"GENETIC VARIABILITY IN CAULIFLOWER (*Brassica oleracea* L. var. *botrytis*) GENOTYPES FOR YIELD AND QUALITY TRAITS UNDER CHHATTISGARH PLAINS"

M.Sc. (Hort.) Thesis

by

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DEPARTMENT OF VEGETABLE SCIENCE

COLLEGE OF AGRICULTURE, RAIPUR

FACULTY OF HORTICULTURE

INDIRA GANDHI KRISHI VISHWAVIDYALAYA

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"GENETIC VARIABILITY IN CAULIFLOWER (*Brassica oleracea* L. var. *botrytis*) GENOTYPES FOR YIELD AND QUALITY TRAITS UNDER CHHATTISGARH PLAINS"

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)

by

Yogita Sonune

IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF

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In

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CERTIFICATE –I

This is to certify that the thesis entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"** submitted in partial fulfillment of the requirements for the degree of **Master of Science** in **Horticulture (Vegetable Science)** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Yogita Sonune** under my/our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by her.

Chairman

Dr. Jitendra Trivedi

Date: 22-12-2020

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

Chairman (Dr. Jitendra Trivedi) _____

Member (Dr. Dhananjay Sharma) _____

Member (Dr. Sunil Nair) _____

Member (Dr. R. R. Saxena) _____

CERTIFICATE – II

This is to certify that the thesis entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"** submitted by **Yogita Sonune** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfillment of the requirements for the degree of **Master of Science in Horticulture (Vegetable Science)** in the **Department of Vegetable Science** has been approved by the external evaluator and Student's Advisory Committee after oral examination, under the chairmanship of head of the Department.

Signature of Head of the Department

(Name: Dr. Neeraj Shukla)

Date: 23-03-2021

Major Advisor

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Approved/Not approved

Director of Instructions

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LIST OF SYMBOLS

Symbols	Description
%	Per cent
@	At the rate
/	Per
˚C	Degree Celsius
Cm	Centimeter
Df	Degree of freedom
et al.	And others/ Co- workers
G	Gram
Ha	Hectare
Hrs	Hours
$h^2_{(bs)}$	Heritability in broad sense
i.e.	That is
Kg	Kilogram
m^2	Square meter
No.	Number
Q	Quintal
var.	Variety
via.	Through
viz.	For example

LIST OF ABBREVIATIONS

Abbreviations	Description
AICRP	All India Coordinated Research Project
CD	Critical difference
CV	Coefficient of variation
Df	Degrees of freedom
Fig.	Figure
FYM	Farm yard manure
GA	Genetic Advance
GCV	Genotypic coefficient of variation
IGKV	Indira Gandhi Krishi Vishwavidyalaya
NPK	Nitrogen, Phosphorus and Potassium
PCV	Phenotypic coefficient of variation
RBD	Randomized block design
RF	Rainfall
RH	Relative humidity
RSS	Replication sum of squares
SE	Standard error

THESIS ABSTRACT

a)	Title of the Thesis	:	**"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"**
b)	Full Name of the Student	:	Yogita Sonune
c)	Major Subject	:	Vegetable Science
d)	Name and Address of the Major Advisor	:	Dr. Jitendra Trivedi, Department of Vegetable Science, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh)
e)	Degree to be Awarded	:	M. Sc. (Hort.)Vegetable Science

Signature of the Student

Signature of Major Advisor

Date: 05/04/2021

Signature of Head of the Department

ABSTRACT

The present investigation was performed on twelve diverse cauliflower genotypes in order to evaluate magnitude of genetic variability, correlation and path analysis among yield and with other contributing components. The experiment was laid out of four replications in a randomized block design, at Horticultural Research cum Instructional Farm, under the project AICRP on vegetable crops, at Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), during the *rabi* 2019-20.

Studies regarding the mean performance of genotypes revealed that genotype 2019/CAUEGENO-8 (252.27 q/ha) recorded highest curd yield per hectare in considerably shorter crop duration, and hence was found most promising than others.

The result of investigation revealed slightly higher magnitude of phenotypic coefficient of variation than corresponding genotypic coefficient of variation, which might be because of interaction of genotypes with environmental factor to certain extent. High estimates of heritability coupled with high genetic advance was recorded for gross plant weight, marketable curd weight and net curd weight.

Evaluation of correlation coefficients between yield and its attributing characters revealed that traits *viz.* marketable curd weight (g), curd width (cm), net curd weight (g) and gross plant weight (g) was significantly positively correlated to curd yield per plot. Also the analysis of path coefficient portrayed positive direct effect of marketable curd weight (g), stalk length (cm), leaf length (cm), curd width (cm) and curd length (cm) on curd yield per plot. Hence it can be concluded that direct selection for these traits would be effective for selecting superior genotypes.

शोध सारांश

- शोध शीर्षक : **"छत्तीसगढ़ के मैदानी इलाकों में उपज और गुणवत्ता लक्षणों के लिए फूलगोभी (ब्रासिका ओलेरासिए अल. किस्म बोट्रीटिस) जीन प्रारूपों में आनुवंशिक परिवर्तनशीलता"**
- विद्यार्थी का पूरा नाम : योगिता सोनुने
- प्रमुख विषय : सब्ज़ी विज्ञान
- प्रमुख सलाहकार का नाम एवं पता : डॉ. जीतेन्द्र त्रिवेदी,
  सब्ज़ी विज्ञान विभाग, कृषि महाविद्यालय
  इंदिरा गाँधी कृषि विश्वविद्यालय, रायपुर (छ. ग.)
- प्रदान की जाने वाली उपाधि : एम. एस. सी. (उद्यानिकी), सब्ज़ी विज्ञान

विद्यार्थी का हस्ताक्षर

प्रमुख सलहाकार का हस्ताक्षर

दिनांक : 05/04/2021

विभागाध्यक्ष का हस्ताक्षर

सारांश

उपज और अन्य घटक लक्षणों के बीच आनुवंशिक परिवर्तनशीलता, सहसंबंध और पथ विश्लेषण की मात्रा का मूल्यांकन करने के लिए बारह विविध फूलगोभी के जीन प्रारूपों पर वर्तमान शोध किया गया था । रबी सत्र 2019-20 के दौरान, उद्यानिकी अनुसंधान सह शैक्षणिक प्रक्षेत्र, वनस्पति विज्ञान विभाग, इंदिरा गांधी कृषि विश्वविद्यालय, रायपुर (छत्तीसगढ़)

में सब्जी फसलों पर अखिल भारतीय समन्वित अनुसंधान परियोजना के तहत, शोध को चार प्रतिकृति के साथ यादृच्छिक खंड अधिकल्पना में लगाया गया था।

जीन प्रारूपों के औसत प्रदर्शन के बारे में अध्ययनों से यह पता चला है कि जीन प्रारूप 2019/सीएयूइजीइएनओ-8 (252.27 क्विंटल प्रति हेक्टेयर) ने काफी कम फसल अवधि में उच्चतम कर्ड उपज दर्ज की, और इसलिए यह दूसरों की तुलना में सर्वश्रेठ पाया गया।

प्ररूपी बिचरण गुणांक का परिणाम सभी लक्षणों के लिए समवर्ती अनुवांशिक रूप गुणांक से अधिक पाया गया, जो सामान्यतः पर्यावरण और जीन प्रारूपों की पारस्परिक क्रिया के कारण अथवा पर्यावरण के प्रभाव के कारण हो सकता है। उच्च आनुवांशिक अग्रिम के साथ युग्मित आनुवांशिकता के उच्च अनुमानों को सकल पौधे का वजन, विपणन योग्य कर्ड वजन और शुद्ध कर्ड वजन जैसे लक्षणों के लिए दर्ज किया गया था।

उपज और इसके अन्य घटक लक्षणों के बीच सहसंबंध गुणांक के मूल्यांकन से पता चला है कि लक्षण जैसे विपणन योग्य कर्ड वजन (ग्रा.), कर्ड चौड़ाई (सेमी), शुद्ध कर्ड वजन (ग्रा.) और सकल पौधे का वजन (ग्रा.), प्रति प्लॉट कर्ड उपज पर सकारात्मक रूप से प्रभाव डालते हैं। इसके अलावा पथ गुणांक के विश्लेषण से यह प्रत्यक्ष होता है कि प्रति प्लॉट कर्ड उपज पर विपणन योग्य कर्ड वजन (ग्रा.), डंठल की लंबाई (से.मी.), पत्ती की लंबाई (से.मी.), कर्ड की चौड़ाई (से.मी.) और कर्ड की लंबाई (से.मी.) सकारात्मक एवं प्रत्यक्ष प्रभाव डालते हैं। इसलिए यह निष्कर्ष निकाला जा सकता है कि इन लक्षणों के लिए प्रत्यक्ष चयन बेहतर जीन प्रारूपों का चयन करने के लिए प्रभावी होगा।

CHAPTER - I
INTRODUCTION

Cauliflower (*Brassica oleracea* L. var. *botrytis*) is amongst the most popular and well known cole vegetable, which is cultivated across the world under varied range of environmental conditions ranging from temperate to tropics, mostly during cold cropping seasons and is generally available throughout the year. The word "Cauliflower" consists of two Latin words *i.e.* '*caulis*', which means stem or stalk and *'floris'*, which means flower. It belongs to family Brassicaceae, which has characteristic petals standing opposite to each other, forming a square cross. The flower has total 6 stamens, 4 of them are long and 2 of them are short. The varieties belonging to *Brassica oleracea* have equal set of chromosome number *i.e.* n=9. It is considered to be a monogenomic species having 'C' genome with chromosome number 2n=2x=18 (Thamburaj and Singh, 2001).

All the cultivated forms of cole vegetable are believed to be evolved from *Brassica oleracea* var. *sylvestris* L., which is commonly renowned as wild cabbage, a leafy kale like plant, about 2000 years ago in Eastern Mediterranean region, through the process of mutation, human selection followed by adaptation (Boriss *et al*., 2006).

The edible part of cauliflower botanically known as prefloral fleshy apical meristem or immature inflorescence or flowering primordial (Nath *et al*., 1994). The head of a cauliflower, known as "curd", is a group of tightly packed flower buds that have not fully developed.

In India, commonly grown cauliflower is classified into two major groups *i.e.* Indian or tropical type and European or temperate commonly renowned as snowball type. In India it is cultivated in an area of 452.6 thousand hectares, giving the total production of 8668.2 thousand tonnes with the productivity of 19.2 metric tonne per hectare (Anon, 2018). To the total production of cauliflower in India, Chhattisgarh contributes for about 5.59% of share. The total cultivated area of cauliflower in

Chhattisgarh occupies about 23868 hectares of land with total production of 482648 metric tonnes (Anon, 2018).

Chhattisgarh is owed to a diversified climate in three agro-climatic regions. This makes it suitable for growing a wide range of tropical, sub-tropical and temperate horticultural crops. Cauliflower is cultivated in all the three regions *viz.* Chhattisgarh plains, Northern hills zone and Bastar plateau. Considering these facts there is immense possibility for improvement of cauliflower crop.

Progress in cauliflower breeding is at lower pace considering both India and Chhattisgarh, thereby yield is not improving to a considerate extent. Genetic variability in a population is of immense importance for biodiversity, hence exploration of the existing genetic variability is pivotal for cauliflower crop improvement, because nature and extent of genetic variability in the germplasm indicates the scope of improvement in the character through selection. Very fewer studies have been conducted to study genetic variability of cauliflower plant in Chhattisgarh, therefore it becomes a matter of great deal to explore more about it and hence creating a vital source for cauliflower improvement through selecting best recombinants with desirable characters.

Also yield is considered of being very complex and polygenic character, which depends upon many other attributes of plant. Hence, improvement of yield contributing characters should also be taken into account while selecting for yield improvement. Hence the studies regarding the correlation of different traits with yield of crop will be an effective tool for selecting desirable traits. Further, greater the amount of variability present in the crop, facilitates selection programmes for yield contributing characters. Path coefficient analysis is highly effective to determine both direct and indirect effect of each and every character towards yield.

Considering all the possibilities for improvement of cauliflower crop, the present investigation entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"** is proposed with following objectives:

1. To identify superior cauliflower genotype for Chhattisgarh plain region.
2. To work out correlation for curd yield and its component characters.
3. To study path coefficient analysis for curd yield and yield parameters in cauliflower.

CHAPTER - II

REVIEW OF LITERATURE

The literature related to various aspects of present study entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"** is provided under following headings-

2.1 Genetic variability and mean performance

2.2 Heritability and Genetic advance

2.3 Correlation coefficient analysis

2.4 Path coefficient analysis

2.1 Genetic variability and mean performance

All the crop improvement programmes are based on variability existing within the crop population. Exploitation of genetic potential for yield is very useful for developing varieties with enhanced productivity of crop (Ameta *et al.*, 2016). Vavilov (1951) was pioneer in realizing that there is greater scope for selecting desired qualities in any crop with broader range of variability. In case of cauliflower both yield and yield contributing characters exhibits enormous genetic variation, therefore studying extent of variability among the traits gives an idea about amount of variation present in the crop for utilization in improvement programmes.

Jamwal *et al.* (1992) studied sixteen cauliflower genotypes. He reported substantial variability for gross weight per plant, curd size index, curd yield per plant and leaf size.

Kumar and Korla (2001) investigated thirteen cauliflower genotypes, the investigation portrayed maximum estimate of genetic variability for gross curd weight. High estimates of both phenotypic coefficient of variation and genotypic coefficient of variation was recorded for traits like curd weight, gross curd weight, stalk length and leaf size.

Kumar (2002) evaluated 22 divergent genotypes of cauliflower. Significant difference was observed for all the traits under study as per the result of analysis of variance. The assessment of PCV and GCV were discovered highest for net curd weight, while they were moderate for the characters like number of leaves per plant and net curd weight.

Ahmed *et al.* (2003) studied ten cauliflower cultivars. Among all the cultivars, one named 'Shiroma-65' recorded maximum whole plant weight i.e. 1916.67g, biggest leaf width i.e. 22.17cm, curd weight (661.67g) and curd yield (18.38 tonnes/ha). Another variety named 'Rakhushi Late' gave highest plant height (68cm), number of leaves at harvest (25.93).

