Biological Forum – An International Journal 13(2): 576-580(2021)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Six Generation Mean Analysis for yield and its Attributing Characters in Flax (*Linum usitatissimum* L.)

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(Received 14 May 2021, Accepted 05 July, 2021)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Linseed varieties with increased yield and omega content are an important strategy to alleviate omega malnutrition. The choice of selection of breeding methods for genetic improvement of any crops is mainly dependent on the knowledge of type and relative amount of genetic component and the presence of epistatic interaction for different traits in the plant materials under investigations. Information on the type of gene action involved in the inheritance of a character is helpful in deciding the breeding procedures to be followed for crop improvement. The study was under taken to know the nature of gene action governing the characters under study. Generation mean analysis is one of the biometrical techniques that provide not only a valid estimate of gene effects (additive, dominance) but also an unambiguous test for presence or absence of epistasis that can help the breeders to decide the breeding programmes that suit for the improvement of traits being analyzed. In majority of the yield traits observed that F_2 mean was lower than their corresponding F_1 means for characters like, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and yield plant^{-1} . Six generations mean analysis in the cross PCL-55 × LLA-5 revealed that dominance genetic variance was documented for the important yield traits like, number of capsules plant^{-1}, 1000 test weight and yield plant^{-1}.

Keywords: Generation means, linseed, gene action, epistasis, variance.

INTRODUCTION

Flax (*Linum usitatissimum* L.), is a self-pollinated crop and commonly known as Alsi in Hindi, Agase in Kannada. It is an oilseed and fibre crop of the tropical as well as temperate regions of the world. Worldwide linseed crop occupies an area of 22.70 lakh ha and production 22.39 lakh tonnes having average productivity of 986 kg per ha. In India production of 1.47 lakh tonnes is produced from an area of 3.38 lakh ha with a low productivity of 435 kg per ha. The major linseed growing states are Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Maharashtra, Bihar, Odisha, Jharkhand and Karnataka accounting for more than 97 per cent of total area (Anon; 2018-19).

Linseed encompasses the potential health suiting nutritional profile in it. The oil possesses a very healthy fatty acid profile and it contains the good amount of omega-3 fatty acid or ALA (Alpha-Linolenic Acid) 58 per cent and it is essential fatty acid and must be directly taken from foods. Omega-3 fatty acid provides beneficial effects in numerous clinical conditions such as cardiovascular disease, blood pressure, heart beat rate, blood clotting and inflammatory disorders.

Gene action governing quantitative characters can be measured by the use of gene models. Fisher, Immer and Tedin (1932) developed different gene models for more than one locus *i.e.*, additive and dominance model. Other models were also developed by Comstock and Robinson (1948) and Mather (1949) to know the relative importance of additive, dominance and epistatic gene effects called as a three parameter model (m, d, h) furthermore, epistatic effects assumed to be very negligible in these models. Anderson and Hayman (1958) believed that epistatic gene effects could be of significance for quantitative characters. Cavalli, (1952) developed a method known as joint scaling testthat estimates various genetic effects and test of fitness of appropriate genetic model (presence or absence of epistasis). The expected and observed generation means were compared by chi square test with the degree of parameters (p) estimated. Hayman (1958) devised six parameter model referring to the additive (*d*), dominance (*h*), additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (l). These parameters were calculated through the means of different generations and called six parameter models. Through this model importance of gene action can be predicted from the mean measurement of six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2. Jinks and Jones (1958) speculated three parameter models and used where epistatic (non- allelic) interactions are absent.

Generation mean analysis is commonly used in inheritance studies of quantitatively inherited characters (Innes *et al.,* 1975). A generation means analysis is one of the biometrical techniques that involve estimation of the magnitude of various genic effects (additive, dominance and epistatic). The gene action of the yield and its contributing traits were documented by many workers in linseed, the genetics of a particular trait may vary with material to material under study and different environmental conditions and therefore it is necessary to study the gene action of quantitative traits before starting of any breeding plan that can help the any plant breeders to judge the breeding procedures better suited for the improvement of trait (s) being studied.

MATERIAL AND METHODS

The two parents *viz.*, PCL-55 and LLA-5 were used for generation of material and these parents were different genotypes concerning to yield, maturity and fatty acid composition. The female parent was crossed with a male parent to generate F_1s during *Rabi* 2017 at experimental field of AICRP (All India Coordinated Improvement Project) on Linseed, MARS (Main Agricultural Research Station), University of Agricultural Sciences, Raichur. Six generations *viz.*, P_1, P_2, F_1, F_2, BCP_1 and BCP_2 of the cross were raised on raised bed during *Rabi* 2018 at experimental blocks of AICRP on Linseed, MARS, UAS, Raichur. The recommended package of practices was followed to raise good crop stand.

