PERFORMANCE OF DIFFERENT GENOTYPES OF CHOW-CHOW [*Sechium edule* (Jacq.) Swartz.] UNDER FOOTHILL CONDITION OF NAGALAND

Thesis
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DOCTOR OF PHILOSOPHY
in

HORTICULTURE (VEGETABLE SCIENCE)

by

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2022

In our Redeemer's Name

This thesis is dedicated to my Mom and Dad.

For their endless love, support and encouragement.

DECLARATION

I, MM Shulee Ariina hereby declare that the subject matter of this thesis is the record of work done by me, that the content of this thesis did not form the basis of the award of any previous degree to me or the best of my knowledge to anybody else and that the thesis had not been submitted by me for any research degree in any other university/institute.

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CERTIFICATE – I

This is to certify that the thesis entitled **"Performance of various genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland"** submitted to Nagaland University in partial fulfillment of the requirements for the award of the degree of Doctor of Philosophy in Horticulture (Vegetable Science) is the record of research work carried out by Mr. M M Shulee Ariina, Registration No. Ph.D./HOR/00238 under my personal supervision and guidance.

The result of the investigation reported in the thesis has not been submitted for any other degree or diploma. The assistance of all kinds received by the student has been duly acknowledged.

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This is to certify that the thesis entitled **"Performance of various genotypes of Chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland"** submitted by MM SHULEE ARIINA, Admission No. Ph.D./HOR/00238 to the NAGALAND UNIVERSITY in partial fulfillment of the requirements for the award of degree of Doctor of Philosophy in Horticulture (Vegetable Science) has been examined by the Advisory Board and External examiner on ……..

The performance of the student has been found **Satisfactory/Unsatisfactory.**

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I own entire responsibility for all the error and omissions.

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LIST OF ABBREVIATTIONS

ANOVA	: Analysis of Variance
@	: at the rate
CD	: Critical Difference
Cm	: centimeter
Df	: Degree of freedom
°C	: Degree Celsius
E	: East
et al.	: Et alilbi and others
FYM	: Farm Yard Manure
GCV	: Genotypic Coefficient of Variation
G	: gram
Ha	: Hectare
Kg	: Kilogram
MSS	: Mean Sum of Square
Max.	: Maximum
Min.	: Minimum
M	: Meter
NPK	: Nitrogen Phosphorous Potassium
/	: Per
%	: Percent
PCV	: Phenotypic Coefficient of Variation
RBD	: Randomized Block Design
SASRD	: School of Agricultural Sciences and Rural Development
SS	: Sum of Square
t	: tones
TSS	: Total Soluble Solute

viz. : namely

Vit. C : Vitamin C

Aug : August

ABSTRACT

The present investigation was conducted during Aug, 2019 to May, 2021 at Horticulture Research Farm, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema with 20 diverse genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.]. The experiment was laid out in Randomized Block Design with three replications. Genetic diversity was studied for twenty one quantitative and qualitative traits *viz*., vine length, days to first flowering, number of nodes at first fruit set, length of internodes, length of leaf, width of leaf, petiole length, no. of fruits per plant, fruit length, fruit weight, fruit diameter, calcium, fat, vitamin C, TSS, moisture, carbohydrate, protein, crude fibre, yield per plant and yield per ha. Data were analyzed statistically for phenotypic and genotypic variance, coefficient of variation, heritability, genetic advance, genetic gain, correlation coefficient, path coefficient, genetic divergence and seed protein banding pattern. Analysis of variance revealed significant differences among the genotypes for all the characters studied. High PCV and GCV, heritability and genetic gain were observed for vine length, days to first flowering, number of nodes at first fruit set, length of internodes, length of leaf, width of leaf, no. of fruits per plant, fruit length, fruit weight, calcium, fat, vitamin C, TSS, moisture, carbohydrate, protein, crude fibre, yield per plant and yield per ha. Correlation studies indicated that fruit yield per plant was positively and significantly correlated with days to first flowering, number of nodes at first fruit set, length of internodes, length of leaf, width of leaf, petiole length, no. of fruits per plant, fruit length, fruit weight, fruit diameter which indicated the importance of these traits in selection for yield. Path analysis revealed that maximum positive direct effect on fruit yield per plant was imposed by fruit weight, number of fruits

per plant and number of nodes at genotypic level. This indicated that these are the real independent characters and have maximum contribution towards increase in fruit yield per plant. Divergence study revealed crude fibre contributed maximum per cent to the diversity followed by Vitamin C, fruit length, yield per plant, protein, carbohydrate, fruit weight, days to first flowering and vine length. Maximum inter cluster distance was observed between cluster II and III which indicated that the genotypes within these clusters were highly divergent. SDS-PAGE analysis showed considerable variation in band number of protein which ranged from 7-11. Protein banding profile showed that the genotype G-15 and G-12 was most distantly related to the rest of the genotypes. Hence, it was recommended that these two genotypes could be utilized for crossing programme to create more genetic diversity. SDS-PAGE marker data provided more sub groupings and revealed higher amount of diversity as compared to morphological data in present study. On the basis of diversity and mean performance of the genotypes for all the traits studied, G-15, G-8 and G-10 were found to be superior for the fruit yield components and quality traits. So, these genotypes can be considered as the best performing genotypes under foothill condition of Nagaland and can be used as parental source in any breeding programme.

Key words: Chow-chow, correlation, divergence, genotypes, cluster, heritability, SDS-PAGE

CHAPTER I

INTRODUCTION

INTRODUCTION

Chow-chow [*Sechium edule* (Jacq.) Swartz.] also known as chayote is an underutilized crop of family Cucurbitaceae, native to Central America and humid tropical region of Mexico. In sub-family sicyoideae, chow-chow is the only cultivated cucurbit. Chow-chow was likely domesticated from its wild related species or from *S. compositum* in Mexico and Guatemala but now it is cultivated in various tropical and sub tropical regions (Newstrom, 1991). In India, this crop was introduced by Christian missionaries and now extends to the border between the Himalayan states and Myanmar, Bhutan and Nepal. (Singh *et al.,* 2012).

Chow-chow is an herbaceous, monoecious, self-compatible, perennial vine with tuberous roots. A thick root generally used for growing this crop which bears fruit on a peduncle. It is primarily used for human consumption. In addition to the fruits; tender stems with soft leaves and tuberous roots are also eaten. It produces large number of fruits, which are single seeded and viviparous. The fruit varies in size shape, color, pulp texture and density of spines. Male and female flowers are almost the same, with a twisted corolla at the base of the hypanthium, 10 nectaries and pollinated by insects (Wille *et al.,* 1983). However, male flowers are borne in racemes and female flowers are solitary. Under cultivation, chow-chow flowers are pollinated by *Apis mellifera* L., bees.

The edible portion has a lower fibre, protein and vitamin content than other plants. However, young stems, roots and seeds have high calorie and carbohydrate content, and the micronutrients and macronutrients contained in fruits are fully adequate. Fruits, especially seeds, are rich in amino acids.

In recent years, the plant has become more important due to its abundance of polyphenols, flavonoids, especially leaves (3.5 mg g^{-1} dry leaves), roots (3.05 mg g^{-1}), and stems (1.93 mg g^{-1}). I am.) has multiple medicinal properties and

sechumin, an anticancer ribosome-inactivating protein. Besides, fruit extract also has antihypertensive effect, antibacterial, antifungal, antioxidant, anti-proliferative properties against cervical carcinoma, mouse lung fibrosarcoma and mouse macrophage leukaemia, antihyperglycemic, anticonvulsant and central nervous system depressant activity (Cadena-Iniguez *et al.*, 2013).

It is very popular among the tribals of NEH region because of its hardiness, minimal care and abundant fruiting, and its wide range of uses. It grows in large quantities in high rainfall conditions. Significant variations are found in chow-chow in respect of fruit size, shape, colour, presence of spines and nutritional composition of the fruits. It is unique among the cultivated cucurbits by bearing a single seeded fruit and expressing vivipary (Aung *et al.*, 1990). So far, it remained a neglected underutilized crop and only few studies have been carried out. Its high yield potential, nutritional, biological and abiotic stress tolerance, and very low cultivation efforts make it a potential crop in changing climate scenarios.

In North East region, chow-chow is grown in kitchen gardens of every tribal as an important component of their daily diet. Fruits of this crop are mainly used as vegetable and it is also used for making sweets and sauce. Though, it is native of Mexico but considerable diversity is found in North East region. Mizoram is the leading state with an estimated area of 845 ha and 10985 MT production (Sanwal, 2008). It is mainly propagated by means of seed (whole fruit with seed)/ sprouted fruits, which are main cause of variation existing in the region.

The importance of genetic diversity in selecting plants for recombinant breeding in crops to get better transgressive segregation has been highlighted by many workers. The genetic diversity of selected plants is not necessarily based on factors such as geographic diversity. Therefore, the characterization of genetic divergence to select appropriate and diverse genotypes should be based on sound statistical techniques such as D^2 statistics and cluster analysis. These methods

characterize genetic differentiation using similarity or dissimilarity criteria based on the overall effect of some economically significant traits.

North East India has good genetic variability for various traits in chow-chow and not much exploration has been taken to tap the diversity till now. So there is need to develop variety(ies) with good qualitative and yield traits, suitable for cultivation in this region. Therefore, the present investigation entitled **"Performance of various genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland''** was undertaken with the following objectives:

1. Morphological characterization of different genotypes of chow-chow based on NBPGR descriptor.
2. To find out the mean performance of yield and quality traits of chow-chow genotypes.
3. To study the genetic variability, heritability and genetic advance.
4. To find out the correlation co-efficient between different pairs of characters.
5. To estimate the direct and indirect effect of yield attributes on fruit yield.
6. To screen out the best chow-chow genotype under foothill condition of Nagaland.

CHAPTER II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

An attempt has been made to collect and review the relevant literatures available on various aspects of work done so far on horticultural traits, quality attributes, genetic variability, character association and divergence association in chow-chow for fruit yield and its component characters. As the relevant literature on some of these aspects is scarce in chow-chow, efforts were made to include review of other cucurbits, wherever it is essential. Literatures on above aspect of the present study are reviewed in this chapter under the following heads.

2.1 Performance of genotypes

2.2 Genetic variability

2.3 Correlation studies and path coefficient analysis

2.4 Genetic divergence

2.5 Protein banding pattern

2.1 Performance of genotypes

Aung *et al.* (1990) reported that chayote (*Sechium edule*), a lesser-known member of the gourd family and among cultivated cucurbits by bearing single-seeded fruits and exhibiting vivipary. Chayote, adaptable to a wide range of climatic conditions, can be grown with relative ease. In addition to its fruits, it yields tender shoots for use as vegetable greens, vines as ornament for fences or as animal fodder, and edible subterranean storage roots. It is worthy of being more widely used because it has good nutritional properties and a firm delectable fruit flesh texture and can be prepared in a variety of ways for consumption.

Merlin *et al.* (2007) reported that one of the most important problems during transport, storage, and marketing of smooth green chayote (*Sechium edule*) export fruits is rot through fungi. Five different diseases were singled out: blister caused by *Colletotrichum gloeosporioides,* anthracnose caused by *C. orbiculare*,

reddish-purple mould provoked by *Fusarium oxysporum*, white mould provoked by *Phytophthora capsici*, and acid rot caused by *Geotrichum sp*. It was also detected that an important source of fungi dissemination was triggered through the manipulation of selection and packing personnel.

Sanwal *et al.* (2010) investigated thirty-eight accessions of chow-chow collected from Meghalaya (20), Mizoram (2) and Sikkim (16). These accessions were grown in augmented design at Barapani (Meghalaya) to study the economic traits both quantitative as well as qualitative. A total of 13 accessions were found without spine and remaining were having spine from soft to hard in nature. The average fruit yield per plant was 7.6 kg. The accessions collected from Meghalaya were early maturing while the accessions collected from Sikkim were late in maturity. Biochemical analysis of fruit revealed that higher TSS content observed for Megha-16 (6.2%), Sikkim-12 (6%) and Sikkim-10 (5.5%) while high level of ascorbic acid 24.7 mg/100gm in Sikkim-1 and followed by 23.4 mg/100gm in Sikkim-13.

Kapoor *et al.* (2014) collected sixteen chow-chow accessions from different locations of Sikkim and studied for fifteen morphological and biochemical characters. Highest fruit weight was recorded in entry S8 (461g). Highest dry matter content was found in the entry S5. Entries S2, S3, S10 and S11 contained higher ascorbic acid content in their fruits.

Lalthansanga and Samanta (2015) investigated the effect of feeding different levels of chayote (*Sechium edule*) meal by replacing standard concentrate mixture (CM) Twenty-four growing indigenous pigs were used to study the effect of feeding chayote (*Sechium edule*) meal on growth performance and nutrient utilization. During the feeding trial of 90 days, it was found that the dry matter (DM) intake decreased as the level of chayote meal increased. For G1, G2, G3, and G4, the ADG (kg) was 0.24±0.04, 0.23±0.03, 0.18±0.02, and 0.18±0.02,

respectively, and the feed conversion efficiency was 5.42±0.44, 4.93±0.17, 5.38±0.05, and 5.74±0.53, respectively. Chayote meal could safely replace the standard grower ration up to 40% in the diet of growing local pigs without causing any adverse effects on growth and nutrient utilization.

Mishra and Das (2015) investigated 10 accessions of *Sechium edule* (Squash) for different physico-chemical parameters. Results indicated that the germplasm collected are rich in important nutritional parameters. The fruits analysed have very high moisture content ranging from 89.3-94.2% but are not a good source of protein which ranged from 0.77-1.05% in the fruits. The juice extracted from the fruits was rich in Vitamin C content and the germplasm GH10 had the highest Vitamin C content (22.3%). Fruits of *Sechium edule* also have significant amount of carbohydrate (4.12-4.98%), crude fibre (4.88-5.89 %) and mineral ash (0.245-0.321%).

Singh *et al.* (2015) reported that chow-chow (*Sechium edule*) is a boon crop of Mizoram and has potential for improving the socio-economic status of the tribal community. It is a popular vegetable grown for its fruits, tender shoots, young leaves and the tuberized roots. Low calorific value of fruits makes it suitable for hospital diets/ baby foods and could also supplement to potatoes for diabetic patients. The vines climbs by clinging with tenacious tendrils, flowers are monoecious, fruits are mostly solitary, pear shaped, single seeded, viviparous with fairly bland taste of potato and cucumber. Mostly it is being cultivated on hilly terrain and the vines are trained over bower system, and even the hills having >100 % slope, where no cultivation is possible, is also under chow-chow cultivation.

Kim *et al.* (2016) studied on two varieties of chayote skin color: green and white. These two varieties of chayote fruit were put in the growing chamber with dry soil for germination. They were transplanted to a non-heated plastic house.

Plant growth, including number of nodes, length of internode, and leaf size, of the green variety was better than that of the white. Brix degree and hardness of fruit compared with the white showed that the green was larger and heavier.

Riviello-Flores *et al.* (2018) investigated the chemical compositions and antioxidant activities from the juice fruits from two commercial varieties of chayote cultivated in Mexico, as well as a proposal for the elaboration of chayote juices with stevia leaves and pineapple juice. The juice of the two varieties differs significantly regarding the concentrations of total soluble solids and total sugars, but not vitamin C. The radical scavenging capacities of VL and NS extracts varied slightly (IC50 = 0.45 to 0.65 mg mL^{-1}), while the antioxidant activities were similar (~80%). The NS variety is particularly promising regarding nutraceutical application.

Das and Mishra (2019) investigated in *Sechium edule* to formulate value added products from this vegetable. Results suggest that vegetable dumplings and tutti-frutti developed have reasonable amount of proximate principles and can be stored up to three months thereby increasing the shelf life of the vegetable. Results indicate that raw vegetable had very high moisture content (87.38%). Value addition to the vegetable led to significant increase in the protein content (21.34 %) and carbohydrate content (56.35 %) in vegetable dumplings and tutti-frutti respectively.

2.2 Genetic variability

Genetic variability is the raw material on which selection acts to evolve superior genotypes or varieties in plant breeding program. The genetic variability for various character available in the breeding populations or materials is systematically subjected to selection to change the genetic architecture of plant characters and consequently of the plant as a whole to develop improved genotype having higher economic yield. The variability exploited in breeding programme is

derived from the naturally occurring variants and the wild relative of crops as well as artificially developed strains and genetic stock by human efforts. The reservoir of variability for different characters of a plant species resulting from available natural or artificially synthesized variants or strains constitute its germplasm. Thus germplasm may include improved strains, primitive cultivars, wild relatives, obsolete cultures, special genetic stocks, seed pollens and vegetative parts etc. Most of the germplasm collections are inadequately evaluated or screened for assessment of genetic variability. Variability in respect of different characters of chow-chow and allied crops is reviewed below. Moreover literatures related to the efficient multivariate techniques for diversity analysis are also reviewed.

Bharathi *et al.* (2006) evaluated genetic variability in 32 genotypes of spine gourd and reported that phenotypic coefficient of variation (PCV) ranged from 15.26 % for fruit girth to 34.28% for fruit weight, while genotypic coefficient of variation (GCV) ranged from 14.38% for fruit girth to 33.52% for fruit weight. High heritability coupled with high genetic advance was recorded for fruit weight, fruit volume and number of fruits per vine.

Cadena-Iniguez *et al.* (2007) reported the importance of chayote is based on the growing commercial demand of the fruit and its large-scale production in Mexico and Costa Rica, and to a lesser extent, in Guatemala, Brazil, Puerto Rico, Algeria, India, New Zealand, and Australia. Chayote comes from the cloud forest of Mexico and Central America, the central region being the State of Veracruz, Mexico, where the largest infraspecific variation has been identified, recently classified in botanical varieties with different shape, color, and flavor. Despite the large variety, only the chayote called smooth green (*Virens levis*) has been utilized for large scale commercial exploitation.

Cadena-Iniguez *et al.* (2008) studied on morphological and anatomical variation analysis was carried out with leaves and fruits of *Sechium edule*,

collected in the central region of Veracruz, Mexico. The collected fruits were classified in eight groups according to their typical characteristics. The results showed that the phenotypical distinction of the studied infraspecific *S. edule* complex is related to morphological and anatomical changes in order to improve the adaptive specialization of the different chayote types with respect to the environment.

Parkash (2008) studied 44 germplasm of ash gourd and observed high heritability along with high genetic advance for fruit yield per plant. In his study it has also been revealed that only number of fruit per plant and fruit weight had high genetic advance.

Pandit *et al.* (2009) studied fifteen genotypes of bottle gourd and reported variability for all traits except fruit/plant. The moderate GCV and genetic advance was observed for fruit length and fruit weight. Thus, improving these characters should be effective and rewarding during selection.

Sharma and Sengupta (2013) reported sixteen genotypes of bottle gourd and reported that high genotypic co-efficient of variation (GCV) was observed for fruit weight (39.48%). In all cases, phenotypic co-efficient variances were higher than the genotypic co-efficient variance. High heritability with high genetic advance percent of mean was observed for all characters.

Koppad *et al.* (2015) studied 16 genotypes of ridge gourd and results revealed that PCV was higher than the GCV for most of the traits. High heritability with moderate to high GCV and PCV was recorded for chlorophyll and proline during 45 DAS and total yield per vine indicated that these characters could be improved by simple selection.

Chinatu *et al.* (2016) studied variability for fruit yield and yield components in 7 varieties of cucumber. Analysis of variance showed that the varieties were significantly different ($P<0.05$) in vine length, number of vines per

plant, number of leaves per plant, fruit length, fruit girth, fruit weight, number of fruits per plant and fruit yield per hectare. All the yield components with the exception of vine length had positive and highly significant ($P<0.01$) coefficients of correlation with fruit yield per hectare. The high genetic coefficient of variation and broad sense heritability estimates deduced for number of vines per plant, number of leaves per plant, and fruit yield per hectare which implied that exploitable variations exist among the varieties.

Cruz-Martínez (2017) studied to develop an efficient protocol for the in vitro regeneration of chayote, an important Mexican crop and the evaluation of the genetic fidelity. This species produces recalcitrant seeds, which complicates germplasm storage and makes in vitro conservation a desirable alternative. Proliferation of axillary shoots was induced from axenic nodal segments obtained from in vitro germinated seedlings. Plant regeneration by organogenesis was optimally achieved when leaf and petiole explants were cultured on MS medium supplemented with 0.1 mg/L BA and 0.05 mg/L gibberellic acid (GA3), obtaining an average of 5.3 ± 1.9 shoots per explant.

Verma *et al.* (2017) studied to assess the genetic variations in the 74 chow–chow landraces collected from the North Eastern Hill region of India. Wide variations for fruit colors, fruit length (6.5–21.5 cm), fruit width (4.2–10.7 cm), fruit weight (60–560 g), vitamin-C (2.6–13.8 mg 100 g^{-1}), reducing sugar (0.18–2.77%), total sugar (1.09–2.94%) and phenol content (0.17–3.85 mg 100 g^{-1} FW) were recorded among the landraces. The grouping of landraces in cluster analysis was found to be independent of their respective geographic locations.

2.3 Correlation studies and path coefficient analysis

The efficiency of selection can be improved by using correlation between different characters. The phenotypic correlation indicates the extent of observed relationship between two characters and this include both hereditary and

environmental influences, while genotypic correlation coefficient provides a real association between two characters and is most useful in selection (Johnson *et al.* 1955).

Qin (2007) studied the resistance correlation between downy mildew and powdery mildew in cucumber. The correlation coefficients of disease index between downy and powdery mildews were extremely significant at the seedling and mature stages, respectively.

Hanchinamani and Patil (2009) studied the correlation coefficients for 20 characters in 45 cucumber genotypes and found that phenotypic and genotypic correlation coefficients for fruit yield per vine was positively and significantly correlated with vine length, inter-nodal length, number of branches per vine, fruit length, number of nodes per vine, fruit diameter, flesh thickness, dry weight of fruit, number of marketable fruits per vine and total number of fruits per vine. Days to first male and female flower appearance, node at which first male and female flower appears and days to first fruit harvest were negatively and significantly correlated with fruit yield per vine both at phenotypic and genotypic levels.

Hossain *et al.* (2010) in a study of path coefficient analysis revealed that the fruit length and diameter, average fruit weight and number of fruits per plant directly contributed towards the yield per plant in the long type cucumber.

Yadav *et al.* (2010) studied path coefficient analysis in bottle gourd and found that length of fruit (cm), weight per fruit (kg) and number of fruits per plant had positive and direct effect on fruit per plant.

Reshmi and Sreelathakumary (2012) study of correlation and path coefficient studies were worked out for 25 genotypes of ash gourd of different geographical origin. Fruit length, fruit girth, average fruit weight, seeds per fruit, 1000 seed weight had positive and positive correlation with yield. The positive

direct effect on yield was revealed by fruit length, average fruit weight and fruits per plant. Therefore, these traits may be considered as the most reliable selection indices for effective improvement in fruit yield in ash gourd.

Golabadi *et al.* (2013) carried out a study to determine the relationships among fruit yield, fruit yield components and morphological traits using 20 different genotypes of cucumber. According to path analysis, among considered traits, fruit number per picking had the greatest positive effect on total fruit yield. Overall, highly significant and positive correlation coefficients as well as high direct effects of fruit number on fruit yield indicated that this trait is simultaneously the most reliable component for selecting high fruit yielding cucumber genotypes.

Kumar *et al.* (2013) studied path coefficient analysis in sponge gourd and reported that average diameter of fruit, number of primary branches, number of fruits per vine, average weight of fruit and total soluble solids showed positive direct effect on total yield per vine. Hence, selection for these traits for improving yield per vine in sponge gourd is suggested.

Hasan *et al.* (2015) studied genetic diversity in commercial cucumber genotypes based on 13 characters. Path analysis revealed that fruits/plant (0.701**)** and fruit weight (0.379) had maximum positive direct effect on yield.

Khan *et al.* (2015) studied correlation and path coefficient for 71 genotypes of bitter gourd. The resulted obtained showed that fruit length showed low direct and positive effect on yield per plant via fruit diameter and average fruit weight. Average fruit weight and number of fruits per plant showed high direct and positive effect on yield per plant. Path analysis revealed that average fruit weight, number of fruits per plant, days to male flowering and fruit length had positive direct effect on fruit yield.

Oliveira and Oliveira (2021) investigated the relationship between the physical properties of chayote fruit of the variety Cambray and their mass, aiming to indicate criteria for direct selection of more attractive fruits. Correlations among these morphological variables were assessed by Pearson's correlation coefficient, and a correlation network was used to express the results graphically. A diagnosis of multicollinearity was performed, and a condition number of 6639 (multicollinearity severe) was found. Path analysis considered the fruit mass as the main dependent variable. Our analyses showed that MAS, FTV, FTA, FTP, and STD are physical attributes with the greatest potential for selection and identification of more attractive chayote fruits of the variety Cambray for commercial purposes.

2.4 Genetic divergence

The concept of D^2 statistics was originally developed by Mahalanobis (1936). Then Rao (1952) suggested the application of this technique for the arrangement of genetic diversity in plant breeding. Now, this technique is extensively used in vegetable breeding for the study of genetic divergence in the various breeding material including germplasm. This analysis also helps in the selection of diverse parents for the development of hybrids. Cluster analysis helps to form groups of closely related individuals which help in determining genetic distance between them.

Kadam and Kale (1987) observed highly significant difference between cultivars suggesting considerable divergence among 30 ridge gourd cultivars. 30 cultivars were grouped in to 20 clusters based on their D^2 values. Cluster A having two cultivars had the lowest intra cluster D^2 values (8.22) while cluster I which had two cultivars with the highest intra-cluster value of 18.59. The highest inter cluster distance was observed between cluster V and XIII (387.11) and it was minimum between cluster IV and VIII (19.79).

Dora *et al.* (2003) studied genetic divergence among 11 characters of pointed gourd genotypes by D^2 Mahalanobis statistics and divided them in to four clusters. Cluster I and II comprised four genotypes each, cluster III comprised 2 genotypes and cluster IV comprised of a single genotype. Their study indicated that numerical taxonomic approach was more potent for clustering biological population over the D^2 statistics.

Bharathi *et al.* (2005) reported the genetic divergence of 32 genotype of spine gourd. Based on the D^2 values all genotypes were grouped in to seen cluster. The maximum number of genotypes (11) were included in cluster III followed by 9 genotypes in cluster IV and 4 genotypes in cluster VI. Three cluster II, V, & VII included two genotypes each.

Abdelnour and Rocha (2008) established protocols for the analysis of genetic diversity in chayote by using isozyme markers, thereby determining the level of genetic diversity present in 42 accessions of chayote from Costa Rica. It was observed that for eight enzyme staining systems: PGM, 6-PGD, PGI, IDH, MDH, SOD, SKD, and EST, and were able to score 14 putative loci. Eight of the 14 loci examined were polymorphic. Five of these multilocus genotypes were homozygous for all loci. This analysis, based on the presence and absence of alleles, revealed that accessions collected in the same location seldom shared the same multilocus genotype.

Sanwal *et al.* (2008) evaluated 38 indigenous collections of chow-chow for eight quantitative and quality traits. High values of genotypic coefficient of variance along with high heritability and genetic advance were recorded for number of fruits plant^{-1}, fruit yield plant^{-1}, TSS, acidity and ascorbic acid. Number of fruits plant^{-1} and average fruit weight showed positive and significant correlation with fruit yield plant^{-1}. The number of fruit plant^{-1} and average fruit weight had high direct effect towards the fruit yield plant^{-1}. On the basis of genetic

divergence, relative magnitude of D^2 values 38 genotypes were grouped into seven clusters. The maximum genetic divergence was observed between cluster III and VII followed by cluster II and VI.

Sreelatha (2010) at Trivandrum studied the genetic diversity of 25 ash gourd genotypes collected from different geographical locations was assessed at the molecular level and compared for morphological traits for degree of divergence. The clustering pattern based on Mahalanobis D^2 statistic indicated that there was no association between geographical distribution of genotype and genetic divergence.

Dewan *et al.* (2013) reported genetic divergence for yield and yield contributing characters of 46 ash gourd genotypes at wide range of variations were found among the ash gourd genotypes in respect of different parameters such as vine length at harvest, fruit length, fruit diameter, sex ratio, number of fruits per plant, average weight per fruit and yield per plant.

Machida-Hirano *et al.* (2015) studied in Chayote that out of 11 microsatellite markers isolated, 10 loci provided 1 to 7 alleles per locus in a set of Mexican chayote accessions. Observed and expected heterozygosities for each locus ranged from 0.00 to 0.85 and 0.00 to 0.73 respectively. The overall genetic diversity detected by microsatellites was compared with that detected by P450-based analogue markers, a genome-wide dominant marker.

Visen *et al.* (2015) studied that the cluster analysis grouped all 31 bottle gourd genotype in to 5 major cluster based on D^2 value. Extreme genetic divergence was estimated among clusters. Maximum number of genotypes were grouped in to cluster V included 10 genotypes whereas, cluster II included eight genotypes. The cluster I had 6 genotypes which is followed by cluster IV and cluster III had only three genotypes in each cluster. Fruit length, fruit girth and average fruit weight contributed maximum towards genetic divergence.

Ene *et al.* (2016) evaluated 16 cucumber genotypes in the early and late planting seasons to estimate the magnitude of their genetic variability and heritability. Genotypes were also classified into groups based on the performance and determination of the highest discriminating trait that accounted for greater variability using cluster analysis. Cluster analysis and its comparison of means showed that 'Beit Alpha', 'Ashely', 'Straight 8', and 'Sumter' from cluster F in the early planting season and 'Beit Alpha' and 'Ashely' from cluster E in the late planting season expressed the best agronomic traits and yield potentials. Hence, selection for any trait would favour genotypes in these clusters.

