

Genetic architecture for growth and flowering traits in gladiolus (*Gladiolus hybridus*. Hort) using diallel analysis

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ABSTRACT

The combining and heterobeltosis analysis was carried out in gladiolus based on 7 x 7 half diallel for growth trait during 2005 to 2007 utilizing seven varieties viz. American Beauty, Sylvia, Melody, Summer Sunshine, Vedanapoli, Magic and Priscilla. Over dominance was exhibited by majority of the growth traits is due to the action and interaction of both additive and dominant gene action. The heritability for flowering traits was very low due to high influence of the environmental component. Unequal distribution of genes with positive and negative effects was observed in the parents with less frequency of dominant alleles and the few number of gene groups are controlling these characters.

Key words : Diallel, Gene effects, Growth, Flowering, Gladiolus.

Gladiolus (*Gladiolus hybridus*. Hort) is an important bulbous cut flower crop and it is famous for its keeping quality and inexhaustive range of colours of spike. The contribution and information available on genetic architecture is very meager. Hence, there is need to work on genetic analysis to unveil the action of genetic components. It also provides necessary information on nature and magnitude of gene effects for growth and flowering traits. Half diallel analysis is useful for preliminary evaluation of genetic stocks with large number for use in hybridization programme and to facilitate a sound breeding programme. So the combining and heterobeltosis analysis was carried out in gladiolus based on 7 x 7 half diallel for growth trait.

MATERIALS AND METHODS

The investigation was carried out utilising seven gladiolus varieties viz. American Beauty, Sylvia, Melody, Summer Sunshine, Vedanapoli, Magic and Priscilla which represents diverse morphological characters. Crossing was done by following half diallel method. The seeds were sown in seed beds and material was carried out for four cycles. The seven selected varieties along with 21 F₁ hybrids were planted during January 2007 at Kittur Rani Channamma College of Horticulture, Arabhavi, (University of Agricultural Sciences, Dharwad) in randomized block design with two replications. The parents along with their F₁ hybrids were planted in raised

beds with a spacing of 30 x 20 cm. The data were collected for five randomly selected plants from each parents and F₁'s.

The genetic analysis was done as per the Hayman's approach model II. Since Hayman's approach is based on some assumptions, it is necessary for the confirmity of the data to those assumptions before interpreting the results. Hayman's approach has been criticized by many investigators because of the assumptions underlying the diallel analysis (Kempthorne, 1956; Arunachalam, 1976 and Baker 1978). Besides homozygous parents and diploid segregation, the independent distribution of genes, no epistasis and absence of material effects. Among the assumptions uncorrelated gene distribution, absence of epistasis and multiple allelism are impossible to satisfy in practice. The non-significance of t² in respect of different traits indicates the confirmity of the data to the diallel assumptions.

RESULTS AND DISCUSSION

The genetic components of variation like D (variation due to additive effect), F (mean of the covariance of additive and dominant effect over arrays), H₁ and H₂ (dominance genetic effects), h² (sum of dominance effect over all loci), E (Environmental component of variation) with their respective standard errors and their ratios and differences viz., (H₁/D)^{1/2} (mean degree of dominance), H₂/4H₁ (the proportion of genes with positive and negative effects on the parents), h²/H₂ (number of group of genes controlling that character and exhibiting dominance), H₁ - H₂ (showing whether positive and negative alleles were