

GENETICS OF RESISTANCE TO WILT IN CASTOR CAUSED BY *FUSARIUM OXYSPORUM* F. SP. *RICINI* NANDA AND PRASAD

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ABSTRACT

Wilt (*Fusarium oxysporum* f. sp. *ricini* Nanda and Prasad) of castor has become a serious problem in Gujarat State, causing at times, heavy losses. The objectives to study the genetics of resistance to wilt in castor, six generations of four crosses were evaluated in the wilt sick plot and through root dip inoculation technique. The mean values of different generations in various crosses revealed that crosses involving both resistant parents gave highly resistant F₁ generation and the level of resistance was maintained even in segregating generations. The inheritance of resistance to wilt of castor appear to be governed by polygenes with dominance and epistasis, therefore, heterosis breeding with choice of superior parents would be advantageous for enhancing the wilt resistance alongwith yield. However, for developing wilt resistant hybrids, both the parents should be wilt resistant. Such heterotic crosses can also be further exploited through breeding following recurrent selection and *inter se* mating in segregating generations for developing wilt resistant high yielding pistillate and inbred male lines of castor.

Key words : Castor, Wilt, Biochemical traits, Generation mean.

INTRODUCTION

The wilt caused by *Fusarium oxysporum* f. sp. *Ricini* Nanda and Prasad, is the most serious disease of castor (*Ricinus communis* L.) recorded in India from Udipur (Rajasthan) in 1975 (Nanda and Prasad, 1974). As the wilt disease is primarily soil-borne, it becomes difficult to manage it through chemical or physical means. Therefore, the only practical solution of this problem lies in the breeding of resistant varieties, for which knowledge of genetics of resistance to wilt pathogen is the basic necessity. The effectiveness of a host-plant resistance in breeding programme largely depends on the development of a reliable screening technique, identification of resistance source(s), selection of breeding procedures to incorporate resistance into

agronomically superior backgrounds and finally the selection of resistant and desirable materials to develop high yielding resistant hybrids/varieties. The ability of a host plant to defend itself against a pathogen is governed by its genetic constitution and the environmental conditions under which the genes operate. Host plant resistance is mostly used to control fungal wilt diseases which usually results in the marked reduction in fungal colonization. Though, castor crop has got great commercial value, the information on genetics of resistance to *Fusarium* wilt invading castor is extremely limited.

MATERIALS AND METHODS

Four resistant (Geeta, SKP-23, JI-258 and 48-1) and two susceptible (VP-1 and JI-35) inbreds based on their previous records were selected for

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the present study. Among them Geeta, VP-1 and SKP-23 were females (pistillate lines) while others were males. Four crosses viz., Geeta x JI-258 (Cross-I), SKP-23 x JI-35 (Cross-II), VP-1 x 48-1 (Cross-III) and VP-1 x JI-35 (Cross-IV) were developed during *kharif*, 2001-2002. Subsequently, these F_1 's were selfed to obtain F_2 and backcrossed to obtain B_1 and B_2 generations during *kharif*, 2002-2003. The entire experimental material comprised 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 four crosses, which were studied during *kharif*, 2003-2004. The details of experimental materials were evaluated in wilt sick plot and through Root dip inoculation techniques (Raof and Rao, 1996) for wilt incidence (%). Six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of four crosses of castor were evaluated in a compact family block design replicated three times with same date of sowing at Main Castor-Mustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *kharif*, 2002-03. The four crosses formed the family block, whereas, six generations of each cross represented individual plots within family. Each block consisted of one row of parents, F_1 s and check, GCH-5, two rows of the backcrosses and four rows of the F_2 Generations. There were ten plants in a row. The recommended inter and intra row spacing of 90 and 60 cm respectively was adopted. Observations on resistant / susceptible plants were recorded from the first appearance of the wilt at an interval of 15 days up to the crop maturity in wilt sick plot. Evaluation of four crosses for reaction to wilt was also simultaneously carried out in pots under green house condition by Root dip inoculation technique given by Raof and Rao (1996). Recommended agronomic practices in vogue alongwith necessary plant protection measures were timely adopted for successful raising of the crop. The data were subjected to different biometrical techniques namely scaling test (Hayman and Mather, 1955) and generation mean analysis by Hayman's six parameter model (Haymen.1958). The heterosis and

inbreeding depression were also estimated by standard statistical formula.