2.5 Protein banding pattern

Seed proteins are used as genetic markers in the study of genetic variation because they are the primary products of structural genes. Any change in the coding sequence of a gene generally reflects the corresponding change in the primary structure of protein (Srivalli *et al.,* 1999). Electrophoresis of seed or seedling extracts followed by appropriate protein or activity stains are all based on the concept that each cultivar is distinct and relatively homogeneous at the genetic level. Thus by screening enough loci one should be able to uniquely define each cultivar. Electrophoresis is basically a process of forced diffusion within an electric field. Protein molecules of the sample are moved through a medium that is gel, paper, or cellulose by applying an electrical gradient. The protein molecules are separated on the basis of their molecular weight or electrical charge. During electrophoresis the lighter molecules move faster and travel more distance in the gel medium and vice-versa. Therefore, the protein molecules with low molecular weight will be stacked at the bottom of the gel. Brief reviews regarding these parameters have been given as under:

Singh and Ram (2001) analysed seed storage protein of 19 cucumber genotypes on single seed basis by sodium dodecyl sulphate polyacrylamide gel

electrophoresis under reduced conditions. The storage protein of seed of 19 germplasm lines could be resolved into a total of 17 bands distributed into 3 zones i.e. A, B and C zones. A zone comprised of 6 bands, zone B had 7 bands and zone C included 4 bands. The 19 germplasm lines could be classified into 8 different groups based on protein profiles. Thus, it was possible to distinguish certain germplasm lines on the basis of protein profiles.

Dudwadkar *et al.* (2015) studied diversity analysis among few cucurbitaceae using seed protein profile. The study endeavours to differentiate the members of cucurbitaceae with eco-agronomical essence at intra and inter genus level by profiling seed storage proteins. About 20-25 unique bands were scored in *C. grandis* and other cucurbitaceae members respectively. Cluster analysis performed based on Jaccard's similarity coefficient and SPSS software (Version 14.0) showed 3 clusters. Similarity matrix showed that the greatest similarity and minimum genetic distance belonged to populations with the similarity coefficient 0.28 and 0.13 respectively.

Mishra and Das (2015) analyzed the fruits of 10 accessions of *Sechium edule* for different physico-chemical parameters. Results indicated that the germplasm collected are rich in important nutritional parameters. The fruits analyzed have very high moisture content ranging from 89.3-94.2% but are not a good source of protein which ranged from 0.77-1.05% in the fruits. The juice extracted from the fruits was rich in Vitamin C content and the Germplasm GH10 had the highest Vitamin C content (22.3%). Fruits of *Sechium edule* also have significant amount of carbohydrate (4.12-4.98%), crude fibre (4.88-5.89 %) and mineral ash (0.245-0.321%).

Jain *et al.* (2017) reported genetic variation of 36 *Sechium edule* accessions collected across 12 states in India was assessed using morphological traits and DAMD markers. Eighteen fruit morphological traits (both qualitative and

quantitative) were evaluated to confirm the variations in the present collection. The DNA analysis performed using DAMD primers were used for deducing the diversity at DNA level. The collection produced 102 bands out of which 97 were polymorphic and the percentage polymorphism ranged between 66.66 and 100 per primer. Discrete pattern of clustering was obtained using UPGMA method of complete linkage percent disagreement revealing high diversity among the collected accessions.

Cruz-Martinez *et al.* (2017) studied to develop an efficient protocol for the in vitro regeneration of chayote (*Sechium edule*), an important Mexican crop and the evaluation of the genetic fidelity. Since somaclonal variation is a potential hindrance to the in vitro propagation of plants, genetic stability was evaluated through RAMP markers using 9 combinations of RAPD and ISSR primers. The amplification products obtained from the regenerated plants were electrophoresed and showed banding patterns similar to that of the mother plant, demonstrating the homogeneity of the individuals obtained through the regeneration protocols reported here.

CHAPTER III

MATERIALS AND METHODS

MATERIALS AND METHODS

The present investigation entitled **"Performance of various genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland''** was carried out at Horticulture Farm, School of Agricultural Sciences and Rural Development, Medziphema, Nagaland University. The details of the materials and methods used and followed during the experiment for recording various observations and analysis is presented below:-

3.1 Geographical situation

Experimental farm situated at School of Agricultural Sciences and Rural Development, Medziphema Campus, Nagaland University, Nagaland. It lies between 25°45'43" N latitude and 93°53'04" E longitude at an elevation of 305 m above the sea level, bringing sub-tropical climate.

3.2 Climatic conditions

The area of the experimental farm has subtropical condition with predominantly high humidity of 70-90%, moderate temperature with medium to high rainfall. The average rainfall varies from 93.22 mm. The temperature ranged between 21^0C to 32^0C during summer and during winter from 10^0C to 15^0C.

3.3 Soil condition

The soil pH of the experimental site was sandy loam, well drained with mean pH of 4.4.

3.4 Field preparation

The preparation of the field was done by tractor-drawn cultivator followed by two cross-harrowing to pulverize the soil and finally the field was leveled with planker. The layout of the prepared field was prepared as per the experimental

design. Field was divided in to treatments replications with randomized block design. The layout of experimental design is shown in PLATE 1.

3.5 Details of treatments

Twenty genotypes of chow-chow from different places of North Eastern Region have been collected to conduct the experiment.

Table 3.1 Meteorological data recorded during the period of crop investigation (September 2019 to June 2021)

Year	Month	Min. temp℃	Max. temp℃	Min. RH%	Max. RH%	Avg. sunshine hour (h)	Total Rainfall (mm)
2019	September	23.9	32.7	72	94	4.1	173.4
	October	21.7	30.3	73	95	5.9	244.8
	November	16.3	28.8	64	97	7.0	52.9
	December	10.4	23.7	62	97	6.1	0.9
2020	January	9.6	22.4	61	97	5.0	18.5
	February	11.1	24.8	51	96	5.2	9.7
	March	14.1	30.1	41	94	6.9	22.5
	April	17.1	30.7	52	90	5.4	153.9
	May	21.1	30.5	64	90	4.8	134.2
	June	23.8	32.4	72	92	3.9	266.2
	July	24.5	32.4	74	94	2.6	199.9
	August	25.0	33.7	70	93	4.4	80.3
	September	24.3	32.5	73	95	4.8	157.6
	October	23.0	31.2	74	95	5.2	175.7
	November	15.6	27.9	59	97	6.7	35.2
	December	9.8	24.5	52	97	7.0	0
2021	January	8.9	24.0	50	96	6.3	3.4
	February	9.7	27.1	40	95	7.2	2.3
	March	14.9	31.1	41	93	6.4	43.5
	April	17.9	33.1	34	87	7.0	59.6
	May	21.9	32.8	58	90	4.7	90.8
	June	24.3	33.1	69	93	3.4	125.5

Source: ICAR, Jharnapani, Nagaland

Table 3.2 Details of the genotypes

Sl. No.	Genotypes	Place of Collection	Latitude, Longitude & Altitude	Farmers Name & Contact No.
1.	G-1	Siiro village, Ziro, Arunachal Pradesh	27°31'9''N, 93°50'23''E, 1706 m	Mr. Narang Dolley, +918787539739
2.	G-2	Tuichang, Champhai Dist., Mizoram	23°15'30''N, 92°57'35''E, 1678 m	Mr. R. Lalhrimte, +917005807685
3.	G-3	Mao-Gate, Senapati Dist., Manipur	25°30'47''N, 94°8'4''E, 2452 m	Ms. Geeta +919862736249
4.	G-4	Hong village, Ziro, Arunachal Pradesh	27°31'18''N, 93°50'41''E, 1702 m	Mr. Narang Dolley +918787539739
5.	G-5	Pfutsero, Phek Dist., Nagaland	25°34'4''N, 94°18'12''E, 2133 m	Mr. Athili Kayina, +917290958315
6.	G-6	Hundung Village, Ukhrul Dist., Manipur	25°4'46''N, 94°21'7''E, 1656 m	Mr. Peing Chipang, +919370047412
7.	G-7	Kohima Village, Kohima Dist., Nagaland	25°40'47''N, 94°6'58''E, 1449 m	Mr. Phokrehrii, +918730014051
8.	G-8	Mawkriah, East Khasi Hills, Meghalaya	25°30'47''N, 91°47'16''E, 1529 m	Ms. Long Langsteih +917005755616
9.	G-9	Nongpiur, East Khasi Hills, Meghalaya	25°32'37''N, 91°48'46''E, 1518 m	Ms. Long Langsteih +917005755616
10.	G-10	Makhel, Senapati Dist., Manipur	25°27'54''N, 94°9'9''E, 2118 m	Ms. Kaisa +918974635289
11.	G-11	Kaibi, Senapati Dist., Manipur	25°28'4''N, 94°9'47''E, 2231 m	Ms. Kaisa +918974635289
12.	G-12	Khoupum, Tamenglong Dist., Manipur	24°41'17''N, 93°26'6''E, 1160 m	Mr. Peter Panmei +918974522972
13.	G-13	Punanamei, Senapati Dist., Manipur	25°31'16''N, 94°9'13''E, 2459 m	Ms. Ela-a Ariina +917627939852
14.	G-14	Tuirot, Namchi, Sikkim	27°9'46''N, 88°22'34''E, 1335 m	Ms. Peggyla Bhutia +919382166284
15.	G-15	Tamei, Tamenglong Dist., Manipur	25°9'44''N, 93°40'53''E, 1330 m	Mr. Peter Panmei +918974522972
16.	G-16	Silesih, Aizawl, Mizoram	23°48'29''N, 92°44'1''E, 1142 m	Mr. Lalhimsanga +918787303354
17.	G-17	Medziphema, Dimapur Dist., Nagaland	25°46'3''N, 93°53'1''E, 368 m	Mr. Rovi Ziekhrii +919436237598
18.	G-18	Tenning, Peren Dist., Nagaland	25°20'43''N, 93°39'42''E, 1503 m	Mr. Moses Newmai +917005544734
19.	G-19	Vidima, Dimapur Dist., Nagaland	25°47'28''N, 93°41'53''E, 157 m	Mr. Moses Newmai +917005544734
20.	G-20	Makhan, Senapati Dist., Manipur	25°26'43'', 94°6'17''E, 1671 m	Ms. Dailu Matia +917629087418

PLATE 1. General view of the experimental field

R1	R2	R3
G-1	G-10	G-15
G-2	G-11	G-16
G-3	G-12	G-17
G-4	G-13	G-18
G-5	G-14	G-19
G-6	G-15	G-20
G-7	G-16	G-1
G-8	G-17	G-2
G-9	G-18	G-3
G-10	G-19	G-4
G-11	G-20	G-5
G-12	G-1	G-6
G-13	G-2	G-7
G-14	G-3	G-8
G-15	G-4	G-9
G-16	G-5	G-10
G-17	G-6	G-11
G-18	G-7	G-12
G-19	G-8	G-13
G-20	G-9	G-14

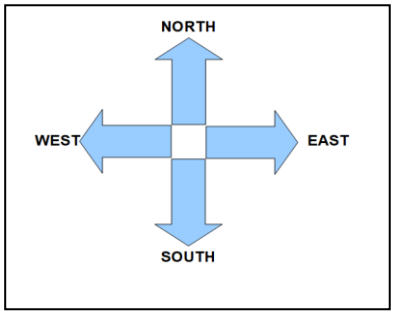

Fig 3.1 Layout plan of experimental field

3.6 Technical programme

1. Design : Randomized Block Design (RBD)
2. Genotypes : 20
3. Replication : 3 (three)
4. Spacing : 1m x 1m

3.7 Experimental Material

Sprouted fruits are sown in hills on raised bed along with channels or furrows. Dig pits of 45 cm x 45 cm x 45 cm at a spacing of 1m x 1m. Fully matured and sprouted fruits collected from high yielding vines were planted in pits @ 1 pit^{-1}.

3.8 Manures and fertilizer application

20t FYM and NPK@100:60:60 kg/ha was given to the crop. The fertilizers are applied in 3 split doses. First during field preparation stage, second was applied at early vine growth stage and third during the early fruiting stage.

3.9 Irrigation

The crop was grown during rainy season hence frequent irrigation was not necessary and not more than once in 7 to 10 days during long gap of the rain. The crop during summer season was irrigated at 4-6 days interval. Water logging condition was avoided with the use of side channels.

3.10 Intercultural operation

2-3 weeding and light hoeing during early stage of vine growth was done.

3.11 Harvesting

Chow-chow fruits were harvested when they attained maturity and the fruits were picked prior to seed development.

3.12 Observations recorded

Observations on quantitative traits were recorded on five randomly selected competitive plants in each genotype from all the three replications and averaged.

3.12.1 Growth parameters

3.12.1.1 Leaf shape

Leaf shape was observed from five randomly selected plants of each plot.

3.12.1.2 Leaf blade margin

Leaf blade margin was observed at 50% flowering stage.

3.12.1.3 Leaf blade; Number of lobes

The number of lobes in leaves was recorded at vegetative stage at 50% flowering stage.

3.12.1.4 Leaf colour

Leaf colour was visually recorded in selected plants at vegetative stage using colour chart.

3.12.1.5 Fruit shape

Fruit shape was observed and recorded when fruit attain marketable maturity.

3.12.1.6 Fruit colour

Fruit colour was visually recorded in selected plants at marketable stage of fruits using colour chart.

3.12.1.7 Spine on fruit skin

Spine on fruit skin was observed in five randomly selected plant of each plot at when fruit reach marketable maturity.

3.12.1.8 Spine distribution

Spine on fruit skin was visually observed in five randomly selected plant of each plot when fruit reached at marketable maturity stage.

3.12.1.9 Spine density

Spine density was divided as sparsely dense, moderately dense and highly dense.

3.12.1.10 Ridges on fruit

Fruit ridges were visually recorded in selected plants at marketable stage of fruits.

3.12.1.11 Groves on fruit surface

Fruit grooves were visually recorded in selected plants at marketable stage of fruits.

3.12.2 Yield and yield attributing parameters

3.12.2.1 Vine length (cm)

The vine length of plant was recorded from main vine of five randomly selected plant of each plot at the time of last picking and average was presented as vine length of plant.

3.12.2.2 Days to first flowering

Days to first flowering appears was recorded as number of days taken from sowing to the opening of first female flower and average value was calculated at initial flowering stage.

3.12.2.3 Number of nodes at first fruit set

The number of nodes at first fruit set was recorded from five randomly selected plant of each plot at the time of first fruit set.

3.12.2.4 Length of internodes (cm)

The internodal length was recorded in nodes from the main vine of five randomly selected plant of each plot at vegetative stage by measuring scale.

3.12.2.5 Length of leaf (cm)

Leaf length was recorded in cm for five fruits from five randomly selected plants of each genotype in each replication and average value was calculated.

3.12.2.6 Width of leaf (cm)

Leaf width was recorded in cm for five fruits from five randomly selected plants of each genotype in each replication and average value was calculated.

3.12.2.7 Petiole length (cm)

Petiole length was recorded at nodes of main vines during vegetative stage at 50% flowering stage.

3.12.2.8 Number of fruits per plant

Number of fruits per plant from five randomly selected plants was recorded throughout the harvest period and their average was worked out.

3.12.2.9 Fruit weight (g)

Five fruits were randomly selected from different tagged plants of a treatment at marketable maturity and their average was worked out to find the average fruit weight.

3.12.2.10 Fruit length (cm)

The fruit was recorded in cm from five fruits of randomly selected plants of each genotype in each replication and average value was calculated.

3.12.2.11 Fruit diameter (cm)

Girth of fruit was recorded in cm of fruits from five randomly selected plants of each genotype in each replication. Girth of the fruit was measured at the centre of the fruits and the average value was recorded as fruit girth in cm. Fruit cut in to two halves and length was measured using measuring scale when fruit attains marketable maturity.

3.12.2.12 Yield per plant (kg)

Yield per plant was worked out by multiplying the average weight of the fruit with total number of fruits per plant. The data was represented in kilogram.

3.12.2.13 Yield per ha (q)

The fruit yield in q/ha was worked out with the help of the following formula:

$$\text{Fruit yield (q/ha)} = \frac{\text{Weight of fruit (kg per plot)}}{\text{Net plot area (sq. m}^2\text{)}} \times \frac{10000}{100}$$

3.12.3 Quality parameters

3.12.3.1 Fat (mg $100g^{-1}$)

Fat was determined by using soxhlet's method. The fresh fruit sample (5 g) was accurately weighed and take extraction flask containing 2/3 organic solvent. Connect these extraction flask and thimble to the condenser unit with heating coil. Put the apparatus on heating mantle and start water supply to the condenser. Regulate the rate of heating to allow continuous volatilization of solvent, its simultaneous condensation. Continue heating slowly till 6-8 siphoning collected in extraction flask. Take out extraction flask from the extraction unit which contains crude fat with little ether. Evaporate excess ether on water bath OR in open air. Keep the flask in the oven at 105^{o}C for 1 hour and evaporate remaining spirit. Cool to the room temperature and weigh it accurately to know the quantity of crude fat / oil extracted**.**

$$\% \text{ Crude fat / oil} = \frac{(W2 - W1)}{5g} \times 100$$

3.12.3.2 Vitamin C (mg $100g^{-1}$)

Vitamin C was determined by using the procedure as outlined by Nielsen (1998). The fresh fruit sample (10 g) was accurately weighed and ground using mortar and pestle with an addition of 20 ml of metaphosphoric acid. The mixture was further ground and strained through muslin and the extract was made up to 100 ml with the metaphosphoric-acetic and mixture. 5 ml of the metaphosphoric-acetic acid solution was pipette in to three of the 50 ml Erlenemayer flask

followed by 2 ml of the sample extract. The sample was titrated separately with the indophenols dye solution until a light rose pink persisted for 5 s. The amount of dye used I the titration were determined and used in the titration were determined and used in the calculation of vitamin C content.

3.12.3.3 Moisture (%)

The moisture content was determined as per the method prescribed by AOAC (1990). 5.0 g of samples were taken in pre-weighed crucible and placed in air oven maintained at 105℃ for 8 hr. The crucibles were transferred immediately to desiccators, cooled and weighed. All the analysis was done in triplicates. The moisture content determined in the fruit sample was calculated as follows:

$$\text{Moisture (\%)} = \frac{\text{Loss in weight (g)}}{\text{Weight of sample (g)}} \times 100$$

3.12.3.4 Carbohydrate (%)

The total carbohydrate content of fruit samples of both the groups was determined as per the Anthrone method (Yemen and Willis, 1954). Fruit sample (0.1g) was extracted in 80% ethanol solution. Dried fruit sample was ground so as to pass through 1 mm sieve and it was shaken for 6 hrs at 60℃. This extract was used for the estimation of carbohydrates. Fruit extract was used for the estimation of carbohydrates. Fruit extract (100 ml) was taken in 25 mL test tubes and 6 mL anthrone reagent was added and then heated in boiling water bath for 10 min and incubated for 20 min at room temperature (25^{o}C). Optical density was read at 625 nm on a UV-Vis spectrophotometer. Blank was also read in the same way. The total carbohydrates were calculated from the standard curve developed by using following the above mentioned method.

3.12.3.5 Protein (%)

Estimation of protein was done as per Lowry's method (Lowry *et al.* 1951). Seeds of 22 germplasm lines were collected and subjected to gel electrophoresis. 1 g of seed sample were macerated in mortar and pestle with 5 ml of buffer (0.06 M Tris-HCl, 2.5% Glycerol, 0.5% SDS, 1.25% β-mercaptoethanol, 0.1% TCA, 10 mM urea, 1 mM EDTA) and transferred to centrifuge tubes. The materials were then centrifuged at 8000 rpm for 20 min. The supernatants were collected and the procedure was repeated 4-5 times. The supernatants were mixed and volume made up to 50 ml with phosphate buffer. 1 ml of 20% TCA was added to 1 ml of the extract and the mixture was kept for 30 min. The mixture was then centrifuged at 8000 rpm for 20 min. The resultant pellets were washed twice with acetone and again centrifuged. The supernatant was then discarded. The pellet was collected and dissolved in 5 ml of 0.1N NaOH till it had dissolved. 1 ml of the aliquot was taken in which 5 ml of freshly prepared alkaline copper sulphate reagent were added and mixed properly. After 10 min, 0.5 ml of Folin's reagent was added and mixed instantaneously and allowed to develop colour for 30 min. Absorbance at 660 nm was recorded after setting the instrument with reagent blank which contained 1 ml of 0.1 N NaOH instead of the sample aliquot.

In another set of tubes, suitable aliquots of BSA solution (in the range of 0-100 µl) were taken and volume made up to 1 ml with 0.1 N NaOH and allowed to develop colour as described above. A standard curve of absorbance at 660 nm versus µg of BSA was drawn and from this standard curve, the amount of protein n the sample tube was determined as protein per gram of the sample.

3.12.3.6 Crude fibre (%)

The determination of crude fibre was done using methods of Association of Official Analytical Chemists (AOAC, 1990). Powdered fruit sample weighing 1.5 gm was digested in 1.25% sulphuric acid, filtered and washed with hot water. The digestion was repeated in 1.25% sodium hydroxide and sample was filtered on a sintered glass filter which was then oven dried and placed in a muffle furnace at

600℃ to ash the sample. The filter was cooked in a desiccator and weighed. Crude fiber content was expressed as percent weight loss resulting from ashing.

3.12.3.7 Calcium (mg/100g)

1 mL of the sample solution was taken and diluted with water in a 50 mL measuring flask to the mark limit. The level of calcium in the sample solution was determined by measuring the absorption with an atomic absorption spectrophotometer. Calcium metal was measured at wavelength 589 nm.

3.12.4 Sodium Dodecyl Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Polyacrylamide gel electrophoresis in presence of denaturing agent (SDS) was carried out as per procedure described by Laemmli (1970) with some modifications.

Reagents

a) **Acrylamide Solution:** 29.2 g acrylamide and 0.8 g bisacrylamide were dissolved in water and the final volume was made up to 100 ml and stored at 4^0C.
b) **Separating Gel Buffer:** 1.5M Tris-HCl of pH 8.8 was prepared and stored at 4^0C.
c) **Stacking Gel Buffer:** 1M Tris-HCl of pH 6.8 was prepared and stored at 4^0C.
d) **Sodium Dodecyl Sulphate solution:** 2% aqueous solution of SDS was prepared.
e) **Ammonium per sulphate solution:** 10% aqueous solution of ammonium persulphate was prepared.
f) **Bromophenol blue solution:** 0.1% aqueous solution of bromophenol blue was prepared.
g) **Electrophoresis buffer:** 3.0 g of Tris base and 14.4 g of glycine was dissolved in water and the final volume was made up to 1liter. The final pH was adjusted to 8.3 with glycine solution.

h) Staining Solution: Staining solution comprised of fixing solution, sensitizing solution, staining solution, developing solution and terminating solution.

- **Fixing Solution:** 50% ethanol, 12% glacial acetic acid, 0.05ml formaldehyde was prepared in double distilled water.
- **Sensitizing Solution:** 0.02% aqueous solution of sodium thiosulphate was prepared.
- **Silver stain solution:** 0.2% Silver nitrate and 0.076% formaldehyde was prepared in double distilled water.
- **Developing Solution:** 6% Sodium carbonate, 0.004% sodium thiosulphate and 0.05% formaldehyde solution was prepared in double distilled water.
- **Terminating/Stopping Solution:** 12% acetic acid solution was prepared.

Formulation for 15% Acrylamide Separating Gel

Water	6.9 ml
30% Acrylamide mixture	15 ml
Separating gel buffer (1.5M Tris-HCl, pH 8.8)	7.5ml
2% SDS	0.3 ml
10 % Ammonium persulphate	0.3 ml
TEMED	0.012 ml

The mixture was transferred to gel cassette by running the solution carefully down one edge between the glass plates till it reaches 1 cm from the bottom of sample loading comb. To ensure that the gel sets with a smooth surface distilled water was run down one edge in the cassette. It was allowed to polymerize.

Formulation for 5% Acrylamide Stacking Gel

Water	5.5 ml
30% Acrylamide mixture	1.3 ml
Separating gel buffer (1.5M Tris-HCl, pH 6.8)	1 ml
2% SDS	0.06ml
10 % Ammonium persulphate	0.06 ml
TEMED	0.008 ml

Preparation of Sample

50mM Tris-HCl (pH 6.8)	100µl
2% SDS	50 µl
0.1% Bromophenol blue solution	30µl
10% Glycerol	120µl
Protein	200µl

The sample was kept in water bath at 90° C for 5 minutes for denaturation of enzyme. Since, the gel run is very slow, SDS-PAGE is performed in refrigerator at 4^0C to prevent overheating of plate.

Procedure

The above polymerized gel was clamped in the electrophoresis assembly and both the tanks were filled with electrode buffer. Desired volume of the purified enzyme and known proteins were placed in previously prepared wells of the stacking gel. Cathode and anode terminals were connected to the electrophoretic power supply and the SDS-PAGE was carried out at a constant current of 25 mA. The gel was run until the bromophenol blue reaches the bottom of separating gel. The power supply was switched off when the tracking dye approached the bottom of the gel. The system was disconnected and the gel was

taken out from the slab. The gel was then subjected to silver staining and the protein bands on the gel were visualized by silver staining.

Silver staining

Silver staining was performed as method described by Mortz *et al.* (2001).

Method

The gel was first sensitized by 0.02% sodium thiosulphate solution for 5 minutes. The gel was then washed twice with double distilled water for 1 minute. It was then transferred to staining solution and kept on gel rocker for 20 minutes in dark. The gel was then washed twice with distilled water for 45 seconds. The gel was then transferred to developing solution and finally the reaction was stopped with 12% acetic acid solution. Gel was washed with double distilled water before visualizing the dark brown band.

3.13 Statistical Analysis

Mean values of data obtained from various experiments are to be subjected to suitable statistical analysis after transformation (if necessary) to test the treatment effect of genotypes and interpretation of the results.

a. Analysis of variance (ANOVA)

The data obtained during the period of investigation were statistically analyzed. Mean, range of variation, standard error of mean and critical difference for each quantitative characters are worked out by method of analysis of variance using Randomized Block Design (ANOVA by Panse and Sukhatme, 1978).

b. Estimation of coefficients of variation

The coefficient of variation for different characters will be estimated by formula as suggested by Burton (1952).

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

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

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

$\overline{X}$ = Mean of character

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The estimates of genotypic and phenotypic coefficient of variance will be classified as low (less than 10%), moderate (10 to 20%) and high (more than 20%).

c. Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The expected advance will be calculated by the formula given by Johnson *et al.* (1955) as described below.

$$GA = K.h^2.\sigma p$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having value of 2.06 at 5% level of selection intensity.

h^2 = Heritability of the character

σp = Phenotypic standard deviation

The genetic advance as percentage of mean was estimated as per the below formula

$$\text{Genetic advance as percent of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \text{ X } 100$$

The magnitude of genetic advance as percent of mean will be categorized as high (more than 20%), moderate (20-10%) and low (less than10%).

d. Estimation of heritability

Heritability in broad sense $h^2_{(bs)}$ defined as the proportion of the genotypic variance to the total variance (phenotypic) will be calculated as per the formula suggested by Burton and De Vane (1952).

$$h^2_{(bs)}\ \% = \frac{\sigma^2_g}{\sigma^2_P} \quad X\ 100$$

Where,

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

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The broad sense heritability estimates were classified as low (<50%), moderate (50-70%) and high (<70%).

e. Estimation of correlation coefficient

Correlation coefficient analysis measures the mutual relationship between various characters at genotypic (g), phenotypic (p) and environmental levels with the help of formula suggested by Miller *et al.* (1958).

1. Genotypic correlation coefficient character x and y

   $$rxy\ (g) = Covxy(g) / \sqrt{varx(g) \times vary(g)}$$

2. Phenotypic correlation coefficient between character x and y

   $$rxy(p) = Covxy(p) / \sqrt{varx(p) \times vary(p)}$$

3. Environmental correlation coefficient between characters x and y

   $$rxy\ (e) = Covxy(e) / \sqrt{varx(e) \times vary(e)}$$

Where,

Covxy (p), covxy (g), covxy (e) = Phenotypic, genotypic & environmental co variances between character x and y, respectively.

Var x (p), var x (g), var x (e) = Phenotypic, genotypic & environmental covariance character x, respectively.

Vary(p), var y(g), var y(e) = Phenotypic, genotypic & environmental covariance character y, respectively.

The significance of correlation coefficient (r) was tested by comparing "t" value at (n-2) degree of freedom

$$t = \sqrt{r\,(n-2\,/\,1-r2)}$$

If calculated "t" is greater than tabulated "t" at (n-2) degree of freedom at given probability level, the coefficient of correlation is taken as significant.

f. Path coefficient analysis

The genotypic correlation coefficients will further partitioned into direct and indirect effects with the help of path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Path co efficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects.

Path coefficient was estimated using, simultaneous equations, the equations showed a basic relationship between correlation coefficient and path coefficient. These equations were solved by presenting them in matrix notations.

$$A = B.C$$

The solution for the vector "C" may be obtained by multiplying both sides by inverse of "B" matrix i.e. B-1 A = C

After calculation of values of path coefficient i.e. "C" vector, it is possible to obtain path values for residual (R). Residual effect was calculated using formula referred from Singh and Chaudhary (1985).

$$R = \sqrt{1 - \text{di x rij}}$$

Where,

Di = direct effect of i^{th} character

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

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

g. Genetic divergence analysis

The Mahalanobis (1936) D^2 statistic is to be used to measure the genetic divergence between the populations. The D^2 value was estimated on the basis of "P" character by the formula:

Formula:

$$D^2 P = \sum_{i=1}^{p} = \sum_{j=1}^{p} = (\lambda ij)\ \lambda i\ \lambda j$$

Where,

(λ ,i,j) is the reciprocal or(λ ,i,j), the pooled common dispersion matrix(i.e. error matrix)

i = the difference in the mean value for the i^{th} character

j = the difference in the mean value for the j^{th} character

For calculating the D^2 values, the variance and covariance will calculated. The genotypes were grouped into different clusters by Torcher's method. The population was arranged in order of their relative distances from each other. For including a particular population in the clusters, a level of D^2 was fixed by taking the maximum D^2 values between any two populations in the first row of the table where D^2 values were arranged in increasing order of magnitude.

h. Data Analysis for protein banding pattern

The gels were scored as presence (1) or absence (0) of protein polypeptide bands. Depending upon the presence or absence of polypeptide bands, similarity

index (SI) (Nei and Li, 1979) between the genotypes was calculated by the following formula:

$$SI = \left(\frac{2Z}{X+Y}\right) X\ 100$$

Where,

Z= Number of similar bands between the genotypes, and

X+Y =Total number of bands in the two genotypes compared.

Cluster analysis UPGMA (Unweighted pair group method with arithmetic mean analysis) by using statistical software SPSS for windows package (Version 16).

