Vegetable Science (2012) 39 (2) : 169-172

Genetic analysis of quality attributes in table pea (*Pisum sativum* L.)

KP Singh, JD Singh, HC Singh and JP Srivastava

Received : October, 2011 / Accepted : July, 2012

Abstract: 10 parental diallel set was used for green pod yield, shelling percentage, harvest index and protein content in F_1 and F_2 generations of pea. The estimates of gca variances were higher than sca variance for harvest index only in F_2 generation while sca variances were higher than gca variance for green pod yield in F_1; for shelling percentage and protein content in both generations. The ratio of gca and sca indicated that additive genes were effective for green pod yield in F_2 generation and for harvest index and protein content in both generations while non-additive genes for shelling percentage. Parents KS 136; Azad P-3 and Azad P-l were found good general combiners for all the traits except shelling percentage for AP3 in F_1. Cross combination KS 226 x Azad P-l was found good specific combiner for green pod yield and harvest index while Azad P-l x Azad P-3 for protein content in both the generations.

Key words: Combining ability, gene effects, quality traits, pea

Introduction

Protein constitutes an important segment of human nutrition. In India, majority of the population is predominantly vegetarian and depends on plants for their protein requirements. The cheapest and richest source of plant proteins are grain legumes, known as pulses. Pea is second most important pulse crops, which is extensively grown throughout the world. Pea is a multipurpose crop which is consumed in different kinds viz. green twigs, green pods, canned peas, *soup, chhola, dhal* and *besan* etc. The table pea is famous for its taste and other qualities among vegetarian people in forms of various dishes. It is also a bridge between huge gap in the availability and requirement of protein for the human population. Hence, the present study was aimed to select suitable parents/crosses for quality traits through combining ability analysis for parents and their hybrids in F_1 and F_2 generations.

Materials and Methods

Ten diverse genotypes of pea were crossed in all possible combinations excluding reciprocals. The parents, their 45 each F_1s sand F_2s were sown in a randomized complete block design with three replications at Vegetable Research Station of C.S.A. University of Agriculture and Technology, Kanpur. Each parents and F_1s in single row and each F_2s in two rows of 3m long were grown with the spacing of 45 x 15 cm between and within rows, respectively. The observations were recorded on ten randomly selected plants from parents and F_1s and 20 plants from F_2s in each replication. Analysis was carried out according to Griffing (1956). After harvesting the crop the protein in seed was determined by Kjeldahl method (AOAC, 1965) and other characters as usual procedure. The data were analysed by method 2 model I of Griffmg (1956).

Results and Discussion

The analysis of variance for combining ability revealed highly significant values both for gca and sca mean sum of squares for all the traits in both F_1 and F_2 generations (Table 1) indicated the existence of sufficient genetic variability in lines and their crosses and the importance of both additive and non-additive genetic component of variation in the expression of these traits. These findings are in agreement of earlier results reported by Gupta and Singh (2004) and Singh and Singh (2003).

If both gca and sca effects are significant in combining ability analysis, it becomes necessary to know how important the interactions are in determining the single cross progeny, the relative importance of gca and sca in determining the progeny performance is better assessed by the ratio $2s^2$ gca/$2s^2$ gca + s^2 sca (Baker, 1978). Lower value of the ratio for shelling percentage and protein content in both generations and for green pod yield in F_1 indicated the role of non-additive gene effects

---

KP Singh, JD Singh, HC Singh and JP Srivastava
Department of Vegetable Science, C.S.A. Univ. of Agri. & Tech., Kalyanpur, Kanpur-208024
E-mail: koshendra63@gmail.com

in the expression of these attributes. Similar results were reported for shelling percentage by Srivastava *et at.* (2007). For harvest index and protein content both additive and non-additive gene effect was observed in both generations. The parents KS-136 & Azad P-l were proved to be as good general combiners for all the traits except Azad P-l for green pod yield in F_1, KS 225 and Azad P-3 for green pod yield, harvest index and protein content, Mutant P-43 for shelling percentage were observed good general combiners in both the generations. These diverse parents can be used in hybridization program depending upon the specific objectives. Alternatively desirable multiple parents can be put into a central gene pool to generate useful segregants (Jenson, 1970).

