Generation Mean Analysis for Seed Yield and Wilt Resistance in Castor (*Ricinus communis* L.)

D.K. Patel, Ankit Patel, C.J. Patel, A.L. Jat

ABSTRACT

Background: Castor is an important non-edible oil seeds crop of Gujarat state. Yield potentiality of this crop has been considerably improved through several breeding techniques. Now days, a wilt (*Fusarium oxysporum* f. sp. *ricini*) of castor has become a serious problem. The present study therefore, was under taken to use populations of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations in each of six crosses of castor. The six crosses were selected in such a way that two crosses in each group of resistance × resistance, resistance × susceptible and susceptible × susceptible made available for detail study of gene effects for wilt resistance.

Methods: The experiment was laid out in a compact family block design with three replications during *kharif*, 2017. The experimental materials consisted of four pistillate lines *viz*., VP-1, Geeta, SKP-84 and SKP-106 and six inbred lines *viz*., VI-9, JI-35, 48-1, SH-72, SKI-215 and PCS-124 selected from the germplasm maintained at the Castor and Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar. Each entry was planted in a single row of 10 dibbles maintaining 120 cm row to row and 60 cm plant to plant distances.

Result: The analysis of variance revealed significant difference among different generations for wilt incidence and seed yield indicating considerable variability in the material tested. The estimation of the gene effects revealed that additive as well as non-additive gene effects were observed for wilt incidence and seed yield in all the six cross. In the cross, VP - 1 × JI- 35 the wilt incidence estimation of scaling test and gene effect was observed non-significant indicating non-allelic interaction was absent for this character, while for seed yield, all the crosses have significant scaling test indicating the presence of non-allelic interactions for this trait.

Key words: Castor, Gene action, Scaling test, Seed yield, Wilt resistance.

INTRODUCTION

Castor (*Ricinus communis* L.) is an important non-edible oil seeds crop of Gujarat state. In Gujarat, the common practice of castor growing is an intercrop under rain fed and as sole crop under irrigated condition. Yield potentiality of castor has considerably increased through exploitation of hybrid vigour on commercial scale and systematic Varietal improvement programme. Due to intensive cultivation, with high inputs, high fertilizers and more number of irrigations without proper crop rotation, wilt disease started its appearance in Gujarat and now, wilt (*Fusarium oxysporum* f. sp. *ricini*) of castor has become a serious problem in India in general and Gujarat in particular which causes serious quantitative and qualitative losses (Patel *et al.*, 2020). As the wilt disease is primarily soil-borne, it becomes difficult to manage it through chemical or physical means.

The character expression is related to the type of gene action involved and its interactions with the environment. The type of gene action *viz*; additive, dominance and epistasis with their relative magnitude determine the breeding methodology to be adopted for the genetic improvement of the characters under study. For the characters governed by the additive type of gene effects, adoption of simple selection procedure would be more rewarding. However, for the characters under the influence of inter-allelic interactions (complimentary or duplicate epistasis) exploitation of heterosis or development of composite and synthetics would be more effective. The value

Castor-Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar-385 506, Banaskantha, Gujarat, India.

Corresponding Author: Ankit Patel, Castor-Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar-385 506, Banaskantha, Gujarat, India. Email: ankitp.patel224@sdau.edu.in

of parents therefore can be determined by the study of gene action which would provide a better guidance to the breeder.

Production of hybrids as opposed to inbreds or open pollinated varieties depends largely on the level of dominance of epistasis (dominance × dominance) or both (Cockerham, 1961). Again level of dominance and forms of epistasis influenced by the selection of parents to develop open pollinated varieties. Thus, estimation of additive, dominance and epistasis components of genetic variances are of paramount for planning part improvement programme.

Number of genetic models assuming basic requirements have been proposed by Fisher and Mackenzie (1918) for the estimation of the gene effects. Hayman (1958), Jinks and Jones (1958), Hayman and Mather (1955) have developed models for estimate relative importance of additive and dominance gene effects. Epistatic gene effects

were assumed to be negligible. Partitioning of total heritable variance in to additive and dominant components ignoring the presence of interallelic gene action would not give a correct picture of the gene action involved. If the epistatic gene action is not separated, they tend to inflate dominance variance and lower the additive variance.

