Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.6084

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (5):** 1615-1618 (2017)

International Journal of Pure & Applied Bioscience

Research Article

OPEN ACCESS

Gene Effects for Yield Contributing Characters in Long Duration Pigeonpea [*Cajanas cajan* (L.) Millspaugh]

Ashutosh[*]**, A. Nishant Bhanu, and M. N. Singh**
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University,
Varanasi (U.P.) India
*Corresponding Author E-mail: ashutoshmishr5766@gmail.com

Received: 15.09.2017 | Revised: 22.10.2017 | Accepted: 24.10.2017

ABSTRACT

Six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of two crosses having one row each of P_1, P_2 and F_1; two rows each of B_1 and B_2 and five rows each of F_2 were grown in Compact Family Block Design with three replications in Kharif, 2016-17 at Agricultural Research Farm , BHU, Varanasi. Geographically, it is situated at 25.18 ^{0}N latitude and 83.03 ^{0}E longitudes in the North Gangetic plain in the eastern part of Uttar Pradesh. The estimates of six parameters model revealed the significant contribution of both additive and dominance gene effects in most of the traits studied. In general, days to maturity, plant height, number of primary and secondary branches, pods plant^{-1}, pod length, seeds pod^{-1}, 100-seed weight and Seed yield plant^{-1}, the relative contribution of dominance gene effect was even higher than those of additive gene effect. The epistatic gene effects were found to play an important role for the inheritance of almost all the characters in variable number of crosses.

Key words: *Additive, Dominance, Generation means, Pigeonpea.*

INTRODUCTION

Pigeonpea is an important component of human diet in developing countries like India where it supplements cereal based foods by improving its nutritional status. Pigeonpea is the fourth most important pulse crop in the world where in, India alone accounts for 85 percent of the world supply. It is commonly known as ‘*Arhar*’ or ‘*Tur*’, generally used in preparing *dal*, which is fairly rich in protein and minerals and eaten by majority of Indian population. It play a vital role in Indian agriculture and are the major source of dietary protein. It can grow under low fertility and harsh conditions due to its ability to use atmospheric nitrogen through biological nitrogen fixation up to 40 kg N ha^{-1}, which is useful in maintaining soil health through increasing nitrogen availability and microbial activities. It is cultivated worldwide in developing countries under tropical and subtropical climatic conditions with variety of cropping systems. Globally, it is cultivated in about 5.52 million hectares area with an annual production of 4.32 million tonnes with an average productivity around 824 kg/ha.

Cite this article: Ashutosh, Bhanu, N.A., and Singh, M.N., Gene Effects for Yield Contributing Characters in Long Duration Pigeonpea [*Cajanas cajan* (L.) Millspaugh], *Int. J. Pure App. Biosci.* **5(5):** 1615-1618 (2017). doi: http://dx.doi.org/10.18782/2320-7051.6084

In India, it is cultivated on 3.78 million hectares area with an annual production of 2.80 million tonnes with productivity around 740 kg/ha which is lower than global average[1]. In India, Gujarat, Andhra Pradesh, Maharashtra, Uttar Pradesh, Madhya Pradesh, Karnataka and Bihar are the major pigeonpea growing states.

The major constraints that limit the production of pigeonpea are non-availability of quality seeds of improved varieties in adequate quantity, poor crop management, biotic and abiotic stresses prevalent in the pigeonpea growing areas, besides socio-economic factors. Seed yield in pigeonpea, same as in all other crops, is due to interaction of many genes with environment, thus, direct selection for it will not be successful. Selection for yield components has been suggested as a solution for further advance in increasing yield. In breeding to increase the inherent yielding potential of a crop plant, the selection criterion may be yield or some of the morphological components of yield. An understanding of the mode of inheritance of the yield components, the correlations among them, and the association between each component with yield is necessary for the intelligent choice of breeding procedures for developing high-yielding varieties. One of the best methods for the estimation of genetic parameters is generation mean analysis, in which epistatic effects could also be estimated. Six basic generations variance components can give an accurate information in relating average dominance ratio and inheritance. Thus, these components can complete the derived information from means [2,3]. The choice of an efficient breeding procedure depends on the knowledge of the genetic controlling system of the character to be selected using generation mean analysis.

