

## Gene action for seed yield, its attributes and wilt resistance in castor (*Ricinus comunis* L.)

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Castor (*Ricinus communis* L.) is an important non-edible oil seed crop of arid and semi-arid regions of India. Like other crops, castor also suffers from many diseases and so far 15 different diseases have been recorded in castor in India. As a result, area under the crop has tremendously increased. 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* Nanda and Prasad) of castor has become a serious problem in India in general and Gujarat in particular which causes serious quantitative and qualitative losses. This indicates the necessity to reduce the wilt incidence for increase the production as well as productivity. The pre-requisite for this is the knowledge of gene action because the genetic constitution of genotype is only way for the control of wilt incidence. This being the motivation, an objective was set to understand the nature and magnitude of gene action involved in controlling the complex traits like seed yield, 100 seeds weight, oil content and yield attributes which would be of considerable importance in planning a sound breeding programme. Ten parents were subjected to diallelic crosses excluding reciprocals. The data obtained indicated that dominant positive genes were responsible for the expression of these traits.

Key words : Castor, Wilt resistance, Gene action, Seed yield, Oil content

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### 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* Nanda and Prasad) of castor has become a serious problem in India in general and Gujarat in particular which causes serious quantitative and qualitative losses. 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 host plant resistance, for which knowledge of genetics of resistance to wilt pathogen is the basic necessity. Our

objective to understand the nature and magnitude of gene action involved in controlling the complex traits like seed yield, maturity, 100 seeds weight, oil content, plant height, length of primary spike, number of capsule on primary spike, number of effective branches per plant which would be of considerable importance in planning a sound breeding programme.

### RESEARCH METHODOLOGY

The experimental material comprised of ten inbred lines/varieties of castor viz., 48-1, SKI 321, SKI 314, JI 321, DCS 89, PCS 124, DCS 9, SKI 291, SKI 281 and SKI 215, 45 hybrids using diallel mating design excluding reciprocals and GCH-5 as standard check were evaluated in Randomized Block Design with three replications during 2007-08 and 2008-09 at Main Castor-Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar in wiltsick plot. Each entry was planted in a single row of 10 dibbles keeping 90 cm row to row and 60 cm plant to plant distance. Recommended package of practices was



followed for raising the normal crop. Observations on five randomly selected competitive plants recovered for 8 traits. (Table 1). However, days to flowering and days to maturity were recorded on plot basis. Component analysis of diallel crosses was done following Hayman (1954), Jink (1956) and Hayman (1958)

## RESULTS AND ANALYSIS

In  $F_1$  analysis, estimates of components of genetic variation revealed that additive as well as dominant components were significant for days to 50 per cent flowering, days to 80 per cent maturity, stem length, number of nodes on main stem, effective raceme length, number of branches per plant, 100-seed weight and wilt incidence and in  $F_2$  generation days to 50 per cent flowering, effective raceme length, number of capsules on primary raceme, number of branches per plant and wilt incidence, revealing importance of both additive as well as non-additive genetic variance. (Table 1). In all above characters, magnitude of dominant components ( $H_1, H_2$ ) were higher than additive component (D). This suggested that all above characters were under control of non-additive genetic variances. The characters *viz.*, number of capsules on primary raceme, seed yield per plant and oil content in  $F_1$  generation and days to 80 per cent maturity, seed yield per plant, 100-seed weight and oil content in  $F_2$  generation only dominant components were these characters purely controlled by non-additive gene action. The average degree of dominance ( $H_1/D$ )<sup>1/2</sup> indicated over dominance for all the traits evaluated thus, on the basis of present study, it is evident that majority of the characters in  $F_1$  generation and  $F_2$  generation are under controlled of non-additive gene action. Over dominance for seed yield per plant have been reported by Giriraj *et al.* (1974), Singh and Yadav (1981), Narkhede *et al.* (1987), Thatikunta *et al.* (2000). The distribution of genes with positive and negative effects in the parents were nearly symmetrical for the traits like days to 80 per cent maturity, stem length, number of nodes on main stem, number of branches per plant, seed yield per plant, 100-seed weight and wilt incidence in  $F_1$  generation and  $F_2$  generation. The significance of F along with  $K_D / K_R$  suggesting that dominant and recessive genes were not in equal proportion in parents for days to 50 per cent flowering, effective raceme length, number of capsules on primary raceme and oil content on the basis of pooled

$F_1$  data. On the other hand, the characters like stem length, number of nodes on main stem, number of branches per plant, seed yield per plant, 100-seed weight and wilt incidence dominant and recessive genes were in equal proportion. The estimates of ratio  $h^2/H_2$  suggested the involvement of one group of genes showing dominance in all the traits except for number of nodes on stem, stem length and seed yield per plant. The estimates of effective factors obtained are likely under estimates of the actual number of genes affecting the traits due to linkage of genes, epistasis and partial dominance at some loci (Jinks, 1956).

The correlation between parental performance and  $W_r + V_r$  values indicate that the characters number of capsules on primary raceme, seed yield per plant and wilt incidence controlled by recessive genes, while remaining characters *viz.*, days to 50 per cent flowering, days to 80 per cent maturity, number of nodes up on main raceme, stem length, number of branches per plant, effective raceme length, 100-seed weight and oil content were controlled by dominant genes.

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