

**EVALUATION OF AONLA (*Emblica officinalis* G.) GENOTYPES
FOR YIELD AND QUALITY TRAITS**

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**KELADI SHIVAPPA NAYAKA UNIVERSITY OF
AGRICULTURAL AND HORTICULTURAL SCIENCES,
SHIVAMOGGA**

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Thesis submitted to the

**KELADI SHIVAPPA NAYAKA UNIVERSITY OF
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In partial fulfillment of the requirements
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**DEPARTMENT OF FRUIT SCIENCE
COLLEGE OF HORTICULTURE, MUDIGERE
KELADI SHIVAPPA NAYAKA UNIVERSITY OF AGRICULTURAL AND
HORTICULTURAL SCIENCES, SHIVAMOGGA**

CERTIFICATE

This is to certify that the thesis entitled 'EVALUATION OF AONLA (*Emblica officinalis* G.) GENOTYPES FOR YIELD AND QUALITY TRAITS' submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (HORTICULTURE) in FRUIT SCIENCE** to the College of Horticulture, Mudigere. Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **Bhagyashree Dundappa Hosur ID. NO. MH2TAI0225** (bhagyadh123@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

**Mudigere
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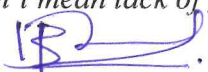
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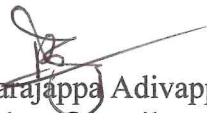
**EVALUATION OF AONLA (*Emblica officinalis* G.) GENOTYPES FOR YIELD
AND QUALITY TRAITS
(BHAGYASHREE DUNDAPPA HOSUR)**

ABSTRACT

An experiment was conducted on evaluation of aonla genotypes for yield and quality traits in Southern Transition Zone, during 2020-21 at Forest Research Station, Govinakovi, Honnali taluk, Davangere district in Karnataka. The experiment was laid out in randomized complete block design with three replications involving 14 vegetatively propagated genotypes (18 years old). The genotypes showed significant variation in terms of fruit, yield and biochemical parameters. With respect to fruit parameters the maximum fruit weight (50.84 g), fruit length (4.15 cm), fruit diameter (4.55 cm), fruit volume (47.33 cc), pulp weight (48.43 g), pulp to seed ratio (20.09) and yield (54.11 kg/plant) was recorded in genotype NA-7. With respect to biochemical parameters the maximum acidity content (2.39 %), vitamin C (403.65 mg/100g), phenol (1.62 %), flavonoid (1.73 mg QE/g) and antioxidant (92.18 %) recorded in K-23 genotype. In general, phenotypic coefficients of variation (PCV) were higher in magnitude than genotypic coefficients of variation (GCV) and narrow difference between them indicates the less environmental influence on expression of trait. High heritability coupled with high genetic advance was observed for all the characters except number of seeds per fruit, phenol and antioxidant. Correlation studies revealed that, yield per tree showed highly significant and positive association with fruit weight, volume, length, diameter and pulp weight at both phenotypic and genotypic levels. Whereas, biochemical parameters showed significant and positive association with yield at genotypic level only. Path analysis for yield per tree showed direct and positive association with fruit diameter, pulp weight, acidity, total sugar and reducing sugar. Among the characters studied, tannin content contributed maximum (18.68 %) to the genetic diversity, followed by vitamin C (17.58 %). Among 14 aonla genotypes, NA-7 is promising genotype for yield parameters followed by NA-6. Whereas, K-23 is superior for quality parameters in Southern Transition Zone of Karnataka.

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ಬೆಟ್ಟದ ನೆಲ್ಲಿಯ ವಂಶವಾಹಿ ರೂಪುಗಳ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಪಟ್ಟ ಗುಣಲಕ್ಷಣಗಳ ಕಾರ್ಯಕ್ರಮತೆ

(ಭಾಗ್ಯಶ್ರೀ ದುಂಡಪ್ಪಾ ಹೊಸೂರ್)

ಸಾರಾಂಶ

೨೦೨೦-೨೧ ನೇ ಸಾಲಿನಲ್ಲಿ ಅರಣ್ಯ ಸಂಶೋಧನಾ ಕೇಂದ್ರ ಗೋವಿನಕೋವಿ ಹೊನ್ನಾಳಿ (ತಾ) ದಾವಣಗೆರೆ (ಜಿ) ಯ, ಕಸಿ ಮಾಡಿದ ಹದಿನೆಂಟು ವರ್ಷದ ಹದಿನಾಲ್ಕು ಬೆಟ್ಟದ ನೆಲ್ಲಿಯ ವಂಶವಾಹಿ ರೂಪುಗಳ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಪಟ್ಟ ಗುಣಲಕ್ಷಣಗಳ ಬಗ್ಗೆ ಅರಿತುಕೊಳ್ಳಲು ಸಂಶೋಧನೆ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಈ ಪ್ರಯೋಗವನ್ನು ಮೂರು ಪುನರಾವರ್ತನೆಯೊಂದಿಗೆ ಯಾದ್ಯಚ್ಛಿಕ ಬ್ಲಾಕ್ ವಿನ್ಯಾಸದಲ್ಲಿ ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಗಿದೆ. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನದಲ್ಲಿ ಎಲ್ಲಾ ವಂಶವಾಹಿ ರೂಪುಗಳ ಇಳುವರಿ ಮತ್ತು ಇಳುವರಿಗೆ ಸಂಬಂಧಿಸಿದ ಗುಣಗಳಲ್ಲಿ ವೈವಿಧ್ಯತೆಯಿದೆ. ಅವುಗಳಲ್ಲಿ ಹಣ್ಣಿನ ತೂಕ (೫೦.೮೪ ಗ್ರಾಂ), ಹಣ್ಣಿನ ಉದ್ದ (೪.೧೫ ಸೆ.ಮೀ), ಹಣ್ಣಿನ ಅಗಲ (೪.೫೫ ಸೆ.ಮೀ), ಹಣ್ಣಿನ ಪರಿಮಾಣ (೪೭.೩೩ ಸಿ.ಸಿ), ಹಣ್ಣಿನ ತಿರುಳುತೂಕ (೪೮.೪೩ ಗ್ರಾಂ) ಮತ್ತು ಇಳುವರಿ (೫೪.೧೧ ಕೆ.ಜಿ ಪ್ರತಿ ಮರಕ್ಕೆ) ಗುಣಗಳನ್ನು ಎನ್‌ಎ-೭ ವಂಶವಾಹಿಯಲ್ಲಿ ಗಮನಿಸಲಾಗಿದೆ. ಜೀವರಾಸಾಯನಿಕ ಗುಣಗಳಲ್ಲಿ ಆಮ್ಲೀಯತೆ (ಶೇ. ೨.೩೯), ವಿಟಮಿನ್ ಸಿ (೪೦೩.೬೫ ಮಿ. ಗ್ರಾಂ ಪ್ರತಿ ೧೦೦ ಗ್ರಾಂ), ಫಿನಾಲ್ (ಶೇ. ೧.೯೨), ಫ್ಲೇವನಾಯ್ಡ್ (೧.೭೩ ಮಿ.ಗ್ರಾಂ ಪ್ರತಿ ಗ್ರಾಂ) ಮತ್ತು ಉತ್ಕರ್ಷಣ ನಿರೋಧಕ (ಶೇ. ೬೨.೧೮) ಗುಣಗಳನ್ನು ಕೆ-೨೩ ವಂಶವಾಹಿಯಲ್ಲಿ ಗಮನಿಸಲಾಗಿದೆ. ಅಧಿಕ ಅನುವಂಶೀಯತೆ ಜೊತೆಗೆ ಹೆಚ್ಚು ಅನುವಂಶೀಕ ಮುಂಗಡದ ಸರಾಸರಿಯನ್ನು ಎಲ್ಲಾ ಗುಣಗಳಲ್ಲಿ ಕಂಡುಬಂದಿದ್ದು ಆದ್ದರಿಂದ ಈ ಮೇಲ್ಕಂಡ ಗುಣಲಕ್ಷಣಗಳನ್ನು ನೇರ ಆಯ್ಕೆಗೆ ಸೂಕ್ತವಾಗಿವೆ. ಸಹಯೋಗ ಅಧ್ಯಯನದ ಫಲಿತಾಂಶದ ಪ್ರಕಾರ ಪ್ರತಿಮರದ ಹಣ್ಣಿನ ಇಳುವರಿಯು, ಹಣ್ಣಿನ ತೂಕ, ಪರಿಮಾಣ, ಉದ್ದ, ಅಗಲ ಮತ್ತು ತಿರುಳಿನ ತೂಕದ ಜೊತೆಗೆ ಅತ್ಯಂತ ಸಹಯೋಗವನ್ನು ವ್ಯಕ್ತಪಡಿಸುತ್ತಿದೆ. ಮಾರ್ಗ ಗುಣಾಂಕದ ಅಧ್ಯಯನದ ಮೂಲಕ ಕಂಡುಬರುವುದೇನೆಂದರೆ ಹಣ್ಣಿನ ಅಗಲ, ತಿರುಳಿನ ತೂಕ, ಶುಗರ್ ಇಳುವರಿಯ ಮೇಲೆ ನೇರ ಸಕಾರಾತ್ಮಕ ಪರಿಣಾಮ ಬೀರಿದೆ. ಮಹಾಲನೊಬಿಸ್ ಡಿ ಅಧ್ಯಯನದಲ್ಲಿ ಟ್ಯಾನಿನ್ ಗುಣವು ವೈವಿಧ್ಯತೆಗೆ ಗರಿಷ್ಠ ಕೊಡುಗೆಯನ್ನು ನೀಡಿದೆ. ಪ್ರಸ್ತುತ ಅಧ್ಯಯನದ ಪ್ರಕಾರ ಎನ್‌ಎ-೭ ಮತ್ತು ಎನ್‌ಎ-೬ ವಂಶವಾಹಿಗಳು ಇಳುವರಿಗೆ ಸೂಕ್ತವಾಗಿದ್ದು, ಕೆ-೨೩ ವಂಶವಾಹಿ ಜೀವರಾಸಾಯನಿಕ ಗುಣಗಳಲ್ಲಿ ಉತ್ತಮವಾಗಿದ್ದು ಇಂತಹ ಗುಣಗಳನ್ನು ಹೊಂದಿರುವ ತಳಿಗಳನ್ನು ಬಿಡುಗಡೆಗೊಳಿಸಲು ಅಥವಾ ಮುಂದಿನ ಅಭಿವೃದ್ಧಿಗೆ ಉಪಯೋಗಿಸಿಕೊಳ್ಳಬಹುದು.

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CONTENTS

CHAPTER NO.	TITLE	PAGE NO.
I	INTRODUCTION	1-3
II	REVIEW OF LITERATURE	4-19
	2.1 Morphological characters of the tree	4-5
	2.2 Fruit and yield parameters	5-7
	2.3 Bio-chemical parameters	8-11
	2.4 Genetic variability parameters	11-13
	2.5 Correlation studies	13-16
	2.6 Path co-efficient analysis studies	16-17
	2.7 Genetic divergence	17-19
III	MATERIAL AND METHODS	20-32
	3.1 Geographical location and weather condition of the experimental site	20
	3.2 Experimental details	20
	3.3 Recording experimental observation	21
	3.4 Fruit and yield parameters	22-23
	3.5 Biochemical parameters	23-28
	3.6 Estimates of genetic variability parameters	28-29
	3.7 Correlation co-efficient analysis	30
	3.8 Path co-efficient analysis	30-31
	3.9 Genetic divergence	31-32
	3.10 Statistical analysis of experimental data	32
IV	EXPERIMENTAL RESULTS	33-61
	4.1 Tree morphological parameters	33-35
	4.2 Fruit and yield parameters	35-39
	4.3 Biochemical parameters	39-43
	4.4 Genetic variability	43-47
	4.5 Correlation studies	47-52
	4.6 Path co-efficient analysis	54-55
	4.7 Genetic divergence	55-59
V	DISCUSSION	62-76
	5.1 Tree morphological parameters	62-63
	5.2 Fruit and yield parameters	63-65
	5.3 Biochemical parameters	66-68
	5.4 Genetic variability	68-70
	5.5 Correlation studies	70-72
	5.6 Path co-efficient analysis	72-73
	5.7 Genetic divergence	73-76
VI	SUMMARY	77-79
VII	REFERENCES	80-88
VIII	APPENDICES	89-90

LIST OF TABLES

TABLE NO.	TITLE	PAGE NO.
1.	List of aonla genotypes used for the experiment	20
2.	Variation in tree height and stem girth of aonla genotypes	34
3.	Variation in tree morphological parameters of aonla genotypes	36
4.	Variation in fruit, seed and pulp parameters of different aonla genotypes	38
5.	Variability in fruit yield of different genotypes of aonla	40
6.	Biochemical parameters in the pulp of aonla genotypes	42
7.	Mean, range and genetic components for fruit and yield parameters of aonla genotypes	45
8.	Mean, range and genetic components for quality parameters of aonla genotypes	48
9.	Phenotypic correlation of co-efficient for yield and quality parameters of aonla genotypes	51
10.	Genotypic co-efficient of correlation for yield and quality parameters of aonla genotypes	53
11.	Phenotypic path co-efficient for yield and quality parameters of aonla genotypes	56
12.	Contribution of different biochemical parameters of aonla genotypes towards total divergence	58
13.	Intra and inter cluster distances for biochemical parameters of 14 aonla genotypes	60
14.	Mean values of clusters for biochemical parameters in 14 aonla genotypes	61

LIST OF FIGURES

FIGURE No.	TITLE	BETWEEN PAGES
1	Dendrogram showing the genetic diversity among 14 genotypes of aonla using Torcher's method	58-59

LIST OF PLATES

PLATE No.	TITLE	BETWEEN PAGES
1.	General view of experimental plot	21-22
2.	Variation in fruit of aonla genotypes	63-64
3.	Variation in pulp of aonla genotypes	65-66
4.	Variation in fruit, pulp and stone of aonla genotypes	65-66

LIST OF APPENDICES

SL. No.	TITLE	PAGE No.
1.	Weather data recorded at Forest Research Station, Govinakovi, Honnali(Tq), Davangere (Dist).	89
2.	List of symbols and abbreviations	90

INTRODUCTION

I INTRODUCTION

The aonla (*Emblica officinalis* G.) is an important fruit and a crop of commercial significance belonging to family Euphorbiaceae. It is also called as amla, nelli, amalaki, amali and amala in different parts of India. It has been cultivated in India since time immemorial and occupies a sacred place in Indian mythology. It was mentioned in the Vedas, Ramayan, Charaksamhita, Sushruta Samhita and literature of Kalidas and Kadambari. It has rich medicinal value and is dominantly used in Ayurvedic and Unani medicinal industry as a raw material. Nutritional, commercial and medicinal significance of aonla fruit makes it popular all over the world (Goyal *et al.*, 2008).

Aonla is native of Tropical India and Southeast Asia, commonly named as Indian gooseberry (Barthakar and Arnold, 1991). The basic chromosome number of aonla is $x = 7$. The cultivated forms of aonla have been identified as polyploid ($2n=28$) (Amal and Raghvan, 1957).

Aonla is a small to medium sized, much branched which behaves as evergreen in tropics and as deciduous in sub-tropical conditions. It bears two types of shoots and on the basis of growth characteristics these have been categorized as long or indeterminate and short or determinate. Size of determinate shoot of aonla is 4.5-114 cm. (Shukla and Singh, 2008). Determinate shoots bear small sized leaves (9-14×2-4 mm) which are compound type. Fruit is fleshy drupe and the pulp of fruit is highly nutritious. They are globose, round to oblate in shape. It is pale green, changing to light yellow or brick-red (rarely) when mature. It consists of 3 sub-dehiscent, 2 to 13 seeded, crustaceous endocarp enclosed in a thick fleshy mesocarp. Fruits of wild aonla are relatively smaller.

The aonla tree bears fruits up to 65 to 70 years. Aonla can be grown in both tropical and subtropical climates. Annual rainfall of 630-680 mm is ideal for its growth. The young plants up to the age of three years should be protected from hot wind during May-June and from frost during winter months. The mature plants can tolerate freezing temperature as well as a high temperature up to 46 °C. It is a dry land fruit crop tolerant to alkalinity and salinity.

The fruit of *Emblica officinalis* is considered as 'wonder fruit for health' because of its unique qualities, namely astringent, cooling anodyne, carminative, digestive, stomachic, laxative, aphrodisiac, diuretic, antipyretic and trichogenous and also useful in the treatment of many diseases including diabetes, cough, asthma, bronchitis, headache, ophthalmic disorder, dyspepsia, colic, flatulence, skin diseases, leprosy, jaundice, scurvy, diarrhea, diabetes and grayness of hair (Anon., 1952). It is also reported to have anticancer properties (Ngamkitidechakul *et al.*, 2010). The vitamin C content in aonla fruit is 500–600 mg 100 g⁻¹, which is next to that of Barbados cherry (Shanker, 1969).

Aonla is a nutritious fruit at low cost. The species is capable of yielding fruits under adverse conditions on marginal land (Gaur, 1999). This will create a very good chance in employment generation, rehabilitation of marginal and wastelands, promotion of large-scale health improvement cottage industries of the people in the tropical to subtropical region of India including Pakistan, Sri Lanka, South-East Asia, China and Malaysia.

Despite being an underutilized fruit, aonla has enormous potential in the world market. Therefore, it is necessary to highlight the nutritional properties of wild-growing population of *Emblica officinalis* fruits. The study of nutritional quality and bioactive contents in aonla which grows in different parts of India, to understand the variation in physical properties and chemical composition of fruits among different populations growing wild. The study would be helpful to recommend the elite germplasm for in-situ conservation and various afforestation and reforestation programs. Now-a-days, cultivation of aonla is gaining popularity due to its high market demand, less management cost coupled with wide adaptability in diverse agro climatic condition.

The knowledge of genetic variability is of great importance for crop improvement programme. Greater the variability in a population, greater the chances of effective selection for desirable types. In fact, most of the present day commercial varieties of aonla are chance selection from natural seedlings. Introduction of novel quality traits into *Emblica officinalis* through genetic transformation is possible only if reliable germplasm for development of promising cultivar is available.

Assessment of genetic variability, nature and magnitude of characters association for quality, yield and yield attributing traits made easy for the success of any crop improvement programme. The study of such variability existing among different varieties enables the breeder to determine the most potential genotypes. Prime importance to a breeder is to develop high yielding varieties through selection or from the superior segregant present in a population.

Divergence analysis is a tool to measure the relative contribution of different components on diversity acting both at intra and inter-cluster levels which helps in the identification of selection parameters to be used as criteria for yield and quality improvement (Mahalanobis, 1936).

Correlation co-efficient analysis measures the mutual relationship between various plant characters and determines the component characters on which, selection can be based for improvement in the yield. Correlation provides information on the nature and extent of relationship between all pairs of characters. Hence, when the breeder applies selection for a particular character, not only it improves that trait, but also other characters and it will provide a reliable measure of genetic association between them which is useful in breeding programmes.

Among the various factors for high production of quality fruits, cultivar/genotype is considered to be the prime ones, as this single factor controlled more than 60 per cent of yield and quality attributing characters. Again, expression of characters of a genotype, which are controlled by genes, depends on environmental factors. For this reason, varietal /genotype specification of crop in a particular agro-climatic condition is the foremost task for commercialization of that crop in a locality or zone.

Identification of suitable genotype for the region is necessary for promoting its productivity, production and quality of the fruits under tropical conditions. In order to identify distinct characters of various aonla cultivars, the morphological characters are also equally important to the fruit characters. In this investigation, the emphasis has been made to study the adaptability of different germplasm. On the basis of yield and quality performance of different germplasm, the suitable varieties/ genotype may be selected for Southern Transition Zone of Karnataka. This will also help the growers in the selection of suitable genotype of this underutilized crop for large-scale cultivation to get higher yield and good quality fruits.

Owing to better prospects of aonla in semi arid regions due to hardy nature of plants, high medicinal and nutritional values, there is a possibility that it will be one of the most important fruit of the future. Therefore, it was felt necessary to evaluate aonla genotypes from the existing orchard at Forest Research Station, Govinakovi. Hence, the present study was conducted to evaluate aonla genotypes on the basis of their yield and quality under Southern Transition Zone of Karnataka.

Objectives:

- 1) To study the genetic variability among the genotypes.
- 2) To assess the association among yield and yield attributing traits.
- 3) To identify superior genotypes for yield and quality attributes.

REVIEW OF LITERATURE

II RIEVIEW OF LITERATURE

Aonla (*Emblica officinalis* G) is one of the important fruit yielding tree which has commercial potential due to its wider adaptability and amplitude of uses. In this view, there is necessary to identify superior elite trees for monoculture plantations without causing genetic erosion. Establishing plantations using genetically improved clones will help to maximize the production per unit area and leads to indirect economic and social benefits. However, in recent times under social forestry schemes efforts have been made to propagate vegetatively and grown in both private and government lands.