Pathania (2003) evaluated twenty divergent cauliflower genotypes for different quality and horticultural traits. Remarkable difference was recorded for all the characters of interest through analysis of variance. The estimates of both PCV and GCV were discovered high for the traits like net curd weight and gross curd weight, whereas values were recorded moderate in case of curd compactness and black rot severity.

Jindal and Thakur (2004) assessed 36 cauliflower genotypes for different types of quality and horticultural traits. Estimates of PCV were discovered higher than GCV for all characters under evaluation. The study shows high genotypic difference for all the traits apart from curd diameter, curd depth and number of leaves per plant.

Kumar *et al.* (2011) studied genetic variability in early maturing Indian cauliflower. Significant difference were observed among genotypes for quality and yield traits. The general estimations of PCV was discovered higher as compared to that of GCV. Highest estimation of GCV was acquired for Vitamin-C content (54.58%) followed by duration of curd availability (49.04%). The genotypes *viz.* DC-98-4, DC-124 and DC-98-10 were observed better over all the remaining varieties for both yield and quality characters.

Singh *et al.* (2013) investigated 24 cauliflower genotypes. Remarkable difference was recorded for all the traits under study. Highest estimate of PCV was obtained for leaf length (21.04) and leaf weight (17.19), though days to maturity showed

minimum variability (7.01), trailed by number of leaves (9.05) and number of inner leaves (9.22).

Yadav *et al.* (2013) studied fifteen cauliflower hybrids for quality, growth and yield traits. Among all the other varieties, Poornima recorded highest number of leaves per plant, plant height, diameter of curd, plant spread, weight of trimmed curd, weight of untrimmed curd, , Vitamin-C content, moisture-dry matter ratio and curd yield. Subsequently the hybrid Poornima was suggested for commercial cultivation in agro-climate of Allahabad conditions.

Elavarasan *et al.* (2014) analyzed the physical characteristics of four cultivated genotypes viz. Basant, Namdhari Seed 60N, Pusa Meghna and Namdhari Seed 133. Study revealed remarkable variations in yield of varieties that ranged from 21 kg/16m^2 to 26.4 kg/16m^2 in hills and 0.78 kg/16m^2 to 1.43 kg/16m^2 in plains. Genotype NS 133 was reported superior over other genotypes for hilly region in terms of early yield and other yield attributes.

Santhosha *et al.* (2014) studied 51 cauliflower genotypes for different yield and quality traits. The investigation portrayed high coefficient of variation for traits like net curd weight, gross curd weight and curd size index. The genotypes which performed better than rest of the genotypes for these parameter were IIHR-263, IIHR-272, IIHR-390 and IIHR-266, showing these particular lines can be used in various breeding programmes as a source of desirable traits for improvement of curd yield and quality or can be directly utilized for cultivation.

Chittora and Singh (2015) studied genetic variability in forty genotypes of early cauliflower for various quantitative and qualitative characters. Genotypes exhibited significance differences for all the traits apart from days to curd maturity, curd depth and days to curd initiation. Moderate estimates of PCV and GCV were recorded in the case of curd yield per hectare, net curd weight, harvest index and marketable curd weight. Among all the genotypes PCF-106, PCF-95, INb-10-1 and INb-9-5 had many desirable characters and were found promising.

Ansari (2017) evaluated ten diverse genotypes of mid-season cauliflower for genetic variability analysis. The analysis revealed that values of PCV were slightly

greater as compared to that of GCV. Estimates of PCV and GCV were found greater in the case of traits like gross plant weight, marketable curd weight, marketable curd yield and net curd weight. The genotype named 2016/CAUMHYB-10 was found superior over others for the traits like gross weight per plant, curd size index and marketable yield per plant.

Kumar *et al.* (2017) studied genetic variability for fifty seven genotypes of mid-season cauliflower. Significant difference was revealed in majority of factors except for plant spread, curd size index and curd length, through analysis of variance. Appreciable level of phenotypic and genotypic coefficient of variation was reported by various traits like stalk length, gross plant weight, marketable curd yield, net curd weight, curd size index, curd yield per hectare and harvest index, while lowest PCV as well as GCV was recorded for days to maturity and number of leaves per plant. The genotypes with more than one desirable traits were INBPCF120, 2013/CAUMVAR-6, PCF-93, PG-5, PCF-7, INBPCF117.

Manaware *et al.* (2017) evaluated thirty genotypes to study genetic diversity. The mean performances of genotypes unveiled broad variability for all the characters under examination. The estimates of PCV were discovered to be higher than that of GCV. The estimate of PCV was found highest for the traits such as core length, curd circumference, curd length, curd width, marketable curd yield, net curd weight, curd yield per plot, curd yield per hectare, total plant weight and curd weight. Similarly, genotypic coefficient of variance was found higher in characters like curd length, curd circumference, core length, curd width, net curd weight, marketable curd yield, curd yield per hectare, total plant weight, curd yield per plot and curd weight.

Chatterjee *et al.* (2018) evaluated twenty cauliflower genotypes, to study nature and magnitude of genetic variability in ten important horticultural traits. For all the traits under study, recorded phenotypic coefficient of variation was observed greater than corresponding genotypic coefficient of variation. Moderate estimate of genotypic coefficient of variation was observed in the case of curd size index (26.51%), leaf number per plant (19.12%), plant height (20.85%), gross weight per plant (19.56%), leaf size index (19.44%), curd depth (15.76%) and marketable yield per plant.

Kindo and Singh (2018) evaluated eleven varieties of cauliflower for their agronomic characters and commercial values. Among all the varieties evaluated, the variety Madhuri recorded highest curd yield (456.45 kg/ha), Vitamin-C (53.57 mg/100g each), plant spread (64.56cm, plant height (25.76cm), number of leaves per plant (21.33), weight of trimmed curd (864g), weight of untrimmed curd (2.84kg), and diameter of curd (18cm).

Sharma *et al.* (2018) evaluated twenty five cauliflower genotypes along with a check called Madhuri. Analysis of variance portrayed significant difference among all the genotypes. Higher estimate of both GCV as well as PCV was obtained for trait curd solidity and moderate estimate for traits like stalk length, ascorbic acid content, curd size index, marketable yield per plant, dry matter content, gross weight per plant and harvest index, which indicates difference in genetic material and growing conditions.

Kumar *et al.* (2019) studied eight genotypes of cauliflower for genetic variability. Evaluation was conducted for fifteen quantitative traits. The investigation revealed that estimates of PCV was significantly higher as compared to GCV, which represents effect of environmental factor for traits expression. High estimates of both GCV as well as PCV was recorded for traits like curd yield, marketable curd weight, net curd weight, curd size index, gross curd weight and harvest index. Therefore, selection for these traits may be helpful for substantial improvement in cauliflower.

2.2 Heritability and genetic advance

Heritability is the ratio of phenotypic and genotypic variation. Genetic variability is largely influenced by heritable variation, so if heritable variation is high, higher is the possibility to fix any character during selection programmes. Any characters having high values of heritability, it becomes easy for the plant breeder to formulate criteria based on phenotypic performance of the plants. While the characters reflecting low heritability, selection becomes very difficult just because of environment provides masking effect on genotypes.

Genetic advance is the expected genetic improvement or gain in the progenies under selection pressure through selecting superior individuals.

Jamwal *et al.* (1992) recorded high heritability in curd size index, leaf size and gross weight per plant. He observed maximum values of genetic advance and heritability for curd yield per plant trailed by leaf size, gross plant weight, curd size index and leaf size.

Kanwar and Korla (2002) studied biparent progenies of cross of late cauliflowers. The result unveiled higher estimates of heritability for traits like net curd weight, stalk length, days to marketable maturity, leaves per plant and harvest index. Moderate values of genetic gain was observed for net curd weight, stalk length as well as number of leaves per plant. Least magnitude of both genetic gain as well as heritability was observed in the case leaf length.

Dubey *et al.* (2003) evaluated sixty five genotypes of cauliflower. The result stated high broad sense heritability for total plant weight, net curd weight and harvest index, whereas moderate estimate of heritability was observed for days to 50% curd maturity, leaf width and curd depth. High genetic advance as percent of mean was recorded for total plant weight, harvest index and net curd weight. Lowest estimate for genetic advance was observed for characters like plant height at 50% curd maturity, days to 50% curd maturity, curd depth and leaf width.

Jindal and Thakur (2004) evaluated genetic advance and heritability for twelve quantitative traits of cauliflower. They recorded highest genetic advance along with high heritability for whole plant weight and harvest index, whilst some traits acquired low genetic advance along with high heritability, these characters were days to curd maturity and plant spread.

Halwai *et al.* (2006) recorded high estimates of genetic advance as percentage of mean along with high heritability for net curd weight, gross curd weight, plant frame and values were low for traits like days to maturity and number of leaves per plant.

Sharma *et al.* (2006) studied thirteen cauliflower genotypes. They concluded higher estimates for both genetic advance and heritability for traits like net curd weight, stalk length and marketable curd yield per plant, indicating that selection of these characters would be effective for improvement of crop. Whereas moderate

estimate was noted for gross plant weight, while leaves per plant and harvest index recorded moderate estimates genetic advance with higher heritability.

Dhatt and Garg (2008) evaluated twenty one genotypes of cauliflower of mid maturing group. The result concluded high heritability and genetic advance for stalk length, gross curd weight and marketable curd weight for consecutive two seasons of experiment.

Kanwar *et al.* (2010) recorded moderate genetic advance with higher heritability values for traits such as net curd weight, days to marketable maturity, curd compactness and number of leaves per plant, indicating presence of additive gene effect.

Kumar *et al.* (2011) evaluated character association for early maturing cauliflower. The result concluded high heritability estimates for traits *viz*. net curd weight, stem length and days to 50% curd formation. The values were recorded moderate to high for traits like duration of curd availability, marketable curd weight, sulphur and potassium content. Higher genetic advance along with high heritability was recorded for net curd weight, Vitamin-C content and curd compactness.

Nimkar and Korla (2011) recorded maximum heritability and genetic advance for traits such as net curd weight and gross curd weigh, whereas low estimates of genetic gain with higher heritability were recorded in the case of days to harvesting and stalk length. All the remaining characters recorded lower to moderate genetic advance, along with moderate heritability showing effect of environmental influence.

Mehra (2013) observed estimates of heritability was maximum for plant diameter, plant height, leaf width and leaf length, while lower most estimates were recorded in case of days to 50% curd initiation, curd depth and curd diameter.

Chittora and Singh (2015) investigated forty genotypes of early cauliflower for 18 quantitative and 5 qualitative characters. The result of investigation showed high estimates for heritability in case of gross plant weight, while moderate estimate of heritability was recorded for curd yield per hectare, marketable curd weight, harvest index, net curd weight, plant diameter, stalk length, curd diameter and leaf length.

Net curd weight recorded highest genetic gain as percent of mean, other characters acquiring high genetic gain were curd yield per hectare, marketable curd weight, gross plant weight and harvest index.

Kumar *et al.* (2017) stated highest estimate of heritability for stalk length, it was followed by net curd weight, curd length, curd size index, with lowest heritability for days to maturity. High estimates of genetic advance was observed in the case of traits such as gross plant weight, net curd weight, marketable curd weight, curd yield per hectare. High heritability with greater genetic gain was observed for gross plant weight, marketable curd weight and net curd weight, which indicates that these characters are governed through additive gene effect with minimum environmental effect.

Manaware *et al.* (2017) investigated thirty cauliflower genotypes. The result of the experiment revealed high values of heritability (broad sense) for curd length, days to harvest, days taken to curd initiation, curd circumference, days taken to 50% curd formation, number of leaves at 45 DAT, curd yield per hectare, marketable curd yield, curd yield per plot, core length, curd weight, total plant weight, number of leaves at 30 DAT, net curd weight and curd width. Genetic advance varied between 13.84% for stalk length at 45 DAT to 103.65% for curd length. The values for genetic advance was found highest for characters like curd length, curd circumference, core length, curd width and total plant weight.

Chatterjee *et al.* (2018) evaluated twenty cauliflower genotypes. The result concluded higher estimate heritability along with higher genetic gain for curd size index, whereas high value of heritability along with moderate genetic gain was observed for marketable yield per plant, gross weight per plant, leaf number per plant, curd depth and leaf size index, showing selection will be efficient for these characters. Traits having moderate values of heritability coupled with lower genetic gain was observed in the case days to marketable curd maturity and curd solidity.

Sharma *et al.* (2018) recorded high estimates of heritability in case of days to curd initiation, ascorbic acid, harvest index, curd size index, days to marketable curd maturity, curd depth, stalk length, percent marketable curd, curd diameter, marketable yield per plant, plant height, gross weight per plant, curd solidity and

TSS. Similarly higher estimates of genetic gain was noted in case of ascorbic acid content. While characters like stalk length, curd size index, marketable yield per plant, harvest index, gross weight per plant, curd depth, curd diameter, dry matter content, days to curd initiation and TSS recorded moderate estimates for both genetic advance and heritability.

Kumar *et al.* (2019) estimated heritability along with genetic advance for fifteen characters in eight cauliflower. According to the results, high estimates of genetic gain with heritability was recorded for curd diameter, days taken to 50% curd maturity, days taken to 50% flowering, days taken to first flowering, days taken to 50% curd initiation, curd size index, net curd weight, curd yield, gross curd weight and marketable curd weight. This indicated that selecting these particular characters would likely to be effective for crop improvement.

2.3 Correlation coefficient studies

Correlation coefficient is a measure of the degree association between the two traits worked out at the same time (Hayes *et al*., 1955). Yield of any particular crop plant is considered to be very complex in nature because it is polygenic and also is affected by fluctuating environment, hence selection based on only yield would not be very effective. The extent of observed relationship between two characters is indicated by phenotypic correlation, which includes both hereditary and environmental influence. While the real association between two characters is indicated by genotypic correlation coefficient which may be useful for selection (Johnson *et al*., 1955).