The present study, therefore, was under taken to use populations of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations in each of six crosses of castor in order to obtain information about digenic epistasis (additive × additive, additive × dominance, dominance × dominance) in addition to additive and dominance gene effects for seed yield and wilt incidence. The six crosses were selected in such a way that two crosses in each group of resistance × resistance, resistance × susceptible and susceptible × susceptible made available for detail study of gene effects for wilt resistance. Our objective to understand the nature and magnitude of gene action involved in controlling the complex traits like seed yield and wilt incidence, which would be of considerable importance in planning a sound breeding programme.

MATERIALS AND METHODS

The experimental materials comprised four pistillate lines *viz.*, VP-1, Geeta, SKP-84 and SKP-106 and six inbred lines *viz.*, VI-9, JI-35, 48-1, SH-72, SKI-215 and PCS-124 selected from the germplasm maintained at Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar. Each entry was sown in a single row keeping 120 cm row to row and 60 cm plant to plant distance with maintaining 10 plants in a row. Six crosses *viz.,* (i) VP-1 × VI-9, (ii) VP-1 × JI-35, (iii) VP-1 × 48-1, (iv) Geeta × SH-72 (v) SKP-84 × SKI-215 and (vi) SKP-106 × PCS-124 were developed during *kharif*, 2015. Subsequently, these F_1's were selfed to obtain F_2 and backcrossed to obtain B_1 and B_2 generations during *kharif*, 2016. The entire experimental material comprised of parents (P_1 and P_2), F_1, F_2, B_1 ($F_1 \times P_1$) and B_2 ($F_1 \times P_2$) generations of all six crosses, which were studied during *kharif*, 2017. Recommended package of practices were followed for raising the normal healthy crop.

The experiment was laid out in a compact family block design with three replications during *kharif*, 2017. The six crosses formed the family block, whereas, six generations of each cross-represented individual plots within family. A single replication comprised of one row of parents and F_1s, two rows of the backcrosses and four rows of the F_2s. There were ten plants in a row with inter and intra row spacing of 120 cm × 60 cm. The sowing was done on 20th August, 2018 in the wilt sick plot. Recommended agronomic practices in vogue along with necessary pest and disease protection measures were timely adopted for successful raising of the crop.

RESULTS AND DISCUSSION

The present investigation was carried out to find out the nature of gene action for seed yield and wilt resistance

through generation mean analysis (P_1, P_2, F_1, F_2, B_1 and B_2) in six crosses under wilt sick plot. Individual scaling tests (A, B, C and D) of Mather (1949) were employed to detect the presence of epistasis (Table 1).

For the seed yield, out of six crosses, all the crosses having three type of gene effects *viz.*, additive, dominance and epistatic were involved in the inheritance of this character. In crosses VP-1 × VI-9 and VP-1 × JI-35 all gene effects *viz.,* additive, dominance and epistatic were significant (Table 2). Here dominance gene effect was greater in magnitude, next in order being additive × additive and additive × dominance effects. In cross, VP-1 × 48-1 wherein dominance, dominance × dominance gene effect was greater in magnitude, next in order being, additive × dominance and additive gene effects. In cross, Geeta × SH-72 for the expression of seed yield per plant, where dominance and additive × additive gene effects were of higher magnitude followed by additive and dominance × dominance gene effects. In cross, SKP-84 × SKI-215, all estimates of gene effects were found highly significant. The magnitude of dominance × dominance gene effect was highest, next in order being additive × dominance, additive × additive and dominance effects, while in the cross SKP-106 × PCS-124, the magnitude of dominance × dominance gene effect was highest, next in order being additive, additive × additive and dominance effects, considering the importance of non-additive gene effect in the inheritance of this character in all above crosses. The opposite signs of dominance and dominance × dominance effects indicated the presence of duplicate epistasis in all above crosses except in cross VP-1 × 48-1 for the inheritance of this trait. In cross VP-1 × 48-1, complimentary type of gene action was present.

