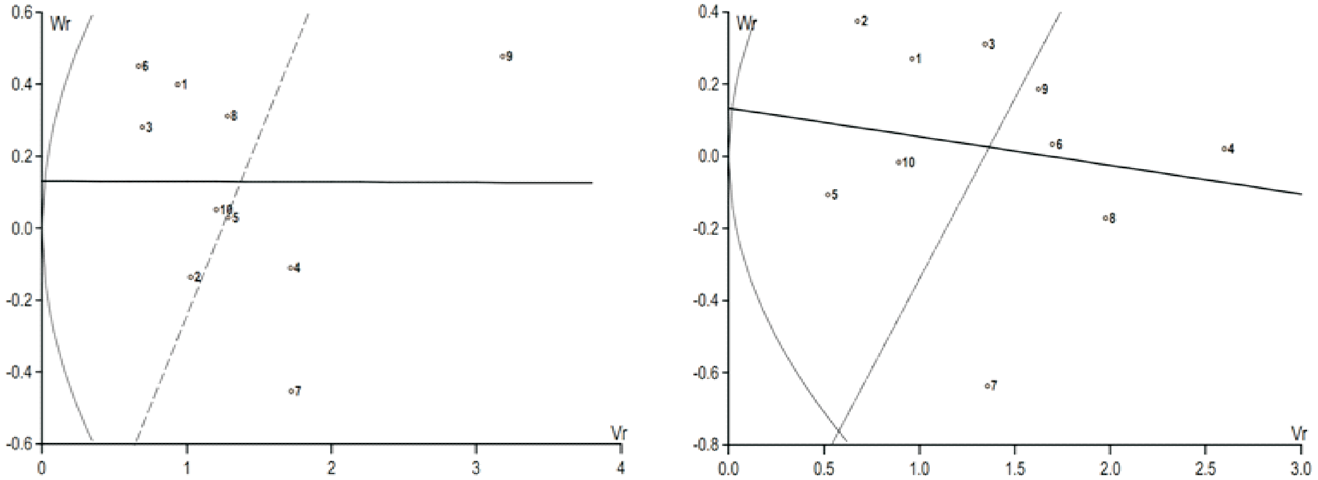
(F_1) (F_2)

Figure 4: Vr-Wr graph for capsules per plant in 10 parent half diallel of linseed.

and E were found to be significant for plant height in both the generations (Table 2). However, the dominant components had greater values than additive component (D) indicating preponderance of non-additive gene action. The unequal values for H_1 and H_2 was observed in both the generations indicated that positive and negative genes were not in equal proportions as also confirmed by the ratio of H2/4H1. Over dominant gene action was depicted for F_1 generation through Vr-Wr graph as the regression line passing below the origin (Fig 2). The array points were scattered around the regression line and genotype Neelum followed by JLS 9 had maximum number of dominant gene. While, genotype GS 234 possessed maximum number of recessive genes. In F_2 generation, the regression line intercepted above the point of origin, which demonstrated partial dominance during inheritance of plant height.