Thamburaj *et al.* (1982) recorded significant and positive correlation between plant weight and foliage weight (0.898), plant weight and curd yield (0.576) and between number of leaves and leaf area (0.569).

Dhiman *et al.* (1983) recorded positive association of marketable yield per plant with curd size index, gross weight per plant and numbers of leaves per plant, while its correlation was found negative with plant height at only genotypic level.

Garg and Lai (2004) evaluated thirty six genotypes of cauliflower. They recorded significant positive correlation of net curd weight with traits like curd size index, equatorial diameter of curd, plant spread, curd compactness index and polar diameter of curd. Also positive correlation was recorded between equatorial diameter of curd and polar diameter of curd, whereas positive correlation was found between curd compactness index and plant spread.

Kumar *et al.* (2005) studied twenty five cauliflower genotypes. They observed positive correlation between net curd weight with plant frame, leaf size index and gross curd weight. Also positive correlation was found between curd depth and gross curd weight, while negative correlation with harvest index.

Kumar *et al.* (2011) recorded that yield was positively and significantly associated to the characters like marketable curd weight, harvest index and net curd weight. While, it was found to have negative correlation with days to 50% curd formation and duration of curd availability. The study also revealed that all the quality attributes showed positive correlation among each other.

Sheemar *et al.* (2012) studied correlation for economic traits of thirty genotypes of cauliflower. The result revealed net curd weight was significantly as well as positively correlated to total plant weight (0.7335) and leaf width (0.5371). Also total plant weight was found to have significant correlation with leaf width, stem length, leaf length, curd compactness index and number of leaves per plant. The result also portrayed significant correlation of curd depth, curd diameter, net curd weight towards mineral matter content and days to 50% curd maturity

Singh and Dogra (2013) studied twenty three cauliflower genotypes for seven quantitative traits. Results revealed positive and significant correlation between net curd weight with leaf area and gross curd weight. Also plant frame and leaf area were found to have positive correlation with days to curd maturity.

Singh *et al.* (2014) investigated correlation and multiple regression on cauliflower cultivar PUSHI for different characters. They observed that yield has highly significant and positive correlation with curd depth, weight of curd, curd diameter, plant girth, plant height and weight of plant.

Santhosha *et al.* (2015) also reported high significant as well as positive correlation of marketable curd weight with leaf length, plant weight, leaf breadth, leaf weight, curd diameter, curd size, leaf number, net curd weight, yield per hectare and net plot yield at both genotypic as well as phenotypic levels.

Ansari *et al.* (2017) recorded positive as well as significant correlation between yield per plot and marketable curd yield, curd yield, leaf length, harvest index, leaf width, gross plant weight and marketable curd weight, both at genotypic as well as phenotypic level. While positive and significant correlation was observed between leaves attached to curd and curd yield per plot at genotypic level only.

Kumar *et al.* (2017) evaluated fifty seven genotypes of cauliflower for assessing correlation coefficient. The genotypic correlation coefficient was found greater than phenotypic correlation coefficient for all the corresponding traits. The estimates of correlation coefficient unveiled that curd yield per hectare was highly positive and significantly correlated to net curd weight, marketable curd weight, number of leaves per plant, gross plant weight and curd diameter,.

Manaware *et al.* (2017) studied correlation pattern in thirty genotypes of cauliflower. The evaluation revealed stalk length at 45 DAT shows significant but negative correlation with days to 50% curd formation, number of leaves per plant at 45 DAT and curd initiation. Also number of leaves per plant at 45 DAT was found to have significant and positive correlation to curd circumference, curd width, days to curd initiation, curd length, total plant weight, curd weight, days to 50% curd formation, days to harvest and core length. Also net curd weight was positively and significantly associated with curd weight.

Sharma *et al.* (2017) studied association for yield and other attributing characters in cauliflower. Estimation of phenotypic and genotypic correlation coefficients concluded that a significant and positive correlation exists between marketable yield per plant and gross weight per plant, curd size index, curd compactness, curd solidity, stalk length, curd diameter, harvest index and number of leaves per plant.

Vanlalneihi *et al.* (2017) recorded positive and significant association for all the characters like curd polar diameter, plant height, curd equitorial diameter, net curd weight and marketable curd weight with curd yield. The outcomes also portrayed that curd polar and equitorial diameter has positively and significantly associated with net cut weight and marketable curd weight, at both genotypic as well as phenotypic level. They also concluded that marketable curd weight has maximum direct and positive contribution towards curd yield.

2.4 Path coefficient analysis

Path coefficient analysis allows the partitioning of correlation coefficient into direct and indirect effect of the traits contributing towards the dependent variable (Wright, 1921). Dewey and Lu (1959) were pioneer for suggesting the adoption of path coefficient analysis in any breeding programme.

Garg and Lai (2004) reported positive direct effect on marketable curd weight was due to curd size index, equitorial diameter of curd and curd compactness index.

Kumar *et al.* (2005) stated highest positive direct effect on marketable curd weight was due to gross curd weight, which is followed by harvest index and stalk length, while highest indirect effect was contributed by leaf size index via gross curd weight followed by plant frame and curd depth (0.362).

Dhatt and Garg (2008) observed that days to curd maturity showed negative direct and indirect effect on net curd weight with considerable magnitude.

Kumar *et al.* (2011) analyzed path coefficient for eleven traits of cauliflower. Recorded result revealed that highest direct effect over yield was contributed through net curd weight. Remaining characters, which had indirect influence on yield were curd compactness and net curd weight. Maximum negative direct effect was recorded in case of gross plant weight followed by harvest index and dry matter in case of early maturing group, and dry matter, harvest index, days to 50% curd formation in case of mid maturing group.

Sheemar *et al.* (2012) recorded maximum positive direct effect of total plant weight on net curd weight, followed by harvest index and curd depth.

Jha *et al.* (2014) showed highest positive direct effect was contributed *via* leaf count followed by curd weight, plant height along with curd depth, while direct negative effect was shown by plant spread, leaf area and curd diameter.

Ansari *et al.* (2017) concluded that gross plant weight showed highest positive direct effect followed by days to first harvest, marketable curd yield, harvest index, net curd weight, curd yield per plot, stalk length, duration of crop, leaf width, leaves attached to the curd, number of leaves per plant and curd index on curd yield (q/ha), therefore selection based on these characters would be effective in breeding programmes.

Kumar *et al.* (2017) assessed path coefficient analysis for mid-season cauliflower. The result revealed that net curd weight had high positive direct effect towards the total yield, while harvest index had negative direct effect on curd yield per hectare.

Sharma *et al.* (2017) reported high positive direct effect on marketable yield per plant was contributed by curd size index, gross weight per plant, days to marketable curd maturity from transplanting date, curd solidity, stalk length and percent marketable curd. According to the result, these traits should be given primary importance as selection criterion to enhance marketable yield per plant.

Chatterjee *et al.* (2018) found that number of leaves per plant (0.995) had highest positive direct effect on marketable curd yield per plant, followed by curd size index (0.411), days to marketable curd maturity (0.376), plant height (0.371), leaf size index (0.363), curd depth (0.164) and curd solidity (0.140), however maximum negative direct effect was recorded for gross weight per (-0.133) followed by stalk length (-0.908).

CHAPTER - III

MATERIALS AND METHODS

This particular chapter compiles complete information regarding the materials utilized and also all methods involved to carry out the present investigation, which is entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains".** The detailed information of experimental materials utilized, various observations recorded, the methods and the techniques adopted throughout this particular course of investigation is provided in this chapter under subsequent headings:

3.1 Location of experimental site

The investigation work was carried at Horticultural Research cum Instructional Farm, Department of Vegetable Science, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), during the *Rabi* 2019-20.

3.2 Geographical situation

Raipur is located in the middle-eastern areas of Chhattisgarh, from 22˚33' N to 21˚14' N latitude and 82˚6' E to 81˚38' E longitude and at an altitude of about 289.56 meters above mean sea level. The region falls under Agro-climatic zone-7, which is Eastern plateau and hills region. Chhattisgarh state has three agro-climatic zones, from which Raipur falls under Chhattisgarh Plain zone.

3.3 Climate and weather

Raipur belongs to 7th Indian Agro-climatic zone i.e. Eastern plateau and hills region, which has characteristic sub-humid weather in general with summer being hot and winters being cold. Chhattisgarh receives its rainfall from South-west monsoon winds. It receives an average rainfall of about 1200-1400 mm per annum, 85% of which is received from months of June to September. Sometimes light showers may occur in winters and occasionally in summers. Tropical wet and dry

climate prevails in the month of March to June in Raipur and winters lasts from November to January. Among all, May is being the hottest month of the year and December being the coolest. It records maximum annual temperature of 48˚C and minimum temperature falls up to 6˚C during winters. From month June to October, Raipur experiences high relative humidity along with higher wind velocity in the months of May to August, with the highest of velocity in June-July. The soil confined within experimental area was found to be of clay-loamy texture, locally called as “Kanhar”.

3.4 Weather conditions during crop growing period

The weekly average meteorological data was recorded for temperature, precipitation, relative humidity and hours of sunlight in the Meteorological Observatory unit, Department of Agrometeorology, IGKV Raipur, during the entire period of investigation from the day of transplanting to harvesting and are represented in Appendix-I and are illustrated graphically in figure 3.1.

3.5 Experimental materials

The experimental material utilized for present study consists of twelve genotypes of cauliflower (*Brassica oleracea* L. var. *botrytis*). These genotypes were obtained from project AICRP on Vegetable Crops to conduct the study programme. The treatment details are summarized in Table 3.1.

3.6 Experimental design

The experiment was laid out in Randomized block design (RBD) having four replications. The investigation was conducted during *rabi* 2019-20. The details regarding layout of experiment is presented in Table 3.2.

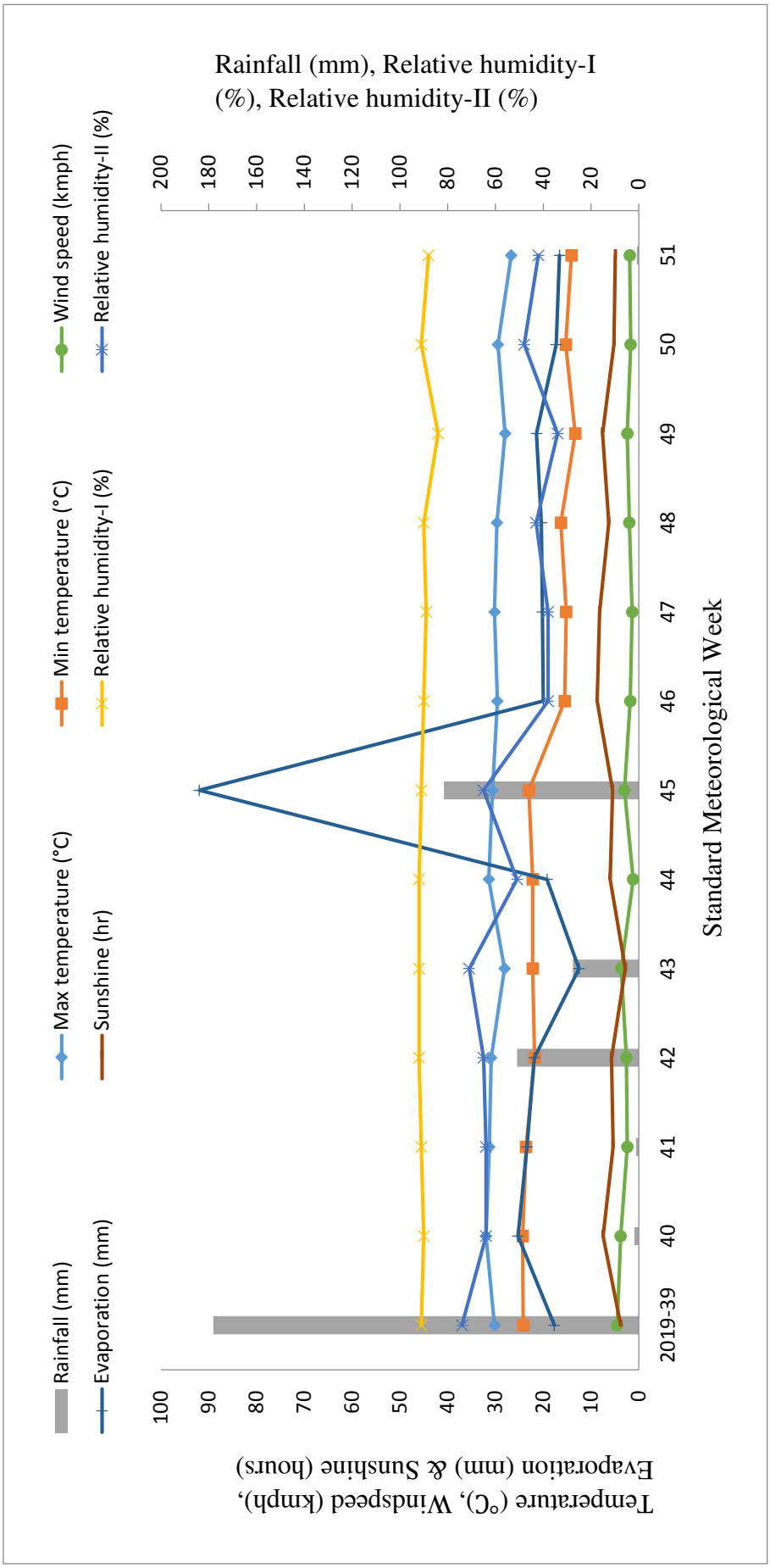

Fig. 3.1 Weekly meteorological data during crop growth period of cauliflower in *rabi* 2019

Table 3.1- Detail of genotypes

S. No.	GENOTYPES	SOURCE
01	2019/CAUEGENO-1	AICRP on Vegetable Crops, Raipur
02	2019/CAUEGENO-2	AICRP on Vegetable Crops, Raipur
03	2019/CAUEGENO-3	AICRP on Vegetable Crops, Raipur
04	2019/CAUEGENO-4	AICRP on Vegetable Crops, Raipur
05	2019/CAUEGENO-5	AICRP on Vegetable Crops, Raipur
06	2019/CAUEGENO-7	AICRP on Vegetable Crops, Raipur
07	2019/CAUEGENO-8	AICRP on Vegetable Crops, Raipur
08	2019/CAUEGENO-9	AICRP on Vegetable Crops, Raipur
09	2019/CAUEGENO-10	AICRP on Vegetable Crops, Raipur
10	2019/CAUEGENO-6	AICRP on Vegetable Crops, Raipur
11	2019/CAUEGENO-11	AICRP on Vegetable Crops, Raipur
12	2019/CAUEGENO-12	AICRP on Vegetable Crops, Raipur

Table 3.2- Details of experiment

1.	Experimental design	Randomized Block Design
2.	Crop	Cauliflower (*Brassica oleracea* L. var. *botrytis*)
3.	Number of genotypes	12
4.	Number of replications	4
5.	Number of plots	48
6.	Plot size	3m × 2m
7.	Spacing	60cm × 50cm
8.	Check variety	2019/CAUEGENO-6 2019/CAUEGENO-11 2019/CAUEGENO-12
9.	Sowing date	23rd August, 2019
10.	Transplanting date	24th September, 2019

3.7 Cultural operations

All the cultural practices adopted for experiment was in accordance to the recommendations in the package of practices of vegetable crops. A total of twelve genotypes of cauliflower were included for conducting the experiment in the present study.