MATERIALS AND METHODS

Six basic generations *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 derived from two crosses *viz.*, MA-6 × BSMR 846 and MAL-13 × BDN 2029 were produced and evaluated in a Compact Family Block Design with three replications during *Kharif* season at Agricultural Research Farm. Each plot consisted of a single row of parents and F_{1s} each, two rows of B_1 and B_2 each and five rows of F_2 generation (20 plants in parents and F_1generation, 50 plants in B_1 and B_2 generation and 200 plants in F_2 generation). Recommended package of practices were followed throughout the crop season. Data were recorded on ten randomly selected plants from each row excluding border plants. Each row was consisted of 4m length and row to row and plant to plant distance being 75 and 25 cm, respectively. All the agronomic practices were followed to raise a good crop. For each family the plot means values in each generation were averaged over replication to obtained generation means. These generations mean formed the basis of calculation of various genetic parameters. The means, variance, variances of mean and standard errors of each of the six generations were estimated. Analysis of data was performed following six parameter model[4,5.]

RESULTS AND DISCUSSION

Assessment of relative magnitude of various gene effects including epistasis is of great importance in formulating the appropriate breeding procedure for further improvement. Considering the significant deviation of scale (s), (A, B, C and D) from zero indicated the evidence of epistasis in all the crosses for all the traits (Table 1) and hence, six parameter model was extended for their practical implication. The estimates of six parameters model revealed the significant contribution of both additive and dominance gene effects in most of the traits studied (Table 2). In general, for days to maturity, plant height, number of primary and secondary branches, pods plant^{-1}, pod length, seed pod^{-1}, 100-seed weight and seed yield plant^{-1}, the relative contribution of dominance gene effect was even higher than those of additive gene effect. Further, higher frequency of duplicate type of epistasis for each of above traits further confirms the predominance of dominant gene effects for the expression of traits studied which was in conformity with earlier reports in this crop [6,7,8]. On the other hand, for 100-seed weight, additive gene effect while for plant height, pod plant^{-1} and secondary branches both additive and dominance gene effects were almost equally important for the inheritance of these traits. The epistatic gene effects were found to play an important role for the inheritance of almost all the characters in variable number of crosses. Considering the importance of epistatic gene interaction, dominance × dominance effect appeared to contribute maximum followed by additive × additive and additive × dominance effects. It may be concluded that the complex character like yield per plant followed by pods per plant were under the controlled of relatively higher proportion of dominance gene effect whereas an important yield component *viz.*, 100 seed weight exhibited relatively higher proportion of additive gene effect which was in conformity with earlier reports [9,10]. It indicated that as the inheritance of quantitative characters becomes more complex, the contribution of dominance gene effect for their inheritance becomes greater. However, the additive gene effects are greater in the traits which are assumed to have less complex inheritance.

Table 1&2: Test of significance of A, B, C and D scales & Estimation of gene effects through generation mean analysis

CROSSES	A	B	C	D	$\hat{m}$	$\hat{d}$	$\hat{h}$	$\hat{i}$	$\hat{j}$	$\hat{l}$	
DAYS TO MATURITY											
MAL-13 × BSMR-846	534.8**	-13.2**	65.3**	12.4**	230.67**	-25.56**	61.50**	-21.67**	32.90**	-20.10**	C
MA-6 × BDN-2029	16.2**	-1.7*	43.9**	16.1**	235.47**	-22.00**	-39.43**	-28.56**	7.98**	16.33**	D
PLANT HEIGHT											
MAL-13 × BSMR-846	-4.27*	1.70*	65.8**	34.3**	183.68**	-40.78**	-56.91**	-65.53**	-2.43*	69.20**	D
MA-6 × BDN-2029	-2.29**	-7.73**	46.8**	28.4**	171.20**	36.90**	-51.30**	-55.80**	2.34*	64.71**	D
PRIMARY BRANCHES											
MAL-13 × BSMR-846	-4.60**	0.25	-1.10	1.25*	13.43**	-1.53**	-2.77	-2.41*	-1.92	5.90**	-
MA-6 × BDN-2029	-4.53**	-1.49**	-5.6**	0.08	13.34**	-1.17**	-3.21*	-0.18	-1.23	5.63**	D
SECONDARY BRANCHES											
MAL-13 × BSMR-846	-1.34*	3.56**	-1.6*	-1.8**	4.95**	-5.67**	6.65**	3.63**	-2.37*	-5.7**	D
MA-6 × BDN-2029	-1.89**	-4.90**	-3.3*	1.77**	4.57**	-6.43*	-4.97**	-3.72**	1.69	10.3**	D
POD PER PLANT											
MAL-13 × BSMR-846	-39.66**	-65.7**	-98.6**	1.34	107.67**	27.00**	57.67**	-2.60	15.00**	105.00**	C
MA-6 × BDN-2029	-34.00**	-19.9**	20.3 **	36.4**	139.00**	-94.39**	-67.00**	-73.67**	-6.69**	127.33**	D
POD LENGTH											
MAL-13 × BSMR-846	-0.02	0.15**	-0.6**	-0.4**	4.46**	0.34**	4.10**	0.76**	-0.09	-0.84**	D
MA-6 × BDN-2029	-1.03**	-1.33**	-0.2*	1.10**	4.70**	-0.18**	-2.80**	-2.21**	0.16	4.58**	D
SEED PER POD											
MAL-13 × BSMR-846	-1.20**	-0.69**	-1.9**	-0.02	3.80**	0.19**	2.66**	0.06	-0.27	2.87**	C
MA-6 × BDN-2029	-0.68**	-0.53**	-2.3**	-0.5**	2.98**	-0.13**	1.24**	1.80**	-0.08	0.17	-
100 SEED WEIGHT											
MAL-13 × BSMR-846	0.90**	-1.00**	-4.7**	2.3**	13.60**	-4.34**	0.34**	4.70**	0.98	-4.57**	D
MA-6 × BDN-2029	1.17**	0.37**	-0.9**	-1.2**	13.39**	-2.67**	1.10**	2.46**	0.44	-3.98**	D
YIELD PER PLANT											
MAL-13 × BSMR-846	-10.9**	-12.1**	-20**	1.27	38.31**	7.37**	28.95**	-2.63	0.56	25.50**	C
MA-6 × BDN-2029	-15.3**	-17.4**	-15**	8.47**	36.90**	-2.40**	-11.35**	-16.97**	1.06	49.67**	D