CHAPTER IV

RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

The results and discussion of the present investigation, "Performance of different genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland" are presented in this chapter. In order to make the findings more comprehensive, the results obtained from the present studies have been duly supported by respective tables and figures.

4.1 Growth attributes

Performance of growth and growth attributes of various chow-chow genotypes.

4.1.1 Leaf shape

Leaf shape of 20 chow-chow genotypes were visually recorded during 50% flowering stage as shown in the table 4.1. Most of the genotypes were found to have cordate leaves except for genotype G-7, G-10, G-15 and G-20 which was found to have palmately lobed leaves. Similar findings were also reported by Jain *et al.* (2017).

4.1.2 Leaf blade margin

The data leaf blade margin was recorded as shown in table 4.1. Genotype G-6, G-16 and G-20 were found to have crenate leaf blade margin while it was entire for the rest of the genotypes. Similar findings were also reported by Cadena-Iniguez *et al.* (2008).

4.1.3 Leaf blade; no. of lobes

The result obtained by visual observation on number of lobes on leaf blade has been presented in table 4.1. The observation was recorded at active vegetative stage of the plants. Among the twenty genotypes, all the genotypes had 5 lobes. The genes controlling this character may be commonly present in chow-chow

plants due to which all the genotypes have same observation. Similar findings were also reported by Cadena-Iniguez *et al.* (2008).

4.1.4 Leaf colour

The data obtained by visual observation of leaf colour was recorded as shown in table 4.1. Genotype G-1, G-6, G-13 and G-15 were found to have green colour while it was dark green in the rest of the genotypes.

4.1.5 Fruit shape

The observations related to fruit shape of chow-chow genotypes have been presented in the table 4.1. The chow-chow genotypes recorded three kinds of fruit skin namely round, obovoid and pyriform. Three genotypes G-1, G-5 and G-11 were found to have round shape, eight genotypes G-2, G-4, G-10, G-14, G-16, G-17, G-18 and G-19 were found to have obovoid shape and the rest of the genotypes were found to have pyriform shape. Similar findings were also reported by Saade (1996), Kapoor *et al.* (2014) and Jain *et al.* (2017).

4.1.6 Fruit colour

The observation related to fruit colour of chow-chow genotypes have been presented in table 4.1. The chowchow genotypes recorded four types of fruit colour namely pale yellow, light green, green and dark green. Most of the genotypes expressed green colour but genotypes G-2, G-5, G-8 and G-15 expressed pale yellow colour, genotypes G-10, G-11 and G-14 expressed dark green colour while G-1 and G-16 expressed light green colour. Similar findings were also reported by Saade (1996), Sanwal *et al.* (2010), Kapoor *et al.* (2014), Mishra and Das (2015) and Jain *et al.* (2017).

4.1.7 Spine on fruit skin

The data of spine on fruit skin was recorded as shown in table 4.1. Genotype G-3, G-11, G-12, G-14 and G-20 were found to have spines present on

fruit skin while it was absent in the rest of the genotypes. Similar findings were also reported by Sanwal *et al.* (2010), Kapoor *et al.* (2014) and Mishra and Das (2015).

4.1.8 Spine distribution

The data of groove on spine distribution was recorded as shown in table 4.1. Genotype G-3, G-11 and G-20 were found to have high spine distribution while G-12 was found to have moderate distribution of spine and low spine distribution in G-14. Similar findings were also reported by Saade (1996) and Jain *et al.* (2017).

4.1.9 Spine density

The data of spine density was recorded as shown in table 4.1. Genotype G-3, G-11 and G-20 were found to have high spine density (more than 7 spines in 1 cm^2) while G-12 was found to have moderately dense spine (3-7 spines in 1 cm^2) and low spine density in G-14 (below 3 spines in 1 cm^2). Similar findings were also reported by Jain *et al.* (2017).

4.1.10 Ridges on fruit: profile of apical part

The observation related to ridges on fruit of chow-chow genotypes have been presented in table 4.1. In the study G-1, G-4, G-5, G-7, G-8, G-9, G-10, G-12, G-13, G-15 and G-18 were found to have prominent ridges on the fruit while the remaining genotypes were found to have moderate ridges on the fruit surface. Similar findings were also reported by Jain *et al.* (2017).

4.1.11 Groove on fruit surface

The groove on fruit surface was recorded as shown in table 4.1. Genotype G-1, G-2 and G-10 were found to have groove on fruit surface while it was absent in the rest of the genotypes. Similar findings were also reported by Jain *et al.* (2017).

Table 4.1 Growth attributes of various characters of chow-chow genotypes

Genotypes	Leaf shape	Leaf blade margin
Genotype-1	Cordiform	Entire
Genotype-2	Cordiform	Entire
Genotype-3	Cordiform	Entire
Genotype-4	Cordiform	Entire
Genotype-5	Cordiform	Entire
Genotype-6	Cordiform	Crenate
Genotype-7	Palmately Lobed	Entire
Genotype-8	Cordiform	Entire
Genotype-9	Cordiform	Entire
Genotype-10	Palmately Lobed	Entire
Genotype-11	Cordiform	Entire
Genotype-12	Cordiform	Entire
Genotype-13	Cordiform	Entire
Genotype-14	Cordiform	Entire
Genotype-15	Palmately Lobed	Entire
Genotype-16	Cordiform	Crenate
Genotype-17	Cordiform	Entire
Genotype-18	Cordiform	Entire
Genotype-19	Cordiform	Entire
Genotype-20	Palmately Lobed	Crenate

Table 4.2 Growth attributes of various characters of chow-chow genotypes

Genotypes	No. of lobes	Leaf colour
Genotype-1	5	Green
Genotype-2	5	Dark Green
Genotype-3	5	Dark Green
Genotype-4	5	Dark Green
Genotype-5	5	Dark Green
Genotype-6	5	Green
Genotype-7	5	Dark Green
Genotype-8	5	Dark Green
Genotype-9	5	Dark Green
Genotype-10	5	Dark Green
Genotype-11	5	Dark Green
Genotype-12	5	Dark Green
Genotype-13	5	Green
Genotype-14	5	Dark Green
Genotype-15	5	Green
Genotype-16	5	Dark Green
Genotype-17	5	Dark Green
Genotype-18	5	Dark Green
Genotype-19	5	Dark Green
Genotype-20	5	Dark Green

Table 4.3 Growth attributes of various characters of chow-chow genotypes

Genotypes	Fruit shape	Fruit colour
Genotype-1	Spheroid	Light Green
Genotype-2	Obovoid	Pale Yellow
Genotype-3	Pyriform	Green
Genotype-4	Obovoid	Green
Genotype-5	Spheroid	Pale Yellow
Genotype-6	Pyriform	Green
Genotype-7	Pyriform	Green
Genotype-8	Pyriform	Pale Yellow
Genotype-9	Pyriform	Green
Genotype-10	Obovoid	Dark Green
Genotype-11	Spheroid	Dark Green
Genotype-12	Pyriform	Green
Genotype-13	Pyriform	Green
Genotype-14	Obovoid	Dark Green
Genotype-15	Pyriform	Pale Yellow
Genotype-16	Obovoid	Light Green
Genotype-17	Obovoid	Green
Genotype-18	Obovoid	Green
Genotype-19	Obovoid	Green
Genotype-20	Pyriform	Green

Table 4.4 Growth attributes of various characters of chow-chow genotypes

Genotypes	Spine on fruit skin	Spine distribution	Spine density
Genotype-1	Absent	Nil	Nil
Genotype-2	Absent	Nil	Nil
Genotype-3	Present	Many	Highly Dense
Genotype-4	Absent	Nil	Nil
Genotype-5	Absent	Nil	Nil
Genotype-6	Absent	Nil	Nil
Genotype-7	Absent	Nil	Nil
Genotype-8	Absent	Nil	Nil
Genotype-9	Absent	Nil	Nil
Genotype-10	Absent	Nil	Nil
Genotype-11	Present	Many	Highly Dense
Genotype-12	Present	Medium	Moderately Dense
Genotype-13	Absent	Nil	Nil
Genotype-14	Present	Few	Sparsely Dense
Genotype-15	Absent	Nil	Nil
Genotype-16	Absent	Nil	Nil
Genotype-17	Absent	Nil	Nil
Genotype-18	Absent	Nil	Nil
Genotype-19	Absent	Nil	Nil
Genotype-20	Present	Many	Sparsely Dense

Spine Density (in 1 cm^2)	No. of spines present
Sparsely Dense	<3
Moderately Dense	3-7
Highly Dense	7>

Table 4.5 Growth attributes of various characters of chow-chow genotypes

Genotypes	Ridges on fruit: Profile of apical part	Groove on fruit surface
Genotype-1	Depressed	Present
Genotype-2	Flat	Present
Genotype-3	Depressed	Absent
Genotype-4	Flat	Absent
Genotype-5	Depressed	Absent
Genotype-6	Depressed	Absent
Genotype-7	Depressed	Absent
Genotype-8	Flat	Absent
Genotype-9	Flat	Absent
Genotype-10	Depressed	Present
Genotype-11	Depressed	Absent
Genotype-12	Flat	Absent
Genotype-13	Flat	Absent
Genotype-14	Depressed	Absent
Genotype-15	Flat	Absent
Genotype-16	Flat	Absent
Genotype-17	Depressed	Absent
Genotype-18	Flat	Absent
Genotype-19	Depressed	Absent
Genotype-20	Flat	Absent

4.2 Yield attributing, yield and quality parameters

4.2.1 Vine length (cm)

Vine length of 20 chow-chow genotypes were recorded as shown in table 4.6 and fig 4.1 during full maturity stage using measuring scale. The maximum vine length was observed in G-12 (346.33 cm) followed by G-2 (343.83 cm) and G-8 (343.17 cm). However, minimum vine length was recorded for G-13 (180.67 cm).

4.2.2 Days to first flowering

The data of days to first flowering of different genotypes was recorded as the number of days taken for initiation of flower from the date of sowing as shown in table 4.7 and fig 4.2. Different genotype showed variable behavior on days to first flowering. The minimum days taken to first flowering was recorded in G-4 (133.33), G-9 (149.5) and G-13 (150.5). However, maximum days taken to first flowering was recorded in G-17 (166.67) followed by G-9 (149.5). Similar findings were also reported by Kim *et al.* (2016).

4.2.3 Number of nodes at first fruit set

The data taken for number of nodes at first fruit set are given in the table 4.8 and fig 4.3. Number of nodes at fist fruit set was recorded at the stage when fruit set first appear. Among the genotypes, G-12 (42.75) recorded highest number of nodes at first fruit set followed by G-2 (40.5) and G-10 (40). However, minimum number of nodes at first fruit set was recorded in G-17 (25.83). Similar findings were also reported by Kim *et al.* (2016).

Table 4.6 Performance of various genotypes of chow-chow on vine length (cm)

Vine length			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	277.67	289.67	283.67
Genotype-2	338.33	349.33	343.83
Genotype-3	270.33	271.33	270.83
Genotype-4	192.67	202.67	197.67
Genotype-5	240	246.33	243.17
Genotype-6	190.33	199	194.67
Genotype-7	268.67	279.67	274.17
Genotype-8	338.67	347.67	343.17
Genotype-9	253	263	258
Genotype-10	293	305.33	299.17
Genotype-11	293.67	307.67	300.67
Genotype-12	337	355.67	346.33
Genotype-13	181.67	179.67	180.67
Genotype-14	275.33	282.33	278.83
Genotype-15	222	218.33	220.17
Genotype-16	233.33	237.33	235.33
Genotype-17	182.67	184.67	183.67
Genotype-18	244.67	243.33	244
Genotype-19	228.67	236.33	232.5
Genotype-20	186	191.33	188.67
Mean			255.96
SEm(±)			4.12
CD at 5%			11.79
CV(%)			2.78

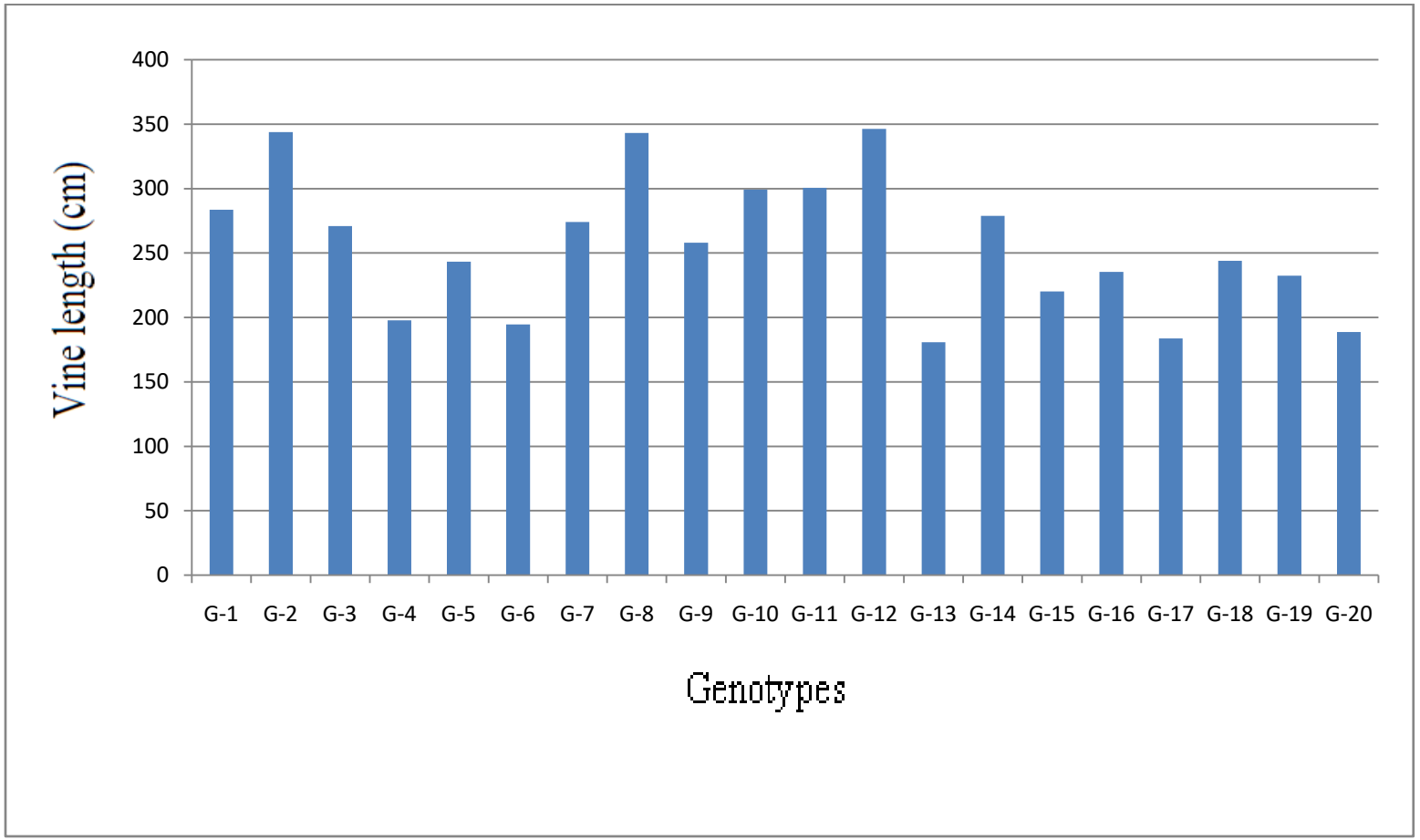

Fig 4.1 Performance of various genotype of chow-chow on vine length (cm)

Table 4.7 Performance of various genotypes of chow-chow on days to first flowering

Days to first flowering			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	154	153	153.5
Genotype-2	162.67	163.33	163
Genotype-3	155.33	152.67	154
Genotype-4	134	132.67	133.33
Genotype-5	157.33	156.33	156.83
Genotype-6	152.67	151.33	152
Genotype-7	154.33	151.33	152.83
Genotype-8	160	158	159
Genotype-9	151.33	147.67	149.5
Genotype-10	158.67	156.67	157.67
Genotype-11	158	157	157.5
Genotype-12	165.33	162.33	163.83
Genotype-13	151.33	149.67	150.5
Genotype-14	156	154	155
Genotype-15	157.33	155.67	156.5
Genotype-16	153.67	153	153.33
Genotype-17	168.67	164.67	166.67
Genotype-18	156	153.3	154.67
Genotype-19	153.33	153	153.17
Genotype-20	161	159.67	160.33
Mean			155.16
SEm(±)			0.65
CD at 5%			1.86
CV(%)			0.72

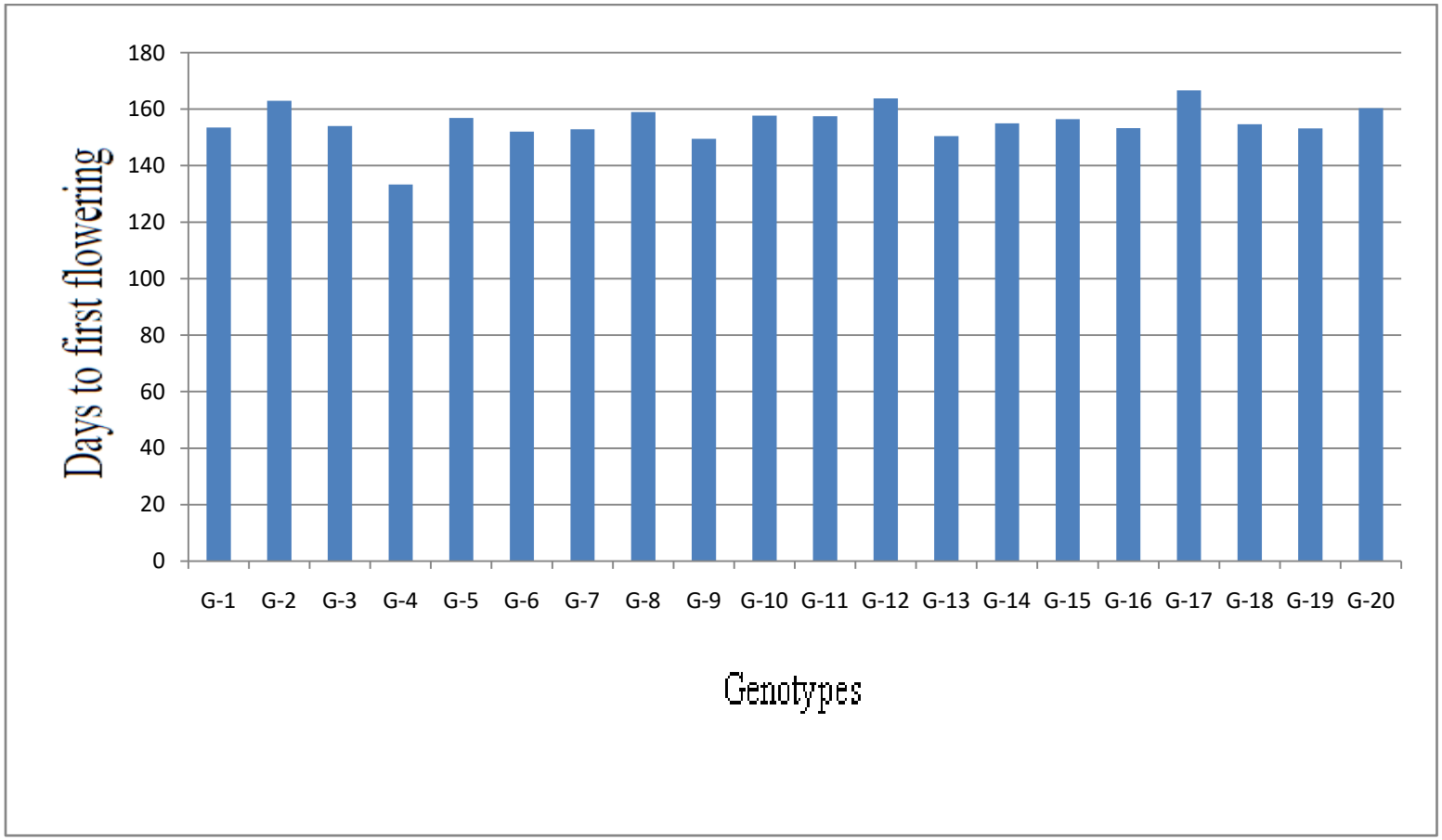

Fig 4.2 Performance of various genotype of chow-chow on days to first flowering

Table 4.8 Performance of various genotypes of chow-chow on number of nodes at first fruit set

Number of nodes at first fruit set			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	35.83	37.33	36.58
Genotype-2	40.67	40.33	40.5
Genotype-3	36.17	36.5	36.3
Genotype-4	25.67	26.83	26.25
Genotype-5	39.17	38.83	39
Genotype-6	32.5	32	32.5
Genotype-7	34	33.67	33.83
Genotype-8	43.5	34.17	38.83
Genotype-9	30.5	30.83	30.67
Genotype-10	40	40	40
Genotype-11	37.67	38.33	38
Genotype-12	41.83	43.67	42.75
Genotype-13	31.33	32	31.67
Genotype-14	35.5	36.67	36.08
Genotype-15	36.3	34	35.17
Genotype-16	32.5	33.33	32.92
Genotype-17	25.33	26.33	25.83
Genotype-18	29.33	27.33	28.33
Genotype-19	31.5	21.67	26.58
Genotype-20	31.97	31.33	31.65
Mean			34.16
SEm(±)			0.48
CD at 5%			1.37
CV(%)			2.43

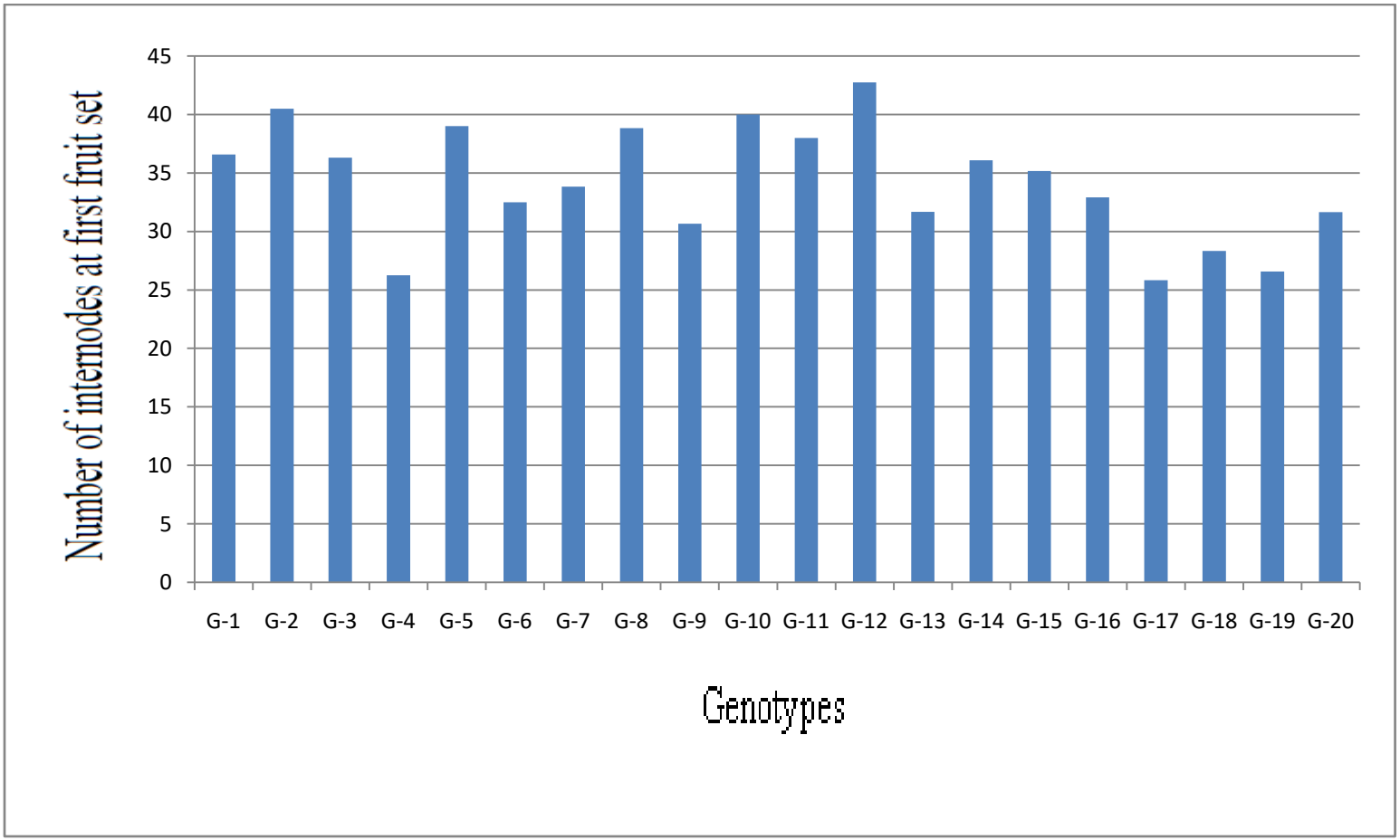

Fig 4.3 Performance of various genotype of chow-chow on number of internodes at first fruit set

4.2.4 Length of internodes (cm)

Table 4.9 and fig 4.4 depicted data on length of internodes (cm) measured using measuring scale. The depicted data shows that the genotypes differ significantly for internodal lengths. Highest internodal length was exhibited by G-12 (11.67 cm) followed by G-8 (11.17 cm) and G-2 (11.1 cm). However, minimum intermodal length was found in G-4 (9.03 cm). Similar findings were also reported by Kim *et al.* (2016).

4.2.5 Length of leaf (cm)

The data on length of leaf of different genotypes are shown in table 4.10 and fig 4.5. Different genotypes showed variable behavior for the length of leaf. The maximum leaf length was recorded from G-15 (22.8 cm) followed by G-8 (21.83 cm) and G-10 (21.18 cm). However, minimum length of leaf was found in G-4 (16.67 cm). Similar findings were also reported by Kim *et al.* (2016).

4.2.6 Width of leaf (cm)

The data on leaf width of different genotypes are shown in table 4.11 and fig 4.6. Leaf width of twenty chowchow genotypes were recorded using measuring scale and showed variable behavior for the leaf width. The maximum leaf width was recorded from G-15 (20.18 cm) followed by G-8 (18.36 cm) and G-10 (18.28 cm). However, minimum leaf width was found in G-17 (13.18 cm). Similar findings were also reported by Kim *et al.* (2016).