The vegetatively propagated clones are known to start bearing as early as in 4 to 5 years of planting. Many plus trees have been identified which were of seedling origin. These were multiplied vegetatively and maintained in the gene bank. They were assessed for fruit traits and yielding capacities. In this chapter, attempts has been made to review the available literature on aonla with respect to variation in morphological, fruit and bio-chemical parameters and presented below with the following sub headings

2.1 Morphological parameters of the tree

2.2 Fruit and yield parameters

2.3 Bio-chemical parameters

2.4 Genetic variability parameters

2.5 Correlation studies

2.6 Path co-efficient analysis studies

2.7 Genetic divergence

2.1 Morphological parameters of the tree

Aulakh *et al.* (1997) studied four cultivars of aonla *viz.*, Banarasi seedling, Banarasi (grafted), Chakaiya and Francis at Regional Research Station for Kandi Area (RRSKA) Balachur were analyzed for growth parameters. They found that the Banarasi seedling cultivar attained the maximum plant height (5.39 m) followed by Francis (4.60 m). Whereas, Banarasi grafted attained minimum plant height (3.30 m).

Aulakh *et al.* (2006) revealed that stem girth of aonla cultivars growing in Shivalik foothills of Punjab varied between 78 cm to 106 cm. It was recorded maximum (106 cm) in Banarasi seedling and minimum (78 cm) in Banarasi grafted.

Krishnamoorthy (2009) studied growth parameters of five aonla varieties *viz.*, BSR-1, Kanchan, Krishna, Chakaiya and NA-7 at Department of Horticulture, TNAU, Coimbatore during 2001-2006. BSR-1, recorded higher plant height (5.40 m) followed by NA-7.

Rao and Subramanyam (2009) studied growth parameters of seven varieties under scarce rainfall zone at Horticultural Research station, Anantapur. Highest plant height (4.2 m) was recorded in NA-10 followed by Kanchan (3.9 m). The maximum stem girth (73.2 cm) in Kanchan followed by NA 10 (65.5 cm) whereas, it was recorded lowest (33 cm) in Chakaiya.

Shukla *et al.* (2010) studied growth parameters of seven cultivars *viz.*, Kanchan, Krishna, Chakaiya, NA-6, NA-7, NA-10 and Anand-1 at Central Institute for Arid Horticulture, Bikaner. The plant height was recorded maximum in NA-7 (3.46 m) whereas, minimum in Anand-1 (2.1 m).

Singh *et al.* (2015 a) studied on evaluation of different aonla varieties for their vegetative and fruit characters under rainfed hot semi-arid ecosystem of western India during the years 2012-14. Among the cultivars, growth habit was varied *viz.*, upright spreading, tall upright, tall spreading, tall drooping and tall semi- spreading. Also studied on leaf characters, the foliage was visualized as dense and sparse among all the cultivars. The leaflet colour (green to pale yellowish green), shape (oblong, oval oblong and elliptical), apex (obtuse and acute) also varied among the cultivars. The size of leaves in terms of length and breadth ranged between 1.25 cm to 1.47 cm and 0.23 cm to 0.37 cm respectively.

Kumar *et al.* (2016) reported that all cultivars behaved differently in their growth characteristics under hot semi-arid conditions of Panchmahal, Gujarat. The growth habit was observed tall drooping in Francis, upright spreading in Chakaiya, tall semi-spreading in NA-7 and Goma Aishwarya and tall upright in Anand-2. The foliage in Francis and NA-7 was observed sparse. Whereas, Chakaiya, Goma Aishwarya and Anand-2 had dense foliage.

Tripathi *et al.* (2016) observed that the popular cultivars of north India produced lesser vegetative growth as compared to cultivar BSR-1 under the humid conditions of western Ghats. The plant height was recorded maximum (6.32 m) in BSR-1 and minimum (3.71 m) in Chakaiya.

2.2 Fruit and yield parameters

2.2.1 Fruit parameters

Singh and Arora (1967) studied the physical parameters of Banarasi and Chakaiya cultivars of aonla and observed that fruit weight (32.50 g) and fruit diameter (4.12 cm) was maximum in Banarasi as compare to Chakaiya (29.70 g weight and 3.91 cm diameter).

Teaotia *et al.* (1968) reported that the maximum length, diameter and weight of aonla fruit in cultivar Banarasi was 3.74 cm, 4.5 cm and 49.68 g respectively and in cultivar Chakaiya it was 3.2 cm, 3.9 cm and 30.0 g respectively.

Kumar *et al.* (2003) studied on performance of different cultivars of aonla for quality and yield parameters. They found that bigger fruit size in the variety Krishna and NA-7 was due to their increases in fruit length (3.6 cm and 3.4 cm) and fruit diameter (13.2 cm and 13.0 cm), respectively.

Patel *et al.* (2003) compared varieties of aonla for fruit growth parameters and maximum fruit size (31.76 g) was recorded in variety Francis and lowest fruit weight (23.66 g) in Aonla-I.

Jaiswal *et al.* (2007) studied fruit characteristics of seven aonla cultivars namely, Krishna, Kanchan, NA-6, NA-7, NA-10, Francis and Chakaiya during 2004-05 under Varanasi conditions. Cultivar NA-6 had maximum pulp content (94.25%) followed by NA-10 and Krishna.

Rao and Subramanyam (2009) reported the highest fruit weight (30.7 g) in aonla cultivar NA 10 followed by Kanchan (30.2 g) whereas, it was lowest (16.18 g) in chakaiya. The fruit volume of aonla cultivars ranged from 1.01 to 1.51 cc, it was maximum (1.51 cc) in NA-6 and minimum (1.01 cc) in Kanchan, under scarce rainfall zone conditions of Anantapur, Andhra Pradesh.

Yadav and Yadav (2010) studied on performance of eight cultivars of aonla namely, Krishna, Kanchan, Chakaiya, NA-7, Balwant Bold, Banarasi, Francis, and NA 10 at Mathura, Uttar Pradesh. A wide range of variation was observed in the length and diameter of fruit, it was ranged from 2.90 to 4.80 cm and 2.60 to 4.30 cm, respectively in Chakaiya to Balwant Bold cultivars.

Bakshi *et al.* (2015) studied on evaluation of different aonla (*Emblica officinalis*) cultivars under rainfed conditions of lower Shivalik foothills of Himalayas. The results revealed that fruit weight was maximum (41.46 g) in Neelam, followed by Banarasi (36.42 g). While, in Desi recorded minimum fruit weight (13.6 g). The length and diameter of aonla fruits ranged from 2.64 to 3.73 cm and 2.84 to 4.42 cm, respectively, in Desi and Neelam cultivars. The fruits of cultivar Neelam showed maximum volume (39.80 cc), whereas, it was minimum (12.01 cc) in Desi. The maximum specific gravity (1.13) was recorded in Desi variety whereas, it was minimum (1.03) in variety Chakaiya. The results revealed that Neelam had maximum stone weight (1.89 g), whereas, minimum (1.04 g) stone weight was obtained in Desi.

Parveen and Khatkar (2015) studied on various physico-chemical characteristics of five different cultivars of aonla i.e., NA-7, Banarasi, Kanchan, Chakaiya and Desi at Hisar, Haryana and observed minimum (14.27 g) fruit weight in cultivar Banarasi and maximum (49.97 g) in Desi.

Kumar *et al.* (2016) reported that the fruit weight of aonla cultivars ranged from 27.75 to 34.85 g, it was recorded maximum (34.85 g) in NA-7 and minimum in Anand 2 (27.75 g). Fruit length (3.65 cm) was highest in NA 7, followed by Goma Aishwarya

(3.56 cm) and lowest in Francis (3.08 cm). Among cultivars fruit width was observed maximum (4.05 cm) in Chakaiya, whereas, it was minimum (3.44 cm) in Francis.

Tripathi *et al.* (2016) studied on evaluation seven aonla cultivars under humid tropical condition at Chettahalli, Karnataka. Observed that the pulp per cent was maximum (95.5 %) in NA 6, however, it was minimum (91.34 %) in BSR-1.

2.2.2 Yield parameters

Supe *et al.* (1997) studied on yield parameters of five aonla cultivars *viz.* Kanchan, Krishna, Chakaiya, NA-7 and Francis grown at MPKV, Rahuri during 1995. Maximum yield was observed (116 kg / tree) in Kanchana followed by Krishna (73.80 kg / tree). Whereas, Chakaiya recorded minimum yield (41.61 kg / tree), higher yield in Kanchan and Krishna could be attributed to spreading growth growth of these cultivars.

Bahaduria *et al.* (2004) studied on seven cultivars *viz.* Balwant, Chakaiya, Kanckan, NA-7, Krishna, Banarasi and Francis grown in alkali soil at Mainpuri district. The result revealed that Banarasi yielded maximum fruit (102.8 kg/tree) and the weight of single fruits was also maximum (77.9 g).

Krishnamoorthy (2009) studied on yield parameter of five aonla varieties *viz.* BSR-1, Kanchan, Krishna, Chakaiya and NA-7 under sodic soil at Department of Horticulture, TNAU, Coimbatore. BSR-1 recorded maximum number of fruit per tree (6718 fruits) with higher fruit weight per tree (139.80 kg)

Rao and Subramanyam (2009) studied yield parameters of seven aonla varieties under scarce rainfall zone. Highest fruit yield per tree was recorded in Kanchan (76.10 kg / tree) followed by NA-10 (74.80 kg / tree). The maximum number of fruits was observed observed in NA-10 under scarce rainfall zone under rainfed conditions

Shukla *et al.* (2009) studied on yield attributes traits of eight cultivars of aonla *viz.*, Kanchan, Krishna, Chakaiya, NA-6, NA-7, NA-10, Anand-1 and Anand-2 under arid eco-system. The fruit yield per tree was recorded maximum in NA-7 (105 kg / tree). Whereas, minimum fruit yield per tree was recorded in Anand-1 (25.3 kg / tree).

Aulakh *et al.* (2013) reported that, Kanchan and Amrit were early maturing cultivars, Balwant, Krishna and Neelam are mid-season and Chakaiya was late maturing under Punjab conditions. Maximum fruit yield (85.33 kg/tree) was recorded in cultivar Balwant, followed by Neelam (76.13 kg/tree) and the lowest fruit yield (0.22 kg/tree) was recorded in Krishna cultivar.

2.3 Biochemical parameters

Srivastava and Srivastava (1964) observed that fresh aonla (*cv.* Banarasi) fruit contained 2.59 per cent acidity, 15.57 per cent reducing sugar, 682 mg vitamin C per 100 g pulp and 4.45 per cent tannin.

Teaotia *et al.* (1968) reported highest TSS content (15.2 B^o) and acidity (2.58 %) in Desi cultivar and lowest in Chakaiya (9.0 ^oB and 2.17 %, respectively). While, the cultivar Banarasi showed highest ascorbic acid content (665 mg/ 100 g pulp). They also observed that the total sugar reducing and non- reducing sugar of aonla fruit varies from 7.30 per cent (*cv.* Francis) to 9.60 per cent (*cv.* Chakaiya). 1.04 per cent (*cv.* Bamirasi) to 4.09 per cent (*cv.* Francis) and 3.05 per cent (*cv.* Francis) to 7.23 per cent (*cv.* Chakaiya), respectively among various aonla cultivars.

Ojha and Pathak (1993) observed that tannin content of aonla fruit varied between 2.3 and 3.40 per cent among evaluated ten aonla cultivars under Faizabad (Uttar Pradesh) conditions.

Singh *et al.* (1994) reported that TSS, acidity and ascorbic acid content of aonla fruit cultivars, Kanchan and Krishna were 13 and 14.0 per cent, 2.2 and 2.0 per cent and 711 and 783 mg per 100 g fruit pulp at maturity respectively.

Kumar and Singh (2002) studied ten aonla cultivars *viz.*, Banarasi, Francis, Krishna, Kanchan, Chakaiya, NA-6, NA-7, NA-5, NA-9, and NA-10 were evaluated for their physico- chemical constituents at Department of Horticulture, ND University, Faizabad. The average value of fruit weight (29.5g to 46.4 g), edible portion (92.85 to 94.9 %), seed (4.2 to 6.07 %), fibre (4.2 to 6.07 %), TSS (7.5 to 15 %), acidity (1.6 to 2.4 %), pectin (2.3 to 3.4 %) and total sugar varied from (3.5 to 4.9 %) respectively. The vitamin C content ranged from 305.7 (NA- 6) to 700 (Chakaiya) mg per 100 g. The range of phenol content was varied from 162.2 to 175.7 mg per 100 g.

Mehta *et al.* (2002) studied on the physico-chemical composition of different cultivars of aonla *viz.*, Banarasi, Chakaiya, Krishna, Kanchan and local seedlings, maximum total sugar (11.09 %) was observed in Banarasi and minimum in local seedling. The maximum (583.09 mg/100g) ascorbic acid and acidity (2.49 %) were observed in local seedling followed by Banarasi (548.77 mg/100g), which was significantly higher than rest of the cultivars.

Patel *et al.* (2003) evaluated nine varieties of aonla grown in arid zone of North Gujarat for fruit quality and they estimated the highest TSS content in variety Krishna (13.28 ^oB) while least in variety Chakaiya (8.03 ^oB).

Jaiswal *et al.* (2007) reported significant variation with respect to ascorbic acid content in different cultivars of aonla growing under Faizabad, Uttar Pradesh conditions. It varied from 465.0 to 500.5 mg per 100 g pulp in different cultivars. It was

registered maximum in cultivar NA-6, followed by NA-7 whereas, it was recorded minimum in Chakaiya.

Hazarika *et al.* (2009) evaluated fourteen genotypes collected from forests of Jorhat, Assam. The reducing sugars was recorded maximum (11.36 %) in AA-13 and minimum (3.76 %) in AA-6. Similarly, the highest total sugars (12.15 %) was observed in AA-13 and the lowest (5.57%) in AA-6. The highest titratable acidity (4.61 %) was found in AA-12 and minimum was in AA-3 (2.29 %).

Singh *et al.* (2009) studied on the performance of eight aonla cultivars *viz.*, Banarasi, Chakaiya, Francis, Kanchan, Krishna, NA-6, NA-7 and NA-10 under Chattisgarh conditions. At maturity, the ascorbic acid content in different cultivars varied from 702.48 to 882.11 mg per 100g of pulp. Among the cultivars studied, it was found highest (882.11 mg/100g pulp) in Banarasi, while lowest (702.48 mg/100g pulp) in Kanchan.

Shukla *et al.* (2010) reported that the TSS ranged from 14.90 to 19.30 per cent in aonla cultivars under subtropical conditions. It was maximum (19.30 %) in NA 6 and minimum (14.90 %) in Kanchan.

Yadav and Yadav (2010) studied on the performance of eight aonla cultivars namely, Krishna, Kanchan, Chakaiya, NA-7, Balwant Bold, Banarasi, Francis, and NA 10 at Mathura, Uttar Pradesh. The highest tannin content (3.35 %) was recorded in Chakaiya variety however, it was recorded lowest (2.60 %) in Banarasi. They also reported the highest titratable acidity (2.24 %) in Chakaiya whereas, it was lowest (1.90 %) in Krishna. The total sugars in different aonla cultivars varied from 2.40 to 3.70 per cent, lowest and highest values observed in Chakaiya and Krishna cultivars, respectively.

Kumar *et al.* (2011 a) reported that aonla genotype G-6 had significantly higher level of reducing sugars (3.50 %), non-reducing sugars (2.50 %) and total sugars (6.00 %). However, the minimum reducing sugars (1.80 %) were determined in G-1 and lowest non-reducing (1.36 %) as well as total sugars (3.23 %) were recorded in G-7.

The total soluble solids in aonla fruits were recorded maximum (14 %) in cultivar BSR-1 and minimum (7.6 %) in cultivar Krishna under Coorg conditions (Kumar *et al.*, 2011 b)

Bakshi *et al.* (2015) reported that Neelam resulted higher total sugars (5.71 %), reducing sugars (3.41 %) and non-reducing sugars (2.19 %), followed by Banarasi (5.69 % total sugars, 3.37 % reducing sugars and 2.14% non-reducing sugars). The least total sugars (5.38 %), reducing sugars (3.07 %) and non-reducing sugars (1.78%) were recorded in Desi. The maximum vitamin C content (596.03 mg/100g pulp) was recorded in cultivar Neelam followed by Banarasi (584.00 mg/100g of pulp) and

Kanchan (580.13 mg/100g pulp). Minimum vitamin C content (480.20 mg/100g pulp) was recorded in Desi.

Parveen and Khatkar (2015) studied on physico-chemical properties and nutritional composition of aonla (*Emblica officinalis*) varieties. Proximate, chemical and nutritional profiles of fresh aonla fruits of five varieties viz., Banarasi, Chakaiya, Kanchan, NA-7 and Desi were studied. Fruits of Desi variety had the highest fat content (0.48 %) followed by Chakaiya, Kanchan, NA-7 and lowest (0.36 %) in Banarasi. Crude fibre was observed maximum (22.35 %) in the fruit of Desi variety and minimum (7.18 %) in Banarasi.

Singh *et al.* (2015 a) noticed that, TSS to acid ratio ranged from 3.61 to 6.74, being maximum in Krishna (6.74), followed by NA-7 (5.60) and Anand-1 (5.51) whereas, it was minimum in Banarasi (3.61).

Kishore *et al.* (2016) revealed that the aonla genotypes showed significant variation in TSS content under eastern tropical region of Bhubaneswar. The cultivar NA-7 (10.36 %) and NA-10 (10.06 %) had relatively high TSS whereas, NA-6 (7.17 %), Banarasi (7.20 %) and Kanchan (7.88 %) had low TSS recorded. The cultivar Krishna was the most acidic (2.65 %) whereas, Francis (1.89 %) was the least acidic under eastern tropical region of Bhubaneswar.

Kumar *et al.* (2016) observed that the TSS to acid ratio was varied from 4.05 to 5.66, it was maximum in NA 7 (5.66) followed by Goma Aishwarya (5.55), Chakaiya (5.08) and Anand 2 (5.05) and minimum (4.05) in Francis.

Kumari and Khatkar (2016) evaluated five different varieties of aonla for phenolic content and antioxidant activities. Total polyphenolic content in fresh aonla fruit extracts varied from 70.6 to 159.4 mg GAE per g and their EC 50 (effective concentration) values for antioxidant activity ranged from 46.72 to 359.7 lg per ml.

Tripathi *et al.* (2016) reported the maximum TSS (11.50 %) in cultivar BSR-1 and minimum (7.90 %) in cultivar Krishna under humid tropical conditions of Western Ghats. The highest acidity (3.53 %) was observed in aonla cultivar BSR-1 and it was lowest (2.12 %) in Chakaiya, under humid tropical conditions at Chettalli (Karnataka).

Kumari *et al.* (2017) studied the performance of aonla cultivars on the antioxidant activity. Among the various cultivars studied, maximum free radical scavenging activity was observed in cv. Kanchan (73.1 %) followed by cv. Krishna (70.7 %). Whereas, minimum free radical scavenging activity was observed in cv. Hathijhul (58.8 %) followed by cv. Banarasi (59.8 %).

Kumari *et al.* (2017) evaluated the cultivars of aonla on flavonoid and phenol content. Among the various cultivars studied, maximum flavonoid content was observed in cv. kanchana (1.55 mg/g) whereas, minimum in cv. chakiya (1.20 mg/g)

and also observed that phenols highest in cv. Chakiya (1.90%) and lowest in cv. Banarasi (1.63 %).

2.4 Genetic variability

Genetic variability studies help the plant breeder to make an effective and efficient selection of genotypes from the available material which can be utilized for the further crop improvement programme. The success of any breeding programme mainly depends on the extent of genetic variability available in the population. Genotypic coefficient of variation indicates the relative magnitude of genetic diversity present in the material and helps to compare the genetic variability of different characters.

The phenotype of any plant is influenced by the genotype, environment and the interaction between the two. Further, the variation in a segregating population is attributed by both heritable and non-heritable components and the variation in a pure line by only environmental factors.

Heritability and genetic advance are important selection parameters. Heritability estimates provide information on the degree of inheritance of characters from parent to progeny. Knowledge on the heritability of different characters in relation to their contribution towards yield is a pre-requisite for an efficient breeding programme. Genetic advance is another important genetic parameter for determining the amount of expected change that could occur due to selection.

Singh *et al.* (2012) studied on morpho-chemical characters of *P. emblica* exhibited considerable genetic variability in fruit morphology, especially those based on fruit weight, which has high genotypic variation, higher heritability and greater potential for genetic gain, vitamin C had moderate genetic variance, moderate heritability but greater genetic gain. Highest phenotypic (9375.77) and genotypic (8773.12) variance was found in fruit weight. However, the lowest values (0.016 and 0.011) were found in fruit length and fruit diameter for genotypic and phenotypic variance, respectively. The heritability (broad sense) values were highest (0.99) for sugar content whereas, lowest (0.42) for fruit diameter. Genetic advance was found to be maximum (187850.27) for fruit weight and minimum (13.92) for fruit diameter. On the other hand, the highest genetic gain was for sugar (4655.58 %) and least (282.29 %) for moisture content in aonla fruit crop.