These six generations were evaluated for yield contributing characters to know the nature of gene action and data obtained for yield and yield attributing traits were subjected for six generation mean analysis, as followed by Hayman (1958), to detect additive, dominance and epistatic variance for metric traits was followed in the present study.

Mather's scaling tests: The scaling test was used to calculate generation means and their variances. The three scales, their variances and their standard errors were calculated as follows:

A = 2 B1 – P1 – F1
B = 2 B2 – P2 – F2
C = 4 F2 – 2 F1 - P1 – P2
D = 2 F2 - B1 - B2

Whereas,

P1, P2, F1, F2, BC1 and BC2 are the mean values of respective generations. Significant deviation of A, B and C values from zero indicated the presence of epistasis.

The variance of different scale effects was estimated as follows:

$$V_A = 4V(B_1)+V(P_1)+V(F_1)$$

$$V_B = 4V(B_2)+V(P_2)+V(F_1)$$

$$V_C = 16V(F_2)+4V(F_1)+V(P_1)+V(P_2)$$

$$V_D = 4V(\overline{F_2})+V(\overline{B_1})+V(\overline{B_2})$$

The standard errors of different scale effects for 't' tests computed as follows :

$$\text{S.E. (A)} = (V_A)^{1/2}$$

$$\text{S.E. (B)} = (V_B)^{1/2}$$

$$\text{S.E. (C)} = (V_C)^{1/2}$$

$$\text{S.E. (D)} = (V_D)^{1/2}$$

Now, the't' value computed as follows:

$t_{(A)}$= A/S.E.$_A$
$t_{(B)}$= A/S.E.$_B$
$t_{(C)}$= A/S.E.$_C$
$t_{(D)}$= A/S.E.$_D$

The calculated values of 't' are correlated with the tabulated value of 't' at 5 percent level of significance.

Computation of gene effects by six generation means: The generation means were evaluated by the method speculated by Hayman (1958) to give information on the inheritance of various traits. The generation means were used to calculate the six genetic parameters like. *m*, *d*, *h*, *i*, *j* and *l* of digenic interaction model representing F2 means, additive gene effect, dominance gene action, additive × additive gene effect, additive × dominance gene effect and dominance × dominance gene interaction effects, respectively domineering that no linkage and no higher order gene interaction exists.

Estimation of gene effects

$$m = \frac{1}{2}\overline{P_1} + \frac{1}{2}\overline{P_2} + 4\overline{F_2} - 2\overline{B_1} - 2\overline{B_2}$$

$$d = \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2}$$

$$h = 6\overline{B_1} + 6\overline{B_2} - 8\overline{F_2} - \overline{F_1} - \frac{3}{2}\overline{P_1} - \frac{3}{2}\overline{P_2}$$

$$i = 2\overline{B_1} + 2\overline{B_2} - 4\overline{F_2}$$

$$j = 2\overline{B_1} - \overline{P_1} - 2\overline{B_2} + \overline{P_2}$$

$$l = \overline{P_1} + \overline{P_2} - 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$$

The gene effects involving the variances of means of the different generations were computed as follows.

$$V_m = \frac{1}{4}V(\overline{P_1}) + \frac{1}{4}V(\overline{P_2}) + 16V(\overline{F_2}) + 4V(\overline{B_1}) + 4V(\overline{B_2})$$

$$V_d = \frac{1}{4}V(P_1) + \frac{1}{4}V(P_2)$$

$$V_h = 36V(\overline{P_1}) + 36V(\overline{P_2}) + 64V(\overline{F_2}) + V(\overline{F_1}) + \frac{9}{4}V(\overline{B_1}) + \frac{9}{4}V(\overline{B_2})$$

$$V_i = 4V(\overline{B_1}) + 4V(\overline{B_2}) + 16V(\overline{F_2})$$

$$V_j = 4V(\overline{B_1}) + \frac{1}{4}V(\overline{P_1}) + V(\overline{B_2}) + \frac{1}{4}V(\overline{P_2})$$

$$V_l = V(\overline{P_1}) + V(\overline{P_2}) + 4V(\overline{F_1}) + 16V(\overline{F_2}) + 16V(\overline{B_1}) + 4V(\overline{B_2})$$

Square roots of the variance provided respective standard errors. B1 = Back cross 1 and B2 = Back cross 2. The standard errors were used to estimate the 't' values for testing significance of the corresponding variances, for an instance.

t (d) = $\sqrt{2}$ SE (d), where, SE (d) = [V (d)]½

RESULT AND DISCUSSION

Yield traits are complex with low inheritance and involve several quantitative attributes. An understanding of the inheritance of characters is pre-requisite for its genetic improvement. Detection of the type of gene action provides quite relevant and vital information that is of direct utility to plant breeding problems.

