Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; SP1: 218-222

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Study of genetic component of variance in seven parents half diallele of oats (*Avena sativa* L.) for grain yield, its components and protein content

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Abstract
Twenty-one progenies with their seven parent cultivars of Avena sativa L. (2n = 6x = 42) along with two checks were taken with a view to estimate genetic components of variance indicating different types of gene effects. The present work aimed at estimating the genetic component of variance in oats involving in the character grain yield, its components and protein content through 7×7 half diallele analysis to provide tools for the selection of high yielding genotypes at very early selfing generations exploiting the fixable effects. To utilize both types of genetic effects breeding methods like modified recurrent selection i.e. alternating pedigree and recurrent selection cycles, diallele selective mating, multiple crossing and early generation selection followed by intermating among F_2/F_3 generation selected plant. The experiment was laid down in Randomized Complete Block Design with three replication at Livestock Research Centre of G.B.P.U.A.&T., Pantnagar. Observations were recorded on twenty three quantitative characters namely days to 50 % heading, plant height at 50% heading, number of tillers per plant, number of leaves per plant, leaf length, leaf width, leaf area, flag leaf length, flag leaf width, flag leaf area, days to maturity, plant height at maturity, panicle length, number of spikelet per panicle, biological yield, grain yield, harvest index, 100- grain weight, 10- groat weight, groat protein content, protein yield, straw yield and growth rate. Genetic component of variance showed the preponderance of non-additive genetic variance and over dominance for all the characters except flag leaf width whereas the importance of genetic variance present with partial dominance was observed and the value (KD/KR) indicated the presence of dominant alleles in excess for most of the traits.

Keywords: genetic component, half diallele of oats, grain yield, protein content

Introduction
Oats (*Avena sativa* L.) is one of the most important winter fodder and grain crop grown throughout world both for animal and human consumption. It is a quick growing, palatable, succulent and nutritious fodder crop which forms an excellent combination when fed along with other cool season legumes inadequate supply of quality feed and fodder is the primary cause of lower productivity of milch animals in India (Patel et al., 2011). With the advent of intensified dairy industry in the country especially with the cross-bred livestock, the oat fodder is gaining significance and the oat crop is catching up in a supplement the high dry matter content and quality in mixture with berseem and Lucerne fodder. Oat grain also makes a good balanced concentrate in the Lucerne fodder in the ration of young animals, poultry, dairy cattle and other animals. Although cereal grains in general have a low percentage and are deficient in some essential amino acids especially lysine. However, Oat (*Avena spp*) have a high percentage of good quality protein in relation to other cereals (Briggle, 1973) it is considered to be one of the safest cereal to be fed to the animals because it is one of the highly nutritious cereal specially rich in fat (20.41%), protein (14.63%), vitamin, phosphorous (0.33%) and iron. As per national estimate, by 2015 and 2025 A.D., sixty crores animals will need 1097 and 1170 million tonnes of green fodder, respectively. Deficiency of green fodder will be about 64.9% and for dry fodders it may go to up to 24.9% in 2025 A.D. (Anonymous, 2009) Diallele analysis is the most popular way and has been extensively used in both self and cross pollinated crops to estimate the combining ability effects of parents and the crosses (Griffing 1956 a, b) it also helps in estimating the genetic components of variance, the degree of dominance, the proportion of dominance and recessive alleles, the distribution of genes with positive and negative effects and the blocks of genes/effective factors governing the expression of a particular trait. For an effective breeding programme in a self-pollinated crop like oat, there is need to develop strategy which allows the accumulation of fixable gene effects in a homozygous line. In order to exploit different types of gene action present in the population,

information regarding magnitude of genetic variance and combining ability for important traits are essential. Such information will be of great importance to oat breeders for the development of suitable breeding procedures and involvement of desirable parental lines in the hybridization nursery. The identification of superior parents is an important pre-requisite for the development of high yielding cultivars. A wrong choice of parents at this stage may undo a meticulously planned and well executed follow-up breeding programme. Combining ability helps in the evolution of parents in terms of their genetic value and in the selection of suitable parents for hybridization. Further this analysis may be transplanted to depict the nature and magnitude of various types of gene effects involved in the expression of economically desirable quantitative traits.