Rabha *et al.* (2013) studied on variability, heritability, genetic advance as percentage of mean in 32 citrus genotypes. The genotypes exhibited significant differences for all the characters under study. A wide range of variability in PCV and GCV was observed for leaf lamina, leaf thickness, fruit length, fruit breadth, fruit weight, rind weight, rind thickness, juice content, number of seed per fruit, seed weight, seed length, seed breadth, TSS, acidity, ascorbic acid, reducing sugar, total sugar and

yield. High heritability and high genetic gain were observed for leaf lamina length, leaf lamina width, leaf thickness, fruit length, fruit breadth, fruit weight, rind weight, rind thickness, juice content, number of seeds per fruit, seed weight, seed length, seed breadth, TSS, acidity, ascorbic acid, reducing sugar, total sugar and yield.

Gill and Navprem (2015) assessed the nature and genetic parameters to select superior genotypes of mango (*Mangifera indica* L.) The moderate estimates (>7.0%) of genotypic co-efficient of variation (GCV) recorded for fruit yield/plant (11.70), fruit weight (7.18), pulp weight (8.73) and peel weight (9.69) signified the presence of adequate variation among the genotypes. Physical fruit attributes viz., fruit yield/tree, fruit weight, pulp weight and peel weight had substantially higher heritability coupled with high genetic advance and confirmed that these traits are under the control of additive gene action.

Gupta *et al.* (2015) recorded higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for bunch weight, berry weight, bunch number and fruit yield per vine. These traits indicated the presence of adequate genetic variation among the genotypes and suitability for further improvement by selection

Mishra *et al.* (2015) found significant variance among genotypes of all traits of strawberry. The phenotypic coefficient of variation (PCV) for all the characters was slightly higher than genotypic coefficient of variation (GCV), which signified the presence of environmental influence to some degree in the phenotypic expression of characters. Dry fruit weight had the highest PCV (52.47) and GCV (48.26).

Lal *et al.* (2016) studied on 24 peach genotypes and reported that TSS to acid ratio and fruit weight recorded maximum variability. High heritability coupled with high genetic advance was obtained with acidity, TSS to acid ratio, fruit weight and yield per plant.

Patel *et al.* (2016) studied on 20 mango genotypes for genetic variability, heritability and genetic advance. The highest range of variation was exhibited by fruit yield per tree followed by number of fruits per tree, fruit volume, peel weight and stone weight. High estimates of genotypic and phenotypic coefficient of variation were recorded for all the characters except fruit width, TSS, non-reducing sugar and total sugar, which indicated the presence of sufficient variability among selected coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). High heritability estimates coupled with high genetic advance were observed for all the characters except tree canopy, indicating predominance of additive gene action in the inheritance of these traits, hence simple selection would be effective for genetic improvement of said characters in desired direction.

Rao *et al.* (2016) studied on genetic variability in fifty genotypes of bael fruit at Horticulture Research Centre and laboratory of the Department of Horticulture,

SVPUA&T, Meerut. Results revealed that high values of GCV and PCV were observed for yield per tree, fruit pulp weight, fruit weight, seed weight, number of fruits per tree, ascorbic acid, skull weight, and reducing sugar. High heritability (in broad sense) along with high estimates of genetic advance (% of mean) was observed for almost all the characters *viz.*, yield per tree, fruit weight, fruit pulp weight, skull weight, seed weight per fruit, T.S.S., ascorbic acid and total sugar.

Marboh *et al.* (2018) studied on 22 litchi genotypes and assessed for the variability, heritability and genetic advance. High phenotypic and genotypic coefficients of variation were recorded for pulp weight (32.86 and 31.11%), seed weight (30.56 and 27.93 %), peel thickness (25.07 and 20.21 %), pulp thickness (24.79 and 22.22 %) and fruit weight (22.65 and 21.17 %).

Sridhar *et al.* (2018) carried out studies to assess the genetic variability, heritability and genetic advance for different characters in 16 diverse cultivars of mango. The high phenotypic coefficient of variation and genotypic coefficient of variation were observed for petiole length, inflorescence width, fruit weight, pulp content, stone weight, seed width, seed weight, reducing sugars, non-reducing sugars, titratable acidity, TSS: acid ratio, ascorbic acid and yield. High heritability was recorded for majority of the characters *viz.*, tree height (99.51), inflorescence length (95.36), inflorescence width (95.32), fruit diameter (94.53), fruit weight (91.81), fruit skin thickness (93.16), pulp content (99.07), stone length (97.31), stone weight (96.72), seed width (95.46), seed weight (97.52), TSS (94.06), reducing sugars (93.61), ascorbic acid (94.88) and yield per plant (96.59).

Gupta and Kour (2019) studied on genetic variability and heritability in guava, estimated the high GCV and PCV were recorded for fruit yield per plant, fruit weight, plant height, petiole size, acidity and number of seeds per fruit while low GCV and PCV were expressed by E-W plant spread, leaf length, fruit breadth and N-S plant spread. Heritability estimates revealed that all the characters under study ranged from 99.97 for leaf breadth to 61.99 for TSS. Genetic advance as per cent of mean varied from 15.13 (fruit breadth) to 70.73 (number of seeds per fruit). High heritability coupled with high genetic advance as percent of mean was recorded for fruit yield, plant height, fruit weight, acidity and number of seeds per fruit indicating that these traits are under the control of additive gene action and phenotypic selection for their improvement will be effective.

2.5 Correlation studies

Correlation studies establish the extent of association between yield and its attributes. These yield components may form additional criteria for selection in the breeding programme. Yield is a complex entity associated with many characters, which are themselves inter-related. Such inter-relationships of various yield components are

essential to understand the relative importance of each factor involved. Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between essential characters, which are of immense help in the selection of suitable clones.

Inamdar (2000) observed that the fruit yield in Jamun had significantly positive correlation with fruit volume, seed volume, fruit length, fruit breadth, seed length, pulp weight, pulp to seed ratio, pulp per cent, pulp thickness and fruit size, while it had negatively correlation with fruit weight and seed per cent, at Gilihosur in Karnataka.

Sawant *et al.* (2003) revealed that fruit weight was significantly and positively associated with fruit diameter, fruit length, pomace content, seed weight per fruit and weight of single seed and negatively associated with seed number, TSS, moisture percentage and fruit number in karonda.

Srinivas *et al.* (2010) studied the correlation co-efficient for different characters in kagzi lime such as fruit weight, quality and yield characters. The result showed that fruit yield had a positive and significant association with an equatorial diameter of fruit, polar diameter, fruit size, fruit volume, TSS: acid ratio and fruit weight, However, it was found negatively significant association with ascorbic acid.

Jambhale *et al.* (2014) revealed that considerable amount of variation on papaya genotypes in their mean performances with respect to the characters studied except TSS (0.267), it indicates presence of sufficient variability for breeding of superior desirable genotypes. Yield per plant exhibited highly significant positive correlation with fruit cavity (0.88 and 0.68), number of fruits per plant (0.87 and 0.85), average fruit weight (0.77 and 0.67) and pulp thickness (0.63 and 0.54) at both genotypic and phenotypic levels respectively.

Gill and Navprem (2015) estimated the correlation co-efficient. The results showed that positive significant association of fruit yield per plant with fruit breadth (0.72) and fruit weight (0.66), while it was negatively associated with acidity (-0.076).

Jana *et al.* (2015) reported that fruit weight was positively and significantly correlated with fruit size ($r=0.860$) and fruit volume ($r=0.981$). T.S.S. was positively and significantly correlated with reducing sugar ($r=0.586$) and total sugars ($r=0.683$). Acidity also positively and significantly correlated with reducing sugar ($r=0.497$) and total sugars ($r=0.417$). Reducing sugar was positively and significantly correlated with total sugars ($r=0.888$). Yield was significantly and positively correlated with fruit size, weight and fruit volume ($r=0.327$) in guava

Lal *et al.* (2016) revealed correlation studies on peach, they reported that fruit weight ($r = 0.797$), fruit length ($r = 0.481$), fruit diameter ($r = 0.559$), fruit pulp thickness ($r = 0.630$) and stone diameter ($r = 0.352$) were the most important traits, which possessed significant positive association with fruit yield per plant.

Patel *et al.* (2016) reported that fruit yield per tree showed significant and positive correlation with number of fruits per tree at both genotypic and phenotypic levels. The significant and positive association of fruit length with fruit width, fruit volume, fruit weight and pulp weight; fruit width with fruit volume, fruit weight and pulp weight; fruit volume with fruit weight and pulp weight; fruit weight with pulp weight, peel weight and stone weight; pulp weight with peel weight and stone weight; peel weight with stone weight; stone weight with stone percentage and total sugar; stone percentage with total sugar; reducing sugar with total sugar; non-reducing sugar with total sugar and tree height with tree canopy at both genotypic and phenotypic levels.

Krishna *et al.* (2017) revealed correlation studies in mango with different physical parameters were carried out during 2015-16 at Fruit research station, Sangareddy, Telangana. Among the physical parameters per cent flowering was negatively correlated with vegetative buds per cent (-0.861**) and days taken for panicle initiation (-0.865**) and positively correlated with number of fruits per tree (0.756*). Among the quality parameters the data showing that yield is positively correlate with total sugars (0.824*) and TSS: acidity ratio (0.853*) whereas negatively correlate with ascorbic acid (-0.939**).

Reeta (2017) reported that correlation studies in aonla, fruit weight shown significant positive correlation with fruit volume (0.996**), pulp thickness (0.932*), pulp weight (1.000**) and juice content (0.999**) but it was non significantly positive correlation with stone weight (0.357) and yield (0.73).

Correlation studies by Bhogave *et al.* (2018) on different fruit and yield characters in 26 tamarind genotypes revealed that, the pod weight showed highly significant and positively correlation with pulp weight ($r = 0.942$), seed weight ($r = 0.866$), shell weight ($r = 0.913$), fibre weight ($r = 0.835$) and seed number ($r = 0.651$). However, yield per plant possessed positive correlation with pod width ($r = 0.215$), pod weight ($r = 0.290$), pulp weight ($r = 0.323$), seed weight ($r = 0.254$), shell weight ($r = 0.139$) and rag weight ($r = 0.128$). Whereas, yield per plant had highly significant association with pod length ($r = 0.497$) and seed number ($r = 0.555$).

Gupta and Kour (2019) revealed that fruit yield per plant showed significant positive association with number of seeds per fruit (0.4415) and acidity in fruits (0.4267) and negative association with petiole size (-0.4608). Fruit weight showed significant positive association with fruit length (0.6134) and fruit breadth (0.7622). Plant height showed significant positive association with N-S plant spread (0.6584) and negative association with (-0.5535) fruit length. Fruit length has positive association with fruit breadth (0.6914) and number of seeds per fruit in guava.

Lal Nag *et al.* (2020 a) revealed that, the character total soluble solids exhibited highly significant positive correlation with total sugar, reducing sugar, keeping days,

pulp ratio, pulp-seed ratio, peel per cent and fruit yield per plant with both the genotypic and phenotypic level, while highly significant negative correlation was found with acidity at both the phenotypic and genotypic level.

Parmar *et al.* (2020) observed that fruit yield had significant and positive correlation for shoot length and fruit diameter at genotypic and phenotypic levels, average fruit weight had positive and highly significant correlation with average number of seeds per fruit and acidity at genotypic and phenotypic levels. Number of fruits per tree had highly significant and positive correlation with total soluble solids at genotypic and phenotypic levels in sapota.

2.6 Path co-efficient studies

Path co-efficient analysis is a tool in genetic analysis for partitioning the association of the components on yield into direct and indirect effect of the characters through other components. The path co-efficient analysis was used to study the cause and effect relationship, diagrammatically.

Jambhale *et al.* (2014) reported that number of fruits per plant had the highest direct effect (0.97) on yield per plant followed by average fruit weight (0.56), length of fruit (0.19) indicating importance of these characters and which can be strategically used to improve the yield of papaya.

Gill and Navprem (2015) Path analysis revealed that fruit weight (1.60) and fruit breadth (0.41) had moderately higher direct effects on fruit yield. Fruit weight showed indirect contribution *via* all the traits except fruit juice acid content signifying that fruit weight is the major contributor towards fruit yield/plant in mango.

Lal *et al.* (2016) studied on path coefficient analysis on peach, they revealed that fruit weight (0.9786) followed by TSS (0.299), fruit pulp thickness (0.211), stone diameter (0.1933) and ascorbic acid (0.0028) influenced direct effect on fruit yield per tree. The direct effects of these traits on fruit yield were found positive and considerably high. Moreover, fruit length, fruit diameter had positive and higher indirect effect on fruit yield through fruit weight in peach.

Phenotypic path coefficient analysis on guava studied by Gupta and Kour (2019) revealed that positive direct effect on yield was exhibited by fruit length (1.950) followed by N-S plant spread (1.273), acidity (0.328), leaf length (0.306), number of seeds per fruit (0.166) and very low magnitude with fruit weight (0.039), plant height (0.075) and petiole size (0.006) indicating good scope for improvement in fruit yield. Fruit length also showed indirect contribution *via* fruit weight (1.196) and fruit breadth (1.348).

Lal Nag *et al.* (2020 a) studied on path analysis of different qualitative traits in sapota, revealed that reducing sugar had highest positive direct effect (0.742)

relationship with fruit yield per plant followed by pulp- seed ratio (0.556), peel percentage (0.082) and non-reducing sugar (0.067). The quality character, total soluble solid showed low negative direct effect on fruit yield per plant due to low positive indirect effect *via* acidity, non-reducing sugar and low negative indirect effect *via* pulp ratio, peel per centage, reducing sugar, pulp- seed ratio, total sugar and keeping days. Total sugar had shown high negative direct effect on fruit yield per plant due to high positive indirect effect *via* acidity and low positive indirect effect *via* non-reducing sugar. Reducing sugar showed high positive direct effect on fruit yield per plant due to high positive.

Parmar *et al.* (2020) reported that the fruit weight had highest positive direct effect on fruit yield followed by number of fruits per tree. Positive direct effect on fruit yield was recorded for fruit length, chlorophyll content, canopy spread North – South, canopy spread East – West, fruit retention at harvest, acidity, plant height and number of flowers per shoot on sapota.

2.7 Genetic divergence

The success of a breeding program depends upon the selection of parents. It has been found that the progenies derived from crossing divergent parents give divergent and useful progenies. The multivariate analysis based on Mahalanobis D^2 statistics is employed as a powerful tool for measuring genetic divergence among the tested genotypes.

Rekha *et al.* (2011) studied on cluster analysis in sapota, experiment includes two main clusters, further divided into two sub clusters i.e., a total of four sub-clusters. The first sub-cluster comprised seven varieties, the second sub-cluster included six accessions. The third sub-cluster had two accessions which were distinct. The fourth sub-cluster was composed of five accessions. All accessions within each cluster showed a close relationship. The first cluster (including sub clusters 1 and 2) had 13 accessions comprising of small, oval fruit types. The first sub-cluster included the accessions Calcutta Round, CO-2, Vavivalsa, Kirtibarti, Mohangooti, Seedless, and an unknown collection from Gujarat. The second sub-cluster included varieties like Gutti, Oval, Jhumakiya, Pilipatti, Pakala oval and Dwarapudi.

Sharma *et al.* (2013) studied on genetic diversity, results revealed that, all the genotypes, on the basis of total variability were grouped into four distinct clusters. Maximum number of cultivars were accommodated in cluster IV (Fuji, Gala, Jonadel, Jonagold, Red Fuji, Royal Gala and Spijon) followed by cluster I (Arlet, Ruspippin, Sinta and Summerred), cluster III (Crimson Gold, Elstar and Neomi) and cluster II (Spartan and Quinte). Cluster IV had highest intra cluster value so was most divergent and Cluster I having least intra cluster value was least divergent. Highest value for inter cluster distance was recorded between cluster I and II while it was lowest between

cluster III and IV. Cluster means were maximum in cluster II followed by clusters I, III and IV. Neomi is best cultivars for fruit yield per plant, fruit length, fruit diameter, fruit weight, total sugars and non-reducing sugars. However, Jonagold is best for TSS. Cultivars Spartan, Elstar, Royal Gala, Jonagold and Summerred would prove best for different vegetative characters.

Singh *et al.* (2015 b) studied on genetic diversity and results revealed that tested genotypes were grouped into six clusters, cluster III and V showing maximum inter cluster distance. Cluster I, cluster IV, cluster V and cluster VI showed intra cluster distance of 55.12, 55.40, 50.70 and 61.84, respectively, indicating that the genotypes in these clusters have dissimilarity for morphological features and performance. Cluster III had highest mean value for fruit weight (312.39 g), fruit length (109.60 mm), fruit width (72.88 mm) and fruit outer flesh thickness (17.95 mm) and least mean values for seed weight per 100 g of fruit (0.933 g). Cluster V was characterized by minimum mean value for 100-seed weight (1.017 g) and maximum value for total soluble solids (11.60 %) and titratable acidity (0.486 %). Contribution towards observed diversity was found to be 47.90, 16.73, 13.11 and 10.76 per cent for seed weight per fruit, fruit diameter, 100-seed weight and leaf width. Genotypes from Cluster III, V and IV may be chosen for intercrossing to get the desired trait combinations through high heterotic response and superior recombinants in their progenies.

Baswal *et al.* (2017) studied on genetic diversity in pummelo, results revealed that, the tested genotypes were grouped into four clusters, indicating that the genotypes in these clusters have dissimilarity for morphological features and performance. Cluster I was recorded with no fruiting, while cluster III had the highest mean value for fruit weight (1218.17 g), fruit diameter (175.93 mm), fruit length (151.36 mm), fruit rind thickness (21.86 mm) and number of segments per fruit (15.50) and least mean value for total soluble solids (7.720 °Brix) and 20 seeds weight (5.86 g). Cluster II was characterized by maximum value for titratable acidity (0.89 %), 20 seeds weight (6.44 g), seed width (8.47 mm) and least mean value for fruit diameter (134.05 mm), fruit rind thickness (15.55 mm) and seed number (84.5).

Kumar and Deepika (2018) studied on cluster analysis, results revealed that cluster I had maximum number of collections (8) and cluster II and V had the minimum number of collection (1). Diversity was observed with respect to fruiting season (March-April and April-May), days from flowering to fruit maturity (62 days to 68 days), fruit set to maturity (58 days to 64 days), fruit clustering habit (solitary and cluster), fruit weight (5.91 g to 12.28 g), fruit volume (5.32 cc to 11.40 cc), number of fruits per cluster (3 to 12), specific gravity (0.91 to 1.23), fruit length (1.61 cm to 3.10 cm), fruit width (1.24 cm to 2.41 cm), fruit shape (oblong), fruit colour (blackish purple), firmness to softness (4.09 kg cm⁻² to 9.94 kg cm⁻²), juice content (14 % to

44 %), pulp content (77.50 % to 90.39 %), seed weight (9.60 % to 22.49 %), pulp to seed ratio (3.24 to 9.41) and yield per plant (10 kg plant⁻¹ to 54 kg plant⁻¹).

Kumar *et al.* (2020) conducted experiment on grouping of jamun genotypes based on fruit quality parameters, results indicated that, genotype Konkan Bahadoli showing maximum fruit length (3.55 cm), fruit width (2.5 cm), and fruit weight (13.16 g). Lowest recorded in Dharwad-12. The genotype Konkan Bahadoli given maximum seed length (2.5cm), width (1.5cm) and weight (3.05 g). The highest TSS content (28.2°Brix) in Dharwad-3a and lowest (14.5° Brix) was recorded in Patna. The genotype Selection-58' was recorded lowest titratable acidity content (0.82 %), whereas the highest acidity content (3.52 %) in Dharwad-12. Among the genotypes, Kaithanal, Dharwad-4, Dhanwad-8, 1C-715 was showing the distinctive from other genotypes in cluster analysis with respect to biochemical parameters.

Lal Nag *et al.* (2020 b) studied on cluster analysis for qualitative traits, results showed that all genotypes were grouped into 8 clusters using non- hierarchical Euclidean cluster analysis. For qualitative parameter, maximum number of genotypes were grouped into cluster VIII (14) followed by cluster III (12). Intra and Inter- Cluster distances among 8 clusters for qualitative traits in custard apple. The highest intra-cluster distance was recorded for cluster VI (48.65) followed by cluster II (46.79) and the smallest intra cluster distance was recorded in cluster III (0.00) followed by cluster V (8.15) for qualitative traits.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The present investigation on “Evaluation of aonla genotypes for yield and quality traits” was carried at Forest Research Station, Govinkovi, Honnali taluk, Davangere district during 2020-21. The details of the experimentation, geographical location, agro-climatic conditions and techniques adopted in the present investigation are furnished in this chapter.