The mode of gene action controlling the inheritance of quantitative characters could be unraveled using, first degree based statistics. First-degree statistics in the form of basic generations not only provide estimates of all the main genetic and digenic epistatic gene effects but also provide powerful tests of the adequacy of genetical model, in particular to test for complex effects such as epistasis. The detection, computation and interpretation of non-allelic interactions have advanced much further at the level of first-degree statistics. Further, first-degree statistics-based gene effects are less affected by non-genetic sources of variation than those based on second-degree statistics. Hence estimates of gene effects based on first-degree statistics are more precise compared to those based on second-degree statistics.

Six generation means performance for yield and yield attributing traits: The generations mean analysis for six basic generations of the cross PCL-55 x LLA-5 was used to estimate the components of epistasis, besides additive and dominance components of total genetic variances. Mean values and their standard error for the seven quantitative traits presented in Table 1.

Table 1: Generation means for yield and yield component in linseed cross PCL-55 x LLA-5.

Generations	X_1	X_2	X_3	X_4	X_5	X_6	X_7
	Mean ± SE	**Mean ± SE**	**Mean ± SE**	**Mean ± SE**	**Mean ± SE**	**Mean ± SE**	**Mean ± SE**
P_1	55.13±2.05	45.53±1.82	4.80±0.22	58.96±3.28	6.50±0.13	6.50±0.00	2.50±0.14
P_2	35.93±1.18	24.60±1.18	4.23±0.21	50.06±3.41	5.96±0.11	6.20±0.00	1.84±0.13
F_1	43.66±0.36	32.33±0.45	4.46±0.27	66.40±2.64	6.76±0.14	6.70±0.00	3.00±0.12
F_2	51.56±0.79	41.11±0.79	5.48±0.17	50.72±2.27	6.42±0.06	6.20±0.01	2.00±0.09
BCP_1	49.85±1.11	40.02±1.14	5.15±0.19	55.42±3.23	6.57±0.10	6.12±0.02	2.21±0.12
BCP_2	40.90±0.95	30.74±0.95	4.87±0.17	51.40±3.17	6.22±0.07	6.14±0.01	1.96±0.12

P_1-PCL-55; P_2-LLA-5; F_1-PCL-55 X LLA-5 ; F_2- (PCL-55 X LLA-5) selfed; BCP_1- (PCL-55 X LLA-5) X PCL-55; BCP_2- (PCL-55 X LLA-5) X LLA-5; X1=Plant height (cm); X2=Technical plant height (cm); X3=Number of branches plant^{-1} ; X4=Number of capsules plant^{-1}; X5=Number of seeds capsule^{-1}; X6=1000 seed weight (g); X7=Seed yield plant^{-1} (g)

The F_1 mean for most of the characters differed from that of its parental means. The majority of yield components revealed that F_2 mean is lower than their corresponding F_1 means for number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and yield plant^{-1} indicating the role of dominance gene action in the inheritance. In contrast plant height, technical plant height and number of branches plant^{-1} recorded higher F_2 mean than their corresponding F_1 means.

The mean of BCP_1 was very close towards parent-1 (P_1) for plant height, technical plant height, number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and yield plant^{-1}. The mean of BCP_2 was resembled towards parent-2 (P_2) for plant height, technical plant height, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight and yield plant^{-1}.

Scaling tests and gene action: Scaling test and gene effects of six generations for yield and yield contributing characters of the cross PCL-55 x LLA-5 is presented in Tables 2 and 3. Significant deviation of 'A', 'B', 'C' and 'D' scales from zero, the cross PCL-55 x LLA-5 revealed the inadequacy of the additive dominance model and thus, the presence of epistatic interaction was indicated in that cross.

Computation of gene effects using six parameters model revealed that significant interaction for all yield attributing traits. The six generation model was applied for estimation of gene effects in view of epistasis as indicated by A, B, C and D scaling tests (Table 2).

Significant additive x additive (i) effect was observed for number of branches per plant and clearly indicated the significant contribution of additive gene effects in the inheritance of this character. While, majority of traits exhibited dominance x dominance type of gene interaction therefore magnitude of dominance × dominance based interaction was high.

The traits, plant height and technical plant height were exhibited dominance × dominance gene effects and duplicate type of gene interaction was observed for both the characters. The results are in accordance with Sood (2004), Kiran *et al.* (2012) and Yadav *et al.* (2018).