Materials and Method

The basic material for the present study consisted of 07 diverse genotypes of oats (Avena sativa L.) viz: (OX788)5-1, UPO 259. UPO 268, UPO 254, Wright, UPO 252 and UPO 256 selected from the ongoing oats breeding research programme at GBPUAT, Uttarakhand. Twenty one F_1 crosses (excluding reciprocals) generated through a diallele mating design were evaluated for forage quality and grain yield in a GBPUAT, Uttarakhand (India) during. The experiment was laid out in a completely randomized block design with three replications. The experimental plot comprised of two rows each of 1m length. Plant spacing was maintained at 30 cm x 10 cm. Observations were recorded on twenty three quantitative traits viz. days to 50%heading, plant height ai 50% heading, number of tillers per plant, number of leaves per plant, leaf length (cm), leaf width (cm), leaf area (cm^2), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm^2), days to maturity, plant height at maturity, panicle length (cm), number of spikelets per plant, biological yield, grain yield per plant,, harvest index, 100-grain weight, 1000-grain weight, groat protein content (%), protein yield, straw yield and growth rate (gm/day/plant). Data was subjected to analysis of variance to find significant differences among genotypes for the recorded data.

Results and Discussion

The diallele analysis described by Hayman (1954) was used to estimate the genetic parameters involved in the expression of different character studied. The genetic components of variation and various estimates regarding the distribution of genes and degree of dominance have been presented in (tables 1 A, and 1 B) and details of results for characters are described as follows

Table 1 A: Estimates of genetic components of variance for different quantitative traits in oats (*Avena sativa* L.)

Components	Days to 50% heading	Plant height at 50% heading	Numbers of tiller per plant	Numbers of leaves plant	Leaf length (cm)	leaf width leaf area (cm)	Leaf area (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm)	Days to maturity	Plant height at maturity
D	0.4743 ±15.04	74.81 ±58.17	1.26 ±3.88	11.52 ±150.95	1.17 ±10.72	0.008** ±0..0062	101.76 ±64.24	6.05 ±4.44	0.029 ±0.037	122.75* ±41.08	0.49 ±3.02	34.03 ±26.91
H_1	2.59 ±12.15	231.69 ±140.05	18.83* ±9.34	8877.66* ±360.40	38.61 ±25.82	0.43* ±0.0194	654.18** ±154.66	56.15** ±10.69	0.245* ±0.089	736.84** ±98.92	79.3** ±7.26	.294.70** ±64.78
H_2	1.98 ±2.86	152.98 ±123.41	7.97* ±8.224	846.41* ±320.21	35.67 ±22.75	0.033* ±0.013	607.29** ±36.28	45.84** ±9.43	0.23* ±0.078	609.55** ±87.16	80.82** ±6.39	233.25 ±57.08
F	2.86 ±7.19	74.37 ±82.88	5.10 ±5.53	320.05 ±215.07	41.42* ±5.28	0.020* ±0.0088	276.08 ±91.53	6.45 ±6.33	0.188** ±0.052	170.58* ±58.54	414.49** ±4.29	527.42** ±38.34
E	7.23 ±12.11	146.65 ±139.56	0.88 ±9.32	38.69 ±362.12	5.56 ±25.73	0.015 ±0.149	119.55 ±154.12	10.83 ±0.66	0.026 ±0.089	170.83 ±98.57	2.63 ±7.23	51.69 ±94.55
	7.12** ±1.79	37.22 ±20.57	1.27 ±1.37	33.53 ±53.37	3.54 ±3.79	0.024** ±0.0022	4.90 ±22.71	22.09** ±1.57	0.13** ±0.013	256.54** ±14.53	3.08* ±1.06	4.88 ±9.51
(H_1\D5)	2.34	1.76	3.87	8.73	5.75	2.31	2.54	3.05	2.89	2.45	12.37	2.94
H_2\ $4H_1$	0.192	0.17	0.239	0.24	0.23	0.19	0.23	0.20	0.23	0.21	0.25	0.19
KD\KR	5.25	3.51	1.02	0.99	1.03	0.83	1.00	0.98	0.05	0.99	0.97	1.00

Table 1B: Estimates of genetic components of variance for different quantitative traits in oats (*Avena sativa* L.)