3.1 Geographical location and weather condition of the experimental site

The experimental site is located in Govinkovi, Davanagere district, which is situated on 140 25' North latitude and 750 67' East longitude, with an elevation of 540 m above mean sea level (MSL). The meteorological data on monthly average maximum and minimum temperature, relative humidity and rainfall of experimental period was presented in Appendix I.

3.2 Experimental details

- Experimental Design: R C B D (Randomized Complete Block Design)
- Treatments or Genotypes : 14
- Replications: 03
- Location : Forest Research station, Govinakovi, Honnali (Tq), Davangere (Dist)
- Number of Genotypes: 14 genotypes (Grafted). It is depicted in Table 1.
- Age of tree: 18 years

Table 1. List of aonla genotypes used for the experiment

SI No.	Genotypes	Location
1	NA-6	Forest Research Station, Govinakovi, Honnali(Tq), Davangere (Dist)
2	NA-7	
3	S-2	
4	S-4	
5	S-5	
6	S-7	
7	S-9	
8	K-16	
9	K-17	
10	K-19	
11	K-18	
12	K-23	
13	V-11	
14	K-7	

3.2.1 Treatment details

The experiment was laid out with randomized complete block design (RCBD) with 14 genotypes and replicated thrice. The genotype in each replication were allotted randomly.

The methods used for the estimation of various morphological traits and biochemical parameters of 14 aonla genotypes are presented below.

3.3 Recording experimental observation

Five trees were selected randomly in each genotype per replication for the purpose of recording observations on growth, quality and yield. The average value of data was worked out for the purpose of statistical computation. The details of experimental observation are as follows

3.3.1 Tree morphological parameters

3.3.1.1 Tree shape

Tree growth habit was recorded visually based on guidelines by Protection of Plant Varieties and Farmer's Rights (PPV and FR). It was observed that there were 3 types of plant growth habits : erect, spreading and drooping.

3.3.1.2 Stem girth (cm)

The girth of the tree trunk was measured by using a measuring tape and the average reading was expressed in terms of centimeters.

3.3.1.3 Tree height (m)

Tree height of the genotypes measured using Ravi altimeter. It is a portable instrument for measuring height of trees without the trigonometric tables and formulae as required for determination of Abney's level. It consists of four scales viz, 20 m, 30 m, red scale for slope correction and per cent scale. For the measurement of tree height 20 m scale is used. The observer must stand about 20 m of horizontal distance from tree to get height of the tree above the eye level directly. Since, the scales are in units, the height of the tree is indicated in the same unit in which the horizontal distance is taken. The height can be read through a longitudinal window in the metal case, which is covered by glass. The instrument has a pistol grip. A lever, on one side of instrument releases a button below the index finger and locks the movement of the pointer on the scales. While releasing the lever, the instrument is pointed to the tip of the tree through the eye-view and the target. The button is pressed when the eye, the target and the tip of the tree are in line. The button should be pressed when the movement of the pointer stops.

$$\text{Tree height (m)} = \text{Top reading} + \text{Base reading}$$



Plate 1. General view of experimental plot

3.3.1.4 Trunk colour

Trunk colour of the trees recorded based on guidelines by PPV and FR. The colour of the trunk varied from grey colour, whitish grey and brownish grey among the genotypes.

3.3.2 Leaf characters

3.3.2.1 Leaf shape

The leaf shape of the trees recorded based on guidelines by PPV and FR. There were 3 leaf shapes viz., elliptical, oblong and ovate.

3.3.2.2 Leaf colour

Leaf colour of the genotypes were identified with the help of colour chart of Royal Horticultural Society.

3.4.2.3 Leaf apex

The leaf apex of the trees recorded based on guidelines by PPV and FR. Leaf apex was varied and observed. i.e Acute and obtuse in aonla genotypes.

3.4 Fruit and yield parameters

3.4.1 Fruit parameters

3.4.1.1 Fruit length (cm)

After harvest, length of the individual fruit was measured with help of vernier calliper and the mean was worked out and expressed in centimeters.

3.4.1.2 Fruit diameter (cm)

The diameter of the individual fruit was measured with the help of vernier calliper and the mean was worked out and expressed in centimeters.

3.4.1.3 Fruit volume (cc)

Volume of the fruits of various genotypes were recorded using water displacement method.

3.4.1.4 Fruit weight (g)

Fruit weight was recorded by weighing fresh fruit on weighing balance and average fruit weight was calculated and represented in grams.

3.4.1.5 Pulp weight (g/fruit)

Pulp of single fruit was extracted and weighed using electronic weighing balance of different genotypes. The average was worked out and expressed in grams.

3.4.1.6 Number of seeds per stone

Seeds were extracted from the stone of the desirable genotype. Individual

number of seed per stone was counted and expressed in number.

3.4.1.7 Stone weight (g)

Stone was extracted from the individual fruit, average was worked out and recorded in gram using electronic weighing balance.

3.4.1.8 Stone: Pulp ratio

The ratio of stone to pulp was calculated and recorded for all genotypes.

3.4.1.9 Pulp: stone

The ratio of pulp to stone was calculated and recorded for all genotypes.

3.4.2 Yield parameters

3.4.2.1 Yield per tree (kg)

The fruit yield per tree was recorded at different intervals of harvest and expressed in kilograms.

3.4.2.2 Yield per hectare (ton)

The fruit yield per tree was recorded randomly from the tagged trees and it was expressed in yield (ton) per hectare.

3.5 Biochemical parameters

3.5.1 Total soluble solids (°Brix)

Total soluble solids recorded by using hand refractometer. A small amount of fruit juice is taken and kept on the respected area, later the readings were taken and analyzed.

3.5.2 Acidity (%)

The acidity content of different genotypes was estimated (Ranganna, 1986). Clear homogenized juice was taken in 100ml conical flask. One to two drops of phenolphthalein indicator was added to it. Then the diluted sample was titrated against 0.1N sodium hydroxide solution taken in a burette. The end point of titration was indicated by a faint pink colour. Titration was continued till three current readings were obtained. Percentage of acidity is calculated by using the formulae with the obtained titrated values. The acidity percentage of the juice in terms of citric acid was calculated adopting the following formula and expressed in arc sign values.

$$\text{Titrateable acidity (\%)} = \frac{\text{Titre value} \times \text{Normality of NaOH} \times \text{Vol. make up (ml)}}{\text{Gram of sample} \times \text{Vol. of sample}} \times 100$$

Note: Meq of citric acid = 0.06404

3.5.3 Vitamin C (mg/ 100 g)

Presence of amount of vitamin C in different genotypes was estimated based on the procedure discussed by Ranganna (1986). About 5 ml of sample filtrate was taken which is diluted with the 4 per cent oxalic acid and made up to 100 ml using distilled water. Pipette out 5 ml of the supernatant, for this add about 10 ml of 4 per cent oxalic acid and titrated against the dye.

Preparation of solutions:

- Four per cent Oxalic acid: About 4 g of oxalic acid was dissolved in little quantity of water and final volume made to 100 ml using distilled water.
- Standard stock solution: Dissolve 100 mg ascorbic acid in 100 ml of 4 per cent oxalic acid solution in standard flask (1 mg / ml).
- Working standard solution: Dilute about 10 ml of stock solution with 4 per cent oxalic acid. The concentration of working standard solution is 100 µg per ml.
- Dye solution: Dissolve about 50 mg of sodium salt of 2, 6-dichlorophenol indophenols in approximately 150 ml of hot distilled water containing about 42 mg of sodium bicarbonate. Later cool and dilute with distilled water to 200 ml. Store in a refrigerator and standardize every day.
- Standardization of dye: Take about 5 ml of working standard ascorbic acid solution and 10 ml of 4 per cent oxalic acid in a 25 ml conical flask. Fill a micro burette with dye. Later titrate the solution in the conical flask against the dye solution till the solution in the flask turns to pink which persists for 15 seconds. Determine the dye factor *ie.*, mg of ascorbic acid per ml of the dye using formulae;

$$\text{Dye factor} = \frac{0.5}{\text{Titre value}}$$

$$\text{Abscorbic acid (mg/100g)} = \frac{\text{Titre value} \times \text{Dye factor} \times \text{Vol. makeup (ml)}}{\text{Aliquot taken for estimation} \times \text{Vol. of sample taken}} \times 100$$

3.5.4 Reducing sugars (%)

Dinitrosalicylic (DNSA) method

- DNSA reagent preparation: One gram of DNSA was dissolved in 50 ml of water. To this solution 30 g Sodium potassium tartarate tetrahydrate was added. Then, the solution turns milky white. Add 20 ml of 2N NaOH which turns the solution to transparent orange yellow colour and made volume to 100 ml with distilled water.
- Standard glucose curve: 100 mg of glucose was dissolved in some quantity of water and volume made to 100 ml (1 mg / ml). Later 0, 0.2, 0.4, 0.6, 0.8 and 1 ml of glucose solution was added to different test tubes, made volume to 2 ml using distilled water. 1 ml of DNSA to each test tube was added and mixed well. Then,

the test tubes were kept for boiling in water bath for five minutes. Cool the test tubes and made up the volume to 10 ml, using distilled water. The absorbance was recorded at 540 nm using spectrophotometer. Clean and dried test tubes were taken, to which 0.1 ml of prepared sample was added and O.D was measured at 540 nm. The amount of reducing sugar present in sample was calculated using standard graph and expressed in arc sign values. (Ranganna, 1986).

$$\text{Reducing sugar (\%)} = \frac{\text{Glucose (mg)in sample from standard curve}}{\text{Aliquot taken for test (ml)}} \times \frac{\text{Vol.made(ml) after alcco hol evaporation}}{\text{Vol.taken for alcohol evaporation}} \times \frac{\text{Vol.made (ml)after sample extraction}}{\text{sample taken for extraction(mg)}} \times 100$$

3.5.5 Total sugars (%)

Anthrone reagent method

- Preparation of Anthrone reagent: 100 ml of chilled H₂SO₄ was taken in a beaker and 200 mg of anthrone was dissolved in concentrated sulphuric acid and the solution was prepared fresh just before using.
- Standard glucose solution: Preparation of standard glucose curve was done (100 mg of glucose in 100 ml of water) by taking 0, 0.2, 0.4, 0.6, 0.8 and 1 ml of standard glucose solution and was added to different test tubes and made the volume up to 2.5ml using distilled water. All the test tubes were kept in ice bath and 4 ml of anthrone reagent was added to each test tubes slowly and stirred the content gently with glass rod. Later the test tubes were kept in boiling water bath for exactly 7.5 minutes and they were cooled immediately using ice bath. After cooling, the absorbance of the solution were measured at 630 nm against the blank.

Clean and dried test tubes were taken, to which 0.1 ml of prepared sample was added and O.D was measured at 630 nm. The amount of total sugar present in sample was calculated using standard graph and expressed in arc sign values (Ranganna, 1986).

$$\text{Total sugar (\%)} = \frac{\text{Glucose (mg)in sample from standard curve}}{\text{Aliquot taken for test (ml)}} \times \frac{\text{Vol.made after hydrolysis (ml)}}{\text{Vol. taken for alcohol hydrolysis (ml)}} \times \frac{\text{Vol.made(ml) after alcco hol evaporation}}{\text{Vol.taken for alcohol evaporation}} \times \frac{\text{Vol.made (ml)after sample extraction}}{\text{sample taken for extraction(mg)}} \times 100$$

3.5.6 Non- reducing sugars (%)

Non-reducing sugar was calculated by deducting the quantity of reducing sugars from total sugars and multiplied by constant factor 0.95 and the results were expressed as per cent of non-reducing sugar and expressed in arc sign values (Ranganna, 1986).

3.5.7 TSS : Acid

The ratio of total soluble solids and acidity content of the genotypes were calculated and recorded.

3.5.8 Estimation of Tannins (%)

Total tannin content was estimated by titrimetric method. By preparing standard solution of Indigo carmine and titrate against 0.1N aqueous solution of KMnO_4 . One gram sample was taken and 50 ml of distilled water was added and incubated at room temperature for 2 hours. Solution was filtered and make up the volume to 100ml with distilled water. 1 ml of Indigo carmine solution was added to sample solution later titrated against KMnO_4 . Noted down the titrate value (AOAC, 1980).

$$\text{Tannin content (\%)} = \frac{(V - V_0) \times 0.004157 \times \text{total volume made up} \times 100}{\text{weight of the sample} \times \text{volume of the indigo solution}} \times 100$$

V = Initial titration value of the sample

V_0 = Final titration value of the sample

3.5.9 Determination of fat content (%)

The 5 g ground sample was defatted with petroleum ether in Soxhlet apparatus for 10-11 hours at 60°C. The resultant ether extract was evaporated and lipid content was calculated (AOAC, 1980)

$$\text{Fat (\%)} = \frac{\text{Final weight of flask} - \text{Empty weight of flask Crude}}{\text{weight of the fat free sample}} \times 100$$

3.5.10 Crude fiber (%)

Crude fiber was estimated by the acid alkali digestion method. Fat free sample was hydrolysed with sulphuric acid (0.255 N) and sodium hydroxide (0.313). The residue obtained after digestion was dried in a crucible and its weight was recorded (We). The dried residues were then ashed in a muffle furnace at 600⁰ C for 2 to 3 hours and its weight (Wa) was recorded. The difference between these two digits (We-Wa) was calculated divided by weight of fat free sample taken for the estimation of crude fiber and expressed in terms of per cent (AOAC, 1980).

$$\text{Crude fiber (\%)} = \frac{\text{We} - \text{Wa}}{\text{Weight of the free sample}} \times 100$$

Where,

We = Weight of residues with crucible

Wa = Weight of ash with crucible

3.5.11 Determination of total flavonoid content (mg QE/g)

Total flavonoid content was measured with the aluminium chloride colorimetric assay. 1ml of aliquot and 1ml standard quercetin solution (100, 200, 400, 600, 800,

1000 µg/ml) was positioned into test tubes and 4ml of distilled water and 0.3 ml of 5 per cent sodium nitrite solution was added into each. After 5 minutes, 0.3 ml of 10 per cent aluminum chloride was added. At 6th minute, 2 ml of 1 M sodium hydroxide was added. Finally, volume was made up to 10 ml with distilled water and mixed well. Orange yellowish color was developed the absorbance of the solution was measured at 510 nm in spectrophotometer. The blank was performed using distilled water. The calibration curve was plotted using standard quercetin. The data of total flavonoid was expressed as mg of quercetin equivalents per g of dry mass (Lee & Ismail, 2012).

$$\text{Total flavonoid content (mg QE/g)} = c \frac{V}{m}$$

where,

c= concentrations of quercetine obtained from calibration curve (mg/ml)

V= volume of extract in (ml)

m= mass of extract in (gram)

3.5.12 Determination of total phenol content (%)

The total phenolic content of fruit extract was determined by using Folineciocalteu reagent, based on the method described by (Sadasivam and Manikam, 1991). One milliliter of extract solution was added into a flask containing 9 ml of distilled water. The extract solution was thoroughly mixed with 1 ml of Folin-ciocalteu's phenol reagent. Afte 5 min, 10ml of 7 per cent Na₂CO₃ was added. The mixture was further shaken and made up to 25 ml with addition of 4 ml of distilled water. Then, the absorbance was measured at 750 nm after 90 min of incubation at room temperature using spectrophotometer. The total phenolic content was expressed as mg of gallic acid equivalents (GAE) per g dry matter.

$$\text{Polyphenolic content (mg GAE/ g)} = c \frac{V}{m}$$

where,

c= concentrations of gallic acid obtained from calibration curve in mg/ml

V=volume of extract in ml

m=mass of extract in gram

3.5.13 Determination of antioxidant content (%)

Scavenging activity (DPPH) assay

The free radical scavenging activities of the extracts were determined by using 2, 2- Diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging method. A fresh 0.002 per cent solution of DPPH was prepared in methanol and its absorbance was recorded at 515 nm. 50 µl of pure extracts was mixed with 3 ml solution of DPPH and

allowed to stand in darkness for 15 minutes. The absorbance was again recorded at 515 nm. The control was prepared as above without sample solution, the scavenging activity was estimated based on the percentage of DPPH radical scavenged, and the scavenging effect (%) was calculated by the following equation (Maizura *et al.*, 2011)

$$\text{Scavenging effect \%} = \frac{(1 - \text{Absorbance of sample})}{(\text{Absorbance of control})} \times 100$$

3.6 Estimates of genetic variability parameters

3.6.1 Genotypic, phenotypic and environmental variance

The variance due to genotype, phenotype and environment were computed as follows.

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{MS due to genotypes (adj)} - \text{MS due to error (intra block)}}{\text{Replication (r)}}$$

$$\text{Environmental variance } (\sigma e^2) = \text{Error mean sum of squares}$$

$$\text{Phenotypic variance } (\sigma p^2) = g^2 + e^2 \text{ (MS due to error)}$$

Where, 'r' is number of replications

3.6.2 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) based on the estimate of genotypic and phenotypic variance.

Genotypic coefficient of variation (GCV)

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

Phenotypic coefficient of variation (PCV)

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

Where,

\bar{X} = General mean

r = Number of replications

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

PCV and GCV were classified (Subramaniyan and Memon, 1973) as mentioned below,

0 – 10 % = Low

>10 – 20 % = Moderate

>20 % and above = High

3.6.3 Heritability

The broad sense heritability (h^2 bs) was estimated by following the procedure suggested by Weber and Moorthy (1952) as indicated here below.

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where, h^2 (%) = Heritability (Broad sense)

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability was categorized (Robinson *et al.*, 1949) as mentioned below

0 – 30 % = Low

>30 – 60 % = Moderate

>60 % and above = High

3.6.4 Expected genetic advance

Genetic advance for each character was predicted by the formula given by Johnson *et al.* (1955).

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

Where, k = Selection differential at 5 per cent selection intensity

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

3.6.5 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent over mean was worked out as suggested by Johnson *et al.* (1955). Where, GA = Genetic advance \bar{x} = General mean

$$GAM = \left(\frac{GA}{\bar{x}} \right) \times 100$$

Where, GA = Genetic advance

\bar{x} = General mean

The genetic advances as per cent of mean (GAM) was categorized as suggested by Johnson *et al.* (1955) and are mentioned below,

0 – 10 % = Low

>10 – 20 % = Moderate

>20 % and above = High

3.7 Correlation coefficient analysis

The correlation coefficient among all possible character combinations at phenotypic (rp) and genotypic (rg) level were estimated employing formula (Al- Jibouri *et al.*, 1958).

$$\text{Phenotypic correlation} = r_{xy}(P) = \frac{\text{Cov}_{xy}(p)}{\sqrt{V_x(p) \times V_x(p)}}$$

$$\text{Genotypic correlation} = r_{xy}(G) = \frac{\text{Cov}_{xy}(g)}{\sqrt{V_x(g) \times V_x(g)}}$$

Where,

$\text{Cov}_{xy}(g)$ = Genotypic covariance between x and y

$\text{Cov}_{xy}(p)$ = Phenotypic covariance between x and y

$V_x(g)$ = Genotypic variance of character 'x'

$V_x(p)$ = Phenotypic variance of character 'x'

$V_y(g)$ = Genotypic variance of character 'y'

$V_y(p)$ = Phenotypic variance of character 'y'

The test of significance for the association between characters was done by comparing table 'r' values at (n-2) error degrees of freedom for phenotypic and genotypic correlations with estimated values, respectively.

3.8 Path coefficient analysis

Path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959) was carried out to know the direct and indirect effect of the morphological traits on plant yield. The following set of simultaneous equations were formed and solved for estimating various direct and indirect effects.

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{1i}i$$

$$r_{2y} = a + r_{21}a + b + r_{23}c + \dots + r_{2i}i$$

$$r_{3y} = r_{31}a + r_{32}b + c + \dots + r_{3i}i$$

$$r_{1y} = r_{11}a + r_{12}b + r_{13}c + \dots + I$$

Where,

r_{1y} to I_{1y} = Coefficient of correlation between causal factors 1 to I with dependent characters y.

r_{12} to r_{1i} = Coefficient of correlation among causal factors a, b, c,.....

i = Direct effects of characters 'a' to 'I' on the dependent character 'y'.

Residual effect (R) was computed as follows.

$$\text{Residual effect(R)} = 1 - \sqrt{a^2 + b^2 + c^2 \dots \dots i^2 + 2abc12 + 12acr13 \dots}$$

3.9 Genetic divergence

Mahalanobis (1936) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasm. Mahalanobis generalized distance (D^2) between any two populations is given by the formulas

$$D^2 = \sum \lambda_{ij} \sigma_i \sigma_j$$

Where, D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal index

$$\sigma_i = \mu_{i1} - \mu_{i2}$$

$$\sigma_j = \mu_{j1} - \mu_{j2}$$

μ = General mean

Since the formula for computation requires the inversion of higher-order determinants, the transformation of the original correlated unstandardized character means (Xs) to standardize uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.9.1 Clustering D^2 values

All the $n(n-1)/2$ D^2 values were clustered using Tocher's method (Rao, 1952).