The present findings are akin to the results obtained by (Natarajan *et al.* 1993; Patel 1996; Gondaliya *et al.* 2001; and Solanki *et al.* 2003), who reported the role of both additive and non-additive gene effects in the expression of wilt, while Dhapke *et al.* (1992) and Goyani *et al.* (1993) reported the importance of additive gene effects for the inheritance of this trait. However, Vindhiyavaraman and Ganesan (1995), Solanki and Joshi (2000), Kavani *et al.* (2001), Ramu *et al.* (2002) and Lavanya and Chandramohan (2003) observed the role of non-additive gene effects in the expression of seed yield per plant.

For wilt incidence, out of six crosses, only one cross VP-1 × JI-35 was subject to scaling tests and estimation of gene effects owing to non-significant of generation means (Table 2). In cross VP-1 × VI-9, all the gene effects were found highly significant for the expression of this trait, where dominance effect was greater in magnitude, next in order being additive × additive, additive and additive × dominance effects, while in the cross VP-1 × 48-1, where the magnitude of dominance was the highest followed by being additive × additive, additive and additive × dominance, effects. In the cross Geeta × SH-72 all other gene effects, were significant, where the magnitude of dominance was the highest followed

Generation Mean Analysis for Seed Yield and Wilt Resistance in Castor (*Ricinus communis* L.)

Table 1: Analysis of variance of generation means of six crosses for various characters in castor.

Source	d.f.	VP-1×VI-9	VP-1×JI-35	VP-1×48-1	Geeta×SH-72	SKP-84×SKI-215	SKI-106×PCS-124
				Seed yield per plant (g)			
Replication	2	45.5	66.5	57.55	2.16	40.05	7.38
Generation	5	429.3**	563.5**	2735.68**	855.73**	2890.05**	726.35**
Error	10	19.7	19.76	62.48	41.1	32.58	39.98
				Wilt incidence (%)			
Replication	2	30.84	152.76	2.80	213.6*	13.38	53.29**
Generation	5	244.83**	212.54	2073.17**	1125.06**	69.29*	151.06**
Error	10	42.86	126.99	49.08	40.114	20.58	3.00

Table 2: Estimates of gene effects for various characters of six castor crosses.

Gene effects	Crosses					
	VP-1×VI-9	VP-1×JI-35	VP-1×48-1	Geeta×SH-72	SKP-84×SKI-215	SKI-106×PCS-124
			Seed yield per plant (g)			
m	46.83** ± 2.65	30.33** ± 2.599	78.00 **± 5.297	28.67** ± 2.831	104.83** ± 4.07	100.83** ± 4.606
(d)	-7.83** ± 0.667	-10.33** ± 0.718	-31.00** ± 0.556	3.33** ± 0.819	-26.17** ± 0.915	-4.17** ± 0.861
(h)	27.5** ± 7.838	82.00** ± 7.724	30.33* ± 15.268	189.00** ± 8.025	-22.17* ± 9.476	-97.50** ± 10.071
(i)	5.33* ± 2.565	28.00** ± 2.498	2.00 ± 5.268	74.67** ± 2.71	-12.67** ± 3.966	-20.00** ± 4.524
(j)	-4.17** ± 1.381	-3.00* ± 1.371	-2.67 ± 2.473	2.00 ±1.386	-12.17** ± 1.32	-1.83 ± 1.157
(l)	5.67 ± 5.775	-24.00** ± 5.982	27.33** ± 10.551	-72.67** ± 6.404	73.00** ± 5.911	111.67** ± 5.851
			Wilt incidence (%)			
m	46.868** ± 2.164		-5.392 ± 3.83	-7.142 ± 4.068	-1.595 ± 1.59	-0.01 ± 1.877
(d)	-7.015** ± 1.189		26.595** ± 1.076	-26.902** ± 1.766	4.478** ± 0.917	0.61 ± 0.528
(h)	55.325** ± 6.732		116.908** ± 11.469	128.878** ± 12.141	38.808** ± 4.795	74.10** ± 5.016
(i)	36.533** ± 1.808		31.987** ± 3.675	44.127** ± 3.665	6.073** ± 1.299	14.99** ± 1.801
(j)	-9.878** ± 1.473		5.452* ± 2.121	5.712* ± 2.526	1.465 ± 1.098	0.36 ± 0.849
(l)	-26.683** ± 5.962		-38.823** ± 7.692	-74.137** ± 8.16	-31.13** ± 3.856	-45.17** ± 3.606