Table 4.9 Performance of various genotypes of chow-chow on length of internodes (cm)

Length of internodes (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	9.93	10.17	10.05
Genotype-2	10.87	11.33	11.1
Genotype-3	10.3	10.87	10.6
Genotype-4	9.03	9.03	9.03
Genotype-5	9.73	9.83	9.78
Genotype-6	9.23	9.8	9.52
Genotype-7	9.47	9.9	9.68
Genotype-8	11.73	10.6	11.17
Genotype-9	9.17	9.33	9.25
Genotype-10	9.8	10.13	9.67
Genotype-11	10.3	10.3	10.3
Genotype-12	11.8	11.53	11.67
Genotype-13	9.4	9.5	9.45
Genotype-14	9.63	9.73	9.68
Genotype-15	9.87	9.87	9.87
Genotype-16	9.87	10.3	10.08
Genotype-17	9.03	9.33	9.18
Genotype-18	9.33	9.33	9.33
Genotype-19	9.27	9.4	9.33
Genotype-20	8.93	9.17	9.05
Mean			9.91
SEm(±)			0.10
CD at 5%			0.29
CV(%)			1.79

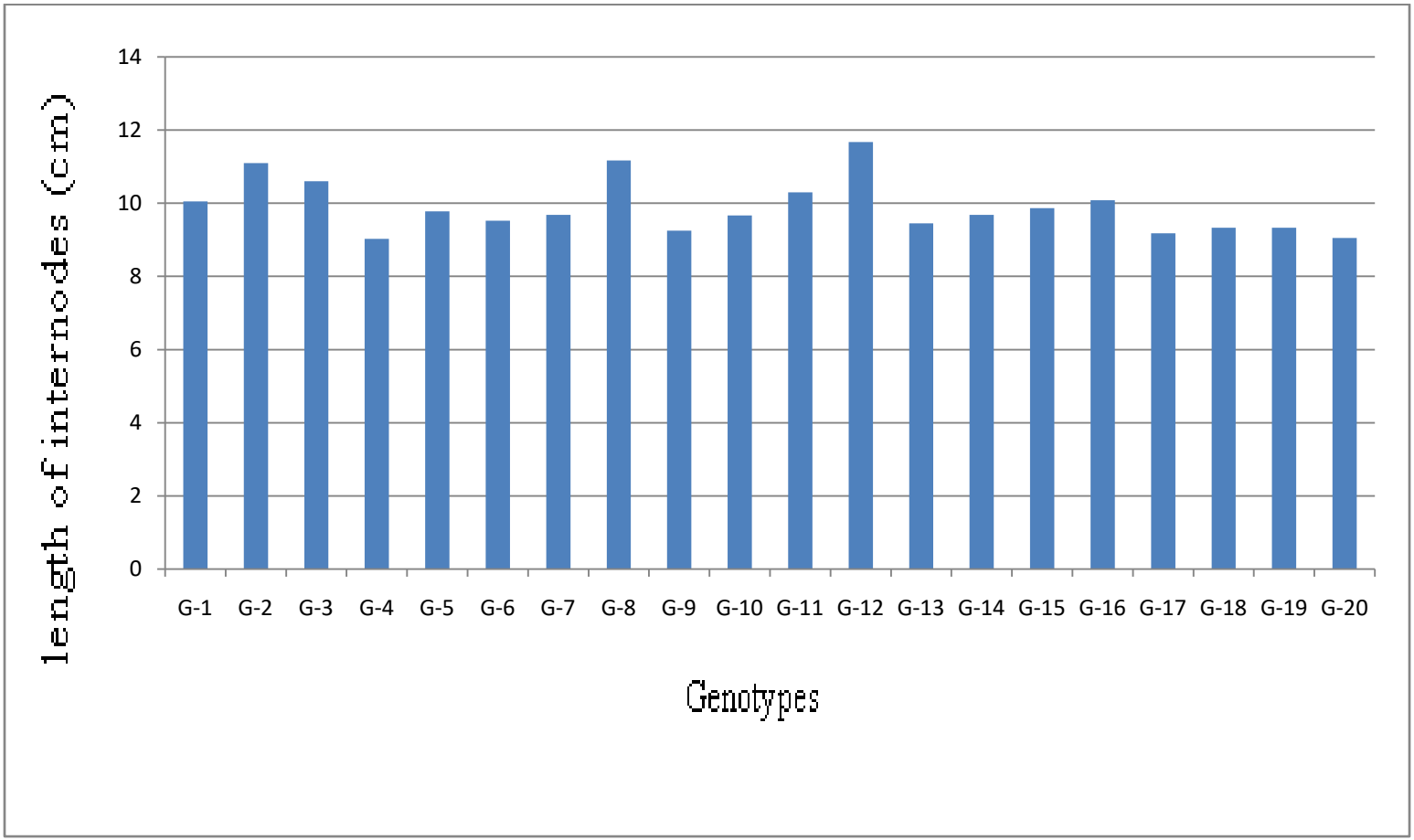

Fig 4.4 Performance of various genotype of chow-chow on length of internodes (cm)

Table 4.10 Performance of various genotypes of chow-chow on length of leaf (cm)

Length of leaf (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	19.2	19.27	19.23
Genotype-2	20.5	20.63	20.57
Genotype-3	18.9	18.97	18.93
Genotype-4	16.63	16.7	16.67
Genotype-5	20.8	21.07	20.93
Genotype-6	17.77	17.8	19.83
Genotype-7	18.43	18.43	18.43
Genotype-8	21.8	21.87	21.83
Genotype-9	17.67	17.6	17.63
Genotype-10	21.07	21.3	21.18
Genotype-11	19.73	19.67	19.85
Genotype-12	21.07	21.1	21.08
Genotype-13	17.3	17.3	17.3
Genotype-14	19.7	20.03	19.87
Genotype-15	22.73	22.87	22.8
Genotype-16	17.6	17.7	17.65
Genotype-17	16.63	16.93	16.78
Genotype-18	18.03	18.1	18.07
Genotype-19	18.9	19.03	18.97
Genotype-20	18.07	18.1	18.08
Mean			20.12
SEm(±)			0.26
CD at 5%			0.77
CV(%)			2.43

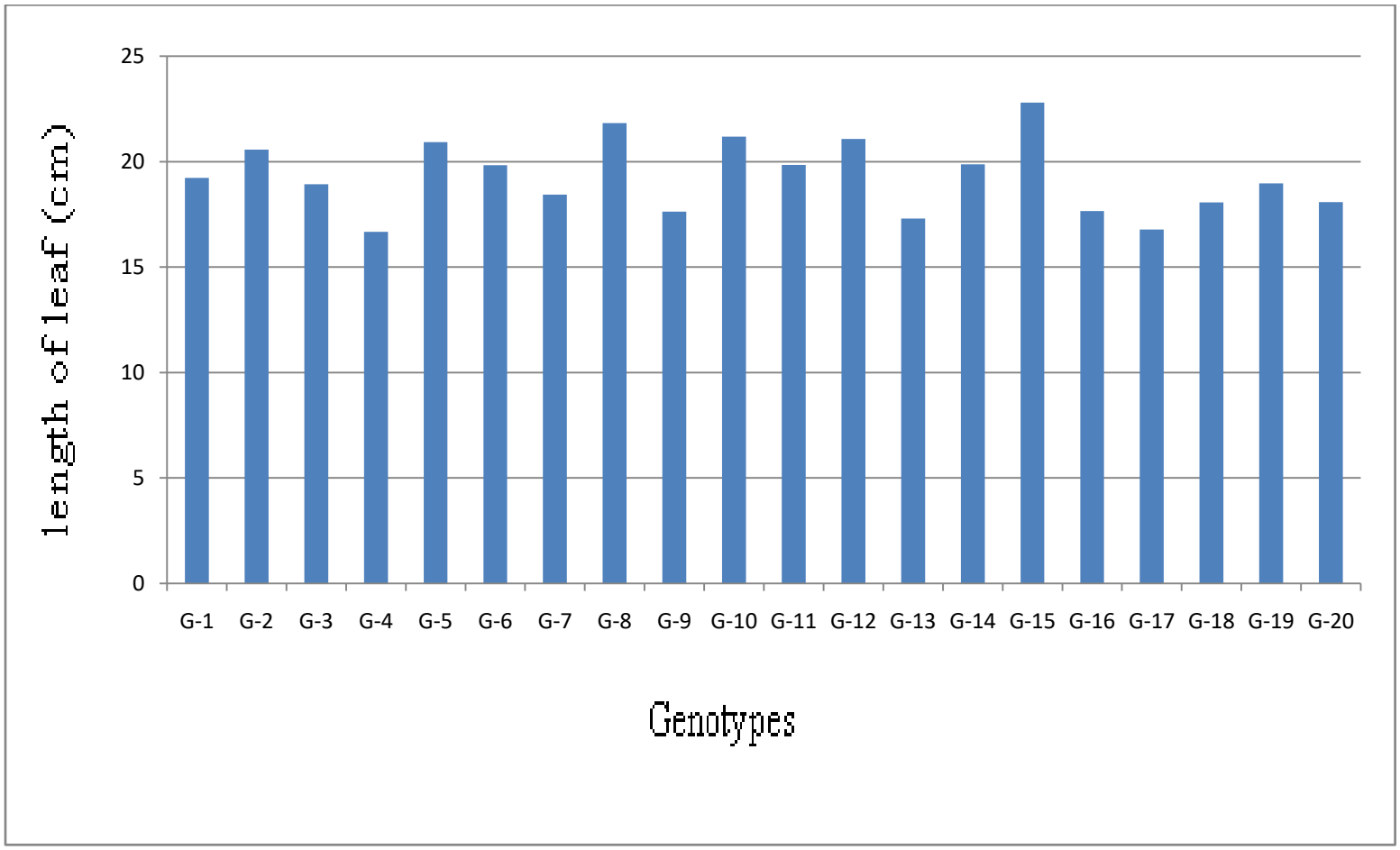

Fig 4.5 Performance of various genotype of chow-chow on length of leaf (cm)

Table 4.11 Performance of various genotypes of chow-chow on width of leaf (cm)

Width of leaf (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	16.1	16.2	16.15
Genotype-2	16.77	16.83	16.8
Genotype-3	13.63	13.77	13.7
Genotype-4	13.67	13.73	13.7
Genotype-5	16.87	16.93	16.9
Genotype-6	14.4	14.47	14.43
Genotype-7	15.97	16.03	16
Genotype-8	18.3	18.42	18.36
Genotype-9	14.5	14.53	14.52
Genotype-10	18.23	18.33	18.28
Genotype-11	16.23	16.33	16.28
Genotype-12	17.37	17.4	17.38
Genotype-13	14.23	14.27	14.25
Genotype-14	16.3	16.37	16.3
Genotype-15	20.17	20.2	20.18
Genotype-16	14.9	14.9	14.9
Genotype-17	13.33	13.23	13.18
Genotype-18	13.87	13.87	13.8
Genotype-19	13.33	13.4	13.67
Genotype-20	15.13	15.2	15.17
Mean			15.70
SEm(±)			0.16
CD at 5%			0.47
CV(%)			1.82

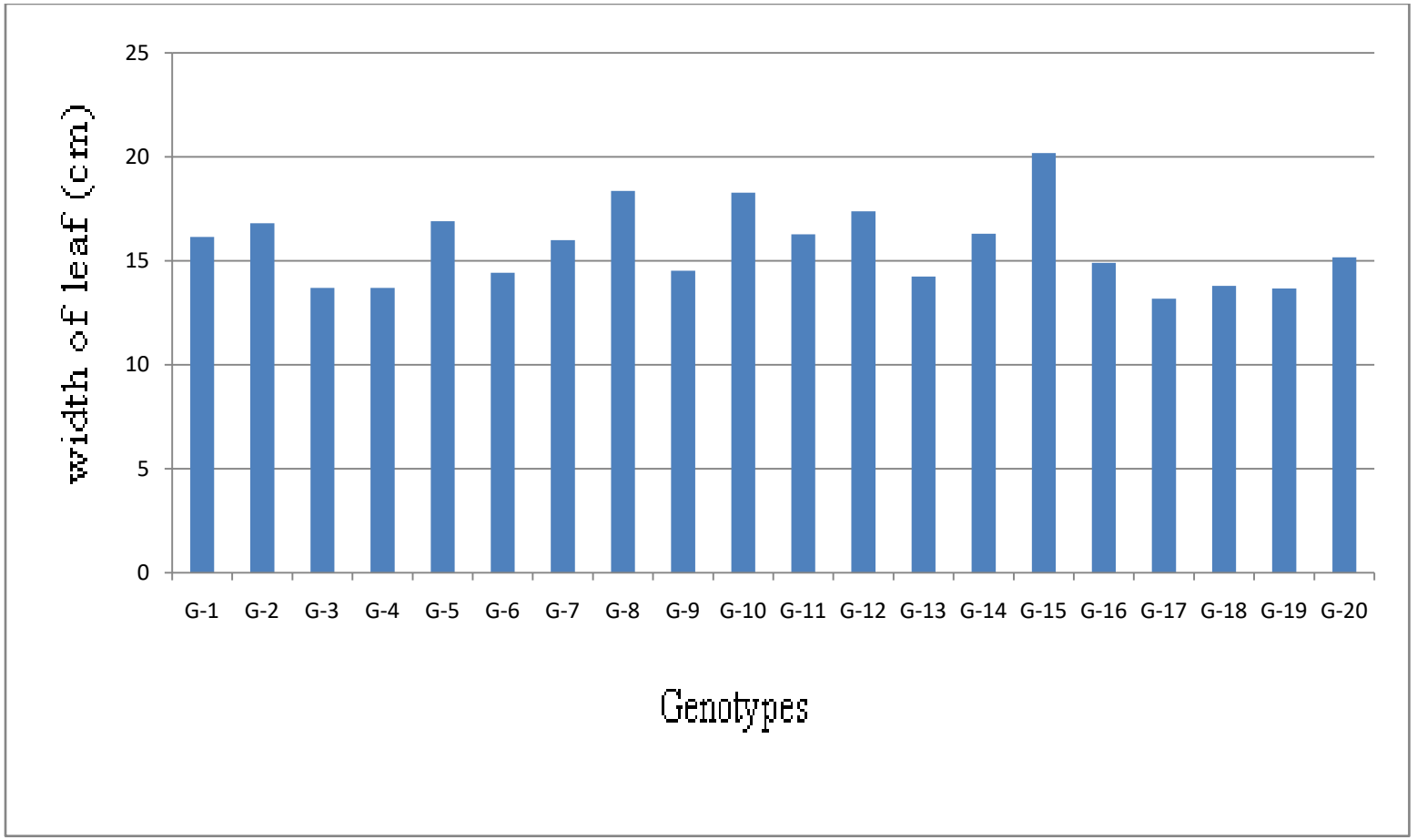

Fig 4.6 Performance of various genotype of chow-chow on width of leaf (cm)

4.2.7 Petiole length (cm)

The observations taken for petiole length are given in table 4.12 and fig 4.7. Petiole length of twenty chowchow genotypes were visually recorded using measuring scale and ranged from 9.82 cm to 12.25 cm. Maximum petiole length was recorded in G- 8 (12.25 cm) and minimum was recorded in G-18 (9.82 cm). Similar findings were also reported by Kim *et al.* (2016).

4.2.8 Number of fruits per plant

The data pertaining to number of fruits per plant of chow-chow genotypes has been presented in table 4.13 and fig 4.8. The pooled results recorded significant variation in number of fruits per plant and it ranged from 5.92 to 11.42. The maximum number of fruits per plant was recorded in G-14 (11.42) and G-18 (11.42) followed by G-17 (11.00) and G-1 (10.83) while the minimum was recorded in G-20 (5.92). Similar findings were also reported by Sanwal *et al.* (2008) and Sanwal *et al.* (2010).

4.2.9 Fruit weight (g)

The data pertaining to fruit weight has presented in the table 4.14 and fig 4.9. The pooled results recorded significant variation in number of fruits per plant and it ranged from 64.33 g to 474 g. The maximum average fruit weight was recorded in G-15 (474 g) followed by G-8 (465.83 g) and G-12 (345.33 g) while minimum fruit weight was recorded in G-4 (64.33 g). Similar findings were also reported by Sanwal *et al.* (2008), Sanwal *et al.* (2010), Kapoor *et al.* (2014), Mishra and Das (2015), Kim *et al.* (2016) and Verma *et al.* (2017).

Table 4.12 Performance of various genotypes of chow-chow on petiole length (cm)

Petiole length (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	11.67	12.17	11.92
Genotype-2	11.93	12.03	11.98
Genotype-3	11.4	11.63	11.52
Genotype-4	10.43	10.53	10.48
Genotype-5	11.1	11.17	11.13
Genotype-6	10.53	10.87	10.7
Genotype-7	10.27	10.73	10.5
Genotype-8	11.97	12.53	12.25
Genotype-9	10.87	11.13	11
Genotype-10	11	11	11
Genotype-11	10.08	11.03	10.92
Genotype-12	11.43	11.6	11.52
Genotype-13	10.33	10.6	10.47
Genotype-14	10.1	10.2	10.15
Genotype-15	11.57	11.47	11.52
Genotype-16	10.93	11.2	11.07
Genotype-17	10.8	10.53	10.67
Genotype-18	9.6	10.03	9.82
Genotype-19	9.93	9.67	9.95
Genotype-20	10.4	10.6	10.5
Mean			10.95
SEm(±)			0.26
CD at 5%			0.74
CV(%)			4.13

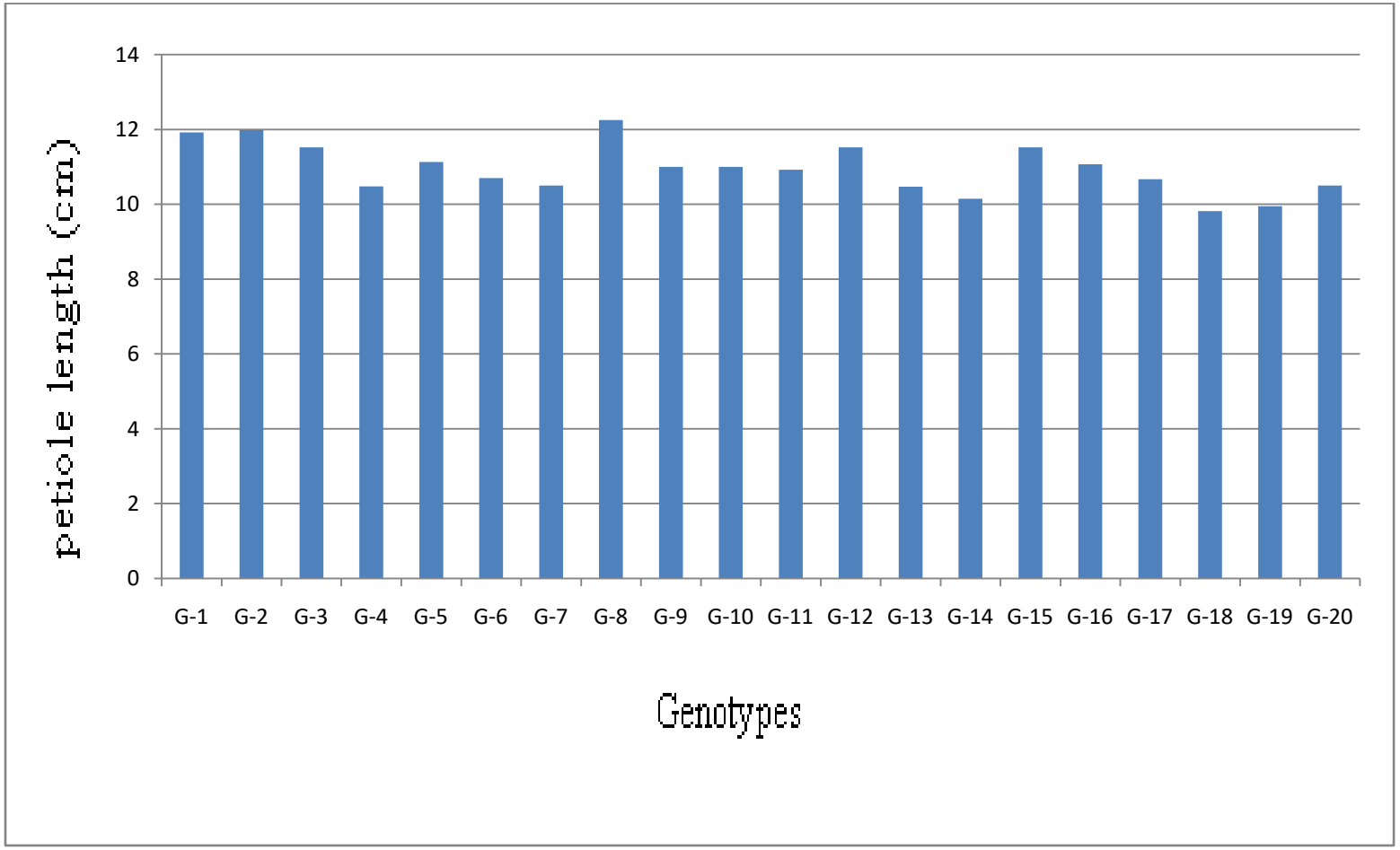

Fig 4.7 Performance of various genotype of chow-chow on petiole length (cm)

Table 4.13 Performance of various genotypes of chow-chow on number of fruits per plant

Number of fruits per plant			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	10.83	10.83	10.83
Genotype-2	7.3	7.83	7.58
Genotype-3	6.5	6.83	6.67
Genotype-4	9.3	9.83	9.58
Genotype-5	8.17	8.33	8.25
Genotype-6	8.67	9	8.92
Genotype-7	9.17	9.33	9.25
Genotype-8	6.17	6.5	6.33
Genotype-9	8.17	8.33	8.25
Genotype-10	8.33	8.67	8.5
Genotype-11	10	10.17	10.08
Genotype-12	6.83	7.17	7
Genotype-13	6.17	6.33	6.25
Genotype-14	11.33	11.5	11.42
Genotype-15	6.17	6.5	6.33
Genotype-16	8.17	8.33	8.25
Genotype-17	10.83	11.17	11
Genotype-18	11.33	11.5	11.42
Genotype-19	6.17	6.33	6.25
Genotype-20	5.83	6	5.92
Mean			8.40
SEm(±)			0.28
CD at 5%			0.82
CV(%)			5.90

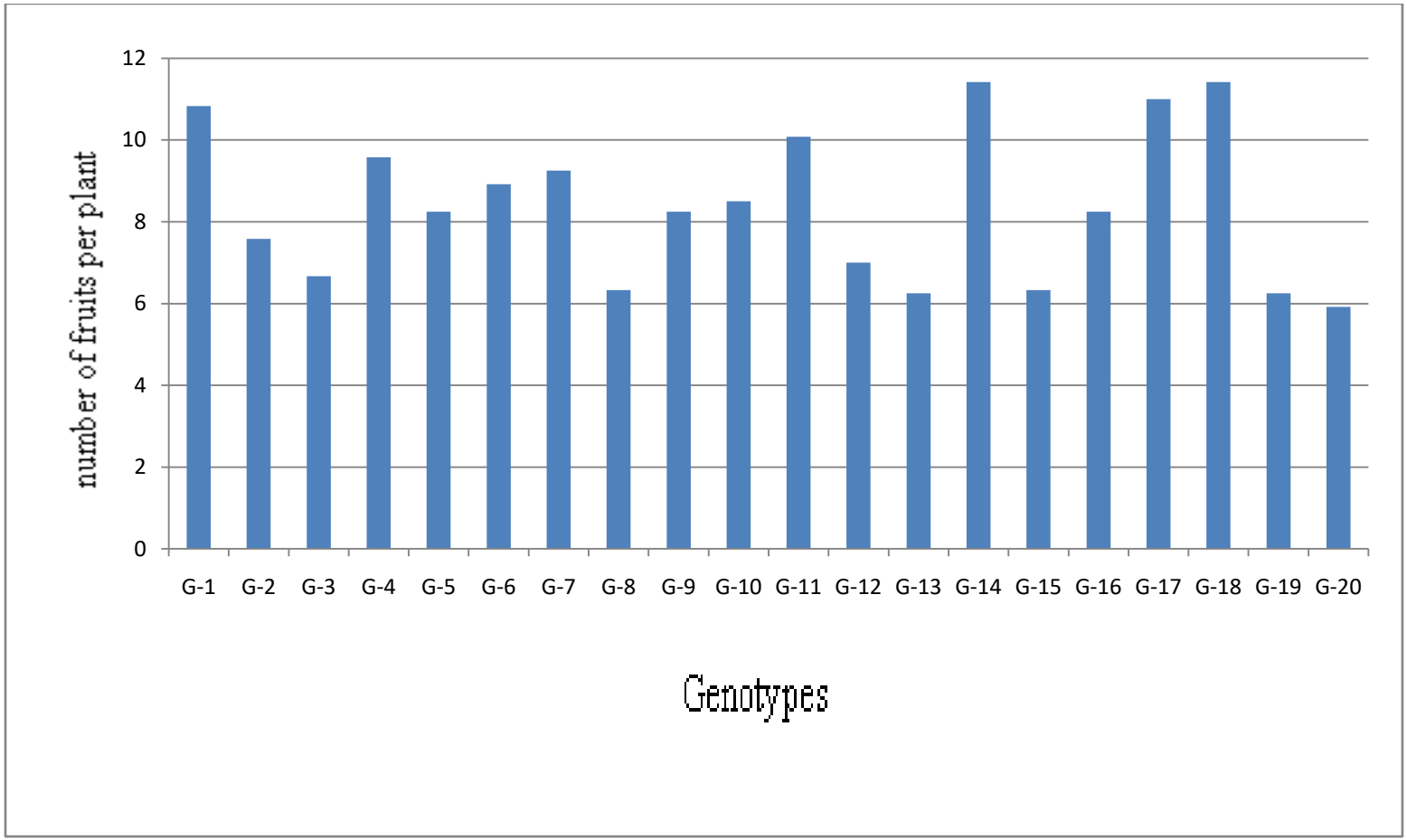

Fig 4.8 Performance of various genotype of chow-chow on number of fruits per plant

Table 4.14 Performance of various genotypes of chow-chow on fruit weight (g)

Fruit weight (g)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	101	101.67	101.33
Genotype-2	306.67	307.33	307
Genotype-3	215	219	217
Genotype-4	64	64.67	64.33
Genotype-5	225	223.33	224.17
Genotype-6	123.33	124.67	124
Genotype-7	251	256.67	253.83
Genotype-8	461	470.67	465.83
Genotype-9	291.67	294.67	293.17
Genotype-10	237.67	243.33	240.5
Genotype-11	212.67	217.33	215
Genotype-12	344	346.67	345.33
Genotype-13	251	256.67	253.83
Genotype-14	152.67	153.67	153.16
Genotype-15	468.67	479.33	474
Genotype-16	197.67	204.67	201.67
Genotype-17	163.67	168.33	166
Genotype-18	169.67	172.67	171.17
Genotype-19	266.67	271.33	269
Genotype-20	247	253.33	250.17
Mean			239.52
SEm(±)			3.77
CD at 5%			10.81
CV(%)			2.73

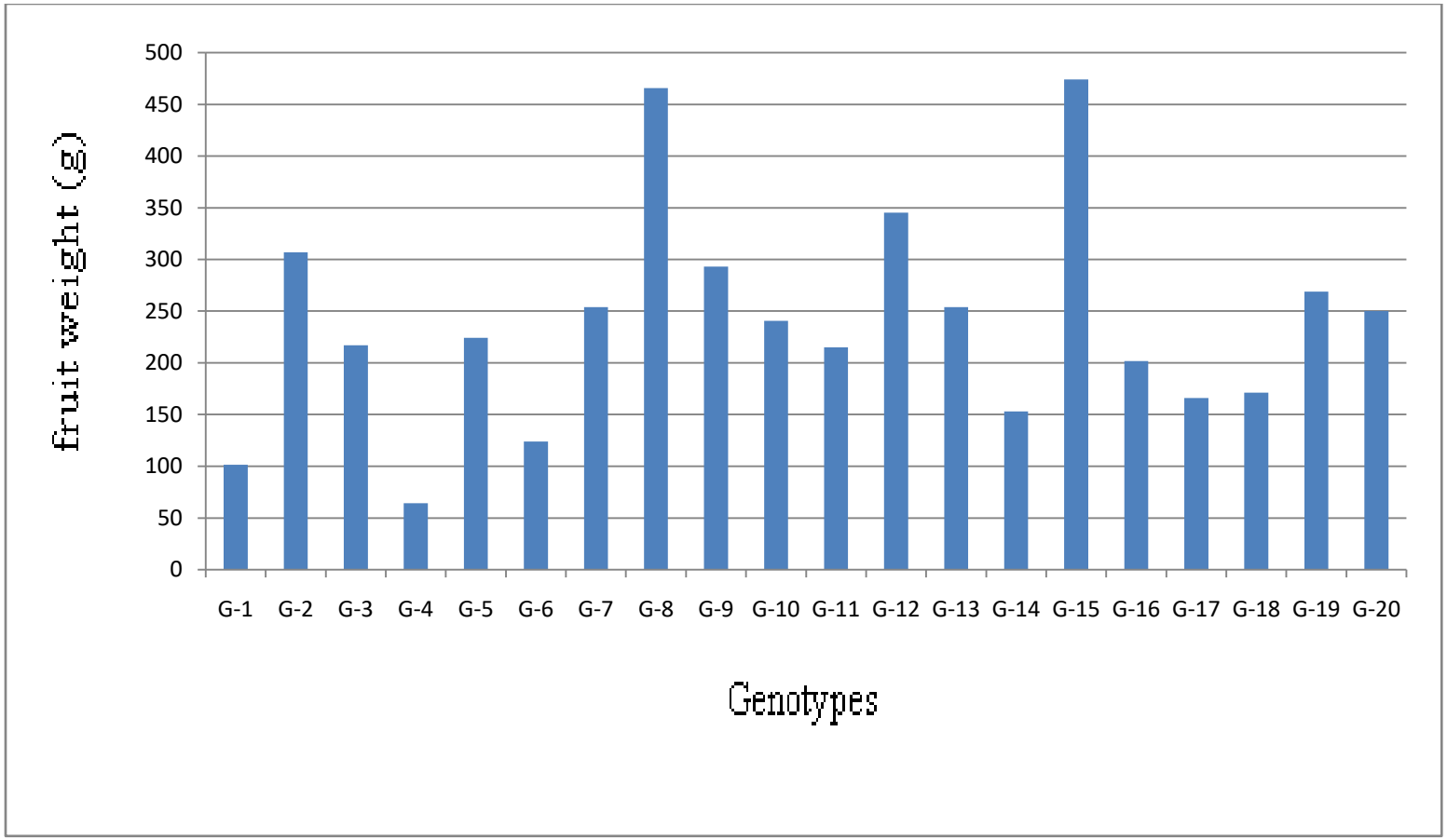

Fig 4.9 Performance of various genotype of chow-chow on fruit weight (g)

4.2.10 Fruit length (cm)

Fruit length of 20 chow-chow genotypes is presented in the table 4.15 and fig 4.10. The fruit was cut in to two halves and length was measured using measuring scale. The maximum fruit length was recorded in G-15 (20.00 cm) followed by G-8 (18.63 cm) and G-5 (17 cm). However, minimum fruit length was recorded in G-4 (6.95 cm). Similar findings were also reported by Sanwal *et al.* (2008), Sanwal *et al.* (2010), Kapoor *et al.* (2014), Mishra and Das (2015), Kim *et al.* (2016) and Verma *et al.* (2017).

4.2.11 Fruit diameter (cm)

Fruit diameter of 20 chow-chow genotypes were recorded using vernier caliper when the fruit attain marketable maturity is as shown in table 4.16 and fig 4.11. The fruit was cut in to two halves and diameter was measured using measuring scale. The maximum fruit diameter was recorded in G-11 (10.62 cm) followed by G-5 (10.53 cm) and G-20 (10.23 cm). However, minimum fruit length was found in G-4 (6.02 cm). Similar findings were also reported by Sanwal *et al.* (2008), Sanwal *et al.* (2010), Mishra and Das (2015) and Verma *et al.* (2017).

4.2.12 Fat (mg $100g^{-1}$)

Fat content of 20 genotypes of chow-chow is presented in the table 4.17 and fig 4.12. Maximum fat content was recorded in G-3 (141.67 mg $100g^{-1}$), G-8 (137.33 mg $100g^{-1}$), G-16 (135.83 mg $100g^{-1}$) and minimum was recorded in G-9 (103.33 mg $100g^{-1}$). Similar findings were also reported by Saade (1996), Cadena-Iniguez *et al.* (2007), Singh *et al.* (2015) and Verma *et al.* (2017).