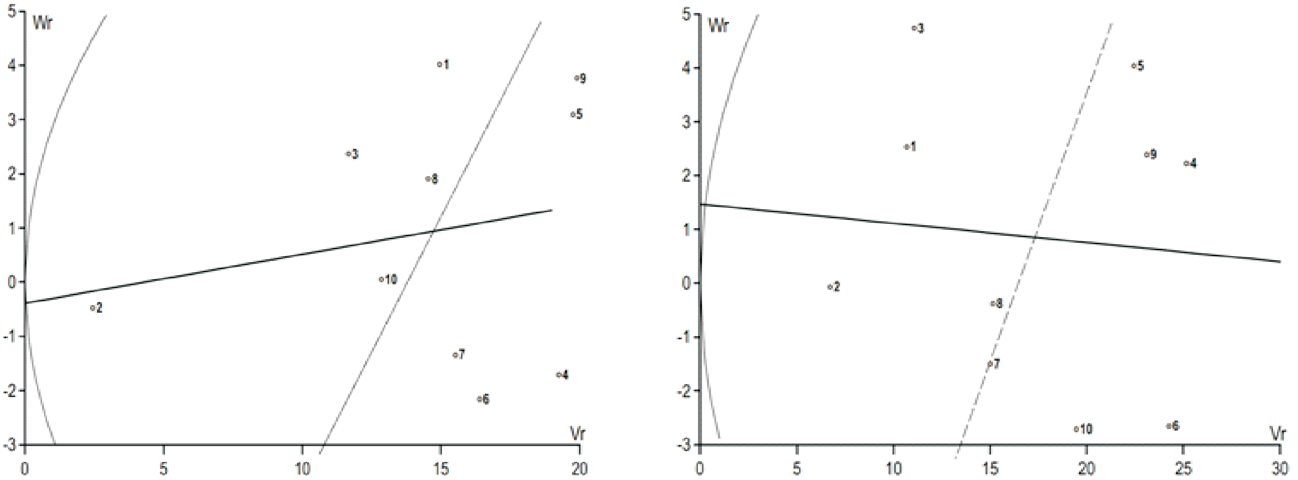
Branches/plant

The genetic components of variance indicated that only H_2 and h^2 were positive and significant while D, F, H_1 and E were non-significant in F_1 and F_2 generations (Table 2). The dominant components H_1 and H_2 had higher values than additive components (D) suggesting importance of non-additive gene action in inheritance of branches/plant. Average degree of dominance was greater than 1 in both the generations which represents the presence of overdominance and showing that dominant genes were in increasing proportion as confirmed by positive and significant values of h^2. The values for H_1 and



(F_1) (F_2)

Figure 5: Vr-Wr graph for seeds per capsule in 10 parent half diallel of linseed.



(F_1) (F_2)

Figure 6 : Vr-Wr graph for capsule weight in 10 parent half diallel of linseed.

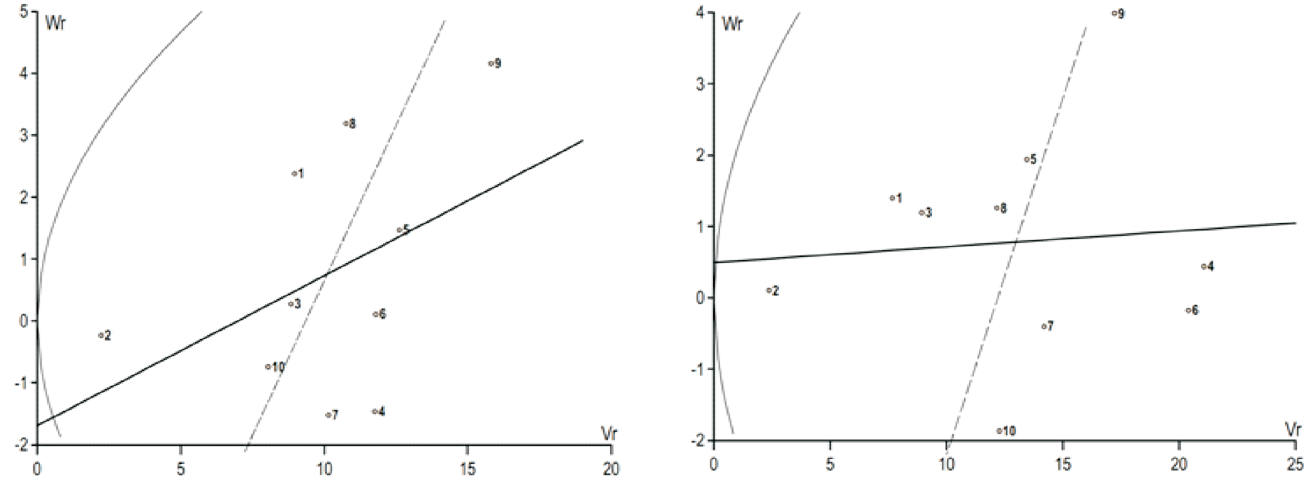
H_2 were not equal indicating asymmetrical distribution of positive and negative genes as supported by $H_2/4H_1$ values ($<.25$) in both the generations. In F_1 and F_2 generation, large number of dominant genes was present in parental genotypes as demonstrated by positive values of F and the same was confirmed by the ratio of dominant and negative genes in the parents.