*Significance at P=0.05, ** Significance at P=0.01
E=Epistasis, D = Duplicate type of epistatic interaction, C = Complementary type of epistatic interactions

CONCLUSION

Scaling tests and Six generation model have revealed that both intra (dominance gene action)and inter-allelic (epistasis) interaction play an important role in the inheritance of all the traits studied. Under such a situation, improvement in such characters may be expected through standard selection procedure which may first exploit additive gene effects. In this situation recombination breeding could be followed by postponing selection to later generations. Simultaneously, care should be taken that dominant gene effects are not dissipated, rather they should be concentrated. Under such circumstances, the reciprocal recurrent selection breeding procedure seems to be the best available method, as it will utilize simultaneously all three types of gene effects resulting for the isolation of desirable recombinants in advanced generations.

REFERENCES

1. Economic survey, An annual document of the Ministry of Finance, Government of India, New Delhi. pp. 100 (2015-16).
2. Mather, K. and J. L. Jinks., Biometrical genetics, the study of continuous variation, third ed., 396 S., Chapman and Hall, London, New York (1982).
3. Kearsey, M.J., Pooni, H.S., The genetic analysis of quantitative traits. Chapman and Hall, London (1996).
4. Hayman, B.I., The separation of epistatic from additive and dominance variation in generation means. *Heredity*. **12:**371–390(1958).
5. Jinks, J.L. and Jones, M., Estimation of components of heterosis. *Genetics*. **43:** 223-234 (1958).
6. Singh, J. and Bajpai, G.C., Analysis of gene effects for yield and yield attributing traits in inter specific crosses of Pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Indian Journal of Genetics and Plant Breeding*. **65(2):** 133-134 (2005).
7. Kumar, C.V.S., Sreelakshmi, Ch., Shivani, D. and Suresh, M., Gene effects for yield contributing characters in Pigeonpea [*Cajanus cajan* (L.) Millsp.] by generation mean Analysis. Journal Research ANGRU. **37(3-4):**71-76 (2009).
8. Ajay, B.C., Gnanesh, B.N., Ganapathy, K.N., Byre, G.M., Prasad, P.S.,Veerakumar, G.N., Venkatesha, S.C., Abdul, F.R. and Ramya, K.T., Genetic analysis of yield and quantitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Euphytica.* **186:** 705-714 (2012).
9. Oommen, A., Namboodiri, K.M.N. and Unnithan, V.K.G., Genetic analysis of yield and yield components in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Journal of Tropical Agriculture.* **37(1-2):** 12-16(1999).
10. Hooda, J.S., Tomar, Y.S., Vashishtha, R.D. and Phogat, D.S., Generation mean analysis in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Annals of Biology (Ludhiana).* **16(1):** 105-109 (2000).