# Genetic analysis in okra [Abelmoschus esculentus (L.) Moench] through Hayman's method

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**Abstract**: In present investigation, 28 F<sub>1</sub> obtained from 8 x 8 diallel mating design excluding reciprocals for yield and its components in okra [Abelmoschus esculentus (L.) Moench]. The genetic study revealed that estimation of variance due to additive (D) and dominance (H) both were involved in the inheritance of most of the traits studied with preponderance of non-additive gene action for all characters. These finding were also confirmed by the values of average degree of dominance estimates (H/D)<sup>0.5</sup>, which was found in the range of over dominance for all the traits except days to flowering, days to first picking and internodal length. The estimates of narrow sense heritability were low for fruit yield per plant and most of the other traits except for days to flowering, days to first picking, fruit girth and crude fiber content which had moderate heritability.

Key Words: Heterosis, Okra, Hayman's method

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## Introduction

Okra [Abelmoschus esculentus (L.) Moench] is one of the most important vegetable crops grown extensively throughout the country during summer and rainy seasons. A good knowledge of the nature and mode of inheritance of quantitative characters of economic importance is helpful to formulate a more pragmatic breeding programme. Diallel analysis is useful device for obtaining rapid overall picture of gene action involved in the inheritance of different quantitative characters. Different workers have studied the nature of gene action for a number of biometric traits in okra. However, as the gene action differs from genetic material to material.

#### MATERIALS AND METHODS

A set of 28 hybrids were developed using 8 parents (Gujarat Okra 2, Parbhani Kranti, Arka Bahar, Arka Abhay, Pusa Sawani, Panjab 7, AOL-03-1, and JOL-04-08) of okra through diallel mating design excluding reciprocals during Summer-2009. The trials consisting of 28 hybrids and their 8

parents were raised in randomized block design with three replications at Department of Genetics and Plant Breeding, C.P. College of Agriculture, S.D. Agricultural University, Sardarkrushinagar during *Kharif*, 2009. Each entry was sown in 3.0 m long single row plot at 60 x 30 cm spacing. Observations on five randomly selected competitive plants were recorded for days to flowering, days to first picking, fruit length, fruit girth, number of nodes on main stem, internodal length, plant height, fruit yield per plant, crude protein content, crude fiber content and vitamin C content. The data were subjected to statistical analysis as per the method suggested by Panse and Sukhatme (1967).

## RESULTS AND DISCUSSION

The estimates of genetic parameters and their ratios for yield and its components are presented in Table 1. The estimates of D, which measure the variance due to additive gene effects, were significant for all the traits except number of nodes on main stem, plant height and crude fiber content. The H1, which measure the variance due to non-additive

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