In Vr-Wr graph, positive intercept of regression line indicated that the trait branches per plant is controlled by additive gene action with partial dominance (Fig 3). Parents were scattered all along the regression line which shows presence of genetic diversity among parents. The position of array points on regression line arranged parental genotypes in the order of dominance as Garima, GS 234, LC 185, Mukta, JLS 9, Neelum, EC 1392, Hira, Neela and Jawahar 17 in F1 generation. In F_2 generation, genotype Neela had maximum number of dominant genes followed by GS 234 while genotype Mukta had maximum recessive genes.

Capsules/plant

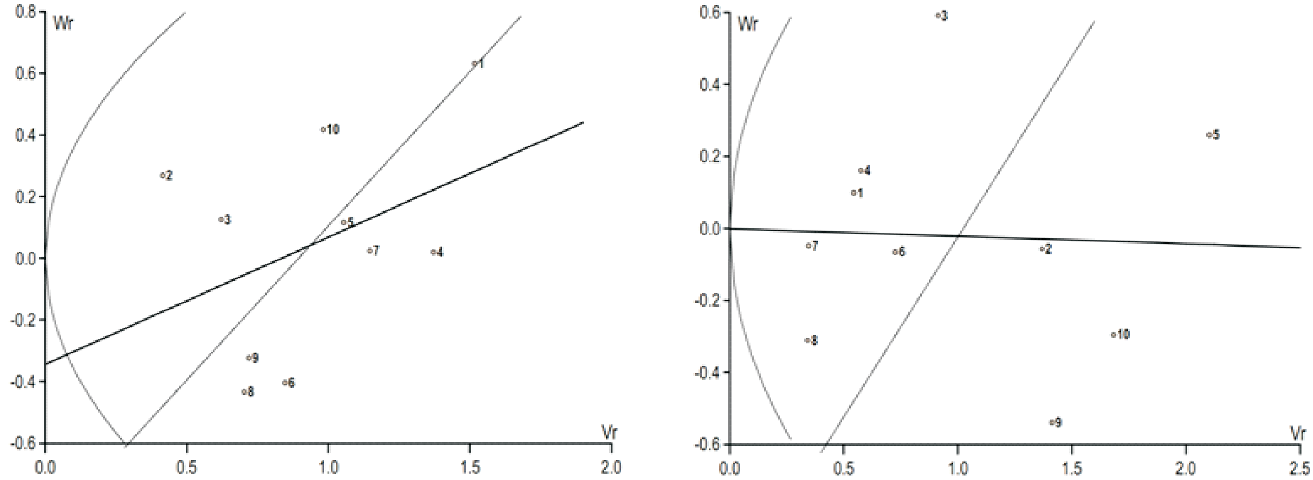
The estimates of all the genetic components of variance were positive and significant in both the generations (Table 2). The preponderance of non-additive gene action was observed due to higher values of dominant components (H_1 and H_2) than additive component (D). The average degree of dominance was greater than unity implicates presence of overdominance type of gene action. Greater value of H_1 than H_2 and ratio of $H_2/4H_1$ indicated that distribution of positive and negative alleles was different among parental genotypes. Positive and significant values of h^2 and F in both the generations indicated that dominant genes were in increasing proportions as also confirmed by ratio of dominant and recessive genes in parents.

