

## TO STUDY THE GENETIC VARIABILITY IN *C. CORONARIUM* AND ITS DIFFERENT MUTANTS

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### ABSTRACT

Genetic variability, heritability and expected genetic advance studied for quantitative characters for species *C. coronarium* and its different mutants. The results of the experiment revealed that number of disc florets followed by number of ray florets, ray floret weight, disc floret weight, flower head height and ray floret length recorded high phenotypic and genotypic coefficient of variation whereas, narrow phenotypic and genotypic coefficient of variation were recorded for plant spread (E-W) followed by leaf area, plant spread (N-S), leaf length, flower head diameter and leaf width that indicating less environmental interference on the expression of the traits. High heritability with magnitude of high genetic advance were recorded for number of disc florets and number of ray florets indicating preponderance of additive gene action and greater scope for improvement of these traits through selection however, ray floret width and disc floret weight showed higher heritability and low genetic advance and this could be due to non-additive gene action (dominant/epistemic) and/or less genetic variability for these traits.

**KEYWORDS:** Genetic Advance, Heritability, Variability, *C. Coronarium* and Mutants

### INTRODUCTION

Among the flowers, chrysanthemum (*chrysos* means 'golden' and *anthos* means 'flower') is a popular flower crop of commercial importance. *Chrysanthemum* belongs to family Asteraceae or Composite also called the aster, daisy, or sunflower family. The name Asteraceae is derived from the type genus Aster, which is Greek term, meaning "star" (<http://www.merriam-webster.com>). It has approximately 1,620 genera and more than 23,600 species (Stevens, 2001). In India, 900 species in 167 genera (Hajra *et al.* 1995) are reported. The family is further subdivided into 12 subfamilies, dominated by the large subfamily asteroidean that contains more than 70 per cent of the species of the family. It is popular commercial cut flower but also grown as pot plant (pot mum). In international florists' trade, chrysanthemum ranks third as a cut flower and fifth as pot plant (Anonymous, 2008). The genus *Chrysanthemum* is characterized by annual or perennial herb or woody nature. *Chrysanthemum coronarium* is the commonest of all annual chrysanthemums. It is a leafy, vigorously growing robust and hardy herbaceous annual, with much branched and erect stem which imparts bushy appearance. It can be cultivated as an ornamental plant in the garden for border planting or in background of flower bed and blooms can be used as cut flower.

The industry must meet the demand of consumers by providing new value added flowers which are cost effective and unique in flower characteristics e.g., flower shape, flower color and have long shelf life. Mutation assisted breeding

(MAB) together with biotechnology can contribute greatly for genetic improvement of ornamental plants and in uplifting the socio-economic benefits in the developing countries (Jain, 2006). The primary objective of any breeding programme is to create variability so selection of desirable characters can be achieved by measurement of genetic variability present in the base population. So, for a sound breeding programme, critical assessment of the nature and extent of genetic variability, heritability and genetic advance of the important quantitative characters in a crop species is essential (Nazir and Dwivedi, 2006). Hence, the present investigation was conducted to study the genetic variability in *C. coronarium* and its different mutants.

## MATERIALS AND METHODS

The present investigation was conducted at the Model Floriculture Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, District Udham Singh Nagar (Uttarakhand) during September, 2012 to June, 2013. Pantnagar is situated at the foothills of Himalayas at 29° North Latitude and 79.3° East Longitude. The altitude of the place is 243.84 m above the mean sea level. In the present investigation, the mutant lines of species *C. coronarium* were grown under open field conditions by raising nursery on seed beds and then transplanting about 30 days old seedlings at 50 cm X 30 cm spacing. The experiment was laid out in a randomized block design with three replications. Soil of experimental site was brought to a fine tilth by two deep ploughing and leveled properly. All weeds and left over crop residue were removed. The field was divided into three blocks, each block having 36 plots for allotment of various treatments. Each individual plot consisting of 30 plants in 6 row of 1.5 m long. The seeds of mutants of species *C. coronarium* were sown on raised nursery beds during second week of September and seedlings (about 30 days old seedling at four leaf stages) were transplanted in experimental plot on October, 2012. Depending upon the requirements, hoeing was done and crop varieties. Staking was done in plants which were prone to lodging. Plants were supported with the help of the wooden stakes. Wooden stakes are fixed at side of the plant to give them proper support and also protect the plant from the wind. The various observations were recorded on two middle row plants of species *Chrysanthemum coronarium* and its selected mutants.