Components	Panicle length (cm)	No. of spikeletes per panicle	Biological yield (gm/plant)	Grain yield (gm/plant)	Harvest index	100 grain weight (gm/plant)	100 groat weight (gm/plant)	Groat protein content (%)	Protein yield (gm/plant)	Straw yield (gm/plant)	Growth rate (gm/day/plant)
D	2.43 ±2.51	127.46 ±80.94	122.44 ±16.22	31.64 ±19.99	3.31 ±2.79	0.05 ±0.026	0.08* ±0.036	0.465* ±0.144	0.249 ±0.260	132.1 ±213.98	0.009 ±0.013
H_1	13.34* ±6.04	407.04* ±194.87	1662.12** ±397.76	96.72 ±48.14	28.97** ±6.74	0.092 ±0.064	0.125 ±0.087	2.06 ±0.347	2.35** ±0.627	3086.46** ±515.14	0.226** ±0.031
H_2	13.03* ±5.33	487.46* ±171.71	1322.32** ±350.49	102.34* ±42.42	17.71* ±5.94	0.17* ±0.056	0.20* ±0.077	1.765** ±0.305	2.249* ±0.553	2698.31** ±453.91	0.21** ±0.027
F	4.26 ±3.58	159.06** ±115.33	346.72 ±235.40	26.18 ±28.49	2.58 ±3.99	2.27** ±0.2037	2.77** ±1.05	8.22** ±0.20	2.79** ±2.371	36067.73** ±304.87	0.275** ±0.0185
E	0.569 ±6.02	165.47 ±194.18	305.23 ±396.36	55.33 ±47.97	6.49 ±6.72	0.11 ±0.1064	0.11 ±0.087	0.66 ±0.35	0.049 ±0.625	436.85 ±513.32	0.018 ±0.031
	1.86* ±0.887	146.38** ±28.62	8.63 ±58.41	58.42 ±7.07	2.52* ±0.989	0.124** ±0.0094	0.138** ±0.013	0.108* ±0.050	0.119 ±0.092	20.93 ±75.65	0.00087 ±0.46
(H_1\D5)	2.34	1.79	3.68	1.75	2.95	1.32	1.24	2.10	3.06	4.83	4.99
H_2\ $4H_1$	0.24	0.29	0.19	0.26	0.15	0.463	0.41	0.21	0.24	0.22	0.23
KD\KR	1.01	1.00	1.00	0.99	1.03	1.38	-2.19	1.42	1.04	1.00	-2.69

***=Significant at 5% and 1% probability level, respectively.

Table 2A: Component of variance ratio for different characters – An overview

Characters	Variance component fraction				Ratio		
	D	H_1	H_2	h^2	$(H1\backslash D)^{0.5}$ (Degree of dominance)	$H_2 \backslash 4H_1$ (Ratio of positive and negative alleles)	KD\KR (Ratio of dominant and recessive genes)
Days to 50% heading	ns	ns	ns	ns	Overdominance	Unequal	Dominant genes
Plant height at 50% heading	ns	ns	ns	ns	Parital dominance	Unequal	Excess of dominant geens
Numbers of tiller per plant	ns	S	S	ns	Overdominance	Unequal	Excess of dominant genes
Numbers of leaves oper plant	ns	S	S	ns	Overdominance	Unequal	Recessive genes
Leaf length(cm)	ns	ns	ns	S	Overdominance	Unequal	Excess of dominant genes
Leaf width (cm)	S	S	S	S	Overdominance	Unequal	Recessive genes
Leaf area (cm)	ns	S	S	ns	Overdominance	Asymetrical	Dominant genes
Flag leaf width (cm)	ns	S	S	ns	Overdominance	Asymmetrical	Recessive genes
Flag leaf area (cm)	ns	S	S	S	Overdominance	Asymmetrical	Recessive genes
Days to maturity (cm)	S	S	S	S	Overdominance	Asymmetrical	Recessive genes
Plant height (cm)	ns	S	S	S	Overdominance	Asymmetrical	Dominant genes