The additive gene action plays important role in controlling capsule/plant as the regression line intercepted the Wr axis above the point of origin which supports partial dominance (Fig 4). Varietal positions on regression line in F_1 and F_2 generation demonstrated that genotype Garima was nearest to the origin with maximum dominant genes while genotype EC 1392 was farthest from the origin and had maximum recessive genes. However, distribution of parents on regression line was more scattered in F_2 generation than F_1



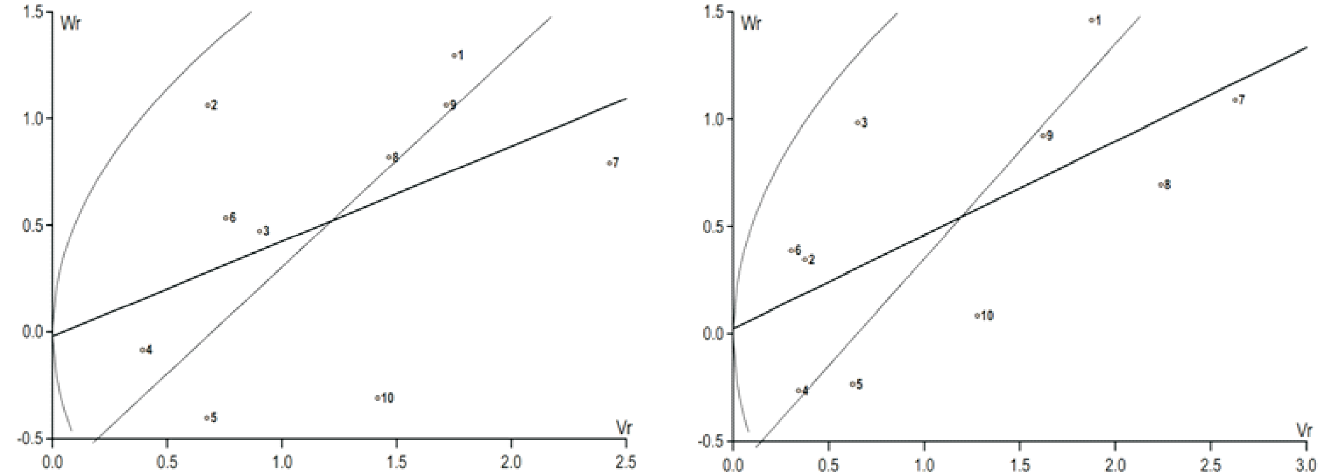
(F$_1$) (F$_2$)

Figure 7: Vr-Wr graph for seed weight in 10 parent half diallel of linseed.



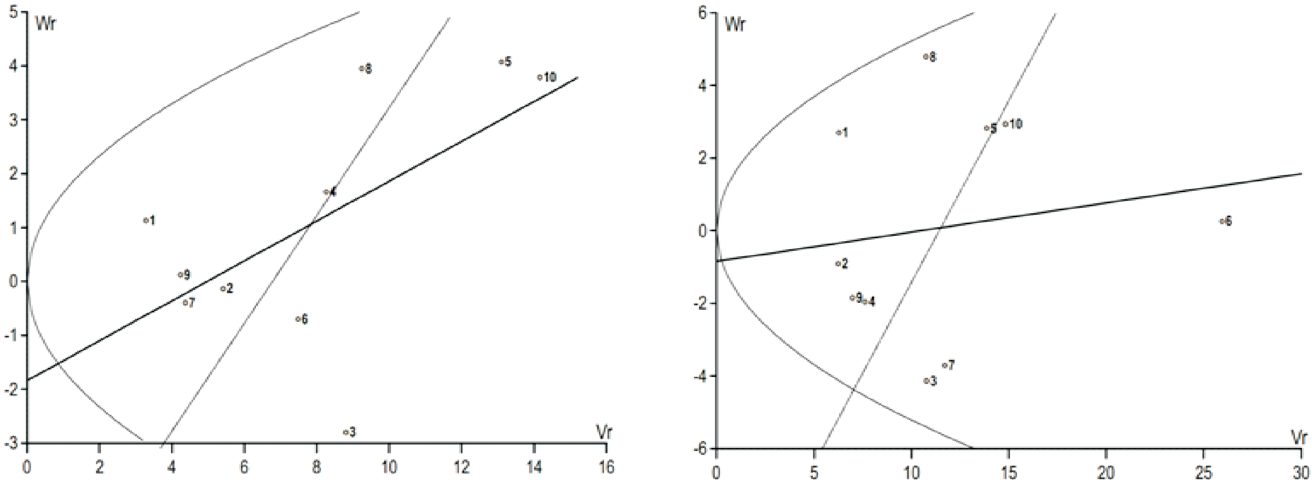
(F$_1$) (F$_2$)