Table 4.15 Performance of various genotypes of chow-chow on fruit length (cm)

Fruit length (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	10.93	11.03	10.98
Genotype-2	16.17	16.23	16.2
Genotype-3	12.83	12.9	12.87
Genotype-4	6.9	7	6.95
Genotype-5	16.97	17.03	17
Genotype-6	12.03	12.1	12.07
Genotype-7	12.5	12.67	12.58
Genotype-8	18.53	18.73	18.63
Genotype-9	15.9	16	15.9
Genotype-10	11.2	11.33	11.27
Genotype-11	11.8	11.87	11.83
Genotype-12	15.5	15.6	15.55
Genotype-13	14.57	15	14.78
Genotype-14	10.43	10.6	10.52
Genotype-15	19.8	20.2	20
Genotype-16	13.8	13.87	13.83
Genotype-17	10.4	10.57	10.48
Genotype-18	14.03	14.13	14.08
Genotype-19	14.77	14.97	14.87
Genotype-20	13.3	13.3	13.3
Mean			13.68
SEm(±)			0.55
CD at 5%			1.58
CV(%)			7.00

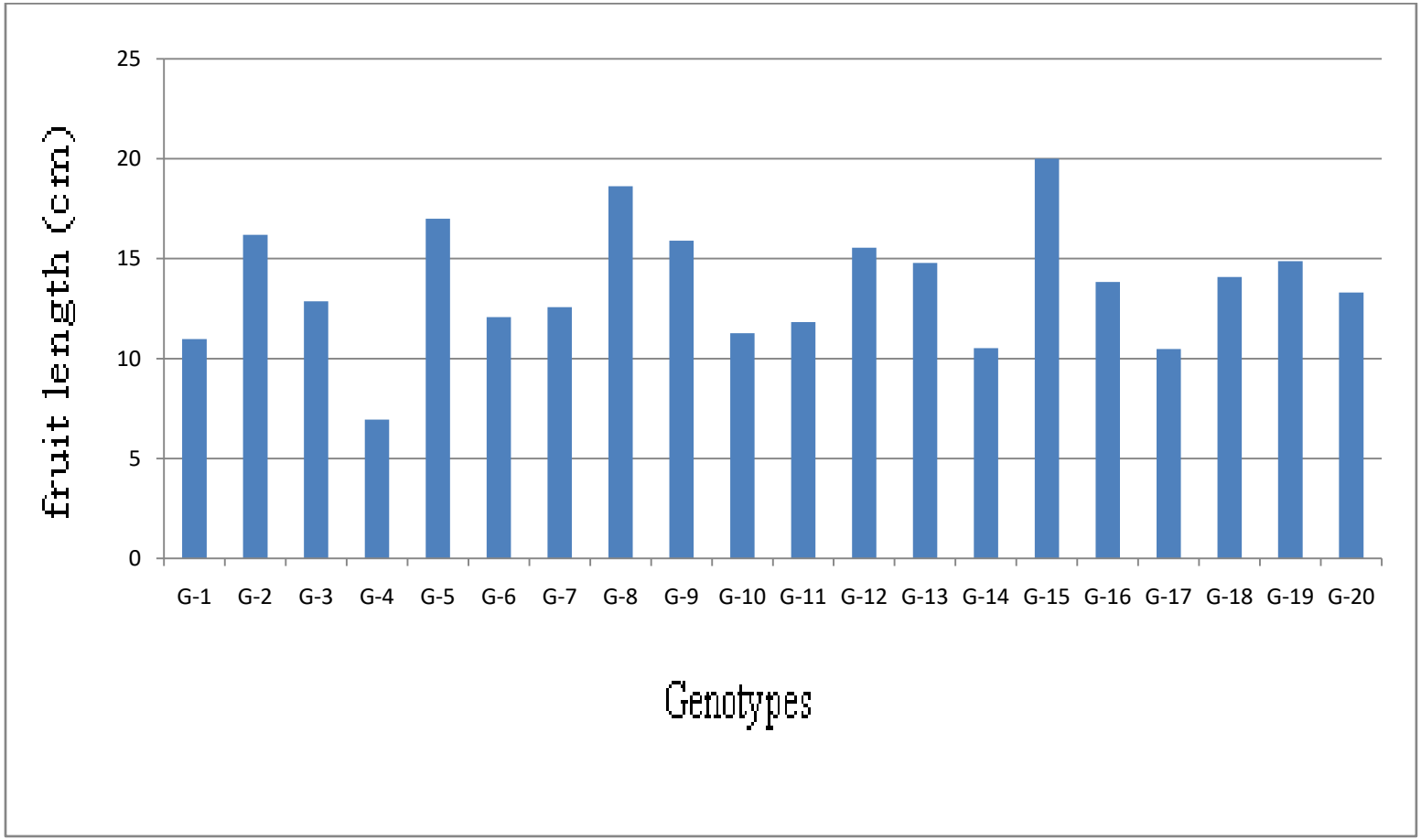

Fig 4.10 Performance of various genotype of chow-chow on fruit length (cm)

Table 4.16 Performance of various genotypes of chow-chow on fruit diameter (cm)

Fruit diameter (cm)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	6.23	6.27	6.25
Genotype-2	7.87	8.03	7.95
Genotype-3	6.57	6.63	6.6
Genotype-4	6	6.03	6.02
Genotype-5	10.43	10.63	10.53
Genotype-6	8.17	8.27	8.22
Genotype-7	8.83	8.63	8.73
Genotype-8	9.23	9.3	9.27
Genotype-9	8.53	8.63	8.58
Genotype-10	8.13	8.2	8.17
Genotype-11	10.57	10.67	10.62
Genotype-12	8.13	8.17	8.15
Genotype-13	6.67	6.73	6.7
Genotype-14	6.9	6.93	6.92
Genotype-15	9	9.03	9.02
Genotype-16	8.4	8.23	8.32
Genotype-17	6.43	6.23	6.33
Genotype-18	7.23	7.33	7.28
Genotype-19	8.67	8.73	8.7
Genotype-20	6.97	13.5	10.23
Mean			8.13
SEm(±)			0.62
CD at 5%			1.77
CV(%)			13.40

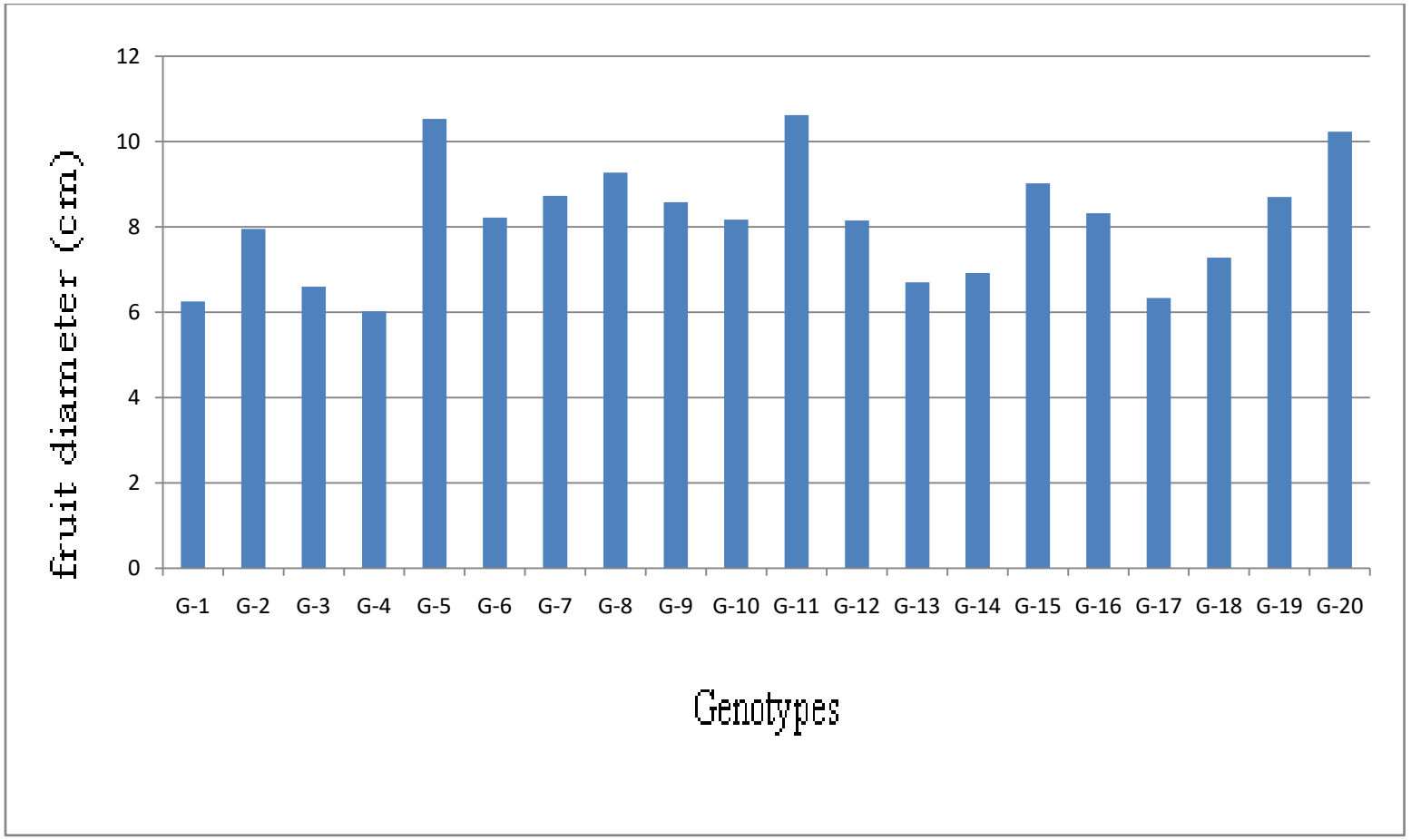

Fig 4.11 Performance of various genotype of chow-chow on fruit diameter (cm)

Table 4.17 Performance of various genotypes of chow-chow on fat (mg $100g^{-1}$)

Fat (mg $100g^{-1}$)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	122	123	122.5
Genotype-2	115.67	115.67	115.67
Genotype-3	143	140.33	141.67
Genotype-4	134	133	133.5
Genotype-5	124.33	124.67	124.5
Genotype-6	119.33	118.33	118.83
Genotype-7	106	105.67	105.83
Genotype-8	138	136.67	137.33
Genotype-9	104.67	102	103.33
Genotype-10	112	111.33	111.67
Genotype-11	113.67	112.33	113
Genotype-12	114.67	112	113.33
Genotype-13	107	107.33	107.17
Genotype-14	113.33	114.33	113.83
Genotype-15	105.33	104.67	105
Genotype-16	135	136.67	135.83
Genotype-17	124	123	123.5
Genotype-18	116.33	118	117.17
Genotype-19	123.67	124.33	124
Genotype-20	117	117	117
Mean			119.23
SEm(±)			0.16
CD at 5%			0.48
CV(%)			2.00

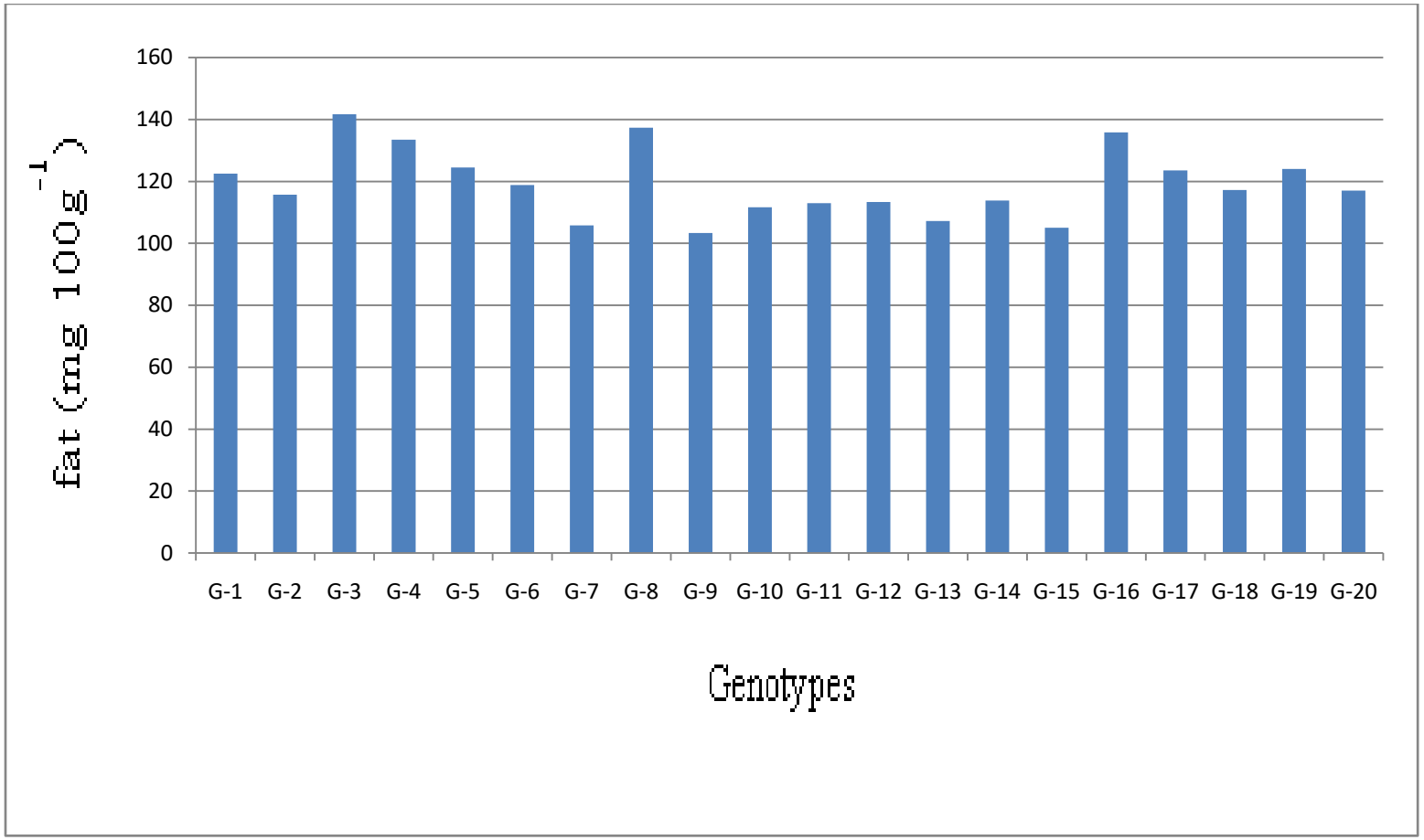

Fig 4.12 Performance of various genotype of chow-chow on fat (mg $100g^{-1}$)

4.2.13 Vitamin C (mg $100g^{-1}$)

The data pertaining to ascorbic acid of chow-chow genotypes has been presented in the table 4.18 and 4.13. The pooled results recorded maximum Vitamin C (22.1 mg $100g^{-1}$) in G-9 followed by G-13 (21.80 mg $100g^{-1}$), G-14 (21.62 mg $100g^{-1}$) and minimum was recorded in G-16 (10.23 mg $100g^{-1}$). Similar findings were also reported by Saade (1996), Sanwal *et al.* (2008), Sanwal *et al.* (2010), Mishra and Das (2015), Singh *et al.* (2015) and Verma *et al.* (2017).

4.2.14 Moisture (%)

The data pertaining to moisture content of chow-chow genotypes has been presented in the table 4.19 and fig 4.14. The pooled results recorded maximum moisture content in G-8 (94.18%) followed by G-12 (93.45%), G-6 (93.42%) and minimum was recorded in G-7 (90.7%). Similar findings were also reported by Cadena-Iniguez *et al.* (2007), Mishra and Das (2015) and Singh *et al.* (2015).

4.2.15 Carbohydrate (%)

The data pertaining to carbohydrate content of chow-chow genotypes has been presented in the table 4.20 and fig 4.15. The pooled results recorded maximum carbohydrate content in G-15 (4.81%), G-12 (4.78%), G-18 (4.72%) and minimum was recorded in G-14 (4.19%). Similar findings were also reported by Cadena-Iniguez *et al.* (2007), Mishra and Das (2015) and Singh *et al.* (2015).

Table 4.18 Performance of various genotypes of chow-chow on vitamin C (mg $100g^{-1}$)

Vitamin C (mg $100g^{-1}$)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	14.33	14.47	14.4
Genotype-2	16.87	16.77	16.82
Genotype-3	12.63	12.6	12.62
Genotype-4	16.73	16.83	16.78
Genotype-5	17.23	17.27	17.25
Genotype-6	16.9	16.93	16.92
Genotype-7	16.47	16.63	16.55
Genotype-8	12.57	12.4	12.48
Genotype-9	21.97	22.23	22.1
Genotype-10	18.77	18.93	18.85
Genotype-11	17.23	17.13	17.18
Genotype-12	17.33	17.37	17.35
Genotype-13	21.77	21.83	21.8
Genotype-14	21.53	21.7	21.62
Genotype-15	19.3	19.43	19.37
Genotype-16	10.17	10.3	10.23
Genotype-17	19.23	19.27	19.25
Genotype-18	17.67	17.8	17.73
Genotype-19	18.37	18.3	18.33
Genotype-20	19.3	19.43	19.37
Mean			17.35
SEm(±)			1.47
CD at 5%			4.23
CV(%)			2.14

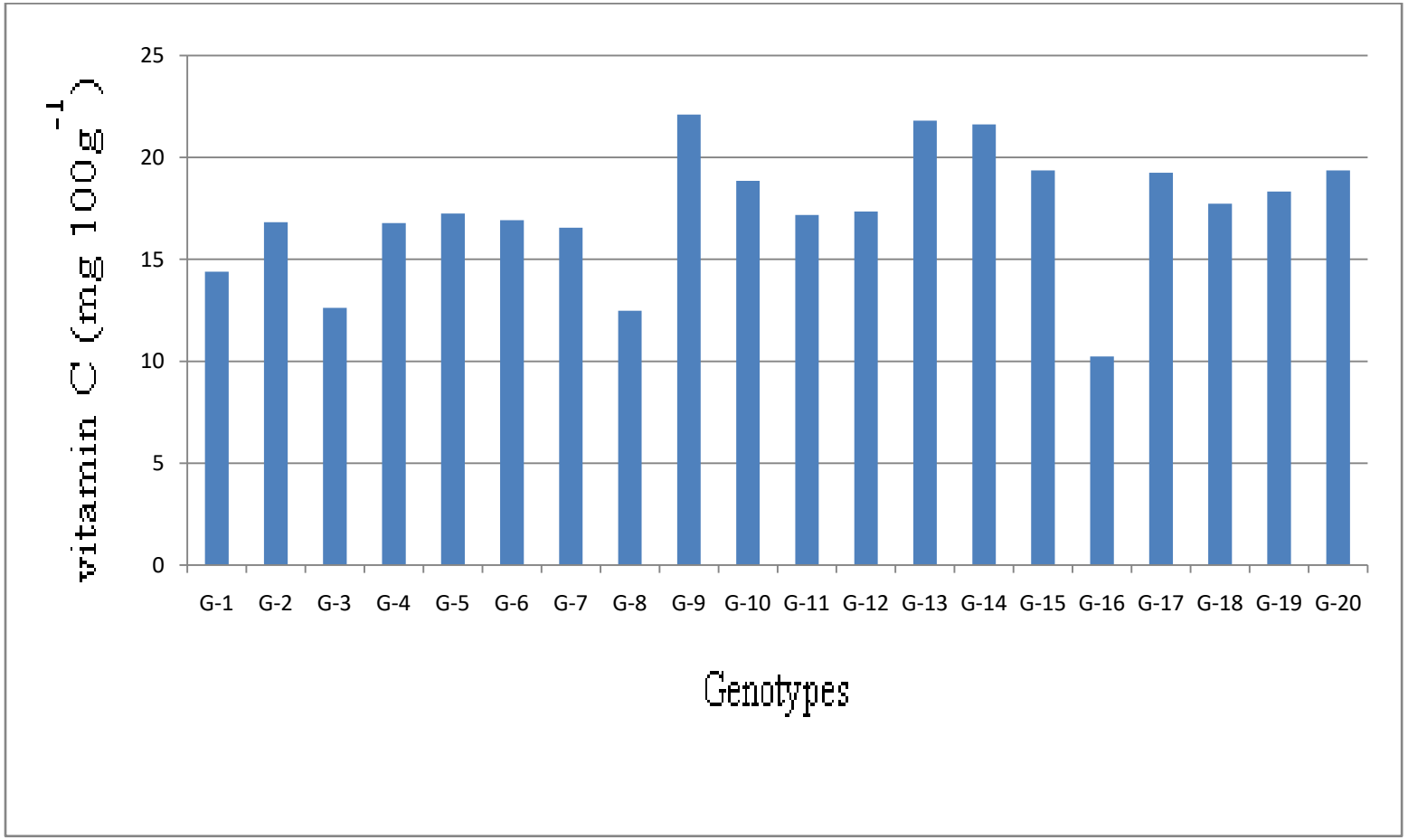

Fig 4.13 Performance of various genotype of chow-chow on vitamin C (mg 100g^{-1})

Table 4.19 Performance of various genotypes of chow-chow on moisture (%)

Moisture (%)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	91.17	91.3	91.23
Genotype-2	90.9	91.03	90.97
Genotype-3	93.1	93.13	93.12
Genotype-4	92.63	92.37	92.5
Genotype-5	91.6	92.1	91.85
Genotype-6	93.4	93.43	93.42
Genotype-7	90.5	90.9	90.7
Genotype-8	94.4	93.97	94.18
Genotype-9	91.1	91.17	91.13
Genotype-10	91.53	90.77	91.15
Genotype-11	90.87	91.07	90.97
Genotype-12	93.57	93.33	93.45
Genotype-13	92.57	92.27	92.42
Genotype-14	92.7	92.57	92.63
Genotype-15	93.17	93.5	93.33
Genotype-16	91.3	91.57	91.43
Genotype-17	93.17	93.43	93.33
Genotype-18	92.13	92.43	92.28
Genotype-19	91.57	92.13	91.85
Genotype-20	91.07	91.4	91.23
Mean			92.16
SEm(±)			0.08
CD at 5%			0.25
CV(%)			0.87

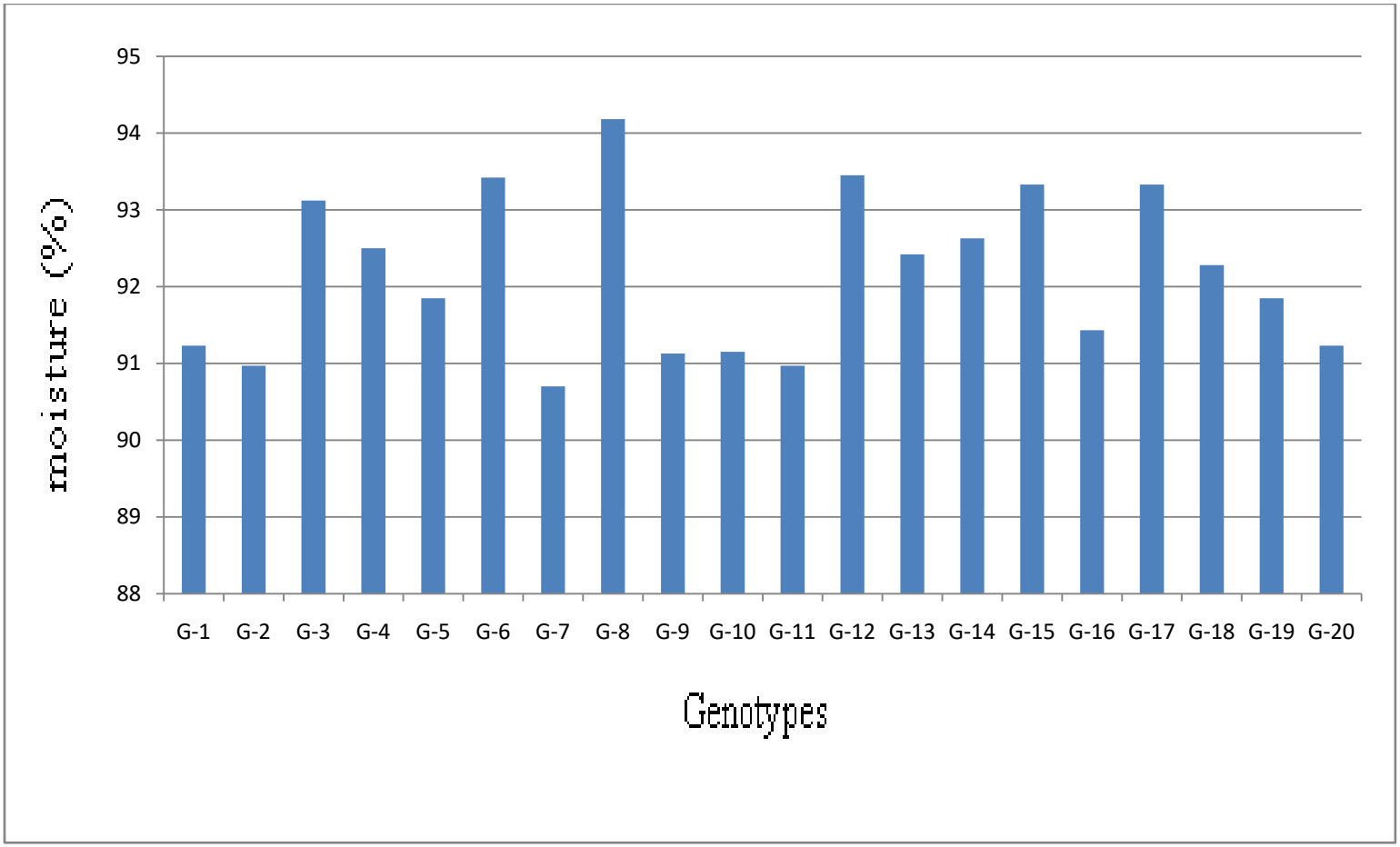

Fig 4.14 Performance of various genotype of chow-chow on moisture (%)

Table 4.20 Performance of various genotypes of chow-chow on carbohydrate (%)

Carbohydrate (%)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	4.23	4.23	4.23
Genotype-2	4.28	4.29	4.29
Genotype-3	4.26	4.26	4.26
Genotype-4	4.68	4.67	4.67
Genotype-5	4.44	4.44	4.44
Genotype-6	4.53	4.52	4.53
Genotype-7	4.4	4.4	4.4
Genotype-8	4.19	4.2	4.2
Genotype-9	4.43	4.44	4.44
Genotype-10	4.23	4.22	4.22
Genotype-11	4.51	4.5	4.51
Genotype-12	4.78	4.78	4.78
Genotype-13	4.38	4.38	4.38
Genotype-14	4.19	4.19	4.19
Genotype-15	4.81	4.8	4.81
Genotype-16	4.66	4.67	4.66
Genotype-17	4.42	4.42	4.42
Genotype-18	4.72	4.71	4.72
Genotype-19	4.4	4.42	4.41
Genotype-20	4.39	4.4	4.39
Mean			4.45
SEm(±)			0.02
CD at 5%			0.08
CV(%)			1.07

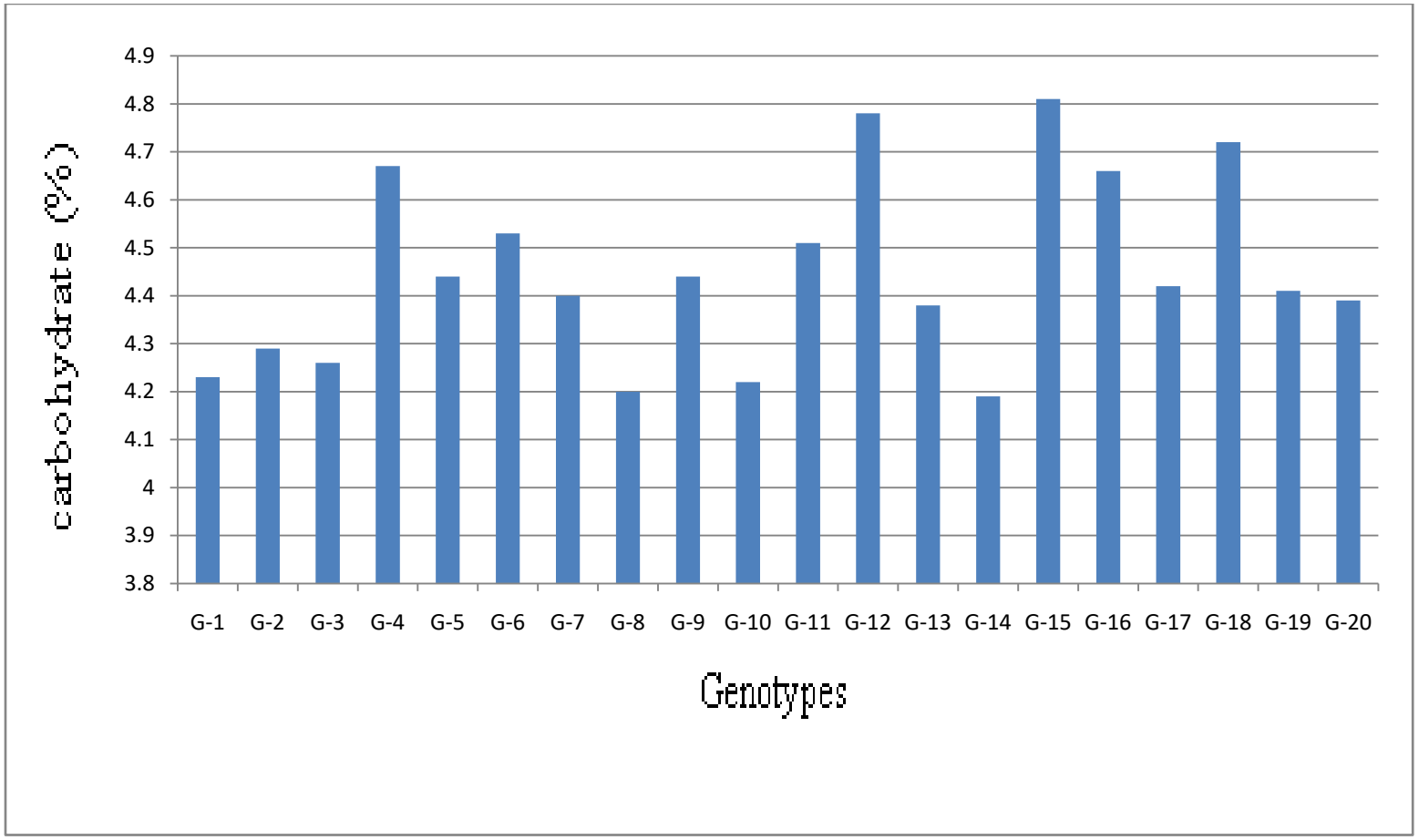

Fig 4.15 Performance of various genotype of chow-chow on carbohydrate (%)

4.2.16 Protein (%)

The observation on protein content of chow-chow genotypes has been presented in the table 4.21 and fig 4.16. The pooled results recorded maximum protein content (1.03%) in G-9 followed by G-13 and G-14 with (1.02%). Minimum content was recorded from G-1 and G-16 with (0.78%). Similar findings were also reported by Saade (1996), Cadena-Iniguez *et al.* (2007), Mishra and Das (2015) and Singh *et al.* (2015).