RESULTS AND DISCUSSION

Mean performance : To study the genetics of resistance to wilt caused by *Fusarium oxysporum* f. sp. *ricini* in castor, six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of four crosses were evaluated, in wilt sick plot and through root dip inoculation technique under green house condition. Mean values of per cent wilt incidence were recorded for six generations in four crosses (Table 1). Among the four crosses studied, two crosses viz., SKP-23 x JI-35 and VP-1 x 48-1 showed significant differences among generations for resistance to wilt of castor, which indicated the presence of good deal of genetic variability for this trait in the experimental materials. The remaining two crosses viz., Geeta x JI-258 and VP-1 x JI-35 showed non-significant differences among generations for resistance to wilt of castor; hence these crosses were dropped from further analysis for the estimation of gene effect. It is interesting to note that these two crosses were derived either by crossing highly resistant parents (Geeta x JI-258) or highly susceptible parents (VP-1 x JI-35), the former gave highly resistant plant progenies, while the latter produced highly susceptible progenies. This may be due to lack of genetic variability/diversity among the parents involved in two crosses, which in turn could have resulted from the fixation of genes for resistance/susceptibility in the similar direction. These results are akin to those of Abdel-Raheem *et al.* (1974) and Ylyasov (1974) for wilt of cotton (*F. oxysporum* f. sp. *vasinfectum*) and Desai *et al.* (2001) for wilt of castor (*F. oxysporum* f. sp. *ricini*).

Gene effect : The results summarized in Table 2 revealed that scaling tests in crosses-II and III were found significant, which suggested the involvement of non-allelic interactions for expression of resistance to wilt in castor. In cross-II, all the gene effects were found highly significant for the expression of this trait, where additive x dominance, additive and dominance x dominance gene effects

were of higher magnitude in that order. All the gene effects, viz., additive, dominance and epistatic were significant in cross-III, where the magnitude of dominance x dominance was the highest, next in order being dominance, additive and additive x additive effects. The preponderance of non-additive gene action was observed in both the crosses where dominance and dominance x dominance components were in opposite direction, indicating the presence of duplicate type of epistasis in crosses-II and III. Through root dip inoculation techniques, the results on the estimates of gene effects in cross-II, all the gene effects were found significant for the expression of this trait, where dominance x dominance, additive x additive and additive gene effects were of higher magnitude. All the gene effects viz., additive, dominance and epistatic were highly significant in cross-III, where the magnitude of dominance x dominance was the highest. The predominance of non-additive gene action was observed in which dominance and dominance x dominance components were in opposite direction, indicating the presence of duplicate type of epistasis in cross-II and III.

These results revealed the involvement of both additive and non-additive gene actions for the inheritance of resistance to wilt in crosses-II and III. Hence, the cyclic method of breeding/recurrent selection can profitably be utilized to take advantage of both types of gene actions to evolve highly wilt resistance genotypes of castor from these crosses. Wilt of castor is a serious problem, which leads to a substantial reduction in yield in castor crop. The present findings revealed that the crosses involving highly resistant parents (Geeta x JI-258) or highly susceptible parents (VP-1 x JI-35) resulted in non-significant difference among their generations. These results are akin to those of Salgado *et al.* (1995) for wilt of common bean (*F. oxysporum* f. sp. *phaseoli*) and 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 polygenes. The present findings are

Table 1 : Mean values of wilt incidence (%) in different generations of castor in four crosses of castor.

Crosses	Generations						S.Em.	C.D.(0.05)	C.V.%
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂			
Wilt sick plot									
I	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	0.0	NS	0.03
II	4.05(0.0)	73.92(91.84)	50.92(59.72)	49.68(57.60)	42.06(44.43)	54.39(65.56)	1.86	5.84	7.03
III	71.66(89.35)	4.05(0.0)	47.19(53.33)	46.30(51.79)	71.33(88.36)	35.41(33.30)	2.79	8.76	10.50
IV	72.52(89.79)	67.65(84.47)	73.90(91.81)	76.84(94.16)	73.78(91.37)	75.24(92.84)	2.75	NS	6.49
Check			48.33(56.08)						
Through Root dip transplantation Technique									
I	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	4.05(0.0)	0.0	NS	0.03
II	4.05(0.0)	69.27(86.67)	40.12(41.11)	44.96(49.46)	41.48(44.28)	49.83(57.88)	2.39	7.49	9.91
III	76.65(93.00)	4.05(0.0)	44.96(49.46)	43.35(46.67)	81.28(96.00)	37.51(36.67)	2.67	8.37	9.63
IV	51.24(89.67)	69.30(86.67)	76.65(93.00)	81.28(96.00)	66.52(83.33)	76.65(93.00)	8.12	NS	20.02
Check(GCH-5)			47.83(53.33)						

* Average of three replications

Figure in parenthesis are retransformed values from Arc sin transformation.

further in conformity with those of Desai *et al.* (2001).