Figure 8: Vr-Wr graph for husk weight in 10 parent half diallel of linseed.



(F$_1$) (F$_2$)

Figure 9: Vr-Wr graph for test weight in 10 parent half diallel of linseed.



(F$_1$) (F$_2$)

Figure 10: Vr-Wr graph for oil content in 10 parent half diallel of linseed.

generation which indicates presence of more diversity among them.

Seeds/capsules

For seeds/capsules, genetic components of variance *i.e* H1, H_2 and h^2 were positive and highly significant while D, F and E were non-significant in F_1 generation (Fig 5). However, except D and E all other genetic components of variance were observed significant in F_2 generation. The values for H_1 and H_2 were higher than D showing importance of non-additive gene action. Unequal distribution of positive and negative genes was reflected through different values of dominant components (H_1 and H_2) along with less than 0.25 values of $H_2/4H_1$ ratio. The abundance of dominant genes were reflected by positive and significant values of F and greater than 1 values for ratio of dominant and recessive genes in parents in F1 and F_2 generations. Number of gene groups (h^2/H_2) responsible for seeds per capsule was more than one in F_1 while only one gene group was involved in F_2 generation. In Vr-Wr graph the regression line cuts the Wr axis above the origin on positive side which suggests additive type of gene action with partial dominance (Fig 6). From the position of array points on regression line, it was observed that the genotype JLS 9 possessed maximum dominant genes being nearest to the origin while genotypes Mukta and LC 185 had minimum dominant genes as farthest from the origin in F_1 generation. In F_2 generation, JLS 9 was nearer to origin due to which it had maximum dominant genes and genotype Garima had maximum recessive genes for being farthest from the origin.

Capsule weight/plant

All the genetic components of variance *i.e.* D, F, H1, H2 and h^2 were found highly significant and positive except E in both the generations (Table 2). The dominance components (H_1 and H_2) were found dominating over additive components (D) and the average degree of dominance was more than unity suggesting the role of non-additive gene action . The positive and significant values of F indicate increasing proportion of dominant genes which is justified through ratio of dominant and recessive genes in parents. The different values of H1 and H_2 also depicts asymmetrical distribution of dominant and recessive genes in parents and confirmed by low values of $H_2/4H_1$ ratio in both generations. Significant and positive values for h^2 reflected abundance of dominant genes suggesting importance of non-additive gene action for capsule weight in F_1 and F_2 generations.

The partial dominance was noticed as the regression line passed much above the origin. Varietal positions on regression demonstrated that parent Garima had maximum dominant genes and parent Mukta had maximum recessive genes in F_1 generation while same as F_1 parent Garima possessed maximum dominant genes but parents Jawahar 17 had maximum recessive genes in F_2 generation.