3.7.1 Raising of seedlings in nursery bed

Suitable site was selected for preparation of nursery beds and ploughed to a good tilth. Unwanted materials such as stones and weeds were removed for better growth of seedlings. Nursery beds of size 18 × 1 × 0.15 m were prepared keeping distance of 30 cm between the beds. Well-rotten farm yard manure (FYM) was incorporated into the nursery beds @25 tonne/ha. The seeds were sown 2-3cm deep in the lines, which are 10cm apart of each other, at the rate of 500g of seeds/hectare. The seeds of two genotypes were separated by each other with the distance of 10cm among them. The genotype were sown in the date 23/08/2019. After the seeds were sown, the beds were covered with sieved and well rotten farm yard manure. The beds were watered with the help of watering can at regular interval.

3.7.2 Field preparation

The field selected for experiment was prepared by one deep ploughing with the help of tractor drawn cultivator, which was followed by two cross harrowing for pulverization of soil. Well rotten farm yard manure was incorporated in soil @25 t/ha before harrowing. At last, the field was levelled with the help of leveler. A proper planning of field was prepared in accordance with the experimental design and small plots were laid out based on the number of treatments and replications.

3.7.3 Transplanting

The healthy, robust and uniform growing seedlings, which were about thirty days old, were transplanted in the experimental field. The seedlings were planted in straight lines maintaining 60cm distance between the rows and 50cm between the plants. The genotypes were transplanted on the date 24/09/2019. Plots of 3m × 2m size were prepared for each genotype, keeping 50cm distance between each plot.

3.7.4 Fertilizer application

The recommended dose of nutrients *viz.* 120 kg N, 100 kg P_2O_5 and 80 kg K_2O per hectare was provided in the form of Urea, Single super phosphate and Muriet of potash, respectively. Full dose of phosphorus and potash along with half dose of nitrogen was applied as basal dose at the time of planting. Remaining amount of nitrogen was provided as top dressing in two equal splits. All the fertilizers were applied through manual mean to the plots.

3.7.5 Gap filling

Mortality of some seedlings were observed in certain experimental plots, hence gap filling was done at 8 to 10 days after transplanting, to maintain optimum plant population and uniformity among the plots.

3.7.6 Irrigation

The nursery beds were lightly irrigated one day before transplanting to facilitate convenient uprooting of seedlings with minimum damage. Further, a light irrigation was provided immediately after transplanting. Subsequently, plots were irrigated three times as per the need of crop, during the entire experimental period.

3.7.7 Intercultural operations

Initially weeds were removed completely during the time of field preparation. Further at later growth stages, weeds were managed with the help of two hand weeding at 15 and 45 days of transplanting to ensure weed free plots.

3.7.8 Plant protection measures

In order to protect the crop from major insect-pests and diseases, suitable plant protection measures were adopted throughout entire experimental period. Infestation of cauliflower aphid was observed in case of certain experimental plots, which was controlled by spraying Imidachlorpid @0.25% as per the need of crop.

3.7.9 Harvesting

The cauliflower plants were uprooted with intact curd for the very first time at the stage of 50% maturity at optimum phase of plant. Later the plants were uprooted

at an interval of 8 to 10 days, as the curds attain harvestable maturity. For studying various yield and quality attributes, curd of five randomly selected plants were picked separately. The net plot yield was recorded carefully at every picking.

3.8 Observations recorded

Five plants were randomly selected and tagged within each experimental plots at the beginning of the experiment. The observations were recorded from these randomly selected plants at every plot in all replications, for all the traits separately.

3.8.1 Growth and yield characters

3.8.1.1 Plant height (cm)

Plant height was measured by calculating the vertical distance between the stem base at the ground level and the upper boundary of main shoot. Height of five selected plants was averaged to calculate plant height of particular genotype.

3.8.1.2 Number of leaves per plant

The total number of leaves of five randomly selected plants was counted at the marketable stage and average was calculated for each genotype.

3.8.1.3 Leaf length (cm)

The average length of middle leaf of five randomly selected plants has been recorded at the marketable stage and average were calculated for each genotype.

3.8.1.4 Leaf width (cm)

The average width of middle leaf of five randomly selected plants has been recorded at marketable stage and average were calculated for each genotype.

3.8.1.5 Plant spread (cm)

Plant spread is measure of canopy of plant in uniform direction. Plant spread of five randomly selected plants has been measured at marketable stage and average were calculated for each genotype.

3.8.1.6 Stalk length (cm)

The length of the curd stalk was recorded from ground level to the tip of stalk for at least five randomly selected plants at marketable stage and the average of stalk length was worked out for each genotype.

3.8.1.7 Days to curd initiation

Days taken for curd initiation was recorded for five randomly selected plants from the date of transplanting to the date of curd initiation on an average basis for each genotype.

3.8.1.8 Days to marketable curd maturity

It was calculated by the number of days taken from the date of transplanting to the date when 50% plants from the plot attained marketable curd size and the average of the days required to curd maturity were worked out for each genotype.

3.8.1.9 Days taken to first harvest

Days taken to first harvest was recorded for five randomly selected plants from the date of transplanting and expressed as mean for each genotype.

3.8.1.10 Curd width (cm)

Curd width or curd diameter is equatorial length of the widest part of the curd. It was calculated on an average basis for five randomly selected plants at the time of harvest for each genotype.

3.8.1.11 Curd length (cm)

Curd length was recorded as average of five randomly selected curds at marketable stage. It was measured as the length from the base to the tip of curd.

3.8.1.12 Gross plant weight (g)

Gross plant weight was recorded as entire weight of plant after removing the soil adhered to the roots, with leaves and stalk intact, at the time of harvesting.

3.8.1.13 Marketable curd weight (g)

The marketable curd weight was recorded as average weight of curd after removing the root, with leaves pruned at curd level, of five randomly selected curds at marketable stage and the average were calculated.

3.8.1.14 Net curd weight (g)

The net curd weight was recorded as average weight of five randomly selected curds excluding all the leaves and stalk, at marketable stage and average were worked out for each genotype.

3.8.1.15 Curd yield per plot (kg)

The weight of curd from each plot was recorded and expressed in the form of mean. The curd yield per experimental plot was averaged over all replications.

3.8.1.16 Duration of crop (days)

Duration of crop was calculated as average for five randomly selected plants from the date of sowing to the date of final harvesting.

3.8.1.17 Curd yield (q/ha)

The curd yield in quintals per hectare was calculated for each plot with the help of data recorded for curd yield per plot and expressed as mean curd yield averaged over all replications.

3.8.2 Quality characters

3.8.2.1 Curd compactness

Curd compactness was determined visually at marketable stage. Curds were classified as loose, compact, medium compact and very compact.

3.8.2.2 Curd colour

Curd colour was recorded at marketable stage by visual means and curds were classified into four categories i.e. snow white, white, creamy white and yellow.

3.9 Statistical and biometrical analysis

For statistical analysis, average values of each genotype in each replication were used for every trait of interest. The outline of procedure followed for estimation of different statistical parameters is represented below:

3.9.1 Analysis of variance (ANOVA)

For each character of interest, the analysis of variance was carried out separately, using the method of Panse and Sukhatme (1967). For all the genotypes under study, significance of difference was tested using following procedure:

ANOVA table for RBD

Sources of variation	Degrees of freedom	Sum of squares	Mean sum of squares	F value	
				Calculated	Tabulated
Replication	(r-1)	RSS	RMS	RMS/EMS	Table value of F
Treatment	(t-1)	TrSS	TrMS	TrMS/EMS	
Error	(r-1) (t-1)	ErSS	EMS	(*Significant at 5% **significant at 1%)	

Where,

r = Number of replications

t = Number of treatments (genotypes)

RSS = Replication sum of squares

TrSS = Treatment sum of squares

ErSS = Error sum of squares

RMS = Replication mean sum of squares

TrMS = Treatment mean sum of squares

EMS = Error mean sum of squares

Test of Significance-

The calculated value of 'F' is compared with tabulated value of 'F' at either 5% or 1% level of significance, to determine significance of treatment differences. The 'F' value is said to be significant, if calculated value of 'F' ratio is greater than the tabulated value. If not, it is considered as non-significant.

If 'F' value is found significant, Standard Error (SE), Critical Difference (CD) and Coefficient of Variation (CV) was calculated to find out superiority of treatments upon one another.

$$SE(m)\pm = \sqrt{\frac{EMS}{r}}$$

$$SE(d)\pm = \sqrt{\frac{2EMS}{r}}$$

$$CD_{(0.05)} = SE(d) \times \text{table value of } t_{(0.05)} \text{ at error degree of freedom}$$

Where,

SE(m) = Standard error of mean

SE(d) = Standard error of mean difference

$CD_{(0.05)}$ = Critical difference at 5% level of significance

3.9.2 Biometrical parameter of variation

Different biometrical parameters adopted for this particular investigation are Mean, Range, Genotypic and Phenotypic coefficient of variation, Heritability and Genetic advance.

3.9.2.1 Mean

It is estimated by summing up all the observations for any character and dividing it with total number of observations.

$$\overline{X} = \frac{\sum X_i}{N}$$

Where, $\sum X_i$ = Sum of all the observations

N = Total number of observations

$\overline{X}$ = Mean of observations (Average)

3.9.2.2 Range of variation

Range is estimated as difference between largest and smallest value of each observations.

3.9.2.3 Genotypic and Phenotypic coefficient of variation

Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) was estimated with the help of formula given by Burton and De Vane (1953)

1) **Genotypic coefficient of variation (GCV) –**

$$GCV\ (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where, $\sigma^2 g$ = genotypic variance

$\bar{X}$ = Mean of characters

2) **Phenotypic coefficient of variation (PCV) –**

$$PCV\ (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where, $\sigma^2 p$ = phenotypic variance

$\bar{X}$ = Mean of characters

Siva subramanian and Menon (1973) suggested classification of the values of GCV and PCV as low, moderate and high according to following:

0-10 % = Low

10-20 % = Medium

>20 % = High

3.9.2.4 Heritability

Formula given by Johnson *et al.* (1955) was used for estimation of heritability in broad sense, which is as follows:

$$h^2_{(bs)}\ (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, $h^2_{(bs)}$ = Heritability in broad sense

Estimates of broad sense heritability were classified as low, moderate and high as per suggested by Robinson (1966).

0-50% = Low

51-70% = Moderate

>70% = High

3.9.2.5 Genetic advance

3.9.2.5.1 Expected genetic advance –

It was estimated by formula given by Johnson *et al*. (1955), which is as follows:

$$GA = k\ \sigma_p\ h^2$$

Where, k = Selection intensity at 5% i.e. 2.06 (constant)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance was classified into high, moderate and low as suggested by Johnson *et al*. (1955)

>20% = High

10-20% = Moderate

<10% = Low

3.9.2.5.2 Genetic advance as percentage of mean –

It was estimated by the formula -

$$GA\ (\%) = \frac{GA}{\overline{X}} \times 100$$

Where, $\overline{X}$ = Mean of character

3.9.3 Correlation coefficient

Correlation coefficient for all the possible combinations of characters at phenotypic and genotypic level was calculated by using procedure given by Searle (1961)-

1) Phenotypic correlation between character X and Y-

$$R_{xy}(p) = \frac{cov_{xy}(p)}{\sqrt{(var\ x(p) \times var\ y(p)}}$$

2) Genotypic correlation between character X and Y-

$$R_{xy}(g) = \frac{cov_{xy}(g)}{\sqrt{(var\ x(g) \times var\ y(g)}}$$

Where, Cov(xy) = Covariance between X and Y character

Var(x) = Variance of character X

Var(y) = Variance of character Y

The significance of correlation coefficient was tested by comparing with Fisher's table value for (g-2) degrees of freedom, where 'g' is number of genotypes at 5% or 1% level of significance.

3.9.4 Path coefficient analysis

The Path-coefficient analysis is equipped for further partitioning of genotypic correlation coefficient into direct and indirect effect as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). All the important characters which consider yield as dependent variable, the path-coefficient was calculated separately for them.

Path-coefficient was calculated using simultaneous equation. These equations represents a basic relationship between correlation coefficient and path coefficient. These equations were solved by presenting them in matrix notation

$$A = B \cdot C$$

The solution for the vector 'C' may be obtained by multiplying both sides with inverse of 'B' matrix i.e.

$$B^{-1} A = C$$

After calculation of values of path coefficient i.e. 'C' vector, we can obtain path values for residual (R). The Residual effect was estimated by using the formula suggested by Singh and Choudhary (1985).

$$R = \sqrt{1 - \sum d_i \times r_{ij}}$$

Where, d_i = direct effect of i^{th} character

r_{ij} = Correlation coefficient of i^{th} character with j^{th} character

The direct and indirect effect of different characters on yield was calculated at genotypic level.

