J. Soils and Crops 28 (1) 189-194, June 2018

ISSN 0971-2836
NAAS Rating - 4.46
Scientific Journal Impact Factor (2017) 4.338

LINE X TESTER ANALYSIS IN LATHYRUS

Ramjan A. Sayyad[1], Vasant S. Jayade[2], Shanti R. Patil[3], Nitin H. Lande[4], Priyanka N. Taksande[5],
Sandeep R. Kamdi[6] and Suresh K. Dhapke[7]

ABSTRACT

The research work entitled "Line x Tester analysis in lathyrus (*Lathyrus sativus* L.)" was conducted during *rabi* 2015 and 2016 at the experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur, where twenty one F_1 crosses obtained by crossing three testers and seven lines in a line x tester fashion were used to study the general and specific combining ability of parents and crosses, respectively and to select good combiner parents and crosses for studying them in the next generation. These crosses were grown in randomized complete block design replicated thrice and observation on days to first flower, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight, yield plant^{-1} and protein content were recorded. Analysis of variance for combining ability indicated that the mean squares due to lines were significant for all the characters. Mean squares due to testers were significant for all the characters studied except days to maturity, number of primary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and protein content. The mean squares due to line x tester were significant for all the characters under study except for days to maturity and protein content. Both gca and sca effects were found important for most of the characters studied. The parents NLK-06, NLK-17 and Prateek were identified as good general combiners. The crosses NLK-06 x Ratan, NLK-17 x NLK-40 and NLK-17 x Prateek had high mean performance for yield plant^{-1} and number of pods plant^{-1}. The criteria for selecting potential parents in this study was based on their combining ability and the potentiality of crosses to be forwarded to next generation was decided on the basis of high mean performance, high gca of one or both parents involved in the cross with negative sca effects. NLK-06 x Prateek and NLK-17 x Ratan were identified as potential crosses for forwarding to the next generation to explain additive genetic variance by following simple selection method.

(Key words: Combining ability, grasspea, Khesari, Lathyrus, Line x tester)

INTRODUCTION

The *Lathyrus sativus* (L.) (2n = 14) locally called as grass pea, khesari dal, peavine or chana matra. It belongs to family Leguminoceae, sub family Papilionoideae. This is cultivated as herbaceous annual pulse crop. The states which cultivate grass pea are Maharashtra, Madhya Pradesh, Bihar, West Bengal and Eastern Uttar Pradesh, contributing about 4.5% towards the total pulse production of the country (Anonymous, 2013).In Maharashtra it is cultivated in Bhandara, Chandrapur, Gadchiroli and Nagpur districts of eastern Vidarbha, accounting to 48,877 hectares area (Anonymous, 2016). Grasspea is a highly nutritive crop thus, seeds are used as complimentary or sole source of calories 351 cal 100 g^{-1} of seed and endowed with 58 % carbohydrates, 28-32 % protein, 0.6 % fat and 3 g minerals 100^{-1} g of seeds (Aykroyd and Doughty, 1964). It also contains calcium (110 mg), iron (5.6 mg), phosphorus (500 mg) and vitamin B_1 (0.45 mg), B_2 (0.41 mg), and niacin (1.8 mg) 100^{-1} g of seeds (Sharma and Padmanaban, 1969). The excessive consumption of *Lathyrus sativus* seeds for prolonged periods of 3-4 months has long been known to be associated with a crippling disease "lathyrism" which was endemic to certain part of India (Ganpathy and Dwivedi, 1961). Lathyrus varieties generally have low yield potential, poor plant type and high neurotoxin content which is unstable over environment (Ramanujam *et al.,* 1980).The cause of relatively poor success in grain legume in achieving substantial progress is the lack in genetic diversity. On other hand, there have been reports where heterosis is not observed even when diverse parents are crossed.

To achieve these objectives, it is essential to know the nature and magnitude of gene action and combining ability of parental lines. The common approaches of selecting the parents based on *per se* performance, does not necessarily lead to fruitful results (Allard, 1960).Therefore, the choice of parents for hybridization has to be based on complete genetic information and combining ability of parental lines. Similarly the utility of heterosis for increased yield is now well recognized in self-pollinated crops.