Seed weight/plant

Both additive and non-additive types of gene action were involved in the inheritance of seed weight/plant as indicated by the significant additive and dominance variances in F_1 and F_2 generations. The non-additive gene effect was more pronounced due to higher magnitude of H_1 and H_2 than D. Positive and significant F values reflected larger frequency of dominant alleles than recessive alleles supported by more than unity values of average degree of dominance in both the generations. The proportion of $H_2/4H_1$ was less than 0.25 indicating that positive and negative alleles were not distributed equally in the parental genotypes as also confirmed by unequal values of dominance components (H_1 and H_2). Positive and significant h^2 values along with higher values for ratio of dominant and recessive genes in parents implied towards abundance of dominant genes in both generation. The ratio of h^2/H_2 suggested that there might be more than one gene group controlling this character. The Vr-Wr graph showed that the regression line was cutting the Wr axis above the origin demonstrating additive gene action with partial dominance in F_1 and F_2 generation (Fig 7). The position of array points on regression line revealed that parent Garima had most dominant genes while parent Mukta had most recessive genes for this trait in both generations. However, in F_2 generation scattering of parents on regression line was more than F_1 generation indicating high genetic diversity.

Husk weight/plant

The dominance components of variance *i.e.* H_1 and H_2 were significant while additive component (D) was non-significant in F_1 and F_2 generations (Table 2). This indicates that expression of husk weight is mainly controlled by non-additive gene action. F values were found to be positive and significant in F_2 generation while in F_1 generation it was non-significant. Therefore, in F_2 preponderance of dominant genes were observed as confirmed by greater than unity values of average degree of dominance in both generations. The magnitude of H_1 and H_2 were not in equal proportion which implies towards unbalanced distribution of dominant and recessive alleles in F_1 and F_2 generations. Ratio of dominant and recessive genes in parents also revealed their asymmetrical distribution. The values of $H_2/4H_1$ reflected that dominant genes having increasing and decreasing effects on husk weight were irregularly distributed in parents. In F_1 generation, more than one gene group was involved but in F_2 generation only one gene group was responsible for controlling husk weight. The Vr-Wr graph for husk weight/plant showed that the regression line passed above the point of origin which indicated the presence of partial dominance (Fig 8). The position of array points on regression line demonstrated that parents were diffused all over the line which represents high genetic diversity among parents. Genotype Hira had most dominant gene for both F_1 and F_2 generations as it fell near to the point of origin. However, genotype Neelum in F_1 and Genotype Jawahar 17 in F_2 generation had maximum frequency of recessive genes as the fell farthest from the point of origin.

Test weight

Both additive (D) and dominant (H_1 and H_2) components of variance were positive and significant (Table 2) indicates both additive and dominance gene action. However, the magnitudes of dominance components (H_1 and H_2) were higher than additive component indicating role of non-additive gene action in inheritance of test weight. Average degree of dominance was greater than unity indicating high level of dominance of the loci effecting this trait and showing non-additive type of gene action with increasing pattern of dominant genes as justified through positive values of h^2. Different magnitudes of dominant components of variance *i.e.* H_1 and H_2 revealed asymmetrical distribution of dominant and recessive genes supported by significant F values and ratio of dominant and recessive genes in parents for both generations. Proportion of dominant genes with positive and negative effect ($H_2/4H_1$) also unequally distributed as it was deviated from standard values (.25). The Vr-Wr graph showed negative intercept as the regression line cut Wr axis below the point of origin in F_1 and F_2 generations (Fig 9). This negative intercept confirms presences of non-additive gene action with over-dominance. The genotype Neela and EC 1392 had maximum dominant genes in both generations being nearest to the origin while genotype Neelum and JLS 7 had maximum recessive genes being farthest from the origin.

Oil content

In F_1 and F_2 generation both additive and dominant components of variance were positive and significant (Table 2). However, higher magnitude of H_1 and H_2 than D reflected that the oil content is mainly governed through non-additive gene action. Average degree of dominance was greater than one in both generations indicating that over-dominance is present for this trait, also confirmed by positive and significant values of F which reflected higher number of dominant alleles than recessive alleles. The proportion of $H_2/4H_1$ was less than .25 indicating that positive and negative alleles were not distributed equally in the parental genotypes as confirmed by unequal values of dominance components (H_1 and H_2). Preponderance of dominant genes was demonstrated through positive and significant h^2 values along with high ratio of dominant and recessive genes in parents. Number of genes or groups governing this trait might be more than one in F_1 and F_2 generations.