CHAPTER - IV

RESULTS AND DISCUSSION

Improvement of different crop plants is amongst the most important goals of many plant breeders with the sole aim of developing varieties or hybrids, which have high yielding characteristics and also are widely adaptive to various environmental conditions. Genetic variability available in the existing crop facilitates breeders to adopt various improvement methodologies to achieve their goals.

The present investigation was performed to evaluate twelve genotypes of cauliflower (*Brassica oleracea* L. var. *botrytis*) of early group, for various horticultural traits to obtain the information regarding nature and magnitude of variability present among them and also association operating among various economic traits, in order to facilitate plant breeders for exercising effective selection programme for genetic improvement. The results obtained are discussed and presented under following heading:

4.1 Analysis of variance

4.2 Mean performance

4.3.1 Genetic Variability

4.3.2 Heritability and genetic advance

4.4 Correlation coefficient (phenotypic and genotypic)

4.5 Path Coefficient analysis

4.1 Analysis of variance

The analysis of variance is represented in the table (Table 4.1) below for all the traits under study. Analysis of variance revealed that mean sum of squares was highly significant for all of the traits under investigation, pointing out the existence of significant genetic variability among all the genotypes evaluated.

Table - 4.1 Analysis of variance for curd yield and its component characters in cauliflower.

S. No.	Characters (df)	Mean sum of squares		
		Replication (3)	Treatment (11)	Error (33)
1.	Plant height (cm)	21.068	21.468**	5.395
2.	No. of leaves per plant	0.193	5.767**	0.954
3.	Leaf length (cm)	3.083	4.525**	1.561
4.	Leaf width (cm)	0.388	4.965**	0.787
5.	Plant spread (cm)	4.562	13.092**	1.016
6.	Stalk length (cm)	3.887	6.750**	0.869
7.	Days to curd initiation	16.595	18.269*	6.730
8.	Days to marketable curd maturity	18.366	9.922*	4.563
9.	Days taken to first harvest	15.799	25.981**	6.625
10.	Curd width (cm)	0.764	2.922**	0.298
11.	Curd length (cm)	0.225	0.953**	0.118
12.	Gross plant weight (g)	24,588.922	134,869.763**	4,753.361
13.	Marketable curd weight (g)	4,520.063	60,890.753**	4,776.166
14.	Net curd weight (g)	2,600.948	31,072.176**	2,879.169
15.	Curd yield per plot (kg)	5.396	8.544**	2.642
16.	Duration of crop	8.811	14.607*	5.969
17.	Curd yield (q/ha)	1,499.002	2,372.298**	733.503

* **Represents significant at 0.05,** ** **represents significant at 0.01**

4.2 Mean performances

For calculating mean performances of different characters like yield and its attributing components, observations were recorded for five randomly selected plants of each genotype in all the four replications. The observations recorded for five randomly tagged plants were first averaged out for each genotype within all four replications and later average was worked out for all four replications. The mean

performance of each genotype is displayed for different characters in Table 4.2 and described below.

4.2.1 Plant height (cm)

Variation obtained in plant height ranged between 25.56 cm to 32.64 cm for all the genotypes, with the general mean of 28.80 cm. The maximum value for plant height was recorded for genotype 2019/CAUEGENO-11 (32.64 cm) followed by 2019/CAUEGENO-7 (31.59 cm), 2019/CAUEGENO-5 (31.33 cm), 2019/CAUEGENO-10 (30.10 cm) and 2019/CAUEGENO-6 (30.04 cm). While, minimum plant height was recorded for genotype 2019/CAUEGENO-1 (25.56 cm).

4.2.2 Number of leaves per plant

Average value for number of leaves per plant ranged from 16.13 to 19.95 for all genotypes with overall mean of 18.23. Highest number of leaves per plant was obtained in the case of 2019/CAUEGENO-10 (19.95), followed by 2019/CAUEGENO-9 (19.75), 2019/CAUEGENO-12 (19.10), 2019/CAUEGENO-11 (19.00), 2019/CAUEGENO-1 (18.75). Whereas lowest value was observed for 2019/CAUEGENO-3 (16.13).

4.2.3 Leaf length (cm)

Leaf length for all the genotypes ranged from 16.74 cm to 20.80 cm. Highest value of leaf length was recorded for genotype 2019/CAUEGENO-10 (20.80 cm) followed by 2019/CAUEGENO-1 (20.54 cm), 2019/CAUEGENO-12 (20.22 cm), 2019/CAUEGENO-6 (19.88 cm), 2019/CAUEGENO-9 (19.57 cm). While, genotype 2019/CAUEGENO-8 (16.74 cm) recorded shortest average leaf length. The overall average recorded for all the genotypes was 19.29 cm.

Table - 4.2 Mean performances for curd yield and its components in cauliflower genotypes.

GENOTYPES	Characters																
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
2019/CAUEGENO-1	25.56	18.75	20.54	16.34	39.99	9.60	63.15	81.25	80.05	13.71	6.80	944.75	547.50	370.00	10.70	112.05	178.38
2019/CAUEGENO-2	27.88	17.60	18.94	15.42	42.77	11.68	58.00	81.00	76.35	14.58	6.90	847.50	554.00	422.00	11.99	108.35	199.79
2019/CAUEGENO-3	28.43	16.13	18.87	16.58	42.91	10.69	60.93	84.50	81.77	14.33	5.62	1060.50	713.65	451.65	10.75	111.93	179.22
2019/CAUEGENO-4	27.73	17.95	19.07	13.55	41.53	11.82	58.00	82.38	77.00	15.24	7.06	1189.13	768.50	556.75	10.08	109.00	168.02
2019/CAUEGENO-5	31.33	16.90	18.66	14.99	42.77	13.52	60.35	82.00	79.60	16.06	6.78	1210.50	776.50	585.50	12.51	112.80	208.42
2019/CAUEGENO-7	31.59	18.60	19.01	13.99	45.56	14.46	55.05	80.75	75.00	16.46	6.71	1413.00	950.25	663.25	12.68	107.50	211.38
2019/CAUEGENO-8	25.89	16.75	16.74	13.00	38.96	11.34	56.25	81.50	76.65	15.57	6.36	1326.00	825.00	575.00	15.14	108.65	252.27
2019/CAUEGENO-9	27.85	19.75	19.57	14.31	43.06	12.08	58.05	82.75	75.95	16.06	7.01	1256.00	797.75	610.75	12.21	107.95	203.56
2019/CAUEGENO-10	30.10	19.95	20.80	14.65	42.48	13.45	57.40	84.00	81.35	15.69	6.46	1335.25	793.75	561.75	12.08	109.10	201.25
2019/CAUEGENO-6	30.04	18.25	19.88	14.85	44.64	12.28	58.35	78.50	73.80	16.32	7.16	1439.00	943.50	637.25	14.27	107.80	237.83
2019/CAUEGENO-11	32.64	19.00	19.23	13.49	43.35	11.88	57.90	81.50	75.85	14.84	6.54	1054.50	733.00	512.50	13.44	107.15	224.06
2019/CAUEGENO-12	26.59	19.10	20.22	15.37	41.51	12.18	58.35	82.75	77.10	15.70	5.75	1238.00	776.75	560.50	12.62	109.10	210.38
MEAN ($\bar{X}$)	28.80	18.23	19.29	14.71	42.46	12.08	58.48	81.91	77.54	15.38	6.59	1192.84	765.01	542.24	12.37	109.28	206.21
SE (m)+	1.16	0.49	0.62	0.44	0.50	0.47	1.30	1.07	1.29	0.27	0.17	34.47	34.55	26.83	0.81	1.22	13.54
CD	3.34	1.40	1.80	1.28	1.45	1.34	3.75	3.07	3.70	0.79	0.49	99.19	99.42	77.19	2.34	3.51	38.96
CV	8.06	5.36	6.48	6.03	2.37	7.72	4.44	2.61	3.32	3.55	5.20	5.78	9.03	9.90	13.13	2.24	13.13

1. Plant height (cm)
2. No. of leaves per plant
3. Leaf length (cm)
4. Leaf width (cm)
5. Plant spread (cm)
6. Stalk length (cm)
7. Days to curd initiation
8. Days to marketable curd maturity
9. Days taken to first harvest
10. Curd width (cm)
11. Curd length (cm)
12. Gross plant weight (g)
13. Marketable curd weight (g)
14. Net curd weight (g)
15. Curd yield per plot (kg)
16. Duration of crop
17. Curd yield (q/ha)

4.2.4 Leaf width (cm)

Average value for leaf width ranged between 13.00 cm to 16.58 cm, with general average of 14.71 cm. Highest value for mean leaf width was observed for genotype 2019/CAUEGENO-3 (16.58 cm) followed by 2019/CAUEGENO-1 (16.34 cm), 2019/CAUEGENO-2 (15.42 cm), 2019/CAUEGENO-12 (15.37 cm) and 2019/CAUEGENO-5 (14.99 cm). Lowest value for average leaf width was observed for 2019/CAUEGENO-8 (13.00 cm).

4.2.5 Plant spread (cm)

The variation obtained in plant spread ranged between 38.96 cm to 45.56 cm, with general mean of 42.46 cm. Maximum plant spread was measured in genotype 2019/CAUEGENO-7 (45.56 cm) followed by 2019/CAUEGENO-6 (44.64 cm), 2019/CAUEGENO-11 (43.35 cm), 2019/CAUEGENO-9 (43.06 cm) and 2019/CAUEGENO-3 (42.91 cm). While, minimum plant spread was observed in case of 2019/CAUEGENO-8 (38.96 cm).

4.2.6 Stalk length (cm)

Average value of stalk length varied between 9.60 cm to 14.46 cm, with general mean of 12.08 cm for all the genotypes. Maximum stalk length was measured is case of 2019/CAUEGENO-7 (14.46 cm) followed by 2019/CAUEGENO-5 (13.52 cm), 2019/CAUEGENO-10 (13.45 cm), 2019/CAUEGENO-6 (12.28 cm) and 2019/CAUEGENO-12 (12.18 cm). Lowest value was recorded for genotype 2019/CAUEGENO-1 (9.60 cm).

4.2.7 Days to curd initiation

Days to curd initiation ranged between 55.05 days to 63.15 days, with the general average of 58.48 days. The genotype 2019/CAUEGENO-7 (55.05 days) taken shortest time to initiate curding, followed by 2019/CAUEGENO-8 (56.25 days), 2019/CAUEGENO-10 (57.40 days) and 2019/CAUEGENO-11 (57.90 days). The genotype which taken maximum days to curd initiation was 2019/CAUEGENO-1 (63.15 days).

4.2.8 Days to marketable curd maturity

The variation in days to marketable curd maturity varied between 78.50 days to 84.50 days with 81.91 days as general mean for all the genotypes. The genotype 2019/CAUEGENO-6 (78.50 days) taken minimum days to attain marketable curd maturity, followed by 2019/CAUEGENO-7 (80.75 days), 2019/CAUEGENO-2 (81.00 days), 2019/CAUEGENO-1 (81.25 days), 2019/CAUEGENO-8 and 2019/CAUEGENO-11 (81.50 days). The genotype which acquired maximum days to attain marketable curd maturity was 2019/CAUEGENO-3 (84.50 days).

4.2.9 Days taken to first harvest

Mean value for days taken to first harvest varied between 73.80 days to 81.77 days, with 77.54 days as overall average. The genotype 2019/CAUEGENO-6 (73.80 days) taken minimum days to first harvest, followed by 2019/CAUEGENO-7 (75.00 days), 2019/CAUEGENO-11 (75.85 days), 2019/CAUEGENO-9 (75.95 days) and 2019/CAUEGENO-2 (76.35 days). The genotype which recorded maximum days to first harvest was 2019/CAUEGENO-3 (81.77 days).

4.2.10 Curd width (cm)

Mean value for curd width varied between 13.71 cm to 16.46 cm with general average of 15.38 cm for all the genotypes. Highest curd width was recorded for genotype 2019/CAUEGENO-7 (16.46 cm) followed by 2019/CAUEGENO-6 (16.32 cm), 2019/CAUEGENO-5 and 2019/CAUEGENO-9 (16.06 cm), 2019/CAUEGENO-12 (15.70 cm) and 2019/CAUEGENO-10 (15.69 cm). Minimum curd width was recorded for genotype 2019/CAUEGENO-1 (13.71 cm).

4.2.11 Curd length (cm)

Mean value for curd length ranged from 5.62 cm to 7.16 cm for all the genotypes, with 6.59 cm as overall average. Highest curd length was measured in case of 2019/CAUEGENO-6 (7.16 cm) followed by 2019/CAUEGENO-4 (7.06 cm), 2019/CAUEGENO-9 (7.01 cm), 2019/CAUEGENO-2 (6.90 cm) and 2019/CAUEGENO-1 (6.80 cm). Lowest curd length was recorded for genotype 2019/CAUEGENO-3 (5.62 cm).

4.2.12 Gross plant weight (g)

Mean value of gross plant weight varied between 847.50 g to 1439.00 g, with the general mean of 1192.84 g. Maximum gross plant weight was observed for genotype 2019/CAUEGENO-6 (1439.00 g), followed by 2019/CAUEGENO-7 (1413.00 g), 2019/CAUEGENO-10 (1335.25 g), 2019/CAUEGENO-8 (1326.00 g), 2019/CAUEGENO-9 (1256.00 g). Genotype 2019/CAUEGENO-2 (847.50 g) acquired lowest gross plant weight.

4.2.13 Marketable curd weight (g)

Mean value of marketable curd weight ranged between 547.50 g to 950.25 g with general mean of 765.01 g. Maximum marketable curd weight was recorded for 2019/CAUEGENO-7 (950.25 g) followed by 2019/CAUEGENO-6 (943.50 g), 2019/CAUEGENO-8 (825.00 g), 2019/CAUEGENO-9 (797.75 g), 2019/CAUEGENO-10 (793.75 g). Minimum marketable curd weight was observed for 2019/CAUEGENO-1 (547.50 g).