Heterosis and inbreeding depression : The estimates of heterosis expressed as percentage over mid parent (relative heterosis), over better parent (heterobeltiosis) and over standard check, GCH-5 (standard heterosis) in F_1 hybrids and inbreeding depression in F_2 generation for various characters in four crosses were estimated and presented in Table 3. The parent showing less disease incidence was taken as a better parent.

In wilt sick plot, The magnitude of relative heterosis for wilt incidence ranged from 0.0 % (cross-II) to 30.60 % (cross-II). None of the crosses showed negative relative heterosis, which is desirable. The estimates of heterobeltiosis for this trait ranged from 0.0 % to 1156.18 % (cross-II). None of the crosses showed negative heterobeltiosis, which is desirable. The estimates of standard heterosis varied from -91.75 % (cross-I) to 63.71 % (cross-IV). Out of the four crosses, only cross-I (-91.75 %) demonstrated significant desirable negative standard heterosis, which indicated its superiority for wilt, as compared to standard check, GCH-5. Through root dip inoculation technique, the magnitude of relative heterosis for wilt incidence ranged from 0.0 % (cross-I) to 27.21 % (cross-IV). None of the crosses showed negative heterosis, which is desirable. The estimates of heterobeltiosis varied from 0.0 % (cross-I) to 1009.25 % (cross-III) and none of the crosses showed negative heterobeltiosis, which is desirable. The magnitude of standard heterosis ranged from -91.44 % (cross-I) to 74.39 % (cross-IV). Cross-I (-91.44 %) and cross-II (-22.91 %) showed highly significant negative heterosis over standard check, GCH-5.

The perusal of the data revealed that the estimates of inbreeding depression in wilt sick plot, ranged from -3.99 % (cross-IV) to 2.42 % (cross-II). Only one cross, SKP-23 x JI-35 showed significant positive inbreeding depression which indicating decrease in wilt incidence of F_2 generations over their respective F_1 generations.

Table 2 : Estimates of scaling tests and gene effects for wilt incidence (%) in four crosses of castor.

Crosses	GENE EFFECTS											
	Scaling tests				Six parameter model							
	A	B	C	D	m	d	h	i	j	I		
Wilt sick plot												
I	Not significant											
II	29.15**	-16.06**	18.92**	2.92**	49.68**	-12.33**	6.10**	-5.83**	22.60**	-7.26**		
III	23.80**	19.57**	15.09**	-14.14**	46.30**	35.92**	37.62**	28.28**	2.12*	-71.65**		
IV	Not significant											
Through Root dip Transplantation Techniques												
I	Not significant											
II	39.80**	-9.71**	26.30**	-1.89*	44.96**	-7.86**	7.23**	3.78*	24.75**	-33.88**		
III	40.95**	26.00**	2.77	-32.09**	43.35**	43.77**	68.79**	64.18**	7.47**	-131.14**		
IV	Not significant											

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

Table 3 : Heterosis, Heterobeltiosis, Standard heterosis and Inbreeding depression for wilt incidence (%) in four crosses of castor.

Crosses	Heterosis (%)		Inbreeding depression (%)	
	Mid parent	Better parent	Standard check(GCH-5)	
Wilt sick Plot				
I	0.00	0.00	-91.75**	0.00
II	30.60**	1156.18**	6.49	2.42**
III	24.67*	1064.38**	-4.90	1.90
IV	5.44	9.24	63.71**	-3.99
Through Root dip transplantation Technique:				
I	0.00	0.00	-91.44**	0.00
II	9.41	889.57**	-22.91**	-12.09**
III	11.42	1009.25**	-7.26	3.59
IV	27.21	49.58	74.39**	-6.04

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

Through root dip inoculation technique, inbreeding depression estimates ranged from – 12.09 % (cross-II) to 3.59 % (cross-III). Out of four crosses, only cross-II (-12.09 %) showed significant negative inbreeding depression indicating increase in resistance of F_2 generations

over their respective F_1 generations and also suggesting the possibility of making selection for resistant recombinants in segregating generations. The results also indicated that to develop wilt resistant castor hybrid, both the parents should be resistant to wilt.

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