Table 2B: Continued……

Characters	Variance component fraction				Ratio		
	D	H1	H2	h^2	$(H1\backslash D)^{0.5}$ (Degree of dominance)	$H_2 \backslash 4H_1$ (Ratio of positive and negative alleles)	KD\KR (Ratio of dominant and recessive genes)
Panicle length (cm)	ns	s	S	ns	Overdominance	Asymmetrical	Dominnt genes
No.of spikeletes per panicle	S	s	S	ns	Overdominance	Equal	Dominant genes
Biological yield (gm/plant	ns	s	S	ns	Overdominance	Asymmetrical	Dominant genes
Grain yield(gm/plant)	ns	ns	S	ns	Overdominance	Equal	Recessivegenes
Harvest index	ns	S	S	ns	Overdominance	Unequal	Recessive genes
100 grain weight (gm/plant)	ns	ns	S	S	Overdominance	Symmetrical	Dominant genes
100 groat weight (gm/plant)	ns	ns	S	S	Overdominance	Symmetrical	Dominance genes
Groat protein content (%)	S	ns	S	S	Overdominance	Unequal	Domoinant genes
Protein yield (gm/plant)	S	S	S	S	Overdominance	Unequal	Dominant genes
Straw yield (gm/plant)	ns	S	S	S	Overdominance	Unequal	Dominant genes
Growth rate (gm/day/plant)	ns	S	S	S	Overdominance	Unequal	Dominant genes

Days to 50% heading

The estimates of variance components D_1 H_1, H_2 and h^2 were non significant for days to 50 % heading however value of H_1 (2.59) was higher as compared to D (0.474) indicated that non – additive variance was more important than additive genetic variance for this trait. The value of $(H_1/ D)^{0.5}$ which was greater than one (2.34) showed the presence of over dominance. The calculated value for the proportion and negative alleles ($H_2/4H_1$) was 0.19 and being less than 0.25 indicated that unequal proportion of positive and negative alleles present in the parents. The ratio of KD \ KR (5.25) was greater than one indicated larger proportion of dominant allele in the parents.

Plant height at 50% heading

The variance components D_1 H_1, H_2 and h^2 were non-significant in the expression of this character. However the value of H1 (231.69) was higher as compared to D (74.81) indicated that non-additive variance was more than additive genetic variance for plant higher at 50% heading. The estimate of average degree of dominance $(H_1/ D)^{0.5}$ was less than unity (0.17) which suggested partial dominance. The proportion of genes with positive and negative effects in the parent estimated, as ($H_2/4H_1$) was 0.17 being less than 0.25 indicated unequal proportions of positive and negative alleles in the parent. The ratio of dominant and recessive genes in the parents (KD/KR) was greater than one (3.51), indicated an excess of dominant alleles in the parents.

Number of tillers per plant

Only two values of variance components i.e. H_1 and H_2 were significant for number of tillers per plant. Values of H_1 was higher than the value of D which showed that non-additive genetic variance was important than additive genetic variance. The value of average degree of dominance $(H_1/ D)^{0.5}$ more than unity, (3.87) indicated the presence of overdominanace. The $H_2\backslash 4H_1$ ratio of 0.24, showed unequal proportion of positive and negative alleles in the parents whereas the ratio of KD/KR (1.02) was greater than one thus indicated the excess of dominant alleles in the parents.

Number of leaves per plant

The two variance component H_1 and H_2 were significant for number of leaves per plant. Higher value of dominant variances (H_1) than that of additive genetic variance (D) showed the importance of non additive genetic variance than additive genetic variance. The average degree of dominance $(H_1/ D)^{0.5}$ was more than one (8.73) hence indicated the presence of over dominance. The ratio of $H_2/ 4H_1$ (0.24) being less than 0.25 indicated the presence of unequal proportion of positive and negative alleles in the parents. The value for KD/KR ratio was less than one (0.99) indicated that recessive gene was present for this character.

Leaf length

The estimate of h^2 was significant for leaf length however, value of H_1 (38.61) was higher as compared to D (1.17) indicated that non- additive variance was more important than additive genetic variance for leaf length. The dominance ratio of $(H_1/ D)^{0.5}$ more than one (5.75), indicated that over dominance was present. The proportion of genes ($H_2/ 4H_1$) with positive and negative effects (0.23) indicated unequal proportion of both positive and negative alleles in the parents. The ratio of dominant and recessive genes (1.03) in the parents showed excess of dominant alleles in the parents.

Leaf width

Variance component of D, H_1, H_2 and, h^2 showed significant

values. H_1 showed higher value as compared to D indicated that non- additive genetic variance was more important in the control of leaf width. Ratio of $(H_1/ D)^{0.5}$was greater than unity thus showed the presence of over dominance and the ratio of KD/KR (0.83) was less than unity revealed the presence of larger proportion of recessive alleles in the parents for leaf width. The $H_2/ 4H_1$ ratio (0.19) indicated unequal proportion positive and negative alleles in the parents.