4.2.14 Net curd weight (g)

Mean value for net curd weight ranged between 370.00 g to 663.25 g for all the genotypes with general mean of 542.24 g. Maximum net curd weight was recorded for 2019/CAUEGENO-7 (663.25 g) followed by 2019/CAUEGENO-6 (637.25 g), 2019/CAUEGENO-9 (610.75 g), 2019/CAUEGENO-5 (585.50 g), 2019/CAUEGENO-8 (575.00 g). Minimum net curd weight was recorded for genotype 2019/CAUEGENO-1 (370.00 g).

4.2.15 Curd yield per plot (kg)

The variation in curd yield per plot ranged between 10.08 kg to 15.14 kg, with general mean of 12.37 kg. Highest curd yield per plot was obtained for 2019/CAUEGENO-8 (15.14 kg) followed by 2019/CAUEGENO-6 (14.27 kg), 2019/CAUEGENO-11 (13.44 kg), 2019/CAUEGENO-7 (12.68 kg), 2019/CAUEGENO-12 (12.62 kg). Minimum curd yield per plot was observed for 2019/CAUEGENO-4 (10.08 kg).

4.2.16 Duration of crop (days)

Duration of crop for all genotypes ranged between 107.15 days to 112.80 days, with general mean of 109.28 days. The genotype which recorded shortest crop duration was 2019/CAUEGENO-11 (107.15 days), followed by 2019/CAUEGENO-7 (107.50 days), 2019/CAUEGENO-6 (107.80 days). The genotype 2019/CAUEGENO-5 (112.80 days) exhibited longest of crop duration among all the other genotypes.

4.2.17 Curd yield (q/ha)

Curd yield for all genotypes ranged from 168.02 q/ha to 252.27 q/ha with general mean of 206.21 q/ha. Highest curd yield was recorded for genotype 2019/CAUEGENO- 8 (252.27 q/ha) followed by 2019/CAUEGENO-6 (237.83 q/ha), 2019/CAUEGENO-11 (224.06 q/ha), 2019/CAUEGENO-7 (211.38 q/ha), 2019/CAUEGENO-12 (210.38 q/ha). Lowest curd yield was recorded for genotype 2019/CAUEGENO-4 (168.02 q/ha).

Table - 4.3 Morphological characteristics of cauliflower genotypes.

S.No.	Genotypes	Curd compactness	Curd colour
1.	2019/CAUEGENO-1	Medium compact	Creamy white
2.	2019/CAUEGENO-2	Compact	Creamy white
3.	2019/CAUEGENO-3	Compact	Creamy white
4.	2019/CAUEGENO-4	Compact	Creamy white
5.	2019/CAUEGENO-5	Compact	Creamy white
6.	2019/CAUEGENO-7	Medium compact	Creamy white
7.	2019/CAUEGENO-8	Compact	Creamy white
8.	2019/CAUEGENO-9	Compact	Creamy white
9.	2019/CAUEGENO-10	Medium compact	Creamy white
10.	2019/CAUEGENO-6	Medium compact	Creamy white
11.	2019/CAUEGENO-11	Medium compact	Creamy white
12.	2019/CAUEGENO-12	Compact	Creamy white

4.3.1 Genotypic and phenotypic coefficient of variation

The most basic variability parameters are genotypic and phenotypic coefficients of variation, which are widely used to measure the degree of variability present in any genetic population. Hence computation of both genotypic and phenotypic coefficient of variation are considered as must to measure genetic variability. For the current investigation, genotypic and phenotypic coefficient of variation calculation showed that phenotypic coefficient of variation (PCV) values were slightly higher for all the characters under observation than the corresponding genotypic coefficient of variation (GCV), which indicates the presence of environmental influence in character's expression.

According to Sivasubramanian and Madhavamenon (1973), measures of the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV) are graded as low (less than 10%), moderate (10-20%) and high (more than 20%). Moderate magnitude of both phenotypic as well as genotypic coefficient of variation was obtained for characters *viz.* net curd weight (18.38 and 15.48), marketable curd weigh (17.93 and 15.48), gross plant weight (16.19 and 15.12) and stalk length (12.66 and 10.04). It implies the existence of significant variability for these characters within the population, so selection of characters must be given priority for cauliflower improvement.

Some characters recorded moderate magnitude of phenotypic coefficient of variation (PCV) but lower magnitude of genotypic coefficient of variation (GCV). Such characters were curd yield (16.40 and 9.82), curd yield per plot (16.40 and 9.82) and plant height (10.65 and 6.96).

Remaining characters acquired low magnitude of both PCV and GCV. These characters were leaf width (9.20 and 6.95), curd length (8.67 and 6.93), number of leaves per plant (8.06 and 6.02), leaf length (7.87 and 4.46), curd width (6.35 and 5.27), days to curd initiation (5.30 and 2.90), plant spread (4.73 and 4.09), days taken to first harvest (4.37 and 2.84), days to marketable curd maturity (2.97 and 1.41) and crop duration (2.61 and 1.31). Similar findings were also reported by Chittora and Singh (2015), Kumar *et al*. (2017), Manaware *et al*. (2017), Vanlalneihi *et al*. (2017),

Chatterjee *et al*. (2018), Sharma *et al*. (2018), Gariya *et al*. (2019) and Kumar *et al*. (2019).

For all the corresponding characters, the estimates of the phenotypic coefficient of variation (PCV) were found to be higher than those of the genotypic coefficient of variation (GCV), suggesting the effect of the environmental factor in the expression of those character. The larger the discrepancy between the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV), the greater the sensitivity of the characters to environmental fluctuations, while the slight difference represents lesser sensitivity of the characters.

Nursery layout and nursery beds of cauliflower

Plate I – General view of the experimental site

2019/CAUEGENO-1

2019/CAUEGENO-2

2019/CAUEGENO-3

2019/CAUEGENO-4

2019/CAUEGENO-5

2019/CAUEGENO-6

2019/CAUEGENO-7

2019/CAUEGENO-8

2019/CAUEGENO-9

2019/CAUEGENO-10

2019/CAUEGENO-11

2019/CAUEGENO-12

Plate II – Variability for curd characters in cauliflower

Table – 4.4 Genetic parameters of variation for curd yield and its component characters in cauliflower.

S. No.	Characters	Mean	Range		Coefficient of variation (%)		Heritability (h^2 %)	Genetic advance as % of mean
			Minimum	Maximum	Phenotypic	Genotypic		
1.	Plant height (cm)	28.80	25.56	32.64	10.65	6.96	42.69	9.37
2.	No. of leaves per plant	18.23	16.13	19.95	8.06	6.02	55.79	9.26
3.	Leaf length (cm)	19.29	16.74	20.80	7.87	4.46	32.19	5.22
4.	Leaf width (cm)	14.71	13.00	16.58	9.20	6.95	57.03	10.81
5.	Plant spread (cm)	42.46	38.96	45.56	4.73	4.09	74.83	7.29
6.	Stalk length (cm)	12.08	9.60	14.46	12.66	10.04	62.86	16.39
7.	Days to curd initiation	58.48	55.05	63.15	5.30	2.90	30.00	3.28
8.	Days to marketable curd maturity	81.91	78.50	84.50	2.97	1.41	22.70	1.39
9.	Days taken to first harvest	77.54	73.80	81.77	4.37	2.84	42.21	3.80
10.	Curd width (cm)	15.38	13.71	16.46	6.35	5.27	68.76	9.00
11.	Curd length (cm)	6.59	5.62	7.16	8.67	6.93	63.96	11.42
12.	Gross plant weight (g)	1192.84	847.50	1439.00	16.19	15.12	87.25	29.09
13.	Marketable curd weight (g)	765.01	547.50	950.25	17.93	15.48	74.60	27.55
14.	Net curd weight (g)	542.24	370.00	663.25	18.38	15.48	71.00	26.87
15.	Curd yield per plot (kg)	12.37	10.08	15.14	16.40	9.82	35.84	12.11
16.	Duration of crop	109.28	107.15	112.80	2.61	1.35	26.57	1.43
17.	Curd yield (q/ha)	206.21	168.02	252.27	16.40	9.82	35.84	12.11

4.3.2 Heritability and genetic advance as percent of mean

Resemblance of progenies with their parents is regulated by heritability, while genetic advance provides the information regarding the magnitude of expected gain for any particular trait following the selection. The knowledge of heritability along with genetic advance facilitates to draw out conclusions to perform effective selection depending upon phenotypic performances. Estimates of broad sense heritability provides valuable knowledge about relative magnitude of genetic variation and environmental variation present in the population. Meanwhile, genetic advance represents the improvement in genetic value of the new population over original one. Hence, estimation of both heritability and genetic advance is matter of great deal for breeders to develop appropriate selection strategy. Estimation of heritability in broad sense was worked out for present investigation, and was classified as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966).

Estimates of broad sense heritability along with genetic advance as percentage of mean has been represented in Table 4.4. High estimate of broad sense heritability was recorded in the case of characters *viz.* gross plant weight (87.25%), plant spread (74.83%), marketable curd weight (74.60%) and net curd weight (71.00%). Five of the characters acquired moderate estimate of heritability, they were curd width (68.76%), curd length (63.96%), stalk length (62.86%), leaf width (57.03%) and number of leaves per plant (55.79%).

Remaining traits recorded low estimates of heritability in broad sense, these traits were plant height (42.69%), days taken to first harvest (42.21%), curd yield per plot and curd yield (35.84%), leaf length (32.19%), days to curd initiation (30.00%), duration of crop (26.57%) and days to marketable curd maturity (22.70%). The result recorded for gross plant weight, marketable curd weight, net curd weight and stalk are in consonance with the result of earlier researchers *viz.* Chittora and Singh (2015), Ansari *et al*. (2017), Manaware *et al*. (2017), Chatterjee *et al*. (2018), Sharma *et al*. (2018), Gariya *et al*. (2019) and Kumar *et al*. (2019). Findings of days to curd initiation, days to marketable curd maturity and curd width are in line with the findings of Chittora and Singh (2015). Estimates of curd length

supports the finding of Dubey *et al*. (2003), Ansari *et al*. (2017) and Kumar *et al*. (2019). High heritability recorded for plant spread is in accordance with the findings of Kumar *et al*. (2017).

Estimation of heritability alone do not provide sufficient information about the magnitude of genetic improvement that would probably result from selecting superior genotype. So in order to compare the improvement in different characters of various genotypes, genetic advance was calculated as a percentage of the mean. As suggested by Johnson *et al*. (1955), the magnitude of genetic gain as a percentage of mean is classified as high (> 20%), moderate (10-20%) and low (< 10%).

High estimate for genetic advance as percentage of mean was recorded for characters *viz.* gross plant weight (29.09%), marketable curd weight (27.55%) and net curd weight (26.87%). Whereas, five of the characters *viz*. stalk length (16.39%), curd yield per plot (12.11%), curd yield (12.11%), curd length (11.42%) and leaf width (10.81%) recorded moderate genetic advance. Low genetic advance as percentage of mean was recorded for remaining traits *viz*. plant height (9.37%), number of leaves per plant (9.26%), curd width (9.00%), plant spread (7.29%), leaf length (5.22%), days taken to first harvest (3.80%), days to curd initiation (3.28%), duration of crop (1.43%) and days to marketable curd maturity (1.39%).

High estimate recorded for gross plant weight, marketable curd weight and net curd weight is in accordance with the findings of earlier researchers *viz.* Chittora and Singh (2015), Ansari *et al*. (2017), Vanlalneihi *et al*. (2017), Sharma *et al*. (2018), Gariya *et al*. (2019) and Kumar *et al*. (2019). Similar result of stalk length was reported by Kanwar and Korla (2002), Chittora and Singh (2015), Ansari *et al*. (2017) and Manaware *et al*. (2017). Results similar to the estimates of days to marketable curd maturity and days to curd initiation were reported by Halwai *et al*. (2006), Chittora and Singh (2015), Vanlalneihi *et al*. (2017) and Sharma *et al*. (2018). Ansari *et al*. (2017), reported similar results for curd length, curd width and duration of crop.

The traits for which high values of genetic advance was recorded indicates that these traits are governed through additive genes and selecting of these traits would probably result in successful improvement of crop. Moderate estimates of genetic

advance indicates the presence of both additive and non-additive gene effect, while the characters acquiring low genetic advance exhibits significant non-additive gene effect. Considering both heritability and genetic advance values for selecting best genotypes is rather more appropriate than considering value of heritability alone.

In present investigation, high heritability coupled with higher genetic gain was reported for gross plant weight, marketable curd weight and net curd weight, suggesting that heritability is most likely attributable to additive gene effect and hence selection of these characters based on phenotypic performances will be quite successful. These findings are in concordance to earlier researchers like Dhatt and Garg (2008), Nimkar and Korla (2011), Ansari *et al*. (2017), Manaware *et al*. (2017), Chatterjee *et al*. (2018), Sharma *et al*. (2018) and Kumar *et al*. (2019).

Low heritability along with low genetic advance was recorded for several characters *viz.* plant height, days taken to first harvest, leaf length, days to curd initiation, duration of crop and days to marketable curd maturity, which indicates influence of non-additive gene effect in heritability of these particular characters. Remaining characters acquired moderate to low heritability along with moderate to low genetic advance, which indicates the influence of non-additive gene action in these character's expression. Similar recordings were also reported by Chittora and Singh (2015), Ansari *et al*. (2017) and Kumar *et al*. (2019).

4.4 Correlation coefficient (phenotypic and genotypic)

Correlation analysis is considered to be one of the most important and necessary approach in any crop improvement programme, because it helps to draw out the basic idea regarding relationship existing between different characters and also facilitates in determining various component characters, which in turn help selecting of any desirable trait. Effectiveness of any selection programme majorly depends upon degree of association existing among various characters. For the very first time, Galton (1889) proposed the degree of association between dependent and independent variables, while Pearson (1904) formulated the theory. Searle (1961) proposed the mathematical use of correlation at the phenotypic, genotypic and environmental level.