Estimates of scaling tests for various characters of six castor crosses

Scaling tests	Crosses					
			Seed yield per plant (g)			
A	-9.667** ± 2.365	-5.0* ± 2.213	-17.33** ± 2.49	1.00 ± 2.863	-42.33** ± 2.319	-47.67** ± 1.824
B	-1.333 ± 2.399	1.0 ± 2.859	-12.00* ± 4.959	-3.00 ± 2.735	-18.00** ± 2.024	-44.00** ± 1.96
C	-16.333** ± 3.151	-32.0** ± 3.736	-31.33** ± 4.289	-76.67** ± 4.586	-47.67** ± 4.525	-71.67** ± 4.967
D	-2.667* ± 1.282	-14.0** ± 1.249	-1.00 ± 2.634	-37.33** ± 1.355	6.33** ± 1.983	10.00** ± 2.262
			Wilt incidence (%)			
A	-14.803** ± 2.609		8.87** ± 2.346	20.717** ± 2.287	13.993** ± 2.263	15.45** ± 1.393
B	4.953 ± 3.263		-2.033 ± 3.6	9.293* ± 4.59	11.063** ± 1.555	14.73** ± 1.615
C	-46.383** ± 4.841		-25.15** ± 2.384	-14.117** ± 3.798	18.983** ± 3.004	15.193** ± 2.435
D	-18.267** ± 0.904		-15.993** ± 1.838	-22.063** ± 1.832	-3.037** ± 0.65	-7.493** ± 0.901

by being additive × additive, additive × dominance and additive effects. The magnitude of dominance was the highest followed by additive × additive, additive and additive x dominance, effects in the cross SKP-84 × SKI-215, while magnitude of dominance was the highest followed by additive × additive, additive and additive × dominance, effects in the cross SKP-106 × PCS-124. In above five crosses, dominant gene effects is predominant, which indicated non-additive gene effect had a major contribute for inheritance of this trait. The opposite signs of dominance and dominance × dominance in all the five crosses indicated that the interactions were balanced and mainly of duplicate

epistatic in nature. These results are akin to those of Desai *et al.* (2001) for wilt of castor (*F. oxysporum* f. sp. *ricini*).

In the present study, the inheritance of resistance to wilt of castor appears to be governed by non-additive along with additive gene effects (Table 2). The present findings are akin to the result obtained by Desai *et al.* (2001) on castor.

The close examination of resistance parameters *i.e.*, wilt incidence (%) involving of resistance × resistance, resistance × susceptible and susceptible × susceptible combination indicated that dominant and epistasis (dominance, additive × additive and dominance × dominance)

Table 3: Gene effect of wilt incidence parameters in six crosses of castor.

Gene effects	Crosses										
	VP-1 × VI-9		VP-1 × JI-35		VP-1 × 48-1		Geeta × SH-72		SKP-84 × SKI-215		SKP-106 × PCS-124	
	(WS)	(WS)	(WS)	(WS)	(WS)	(WR)	(WS)	(WR)	(WR)	(WR)	(WR)	(WR)
m	S		S		NS		NS		NS		NS	
a	S		S		S		S		S		NS	
d	S		S		S		S		S		S	
aa	S		S		S		S		S		S	
ad	S		S		S		S		NS		NS	
dd	S		S		S		S		S		S	

WS = Wilt susceptible paren; WR = Wilt resistant parent; S = Significant; NS = Non-significant.

were involved in controlling wilt disease (Table 3). However, considering the major role of epistasis variance, selection should be attempted between families and lines carrying resistance genes. Whereas wilt incidence (%) was controlled by the non additive gene action Desai *et al.* (2001).

Over all, the results revealed that different types of gene effects controlled the inheritance of same characters in different crosses and for different characters in the same crosses in castor.