3.9.2 Intra and inter-cluster distance

The intra and inter-cluster distances were calculated by following the formula described by Singh and Choudhary (1977).

$$\text{Square of intracluster distance} = (\sum Di^2)/(N)$$

Where, $\sum Di^2$ = Sum of distances between all possible combinations of the entries included in the cluster

N = Number of all possible combinations

$$\text{Square of inter - cluster distance} = \frac{\sum Dij^2}{n_i n_j}$$

Where,

$\sum Dij^2$ = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster.

n_i = Number of entries in the cluster i

n_j = Number of entries in the cluster j

3.10 Statistical analysis of experimental data

The experimental data recorded on various parameters during the investigation were analyzed statistically using method of analysis of variance (ANOVA) for Randomized Complete Block Design (RCBD) as given by Gomez and Gomez (1984). Whenever 'F' test was found significant for comparing the means of two treatments, critical difference (C.D. at 5%) were worked out.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The data pertaining with respect to 14 genotypes of aonla (*Emblica officinalis* G.) on various morphological and bio-chemical characters were subjected to statistical analysis and the results obtained were presented under the following heads.

4.1 Tree morphological parameters

4.2 Fruit and yield parameters

4.3 Biochemical parameters

4.4 Genetic variability

4.5 Correlation studies

4.6 Path co-efficient analysis

4.7 Genetic divergence

4.1 Tree morphological parameters

4.1.1 Tree parameters

4.1.1.1 Tree height (m)

The data on tree height (Table 2.) showed significant difference during experimental period. Tree height was observed maximum in K-18 (6.46 m) which was *on par* with K-23 (6.25 m), K-19 (6.19 m) and K-16 (5.90 m). However, it was found minimum in V-11 (3.55 m).

4.1.1.2 Stem girth (cm)

The result revealed significant differences on stem girth of aonla genotypes which is depicted in Table 2. The maximum stem girth was recorded in S-4 (86.53 cm) which was statistically *on par* with S- 9 (86.35 cm) and K-23 (85.56 cm). While, it was minimum in V-11 (54.01 cm).

4.1.1.3 Tree shape

Tree shape shows variation among different genotypes. Spreading growth habit was observed in 11 (NA-6, NA-7, S-2, S-4, S-5, S-7, S-9, K-16, K-17 V-11 and K-7) genotypes. Whereas, erect growth habit was observed in three (K-19, K-18 and K23) genotypes, which is furnished in Table 3.

4.1.1. 4 Trunk color

All the genotypes showed whitish grey trunk color during experimental period and it is depicted in Table 3.

Table 2. Variation in tree height and stem girth of aonla genotypes

Genotypes	Tree height (m)	Stem girth (cm)
NA-6	4.23	73.20
NA-7	4.80	82.80
S-2	5.16	79.40
S-4	5.73	86.53
S-5	5.21	54.22
S-7	5.11	79.21
S-9	5.50	86.35
K-16	5.90	69.23
K-17	5.74	80.48
K-19	6.19	79.46
K-18	6.46	83.48
K-23	6.25	85.56
V-11	3.55	54.01
K-7	6.03	67.23
S.Em ±	0.22	1.03
C.D @ 5 %	0.65	2.90

4.1.2 Leaf characters

4.1.2.1 Leaf shape

Leaf shape has shown greater variation among 14 genotypes (Table 3). There were three leaf shapes *viz.*, elliptical, oblong and ovate. The six genotypes (S-2, S-4, S-5, S-9, K-16 and K-17) had shown elliptical leaf shape and only one (V-11) genotype has shown oval leaf shape and oblong shape was observed in seven genotypes (NA-6, NA-7, S-7, K-19, K-18, K-23 and K-7).

4.1.2.2 Leaf apex

Variation in leaf apex was observed among the 14 aonla genotypes (Table 3). Leaf apex varied in two different shapes (Acute and obtuse). Acute leaf apex was observed in 12 genotypes (NA-6, NA-7, S-2, S-4, S-5, S-7, S-9, K-16, K-17, K-19, V-11 and K-7) and obtuse leaf apex was observed in two genotypes (K-18 and K-23).

4.1.2.3 Leaf color

Three groups of leaf color were observed among 14 aonla genotypes (Table 3). Dark yellowish green leaves were observed in two genotypes (NA-6 and NA-7) whereas, moderate yellowish green leaves were observed in eight genotypes (S-2, S-4, S-5, S-7, K-17, K-23, V-11 and K-7) and moderate olive green leaves were found in four genotypes (S-9, K-16, K-19 and K-18).

4.2 Fruit and yield parameters

4.2.1 Fruit parameters

4.2.1.1 Fruit length (cm)

Fruit length had showed significant variation which is enumerated in Table 4. Maximum length of fruit (4.15 cm) was observed in genotype NA-7 which was statistically *on par* with NA-6 (4.10 cm) whereas, minimum length of fruit was observed in genotype V-11 (1.90 cm).

4.2.1.2 Fruit diameter (cm)

Significant difference was observed with respect to fruit diameter. Among the 14 genotypes, maximum diameter of fruit was observed in NA-7 genotype (4.55 cm) which was statistically *on par* with NA-6 (4.44 cm) and minimum was observed in V-11 genotype (2.09 cm) which is presented in Table 4.

4.2.1.3 Fruit weight (g)

Fruit weight had shown significant variation during the experimental period and it is presented in Table 4. Maximum fruit weight was observed in NA-7 (50.84 g) which was statistically *on par* with NA-6 (48.82 g) however, minimum fruit weight was observed in V-11 (6.03 g).

Table 3. Variation in tree morphological parameters of aonla genotypes

Genotypes	Tree shape	Trunk colour	Leaf shape	Leaf apex	Leaf colour
NA-6	Spreading	Whitish grey	Oblong	Acute	Dark yellowish green
NA-7	Spreading	Whitish grey	Oblong	Acute	Dark yellowish green
S-2	Spreading	Whitish grey	Elliptical	Acute	Moderate yellowish green
S-4	Spreading	Whitish grey	Elliptical	Acute	Moderate yellowish green
S-5	Spreading	Whitish grey	Elliptical	Acute	Moderate yellowish green
S-7	Spreading	Whitish grey	Oblong	Acute	Moderate yellowish green
S-9	Spreading	Whitish grey	Elliptical	Acute	Moderate olive green
K-16	Spreading	Whitish grey	Elliptical	Acute	Moderate olive green
K-17	Spreading	Whitish grey	Elliptical	Acute	Moderate yellowish green
K-19	Erect	Whitish grey	Oblong	Acute	Moderate olive green
K-18	Erect	Whitish grey	Oblong	Obtuse	Moderate olive green
K-23	Erect	Whitish grey	Oblong	Obtuse	Moderate yellowish green
V-11	Spreading	Whitish grey	Oval	Acute	Moderate yellowish green
K-7	Spreading	Whitish grey	Oblong	Acute	Moderate yellowish green

4.2.1.4 Fruit volume (cc)

Significant difference was observed in fruit volume among the 14 genotypes studied. Fruit volume was observed highest in genotype NA-7 (47.33 cc) which was statistically *on par* with NA-6 (46.33 cc) and lowest was observed in genotype V-11 (5.90 cc) which is presented in Table 4.

4.2.1.5 Pulp weight (g)

Significant difference in pulp weight was observed among the genotypes (Table 4). Maximum pulp weight was observed in genotype NA-7 (48.43 g) which was statistically *on par* with NA-6 (46.31 g) and minimum (5.28 g) was observed in genotype V-11.

4.2.1.6 Stone weight (g)

Stone weight had shown significant variation among the genotypes which is illustrated in Table 4. Higher stone weight was observed in genotype NA-6 (2.51 g) which was statistically *on par* with NA-7 (2.41 g) and lowest stone weight (0.75 g) was observed in genotype V-11.

4.2.1.7 Pulp: Stone ratio

The data pertaining pulp to stone ratio exhibited significant difference and maximum was found in genotype NA-7 (20.09) followed by genotype NA-6 (18.45) and minimum was found in genotype K-23 (6.76). It is depicted in Table 4.

4.2.1.8 Stone: Pulp ratio

The results of stone to pulp ratio was found significant difference among the genotypes and it is depicted in Table 4. The stone to pulp ratio was maximum in K-23 (0.15) which was *on par* with two genotypes K-16 (0.14) and V-11 (0.14). However, it was found minimum (0.05) in NA-7, NA-6 and S-5.

4.2.1.9 Number of seeds per stone

Significant difference observed among the genotypes with respect to number of seeds per stone. Maximum seeds per stone were observed in eight genotypes (NA-6, NA-7, K-16, K-17, K-19, K-18, K-23 and K-7). However, minimum were observed in genotypes (S-2, S-4, S-5, S-7, S-9 and V-11). It is furnished in Table 4.

4.2.2 Yield parameters

4.2.2.1 Fruit yield (kg/tree)

Fruit yield per tree had shown significant effect on aonla genotypes which is presented in Table 5. The results found that, significantly maximum fruit yield per tree was observed in NA-7 (54.11 kg) and it was followed by NA-6 (49.04 kg)

whereas, minimum was observed in V-11 (25.22 kg).

Table 4. Variation in fruit, seed and pulp parameters of different aonla genotypes

Genotypes	Fruit length (cm)	Fruit diameter (cm)	Fruit weight (g)	Fruit volume (cc)	Pulp weight (g)	Stone weight (g)	Pulp / Stone ratio	Stone / Pulp ratio	Number of seeds / stone
NA-6	4.10	4.44	48.82	46.33	46.31	2.51	18.45	0.05	6.00
NA-7	4.15	4.55	50.84	47.33	48.43	2.41	20.09	0.05	6.00
S-2	2.63	2.90	14.05	12.93	13.08	0.97	13.48	0.07	5.00
S-4	2.59	2.83	13.05	10.87	12.01	1.04	11.55	0.09	5.00
S-5	2.65	3.02	17.32	13.30	16.41	0.91	18.03	0.05	5.00
S-7	2.39	2.69	11.06	9.13	10.03	1.03	9.73	0.10	5.00
S-9	2.15	2.50	8.76	8.00	7.7	1.06	7.26	0.13	5.00
K-16	2.13	2.36	8.17	6.63	7.14	1.03	6.93	0.14	6.00
K-17	2.07	2.34	7.90	7.07	6.94	0.96	7.22	0.13	6.00
K-19	2.33	2.65	10.90	9.53	10.03	0.87	11.53	0.09	6.00
K-18	2.48	3.08	15.46	12.17	14.28	1.18	12.10	0.08	6.00
K-23	2.19	2.55	8.78	7.93	7.65	1.13	6.76	0.15	6.00
V-11	1.90	2.09	6.03	5.90	5.28	0.75	7.04	0.14	5.00
K-7	2.20	2.74	9.36	9.27	8.35	1.01	8.26	0.12	6.00
S.Em ±	0.10	0.11	1.43	1.31	0.97	0.08	0.47	0.001	0.17
C.D @ 5 %	0.31	0.34	4.16	3.80	2.82	0.24	1.36	0.003	0.49

4.2.2.2 Fruit yield (t/ha)

Significant differences were observed in genotypes with respect to fruit yield per hectare (Table 5). Among the 14 genotypes, significantly higher yield was recorded in NA-7 (14.98 t/ ha) which was followed by NA-6 (13.58 t/ha). However, it was observed minimum in V-11(6.98 t/ha).

4.3 Biochemical parameters

4.3.1 Total soluble solids (°Brix)

Significant differences were observed in total soluble solids among aonla genotypes which is furnished in Table 6. The significantly highest total soluble solids were observed in K-7 (16.77 °B) which was followed by K-23 (14.82 °B) and V-11(14.34°B). However, least was recorded in NA-7 (8 °B).

4.3.2 Titratable acidity (%)

During this study, titratable acidity had showed significant difference among the genotypes which is presented in Table 6. Significantly higher acidity was recorded in K-23 (2.39 %) followed by K-18 (2.20 %), V-11 (2.06 %) and K-19 (2.05 %). However, it was observed minimum in S-4 (1.06 %).

4.3.3 TSS : Acid ratio

Significant differences on TSS to acid ratio was observed during the experimental period. Maximum TSS to acid ratio was observed in genotype S-4 (10.08) which was statistically *on par* with genotype K-7 (9.52) and it was observed minimum in genotype NA-7 (4.23) which is illustrated in Table 6.

4.3.4 Ascorbic acid (mg/100 g)

The data on ascorbic acid content of pulp showed significant difference on aonla genotypes which is furnished in Table 6. The maximum ascorbic acid content of pulp was recorded in K-23 (403.65 mg/100 g) followed by K-18 (371.56 mg/100 g), K-16 (366.49 mg/100 g) and V-11 (347.91 mg/100 g). However, it was observed minimum in S-4 (179 mg/100 g).

4.3.5 Total sugar (%)

The result of total sugar content of the pulp showed significant differences which is presented in Table 6. The maximum total sugar content of the pulp was recorded in K-7 (6.80 %) which was statistically *on par* with K-23 (6.54 %). The least total sugar was recorded in NA-7 genotype (4.44 %).

Table 5. Variability in fruit yield of different genotypes of aonla

Genotypes	Fruit yield (kg/tree)	Fruit yield (ton/ha)
NA-6	49.04	13.58
NA-7	54.11	14.98
S-2	39.21	10.86
S-4	37.42	10.39
S-5	41.67	11.54
S-7	35.41	9.80
S-9	32.90	9.11
K-16	31.46	8.71
K-17	29.43	8.15
K-19	34.81	9.80
K-18	40.51	11.22
K-23	33.02	9.14
V-11	25.22	6.98
K-7	33.39	9.24
S.Em ±	1.82	0.42
C.D. @ 5 %	5.31	1.24

4.3.6 Reducing sugar (%)

Significant results were exhibited on reducing sugar content which is depicted in Table 6. The highest reducing sugar per cent of the pulp was recorded in K-7 (4.46 %) which was statistically *on par* with K-23 (4.26 %) and K-18 (4.18 %), it was observed lowest in NA-7 (2.92 %).

4.3.7 Non-reducing sugar (%)

Significant difference was found with respect to non-reducing sugar content of the pulp which is furnished in Table 6. The maximum non-reducing sugar content of the pulp was observed in K-7 (2.34 %) which was statistically *on par* with K-23 (2.28 %) and V-11 (2.20 %) and minimum was observed in NA-7 (1.53 %).

4.3.8 Fat (%)

The data pertaining to fat content on aonla fruits showed significant differences among the genotypes which is furnished in Table 6. Significantly highest fat content was observed in K-17 (1.64 %) followed by S-4 (1.38 %) and lowest was observed in NA-6 (0.39 %) genotype.

4.3.9 Fiber (%)

Variation in fiber content of fruits were significantly observed among the genotypes. Fiber content was observed maximum in S-4 (16.65 %) which was statistically *on par* with K-23 (16.30 %) and S-5 (15.70 %) and minimum fiber content was recorded in K-7 (10.25 %) (Table 6).

4.3.10 Flavonoids (mg /g)

The results of flavonoids showed greater variation on aonla genotypes which is presented in Table 6. The genotype K-23 (1.73 mg/g) had significantly highest content of flavonoids followed by K-17 (1.51 mg/g). Whereas, lowest flavonoid content was observed in NA-6 (1.04 mg/g).

4.3.11 Tannins (%)

Significant difference was observed among the genotypes with respect to tannin content. The highest tannin content of pulp was recorded in K-16 (9.62 %) which was statistically *on par* with K-17 (9.27 %). Whereas, minimum was observed in S-7 (4.91 %) (Table 6).

4.3.12 Phenols (%)

Aonla genotypes had shown significant effect on phenols. It was observed that K-23 (1.62 %) had the highest content of phenols which was statistically *on par* with K-18 (1.56 %) and K-19 (1.52 %) genotypes. Whereas, lowest phenol content was observed in S-4 (1.11 %) (Table 6).

Table 6. Biochemical parameters in the pulp of aonla genotypes

Genotypes	TSS (°B)	Acidity (%)	TSS / Acid ratio	Vitamin C (mg/100 g)	Total sugar (%)	Reducing sugar (%)	Non-reducing sugar (%)	Fat (%)	Fibre (%)	Flavonoid (mg/g)	Tannins (%)	Phenols (%)	Antioxidant (%)
NA-6	8.47	1.77	4.78	298.44	4.55	2.96	1.59	0.39	14.65	1.04	6.46	1.39	86.45
NA-7	8.00	1.89	4.23	319.16	4.44	2.92	1.53	0.56	15.05	1.09	5.33	1.42	86.52
S-2	9.70	1.27	7.63	214.46	5.28	3.45	1.83	0.73	15.05	1.09	6.14	1.26	84.32
S-4	10.69	1.06	10.08	179.00	5.90	3.95	1.95	1.38	16.65	0.81	6.05	1.11	83.20
S-5	10.28	1.40	7.34	236.44	5.60	3.65	1.95	0.57	15.70	1.15	5.23	1.35	84.27
S-7	8.52	1.70	5.01	287.11	4.65	3.02	1.63	0.91	12.60	0.89	4.91	1.42	86.10
S-9	9.16	1.76	5.20	298.94	5.07	3.18	1.89	1.16	13.65	1.09	5.70	1.46	86.78
K-16	9.32	2.17	4.29	366.49	5.20	3.36	1.84	1.16	12.40	1.50	9.62	1.48	87.72
K-17	9.76	1.71	5.70	288.80	5.36	3.52	1.84	1.64	12.50	1.51	9.27	1.44	86.64
K-19	10.30	2.05	5.02	346.22	5.65	3.70	1.95	0.66	12.00	1.26	8.44	1.52	89.28
K-18	13.90	2.20	6.31	371.56	6.25	4.18	2.07	0.92	12.75	1.16	6.09	1.56	91.98
K-23	14.82	2.39	6.20	403.65	6.54	4.26	2.28	0.87	16.30	1.73	8.01	1.62	92.18
V-11	14.34	2.06	6.96	347.91	6.23	4.03	2.20	0.82	12.75	1.18	8.17	1.43	86.25
K-7	16.77	1.76	9.52	297.25	6.80	4.46	2.34	0.50	10.25	1.08	5.26	1.36	86.27
S.E.m ±	0.55	0.06	0.34	9.50	0.17	0.13	0.08	0.03	0.53	0.04	0.25	0.05	1.02
C.D @ 5%	1.60	0.18	0.98	27.62	0.51	0.36	0.23	0.09	1.55	0.10	0.72	0.15	2.95

4.3.13 Antioxidant (%)

The data on antioxidant content showed significant effect on aonla genotypes which is furnished in Table 6. The study revealed that, maximum antioxidant content was recorded in K-23 (92.18%) which was *on par* with K-18 (91.98 %) and K-19 (89.28 %). Whereas, minimum antioxidant was recorded in S-4 (83.20 %).

4.4 Genetic variability

4.4.1 Plant height (m)

In the present investigation, the estimates of GCV (14.49 %) and PCV (16.15 %) were found to be moderate in plant height. The calculated broad sense heritability (80.46 %) and genetic advance as percent mean (26.77 %) were high for this trait. (Table 7)

4.4.2 Stem girth (cm)

The trait stem girth showed a moderate level of GCV (14.21 %) and PCV (14.84 %). The calculated broad sense heritability (91.63 %) was high with high genetic advance as percent mean (28.01 %). It is presented in Table 7.

4.4.3 Fruit weight (g)

The trait fruit weight showed high level of GCV (86.19 %) and PCV (87.47 %). The experimental results also revealed that high broad sense heritability (97.10 %) coupled with genetic advance mean (174.95 %). It is depicted in Table 7.

4.4.4 Fruit volume (cc)

During investigation, the results pertaining to GCV (93.08 %) and PCV (94.34 %) were found to be high for fruit volume. It was also revealed higher percentage of heritability (97.34 %) and genetic advance as percent mean (189.17 %). It is presented in Table 7.

4.4.5 Fruit length (cm)

The magnitude of observed GCV (26.79 %) and PCV (27.76 %) values were high for a trait fruit length. The estimates of heritability (93.18 %) was higher with high genetic advance as percent mean (53.28 %). It is furnished in Table 7.

4.4.6 Fruit diameter (cm)

From the experimental results, the results related to GCV (24.58 %) and PCV (25.57 %) values were high for fruit diameter, the results also showed that accomplishment of broad sense heritability (92.42 %) and higher genetic advance as percent mean (48.68 %). It is depicted in Table 7.

4.4.7 Pulp weight (g)

In the present investigation, the GCV (91.28 %) and PCV (91.94 %) estimates were high for pulp weight. The calculated heritability (98.56 %) and genetic advance as percent mean (186.69 %) were higher for this trait. It is depicted in Table 7.

4.4.8 Stone weight (g)

The variability study revealed that GCV (45.07 %) and PCV (45.08 %) were found to be high for stone weight. It was also revealed that higher percentage of broad sense heritability (99.93 %) and high genetic advance as percent mean (92.81 %). It is presented in Table 7.

4.4.9 Number of seeds per stone

In the present investigation, the results related to GCV (8.73 %) and PCV (10.13 %) were found to be low. Higher percentage of broad sense heritability (74.32 %) and moderate genetic advance as percent mean (15.50 %) observed in this trait. It is furnished in Table 7.