1, 4 & 5. P.G. Students, Agricultural Botany Section, College of Agriculture, Nagpur
2, 3, 6,&7. Asstt. Professors, Agricultural Botany Section, College of Agriculture, Nagpur

Top cross, poly cross, diallel and line x tester are different biometrical approaches which have helped the breeder to choose appropriate parents to be included in the hybridization programme. Of these, line x tester analysis is one of the conveniently and often used biometrical tools that provides information of parents and F_1 s. This is widely employed in estimating the general combining ability (gca) of parents and specific combining ability (sca) of crosses.

Keeping in view the importance of this crop as a rich source of proteins, low requirements for its cultivation and tolerance to various biotic and abiotic stresses, the present study was under taken to assess the nature of individual lines and particular cross combinations.

MATERIALS AND METHODS

Seven lines *viz*., NLK-06, NLK-48, NLK-12, NLK-73, NLK-17, LL-14-2 and LL-14-5 were crossed with broad based three testers *viz*., Ratan, Prateek and NLK-40 in line x testers fashion to generate twenty one cross combinations during *rabi* 2015-16. These twenty one crosses were evaluated in *rabi* 2016-17 in RBD design with three replications at the field of Shanker Nagar farm of Agricultural Botany Section, College of Agriculture, Nagpur. Observations were recorded on five randomly selected plants from each cross on days to first flower, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight (g), yield plant^{-1} (g) and protein content (%).The combining ability analysis was carried out as per standard method given by Kempthorne (1957) and ANOVA as per Panse and Sukhatme (1954).

RESULTS AND DISCUSSION

The data regarding analysis of variance for various characters are presented in table 1. The mean squares of genotypes was highly significant for all ten characters. This indicated the presence of sufficient variability in the material used for this study which allows the exploitation of the material for further analysis. Similar to this result Sawant *et al*. (2011), Borkar (2014) also reported significant mean squares for genotypes in lathyrus. On basis of *per se* performance studied for yield and yield contributing characters among twenty one crosses, the cross NLK-17 x NLK-40 was identified as the top ranking cross as it recorded 16.07 g yield plant^{-1}, and 25.50 pods plant^{-1}, 5.13 primary branches plant^{-1}, 7.60 secondary branches plant^{-1}. This was followed by cross NLK-06 x Ratan which produced 15.20 g yield plant^{-1}, 68.73 number of pods plant^{-1}. This was followed by another cross NLK-17 x Prateek which produced 14.87 g yield plant^{-1}, 49.27 number of pods plant^{-1}. These three crosses viz., NLK-17 x NLK-40, NLK-06 x Ratan and NLK-17 x Prateek were identified as potential crosses for selecting superior segregant in future generation on the basis of *per se* performance of crosses. Similar to this result Sawant (2011) and Patil (2001) also reported that *per se* performance of parents and crosses were not useful alone for identification of superior parents and crosses.

Data regarding analysis of variance for combining ability are presented in table 2. The variation between crosses was partitioned into different components representing mean squares due to lines, testers and lines x testers. The mean squares due to lines were significant for all the characters. Mean squares due to testers were significant for all the characters studied except days to maturity, number of primary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1} and protein content. The mean squares due to lines for all characters *i.e*. days to first flower, days to maturity, plant height at maturity, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, seeds pod^{-1}, 100 seed weight, seed yield plant^{-1} and protein content were higher in magnitude than those due to testers, indicating large diversity among the lines than in testers for these characters. The mean squares due to line x tester were significant for all characters under studied except days to maturity and protein content. The significant mean squares for line, tester and lines x testers were also observed by Sharma *et al*. (2007) in gardenpea, Sawant *et al*. (2011) in lathyrus, Amadabade *et al*. (2014) in chickpea, Wagh (2015) in lathyrus, Pinkidas (2015) in lathyrus.