## RESULTS AND DISCUSSIONS

Phenotypic, genotypic and environment variance, heritability and genetic advance of *C. coronarium* and its different mutants were presented in Table 1.

**Table 1: Genetic Parameters of Morphological Characters of *C. Coronarium* and its Mutants**

Quantitative Characters	gcv	pcv	ecv	ga	h <sup>2</sup>
Plant ht	25.73	25.80	1.91	32.32	99.44
Plant spread (E-W)	13.21	12.28	1.36	15.65	98.93
Plant spread (N-S)	14.91	14.99	1.52	16.02	98.96
Leaf length	15.83	16.16	3.26	1.71	95.92
Leaf width	20.28	20.62	3.76	1.43	96.67
Leaf area	14.77	14.87	1.65	3.14	98.75
No of flowers/plant	26.10	26.20	2.21	15.43	99.28
Flower head diamt	18.31	18.47	2.42	2.18	98.28
Flower disc diamt	66.31	66.51	5.20	2.22	99.38
No. of ray florets	52.45	52.48	1.56	233.84	99.91
No. of disc florets	102.47	102.49	1.88	280.88	99.96
Flower head wt. (g)	24.79	24.93	2.62	1.66	98.88
Ray floret wt. (mg)	50.89	50.96	2.64	12.78	99.73

Disc floret wt. (mg)	33.39	33.63	4.03	0.84	98.56
Ray floret length	27.65	27.96	4.15	1.09	97.78
Ray floret width	23.67	24.03	4.13	0.47	97.04
Flower head ht.	32.01	32.15	3.02	2.02	99.11

It is evident from the data represented in Table 1 that genotypic coefficient of variation varied from 13.21 plant spread (E-W) to 102.47 number of disc florets whereas, phenotypic coefficient of variation varied from 12.28 plant spread (E-W) to 102.49 number of disc florets. However the environment coefficient of variation ranged from 1.36 plant spread (E-W) to 5.20 flower disc diameter. Heritability estimates varied from 95.92 per cent (leaf length) to 99.96 per cent (number of disc florets) among the traits under study. Genetic advance varied from 0.47 per cent for ray floret width to 280.88 per cent for number of disc florets.

The ranged of variability was highest in the characters number of disc florets followed by flower disc diameter, number of ray florets, ray floret weight, disc floret weight, flower head height and ray floret length. Whereas, the lowest PCV and GCV were registered for the plant spread followed by leaf area, plant spread (N-S), leaf length, flower head diameter and leaf width. **Anuradha and Gowda (1990)** also obtained narrow differences between PCV and GCV values in gladiolus for characters like floret length, number of leaves, plant height and spike length thereby suggesting major contribution of genetic variability towards the total variance. **De et al. (1992)** also reported very narrow differences between PCV and GCV for characters like days to flowering, diameter of foremost floret, and plant height in gladiolus. Moderate PCV and GCV were recorded for ray floret width, flower head weight, plant height and number of flowers per plant. Findings recorded for coefficient of variation of *C. coronarium* and its different mutants were exhibited that PCV (phenotypic coefficient of variation) was higher than GCV (genotypic coefficient of variation) indicated less environmental interference on the expression of the traits.

The heritability express the proportion of the total variance that is attributed to the average effect of genes and that is what determines the degree of resemblance between parents and offspring (**Falconer, 1960**). Estimates of heritability and genetic advance are important to find out the heritable portion of variability and genetic gain likely to be achieved in the next generation. Heritability values were highest for number of disc florets followed by number of ray florets, ray floret weight, plant height, and flower disc diameter, number of flowers per plant and flower head height. The genetic advance was found to be highest for number of disc florets followed by number of ray florets and plant height. High heritability and genetic advance were observed for number of disc florets and number of ray florets indicating preponderance of additive gene action (**Panase, 1957**), thus selection would be effective and exhibited greater scope for improvement for that trait. Similar results were reported by **Verma (2004)** in case of gladiolus as he found high heritability and genetic advance for number of shoots per plant. These are in line with the findings of **Punetha et al. (2012)** in chrysanthemum. However, ray floret width and disc floret weight showed higher heritability and low genetic advance and this could be due to the non-additive genes (dominance and epistasis) as suggested by **Panase (1957)**.

## COCLUSIONS

So it can be concluded that higher value of phenotypic coefficient of variation compared to environment coefficient of variation but lower to genotypic coefficient of variation indicating that environmental factors influencing their expression to some degree or other however, estimates of heritability and genetic advance for number of disc florets and number of ray florets are important to find out the heritable portion of variability and genetic gain likely to be achieved

in the next generation.

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