The mechanism behind association among characters is either pleiotropic gene action or linkage or maybe both. The phenotypic correlation consists of both genotypic and environmental effect, and it provides basic knowledge about overall association among phenotypic characters. Genotypic correlation provides measure of genetic association among various characters and is most commonly utilized during selection programmes. The phenotypic and genotypic correlation for curd yield and its component characters in cauliflower are presented in Table 4.5 and the significant correlations only are discussed here.

The curd yield per plot was found highly significant and positively correlated with marketable curd weight (0.628 and 0.383), curd width (0.608 and 0.406), net curd weight (0.594 and 0.393) and gross plant weight (0.591 and 0.390), at both genotypic and phenotypic levels, respectively. While, it also recorded significant positive correlation with plant height (0.464) and stalk length (0.353) at only genotypic level. While, days to marketable curd maturity, leaf width and leaf length was found negatively significantly correlated to curd yield at both genotypic and phenotypic levels. Whereas, days to curd initiation, duration of crop and days taken to first harvest was negatively correlated at only genotypic level.

Duration of crop recorded highly significant positive correlation with days to curd initiation (0.976 and 0.668), days taken to first harvest (0.770 and 0.824) and days to marketable curd maturity (0.370 and 0.393) at both genotypic and phenotypic levels, respectively. Leaf width was found highly significant and positively correlated at genotypic level (0.989 and 0.288). Characters like net curd weight, marketable curd weight, plant spread and gross plant weight were found negatively correlated at both genotypic and phenotypic levels. Characters like curd yield per plot, number of leaves per plant, curd width, stalk length and curd length were found highly significant but negatively correlated at only genotypic level.

Table – 4.5 Genotypic and phenotypic correlation coefficient between curd yield and its components in cauliflower.

S. no.	Characters		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	Plant height (cm)	G	1.000	0.109	0.020	-0.433**	0.922**	0.879**	-0.377**	-0.287*	-0.186	0.546**	0.291*	0.304*	0.517**	0.559**	0.464**	-0.275
		P	1.000	0.147	0.123	-0.006	0.552**	0.391**	-0.228	-0.027	-0.148	0.206	-0.001	0.209	0.305*	0.222	-0.096	-0.206
2	No. of leaves per plant	G		1.000	0.925**	-0.230	0.192	0.254	-0.263	-0.008	-0.245	0.213	0.265	0.211	0.079	0.197	-0.027	-0.677**
		P		1.000	0.475**	-0.045	0.195	0.244	-0.141	0.003	-0.130	0.246	0.228	0.207	0.171	0.232	-0.013	-0.262
3	Leaf length (cm)	G			1.000	0.418*	0.349*	0.015	0.627**	-0.016	0.308*	-0.089	0.096	-0.067	-0.165	-0.169	-0.463**	0.079
		P			1.000	0.560**	0.108	0.022	0.082	0.190	0.109	-0.125	0.032	-0.039	-0.140	-0.141	-0.378**	0.019
4	Leaf width (cm)	G				1.000	0.027	-0.432**	1.159**	0.317*	0.763**	-0.555**	-0.342*	-0.529**	-0.554**	-0.650**	-0.562**	0.989**
		P				1.000	-0.014	-0.352*	0.301*	0.131	0.256	-0.411**	-0.327*	-0.376**	-0.445**	-0.514**	-0.442**	0.288*
5	Plant spread (cm)	G					1.000	0.695**	-0.368*	-0.257	-0.391**	0.538**	0.234	0.304*	0.517**	0.511**	0.100	-0.430**
		P					1.000	0.489**	-0.256	-0.287*	-0.324*	0.345*	0.212	0.279	0.403**	0.359*	-0.022	-0.291*
6	Stalk length (cm)	G						1.000	-0.891**	-0.162	-0.330*	0.904**	0.171	0.690**	0.722**	0.837**	0.353*	-0.461**
		P						1.000	-0.364*	0.015	-0.134	0.678**	0.167	0.519**	0.580**	0.655**	0.178	-0.180
7	Days to curd initiation	G							1.000	0.088	0.601**	-0.894**	-0.113	-0.695**	-0.801**	-0.932**	-0.838**	0.976**
		P							1.000	0.245	0.590**	-0.373**	-0.116	-0.435**	-0.438**	-0.393**	-0.216	0.668**
8	Days to marketable curd maturity	G								1.000	0.969**	-0.349*	-0.851**	-0.219	-0.306*	-0.317*	-0.652**	0.370**
		P								1.000	0.573**	-0.154	-0.409**	-0.148	-0.203	-0.148	-0.382**	0.393**
9	Days taken to first harvest	G									1.000	-0.603**	-0.582**	-0.337*	-0.530**	-0.618**	-0.771**	0.770**
		P									1.000	-0.315*	-0.361*	-0.318*	-0.341*	-0.359*	-0.276	0.824**
10	Curd width (cm)	G										1.000	0.240	0.929**	0.910**	0.996**	0.608**	-0.582**
		P										1.000	0.243	0.754**	0.824**	0.926**	0.406**	-0.236
11	Curd length (cm)	G											1.000	0.081	0.047	0.207	0.048	-0.363*
		P											1.000	0.099	0.160	0.242	0.009	-0.209
12	Gross plant weight (g)	G												1.000	0.977**	0.954**	0.591**	-0.378**
		P												1.000	0.898**	0.837**	0.390**	-0.324*
13	Marketable curd weight (g)	G													1.000	0.958**	0.628**	-0.533**
		P													1.000	0.925**	0.383**	-0.328*
14	Net curd weight (g)	G														1.000	0.594**	-0.619**
		P														1.000	0.393**	-0.305*
15	Curd yield per plot (kg)	G															1.000	-0.784**
		P															1.000	-0.194
16	Duration of crop	G																1.000
		P																1.000

*** Represents significant at 0.05, ** represents significant at 0.01**

Net curd weight recorded highly significant positive correlation with curd width (0.996 and 0.926), marketable curd weight (0.958 and 0.925), gross plant weight (0.954 and 0.837), stalk length (0.837 and 0.655), both at genotypic and phenotypic level, respectively. While in case of plant spread (0.511 and 0.359) highly significant positive correlation was recorded at genotypic level and significant positive correlation at phenotypic level. Plant height (0.559) recorded highly significant positive correlation at only genotypic level. While days to curd initiation, leaf width and days taken to first harvest recorded highly significant negative association at both genotypic and phenotypic levels. Days to marketable curd maturity has negative correlation at genotypic level only.

Marketable curd weight was found highly significant and positively correlated to gross plant weight (0.977 and 0.898), curd width (0.910 and 0.824), stalk length (0.722 and 0.580), plant spread (0.517 and 0.403) and plant height (0.517 and 0.305) at both genotypic and phenotypic levels. While, characters like days to curd initiation, leaf width and days taken to first harvest recorded highly significant negative correlation at both genotypic and phenotypic levels respectively, days to marketable curd maturity recorded significant negative correlation at only genotypic level.

Gross plant weight exhibited highly significant positive correlation with curd width (0.929 and 0.754) and stalk length (0.690 and 0.519) at both genotypic and phenotypic levels, while plant height and plant spread (0.304) recorded significant positive correlation at only genotypic level. Significant negative correlation was established between gross plant weight and characters like days to curd initiation, leaf width and days taken to first harvest.

Curd length recorded significant positive correlation with plant height (0.291) at only genotypic level, while characters like days to marketable curd maturity, days taken to first harvest, leaf width recorded significant negative correlation with curd length. On the other hand curd width was found highly significant and positively correlated to stalk length (0.904 and 0.678) and plant spread (0.538 and 0.345), at both genotypic and phenotypic levels, respectively. While plant height (0.546) recorded highly significant positive correlation with same. Characters like days to

curd initiation, days taken to first harvest and leaf width was found significant and negatively correlated to curd width at genotypic and phenotypic levels and days to marketable curd maturity at only genotypic level.

Days taken to first harvest recorded highly significant positive correlation with days to marketable curd maturity (0.969 and 0.573) and days to curd initiation (0.601 and 0.590) at both phenotypic and genotypic levels, respectively. While, leaf width (0.763) and leaf length (0.308) recorded significant positive correlation at only genotypic level. Characters like plant spread and stalk length recorded significant negative correlation.

Days to marketable curd maturity was found significantly positively correlated with leaf width (0.317) at only genotypic level. Whereas, plant height was negatively correlated at genotypic level and plant spread was correlated at phenotypic level only. Days to curd initiation recorded highly significant and positive correlation to leaf width (1.159 and 0.301) at both genotypic and phenotypic levels, respectively, while leaf length (0.627) was correlated at only genotypic level. Characters like stalk length, plant height and plant spread recorded significant negative correlation to it.

Stalk length recorded highly significant positive correlation with plant height (0.879 and 0.391) and plant spread (0.695 and 0.489) at both genotypic and phenotypic levels, while it established significant negative correlation with leaf width. Plant spread (cm) was found significantly positively correlated to plant height (0.922 and 0.552), at both genotypic and phenotypic levels, while leaf length was observed correlated at only genotypic level. Leaf width (cm) was found positively correlated to leaf length, while negatively correlated to plant height. Leaf length was observed positively correlated to number of leaves per plant (0.925 and 0.475) at both genotypic and phenotypic levels.

The findings of the present investigation indicated that estimates of genotypic correlation were recorded higher than that of phenotypic correlation for almost all the traits under study. Lower values of phenotypic correlation might due to the influence of environmental effect on genotypes. Result recorded for association of curd yield per plot (kg) and other component traits was also recorded by earlier researchers *viz.* Kumar *et al*. (2011), Sheemar *et al*. (2012), Santhosha *et al*. (2015),

Ansari *et al*. (2017), Sharma *et al*. (2017), Kumar *et al*. (2019). Manaware *et al*. (2017), recorded similar findings regarding association of curd width and days to 50% curd formation with other component characters. Association between gross plant weight (g) and curd width (cm) with other component traits was in line with the findings of Kumar *et al*. (2017). Sharma *et al*. (2017) suggested similar findings about association of curd diameter, days to curd initiation stalk length and number of leaves per plant.

The overall study of association among curd yield per plot (kg) and other component traits revealed that marketable curd weight, curd width, net curd weight, gross plant weight, plant height and stalk length has significant positive correlation with curd yield per plot, thus selection of these traits maybe beneficial for selecting superior genotypes among a population to improve yield of cauliflower.

4.5 Path coefficient analysis

Path coefficient analysis is one of the most important operation, which is mainly adopted for partitioning correlation coefficients into direct and indirect effects of various independent variables on to dependent variable. Wright (1921) developed the concept of path analysis and Dewey and Lu (1959) utilized the technique for the very first time for determining component characters of yield, which is useful for indirect selection. If the association between yield and some other character is primarily due to the direct effect of that particular character, so it would be advantageous to improve yield by direct selection of that trait. However, if the correlation coefficient is mostly due to the indirect effect of that character through some other traits, then indirect selection *via* those characters will be rewarding for yield improvement.

The path coefficient analysis divides overall correlation coefficient of various characters into indirect and direct effects on yield in specific way that sum total of all indirect and direct effects is always equal to total genotypic correlation. Genotypic path coefficient analysis was performed by taking curd yield per plot (kg) as dependent variable and remaining characters as independent variables, and is represented in Table 4.6.

Table- 4.6 Genotypic path coefficient analysis for curd yield and its component character in cauliflower.

S. no.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	R
1	**-1.825**	-0.063	0.008	0.252	-0.200	3.192	0.392	0.374	-0.048	0.201	0.029	-0.026	2.729	-4.656	0.103	0.464
2	-0.200	**-0.576**	0.398	0.134	-0.042	0.921	0.274	0.010	-0.062	0.078	0.027	-0.018	0.416	-1.643	0.255	-0.027
3	-0.036	-0.533	**0.431**	-0.243	-0.076	0.055	-0.653	0.021	0.079	-0.033	0.010	0.006	-0.870	1.410	-0.030	-0.463
4	0.791	0.133	0.180	**-0.582**	-0.006	-1.570	-1.207	-0.414	0.195	-0.204	-0.034	0.045	-2.922	5.406	-0.372	-0.562
5	-1.682	-0.110	0.150	-0.016	**-0.217**	2.524	0.384	0.335	-0.100	0.198	0.024	-0.026	2.730	-4.255	0.162	0.100
6	-1.605	-0.146	0.006	0.252	-0.151	**3.630**	0.928	0.211	-0.084	0.333	0.017	-0.059	3.811	-6.964	0.173	0.353
7	0.687	0.152	0.270	-0.675	0.080	-3.236	**-1.041**	-0.115	0.153	-0.329	-0.011	0.059	-4.225	7.760	-0.367	-0.838
8	0.524	0.004	-0.007	-0.185	0.056	-0.589	-0.092	**-1.303**	0.247	-0.128	-0.086	0.019	-1.615	2.642	-0.139	-0.652
9	0.340	0.141	0.133	-0.444	0.085	-1.196	-0.626	-1.263	**0.255**	-0.222	-0.058	0.029	-2.799	5.144	-0.289	-0.771
10	-0.997	-0.123	-0.038	0.323	-0.117	3.282	0.931	0.454	-0.154	**0.368**	0.024	-0.079	4.800	-8.286	0.219	0.608
11	-0.532	-0.152	0.041	0.199	-0.051	0.620	0.118	1.110	-0.148	0.088	**0.101**	-0.007	0.246	-1.722	0.137	0.048
12	-0.555	-0.122	-0.029	0.308	-0.066	2.504	0.724	0.286	-0.086	0.342	0.008	**-0.085**	5.157	-7.937	0.142	0.591
13	-0.944	-0.045	-0.071	0.322	-0.112	2.622	0.834	0.399	-0.135	0.335	0.005	-0.084	**5.276**	-7.973	0.200	0.628
14	-1.021	-0.114	-0.073	0.378	-0.111	3.037	0.971	0.414	-0.158	0.366	0.021	-0.081	5.054	**-8.323**	0.233	0.594
15	0.501	0.390	0.034	-0.576	0.093	-1.674	-1.016	-0.482	0.196	-0.214	-0.037	0.032	-2.810	5.154	**-0.376**	-0.784

Residual Effect = 0.06836; Diagonal and bold values shows direct effect

1. Plant height (cm)
2. No. of leaves per plant
3. Leaf length (cm)
4. Leaf width (cm)
5. Plant spread (cm)
6. Stalk length (cm)
7. Days to curd initiation
8. Days to marketable curd maturity
9. Days taken to first harvest
10. Curd width (cm)
11. Curd length (cm)
12. Gross plant weight (g)
13. Marketable curd weight (g)
14. Net curd weight (g)
15. Duration of crop

The data portrayed that marketable curd weight (5.276) showed highest positive direct effect on curd yield per plot (kg), followed by stalk length (3.630), leaf length (0.431), curd width (0.368), days taken to first harvest (0.255) and curd length (0.101). Whereas, net curd weight (-8.323), plant height (-1.825), days to marketable curd maturity (-1.303), days to curd initiation (-1.041), leaf width (-0.582), number of leaves per plant (-0.576), duration of crop (-0.376), plant spread (-0.217) and gross plant weight (-0.085) showed negative direct effect on curd yield per plot.