The predictability ratios ranged from 0.16 (yield plant^{-1}) to 0.53 (plant height). Predictability ratio was found to be less than 0.50 for days to first flower (0.28), number of primary branches plant^{-1} (0.30), number of secondary branches plant^{-1} (0.46), number of pods plant^{-1} (0.36), number of seeds pod^{-1} (0.21), 100 seed weight (0.42), seed yield plant^{-1} (0.16), protein content (0.44) and predictability ratio was more than 0.50 for other characters *viz*., days to maturity (0.52) and plant height (0.53). The predictability ratio was closer to 0.5 for number of secondary branches plant^{-1} (0.46), 100 seed weight (0.42), protein content (0.44), days to maturity (0.52) and plant height (0.53) which indicated that the additive as well as non-additive genetic components are equally responsible for the development of these characters. Under such situation the performance of the progeny can be judged / predicated on the basis of both general combining ability and specific combining ability for these traits.

The gca effects of ten lines were estimated for all the ten characters and gca effects of testers were estimated for five traits only, except days to maturity, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of seeds pod^{-1} and protein content and data are presented in table 3. Sca effects of 21 crosses for all characters except days to maturity and protein content were calculated and data are presented in table 4. The gca effect of testers for five traits and sca effect of crosses for two characters were not estimated as their respective mean squares were non significant.

Table 1. Analysis of variance for various characters

Sources of variation	d.f.	Mean squares									
		Days to first flower	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)	Protein content (%)
Replications	2	1.59	8.29	7.85	0.06	1.83	52.23	0.06	0.07	4.72	0.048
Genotypes	20	32.20**	15.55**	31.47**	0.53**	2.58**	350.75**	0.16**	1.40**	25.16**	6.60*
Error	40	1.84	6.44	3.30	0.04	0.59	31.45	0.04	0.26	1.82	3.18

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

Table 2. Analysis of variance for combining ability

Sources of variation	d.f.	Mean squares									
		Days to first flower	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)	Protein content (%)
Lines	6	42.99**	23.72**	64.29**	0.85**	4.17**	633.16**	0.16**	1.97**	17.70**	9.08*
Testers	2	15.72**	18.25	20.82**	0.10	2.28*	80.37	0.10	1.59**	13.65**	6.57
Line x Testers	12	29.55**	11.01	16.84**	0.45**	1.84**	254.60**	0.16**	1.08**	30.81**	5.37
Error	40	1.83	6.44	3.30	0.04	0.59	31.45	0.04	0.26	1.82	3.18
Predictability ratio (GCA vs SCA)		0.28	0.52	0.53	0.30	0.46	0.36	0.21	0.42	0.16	0.44

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

Table 3. General combining ability effects of parents for different characters

Sr.No.	Parents	Days to first flower	Days to maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)	Protein content (%)
	Lines										
1	NLK-06	0.78	-0.99	2.81**	0.25*	-0.80**	14.26**	-0.13	-0.97**	1.94**	0.20
2	NLK-48	-2.95**	-1.33	-2.83**	0.05	-0.15	1.12	-0.12	0.37*	0.05	0.31
3	NLK-12	3.34**	1.11	2.23**	0.12	0.16	-6.81**	-0.13	0.34*	-1.39**	0.48
4	NLK-73	0.57	-2.12**	0.79	0.07	0.59	-1.35	-0.00	-0.19	-1.28**	-2.15**
5	NLK-17	-2.38**	-0.44	1.95**	0.29**	0.83**	-11.60**	0.03	0.08	1.58**	-0.25
6	LL-14-2	-0.69	1.99*	-4.10**	-0.61**	0.34	-1.37	0.23*	0.08	-1.33**	0.69
7	LL-14-5	1.33*	1.78*	-0.85	-0.17	-0.97**	5.74**	0.12	0.29	0.43	0.71
	SE(g_i)	**0.54**	**0.77**	**0.55**	**0.09**	**0.27**	**1.57**	**0.084**	**0.16**	**0.39**	**0.56**
	Testers										
1	Ratan	0.91*	-	0.28	-	-	1.06	-	0.21	-0.56*	-
2	Prateek	-0.81*	-	0.83*	-	-	1.20	-	-0.31**	0.92**	-
3	NLK-40	-0.10	-	-1.10**	-	-	-2.26*	-	0.11	-0.36	-
	SE(g_j)	**0.35**	**-**	**0.36**	**-**	**-**	**1.03**	**-**	**0.11**	**0.25**	**-**

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

Note:- gca effect of testers for days to maturity, no. of primary branches plant^{-1}, no. of seeds pod^{-1}, Protein content was not estimated as mean square due to gca was non significant.