The performance of parent and crosses themselves give some indication for their usefulness, long term potentialities of them are least known at the initiation of breeding program. If there is an agreement between combining ability values and *per se* performance, it will not be difficult to make the right choice for selection of parents. In the absence of correlation between two, the question regarding relative importance to be attached to each needs to be addressed. In such conditions, more reliance could not be put on parental mean values as an index of their superiority for inclusion in breeding program aimed at quality improvement (Chauhan and Singh, 1983). But when a character mean is of desirable status, weightage should be given to s^2gca/s^2sca scored depending upon the objective and nature of the crop (Jagdap, 1986).

The top ranking five crosses showed desirable sca effects and high *per se* performance (Table 3) indicates high x high, high x medium, medium x low and low x low general combining ability effects for different quality parameters. The cross combination KS 226/ Azad P-l exhibited good specific combiner for green pod yield and harvest index in both generations having high x high gca pattern. The cross combination KS 195/Azad P-3 for shelling percentage in F_1 and protein content in F_2 exhibited desirable and significant specific combining ability. The crosses having high x high gca coupled with high sca effects might be produced due to involvement of diverse parents and involvement of additive or additive x additive types of gene interaction (Singh and Sharma, 2006).

Crosses involving high x low and low x low general combiners in the present study having high sca effects are of considerable interest as they might be produce transgressive segregants if the additive effects of one parent and complementary effect of the other act in the same direction for maximum expression of the traits. Similar findings have also been reported by Gadag *et at.* (1999) in soyabean. The predominance of non-additive variance leads to bias in favour of heterozygotes in early segregating generations. Therefore, the main objective must be to get homozygosity fast, while reserving selection pressure for later generation in such crosses. The single seed decent method as suggested by Brim (1966) for 2-3 generations per years might be more appropriate.

The results also showed that crosses are promising for different characters. In order to utilize them effectively, an *inter-se* crossing of desirable F_1 S in all possible combinations might be an alternative strategy. Such multiple parent can be put into a central genetic pool which helps in speedy recombination and will also help in breaking tight genetic barriers if present 5 to 6

Table 1. Analysis of variance of combining ability for quality parameters in F_1 and F_2 generations in table pea

S.V.		d.f.	M.S.S.			
			Green pod yield / plant (g)	Shelling %	Harvest index %	Protein content %
gca	F_1	9	2741.31**	40.14**	101.49**	13.12**
	F_2	9	2881.16**	22.95**	107.14**	23.14**
sca	F_1	45	761.23**	9.29**	8.49**	1.49**
	F_2	45	134.86**	6.03**	7.71**	2.24**
Error	F_1	108	14.33	0.02	0.16	0.03
	F_2	108	8.30	0.02	0.18	0.03
σ^2gca	F_1		165.01	2.57	7.75	0.96
	F_2		228.85	1.41	8.28	1.74
σ^2sca	F_1		746.90	9.27	8.33	1.46
	F_2		126.56	6.01	7.53	2.21
σ^2g/σ^2gs	F_1		0.22	0.28	0.93	0.65
	F_2		1.81	0.23	1.09	0.78

** Significant at p – 0.01

Table 2. Estimates of gca effect of parents for quality parameters in F_1 and F_2 generations in table pea