Leaf area

Only two values H_1 and H_2 component were significant for leaf area. The estimate of H_1 was greater than D indicated that non- additive genetic variance was more important for leaf area. The value of $(H_1/ D)^{0.5}$ was more than one (2.54) which suggested the presence of over dominance. The ratio of $H_2/ 4H_1$ (0.23) showed asymmetrical distribution of positive and negative alleles in the parents. The value of KD/KR (1.00) showed the excess of dominant genes for leaf area in the parents.

Flag leaf length

Only two components H_1 and H_2 showed significant estimates for this trait. Dominance variance (H1) was greater than D indicated that non-additive genetic variance was more important for flag leaf length. The value of $(H_1/ D)^{0.5}$ was greater than one (3.05) indicated presence of over dominance. The ratio $H_2/ 4H_1$ (0.20) was less than 0.25 revealed as asymmetrical proportion of positive and negative alleles in the parents. The value of KD/KR (0.98) showed the excess of recessive alleles in the parents for leaf length.

Flag leaf width

Estimates for H_1, H_2 and, h^2 found to be significant component of variance. The value of H_1 was more than D expressed that non- additive genetic variance was more important for leaf width. More than unity value of $(H_1/ D)^{0.5}$ (3.05) expressed over dominance whereas, the ratio of KD/KR was less than one (0.05) thereby expressing the preponderance of recessive alleles in the parents. Unequal proportion of positive and negative alleles has been revealed by less than one value (0.20) of $H_2/ 4H_1$.

Flag leaf area

The genetic parameter D, H_1, H_2 and, h^2 were found to be significant. Greater value of H_1 than D indicates more importance of non- additive genetic variance for flag leaf area (Table 1 A).The ratio of $(H_1/ D)^{0.5}$ was more than one (2.45) which indicated the presence of over dominance. The value of $H_2 \backslash 4H_1$ (0.21) showed unequal proportion of positive and negative alleles. The ratio KD/KR (0.99) being less than one expressed that recessive genes was for this trait were in excess in the parents.

Days to maturity

Estimates of the components, H_1, H_2 and, h^2 were found to be significant for days to maturity. The value of H_1 was higher than D which revealed that non-additive genetic variance was more important for this trait. The ratio of $(H_1/ D)^{0.5}$ was more than one indicating the presence of over dominance. The value of $H_2 \backslash 4H_1$(0.25) showed equal proportion of positive and negative alleles in the parents while the less than unity value of KD/KR ratio (0.97) indicated the excess of recessive alleles for this character.

Plant height at maturity

Only one component of variance viz; H_1 showed significant estimate for this character. Dominance variance (H_1) was in greater magnitude than additive genetic variance. The ratio of $(H_1/ D)^{0.5}$ was greater than one (2.94) thus indicated over dominance. Less than unity (0.19) value for $H_2/4H_1$ ratio indicated asymmetrical distribution of positive and negative alleles among the parents. The value of KD/KR (1.00) showed that dominant alleles were present in the parents for plant height at maturity.

Panicle length

Only two components H_1 and H_2 were significant for this character. Dominance variance (H_1) was greater than additive genetic variance (D) indicating the importance of non-additive genetic variance (D) indicating the importance of non-additive genetic variance for panicle length. The ratio of $(H_1/ D)^{0.5}$ was greater than one (2.34) hence, indicated over dominance. The ratio of $H_2 /4H_1$ (0.24) was less than unity reflected asymmetrical distribution of positive and negative alleles and the value KD/KR(1.01) showed the presence of dominant alleles in the parents for this character.

Number of spikeletes per plant

The components D, H_1 and H_2 were significant and the higher value of H_1 than D indicated that non-additive genetic variance was more important in the expression this trait. The ratio of $(H_1/ D)^{0.5}$ (1.79) indicated that over dominance was present and also the value of KD/KR (1.00) showed the presence of genes in the parents. The ratio of $H_2 /4H_1$ (0.29) (i.e > 0.25) revealed equal proportion of positive and negative alleles in the parents.