4.4.10 Pulp to stone ratio

Pulp to stone ratio exhibited high GCV (40.93 %) and PCV (41.55 %) values for this trait. The results of heritability (97.05 %) and genetic advance as percent mean (83.06 %) were high for this trait. It is furnished in Table 7.

4.4.11 Yield (kg/plant)

The variability study revealed that GCV (20.05 %) and PCV (21.76 %) for yield per tree were high. The values observed for broad sense heritability (84.86 %) and genetic advance as percent mean (38.04 %) were more for this trait. It is furnished in Table 7.

4.4.12 TSS (%)

The experimental results revealed that, the GCV (24.65 %) and PCV (26.13 %) were found to be high for total soluble solids. The calculated heritability (89.00 %) and genetic advance as percent mean (47.90 %) were found to be high for this trait. It is presented in Table 8.

4.4.13 Acidity (%)

The results from the experiment revealed that the obtained values for GCV (20.36 %) and PCV (21.20 %) were found to be high for acidity. The estimated broad sense heritability (92.22 %) was high with high genetic advance as percent mean (40.28 %) (Table 8).

Table 7. Mean, range and genetic components for fruit and yield parameters of aonla genotypes

Parameters	Mean \pm S.Ems	Range	GCV (%)	PCV(%)	h^2 (%)	GA (%)	GAM (%)
Plant height (m)	5.42 \pm 0.22	3.55 - 6.46	14.49	16.15	80.46	1.45	26.77
Stem girth (cm)	75.80 \pm 1.03	54.01- 86.53	14.21	14.84	91.63	21.23	28.01
Fruit weight (g)	16.63 \pm 1.43	6.03-50.83	86.19	87.47	97.10	29.09	174.95
Fruit volume (cc)	14.74 \pm 1.31	5.90 - 47.33	93.08	94.34	97.34	27.89	189.17
Fruit length (cm)	2.57 \pm 0.10	1.90 - 4.15	26.79	27.76	93.18	1.37	53.28
Fruit diameter (cm)	2.91 \pm 0.11	2.09 - 4.55	24.58	25.57	92.42	1.42	48.68
Pulp weight (g)	15.26 \pm 0.97	5.28 - 48.43	91.28	91.94	98.56	28.49	186.69
Stone weight (gm)	1.20 \pm 0.08	0.75-2.51	45.07	45.08	99.93	1.12	92.81
Pulp /stone ratio	11.32 \pm 0.47	6.76 - 20.09	40.93	41.55	97.05	9.40	83.06
No of seeds per fruit	5.57 \pm 0.17	5 - 6	8.73	10.13	74.32	0.86	15.50
Yield (kg/tree)	36.97 \pm 1.82	25.22 -54.11	20.05	21.76	84.86	14.07	38.04

GCV – Genotypic coefficient of variation

h^2 - Heritability

GAM – Genetic advance as per cent mean

PCV - Phenotypic coefficient of variation

GA- Genetic advance

4.4.14 TSS/Acid ratio

The estimated GCV (28.51 %) and PCV (29.99 %) values were found to be high for TSS to acid ratio. The study revealed that heritability (90.38 %) was high with higher genetic advance as percent mean (55.84 %) which is represented in Table 8.

4.4.15 Vitamin C (mg/100g)

The magnitude of observed GCV (20.40 %) and PCV (21.11 %) values were high for trait vitamin C. The experimental results also showed that accomplishment of broad sense heritability (93.42 %) and genetic advance as percent mean (40.62 %) were higher for this trait. It is presented in Table 8.

4.4.16 Total sugar (%)

The variability study revealed that GCV (13.03 %) and PCV (14.12 %) for total sugar were moderate. It was also revealed that higher percentage of broad sense heritability (85.14 %) and genetic advance as percent mean (24.76 %). It is depicted in Table 8.

4.4.17 Reducing sugar (%)

Reducing sugar had recorded moderate magnitude of GCV (13.49 %) and PCV (14.76 %). Heritability (83.50 %) was high with, higher genetic advance as percent mean (25.39 %). (Table 8)

4.4.18 Non -Reducing sugar (%)

In the present experiment the performance of GCV and PCV values were moderate with 12.03 per cent and 14.00 per cent, respectively for this trait. The experiment also revealed that exploit of heritability and genetic advance as per cent mean were more with 73.82 per cent 21.30 per cent respectively. It is presented in Table 8.

4.4.19 Tannins (%)

In the present investigation, the GCV (23.44 %) and PCV (24.28 %) estimates were high for tannins. The calculated broad sense heritability (93.21 %) and higher genetic advance as percent mean (46.62 %) were also high for this trait (Table 8).

4.5.20 Fat (%)

The magnitude of observed GCV (40.39 %) and PCV (40.96 %) values were found to be high for fat content. The higher level of heritability (97.23 %) and higher genetic advance as percent mean (82.04 %) was observed. It is enumerated in Table 8.

4.4.21 Fibre (%)

The variability study revealed that GCV (12.97 %) and PCV (14.60 %) for

fibre content were moderate. It was also revealed that higher percentage of broad sense heritability (78.83 %) and higher genetic advance as percent mean (23.72 %). It is depicted in Table 8.

4.4.22 Flavonoids (%)

Flavonoids content exhibited higher percentage of GCV (20.67 %) and PCV (21.34 %). The values observed for broad sense heritability (93.89 %) and genetic advance as percent mean (41.26 %) were high for this trait. It is depicted in Table 8.

4.4.23 Phenols (%)

The estimates of GCV (8.07 %) and PCV (10.35 %) were found to be low for phenol content. Higher heritability (60.82 %) was coupled with moderate genetic advance as percent mean (12.96 %) was observed in this trait. It is furnished in Table 8.

4.4.24 Antioxidants (%)

The estimates of GCV (3.01 %) and PCV (3.01 %) were found to be low for antioxidant content. The higher heritability (88.93 %) was coupled with low genetic advance as percent mean (6.19 %) was observed for this trait. It is furnished in Table 8.

4.5 Correlation studies.

4.5.1 Phenotypic correlation

4.5.1.1 Fruit weight (g)

The correlation studies revealed that fruit weight had positive and highly significant correlation with fruit volume (0.981**), fruit length (0.962 **), fruit diameter (0.947 **), pulp weight (0.985 **) and yield per tree (0.832 **). While, significant negative correlation for TSS (-0.452 *) and highly significant negative correlation for total sugar (-0.597**), reducing sugar (-0.565**) and non-reducing sugar (- 0.638**). Whereas, non-significant negative correlation of fruit weight was noticed with acidity (- 0.0765) and vitamin C (-0.0788). (Table 9)

4.5.1.2 Fruit volume (cc)

During experimental period, fruit volume showed highly significant and positive correlation with fruit length (0.958**), fruit diameter (0.941**), pulp weight (0.990**) and yield per tree (0.821**). While significant negative correlation for TSS (-0.434*), and highly significant negative correlation for total sugar (-0.587**), reducing sugar (-0.554**) and non-reducing sugar (-0.626**). Whereas, non-significant negative correlation of fruit diameter was noticed with acidity (-0.0559) and vitamin C (-0.0598). (Table 9)

Table 8. Mean, range and genetic components for quality parameters of aonla genotypes

Parameters	Mean \pm S.E.m	Range	GCV (%)	PCV(%)	h^2 (%)	GA (%)	GAM (%)
TSS ($^{\circ}$ Brix)	11.00 \pm 0.55	8 - 16.77	24.65	26.13	89.00	5.27	47.90
Acidity (%)	1.80 \pm 0.06	1.06 - 2.39	20.36	21.20	92.22	0.72	40.28
Vitamin C (%)	303.96 \pm 9.50	179 - 403.65	20.40	21.11	93.42	123.47	40.62
TSS /acid ratio	6.31 \pm 0.34	4.23 - 10.08	28.51	29.99	90.38	3.52	55.84
Total sugar (%)	5.54 \pm 0.17	4.44 - 6.80	13.03	14.12	85.14	1.37	24.76
Reducing sugar (%)	3.62 \pm 0.13	2.92 - 4.46	13.49	14.76	83.50	0.92	25.39
Non- reducing sugar (%)	1.92 \pm 0.08	1.53 - 2.34	12.03	14.00	73.82	0.41	21.30
Tannins (%)	6.76 \pm 0.25	4.91- 9.62	23.44	24.28	93.21	3.15	46.62
Fat (%)	0.88 \pm 0.03	0.39-1.64	40.39	40.96	97.23	0.72	82.04
Fibre (%)	13.74 \pm 0.53	10.25 -16.65	12.97	14.60	78.83	3.26	23.72
Flavonoids (mg/g)	1.18 \pm 0.04	0.81-1.73	20.67	21.34	93.89	0.49	41.26
Phenols (%)	1.42 \pm 0.05	1.11-1.62	8.07	10.35	60.82	0.18	12.96
Antioxidants (%)	87.00 \pm 1.89	83.20- 92.18	3.01	3.01	88.93	5.39	6.19

GCV – Genotypic coefficient of variation

PCV- Phenotypic coefficient of variation

h^2 - Heritability

GA- Genetic advance

GAM – Genetic advance as per cent mean

4.5.1. 3 Fruit length (cm)

The result observed in the study for the association of fruit length was highly significant and positive correlation with fruit diameter (0.972**), pulp weight (0.971**) and yield per tree (0.849**). Whereas significant negative association with TSS (-0.479*) and highly significant negative correlation for total sugar (-0.592**), reducing sugar (-0.553**) and non-reducing sugar (-0.647**). Whereas, non - significant negative correlation with acidity (-0.1607) and vitamin C (-0.1645) which is represented in Table 9.

4.5.1. 4 Fruit diameter (cm)

During the study, fruit diameter exhibited positive and highly significant correlation with pulp weight (0.953**) and yield per tree (0.890**). While significant negative correlation for TSS (-0.375*) and highly significant negative correlation for total sugar (-0.500**), reducing sugar (-0.457*) and non-reducing sugar (-0.561**). Whereas non -significant negative correlation with acidity (-0.1251) and vitamin C (-0.1278). (Table 9)

4.5.1.5 Pulp weight (g)

The results revealed that pulp weight showed highly significant and positive association with yield per tree (0.853**). While significant negative correlation for TSS (-0.449*) and highly significant negative correlation for total sugar (-0.584**), reducing sugar (-0.546**) and non-reducing sugar (-0.634**). Whereas, non-significant negative correlation with acidity (-0.0671) and vitamin C (-0.0704). (Table 9)

4.5.1.6 Total soluble solids (°Brix)

The experimental results showed that TSS was highly significant and positive correlation with total sugar (0.940**), reducing sugar (0.930**) and non-reducing sugar (0.927**). While, positively significant with acidity (0.347*) and vitamin C (0.346*). Whereas, non - significant negative correlation for yield per tree (-0.393*). (Table 9)

4.5.1.7 Acidity (%)

The results revealed that acidity showed highly significant positive correlation with vitamin C (0.994**). Whereas, non -significant positive correlation with total sugar (0.2218), reducing sugar (0.1896) and non-reducing sugar (0.2796). While, non-significant negative correlation for yield per tree (-0.2030) (Table 9).

4.5.1.8 Vitamin C (mg/100g)

During the study, vitamin C showed non - significant positive correlation with total sugar (0.2202), reducing sugar (0.1861) and non-reducing sugar (0.2790). While non-significant negative correlation for yield per tree (-0.2070) (Table 9).

4.5.1.9 Total sugar (%)

The result observed in the study, total sugar showed highly significant and positive correlation with reducing sugar (0.985**) and non-reducing sugar (0.961**). Significant negative correlation with yield per tree (-0.459*). (Table 9)

4.5.1.10 Reducing sugar (%)

The correlation studies revealed that reducing sugar showed highly significant and positive correlation with non-reducing sugar (0.934**) and significant negative correlation with yield per tree (-0.409*). (Table 9)

4.5.1.11 Non-reducing sugar (%)

The results revealed that non-reducing sugar showed highly significant negative correlation with yield per tree (-0.537**). (Table 9)

4.5.2 Genotypic correlation

4.5.2.1 Fruit weight (g)

The correlation study revealed that fruit weight was positive and highly significant with fruit volume (0.985**), fruit length (0.832**), fruit diameter (0.814**), pulp weight (0.987**) and yield per tree (0.715**). While, non-significant positive correlation for TSS (0.1344), total sugar (0.2224), reducing sugar (0.2240) and non-reducing sugar (0.2217). Whereas, significant positive correlation of fruit weight was noticed with acidity (0.335*) and vitamin C (0.334*). (Table 10)

4.5.2.2 Fruit volume (cc)

The trait fruit volume exhibited highly significant and positive association with fruit length (0.816**), fruit diameter (0.797**), pulp weight (0.991**), and yield per tree (0.695**). While non-significant positive correlation for TSS (0.1199), total sugar (0.2006), reducing sugar (0.2031) and non-reducing sugar (0.1998). Whereas, significant positive correlation of fruit volume was noticed with acidity (0.321*) and vitamin C (0.319*). (Table 10)

4.5.2.3 Fruit length (cm)

The experimental study revealed that fruit length was highly significant and had positive association with fruit diameter (0.992**), pulp weight (0.832**) and yield per tree (0.955**). Whereas, fruit length also showed highly significant positive correlation with these biochemical traits viz. TSS (0.562**), total sugar (0.682**), reducing sugar (0.683**), non-reducing sugar (0.682**), acidity (0.696**) and vitamin C (0.695**). (Table 10)

Table 9. Phenotypic correlation of co-efficient for yield and quality parameters of aonla genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
X1	1.0000	0.981**	0.962**	0.947**	0.985**	-0.452*	-0.0765	-0.0788	-0.597**	-0.565**	-0.638**	0.832**
X2		1.0000	0.958**	0.941**	0.990**	-0.434*	-0.0559	-0.0598	-0.587**	-0.554**	-0.626**	0.821**
X3			1.0000	0.972**	0.971**	-0.479*	-0.1607	-0.1645	-0.592**	-0.553**	-0.647**	0.849**
X4				1.0000	0.953**	-0.375*	-0.1251	-0.1278	-0.500**	-0.457*	-0.561**	0.890**
X5					1.0000	-0.449*	-0.0671	-0.0704	-0.584**	-0.546**	-0.634**	0.853**
X6						1.0000	0.347*	0.346*	0.940**	0.930**	0.927**	-0.393*
X7							1.0000	0.994**	0.2218	0.1896	0.2796	-0.2030
X8								1.0000	0.2202	0.1861	0.2790	-0.2070
X9									1.0000	0.985**	0.961**	-0.459*
X10										1.0000	0.934**	-409*
X11											1.0000	-0.537**
X12												1.0000

** indicates highly significant at 1 % * indicates significant at 5 %

X1 - Fruit weight X2- Fruit volume X3- Fruit length X4- Fruit diameter X5 - Pulp weight X6- Total soluble solids X7- Acidity
 X8- Vitamin C X9- Total sugar X10 - Reducing sugar X11- Non- reducing sugar X12- Yield per tree

4.5.2.4 Fruit diameter (cm)

The result observed in the present study revealed that fruit diameter was highly significant and had positive association with pulp weight (0.812**), and yield per tree (0.969**) and also with TSS (0.604**), total sugar (0.711**), reducing sugar (0.713**), non-reducing sugar (0.709**), acidity (0.718**) and vitamin C (0.718**). (Table 10).

4.5.2.5 Pulp weight (g)

The present study revealed that, pulp weight had positive correlation and highly significant with yield per tree (0.717**). While non-significant positive correlation for TSS (0.1270), total sugar (0.2164), reducing sugar (0.2203) and non-reducing sugar (0.2125). Whereas significant positive correlation with acidity (0.331*) and vitamin C (0.329*). (Table 10)

4.5.2.6 Total soluble solids (%)

The experimental study revealed that TSS was highly significant and positive correlation with total sugar (0.962**), reducing sugar (0.962**), non-reducing sugar (0.956**), acidity (0.841**), vitamin C (0.841**) and yield per tree (0.657**). Which is depicted in Table 10.

4.5.2.7 Acidity (%)

The acidity trait studied in the correlation had highly significant and positive association with vitamin C (0.999*), total sugar (0.875**), reducing sugar (0.869**), non-reducing sugar (0.886**) and also with yield per tree (0.746**). (Table 10)

4.5.2.8 Vitamin C (mg/100g)

The experimental study revealed that Vitamin C exhibited positive and highly significant correlation with total sugar (0.876**), reducing sugar (0.869**), non-reducing sugar (0.886**) and yield per tree (0.746**). (Table 10)

4.5.2.9 Total sugar (%)

In the present study, the total sugar was highly significant and had positive association with reducing sugar (0.998**), non-reducing sugar (0.996**) and also with the yield per tree (0.777**). (Table 10)

4.5.2.10 Reducing sugar (%)

The reducing sugar trait studied in correlation exhibited highly significant and positive correlation with non-reducing sugar (0.993**) and yield per tree (0.778**). (Table 10)

4.5.2.11 Non-reducing sugar (%)

The present study revealed that non-reducing sugar showed significant negative correlation with yield per tree (0.773**). (Table 10)

Table 10. Genotypic co-efficient of correlation for yield and quality parameters of aonla genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
X1	1.0000	0.985**	0.832**	0.814**	0.987**	0.1344	0.335*	0.334*	0.2224	0.2240	0.2217	0.715**
X2		1.0000	0.816**	0.797**	0.991**	0.1199	0.321*	0.319*	0.2006	0.2031	0.1998	0.695**
X3			1.0000	0.992**	0.832**	0.562**	0.696**	0.695**	0.682**	0.683**	0.682**	0.695**
X4				1.0000	0.812**	0.604**	0.718**	0.718**	0.711**	0.713**	0.709**	0.969**
X5					1.0000	0.1270	0.331*	0.329*	0.2164	0.2203	0.2125	0.717**
X6						1.0000	0.841**	0.841**	0.962**	0.962**	0.956**	0.657**
X7							1.0000	0.999**	0.875**	0.869**	0.886**	0.746**
X8								1.0000	0.876**	0.869**	0.886**	0.746**
X9									1.0000	0.998**	0.996**	0.777**
X10										1.0000	0.993**	0.778**
X11											1.0000	0.773**
X12												1.0000

** indicates highly significant at 1 % * indicates significant at 5 %

X1 - Fruit weight X2- Fruit volume X3- Fruit length X4- Fruit diameter X5 – Pulp weight X6- Total soluble solids
 X7- Acidity X8- Vitamin C X9- Total sugar X10 – Reducing sugar X11- Non- reducing sugar X12- Yield per tree

4.6 Path co-efficient analysis

4.6.1 Phenotypic path co-efficient analysis

4.6.1.1 Fruit weight (g)

During investigation, fruit weight had showed negative and direct effect (-0.2434) on yield per tree. Whereas, the study exhibits positive indirect effect on TSS (0.1100), acidity (0.0186), vitamin C (0.0192), total sugar (0.1453), reducing sugar (0.1376) and non - reducing sugar (0.1552). While, the negative indirect effect was expressed by fruit length (-0.2341), pulp weight (-0.2305), fruit volume (- 0.2387) and fruit diameter (-0.2305). (Table 11)

4.6.1.2 Fruit volume (cc)

In the present study, the fruit volume had showed negative and direct effect (-0.7975) on yield per tree. Whereas, positive indirect effect exhibited by TSS (0.3464), acidity (0.0446), vitamin C (0.0477), total sugar (0.4681), reducing sugar (0.4416) and non -reducing sugar (0.4993). While, the negative indirect effect was expressed by fruit length (-0.7643) and fruit diameter (-0.7507) and pulp weight (- 0.7893). (Table 11)

4.6.1.3 Fruit length (cm)

In the present study, fruit length showed negative and direct effect (-1.0699) on fruit yield per tree. Whereas, positive and indirect effect exhibited by TSS (0.5120), acidity (0.1719), vitamin C (0.1760), total sugar (0.6329), reducing sugar (0.5912) and non -reducing sugar (0.6920). While, the negative indirect effect was expressed by fruit diameter (-1.0402) and pulp weight (-1.0385). It is depicted in Table 11.

4.6.1.4 Fruit diameter (cm)

Fruit diameter trait on fruit yield per tree was positive and direct effect (1.0217). Whereas positive and indirect effect exhibited by pulp weight (1.2977). While, the negative indirect effect was expressed by TSS (-0.5099), acidity (-0.1704), vitamin C (-0.1741), total sugar (-0.6810), reducing sugar (-0.6218) and non -reducing sugar (-0.7632). It is presented in Table 11.