Partial dominance was observed for oil content as the regression line was intercepted above the point of origin in F_1 and F_2 generations (Fig 9). Diffused arrangement of parents on Vr-Wr graph was observed indicating high genetic diversity among parents for oil content. In F_1 generation, genotype JLS 9 had maximum dominant genes as it fell nearest to the origin while genotype GS 234 has maximum recessive genes being farthest from the origin. However, in F_2 generation genotype Garima was nearest to the origin having maximum dominant genes and genotype LC 185 fell farthest from the origin having maximum recessive genes.

The additive and dominant components of variances were positive and significant in F_1 and F_2 generation for days to 50% flowering, plant height, capsules/plant, capsule weight/plant, seed weight/plant and test weight. Therefore, the exploitation of hybrid vigour for these traits might be useful but development of hybrid varieties is not favourable due to auto-gamous nature of linseed (Sood *et al.*, 2007). The variation due to additive component (D) is heritable and fixable in nature while variation due to dominant components (H_1 and H_2) is non-fixable. In all traits, the magnitude of dominant components exceeded additive component which indicated non-additive gene action as supported by more than 1 values of average degree of dominance in both the generations. Therefore, the selection of superior plants, in terms of plant height, early maturity and other yield related traits should be postponed to later generation where these traits can be improved by making selections among the recombinants within the segregating populations. Kumar and Paul (2015) also observed that plant height, capsule/plant and test weight were governed by non-additive gene action in linseed. Preponderance of non-additive gene action in yield related traits was also reported by Bhateria *et al.* (2006) and Kumar *et al.* (2000). The unequal magnitudes of H_1 and H_2 along with <0.25 values of $H_2/4H_1$ for all the traits demonstrated asymmetric distribution of genes with positive and negative effect in F_1 and F_2 generation. Thus, selection of parents carrying positive genes for the trait of interest would be possible for any crop improvement program. Marame *et al.* (2008) also reported unequal distribution of genes in parents with positive and negative effect for various quantitative traits in hot pepper. The positive and significant magnitude of h^2 for all the traits in F_1 and F_2 generation suggested increasing proportion of dominant genes which could be utilized for hybrid vigour. Shekhar *et al.* (2016) also reported increasing proportion of dominant genes for days to 50% flowering, days to maturity, 1000 seed weight, seed yield/plant and harvest index in linseed.

Highly significant positive values of h^2 for grain yield/plant, ear length, number of row/ear, number of grain/row and 100 grain weight was observed in maize by Haq *et al*. (2009). The relative frequency of dominant allele *i.e.* F was positive and significant for all the traits except branches/plant indicated abundance of dominant genes than recessive genes in the expression of these traits. This availability of surplus dominant genes may be justified by greater than unity values of ratio of dominant and recessive genes in parents. Similar results were also reported by Satar (2017) and Syukur *et al*. (2010) in sunflower and pepper, respectively. More than one group of gene with dominance effect were governing expression of branches/plant, capsule/plant, seeds/capsule, capsule weight/plant and seed weight/plant in F_1 and F_2 generation as suggested by higher values of h^2/H_2.

The Vr-Wr graph for all traits showed presence of partial dominance except days to 50% flowering and plant height in F_1 and F_2 generation. This suggests that additive gene action plays an important role during inheritance of these traits which helps in early generation selection during breeding program. However, there is contradiction between results of genetic components of variation and Vr-Wr graph which could be attributed to the presence of correlated gene distribution (Hayman, 1954). Varietal distribution on the graph reflects the amount of genetic diversity among parents. Since, for most of the traits parents were scattered all over the regression line suggesting high genetic diversity among them in both generations. Selection of parents on the basis of genetic diversity has the potential to derive high yielding varieties. Dubey and Ram (2015) also reported opposite results from genetic components of variance and Vr-Wr graph in bottle guard for 11 quantitative characters.

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