Biological yield

Significant estimates of H_1 and H_2 components were recorded for biological yield. The estimate of H_1 was greater than D indicating preponderance of non-additive genetic variance for biological yield. Higher value (3.68) of $(H_1/ D)^{0.5}$ suggested the presence of over dominance. The ratio of $H_2 /4H_1$(0.19) showed asymmetrical distribution of positive and negative alleles and the value of KD/KR (1.00) indicated the dominant genes were present in the excess in the parent for biological yield.

Grain yield

Only H_2 component was found significant for grain yield however, value of H_1 (96.72) was higher as compared to the (31.46) indicated that non-additive variance was more important than additive genetic variance for grain yield. The $(H_1/ D)^{0.5}$ ratio of 1.75 showed the presence of over dominance. The value of $H_2 /4H_1$ (0.26) showed equal proportion of distribution of positive and negative alleles in the parents. The ratio of KD/KR being less than one indicated the excess of recessive genes in the parents.

Harvest index

Only two components H_1 than H_2 were significant for this character. Greater estimate of H_1 than D indicated that non-additive genetic variance was more important for harvest index. The value of $(H_1/ D)^{0.5}$ which was more than one (2.95) suggested the presence of over dominance. The ratio of $H_2 /4H_1$ (0.51) showed asymmetrical distribution of positive and negative alleles and also KD/KR value (1.03) revealed excess of dominant genes present in the parents for harvest index.

100- Grain weight

The variance components H_1 than H_2 were found significant for 100-grain weight however, value of H_1 (0.092) was greater than D (0.05) indicated that non-additive variance was more important than additive genetic variance for this trait. The ratio $(H_1/ D)^{0.5}$ showed the presence of over dominance. The value of $H_2 /4H_1$ (0.46) showed equal proportion of positive and negative alleles in the parents. Whereas, the KD/ KR ratio (1.38) being more than one indicated the excess of dominance genes.

100 – Groat weight

Three components D, H_2 and h^2 observed significant for this character. The ratio of $(H_1/ D)^{0.5}$ expressed the presence of over dominance. The value of $H_2 /4H_1$ (0.41) showed equal proportion of positive and negative alleles and KD/KR ratio which was more than one indicated presence of dominance genes for 100- groat weight.

Groat protein content (%)

Significant estimates were recorded three components of variances D, H_2 and h^2 for protein content. The ratio $(H_1/ D)^{0.5}$ expressed existence of over dominance. The value of ratio of $H_2 /4H_1$ (0.21) showed unequal distribution of positive and negative alleles and ratio of KD/KR being more than one (1.42) indicated the excess of dominant genes for protein yield per plant.

Protein yield

The components H_1, H_2 and h^2 were found significant for protein yield. The value (3.06) for the ratio of $(H_1/ D)^{0.5}$ indicated over dominance present. The ratio of $H_2/ 4H_1$ (0.24) showed unequal distribution of positive and negative alleles for this trait. The ratio of KD/KR (1.04) indicated excess of dominant genes for protein yield per plant.

Straw yield

The genetic component of variance H_1, H_2 and h^2 were found significant. The value $((H_1/ D)^{0.5}$ indicated over dominance and ratio of $H_2/ 4H_1$ (0.22) showed unequal distribution of positive and negative alleles for this trait. The ratio of KD/KR (1.00) exhibited excess of dominant genes in the parents for straw yield per plant.

Growth rate

The genetic component of variance H_1, H_2 and h^2 were found significant for growth rate. The value of $((H_1/ D)^{0.5}$ indicated over dominance and $H_2/ 4H_1$ (0.23) ratio showed unequal proportion of positive and negative alleles in the parents. The ratio KD / KR exhibited excess of dominant genes present in the parents for growth rate.

Conclusion

Considering the overall results from the present study it is apparent that additive and non additive genetic effects are prevalent for most of the character which may be utilized through selection in the early segregating generations exploiting the fixable effects. To utilize both types of genetic effects breeding methods like modified recurrent selection i.e alternating pedigree and current selection cycles (Khadr and Frey 1965). Diallele selective mating (Jensen, 1970) multiple crossing and early generation selection followed by intermating among F_2/F_3 generation selection followed by intermating among F_2/F_3 generation selected plants (Redden and Jensen, 1974) is proposed for further improvement in the crop. Biparental mating may be useful when linkage between the genes governing the inheritance is pronounced.

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