Parents	Green and yield per plant (g)		Shelling (%)		Harvest index (%)		Protein content (%)	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Rachna	-6.44**	-13.53**	2.60**	1.31**	-4.57**	-3.66**	-1.40**	-2.54**
KPMR-65	-9.38**	-4.45**	1.40**	-0.64**	-0.61**	-3.23**	-1.07**	-1.12**
KPMR-184	-11.74**	-13.52**	0.68**	0.80**	-4.98**	-4.95**	-0.92**	-1.30**
Mutant of P-43	-28.37**	-29.07**	1.93**	1.81**	-1.85**	-1.36**	-0.95**	-0.57**
KS-136	9.78**	7.40**	0.18**	0.53**	1.14**	1.44**	0.64**	0.65**
KS-195	-0.74	7.84**	-0.77**	-0.71**	2.80**	2.55**	1.35**	1.80**
KS-225	17.01**	13.98**	-2.71**	-1.81**	1.27**	1.99**	0.62**	0.89**
KS-226	23.92**	24.20**	-2.91**	-2.52**	1.74**	1.99**	-0.39**	-0.29**
Azad P-1	0.96	5.49**	0.40**	0.71**	2.28**	2.66**	1.00**	1.12**
Azad P-3	5.00**	1.65	-0.80**	0.52**	2.77**	2.57**	1.11**	1.36**
S.E.(gi)±	1.07	0.62	0.001	0.001	0.01	0.01	0.002	0.002
S.E.(gi-gj)±	2.39	1.38	0.003	0.003	0.03	0.03	0.005	0.005

** Significant at p – 0.01

Table 3. Desirable cross combinations on the basis of sca effects for quality parameters in table pea

Combination	*Per se* performance	sca effects	gca effect	
			P_1	P_2
Green pod yield / plant				
F_1				
KS 226/Azad P-1	201.70	34.28**	23.92**	0.96
KPMR 184/KS 136	198.23	57.65**	-11.74**	9.78**
Rachna/ KS 225	197.30	44.20**	-6.44**	17.01**
KS 225/ Azad P-3	195.40	30.85**	17.01**	5.00**
KS 195/KS 226	195.03	29.32**	-0.74	23.92**
F_2				
KS 226/Azad P-1	149.70	15.04**	24.20**	5.49**
KS 195/ KS 225	144.80	18.02**	7.84**	13.98**
KS 226/ Azad P-3	144.40	13.58**	24.20**	1.65
KPMR 65/ KS 226	138.77	14.05**	-4.45**	24.20**
KS 195/ KS 226	136.60	-0.41	7.84**	24.20**
Shelling %				
F_1				
Mutant of P-43/Azad P-1	57.13	3.95**	1.93**	0.40**
KPMR 65/ KS 225	56.37	6.83**	1.40**	-2.71**
KS 195/ Azad P-3	55.23	5.96**	-0.77**	-0.80**
Rachna/ KPMR 184	55.17	1.05**	2.60**	0.68**
Rachna/ KS 195	55.13	2.47**	2.60**	-0.77**
F_2				
KPMR 184/ Mutant ofP-43	55.43	1.88**	0.80**	1.81**
Mutant of P-43/ Azad P-1	55.40	1.94**	1.81**	0.71**
Rachna / KPMR 65	55.37	3.76**	1.31**	-0.64**
Rachna / KS 136	55.17	2.40**	1.31**	0.53**
Mutant of P-43/ Azad P-3	54.70	1.43**	1.81**	0.52**
Harvest index				
KS 226/ Azad P-1	55.43	3.22**	1.74**	2.28**
KS 226/ Azad P-3	55.30	2.59**	1.74**	2.77**
KS 225/ Azad P-1	55.17	3.42**	1.27**	2.28**
KS 195/ Azad P-3	54.20	0.44**	2.80**	2.77**
KS 225/ Azad P-3	53.93	1.70**	1.27**	2.77**
Harvest index				
F_2				
KS 225/Azad P-3	55.63	0.60**	1.99**	2.57**
KS 226/Azad P-1	55.53	2.41**	1.99**	2.66**

KS 136/ KS 226	55.40	3.50**	1.44**	1.99**
KS 226/ Azad P-3	54.73	1.70**	1.99**	2.57**
KS 195/ KS 226	54.70	1.69**	2.55**	1.99**
Protein content %				
F_1				
Azad P-1 / Azad P-3	26.90	1.04**	1.00**	1.11**
KS 136/ Azad P-1	26.53	1.14**	0.64**	1.00**
KS 225/ Azad P-1	26.30	0.93**	0.62**	1.00**
KS 195/ KS 225	26.13	0.41**	1.35**	0.62**
KS 136/ Azad P-3	25.90	0.39**	0.64**	1.11**
F_2				
KS 195/ Azad P-1	27.37	1.06**	1.80**	1.12**
KS 195/ Azad P-3	26.70	0.16**	1.80**	1.36**
Azad P-1/ Azad P-3	26.67	0.80**	1.12**	1.36**
Mutant of P-43/ KS 225	26.47	2.76**	-0.57**	0.89**
Mutant of P-43/ KS 195	26.40	1.78**	-0.57**	1.80**

** Significant at p – 0.01

generation selections should be applied to whole populations over several environments for extracting superior lines.