4.2.17 Crude fibre (%)

The observation on crude fibre of chow-chow genotypes has been presented in the table 4.22 and fig 4.17. The pooled results recorded maximum crude fibre (5.81%) in G-3 followed by G-8 (5.79%) and G-16 (5.78%). Minimum content was recorded from G-15 (4.89%). Similar findings were also reported by Saade (1996), Cadena-Iniguez *et al.* (2007), Mishra and Das (2015) and Singh *et al.* (2015).

4.2.18 Calcium (mg/100g)

The observation on calcium content of chow-chow genotypes has been presented in the table 4.23 and fig 4.18. The pooled results recorded maximum calcium content (16.41 mg) in G-2 followed by G-19 (16.26 mg) and G-7 (16.00 mg). Minimum content was recorded from G-9 (13.23 mg). Similar findings were also reported by Cadena-Iniguez *et al.* (2007), Singh *et al.* (2015) and Kim *et al.* (2016).

Table 4.21 Performance of various genotypes of chow-chow on protein (%)

Protein (%)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	0.78	0.78	0.78
Genotype-2	0.81	0.82	0.82
Genotype-3	0.83	0.8	0.82
Genotype-4	0.88	0.88	0.88
Genotype-5	0.87	0.87	0.87
Genotype-6	0.85	0.85	0.85
Genotype-7	0.83	0.84	0.83
Genotype-8	0.81	0.81	0.81
Genotype-9	1.03	1.03	1.03
Genotype-10	0.92	0.92	0.92
Genotype-11	0.87	0.87	0.87
Genotype-12	0.88	0.89	0.89
Genotype-13	1.02	1.02	1.02
Genotype-14	1.02	1.02	1.02
Genotype-15	0.91	0.89	0.9
Genotype-16	0.78	0.77	0.78
Genotype-17	0.94	0.93	0.94
Genotype-18	0.89	0.9	0.9
Genotype-19	0.9	0.91	0.91
Genotype-20	0.93	0.93	0.93
Mean			0.89
SEm(±)			0.17
CD at 5%			0.50
CV(%)			0.32

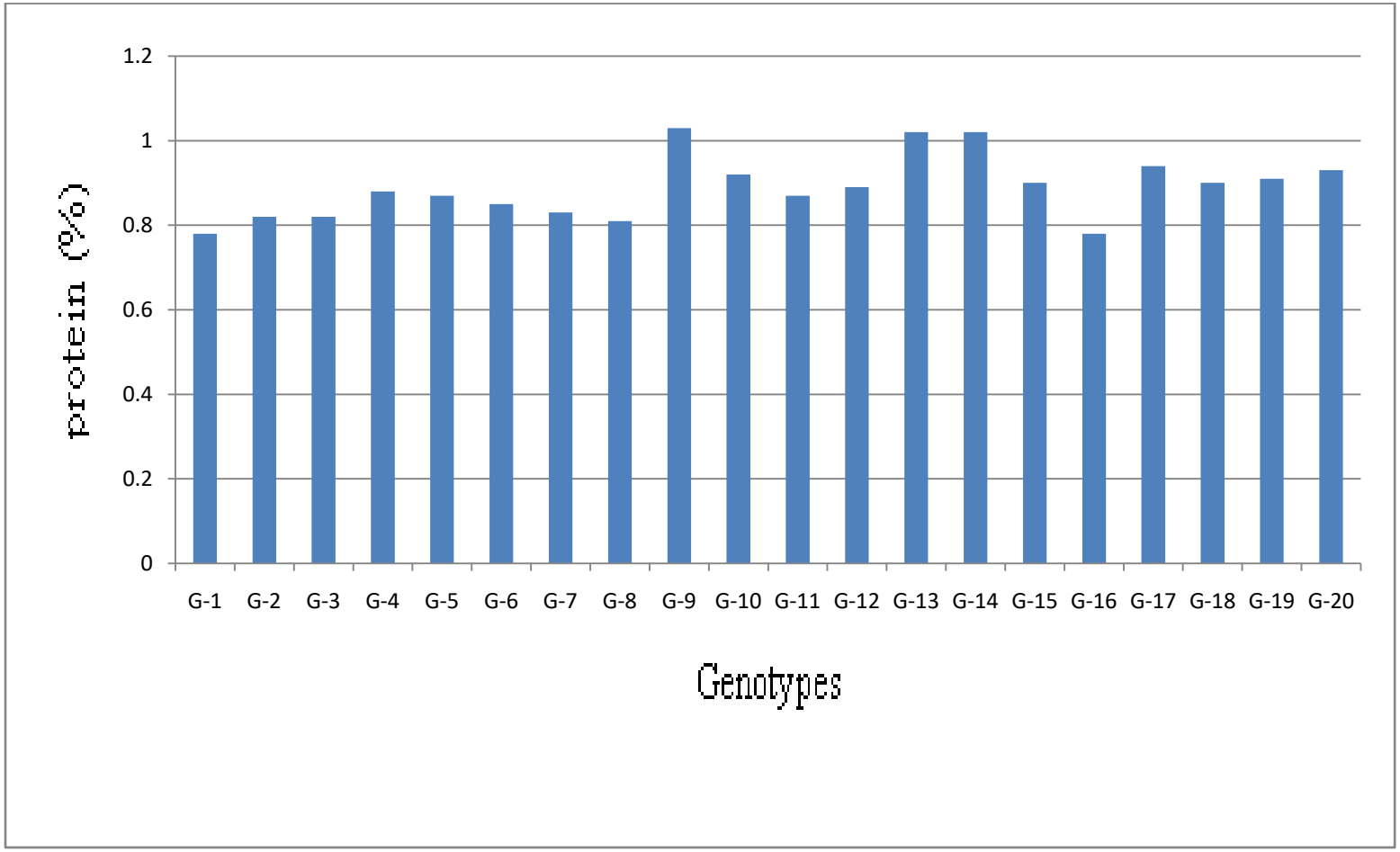

Fig 4.16 Performance of various genotype of chow-chow on protein (%)

Table 4.22 Performance of different genotypes of chow-chow on crude fibre (%)

Crude fibre (%)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	5.68	5.69	5.69
Genotype-2	5.05	5.06	5.06
Genotype-3	5.81	5.81	5.81
Genotype-4	5.6	5.59	5.6
Genotype-5	5.23	5.24	5.24
Genotype-6	5.06	5.07	5.07
Genotype-7	4.94	4.94	4.94
Genotype-8	5.79	5.79	5.79
Genotype-9	4.97	4.97	4.97
Genotype-10	4.98	5	4.99
Genotype-11	5.09	5.09	5.09
Genotype-12	5.11	5.11	5.11
Genotype-13	4.94	4.94	4.94
Genotype-14	4.96	4.97	4.97
Genotype-15	4.88	4.89	4.89
Genotype-16	5.78	5.78	5.78
Genotype-17	5.14	5.14	5.14
Genotype-18	5.45	5.45	5.45
Genotype-19	5.34	5.35	5.35
Genotype-20	5.16	5.16	5.16
Mean			5.25
SEm(±)			0.01
CD at 5%			0.02
CV(%)			0.38

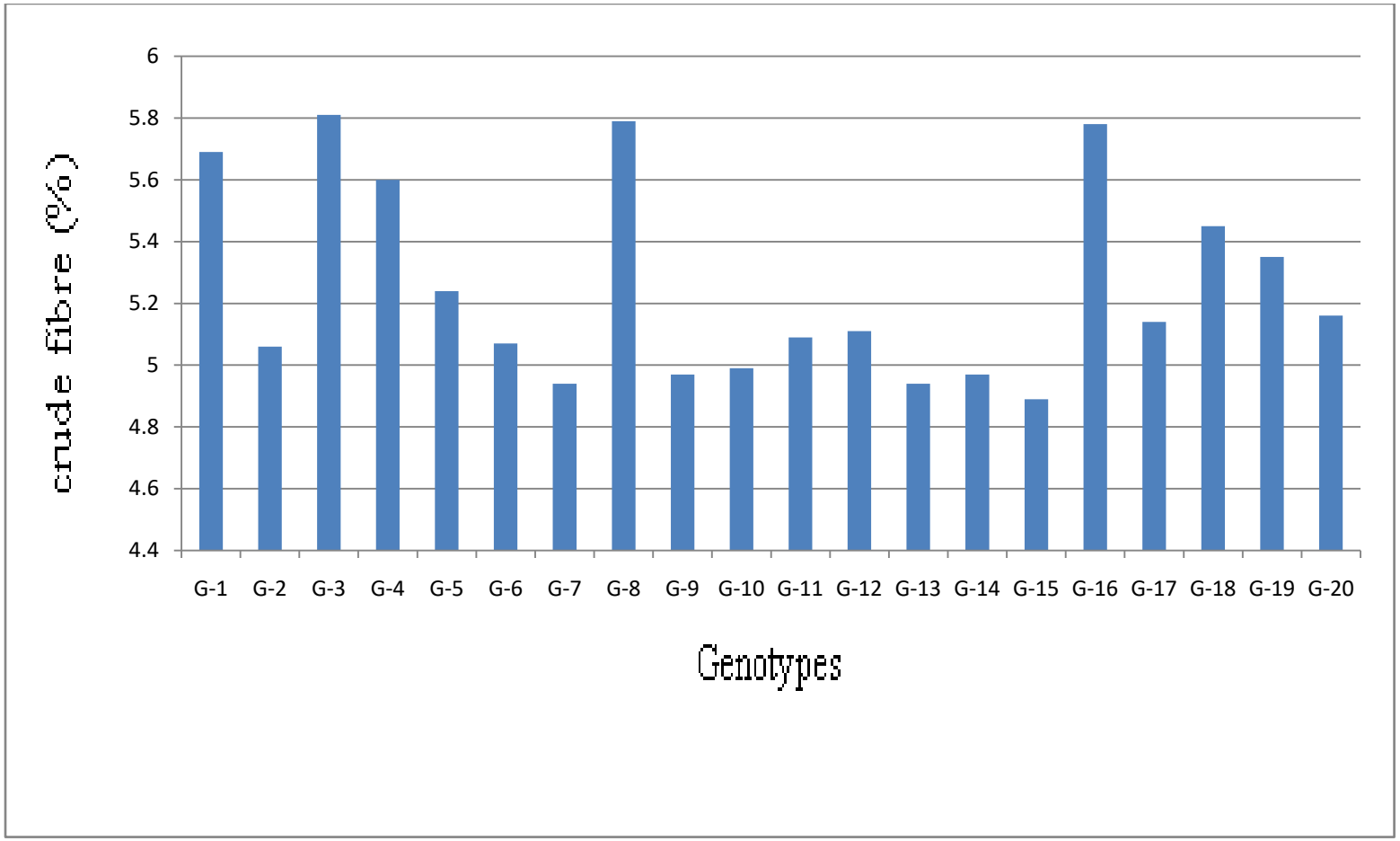

Fig 4.17 Performance of various genotype of chow-chow on crude fibre (%)

Table 4.23 Performance of various genotypes of chow-chow on calcium (mg/100g)

Calcium (mg/100g)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	15.24	15.25	15.25
Genotype-2	16.37	16.44	16.41
Genotype-3	14.62	14.59	14.61
Genotype-4	14.75	14.74	14.74
Genotype-5	15.17	15.11	15.14
Genotype-6	14.76	14.87	14.82
Genotype-7	15.96	16.03	16.00
Genotype-8	14.49	14.51	14.50
Genotype-9	13.32	13.14	13.23
Genotype-10	14.31	14.33	14.32
Genotype-11	14.25	14.25	14.25
Genotype-12	13.62	13.72	13.67
Genotype-13	13.72	13.71	13.72
Genotype-14	13.68	13.73	13.70
Genotype-15	14.10	14.15	14.13
Genotype-16	14.78	14.79	14.79
Genotype-17	14.74	14.75	14.75
Genotype-18	13.95	13.97	13.96
Genotype-19	16.25	16.27	16.26
Genotype-20	15.08	15.11	15.10
Mean			14.67
SEm(±)			0.01
CD at 5%			0.01
CV(%)			1.17

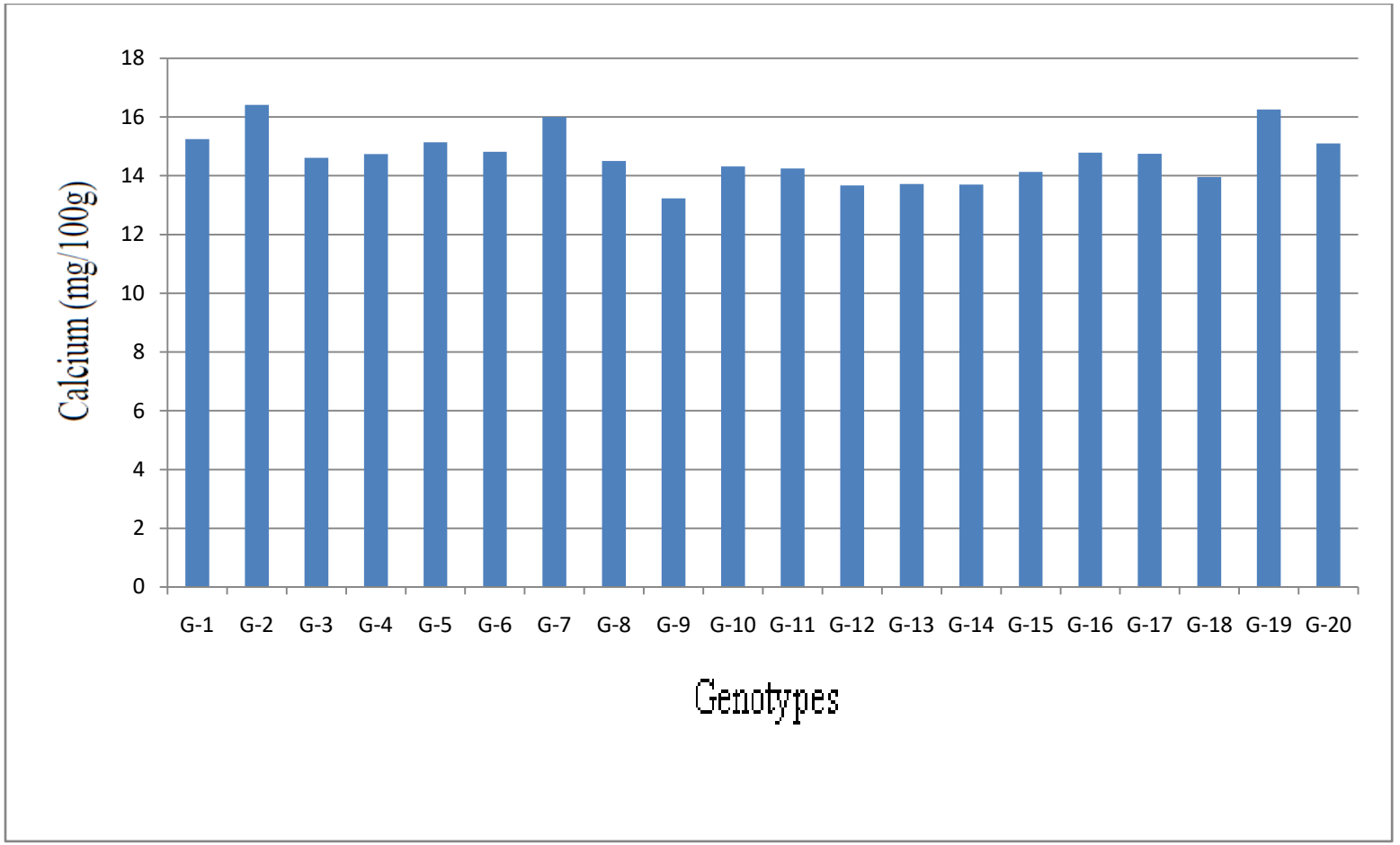

Fig 4.18 Performance of various genotype of chow-chow on calcium (mg/100g)

4.2.19 TSS (˚Brix)

The data pertaining to TSS of chow-chow genotypes has been presented in table 4.24 and fig 4.19. The pooled results recorded maximum TSS (5.17) in G-10 and the minimum TSS (4.12) in G-18. TSS content was noticeable proportion towards sweetness of chowchow. Similar findings were also reported by Sanwal *et al.* (2008), Sanwal *et al.* (2010), Kapoor *et al.* (2014) and Mishra and Das (2015) and Kim *et al.* (2016).

4.2.20 Yield per plant (kg)

The observation on yield per plant of chow-chow genotypes has been presented in the table 4.25 and fig 4.20. The pooled results recorded maximum yield per plant (3.06 kg) in G-15 followed by G-8 (3.01 kg) and G-12 (2.48 kg). Minimum yield was recorded from G-4 (0.63 kg). Fruit yield was a complex character which was shaped through various yield attributing characters.

The findings were in accordance with Sanwal *et al.* (2008), Sanwal *et al.* (2010), Kapoor *et al.* (2014), Kim *et al.* (2016) and Verma *et al.* (2017).

4.2.21 Yield per ha (q)

The observation on yield per hectare of chow-chow genotypes has been presented in the table 4.26 and fig 4.21. The pooled results recorded maximum yield per plant in G-15 (306 q) followed by G-8 (301.23 q), G-12 (247.75 q) and minimum was recorded in G-4 (62.52 q). Fruit yield was a complex character which was shaped through various yield attributing characters. Of which average fruit yield played a pivotal role to harvest high fruit yield.

The variation in fruit yield per plant was also documented by Sanwal *et al.* (2008), Sanwal *et al.* (2010), Kapoor *et al.* (2014), Kim *et al.* (2016) and Verma *et al.* (2017).

Table 4.24 Performance of various genotypes of chow-chow on TSS (˚Brix)

TSS (˚Brix)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	4.97	5.03	5
Genotype-2	5.07	5.1	5.08
Genotype-3	4.57	4.53	4.55
Genotype-4	4.63	4.67	4.65
Genotype-5	5.17	5.13	5.15
Genotype-6	5.07	5.07	5.07
Genotype-7	5.03	5.07	5.05
Genotype-8	4.23	4.27	4.25
Genotype-9	4.27	4.27	4.27
Genotype-10	5.17	5.17	5.17
Genotype-11	5.13	5.17	5.15
Genotype-12	4.3	4.27	4.28
Genotype-13	4.37	4.37	4.37
Genotype-14	4.37	4.63	4.5
Genotype-15	4.67	4.87	4.77
Genotype-16	4.83	4.83	4.83
Genotype-17	4.7	4.67	4.68
Genotype-18	4.17	4.07	4.12
Genotype-19	5.07	5.07	5.07
Genotype-20	4.87	4.87	4.87
Mean			4.74
SEm(±)			0.01
CD at 5%			0.02
CV(%)			0.23

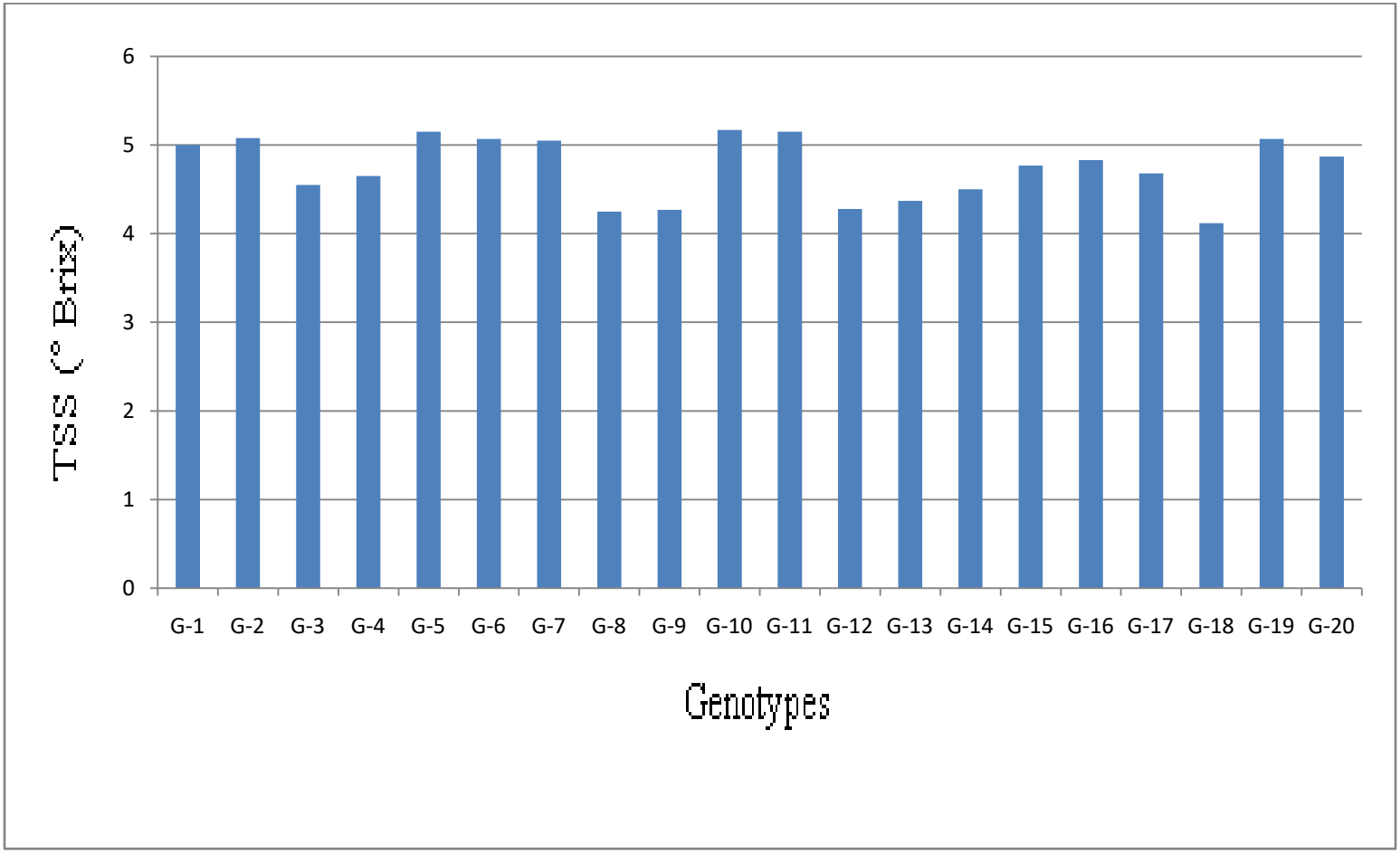

Fig 4.19 Performance of various genotype of chow-chow on TSS

Table 4.25 Performance of various genotypes of chow-chow on yield per plant (kg)

Yield per plant (kg)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	1.13	1.11	1.12
Genotype-2	2.62	2.42	2.34
Genotype-3	1.44	1.51	1.47
Genotype-4	0.61	0.64	0.63
Genotype-5	1.89	1.88	1.88
Genotype-6	1.12	1.16	1.14
Genotype-7	2.35	2.41	2.38
Genotype-8	2.93	3.09	3.01
Genotype-9	2.42	2.5	2.46
Genotype-10	2.02	2.07	2.05
Genotype-11	2.14	2.22	2.18
Genotype-12	2.45	2.51	2.48
Genotype-13	1.57	1.65	1.61
Genotype-14	1.82	1.82	1.82
Genotype-15	2.93	3.2	3.06
Genotype-16	1.66	1.073	1.69
Genotype-17	1.9	1.92	1.91
Genotype-18	1.97	2.05	2.01
Genotype-19	1.7	1.74	1.72
Genotype-20	1.56	1.53	1.55
Mean			1.93
SEm(±)			0.05
CD at 5%			0.16
CV(%)			5.09

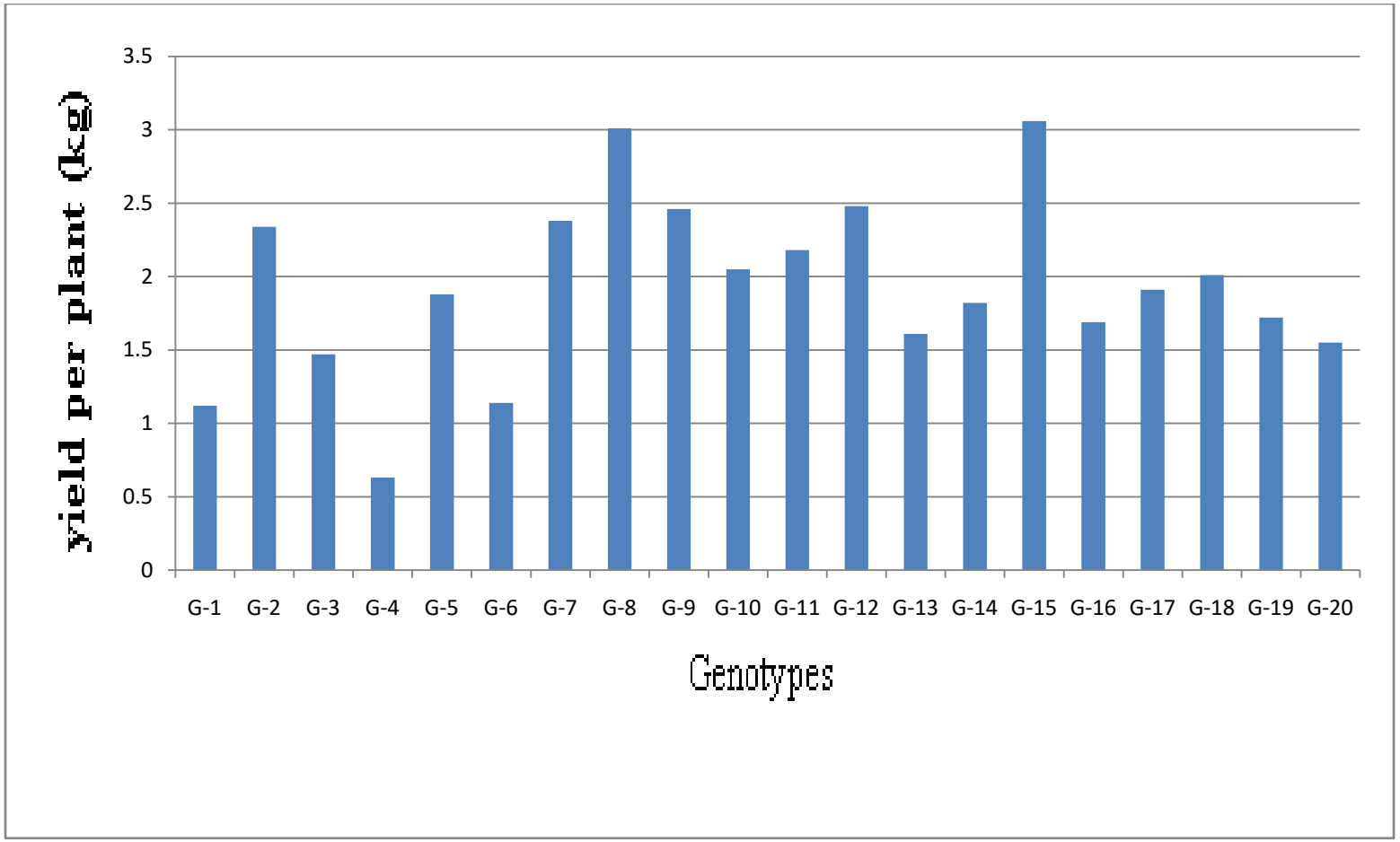

Fig 4.20 Performance of various genotype of chow-chow on yield per plant (kg)

Table 4.26 Performance of various genotypes of chow-chow on yield per ha(q)

Yield per ha(q)			
Genotypes	**2019-20**	**2020-21**	**Pooled**
Genotype-1	113.4	111.37	112.38
Genotype-2	226.2	242.13	234.17
Genotype-3	143.9	150.97	147.43
Genotype-4	60.63	64.4	62.52
Genotype-5	189.03	187.8	188.42
Genotype-6	112.5	116.1	114.3
Genotype-7	235.03	240.6	237.82
Genotype-8	293.23	309.23	301.23
Genotype-9	242.43	250.1	246.27
Genotype-10	201.9	207.4	204.65
Genotype-11	214.47	221.7	218.08
Genotype-12	244.77	250.73	247.75
Genotype-13	157.43	165.33	161.38
Genotype-14	181.73	181.8	181.77
Genotype-15	292.5	319.5	306
Genotype-16	166	172.5	169.25
Genotype-17	189.5	192	190.75
Genotype-18	196.9	205.33	201.12
Genotype-19	170.03	173.97	172
Genotype-20	156.33	153.1	154.72
Mean			192.60
SEm(±)			5.66
CD at 5%			16.22
CV(%)			5.09

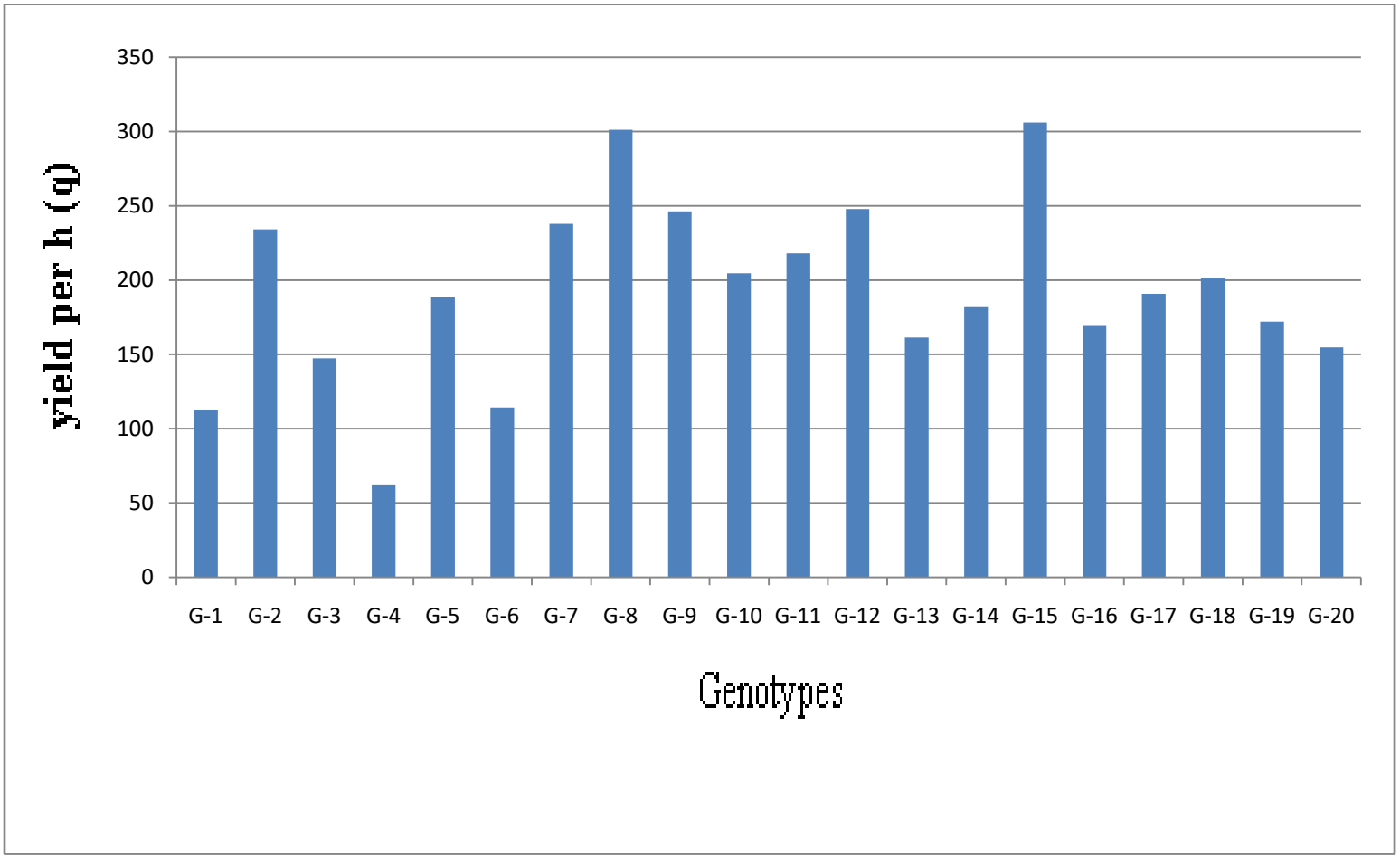

Fig 4.21 Performance of various genotype of chow-chow on yield per h (q)

G-1

G-2

G-3

G-4

G-5

G-6

G-7

G-8

PLATE 2. Glimpses of chow-chow genotypes

G-9

G-10

G-11

G-12

G-13

G-14

G-15

G-16

PLATE 3. Glimpses of chow-chow genotypes

G-17

G-18

G-19

G-20

PLATE 4. Glimpses of chow-chow genotypes

4.3 Estimation of coefficients of variation

We calculated the coefficient of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). It is essential to know about the selection by separating out the environmental influences from total variability. This suggests the accuracy with which genotypes may be diagnosed primarily based on phenotypic performance. Genotype and phenotypic coefficients of variation are simple measures variability of and these measures are commonly used to assess variability. The relative values of these types of coefficients provide an idea of the amount of variation present in the genetic population. Therefore, we compared the coefficient of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The coefficient of variation of the phenotype is slightly higher than the coefficient of variation of the corresponding genotype, indicating the environmental effect on the expression of the studied trait.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are classified as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Sivasubramanian and Madhavamenon (1973).