Table 4. Specific combining ability effects of crosses for different characters

Sr.No.	Parents	Days to first flower	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)
1	NLK-06 x Ratan	1.63	2.43*	0.55**	0.38	6.45*	-0.13	0.04	2.85**
2	NLK-06 x Prateek	1.05	-2.72**	-0.51**	0.37	-16.15**	0.13	-0.64*	-4.10**
3	NLK-06 x NLK-40	-2.68**	0.28	-0.04	-0.75	9.70**	-0.01	0.60*	1.25
4	NLK-48 x Ratan	3.56**	1.15	-0.19	0.93	4.92	-0.20	0.24	3.14**
5	NLK-48 x Prateek	-1.92*	-1.01	0.16	-0.09	-8.48**	0.15	-0.18	-3.68**
6	NLK-48 x NLK-40	-1.64	-0.14	0.02	-0.84	3.57	0.05	-0.06	0.54
7	NLK-12 x Ratan	-1.73	-1.92	-0.05	-0.72	1.92	0.27	0.93**	0.65
8	NLK-12 x Prateek	-2.55*	-0.07	0.16	0.67	-3.22	0.07	0.05	0.63
9	NLK-12 x NLK-40	4.28**	1.99*	-0.11	0.05	1.30	-0.34*	-0.97**	-1.28
10	NLK-73 x Ratan	1.85	-1.68	0.19	0.53	-4.62	-0.28	-0.31	-1.79*
11	NLK-73 x Prateek	-2.90**	0.84	-0.06	-0.36	-0.08	0.01	-0.15	3.12**
12	NLK-73 x NLK-40	1.05	0.84	-0.13	-0.17	4.70	0.27	0.46	-1.33
13	NLK-17 x Ratan	-0.31	-3.03**	-0.50**	-0.38	-5.10	-0.01	-0.67*	-5.26**
14	NLK-17 x Prateek	3.61**	1.88	-0.08	-0.67	12.70**	0.11	0.11	1.39*
15	NLK-17 x NLK-40	-3.30**	1.15	0.58**	1.05*	-7.61**	-0.10	0.56	3.87**
16	LL-14-2 x Ratan	-2.70**	-0.32	0.34*	-0.96	0.40	0.12	-0.14	-0.62
17	LL-14-2 x Prateek	0.39	2.13*	-0.11	0.62	5.54*	-0.16	0.45	1.23
18	LL-14-2 x NLK-40	2.31*	-1.81	-0.22	0.34	-5.94*	0.04	-0.31	-0.62
19	LL-14-5 x Ratan	-2.30*	3.37**	-0.35*	0.22	-3.97	0.23	-0.08	1.03
20	LL-14-5 x Prateek	2.32*	-1.05	0.44*	-0.53	9.69**	-0.31*	0.37	1.41*
21	LL-14-5 x NLK-40	-0.02	-2.32*	-0.09	0.32	-5.72*	0.08	-0.28	-2.44**
	SE (s_{ij}) ±	**0.94**	**0.95**	**0.16**	**0.48**	**2.72**	**0.14**	**0.29**	**0.68**

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

Note:- sca effect of crosses for days to maturity and protein content was not estimated as mean square due to crosses was non significant.

The estimates of gca and sca effects among the parents and crosses showed wide variation in the level of significance for various characters. None of the parents nor crosses had a high and significant gca and sca effects in the desirable direction for all the characters studied. The significant gca and sca effects were also reported by Jaronde (1998), Sawant *et al.* (2011), Borkar (2014), Wagh (2015) and Pinkidas (2015) in lathyrus.

The estimates of gca effects showed that among the testers, Prateek was found to be the best general combiner as it recorded significant and positive gca effects for yield plant^{-1} and plant height. The lines NLK-06 and NLK-17 were found to be good general combiner. NLK-06 line exhibited significant and positive gca effects for four economically important characters *i.e.* yield plant^{-1}, number of pods plant^{-1}, number of primary branches plant^{-1} and plant height and NLK-17 also exhibited significant and positive gca effects for four economically importance characters *i.e.* yield plant^{-1}, number of primary branches plant^{-1} , number of secondary branches plant^{-1} and plant^{-1} , height. These three genotypes Prateek, NLK-06 and NLK-17 were identified as good general combiners and can be used in crossing programme.