सारांश

मटर के दस पित्रों से बनाये गये डायलिल सेट को गुणात्मक लक्षणों जैसे हरी फली उपज सूचकांक तथा प्रोटीन प्रतिशत के आनुवांशिक विश्लेषण हेतु प्रथम एवं द्वितीय पीढ़ियों में मूल्यांकित किया गया। उपज सूचकांक के लिए द्वितीय पीढ़ी में सामान्य संयोजन क्षमता प्रसरण का परिमाण विशिष्ट संयोजन क्षमता प्रसरण से अधिक पाया गया जबकि शेलिंग प्रतिशत एवं प्रोटीन प्रतिशत के लिए दोनों पीढ़ियों में तथा हरी फली उपज के लिए प्रथम पीढ़ी में विशिष्ट संयोजन क्षमता प्रसरण का परिमाण सामान्य संयोजन क्षमता प्रसरण से अधिक पाया गया। सामान्य एवं विशिष्ट संयोजन क्षमता प्रसरण के सापेक्षित अनुपात से भी स्पष्ट है कि हरी फली उपज के लिए द्वितीय पीढ़ी में, उपज सूचकांक एवं प्रोटीन प्रतिशत के लिए दोनों पीढ़ियों में संयोगिक जीन क्रिया प्रभावी थी जबकि शेलिंग प्रतिशत के लिए दोनों पीढ़ियों में असंयोगिक जीन क्रिया प्रभावी पायी गयी। पित्र के एस 136, आजाद पी 1 तथा केवल आजाद पी 3 को शेलिंग प्रतिशत के लिए प्रथम पीढ़ी में छोड़कर, सभी लक्षणों के लिए अच्छे सामान्य संयोजक पाये गये। संकरण के एस 226/आजाद पी 1, हरी फली उपज तथा उपज सूचकांक, आजाद पी 1/आजाद पी 3 प्रोटीन प्रतिशत के लिए दोनों पीढ़ियों में अच्छे विशिष्ट संयोजक पाये गये।

References

AOAC (1965) Official methods of analysis of official agriculturist 9th Ed. Association of Agril Chemist Washington DC.

Baker RJ (1978) Issues in diallel analysis. Crop Science 18 (4): 533-536.

Brim CA (1966) A modified pedigree method of selection in soybeans. Crop Sci 6: 220.

Chauhan VS and Singh BB (1983) Genetic analysis of protein and oil content in soybean. Indian J Agric Sci 53: 634-637.

Gadag RN, Upadhyaya HD and Gond JV (1999) Genetic analysis of yield, protein, oil and other related traits in soybean. Indian J Genet 59 (4): 487- 792.

Griffing B (1956) Concept of general and specific combining ability in relation to diallel crossing system. Australian J Biol Sci 9: 463-493.

Gupta AJ and Singh YV (2004) Line x Tester analysis for early yield components in vegetable pea *(Pisum sativum* L). Veg Sci 31 (1): 17-21.

Jagdap DR (1986) Combining ability in upland cotton. Indian J Agric Sci 56: 833-844.

Jenson NF (1970) A diallel selective mating system from cereal breeding. Crop Sci 10: 629-635.

Singh G and Sharma A (2006) Detection of epistasis and genetic components for quality traits and powdery mildew incidence in garden pea *(Pisum sativum* L). Veg Sci 33 (2): 192-193.

Singh JD and Singh IP (2003) Combining ability analysis in field pea. Indian J Pulses Res 16 (2): 98-100.

Srivastava JP, Singh NP and Srivastava BP (2007) Genetic architecture of quantitative traits in table pea *(Pisum sativum* L). Prog Agric J 7 (1/2): 96-98.