4.6.1.5 Pulp weight (g)

During the study, Pulp weight showed positive and direct effect (1.0340) on fruit yield per tree. While, the negative indirect effect was expressed by TSS (-0.7149), acidity (-0.1069), vitamin C (-0.1122), total sugar (-0.9302), reducing sugar (-0.8692) and non -reducing sugar (-1.0100). (Table 11)

4.6.1.6 Total soluble solids (^oBrix)

During this investigation, TSS showed negative and direct effect (-0.2684) on yield per tree. While, the negative indirect effect was expressed by acidity (-0.0931), vitamin C (-0.0929), total sugar (-0.2521), reducing sugar (-0.2495) and non-reducing sugar (-0.2488). (Table 11)

4.6.1.7 Acidity (%)

The path estimates disclosed that acidity showed positive and direct effect (0.1709) on yield per tree. While positive indirect effect on total sugar (0.0379), reducing sugar (0.0324) and non-reducing sugar (0.0478). (Table 11)

4.6.1.8 Vitamin C (mg/100g)

In the present study it was observed that the vitamin C on yield per tree was direct and negative (-0.2740). While, the negative indirect effect was expressed by total sugar (-0.0603) reducing sugar (-0.0510), non-reducing sugar (-0.0764). It is enumerated in Table 11.

4.6.1.9 Total sugar (%)

During this study, total sugar showed positive and direct effect (0.2179) on fruit yield per tree. While positive indirect effect on reducing sugar (0.2147) and non-reducing sugar (0.2094). (Table 11)

4.6.1.10 Reducing sugar (%)

The path estimates disclosed that, reducing sugar showed positive and direct effect (0.0381) on fruit yield per tree. While positive indirect effect on non-reducing sugar (0.0356). It is depicted in Table 11.

4.6.1.11 Non-reducing sugar (%)

In the present study, non-reducing sugar showed negative and direct effect (-0.0782) on fruit yield per tree. It is presented in Table 11.

4.7 Genetic divergence

4.7.1 Contribution of individual character towards total divergence

The genetic diversity was assessed among the 14 genotypes of aonla by Mahalanobis' D^2 statistics, which resulted in seven clusters using Tocher's method. The trait tannin content contributed maximum towards the total genetic divergence with 18.68 %, followed by vitamin C (17.58 %), antioxidant (15.38 %), acidity (14.29 %), TSS (9.89 %), fibre (8.79 %), flavonoid (6.59 %), total sugar (4.40 %) and TSS to acid ratio (4.40 %). (Table 12)

Table 11. Phenotypic path co-efficient for yield and quality parameters of aonla genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	-0.2434	-0.2387	-0.2341	-0.2305	-0.2396	0.1100	0.0186	0.0192	0.1453	0.1376	0.1552
X2	-0.7823	-0.7975	-0.7643	-0.7507	-0.7893	0.3464	0.0446	0.0477	0.4681	0.4416	0.4993
X3	-1.0291	-1.0253	-1.0699	-1.0402	-1.0385	0.5120	0.1719	0.1760	0.6329	0.5912	0.6920
X4	1.2900	1.2817	1.3238	1.0217	1.2977	-0.5099	-0.1704	-0.1741	-0.6810	-0.6218	-0.7632
X5	1.5690	1.5771	1.5466	1.5185	1.0340	-0.7149	-0.1069	-0.1122	-0.9302	-0.8692	-1.0100
X6	0.1213	0.1166	0.1284	0.1005	0.1204	-0.2684	-0.0931	-0.0929	-0.2521	-0.2495	-0.2488
X7	-0.0131	-0.0096	-0.0275	-0.0214	-0.0115	0.0593	0.1709	0.1700	0.0379	0.0324	0.0478
X8	0.0216	0.0164	0.0451	0.0350	0.5783	-0.0948	-0.2724	-0.2740	-0.0603	-0.0510	-0.0764
X9	-0.1301	-0.1279	-0.1289	-0.1090	-0.1272	0.2047	0.0483	0.0480	0.2179	0.2147	0.2094
X10	-0.0216	-0.0211	-0.0211	0.3223	-0.0208	0.0351	0.0072	0.0071	0.0376	0.0381	0.0356
X11	0.0498	0.0493	0.0509	0.0438	0.0495	-0.0725	-0.0219	-0.0218	-0.0751	-0.0730	-0.0782
r value	0.8320	0.8210	0.8490	0.8900	0.8530	-0.3930	-0.2030	-0.2070	-0.4590	-0.4090	-0.5370

Diagonal values indicate direct effect Residual effect =0.273

X1 - Fruit weight X2- Fruit volume X3- Fruit length X4- Fruit diameter X5 - Pulp weight X6- Total soluble solids
X7- Acidity X8- Vitamin C X9- Total sugar X10 - Reducing sugar X11- Non- reducing sugar

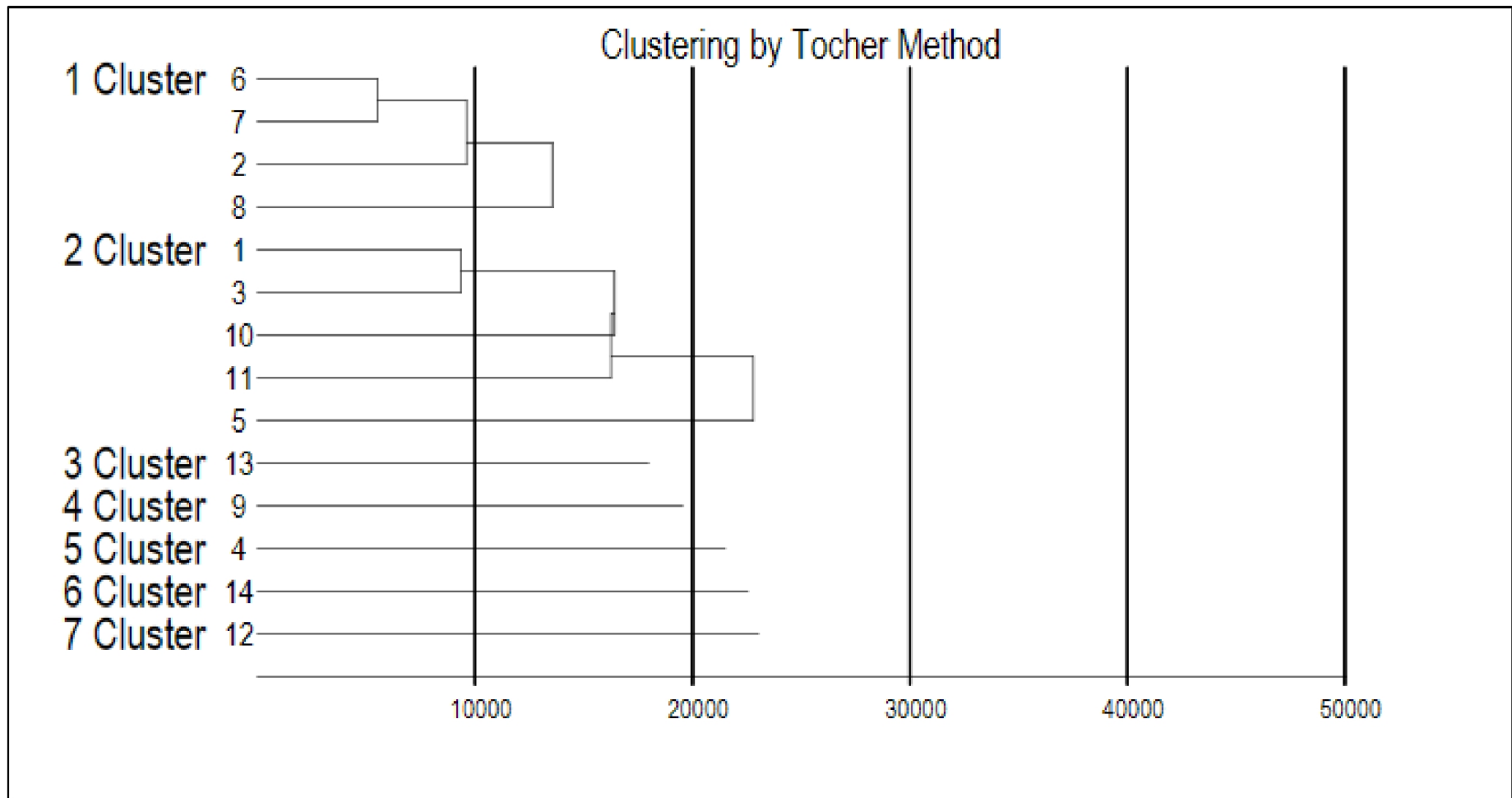


Fig. 1. Dendrogram showing the genetic diversity among 14 genotypes of aonla using Torcher's method

- | | | | | | |
|----------|---------|---------|----------|----------|----------|
| 1. NA-6 | 2. NA-7 | 3. S-2 | 4. S-4 | 5. S-5 | 6. S-7 |
| 7. S-9 | 8. K-16 | 9. K-17 | 10. K-19 | 11. K-18 | 12. K-23 |
| 13. V-11 | 14. K-7 | | | | |

4.7.2 Grouping genotypes into various clusters

Clusters II emerged as the largest cluster with five genotypes, followed by cluster I with four genotypes. Cluster III, IV, V, VI and VII had solitary genotype. (Fig 1)

4.7.3 Inter and intra-cluster distances

4.7.3.1 Inter-cluster distances

Intra-cluster D^2 values were ranged from 0 to 154.16. The highest intra-cluster distance (154.16) was noticed in cluster II, followed by 121.62 in cluster I. Whereas, no intra-cluster distance values were noticed in the clusters III, IV, V, VI and VII (Table 13).

4.7.3.2 Inter-cluster distances

Inter- cluster D^2 values ranged from 158.74 to 237.74. The highest inter-cluster D^2 value was documented between the clusters VI and IV, followed by 211.78 between cluster VI and V and least inter –cluster distance (158.74) was recorded in the clusters in III and I (Table 13).

4.7.4 Cluster means for various characters

The detailed cluster mean values for different quality traits in 14 genotypes are presented in Table 14.

4.7.4.1 TSS ($^{\circ}$ Brix)

The cluster mean values for this trait was higher in cluster VI (16.77), followed by cluster VII (14.82), cluster III (14.34), cluster V (10.69), cluster II (10.53), cluster IV (9.76) and least was observed in cluster I (8.75).

4.7.4.2 Acidity (%)

The results revealed that cluster VII had the highest cluster mean (2.39), followed by cluster III (2.06), cluster I (1.88), cluster VI (1.76), cluster II (1.74), cluster IV (1.71) and least cluster mean (1.06) was observed in cluster V for trait acidity.

4.7.4.3 Vitamin C (mg/100g)

The cluster mean values for vitamin C trait was highest in cluster VII (403.65), followed by cluster III (347.91), cluster I (317.93), cluster VI (297.25), cluster II (293.42), cluster IV (288.80) and least cluster mean (179.00) was observed in cluster V.

4.7.4.4 Total sugar (%)

Total sugar was found highest in cluster VI (6.80), followed by cluster VII (6.54), cluster III (6.25), cluster V (5.90), cluster II (5.47), cluster IV (5.36) and least was observed in cluster I (4.84).

Table 12. Contribution of different biochemical parameters of aonla genotypes towards total divergence

Sl. No.	Parameters	Contribution (%)
1	TSS (^o Brix)	9.89
2	Acidity (%)	14.29
3	Vitamin C (mg/100g)	17.58
4	Total sugar (%)	4.40
5	Reducing sugar (%)	0.00
6	Fat (%)	0.00
7	Fibre (%)	8.79
8	Flavonoid (mg/g)	6.59
9	Tannins (%)	18.68
10	Phenol (%)	0.00
11	Antioxidant (%)	15.38
12	TSS/Acid ratio	4.40

4.7.4.5 Reducing sugar (%)

Reducing sugar was found highest in cluster VI (4.46), followed by cluster VII (4.26), cluster III (4.03), cluster V (3.95), cluster II (3.59), cluster IV (3.52) and least was observed in cluster I (3.12).

4.7.4.6 Fat (%)

The cluster mean values for fat content was highest in cluster IV (1.64), followed by cluster V (1.38), cluster I (0.95), cluster VII (0.87), cluster III (0.82), cluster II (0.65) and least cluster mean (0.50) was observed in cluster VI.

4.7.4.7 Fibre (%)

Fibre content was found highest in cluster V (16.65), followed by cluster VII (16.30), cluster II (14.03), cluster I (13.43), cluster III (12.75), cluster IV (12.50) and least was observed in cluster VI (10.25).

4.7.4.8 Flavonoid (mg/g)

During the study results revealed that flavonoid content was found highest in cluster VII (1.73), followed by cluster IV (1.51), cluster III (1.18), cluster I (1.14), cluster II (1.14), cluster VI (1.08) and least was observed in cluster V (0.81).

4.7.4.9 Tannin (%)

Tannin content was found highest in cluster IV (9.27), followed by cluster III (8.17), cluster VII (8.01), cluster II (6.47), cluster I (6.39), cluster V (6.05) and least was observed in cluster VI (5.26).

4.7.4.10 Phenol (%)

The cluster mean values for phenol content was highest in cluster VII (1.62) followed by cluster IV (1.44), cluster I (1.44), cluster III (1.43), cluster II (1.42), cluster VI (1.36) and least cluster mean (1.11) was observed in cluster V.

4.7.4.11 Antioxidant (%)

Antioxidant content was found highest in cluster VII (92.18), followed by cluster II (87.26), cluster I (86.78), cluster IV (86.64), cluster VI (86.27), cluster III (86.25) and least was observed in cluster V (83.20).

4.7.4.12 TSS/Acid ratio

The cluster mean values for TSS to acid ratio was highest in cluster V (10.08), followed by cluster VI (9.53), cluster III (6.96), cluster II (6.22), cluster VII (6.20), cluster IV (5.70) and least cluster mean (4.68) was observed in cluster I.

Table 13. Intra and inter cluster distances for biochemical parameters of 14 aonla genotypes

Clusters	I	II	III	IV	V	VI	VII
I	121.62	162.50	158.74	159.48	168.50	193.76	182.28
II		154.16	188.07	187.55	183.27	173.37	174.73
III			0.00	159.87	181.04	203.51	202.90
IV				0.00	174.26	237.74	205.88
V					0.00	211.78	203.72
VI						0.00	202.53
VII							0.00

Note: diagonal values indicates intra cluster distances

Table 14. Mean values of clusters for biochemical parameters in 14 aonla genotypes

Sl No.	Parameters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VII	Cluster VII
1	TSS (°B)	8.75	10.53	14.34	9.76	10.69	16.77	14.82
2	Acidity (%)	1.88	1.74	2.06	1.71	1.06	1.76	2.39
3	Vitamin C (mg/100g)	317.93	293.42	347.91	288.80	179.00	297.25	403.65
4	Total sugar (%)	4.84	5.47	6.25	5.36	5.90	6.80	6.54
5	Reducing sugar (%)	3.12	3.59	4.03	3.52	3.95	4.46	4.26
6	Fat (%)	0.95	0.65	0.82	1.64	1.38	0.50	0.87
7	Fibre (%)	13.43	14.03	12.75	12.50	16.65	10.25	16.30
8	Flavonoid (mg/g)	1.14	1.14	1.18	1.51	0.81	1.08	1.73
9	Tannins (%)	6.39	6.47	8.17	9.27	6.05	5.26	8.01
10	Phenol (%)	1.44	1.42	1.43	1.44	1.11	1.36	1.62
11	Antioxidant (%)	86.78	87.26	86.25	86.64	83.20	86.27	92.18
12	TSS/Acid ratio	4.68	6.22	6.96	5.70	10.08	9.53	6.20

DISCUSSION

V DISCUSSION

The present investigation on “Evaluation of aonla genotypes for yield and quality traits” led to some important observations. The salient features of these observations have been discussed and interpreted below in the light of available literature under the following heads

5.1 Tree morphological parameters

5.2 Fruit and yield parameters

5.3 Biochemical parameters

5.4 Genetic variability

5.5 Correlation studies

5.6 Path co-efficient analysis

5.7 Genetic divergence

5.1 Tree morphological parameters

Morphological characters of a tree give a basic idea for preliminary selection of a genotype during the crop improvement programme. Based on the morphological characterization superior genotypes were selected for further studies.

5.1.1 Tree parameters

There was significant differences on stem girth during experimental period. The maximum stem girth was recorded in S-4 (86.53 cm) while, the minimum was recorded in V-11 (54.01 cm). The difference in stem girth might be due to genetic makeup of genotypes and favourable climatic condition. Similar results were observed by Rao and Subramanyam (2009), Aulakh *et al.* (2006) and Pandey *et al.* (2016).

The result revealed significant differences for tree height among the genotypes studied. The maximum tree height was recorded in K-18 (6.46 m) while, the minimum tree height was recorded in V-11 (3.55 m). The difference in tree height might be due to genetic makeup, prevailing climatic condition or the interaction effect of genotypes with environment. These observations were in conformity with the results of Aulakh *et al.* (1997), Krishnamoorthy *et al.* (2009) and Pandey *et al.* (2016).

Tree shape shows greater variation on 14 aonla genotypes. Spreading growth habit was observed in 11 genotypes. Whereas, erect growth habit was observed in three genotypes. The variation in tree shapes might be due to the inherit genetic character of respective genotypes, similar records were observed by Singh *et al.* (2015 a) and Kumar *et al.* (2016).

All genotypes exhibit similar trunk color i.e. whitish grey color. The observation regarding stem color was recorded from DUS (distinctness, uniformity, stability) characterization of aonla. This trunk color was due to inherit genetic character of aonla genotypes.

5.1.2 Leaf parameters

Morphological traits of tree foliage directly affects the nature of growth and development of tree. During the selection of superior genotype, the variations in foliage parameters were also plays a role.

Leaves are the functional units for photosynthesis which greatly influence the growth, yield and quality of the tree. Leaf shape has shown greater variation among the genotypes. Leaf shape was varied in elliptical, oblong and ovate shapes. Among three different leaf shapes, six genotypes has shown elliptical shape, one genotype showed oval leaf shape and seven genotypes has oblong shape. This variation in leaf shape might be due to the genetic character of the genotypes. Similar results were observed by Singh *et al.* (2015 a)

Aonla genotypes shows variation in leaf apex which directly influences the shape of leaves. A greater variation was observed in leaf apex. Leaf apex varied in two different shapes (Acute and obtuse). 12 genotypes have acute leaf shape and obtuse leaf apex was observed in two genotypes. This variation might due to genetic makeup of trees. Similar results were observed by Singh *et al.* (2015 a)

Leaf color is a important character for photosynthetic activity of the tree which ultimately decides the growth and development of the tree. Three groups of leaf color were observed among aonla genotypes. Dark yellowish green leaves were observed in two genotypes whereas, moderate yellowish green leaves were observed in eight genotypes and four genotypes has shown moderate olive-green leaves. Dark green color leaves exhibit higher photosynthetic activities. Variation in leaf color might be due to genetic makeup of the genotypes. Similar records were observed by Singh *et al.* (2015 a)

5.2 Fruit and yield parameters

The ultimate aim of any grower is to get improved fruit, yield and quality which realizes more revenue. Among several parameters which either directly or indirectly influence the yield and quality of aonla like fruit length, fruit volume, fruit weight, pulp weight, seed weight, number of seeds per fruit *etc.*, which ultimately decide the yield and quality which are described in detail here under following headings.