The significant sca effects observed in different crosses for different characters had the combination of either high x high, high x poor, high x average, average x average, poor x high, poor x average and poor x poor combining parents. It is important to note here that among the crosses showing significant sca in desirable direction in respect of all the traits either involved or did not involve one or both the parents as good general combiner for the concerned traits. It was also inferred that all the crosses which exhibited high mean in a desirable direction had either positive or negative sca effects, indicating the involvement of additive and dominance gene action.

Out of twenty one crosses studied, crosses NLK-06 x Ratan, NLK-17 x Prateek and LL-14-5 x Prateek were identified as superior crosses on the basis of high mean performance, positive significant gca of one or both parents involved in the cross with negative significant sca effects.

REFERENCES

Allard, R. W. 1960. Principle of Plant Breeding. John Willey & Son's, Inc. New York.

Amadabade, J., A. Arora and H. Sahu, 2014. Combining ability analysis for yield contributing characters in chickpea. Elect. J. Pl. Breed. **5**(4):664-670.

Anonymous, 2013. FAO Production year book (from www.FAO.org).

Anonymous, 2016. Joint directorate of agriculture, Statistical division, Nagpur (M.S.) India.

Aykroyd, W.R. and J. Doughty, 1964. Legumes in Human Nutrition. F.A.O. Nutritiona Studies No. 19, F.A.O. Rome , pp.67-68.

Borkar, R. R. 2014. Top cross analysis in lathyrus (*Lathyrus sativus* L.) Unpublished M.Sc. thesis submitted to Dr.P.D.K.V., Akola.

Ganpathy, K. T. and M. P. Dwivedi, 1961. Studies on the clinical epidemiology of Lathyrism. Reserved ed. (ICMR), Govt. Reg. Press, Rewa, M.P., India. pp. 1-53.

Jaronde, R. V. 1998. Genetic analysis of yield and yield contributing parameter in lathyrus. M. Sc. Thesis (Unpub.) submitted to Dr. P.D.K.V., Akola.

Kempthorne, O.1957. An Introduction to General Statistics. John Wiley and Sons. Inc. New York. Chapman and Hall Ltd.London. pp.468-470.

Panse, V. G. and P. V. Sukatme, 1954. Statistical methods for Agricultural workers. ICAR. Publication, New Delhi. 2 pp.63-66.

Patil, S. P. 2001. Diallel analysis in lathyrus (*Lathyrus sativus)* Unpublished M.Sc. thesis submitted to Dr. P.D.K.V.,Akola.

Pinkidas. 2015. Genetic analysis and molecular characterization in Grasspea (*Lathyrus sativus* L.) .) Unpublished M.Sc. Thesis, submitted to Deptt. of Plant Breeding and Genetics, IGKV, Raipur, (C.G).

Ramanujam, S., K. L. Sethi and S. L. N. Rao. 1980. Stability of neourotoxin in khesari. Indian J. Genet. **40**:300-304.

Sawant, P.V. and V. S.Jayde, S. R. Patil. 2011. Line x tester analysis in lathyrus. J. Food Legumes, **24**(1):41-45.

Sharma, A., G. Singh, S. Sharma and S. Sood, 2007. Combining ability and heterosis for pod yield and its related horticultural traits in garden pea under mid-hill subtemperate and high-hill dry temperate condition of Himachal Pradesh. Indian J. Genet. **67**(1):47-50.

Sharma, D. S. and Padmanabhan, 1969. Food Science and Tech. Liener, I.E. (ed). Academic press, New York. pp.209-233.

Wagh, B. P. 2015. Diallel analysis in lathyrus (*Lathyrus sativus.* L.). Unpublished. M.Sc. thesis submitted to Dr.P.D.K.V.,Akola.

Rec. on 30.05.2017 & Acc. on 20.06.2017