GENETIC DIVERGENCE STUDIES IN PEA (PISUM SATIVUM L.)

Bhupendra Kumar

Department of Genetics and Plant Breeding, Janta Mahavidyalaya, Ajitmal,

Auraiya (UP) India

Abstract

Genetic divergence for 11 characters in 32 strain / varieties of pea (Pisum sativum L.) were studied. Genetic divergence studies suggested that the parents for hybridization may be selected from cluster number 15, 11, 14, 13, and 4. A cross between the strains of cluster number 15 and 11are likely to produce maximum diversity in the segregating generations.

Keywords: Pea, Pisum Sativum L., Genetic divergence, D^2 analysis

Introduction

Pulses are an important part of Indian dietary. They are an important source of protein particularly for vegetarian population. The consumption ratio of pulses and cereals is 1:3 to meet the essential nutritional needs of human beings. Pulse crops are more drought resistance than other crops and also possess unique potentiality of fixing atmospheric nitrogen and thus improve the soil fertility. Pea is grown all over the world and occupies an area of about 7 million hectares, producing more than 10 million tones annually. It is grown particularly in Asia, Europe and USA. In China and USSR the grain is mostly fed to livestock, while in our country it is used for human consumption as a protein source and occupies a position of considerable value because of its importance in the agriculture economy of the country. India stands next to china and USSR in production. Uttar Pradesh is the largest producers in the country contributing about 345 thousand hectares in the area and 481 thousand tones in production and average productivity is 13.94 quintal/hectare. Other important pea growing states are Madhya Pradesh, Bihar, Haryana, Maharashtra and Rajasthan. The D^2 statistics of Mahalanobis (1928) provide a means of grouping varieties / genotypes in topologically distinct clusters to arrange the genotype in order to their relative distances from each other.

Material and Methods

In the present investigation 32 pea *(Pisum sativum*L.) genotypes were planted in a Randomized Complete Block Design with three replications. The each experimental plot consists of 6 rows of 4 m length with 30 cm distance from row to row and 10 cm from plant to plant. All the recommended agronomic practices were followed to raise a good crop. The observations were recorded on 10 randomly selected plants from each treatments and each replication for days to flowering, plant height number of primary branches, number of secondary branches, days to maturity, number of pods/plant, number of seeds/pod, pod length, yield/plant, 100-grain weight and harvest index. The genetic divergence among 32 strains/ varieties were determined for 11 characters from Mahalanobis's D^2 statistics. D^2 between any two populations were calculated as the sum of squares of differences in the values between pairs of corresponding mean values of the transformed characters.

Result and discussion

Genetic diversity is the first and foremost need for any crop improvement programme. Divergence analysis is perform to identity the diverse genotypes for hybridization purposes. Mahalanobis's D2 statistics has been widely used to determine the extent of genetic diversity In the material in irrespective number of populations. The genotypes grouped together in one cluster are less divergent that the ones which fall into different cluseters.

Sometimes ecological and geographical diversity have also been considered as an index of genetic diversity (Vavilov,1921). Contrary of this, Murty and Arunachalam (1966 , Singh and Singh (1969) Yadav et al.(2010) reported that there is no direct relationship between geographical distribution and genetic diversity.

In the present study, 32 genetically diverse strains/ varieties were grouped into 15 clusters (Table 1).

Cluster 2 had the maximum number of genotypes i.e. , 9. It is thus evident that genotypes with in this cluster are not much divergent. Cluster numbers 4,5,,6,9,10,11,12,13,14 and 15 each retained only one genotypes, showing thereby that these genotypes had considerable differences from the rest of the population.

The maximum value of inter cluster 15 and 11 and 14 and 11 followed by between the cluster 11 and 4 and 13 and 11. This clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity. It is suggested that the superior genotype from the cluster 15, 14 and 13 (KMPR317,ICDMR 309 and ICMPR 272) may be

used as the parents for the hybridization programme with the strain 'KPMR-333' as another parent of cluster number 11 for obtaining superior recombinants. Another hybridization between KPMR-333 (from cluster 11) and KPMR-249 (from cluster 4) would produce a wide range of recombinants. The lowest magnitude of inter cluster distance was observed between cluster number 5 and 6 followed by 7 and 8 and cluster number 6 and cluster number 9. It indicates that genotypes of these cluster had close relationship, therefore, may not be emphasized, Therefore, during the selection of parents the inter cluster distance must be accounted.

Intra cluster D^2 values as par Table 1 range from 0.00 to 42.38 (cluster 8). The lowest D^2 values for clusters indicated that the varieties included within the group were compact in diversity, showing less variability as compared to the varieties included in the cluster number 8, which showed maximum divergence within the group.

The comparision of the cluster 'mean' for eleven characters under study, marked considerable genetic difference between the cluster (Table2). Cluster 11 showed maximum value of cluster mean for days to maturity, number of pods/ plant, number of seeds / pod, pod length and grain yield / plant; thus, this cluster is desirable for these character , means strain KMPR-333 is desirable for days to maturity, number of pods / plant, number of seed / pod, pod length and grain yield / plant. Cluster number 4 ,5, 8, 9,10,14 and 15 have maximum mean values for number of secondary branches, plant height, number of primary branches, harvest index, days to flowering, 100-grain weight and number of secondary branches, respectively; though cluster 1,2,3 and 6 showed moderate mean values for almost all the characters under study.