Phenotypic and genotypic coefficients of variation of different characters are presented in table 4.27. High magnitude of genotypic as well as phenotypic coefficient of variations were recorded for traits viz. vine length (20.896 and 20.833), number of fruits per plant (22.136 and 21.871), fruit weight (43.865 and 43.836), fruit length (22.484 and 22.117), yield per plant (31.575 and 31.437) and yield per hectare (31.575 and 31.437). This high value of PCV and GCV indicated that maximum variability exists in these traits and there is enough scope for further improvement. Similar findings were also reported earlier by Lakshmi *et al.* (2002) in pumpkin and Sanwal *et al.* (2008) in chow-chow.

Moderate PCV and GCV were recorded for suggested existence of considerable variability in the population for the traits viz. number of nodes at first fruit set (14.662 and 14.594), width of leaf (12.194 and 12.149), fruit diameter (12.451 and 9.752) and Vit.C (17.867 and 17.860). Selection for these traits may also be given the importance for improvement programme. Similar findings were also reported earlier by Yadav *et al.* (2013) in bittergourd genotypes.

Low PCV and GCV were found in the character like days to first flowering (4.397 and 4.377), length of internodes (7.464 and 7.392), length of leaf (9.193 and 9.085), petiole length (6.154 and 5.673), calcium (5.873 and 5.758), fat (9.331 and 9.249), TSS (7.405 and 7.379), moisture (1.136 and 1.120), carbohydrate (4.370 and 4.364), protein (8.455 and 8.427) and crude fibre (6.074 and 6.072). Selection for these traits may not have significant effect for improvement programme. Similar findings were also reported earlier by Gayen and Hossain (2006) and Pandit *et al.* (2009) in different cucurbitaceous crops.

Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters indicating that environmental factors were effecting the expression of traits. Narrow difference between phenotypic and genotypic coefficient of variations indicated less environmental influence on the expression of these characters. Traits with high phenotypic and genotypic coefficients of variation are economically important and there is room for improvement of these traits by choice.

Heritability (h^2_{bs}) and Genetic advance (GA)

Heritability governed the resemblance between parents and their progeny whereas, the genetic advance provide the knowledge about expected gain for a particular character after selection. Heritability suggests the comparative role of genetic factors in expression of phenotypes and also acts as an index of transmissibility of a particular character to its off springs. However, the

knowledge of heritability alone does not help to formulate a concrete breeding programme where as genetic advance along with heritability help to find out the possible genetic control for any particular character. The nature and extent of the inherent ability of a genotype for a character is an important parameter deciding the extent of improvement of any crop species. Heritability and genetic advance are the important genetic parameters for selecting a genotype that permit greater effectiveness of selection by separating out environmental influence from total variability.

Heritability estimates provides the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. Heritability estimates along genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However it is not necessary that a character showing high heritability will also express high genetic advance. The heritability usually viewed to be low if it is less than 30%, moderate between (30%-60%) and high heritability if it is more than 60% (Johnson *et al.* 1955).

Among the twenty one characters estimated in this experiment all the characters have shown heritability above 60% in which the highest heritability in broad sense was observed in fruit weight (99.9%), vitamin C (99.9%) and crude fibre (99.9%) as shown in the table 4.27.

The heritability value solely however, provides no indication of the amount of genetic improvement that would result from selection of superior genotypes. To make easier the comparison of progress in various characters of different genotypes, genetic advance was calculated as percentage of mean. The range of genetic advance was calculated as percentage of mean. The range of genetic advance as percent of mean is categorized as low if it is less than 10%, moderate between (10-20%) and high if more than 20% (Johnson *et al.* 1955).

Genetic advance as percentage of mean was observed high for fruit weight (90.24%) whereas yield per plant (64.47%), yield per ha (64.47%), fruit length (44.81%), number of fruits per plant (44.51%), vine length (42.78%), Vit. C (36.77%), number of nodes at first fruit set (29.92%) and width of leaf (24.93%) have shown high genetic advance. Moreover, fat (18.88%), length of leaf (18.49%), protein (17.30%), fruit diameter (15.73%), TSS (15.14%), length of internodes (15.08%), crude fibre (12.50%), calcium (11.62%) and petiole length (10.77%) have shown moderate genetic advance. The high value of genetic advance for these traits showed that these characters are governed by additive genes and selection will be rewarding for improvement of these traits. Moderate genetic advance for the traits suggest that both the additive and non-additive variance are operating in these traits. The results were in conformity with Singh *et al.* (2002), Sanwal *et al.* (2008) in chowchow and Kumar *et al.* (2011) in bottle gourd genotypes.

Heritability estimates along with genetic advance are more useful than the heritability value alone for selecting the best individual. In present experiment it is found that almost all the characters are showing high heritability also high genetic advance except fat, length of leaf, protein, fruit diameter, TSS, length of internodes, crude fibre, calcium and petiole length. However, among these few most suitable characters for selection with high heritability coupled with high genetic advance as percentage of mean were observed for traits like fruit weight (99.9% and 90.24%), yield per plant (99.1% and 64.47%), yield per ha (99.1% and 64.47%), fruit length (96.8% and 44.81%), number of fruits per plant (97.6% and 44.51%), vine length (99.4% and 42.78%), Vit. C (99.9% and 36.77%), number of nodes at first fruit set (99.1% and 29.92%) and width of leaf (99.3% and 24.93%)

Table 4.27 Genetic parameter on growth attributes of twenty chow-chow genotypes

Sl. No.	Characters	Range		Variance		Co. eff. Var.		H%	GA	GA% mean
		Min.	Max.	P	G	PCV	GCV			
1.	Vine length	180.66	346.33	2860.51	2843.53	20.89	20.83	99.4	109.52	42.78
2.	Days to first flowering	133.33	166.66	46.53	46.11	4.39	4.37	99.1	13.92	8.97
3.	Number of nodes at First fruit	26.25	42.75	25.08	24.85	14.66	14.59	99.1	10.22	29.92
4.	Length of internodes	9.033	11.66	0.54	0.53	7.46	7.39	98.1	1.49	15.08
5.	Length of leaf	16.66	22.80	3.11	3.03	9.19	9.08	97.7	3.54	18.49
6.	Width of leaf	13.18	20.18	3.66	3.63	12.19	12.14	99.3	3.91	24.93
7.	Petiole length	9.81	12.25	0.45	0.38	6.15	5.67	85.0	1.18	10.77
8.	No. of fruits/ plant	5.91	11.41	3.45	3.37	22.13	21.87	97.6	3.73	44.51
9.	Fruit weight	64.33	474.00	11036.83	11022.56	43.86	43.83	99.9	216.13	90.24
10.	Fruit length	6.95	20.00	9.47	9.16	22.48	22.11	96.8	6.13	44.81

11.	**Fruit diameter**	6.23	9.63	0.99	0.61	12.45	9.75	61.3	1.26	15.73
12.	**Calcium**	13.23	16.40	0.74	0.71	5.87	5.75	96.1	1.70	11.62
13.	**Fat**	103.33	141.66	123.79	121.60	9.33	9.24	98.2	22.51	18.88
14.	**Vitamin C**	10.23	22.10	9.61	9.60	17.86	17.86	99.9	6.38	36.77
15.	**TSS**	4.11	5.16	0.12	0.12	7.40	7.37	99.3	0.71	15.14
16.	**Moisture**	90.70	94.18	1.09	1.06	1.13	1.12	97.2	2.09	2.27
17.	**Carbohydrate**	4.19	4.80	0.03	0.03	4.37	4.36	99.7	0.39	8.97
18.	**Protein**	0.77	1.03	0.01	0.01	8.45	8.42	99.4	0.15	17.30
19.	**Crude fibre**	4.88	5.81	0.10	0.10	6.07	6.07	99.9	0.65	12.50
20.	**Yield per plant**	0.62	3.06	0.37	0.36	31.57	31.43	99.1	1.24	64.47
21.	**Yield per ha**	62.51	306.00	3698.24	3666.13	31.57	31.43	99.1	124.18	64.47

indicating that most likely the heritability is due to additive gene effects and selection may be effective.

4.4 Correlation studies

The phenotypic and genotypic correlation coefficients among different characters were worked out in all possible combinations (Table 4.28 and 4.29). In general, it was observed that genotypic correlation coefficient (r_g) values were higher in magnitude than phenotypic correlation coefficient (r_p) values.

Vine length showed positive and significant phenotypic correlation (0.5439) as well as genotypic correlation (0.5462) with width of leaf.

Days to first flowering showed positive and significant phenotypic correlation with number of nodes at first fruit set (0.4477) and length of internodes (0.4620). Days to first flowering also showed positive and significant genotypic correlation with number of nodes at first fruit set (0.4492), length of internodes (0.4662) and length of leaf (0.4467). However, days to first flowering showed negative and significant genotypic correlation with fruit diameter (-0.4715) at genotypic level.

Number of nodes at first fruit set showed positive and significant phenotypic correlation with days to first flowering (0.4477). Number of nodes at first fruit set also showed positive and significant genotypic correlation with days to first flowering (0.4492).

Length of internodes showed positive and significant phenotypic correlation with days to first flowering (0.4620), width of leaf (0.5343) and fruit weight (0.4956). Length of internodes also showed positive and significant genotypic correlation with days to first flowering (0.4662), width of leaf (0.5396) and fruit weight (0.5002).

Width of leaf showed positive and significant correlation with vine length (5439), length of internodes (0.5343), fruit length (0.5187) at phenotypic level. At genotypic level, width of leaf showed positive correlation with vine length

(0.5462), length of internodes (0.5396), fruit length (0.5322) and fruit diameter (0.4477).

Petiole length showed positive and significant correlation with fruit weight (0.4735). At genotypic level, petiole length is positively correlated with fruit weight (0.5142) and fruit length (0.4646).

Fruit weight showed positive correlation with length of internodes (0.4956) and petiole length (0.4735) at phenotypic level. Fruit weight also showed positive correlation with length of internodes (0.5002) and petiole length (0.5142) at genotypic level.

Fruit length showed positive correlation with width of leaf (0.5187) at phenotypic level. Fruit length also showed positive correlation with width of leaf (0.5322) and petiole length (0.4646) at genotypic level.

Fruit diameter show no significant positive correlation at phenotypic level but in genotypic level it showed correlation with width of leaf (0.4477) and number of fruits per plant (0.4738) and negative correlation with days to first flowering (-0.4715).

These findings clearly show that genotypic correlation is greater than phenotype, indicating a strong and unique relationship between the examined traits. Low phenotypic values can be due to significant genotype-environment interactions. Therefore, direct selection of these traits may lead to the development of high-yielding chow chow genotypes.

These findings were in conformity with Sanwal *et al.* (2008) and Verma *et al.* (2017) in chow-chow.

Table 4.28 Phenotypical correlation coefficients (r_p) between 12 traits of chow-chow

Character	Vine length	Days to first flowering	No. of nodes at first fruit	Length of internodes	Length of Leaf	Width of leaf	Petiole length	No. of fruits/ plant	Fruit weight	Fruit length	Fruit diameter	Calcium
Vine length	**1.0000**	0.3689	0.7873	0.8473	0.6457	0.5439*	0.5935	-0.0181	0.3929	0.2626	0.1142	0.0393
Days to first flowering		**1.0000**	0.4477*	0.4620*	0.4422	0.3488	0.3174	-0.1078	0.4302	0.4000	-0.3598	0.0829
Number of nodes at first fruit set			**1.0000**	0.8246	0.7773	0.7526	0.6863	-0.2022	0.4105	0.3554	0.0699	-0.0555
Length of internodes				**1.0000**	0.6458	0.5343*	0.7552	-0.2829	0.4956*	0.3996	-0.1912	0.0159
Length of leaf					**1.0000**	0.9072	0.5726	-0.3080	0.6863	0.6037	0.2442	-0.0150
Width of leaf						**1.0000**	0.5813	-0.2288	0.6513	0.5187*	0.3549	-0.1037
Petiole length							**1.0000**	-0.3164	0.4735*	0.4254	-0.1497	0.0738
No. of fruits/plant								**1.0000**	-0.6783	-0.6213	0.3191	-0.1199
Fruit weight									**1.0000**	0.8704	-0.0453	-0.0920
Fruit length										**1.0000**	-0.1388	-0.0460
Fruit diameter											**1.0000**	-0.1203
Calcium												**1.0000**
Yield per plant	**0.5151**	**0.5492**	**0.4309**	**0.4677**	**0.6623**	**0.6582**	**0.3694**	**-0.2804**	**0.8786**	**0.7580**	**0.1147**	**-0.1797**

*5% level of probability, respectively.

Table 4.29 Genotypical correlation coefficients (r_g) between 12 traits of chow-chow

Character	Vine length	Days to first flowering	No. of nodes at first fruit	Length of internodes	Length of Leaf	Width of leaf	Petiole length	No of fruits/ plant	Fruit weight	Fruit length	Fruit diameter	Calcium
Vine length	**1.0000**	0.3670	0.7899	0.8552	0.6530	0.5462*	0.6468	-0.0153	0.3939	0.2704	0.1450	0.0410
Days to first flowering		**1.0000**	0.4492*	0.4662*	0.4467*	0.3500	0.3464	-0.1040	0.4322	0.4119	-0.4715*	0.0850
Number of nodes at first fruit			**1.0000**	0.8284	0.7902	0.7581	0.7448	-0.2054	0.4122	0.3662	0.0961	-0.0506
Length of internodes				**1.0000**	0.6616	0.5396*	0.8221	-0.2915	0.5002*	0.4150	-0.2235	0.0264
Length of leaf					**1.0000**	0.9122	0.6430	-0.3073	0.6954	0.6201	0.2980	-0.0210
Width of leaf						**1.0000**	0.6446	-0.2282	0.6544	0.5322*	0.4477*	-0.1081
Petiole length							**1.0000**	-0.3537	0.5142*	0.4646*	-0.2282	0.0595
No. of fruits/plant								**1.0000**	-0.6850	-0.6326	0.4738*	-0.1261
Fruit weight									**1.0000**	0.8804	-0.0584	-0.0919
Fruit length										**1.0000**	-0.1908	-0.0485
Fruit diameter											**1.0000**	-0.1658
Calcium												**1.0000**
Yield per plant	0.5214	0.5575	0.4349	0.4726	0.6782	0.6667	0.3987	-0.2970	0.8831	0.7726	0.1718	-0.1814

*5% level of probability, respectively.

4.5 Path coefficient analysis

Path coefficient analysis at phenotypic and genotypic level was worked out to study the effect of various traits on yield per plant. The results have been presented in table 4.30 and 4.31.

4.5.1 Path coefficient analysis at phenotypic level

A perusal of phenotypic path coefficient analysis showed that maximum direct positive effect on yield per plant was imposed by fruit weight (1.563) followed by number of fruits per plant (0.677), number of nodes at first fruit set (0.448), fruit diameter (0.062), calcium (0.053), days to first flowering (0.044) and fruit length (0.004). While maximum negative direct effects on yield per plant were recorded for width of leaf (-0.265), length of leaf (-0.183), length of internodes (-0.145) and vine length (-0.027).

The maximum positive indirect effect on yield per plant was imposed by fruit length through fruit weight (1.360), length of internodes through number of nodes (0.370), length of leaf through number of nodes at first fruit set (0.348), width of leaf through number of nodes at first fruit set (0.337), petiole length through number of nodes at first fruit set (0.308) and fruit diameter through number if fruits per plant (0.216). Maximum negative indirect effect on yield per plant was imposed by characters like fruit weight through number of fruits per plant (-0.459), fruit length through number of fruits per plant (-0.420), width of leaf through length of leaf (-0.166) and petiole length through width of leaf (-0.154). Residual effect at phenotypic level was observed to be 0.0988.

4.5.2 Path coefficient analysis at genotypic level

Fruit weight (1.717) had maximum positive direct effect on yield per plant followed by number of fruits per plant (0.752) and number of nodes at first fruit set (0.591). However, maximum negative direct effect on yield per plant was

imposed by width of leaf (-0.340), length of leaf (-0.217) and length of internodes (-0.158).

The maximum and positive indirect effect on yield per plant was imposed by fruit length through fruit weight (1.152), length of internodes through number of nodes at first fruit set (0.490), length of leaf through number of nodes at first fruit set (0.467) and width of leaf through number of nodes at first fruit set (0.448). Maximum negative indirect effect on yield per plant was imposed by characters like fruit weight through number of fruits per plant (-0.515) imposed high negative indirect effect followed by fruit length through number of fruits per plant (-0.475) and fruit weight through width of leaf (-0.222). Residual effect at genotypic level was observed to be 0.0496.

The present study suggest that more emphasis should be given to selecting genotypes having fruit weight, number of fruits per plant, number of nodes at first fruit set, fruit diameter fruit weight, number of fruits per plant, number of nodes at first fruit set and fruit diameter. Directly or indirectly all characters showed positive effect on fruit yield per plant, which is in confirmation to the findings of Ahmed *et al.* (2005) in bottle gourd, Sanwal *et al.* (2008) in chow-chow, Muralidharan *et al.* (2013) and Oliveira and Oliveira (2021).

Overall path analysis confirmed that direct effects of fruit weight, number of fruits per plant, number of nodes at first fruit set, fruit diameter, calcium, days to first flowering and fruit length and indirect effects such as fruit length through fruit weight, length of internodes through number of nodes, length of leaf through number of nodes at first fruit set, width of leaf through number of nodes at first fruit set, petiole length through number of nodes at first fruit set and fruit diameter through number of fruits per plant should be considered simultaneously for amenability in fruit yield of chow-chow.

Table 4.30 Direct and indirect effects of yield components on yield per plant at phenotypic level in chow-chow

No.	Character	Vine length	Days to first flowering	Number of nodes at first fruit	Length of internodes	Length of leaf	Width of leaf	Petiole length	No. of fruits/ plant	Fruit weight	Fruit length	Fruit diameter	Calcium
1	**Vine length**	**-0.0277**	-0.0102	-0.0218	-0.0235	-0.0179	-0.0151	-0.0165	0.0005	-0.0109	-0.0073	-0.0032	-0.0011
2	**Days to first flowering**	0.0165	**0.0447**	0.0200	0.0206	0.0197	0.0156	0.0142	-0.0048	0.0192	0.0179	-0.0161	0.0037
3	**Number of nodes at**	0.3534	0.2010	**0.4489**	0.3701	0.3489	0.3378	0.3081	-0.0908	0.1843	0.1595	0.0314	-0.0249
4	**Length of internodes**	-0.1231	-0.0671	-0.1198	**-0.1452**	-0.0938	-0.0776	-0.1097	0.0411	-0.0720	-0.0580	0.0278	-0.0023
5	**Length of leaf**	-0.1185	-0.0811	-0.1426	-0.1185	**-0.1835**	-0.1664	-0.1051	0.0565	-0.1259	-0.1108	-0.0448	0.0028
6	**Width of leaf**	-0.1445	-0.0927	-0.2000	-0.1420	-0.2410	**-0.2657**	-0.1544	0.0608	-0.1730	-0.1378	-0.0943	0.0275
7	**Petiole length**	-0.0530	-0.0284	-0.0613	-0.0675	-0.0512	-0.0519	**-0.0893**	0.0283	-0.0423	-0.0380	0.0134	-0.0066
8	**No. of fruits/plant**	-0.0123	-0.0730	-0.1370	-0.1916	-0.2086	-0.1550	-0.2143	**0.6773**	-0.4595	-0.4208	0.2161	-0.0812
9	**Fruit weight**	0.6141	0.6724	0.6417	0.7746	1.0728	1.0180	0.7401	-1.0603	**1.5631**	1.3605	-0.0709	-0.1438
10	**Fruit length**	0.0010	0.0016	0.0014	0.0016	0.0024	0.0021	0.0017	-0.0025	0.0034	**0.0040**	-0.0005	-0.0002
11	**Fruit diameter**	0.0071	-0.0224	0.0044	-0.0119	0.0152	0.0221	-0.0093	0.0199	-0.0028	-0.0086	**0.0623**	-0.0075
12	**Calcium**	0.0021	0.0045	-0.0030	0.0009	-0.0008	-0.0056	0.0040	-0.0065	-0.0050	-0.0025	-0.0065	**0.0539**
	Yield per plant	**0.5151**	**0.5492**	**0.4309**	**0.4677**	**0.6623**	**0.6582**	**0.3694**	**-0.2804**	**0.8786**	**0.7580**	**0.1147**	**-0.1797**
	Partial R^2	-0.0143	0.0245	0.1934	-0.0679	-0.1215	-0.1749	-0.0330	-0.1900	1.3734	0.0030	0.0071	-0.0097

R SQUARE = 0.9902, RESIDUAL EFFECT =0.0988

Table 4.31 Direct and indirect effects of yield components on yield per plant at genotypic level in chow-chow

No.	Character	Vine length	Days to first flowering	Number of nodes at first fruit	Length of internodes	Length of leaf	Width of leaf	Petiole length	No. of fruits/ plant	Fruit weight	Fruit length	Fruit diameter	Calcium
1	**Vine length**	**-0.0904**	-0.0332	-0.0714	-0.0773	-0.0591	-0.0494	-0.0585	0.0014	-0.0356	-0.0245	-0.0131	-0.0037
2	**Days to first flowering**	0.0026	**0.0070**	0.0031	0.0033	0.0031	0.0025	0.0024	-0.0007	0.0030	0.0029	-0.0033	0.0006
3	**Number of nodes at**	0.4672	0.2657	**0.5915**	0.4900	0.4674	0.4484	0.4405	-0.1215	0.2438	0.2166	0.0568	-0.0299
4	**Length of internodes**	-0.1352	-0.0737	-0.1309	**-0.1581**	-0.1046	-0.0853	-0.1299	0.0461	-0.0791	-0.0656	0.0353	-0.0042
5	**Length of leaf**	-0.1419	-0.0971	-0.1718	-0.1438	**-0.2174**	-0.1983	-0.1398	0.0668	-0.1512	-0.1348	-0.0648	0.0046
6	**Width of leaf**	-0.1859	-0.1192	-0.2581	-0.1837	-0.3105	**-0.3404**	-0.2195	0.0777	-0.2228	-0.1812	-0.1524	0.0368
7	**Petiole length**	-0.0647	-0.0346	-0.0745	-0.0822	-0.0643	-0.0644	**-0.1000**	0.0354	-0.0514	-0.0464	0.0228	-0.0059
8	**No. of fruits/plant**	-0.0115	-0.0783	-0.1545	-0.2193	-0.2311	-0.1716	-0.2661	**0.7522**	-0.5153	-0.4759	0.3563	-0.0949
9	**Fruit weight**	0.6767	0.7425	0.7082	0.8592	1.1947	1.1241	0.8834	-1.1768	**1.7178**	1.5123	-0.1003	-0.1578
10	**Fruit length**	-0.0050	-0.0077	-0.0068	-0.0077	-0.0115	-0.0099	-0.0086	0.0118	-0.0164	**-0.0186**	0.0036	0.0009
11	**Fruit diameter**	0.0064	-0.0208	0.0042	-0.0098	0.0131	0.0197	-0.0101	0.0209	-0.0026	-0.0084	**0.0441**	-0.0073
12	**Calcium**	0.0033	0.0068	-0.0040	0.0021	-0.0017	-0.0086	0.0047	-0.0100	-0.0073	-0.0039	-0.0132	**0.0795**
	Yield per plant	**0.5214**	**0.5575**	**0.4349**	**0.4726**	**0.6782**	**0.6667**	**0.3987**	**-0.2970**	**0.8831**	**0.7726**	**0.1718**	**-0.1814**
	Partial R^2	-0.0472	0.0039	0.2573	-0.0747	-0.1474	-0.2270	-0.0399	-0.2234	1.5171	-0.0144	0.0076	-0.0144

R SQUARE = 0.9975, RESIDUAL EFFECT =0.0496

4.6 Divergence analysis

The concept of D2 statistics was originally developed by Mahalanobis (1936). Rao (1952) then proposed using this technique to regulate genetic diversity in plant breeding. Today, this technique is also widely used in vegetable breeding to study different parental choices. Chow Chow hybrids can be developed using genetic diversity and parental selection from diverse breeding strains, as well as germ plasm and diverse parents.

