

## Genetic architecture for yield and its composition in castor (*Ricinus communis* L.)

P.B. PATEL\* AND H.C. PATHAK<sup>1</sup>

Department of Plant Breeding and Genetics, C.P. College of Agriculture, S.D. Agricultural University, SARDAR KRUSHINAGAR (GUJARAT) INDIA

### ABSTRACT

The genetic architecture of seed yield and related traits was investigated through generation mean analysis for four crosses in six generations in castor. Involvement of both additive and non-additive gene actions with preponderance of non-additive gene actions for seed yield, its major yield components suggested that hybrid breeding can profitably be utilized for improving seed yield in castor by exploiting dominance / non-additive gene action. However, to exploit both additive and non-additive types of gene actions observed for seed yield, its components, cyclic method of breeding involving conventional breeding approaches for selection of superior recombinants and their *inter se* crossing can alternatively be utilized for the development of high yielding inbred and pistillate lines in castor.

**Key words :** Castor, Genetic architecture, Gene action, Generation mean

### INTRODUCTION

Castor (*Ricinus communis* L.) is an important non-edible oil seed crop of arid and semi-arid regions of India, which belongs to the genus *Ricinus* of Euphorbiaceae family. Yield is the ultimate product of action and interaction of number of yield components, which are governed by a large number of genes having small effects and are greatly influenced by environment. Effect of small individual gene cannot be selected, collective effect of the genes can be estimated any of the attributes. The estimation of gene effects involved in the inheritance of yield contributing or quantitative characters are helpful in planning breeding programs. Through gene effects for seed yield and other traits have been estimated in castor, information on epistatic gene effects is negligible. Thus the present investigation, genetic parameters namely additive, dominance and epistatic gene effects were estimated through generation mean study for nine quantitative traits in four crosses of castor.

### MATERIALS AND METHODS

The material comprised of four hybrids *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) involving six diverse parents. 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 four crosses, which was conducted in compact family block design with three replications at the Main Castor and Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar,

Gujarat during *Kharif*, 2004-2005. The four 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  $F_1$ s, two rows of the backcrosses and four rows of the  $F_2$ s. There were ten plants in a row at inter and intra row spacing of 90 cm x 60 cm, respectively. From each replication data were recorded for nine quantitative characters (Table 1). 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 (Hayman, 1958).

### RESULTS AND DISCUSSION

Significant scaling test for different traits was observed in almost all crosses indicating the presence of digenic or higher order interactions (Table 1). The estimates of gene effects for days to 50 per cent flowering in cross-I indicated that additive, dominance, additive x additive and dominance x dominance were involved in the expression of this trait. The results further revealed that barring additive x additive and dominance x dominance, all other gene effects were found significant in cross-II. All the gene effects were highly significant in cross-III and IV. Thus, predominance of non-additive gene action was observed in which dominance and dominance x dominance components were in opposite direction in cross-I, II and III, indicating the presence of duplicate type of epistasis. The present findings are in close agreement with the results obtained by Bhatt and Reddy

\* Author for correspondence & Present Address : Department of Plant Breeding, Soil and Water Management Research Unit (Navsari Agricultural University) DANTI-UMBHARAT (GUJARAT) INDIA

<sup>1</sup> Directorate of Research, Navsari Agricultural University, NAVSARI (GUJARAT) INDIA