Plant height (cm) showed positive indirect effect on curd yield per plot through characters like stalk length (3.192), marketable curd weight (2.729), days to curd initiation (0.392), days to marketable curd maturity (0.374), leaf width (0.252), curd width (0.201), duration of crop (0.103), curd length (0.029) and leaf length (0.008). While, through remaining characters it recorded negative indirect effect.

Number of leaves per plant recorded positive indirect effect on curd yield per plot *via* characters like stalk length (0.921), marketable curd weight (0.416), leaf length (0.398), days to curd initiation (0.274), duration of crop (0.255), leaf width (0.134), curd width (0.078), curd length (0.027) and days to marketable curd maturity (0.010). While, it caused negative indirect effect *via* remaining characters

Leaf length (cm) exerted positive indirect effect on curd yield per plot through net curd weight (1.410), days taken to first harvest (0.079), stalk length (0.055), days to marketable curd maturity (0.021), curd length (0.010) and gross plant weight (0.006). Rest of the characters caused leaf length to have negative indirect effect on curd yield per plot.

Leaf width (cm) exhibited positive indirect effect on curd yield per plot through characters like net curd weight (5.406), plant height (0.791), days taken to first harvest (0.195), leaf length (0.180), number of leaves per plant (0.133) and gross plant weight (0.045). Through remaining characters it caused negative indirect effect.

Plant spread (cm) caused positive indirect effect on curd yield per plot *via* marketable curd weight (2.730), stalk length (2.524), days to curd initiation (0.384),

days to marketable curd maturity (0.335), curd width (0.198), duration of crop (0.162), leaf length (0.150) and curd length (0.024). While, it exhibited negative indirect effect through remaining characters.

Stalk length (cm) showed positive indirect effect on curd yield per plot *via* various characters *viz*. marketable curd weight (3.811), days to curd initiation (0.928), curd width (0.333), leaf width (0.252), days to marketable curd maturity (0.211), duration of crop (0.173), curd length (0.017) and leaf length (0.006). Remaining characters were responsible for negative indirect effect on curd yield per plot through stalk length.

Days to curd initiation exerted positive indirect effect through various characters *viz.* net curd weight (7.760), plant height (0.687), leaf length (0.270), days taken to first harvest (0.153), number of leaves per plant (0.152), plant spread (0.080) and gross plant weight (0.059). Remaining showed negative indirect effect.

Days to marketable curd maturity recorded indirect positive effect on curd yield per plot *via* net curd weight (2.642), plant height (0.524), days taken to first harvest (0.247), plant spread (0.056), gross plant weight (0.019) and number of leaves per plant (0.004). Remaining characters were found to have indirect negative effect over curd yield per plot.

Days taken to first harvest showed indirect positive effect on curd yield per plot through characters *viz.* net curd weight (5.144), plant height (0.340), number of leaves per plant (0.141), leaf length (0.133), plant spread (0.085) and gross plant weight (0.029). Rest of the traits were recorded to have negative indirect effect.

Curd width exhibited positive indirect effect on curd yield per plot *via* characters like marketable curd weight (4.800), stalk length (3.282), days to curd initiation (0.931), days to marketable curd maturity (0.454), leaf width (0.323), duration of crop (0.219) and curd length (0.024). Rest of the characters caused negative indirect effect on curd yield per plot.

Curd length caused positive indirect effect on curd yield per plot through days to marketable curd maturity (1.110), stalk length (0.620), marketable curd weight (0.246), leaf width (0.199), duration of crop (0.137), days to curd initiation (0.118),

curd width (0.088) and leaf length (0.041). While, it recorded negative indirect effect through rest of the characters.

Gross plant weight showed positive indirect effect on curd yield per plot through marketable curd weight (5.157), stalk length (2.504), days to curd initiation (0.724), curd width (0.342), leaf width (0.308), days to marketable curd maturity (0.286), duration of crop (0.142) and curd length (0.008).Whereas, rest of the characters were having negative indirect effect.

Marketable curd weight recorded positive indirect effect on curd yield per plot *via* characters like stalk length (2.622), days to curd initiation (0.834), days to marketable curd maturity (0.399), curd width (0.335), leaf width (0.322), duration of crop (0.200) and curd length (0.005). While, it recorded negative indirect effect through remaining characters.

Net curd weight showed positive indirect effect on curd yield per plot through marketable curd weight (5.054), stalk length (3.037), days to curd initiation (0.971), days to marketable curd maturity (0.414), leaf width (0.378), curd width (0.366), duration of crop (0.233) and curd length (0.021). Rest of the characters showed negative indirect effect.

Duration of crop caused positive indirect effect on curd yield per plot *via* net curd weight (5.154), plant height (0.501), number of leaves per plant (0.390), days taken to first harvest (0.196), plant spread (0.093), leaf length (0.034) and gross plant weight (0.032). Rest of the characters caused negative indirect impact on curd yield per plot.

In present investigation marketable curd weight, stalk length, leaf length, curd width, days taken to first harvest and curd length showed high positive and direct significant effect on curd yield per plot. Characters like days to marketable curd weight and stalk length showing higher significant direct effect on curd yield per plot, hence these characters should be taken into consideration for improving curd yield. The result presented above is in accordance with the findings of earlier researchers like Ansari *et al*. (2017), Kumar *et al*. (2017), Sharma *et al*. (2017), Vanlalneihi *et al*. (2017) and Chatterjee *et al*. (2018).

CHAPTER - V

SUMMARY AND CONCLUSIONS

The present investigation which is entitled **"Genetic variability in cauliflower (*Brassica oleracea* L. var. *botrytis*) genotypes for yield and quality traits under Chhattisgarh plains"** was performed during the season of *rabi* 2019-20 at Horticultural Research cum Instructional Farm, under the project AICRP on vegetable crops, at Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh).

The investigation consists of total twelve cauliflower genotypes *viz.* 2019/CAUEGENO-1, 2019/CAUEGENO-2, 2019/CAUEGENO-3, 2019/CAUEGENO-4, 2019/CAUEGENO-5, 2019/CAUEGENO-7, 2019/CAUEGENO-8, 2019/CAUEGENO-9, 2019/CAUEGENO-10, with three checks *viz.* 2019/CAUEGENO-6, 2019/CAUEGENO-11 and 2019/CAUEGENO-12.

The experiment was laid out of four replications in randomized block design. Seeds of different genotypes were sown within nursery beds having the size of 18 × 1 × 0.15 m keeping distance of 30 cm between the beds. Plots of 3m × 2m size were prepared for each genotype, keeping 50cm distance between each plots. About one month old seedlings were transplanted in straight lines maintaining 60cm distance between the rows and 50cm between the plants. Following which all the cultural practices were carried out as recommended.

Five plants were randomly selected and tagged within each experimental plots to take various observations regarding different characters under study. Further observations recorded were subjected to different statistical operations to study the mean performances of genotypes, estimates of genetic variability, broad sense heritability, genetic gain along with association studies and path analysis.

The results regarding analysis of variance showed significant mean sum of squares for all the traits under investigation, which points out the presence of considerate variability in studied material for curd yield and attributing traits.

Genotype which recorded highest curd yield (q/ha) as compared to other genotypes was 2019/CAUEGENO- 8 followed by 2019/CAUEGENO-6, 2019/CAUEGENO-11, 2019/CAUEGENO-7, 2019/CAUEGENO-12. Also genotype 2019/CAUEGENO-7 recorded highest marketable curd weight, net curd weight, curd width, plant spread, stalk length along with least days taken to curd initiation.

Moderate magnitude of both phenotypic as well as genotypic coefficient of variation as recorded for traits *viz.* net curd weight, marketable curd weigh, gross plant weight and stalk length. Characters which recorded moderate phenotypic coefficient of variation (PCV) but lower magnitude of genotypic coefficient of variation (GCV) were curd yield, curd yield per plot and plant height. Rest of the characters acquired low magnitude of both phenotypic (PCV) as well as genotypic coefficient of variation (GCV).

High estimates of heritability was recorded in the case of characters *viz.* gross plant weight, plant spread, marketable curd weight along with net curd weight. The characters which acquired moderate estimate of heritability were curd width, curd length, stalk length, leaf width along with number of leaves per plant.

Highest genetic advance was exhibited in case of characters *viz.* gross plant weight, marketable curd weight and net curd weight. Whereas some of the characters *viz*. stalk length, curd yield per plot, curd yield, curd length and leaf width recorded moderate genetic advance.

The curd yield per plot was found highly significant and positively correlated with marketable curd weight, curd width, net curd weight and gross plant weight at both genotypic as well as phenotypic levels. While, it also recorded significant positive correlation with plant height and stalk length at only genotypic level.

The analysis of path coefficient revealed that marketable curd weight showed maximum direct positive effect over curd yield per plot (kg), followed by stalk length, leaf length, curd width, days taken to first harvest and curd length. While, rest of the characters exhibited negative indirect effect on it.

Conclusion

As per the results obtained through present investigation, it can be concluded that sufficient and significant variability exists among all the genotypes as well as characters under evaluation. Estimates of mean sum of squares due to genotypes were recorded significant for all of the traits.

The results of mean performances of genotypes for various traits revealed that genotypes 2019/CAUEGENO-8 recorded greatest curd yield (q/ha) and 2019/CAUEGENO-7 recorded highest marketable and net curd weight, which makes these two genotypes more promising than other genotypes for Chhattisgarh plain regions.

The values of phenotypic coefficient of variation (PCV) recorded marginally higher values as compared to corresponding genotypic coefficient of variation (GCV) in case of all the characters under observation, which indicates interaction of genotypes with environment to certain extent or presence of environmental influence in character's expression.

For gross plant weight, marketable curd weight and net curd weight, high heritability estimates along with high genetic advance were observed, indicating that heritability is most likely due to additive gene effect and therefore selection of these characters based on phenotypic performances would be very effective.

Evaluation of correlation coefficients between yield and its attributing characters revealed that traits *viz.* marketable curd weight, curd width, net curd weight and gross plant weight were significantly positively correlated to curd yield per plot. Thus selection of these traits maybe beneficial for selecting superior genotypes among any population to improve yield of cauliflower.

Also the analysis of path coefficient portrayed positive direct effect of marketable curd weight, stalk length, leaf length, curd width and curd length on curd yield per plot. Which indicates that genotypes showing higher values for these traits should be prioritized when for selecting high yielding varieties.

Suggestions for future research work

Through the results obtained and experience gained throughout the course of investigation, following studies can be suggested to be undertaken in upcoming future:

- The best genotype identified through this particular course of investigation having desirable traits with greater variability, can be further utilized in hybridization programme.
- The genotypes under investigation should also be studied under different agro-climatic zones of Chhattisgarh, to study their stability in varied regions of the state, which would help selecting genotypes for wider adaptability.
- There is a huge need of screening the genotypes against various biotic as well as abiotic stresses.
- There is a scope of utilizing biotechnological tools to incorporate various genes of interest to improve different qualitative traits and nutrient content of cauliflower.
- The local genotypes available in distant regions of Chhattisgarh should also be evaluated to identify valuable genes for desirable characters and should be included in hybridization programmes.
- The genotypes may also be compared with other established varieties and hybrids for their yield potential.
- Genotypes from distant parts of India can be collected and studied for their adaptability for Chhattisgarh region.

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APPENDICES

Appendix I

Weekly Meteorological data during the crop growth period of cauliflower

(*Rabi* 2019)

Date	Wk No.	Temp (°C)		Rainfall (mm)	Relative Humidity		Wind Velocity (Kmph)	Evaporation(mm)	Sun Shine (hours)
		Max.	Min.		I	II			
Sep 24-30	39	30.2	24.2	178.1	91	74	4.5	17.7	3.8
Oct 01-07	40	32	24.3	1.8	90	64	3.8	25.3	7.5
08-14	41	31.3	23.6	1.2	91	64	2.4	23.4	5.4
15-21	42	30.9	21.8	51	92	65	2.6	21.9	5.7
22-28	43	28.1	22.2	27.6	92	71	3.7	12.5	2.8
29-04	44	31.4	22.2	0	92	51	1.2	19.2	6
Nov 05-11	45	30.6	23	81.6	91	65	3	92	5.5
12-18	46	29.6	15.5	0	90	38	1.8	20	8.7
19-25	47	30.2	15.2	0	89	38	1.4	20.2	8.2
26-02	48	29.7	16.3	0	90	43	2	20.4	6.3
Dec 03-09	49	28	13.3	0	84	34	2.4	21.4	7.6
10-16	50	29.5	15.3	0	91	48	1.7	17.3	5.2
17-23	51	26.7	14.1	0.8	88	42	1.9	16.6	4.9

RESUME

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