The genetic diversity among 20 chow-chow genotypes shows that out of 21 characters studied; crude fibre contributed maximum percent to the diversity (37.89%) followed by vitamin C (16.84%), fruit length (12.11%), yield per plant (11.05%), protein (8.42%), carbohydrate (7.89%), fruit weight (2.63%), days to first flowering (2.11%) and vine length (1.05%). (Table 4.14 and Figure 4.1)

Table 4.32 Percentage contribution of important characters towards diversity in chow-chow genotypes

	CHARACTER	CONTRIBUTION (%)
1	Vine length	1.05
2	Days to first flowering	2.11
3	Fruit weight	2.63
4	Fruit length	12.11
5	Vit. C	16.84
6	Carbohydrate	7.89
7	Protein	8.42
8	Crude fibre	37.89
9	Yield per plant	11.05

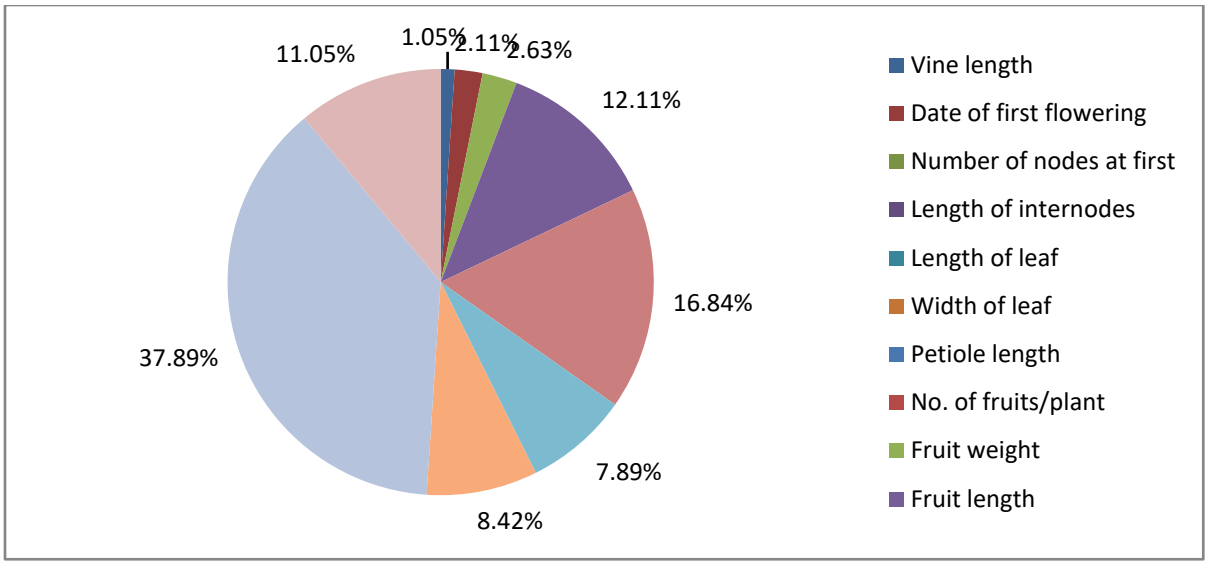

Figure 4.22 Contribution % towards genetic divergence

Based on D^2 value, 20 genotypes were grouped in to 4 clusters. Out of the 4 clusters, cluster I was largest group containing 14 genotypes followed by cluster II with four genotypes, cluster III and IV were solitary containing single genotypes each. (Table 4.33 and figure 4.23)

Table 4.33 Clustering pattern of 20 chow-chow genotypes by Tocher's method

Cluster Number	No. of Genotypes	Genotypes
CLUSTER I	14	G-2, G-5, G-6, G-7, G-9, G-10, G-11, G-12, G-13, G-14, G-17, G-18, G-19, G-20
CLUSTER II	4	G-1, G-3, G-4, G-16
CLUSTER III	1	G-15
CLUSTER IV	1	G-8

Linkage distance

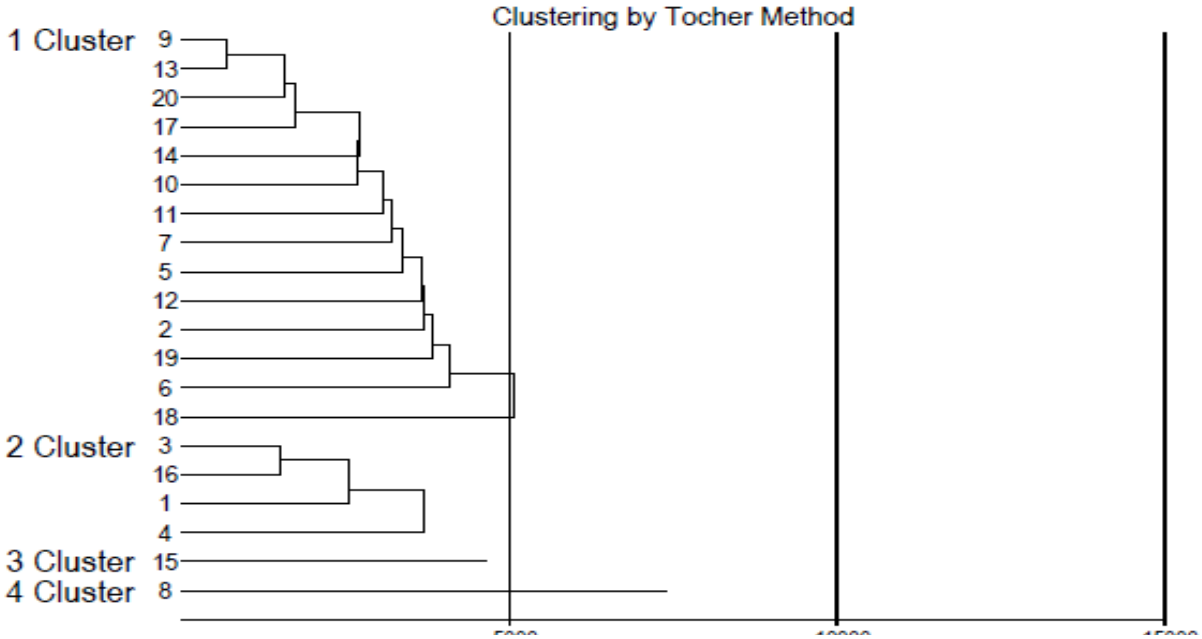

Figure 4.23 Tree diagram of 20 chow-chow genotypes using hierarchical analysis (Tocher's method)

4.6.1 Inter cluster distance

Inter cluster D^2 values are given in the table 4.34. The inter cluster D^2 value was maximum (159.90) between cluster II and III. The minimum (102.05) distance was observed between cluster I and III which indicated close relationship among the genotypes included in these two clusters.

The greater the distance between the clusters in this study, the greater the diversity between breeding lines of different groups. Therefore, it is suggested that genotype crossing from different clusters with high average performance is beneficial for obtaining better recombinants with higher genetic diversity.

4.6.2 Intra cluster distance

Intra cluster was observed only in cluster I and II as the remaining two clusters contain only one constituent genotype. Intra cluster distance was highest in the cluster I (63.52) followed by cluster II (63.19), Intra cluster D^2 values are presented in the table 4.34.

Table 4.34 Average Inter and Intra Cluster distances (D^2) for 20 genotypes

Cluster Number	CLUSTER I	CLUSTER II	CLUSTER III	CLUSTER IV
CLUSTER I	**63.52**	111.26	102.15	130.44
CLUSTER II		**63.19**	159.90	114.55
CLUSTER III			**0.00**	116.48
CLUSTER IV				**0.00**

4.6.3 Cluster mean analysis

Cluster mean analysis was computed in all 4 clusters for 21 characters studied and presented in table 4.17. From the present data it is evident that mean value of vine length was found to be maximum (343.17) in cluster IV and minimum (220.17) in cluster III. With regards to days to first flowering and number of nodes at first fruit set cluster IV was found to be maximum (159.00 & 38.83) and minimum (148.54 & 33.02) in cluster II. Length of internodes was recorded highest (11.17) in cluster IV and lowest (9.81) in cluster I. Length of leaf and width of leaf was found maximum (22.80 & 20.18) in cluster III and minimum (18.12 & 14.61) in cluster II. Petiole length was found to be highest (12.25) in cluster IV and lowest (10.74) in cluster I. Number of fruits per plant was found maximum (8.83) in cluster II and minimum (6.33) in cluster III and IV. Fruit weight and fruit length was found highest (474.00 & 20.00) in cluster III and lowest (145.96 & 11.16) in cluster II. Fruit diameter was found minimum (7.54) in cluster II and maximum (8.80) in cluster IV. Calcium was found highest (14.85) in

Table 4.35 Mean value of clusters for 21 characters studied in chow-chow

Cluster Number	1	2	3	4	5	6	7	8	9	10
Cluster I	254.88	156.68	34.08	9.81	19.04	15.48	10.74	8.57	233.31	13.61
Cluster II	246.87	148.54	33.02	9.94	18.12	14.61	11.25	8.83	145.96	11.16
Cluster III	220.17	156.50	35.17	9.87	22.80	20.18	11.52	6.33	474.00	20.00
Cluster IV	343.17	159.00	38.83	11.17	21.83	18.36	12.25	6.33	465.83	18.63

11	12	13	14	15	16	17	18	19	20	21
8.08	14.67	114.92	18.65	4.77	91.95	4.44	0.91	5.10	1.97	196.66
7.54	14.85	133.38	13.51	4.76	92.07	4.46	0.81	5.72	1.23	122.20
8.40	14.13	105.00	19.37	4.77	93.33	4.80	0.90	4.89	3.06	306.00
8.80	14.50	137.33	12.48	4.25	94.18	4.20	0.81	5.79	3.01	301.23

Where,

1. Vine length 2. Days to first flowering 3. Number of nodes at first fruit set 4. Length of internodes 5. Length of leaf 6. Width of leaf 7. Petiole length 8. No. of fruits/plant 9. Fruit weight 10.Fruit length 11.Fruit diameter 12.Calcium 13.Fat 14. Vit. C 15. TSS 16. Moisture 17. Carbohydrate 18. Protein 19. Crude fibre 20. Yield per plant 21. Yield per ha

cluster II and lowest (14.13) in cluster III. Fat was found highest (137.33) in cluster IV and lowest (105.00) in cluster III. Vit. C was found minimum (12.48) in IV and maximum (19.37) in III. Cluster I and III showed maximum (4.77) for TSS and minimum (4.25) in cluster IV. Moisture was highest (94.18) in cluster IV and minimum (91.95) in cluster I. Carbohydrate was lowest (4.20) in cluster IV and highest (4.80) in cluster III. Protein was found maximum (0.91) in cluster I and minimum (0.81) in cluster II and IV. Crude fibre was highest (5.79) in cluster IV and lowest (4.89) in cluster III. Yield per plant and yield per ha was found maximum (3.06 & 306.00) in cluster III and minimum (1.23 & 122.20) in cluster II. The results were in conformity with Sanwal *et al.* (2008) and Verma *et al.* (2017) in chow-chow.

4.7 Genotype characterization through Seed Protein Profiles

Protein banding pattern of chow-chow genotypes generated by SDS-PAGE is presented in Plate 5. Protein distribution in 20 chow-chow genotypes were studied and summarized in table 4.36 and figure 4.24. Cluster analysis of banding pattern of 20 chow-chow genotypes based on UPGMA resulted in distinct cluster. A total of 31 protein bands as per Rm values were identified by silver staining. The genotypes showed considerable variation in protein band numbers ranging from 7-11. Among the genotypes G-8 and G-12 showed maximum numbers (11) of the protein bands while the minimum numbers (7) of bands were present in G-6, G-9, G-13 & G-18. Band number 9 (Rm=26 kDa) was found to be present in 17 genotypes where as band number 12 (Rm= 32 kDa), 24 (Rm=60 kDa), 26 (Rm=66 kDa), 27 (Rm=68 kDa), 28 (Rm=70 kDa) and 31 (Rm=100 kDa) were found to be present in single genotype each.

Table 4.36 Major cluster produced by SDS-PAGE analysis on 20 genotypes of chow-chow

CLUSTER	SUB CLUSTER	SUB-SUB CLUSTER	GENOTYPES
I	I A	I A 1	G-13, G-6, G-2, G-10, G-18, G-3, G-9, G-14, G-4, G-11, G-1, G-19, G-20 & G-5
		I A 2	G-17
	I B	I B 1	G-7 & G-8
		I B 2	G-6
II	II A	G-12	
	II B	G-15	

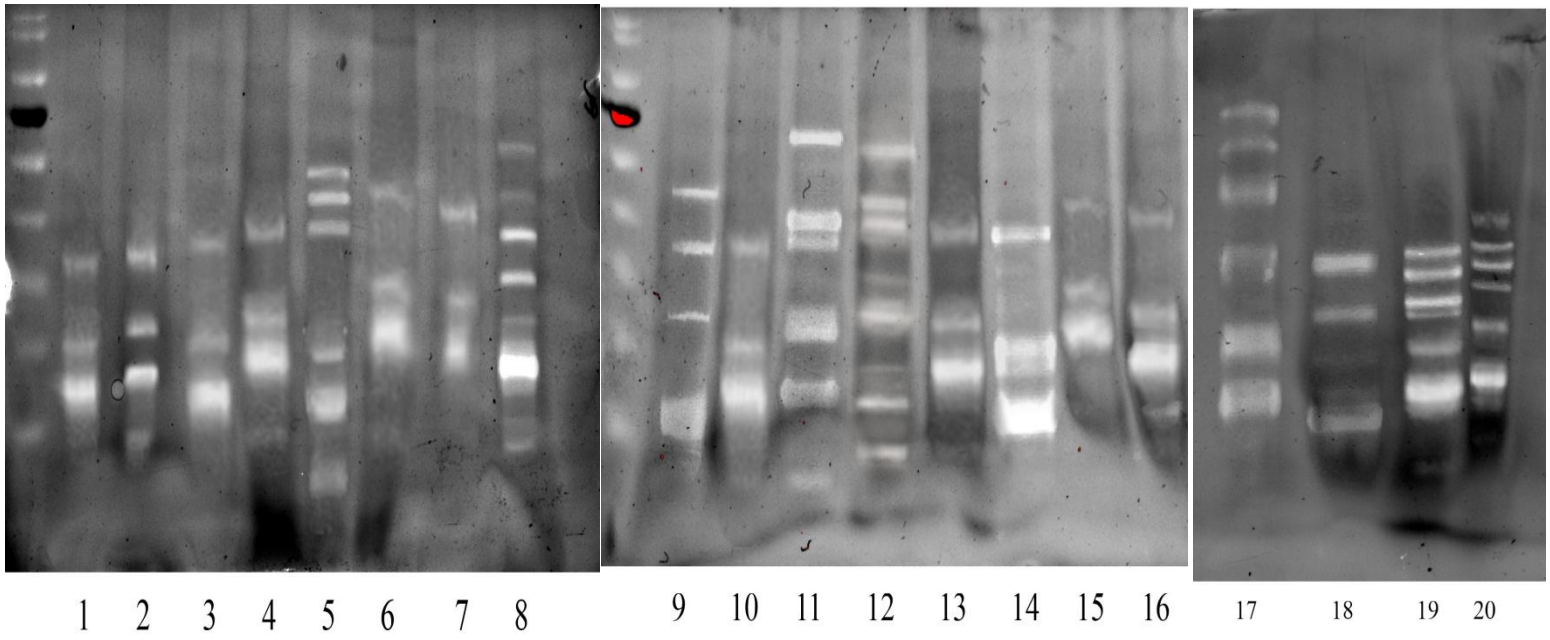

PLATE 5. Protein banding pattern in 20 chow-chow

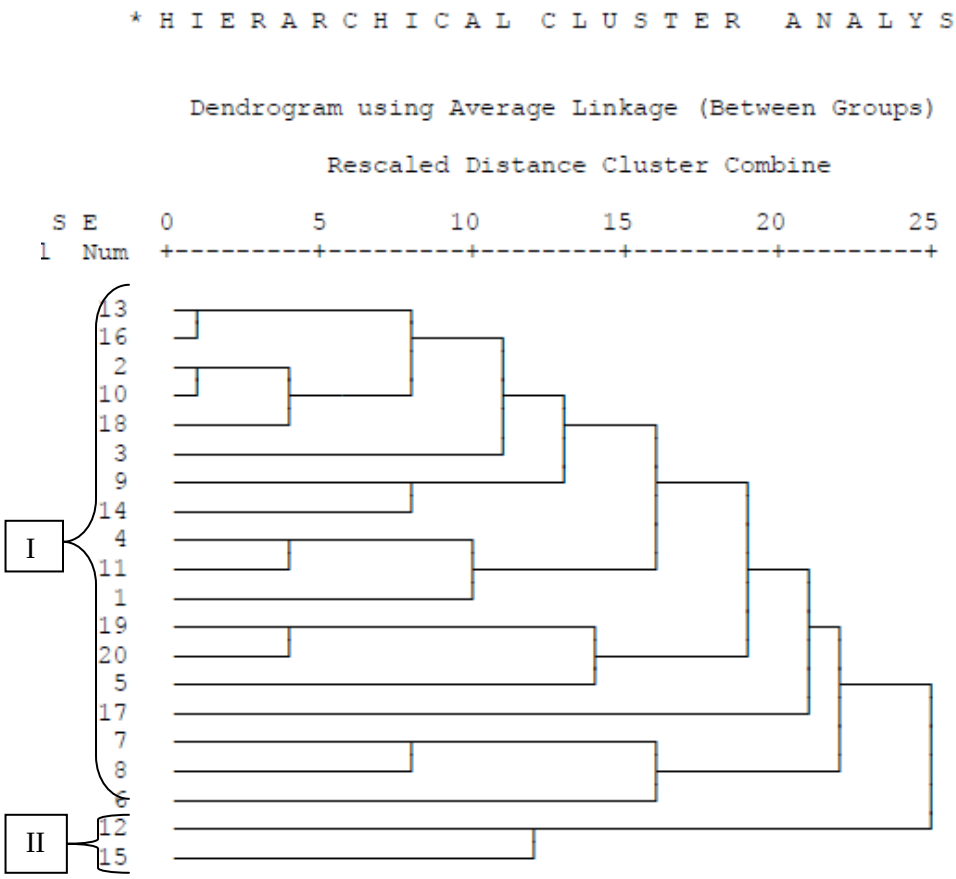

Figure 4.24 UPGMA of 20 chow-chow genotypes based on total seed protein profiles obtained by SDS-PAGE

Genetic relationship

Based on the dendogram, all the genotypes could be grouped into 2 major clusters. Cluster I was further sub divided into 2 sub-cluster, cluster I A was again divided into 2 sub-sub clusters. The distribution of different genotypes in different cluster of the dendogram has been presented in table 4.36. Cluster I was found to contain 18 genotypes while cluster II contain 2 genotypes (G-12 & G-15). The first sub-sub cluster (IA1) was found to be incorporating 14 genotypes *viz.* G-13, G-6, G-2, G-10, G-18, G-3, G-9, G-14, G-4, G-11, G-1, G-19, G-20 & G-5. The second sub-sub cluster (IA2) was found to be incorporating a single genotype G-17. Third sub-sub cluster (IB1) was found to be incorporating two genotypes G-7 & G-8. Fourth sub-sub cluster (IB2) found to contain a single genotype G-6. Genetic diversity analysis, based on seed protein profile using SDS-PAGE was also reported by Mishra and Das (2015) in chow-chow, Chakraborty (2017) in cucumber and Jain *et al.* (2017) in chow-chow.

Table 4.37 Comparison of scorable protein bands among 20 chow-chow genotypes

No.	Rm	G-1	G-2	G-3	G-4	G-5	G-6	G-7	G-8	G-9	G-10	G-11	G-12	G-13	G-14	G-15	G-16	G-17	G-18	G-19	G-20
1	10 kDa	0	0	0	0	1	0	0	1	0	0	0	1	0	0	0	1	0	1	0	1
2	12kDa	0	0	1	0	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0
3	14kDa	1	1	0	1	0	0	1	1	1	1	1	1	1	1	0	1	1	1	0	0
4	16kDa	0	0	0	0	0	1	0	0	1	1	0	0	0	1	0	0	0	0	1	1
5	18kDa	1	0	1	1	1	0	0	0	0	0	1	1	1	0	0	1	1	0	1	1
6	20kDa	1	1	1	0	1	0	0	1	1	1	0	0	1	1	0	1	0	1	1	1
7	22kDa	0	1	1	1	0	0	1	1	0	1	1	0	0	0	0	1	0	0	1	1
8	24kDa	1	0	0	1	1	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0
9	26kDa	0	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
10	28kDa	0	1	1	1	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0	0
11	30kDa	1	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0
12	32kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
13	34kDa	0	1	0	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0
14	36kDa	1	1	1	0	0	1	1	1	1	0	0	0	0	0	1	0	1	1	0	1
15	38kDa	1	1	1	1	1	0	0	0	0	1	1	0	0	1	0	0	1	1	1	1
16	40kDa	0	0	0	1	0	1	1	1	0	1	1	1	1	1	0	1	1	1	1	1
17	42kDa	1	0	1	1	0	0	0	0	1	0	1	1	0	1	1	1	0	0	0	0
18	44kDa	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0
19	48kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	50kDa	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1

21	52kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	54kDa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
23	56kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	60kDa	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
25	64kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	66kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
27	68kDa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
28	70kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
29	76kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	80kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31	100kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Total		**8**	**8**	**9**	**10**	**9**	**7**	**9**	**11**	**7**	**8**	**9**	**11**	**7**	**9**	**8**	**9**	**10**	**7**	**9**	**10**

CHAPTER V

SUMMARY AND CONCLUSIONS

SUMMARY AND CONCLUSIONS

The present investigation entitled **"Performance of various genotypes of chow-chow [*Sechium edule* (Jacq.) Swartz.] under foothill condition of Nagaland"** was carried out at Horticulture Research Farm at School of Agricultural Sciences and Rural Development, Medziphema, Nagaland University during *Kharif* season in the year 2019-20 & 2020-21. The experiment was conducted in Randomized Block Design (RBD) with twenty treatments in three replications of chow-chow collected from different places of North East India to estimate growth, yield and quality parameters along with genetic variability, correlation coefficient, path analysis, genetic divergence and protein banding pattern.

Five randomly selected plants were considered for observation of different character *viz.* leaf shape, leaf blade margin, leaf blade; number of lobes, leaf colour, fruit shape, fruit colour, fruit shape, spine on fruit skin, spine distribution, spine density, ridges on fruit, groves on fruit surface, vine length, days to first flowering, number of nodes at first fruit set, length of internodes, length of leaf, width of leaf, petiole length, number of fruits per plant, fruit weight, fruit length, fruit diameter, fat, vitamin C, moisture, carbohydrate, protein crude fibre, calcium, TSS, yield per plant and yield per ha.

Analysis of variance among the genotypes reveals that the mean sum of square were highly significant for all the traits studied. Yield and Yield attributing characters expressed significant mean sum of square which showed substantial variability in the genotypes studied for the improvement of various characters.

- Growth parameter with respect to length of leaf (22.8 cm), width of leaf (20.18 cm), fruit weight (474 g) and fruit length (20 cm) were recorded maximum in G-15 where as G-4 recorded minimum growth parameter in length of leaf (16.67 cm), fruit weight (64.33 g) and fruit length (6.95 cm).
- Yield attributes with respect to fruit weight (474g), yield per plant (3.06kg) and yield per hectare (306q) was found maximum in G-15.
- Quality attributes with respect to Vit. C (22.1 mg $100g^{-1}$) was found highest in G-9, carbohydrate (4.81%) in G-15, protein (1.03%) in G-9, calcium (16.41g) in G-2, crude fibre (5.81%) in G-3, TSS (5.17°Brix) in G-10 and lowest moisture was recorded in G-7 (90.7%).
- Highest genotypic as well as phenotypic coefficient of variations was recorded for fruit weight (43.865 and 43.836) followed by yield per plant (31.575 and 31.437), yield per hectare (31.575 and 31.437), fruit length (22.484 and 22.117), number of fruits per plant (22.136 and 21.871) and vine length (20.896 and 20.833). High heritability along with high genetic advance were recorded for almost all the parameters except for length of leaf, protein, fruit diameter, TSS, length of internodes, crude fibre, calcium and petiole length where it was found to be moderate to low.
- Correlation studies revealed that characters like length of internodes, width of leaf, fruit weight, fruit length, petiole length and number of nodes at first fruit set had significant positive correlation with fruit yield per plant both at genotypic and phenotypic level which indicated the importance of these traits in selection for yield.
- Path analysis confirmed that direct effects on fruit yield by fruit weight, number of fruits per plant, number of nodes at first fruit set, fruit diameter, calcium, days to first flowering and fruit length and

indirect effects such as fruit length through fruit weight, length of internodes through number of nodes, length of leaf through number of nodes at first fruit set, width of leaf through number of nodes at first fruit set, petiole length through number of nodes at first fruit set and fruit diameter through number of fruits per plant on fruit yield.

- Based on D^2 value, 20 genotypes were grouped in to 4 clusters. Among the 4 clusters, the largest group was found to be cluster I with 14 genotypes, cluster II with 4 genotypes, cluster III and IV were solitary containing single genotypes each. The data reveals that inter cluster D^2 value was maximum (159.90) between cluster II and III and hence can be used in breeding to exploit heterotic expression for fruit yield and its component characters in chow-chow.
- The sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) showed considerable variation in protein band numbers in twenty genotypes. The genotypes G-15 and G-12 was most distantly related to the rest of genotypes. Hence, through breeding programmes these two genotypes can be used as parent to create more genetic diversity of desired characters.

CONCLUSIONS

Analysis of variance shows that there is considerable variability between genotypes for most traits, indicating an opportunity for greater genetic improvement in chow chow. From the present investigation assemblage of twenty different genotypes from different states of north eastern India was done and found out that the mean performance for yield and carbohydrate was highest in G-15, Vitamin C and protein in G-9, fat and crude fibre in G-3 and with respect to Calcium and TSS in G-2 and G-10 respectively. Width of leaf, fruit weight, fruit length, number of fruits per plant, yield per plant and yield per hectare was observed to have high heritability combined with high genetic advance.

Correlation studies revealed that characters like length of internodes, width of leaf, fruit weight, fruit length, petiole length and number of nodes at first fruit set had significant positive correlation with fruit yield per plant. The D^2 values recorded for twenty genotypes indicated the appreciable amount of diversity among the genotypes. The inter-cluster D^2 value was observed maximum between Cluster II and III. High yield potential exhibited by G-15 confirmed that it is the best chow-chow genotype with respect to yield under existing agro-climatic condition. Based on the mean performance of twenty chow-chow genotypes it can be concluded that genotype G-15, G-9, G-3, G-2 and G-10 were the best performing genotype.

Future line of work

- Selected parents with desirable yield per plant with respect to different component traits can be involved in multiple crossing schemes to recombine different productivity components.
- 2-D electrophoresis should be used to further characterize genotypes with similar banding pattern.
- Advanced molecular techniques can be used to find duplicate genotypes for systematic processing of chow-chow genetic resources and to tag important genes available in the germplasm by linkage to DNA markers.
- Next generation genome sequencing can be employed for promising varieties.

CHAPTER VI

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REFERENCES

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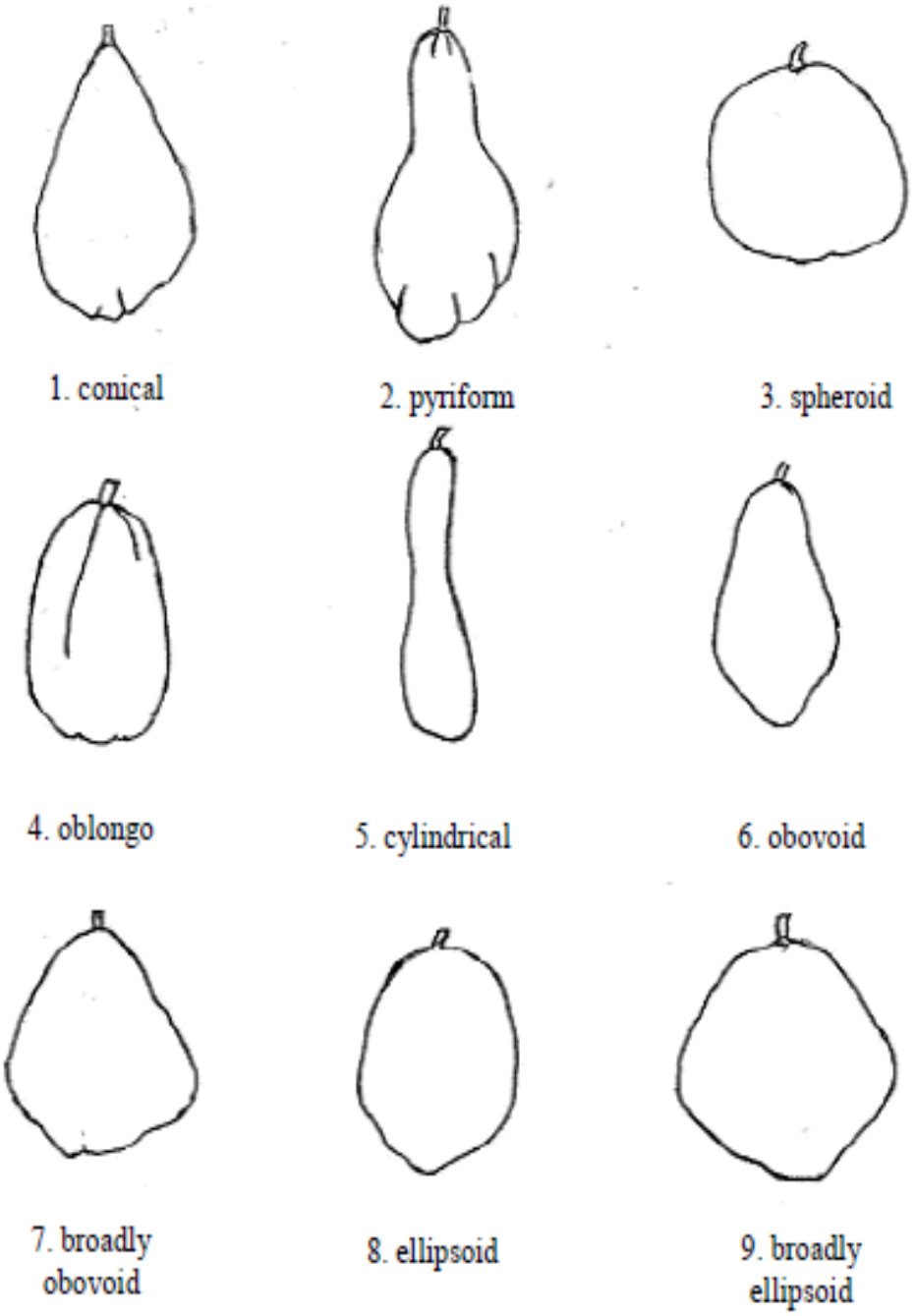
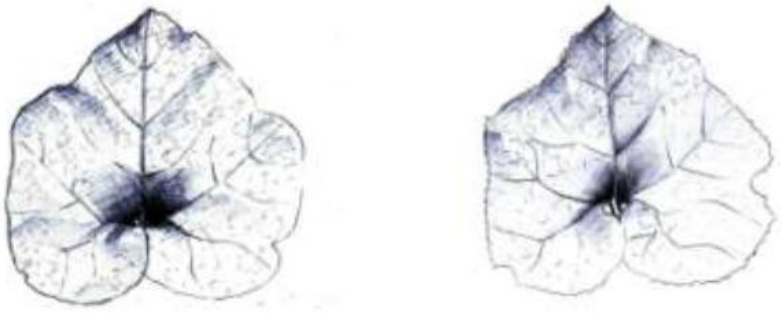
Appendix I

Diagrammatic representation of leaf and fruit shape as per International Union for protection of new varieties of plants (UPOV) and NBPGR guidelines

Ad. 33: Fruit shape

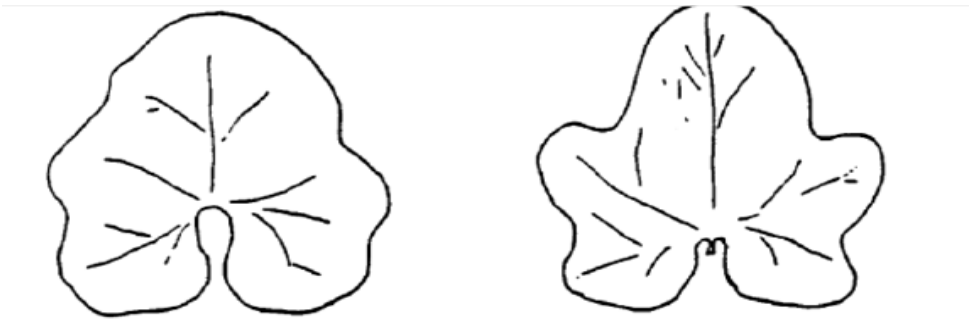


Ad. 10: Leaf blade margin



Entire Crenate

Ad. 16: No. of lobes



Ad. 37: Ridges on fruit: Profile of apical part

Raised Flat Depressed