The lowest mean values of cluster 7 for days to flowering similarly cluster 8 showed lowest mean values for days to maturity. Cluster 10 revealed lowest mean value for two characters I.e.; number of secondary branches and harvest index while cluster 12 also have lowest mean values for two character I.e.; plant height and grain yield / plant. Cluster 13 also show lowest mean values for two cluster i.e.; number of primary branches and number of pods / plant. Cluster 14 also showed lowest mean values for number of seeds /pod and pod length but cluster 15 showed lowest mean values for the 100-grain weight. Rest of the clusters presented almost low values for all the characters under study.

Therefore, hybridization between these cluster (4, 11, 13, 14 and 15) will be more effective for breading selection programme.

Table-1 Intra and inter cluster distance (D²) among fifteen clusters in pea.

Clusters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	(-17.22)	58.82	49.14	84.08	44.35	42.64	95.06	63.36	68.55	55.05	49.84	43.95	91,39	132.71	125.44
2		(-25.5)	84.32	38.06	48.72	38.31	103.02	64.80	51.12	36.48	139.71	72.59	69.55	55.50	62.88
3			(-20.07)	99.40	69.88	90.63	146.89	93.50	92.16	91.39	51.12	79.74	115.34	122.98	177.42
4				(0.00)	70.89	41.99	107.12	34.81	54.90	70.39	184.41	101.60	62.72	70.97	49.14
5					(0.00)	15.52	106.09	36.84	21.43	51.84	122.76	118.15	131.10	48.72	72.93
6						(0.00)	99.40	48.44	18.83	37.94	141.13	96.82	107.12	63.20	39.94
7							(-15.68)	18.83	131.79	120.34	173.97	99.20	61.15	110.25	117.07
8								(-42.38)	42.38	96.82	135.95	120.56	99.00	69.38	71.40
9									(0.00)	81.54	148.35	133.50	153.51	44.48	52.99
10										(0.00)	164.86	56.70	81.90	83.90	73.78
11											(0.00)	89.68	173.18	246.80	270.60
12												(0.00)	49.00	181.17	152.76
13													(0.00)	142.56	129.96
14														(0.00)	62.41
15															(0.00)

Values in parenthesis denots intra cluster distance

Table- 2 Cluster mean of fifteen clusters for eleven traits in pea(Pisum sativumL.)

Traits/Characters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Days to flowering	70.22	69.68	71.02	65.33	69.53	69.60	60.56*	63.66	68.60	73.06**	71.33	69.66	62.53	66.86	68.20
Plant height	150.54	147.48	156.20	152.66	160.00**	156.66	148.50	157.83	135.00	157.00	146.33	120.66*	133.66	131.00	158.00
No. of primary branches	1.72	1.77	1.98	1.86	1.53	1.73	1.93	2.00**	1.73	1.66	1.93	1.80*	1.33*	1.63	1.80
No. of secondary branches	2.14	2.18	2.46	2.53**	2.06	2.00	2.30	2.43	2.33	1.86*	2.40	2.43	2.06	2.20	2.53**
Days to maturity	121.55	124.10	125.98	119.60	119.46	118.60	119.96	118.56*	121.33	120.90	127.53**	121.60	118.80	121.80	122.23
No. pods per plant	19.01	15.71	19.90	13.53	20.30	18.26	20.33	22.93	22.13	13.26	23.20**	15.20	10.80*	19.33	16.80
No. of seeds per pod	5.93	5.04	6.04	5.06	5.03	5.03	5.03	5.06	4.90	5.03	6.86**	6.03	5.36	4.10*	4.16
Pod Length	5.03	4.79	5.20	4.56	4.66	4.86	5.03	5.11	4.50	4.46	5.70**	5.20	5.16	4.16*	4.76
Yield per plant	15.35	12.05	16.46	12.20	18.16	14.60	14.75	17.75	16.06	10.33	18.60**	9.60	10.00	14.76	11.60
100 grain weight	18.66	21.83	24.20	21.66	20.50	18.66	18.58	20.41	20,50	19.33	20.16	18.66	21.66	24.33**	17.83*
Harvest index	39.04	39.51	38.45	44.79	39.86	42.29	36.22	41.74	45.67**	34.28	40.18	34.83	37.20	39.46	42.19

*, ** indicates lower and upper range respectively.

References

Arunachalam,V. and A, Upadhya(1989). On the method of classification using D 2 stasistic and the importance of characters contributing to genetic divergence.Indian J.Genet.49(2):227-230.

Das Gupta, T. and Das, P.K.(1991).Genetic divergence in black gram. Indian J. Agric. Res.25(1):07-13.

Dobhal,V.K.and Harihar Ram(1985).Genetic divergence in pea. Indian J. Agric. Sci.55(2):67-71.

Gupta, K.R.; Singh,K.P.,Lodhi,G.P.,and dhaiya,B.S.(1984).Genetic divergence and hybrid performance in some Indian and exotic cultivars of field pea.Crop Improv.11(2):106-110.

Gupta,A.J. and Singh,Y.V.(2006).Genetic divergence in garden pea(Pisum sativumL.).Indian J.of Geneyics and plant breeding. 66(5):341-342.

Mahalanobis,P.C., majumdar,P.N. and Rao,C.R.(1949).Anthropomotic survey of the united pronounces.A ststistical study ,Sankhya19:201-403.

Murty,B.R. and Arunachalam,V.91966).The nature of divergence in relation to breeding systemin some crop plants.Indian J,Genet.26A:188-198.

Singh, M .N. and Singh, R.B.(1989).Genetic analysis of yield traits I pea. Crop Improv.16(1):62-67.

9, Yadav, K., Singh, B.D., Srivastava, C. P., Chand, R. and Yadav, A.(2010).Analysis of genetic divergencein pea(Pisum sativumL.). using quattitave traits and RAPD markers. Indian J.of Geneyics and plant breeding. 70(4):242-244.