However, the traits like number of capsules plant^{-1}, 1000 seed weight and yield plant^{-1} exhibited positive signs for both dominance [*h*] and dominance ×dominance [*l*] depicting complementary nature of gene interaction. The complementary effect of the traits will contribute for the production of new recombinants capable of improving yield. Dominance effects and dominance by dominance epistasis were found to be more important than additive effects and other Epistatic components. Several earlier scientists like Pali and Mahta (2014) and Yadav *et al.* (2018) reported predominance of non-additive gene effects in expression of yield related traits.

Significant but lower magnitude of additive genetic effects for plant height, technical plant height and number of capsules plant^{-1} and non-significant additive genetic effects in the inheritance of number of branches and 1000 seed weight could be due to either limited role of genes with additive gene effects or different degrees of nullifying effects of genes with smaller/larger increasing and decreasing effects in opposite direction (Mather and Jinks 1982). Conclusions based on the magnitudes of only first degree statistics-based additive effects are not advisable, as may not be a true reflection of actual mode of action of genes controlling quantitative traits (Mather and Jinks 1982).

Table 2: Scaling test for seed yield and its component characters in linseed cross PCL-55 × LLA-5.

Sr. No.	Characters	A	B	C	D
1.	Plant height (cm)	0.91±3.04	2.20±2.27	27.86**±4.03	12.37**±2.16
2.	Technical plant height (cm)	4.19±2.96	4.55**±2.29	31.66**±3.94	11.45**±2.17
3.	Number of branches per plant	1.04**±0.51	1.04**±0.49	3.96**±0.93	0.93**±0.43
4.	Number of capsules per plant	-14.51±7.72	-13.66±7.67	-38.94**±11.55	-5.38±6.42
5.	Number of seeds per capsule	-0.12 ^{NS}±0.28	-0.27 ^{NS}±0.24	-0.29^{NS}±0.42	0.05 ^{NS}±0.18
6.	1000 seed weight (g)	-0.94**±0.04	-0.60**±0.02	-1.27**±0.06	0.14**±0.04
7.	Yield plant^{-1} (g)	-1.07**±0.31	-0.91**±0.31	-2.31**±0.48	-0.16±0.25

** One percent level of significance   * Five per cent level of significance

Table 3: Joint scaling test and estimates of gene effect for seven yield contributing traits in linseed cross PCL-55 × LLA-5.

Sr. No.	Characters	m	d	h	i	j	l	Gene action
1.	Plant height (cm)	51.56** ±0.79	8.95** ±1.46	-26.61** ±4.50	-24.75** ±4.33	-0.64± 1.88	21.63** ±7.12	Duplicate
2.	Technical plant height (cm)	41.11** ±0.79	9.28** ±1.49	-24.65** ±4.51	-22.91** ±4.35	-0.18 ±1.84	14.17** ±7.16	Duplicate
3.	Number of branches plant^{-1}	5.48** ±0.17	0.28±0.25	-1.92* ±0.92	-1.87* ±0.86	0.00± 0.30	-0.21±1.39	Complementary
4.	Number of capsules plant^{-1}	50.72** ±2.27	4.02** ±4.52	22.65** ±13.33	10.76** ±12.84	-0.42 ±5.11	17.41** ±21.48	Complementary
5.	1000 seed weight (g)	6.20** ±0.01	-0.02±0.02	0.06 ± 0.08	-0.28** ±0.08	-0.17± 0.02	1.84** ±0.11	Complementary
6.	Yield plant^{-1} (g)	2.00** ±0.09	0.24±0.17	1.15* ±0.53	0.32 ±0.51	-0.07± 0.20	1.66*±0.86	Complementary

** One percent level of significance   * Five per cent level of significance
Whereas,
m=Mean   d=Additive gene effect ;   h=Dominance gene effect;   i=Additive × additive effects ;   j=Additive × dominance effect
l=Dominance x dominance effect

CONCLUSION

Dominance genetic variance noticed the major part of the genetic variance for the important yield components. The use of intermating of selects followed by visual selection in early segregating generations that would simultaneously exploit the gene effects has been suggested. Further, this approach is likely to break some undesirable linkages resulting in the establishment of rare and useful recombinants. The traits which have shown the additive and/or additive x additive can be improved by simple mass selection. If the more predominance of dominance x dominance gene effects exhibited by traits then, delay the selection in early segregating populations and it can also be exploited through heterosis breeding.

FUTURE SCOPE

The F_2 population of a cross between PCL-55 × LLA-5 can be advanced to succeeding segregating generations for selecting desirable stabilized lines for improved yield.

Conflict of interest. Nil.

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How to cite this article: Rajanna, B., Ajith Kumar K., Shiva Kumar K., Ananda N. and Singh, P.K. (2021). Six Generation Mean Analysis for yield and its Attributing Characters in Flax (*Linum usitatissimum* L.). *Biological Forum – An International Journal, 13*(2): 576-580.