CONCLUSION

Since, different gene effects were responsible for the inheritance of the same traits in different crosses and for different traits in the same crosses, specific handling of individual cross in segregating generation would be advantageous for the improvement of these traits in castor. In general, the characters controlled by additive gene effects can best be improved by adopting various types of selection strategies. Those characters controlled by non-additive gene effects can successfully be improved by adopting utilizing hybrid vigour or following cyclic method of breeding *i.e.* recurrent selection.

REFERENCES

Cockerham, C.C. (1961). Implication of genetic variance in a hybrid breeding programme. Crop Science. 1: 47-52.

Desai, A.G., Dange, S.R.S. and Pathak, H.C. (2001). Genetics of resistance to wilt in castor caused by *Fusarium oxysporum* f. sp. *ricini*. Journal of Mycology and Plant Pathology. 31(3): 322-327.

Dhapke, S.K., Khorgade, P.W. and Narkhede, M.N. (1992). Estimates of genetic variability in castor. Agricultural Science Digest. 12(3): 141-143.

Fisher, R.A. and Mackenzie, W.A. (1918). Studies in crop variation II. The manurial response of different potato varieties. Journal of Agricultural Science. (Camb.). 13: 311-320.

Gondaliya, A.B., Dangaria, C.L., Kavani, R.H. and Golakia, P.R. (2001). Genetic architecture for yield and its components in castor. Journal of Oilseeds Research. 18(2): 150-153.

Goyani, M.B., Makne, V.G. and Salunke, M.R. (1993). Inheritance of oil, hull content and seed yield in castor. Journal of Maharashtra Agricultural University. 18(2): 298-299.

Hayman, B.I. (1958). The theory and analysis of diallel crosses. II. Genetics. 43: 63-85.

Hayman, B.I. and Mather, K. (1955). The description of genetic interaction in continuous variation. Biometrics. 11: 69-82.

Jinks, J.L. and Jones, R.M. (1958). Estimation of the components of heterosis. Genetics. 43(2): 223-224.

Kavani, R.H., Golakia, P.R. and Dhaduk, H.L. (2001). Combining ability analysis in Castor (*Ricinus communis* L.). Journal of Oilseeds Research. 18(1): 24-27.

Lavanya, C. and Chandramohan, Y. (2003). Combining ability and heterosis for seed yield and yield components in castor (*Ricinus communis* L.). Journal of oilseeds Research. 20(2): 220-224.

Mather, K. (1949). Biometrical Genetics. Methuen and Co., London.

Natarajan, C., Palaniswamy, G.A. and Muthiah, A.R. (1993). Diallel analysis of yield and its components in castor. Madras Agricultural Journal. 80(5): 281-283.

Patel, A.A. (1996). Genetic analysis in castor (*Ricinus communis* L.). M.Sc. (Agri.) Thesis (Unpublished) Submitted to Gujarat Agricultural University, Sardarkrushinagar.

Patel, A.M., Patel, D.K., Patel, C.J., Jat, A.L., Shah, S.K., Tejani, D.N., Gangwar, G.P. and Desai, A.G. (2020). A high yielding and wilt resistant castor (*Ricinus communis*) hybrid for India. Indian Journal of Agricultural Sciences. 90(5): 930-33.

Ramu, R., Sreedhar, N., Lavanya, C. and Ramesh, T. (2002). Combining ability studies in castor (*Ricinus communis* L.). Journal of Oilseeds Research. 19(2): 229-230.

Solanki, S.S. and Joshi, P. (2000). Combining ability analysis over environments of diverse pistillate and male parents for seed yield and other traits in castor. Indian Journal of Genetics and Plant Breeding. 60(2): 201-212.

Solanki, S.S., Joshi, P., Gupta, D. and Deora, V.S. (2003). Gene effects for yield contributing characters in castor (*Ricinus communis* L.) by generation mean analysis. Journal of Oilseeds Research. 20(2): 217-219.

Vindhiyavarman, P. and Ganesan, K. (1995). The combining ability in castor. Madras Agricultural Journal. 82(9/10): 545-547.