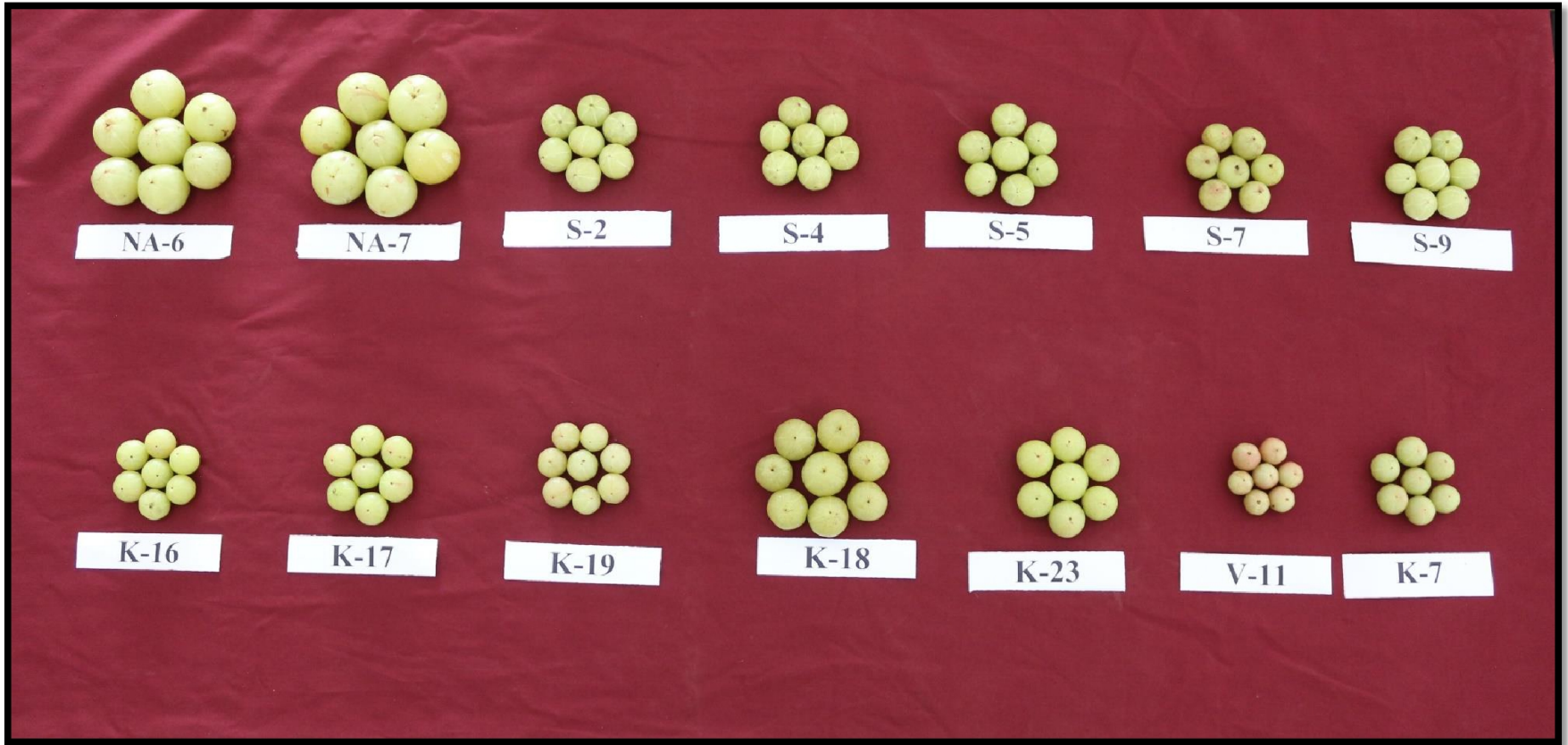


Plate 2. Variation in fruit of aonla genotypes

5.2.1 Fruit parameters

Fruit length is an important trait which impact marketability of fruits. Length of fruit showed significant variation in aonla genotypes which was ranged from 1.90 cm to 4.15 cm. Longest length of fruit (4.15 cm) was observed in genotype NA7 which was statistically *on par* with NA-6 (4.10 cm) and shorter length of fruit was recorded in genotype V-11 (1.90 cm). This variation in fruit length might be governed by genetic character associated with the genotypes and also favourable climatic condition. Similar results were observed by Yadav and Yadav (2010), Bakshi *et al.* (2015), Kumar *et al.* (2016), Singh *et al.* (2016) and Chiranjeevi *et al.* (2018).

Fruit diameter is an important character where it shows the shape of the fruits. Usually, high diameter fruits are round in shape. It was observed that diameter of fruit is higher than the fruit length. In the present research, it was observed that NA-7 had the higher diameter (4.55 cm) and lowest was observed in V-11 (2.09 cm). The similar observations were accordance with Yadav and Yadav (2010), Bakshi *et al.* (2015) and Chiranjeevi *et al.* (2018).

A significant difference was observed in fruit weight, it is desirable character for selection. In the present investigation fruit weight was ranged from 6.03 g to 50.84 g. It was recorded maximum and minimum in NA-7 and V-11 respectively. The variation might be due to genetic variability and favourable climatic condition which significantly increased fruit weight. It may be also due to the increase in fruit length, fruit diameter, pulp and stone weight of the fruits. Similar results were observed by Bakshi *et al.* (2015), Parveen and Khatkar (2015), Kumar *et al.* (2016), Chiranjeevi *et al.* (2018) and Pandey *et al.* (2016).

Fruit volume of aonla genotypes showed significant variation which was ranged between to 5.90 cc (V-11) to 47.33 cc (NA-7). The variation in the fruit volume depends on genotypic character, and it is positively interrelated with fruit weight. Higher volume in NA-7 might be due to more activeness of mesocarp cells, which enlarges the fruit development leads to increase in fruit size and fruit volume. Similar records were observed by Rao and Subramanyam (2009) and Bakshi *et al.* (2015).

Pulp weight is a desirable character as it fetches more demand for processing industry. The results showed that in pulp weight, maximum pulp weight was recorded in genotype NA-7 (48.43 g) and minimum in V-11 (5.28 g). The higher pulp weight might be due to larger fruit weight and it also depends on genotypic character of genotypes. These results are in close conformity with findings of Bakshi *et al.* (2015), Pandey *et al.* (2016) and Chiranjeevi *et al.* (2018).

The significant difference was observed in stone weight. Maximum seed weight was noticed in NA-6 (2.51 g) and minimum in V-11(0.75 g). The difference

in seed weight might be due to differences in the number and size of seeds among the genotypes. The bold seed might have more stored food and larger healthy embryo which may show better germination and survival rate. The results were in accordance with Pandey *et al.* (2014), Bakshi *et al.* (2015), Singh *et al.* (2016), Pandey *et al.* (2016) and Chiranjeevi *et al.* (2018).

Stone to pulp ratio was significantly varied among the genotypes. It was observed that ratio was maximum in K-23 (0.15) and it was found minimum in NA-6, NA-7 and S-5 (0.05). The variation in stone to pulp ratio could be due to the effect of inherited character among the genotypes. Similar results were observed in research of Chiranjeevi *et al.* (2018) and Naithani *et al.* (2020).

Pulp to stone to ratio is important character for selection of genotypes for further research in breeding. Among the genotypes, NA-7 shows maximum pulp to stone ratio (20.09) and minimum was found in V-11 (6.76). The variation with respect to the ratio could be due to the effect of inherit character of genotypes. These results were accordance with Chiranjeevi *et al.* (2018) and Naithani *et al.* (2020).

Number of seeds per stone is important trait for propagation. The significant difference was observed with respect to number of seeds per stone in genotypes. Variation with respect to seeds per stone might be due to genotypic character among the genotypes. Similar results were observed by Chiranjeevi *et al.* (2018).

5.2.2 Fruit yield (kg/tree)

Yield is important character for selection of genotypes for economic cultivation of any crop. It was observed that maximum yield was recorded in NA-7 (54.11 kg) which was followed by NA-6 (49.04 kg) and minimum in V-11 (25.22 kg). Higher yield of NA -7 might be due to greater number of branchlets, number of leaves and leaf area causing more accumulation and transport of more photosynthates resulting in increased fruit weight, better fruit retention and more number of fruits. And also, it could be due to inherited character of genotypes. It was observed that NA-6 and NA-7 genotypes bears fruits two times per year. Similar results observed by Krishnamoorthy (2009), Rao and Subramanyam (2009), Shukla *et al.* (2009) and Aulakh *et al.* (2013).

5.2. 3 Fruit yield (ton/ha)

Significant differences were observed in 14 aonla genotypes with respect to fruit yield per hectare. Among the genotypes NA-7 (14.98 t/ ha) showed highest yield which was followed by NA-6 (13.58 t/ha) and found minimum in V-11(6.98 t/ha). The variation might be due to accumulation of relatively more photosynthates which were synthesized in the trees for better translocation of assimilates from source to sink which in turn increased the fruit yield in aonla.

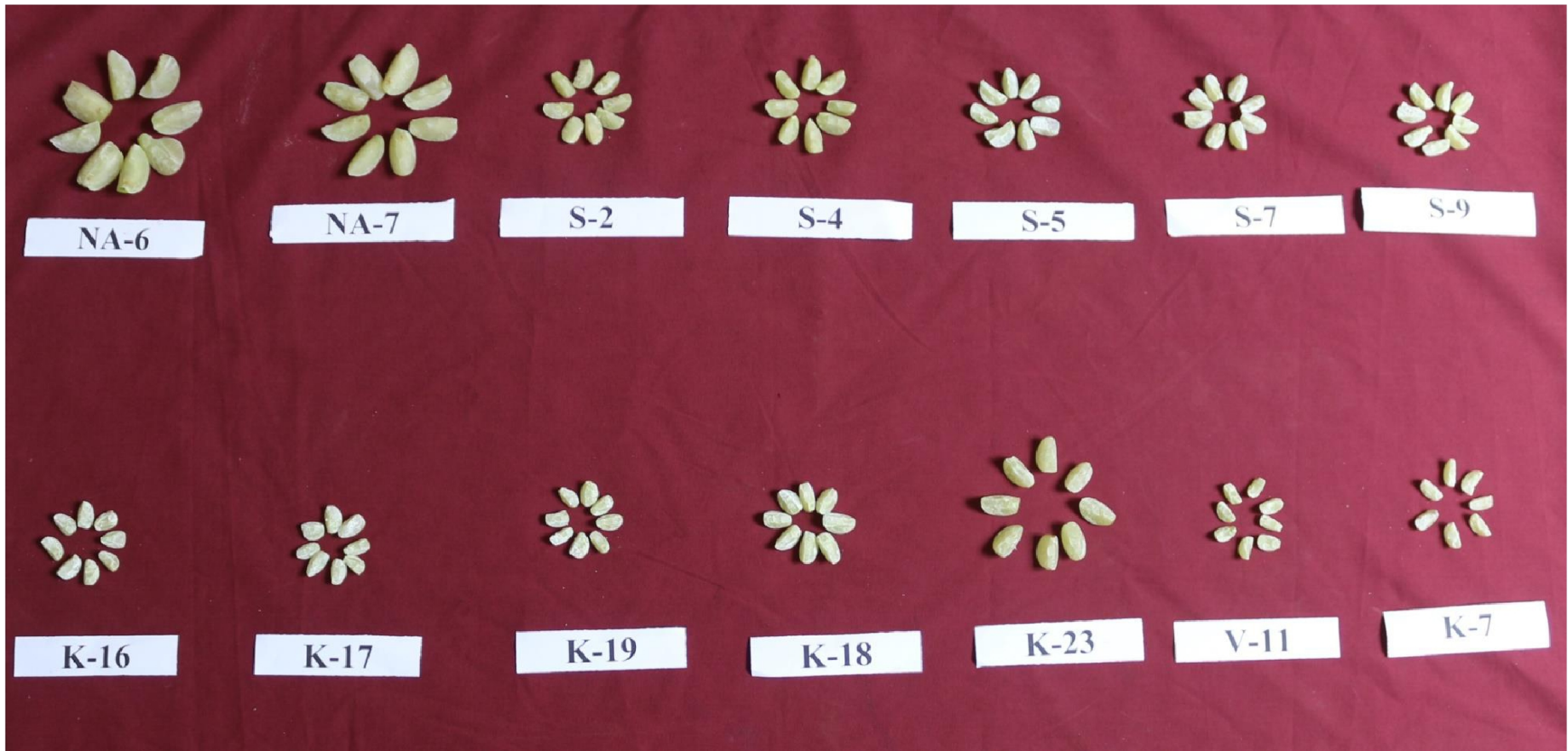


Plate 3. Variation in pulp content of aonla genotypes

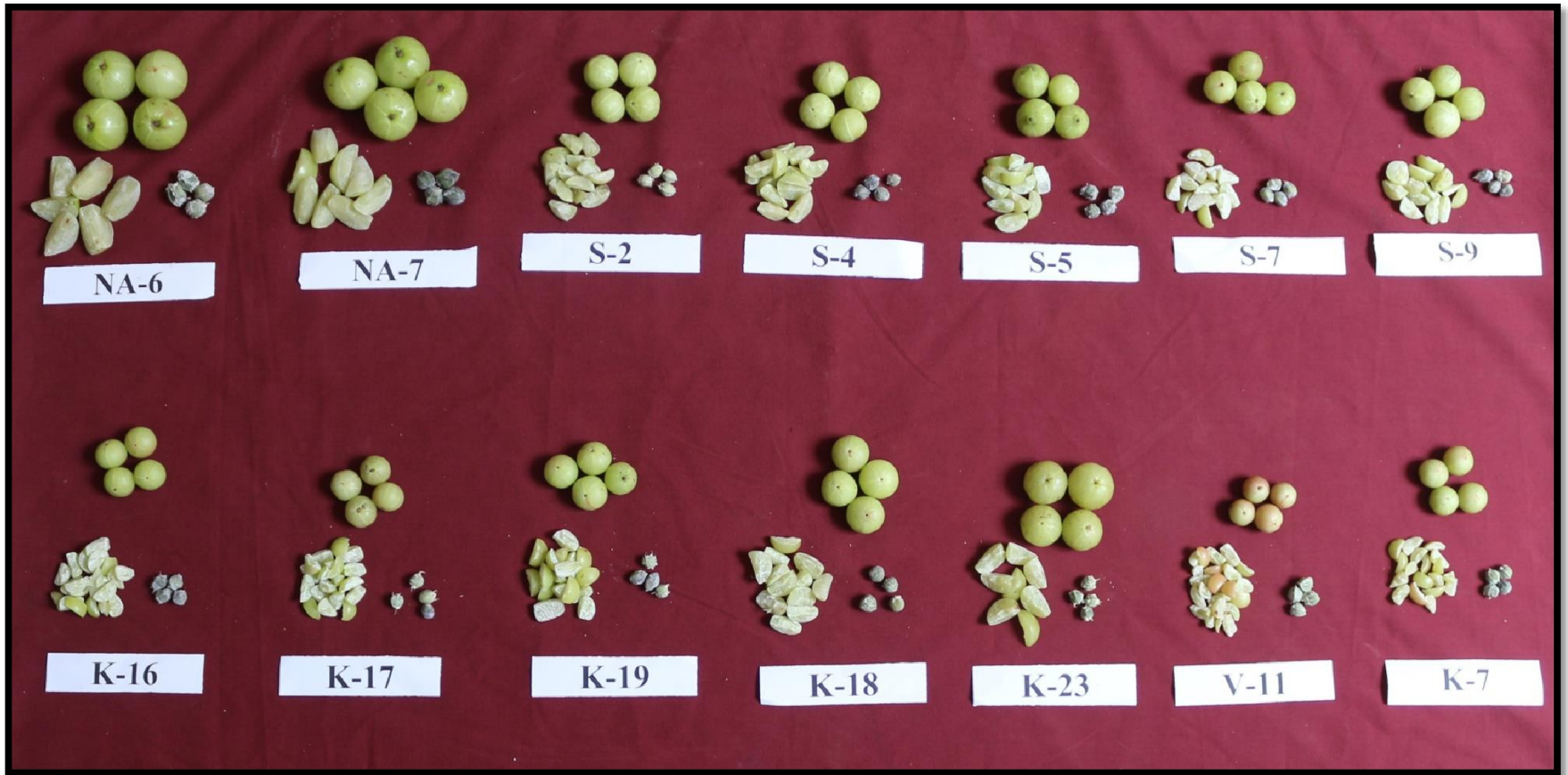


Plate 4. Variation in fruit, pulp and stone of aonla genotypes

5.3 Biochemical parameters

Quality and acceptance of a fruit is mainly depends on the biochemical characters of the fruit pulp.

The total soluble solids (TSS) content of different genotypes varied significantly. The minimum TSS was recorded in NA-7 (8 °B) and maximum TSS was recorded in K-7 (16.77 °B). The variation observed in TSS might be due to existing genetic variability, also due to difference in sugar content of the pulp, low moisture content in the pulp at the time of harvesting. On the other hand, lower TSS content under tropical condition may be attributed to the occurrence of rainfall during fruit maturity i.e., August- September, which might have increased the moisture content in the fruit and dilution of carbohydrates. Similar outcome with respect to TSS was reported by Kumar and Singh (2002), Jadhav *et al.* (2006), Bakshi *et al.* (2015), Tripathi *et al.* (2016) and Naithani *et al.* (2020).

Acidity is important trait in aonla fruit crop, which enumerates the ascorbic acid content. Higher acid content was observed in cultivar K-23 (2.39 %) whereas, it was lowest in S-4 (1.06 %). Wide variation in acidity might be due to greater diversity that exists between genotypes. The maximum acidity might be due to higher synthesis of organic acids. Generally, total acidity in gooseberry was low at immature stage and slowly increased with advancement of maturity. Acidity mainly depends on varietal character and harvesting stage. Similar results were iobserved by with Kumar and Singh (2002), Mehta *et al.* (2002), Bakshi *et al.* (2015), Tripathi *et al.* (2016) and Naithani *et al.* (2020).

TSS to acid ratio is an economically important biochemical parameter, as it determines taste, sugar- acid blend and acceptability of product by consumers in the market. The maximum TSS to acid ratio was obtained in genotype S-4 (10.08) and minimum in NA-7 (4.23). This variation might be due to sugar acid blend in different genotypes. Similar results were in accordance with Bakshi *et al.* (2015), Pandey *et al.* (2014), Singh *et al.* (2015 a) and Kumar *et al.* (2016).

The higher ascorbic acid content is a preferred character, as aonla is mainly consumed for intake of ascorbic acid. Aonla genotypes showed significant difference on ascorbic content during experimental period. The results revealed that the K-23 genotype exhibited highest ascorbic acid content (403.6 mg/100g) and lowest was observed in NA-6 (179 mg/100gm). The variation in ascorbic acid content may be associated with genetic makeup and inherited characters of aonla genotypes. The higher ascorbic acid content might be attributed to the adequate supply of hexose sugars in photosynthetic activity. However, ascorbic acid content was reported low in tropical condition which could be due to high temperature, soil moisture and humidity at the time of fruit maturation that might have affected enzymatic

biosynthesis. Similar results are in accordance with Singh *et al.* (2009), Kumar and Singh (2013), Bakshi *et al.* (2015), Pandey *et al.* (2016) and Naithani *et al.* (2020).

The data showed highest total sugars, reducing sugars and non-reducing sugars (6.80 %, 4.28 % and 2.34 %, respectively) in K-7 genotype. However, total sugars and reducing sugars and non-reducing sugars were observed lowest (4.44 %, 2.92 % and 1.53 %, respectively) in NA-7. Total sugars may increase or decrease in accordance with the increase or decrease in TSS. The variation in sugar content may be attributed to accumulation and translocation of photosynthates from leaves to fruits as carbohydrates are manufactured in the leaves. The increased level of total sugar might be due to degradation of insoluble polysaccharides. Variation in reducing sugar content might be due to breakdown of sucrose to glucose and fructose or inversion of sugars, it also might be due to genetic makeup of genotypes. Similar results were in accordance with Pandey *et al.* (2014), Bakshi *et al.* (2015) and Naithani *et al.* (2020).

Fruits are recommended as a good source of dietary fibers. S-4 genotype showed highest fiber content (16.65 %), and lowest was observed in K-7 (10.25 %). The term crude fiber generally includes polysaccharides, cellulose, hemicelluloses and lignin. Variations in genotypes due to genetic character. The results are in accordance with Parveen and Khatkar (2015), Nimse and More (2018).

The data showed that the K-17 genotype resulted in highest fat content (1.64 %) and lowest was observed in NA-6 (0.39 %). The variation in the fat content among the genotypes of aonla could be attributed to genotypic characters. The present findings were in accordance with those of Nimse and More (2018) and Parveen and Khatkar (2015).

Flavonoid is important trait in aonla which contributes to antioxidant property. Among the genotypes test, Significant results were obtained with respect to flavonoid content in aonla fruits. The data showed that K-23 genotype recorded highest flavonoid content (1.73 %) and lowest was observed in S-4 (0.81 %). Variation in flavonoid content among the different genotypes of aonla could be attributed to genetic characteristics. The results were in accordance with those of Kumari *et al.* (2017).

The higher tannin content is a desired character as it reduces the degradation of ascorbic acid during processing. Tannin i.e., gallotanic acid on hydrolysis yields gallic acid has antioxidant property (Singh *et al.*, 2016). The data showed that K-16 genotypes recorded highest tannin content (9.62 %) and lowest was observed in S-7 (4.91 %). The variation of genotypes might be attributed due to genetic character in aonla. The present findings are in accordance with those of Srivastava and Srivastava (1964), Yadav and Yadav (2010) and Pandey *et al.* (2008).

Antioxidant properties in aonla fruit is due to the presence of phenolic compounds. Aonla genotypes showed significant variation on phenol content. The results revealed that K-23 genotype had highest phenol content (1.62 %) and lowest observed in S-4 (1.11 %). Variation in phenols among the different cultivars of aonla might be due to differential activity of phenylalanine ammonium lyase and polyphenol oxidase enzymes. Varietal difference in total polyphenol content could be partially due to the different maturity stages, genetic and climatic conditions. The present findings were in accordance with those of Kumari *et al.* (2017).

In general, most of the diseases are mainly due to homeostatic imbalance in pro-oxidant and anti-oxidant. Antioxidant is important for good immunity. Cultivar K-23 had highest antioxidant content (92.18 %) and lowest was observed in S-4 (83.20 %). Variation in antioxidant may be due to genotypic characters. There are some invitro studies indicating that the antioxidant activities of aonla could be attributed to ascorbic acid and the overall effect was also due to the presence of other polyphenols such as ellagic acid, gallic acid, tannins and flavonoids. The present findings were in accordance with those of Kumari *et al.* (2017) and Haripriya *et al.* (2012).

5.4 Genetic variability

Assessment of genetic variability, nature and magnitude of characters association for quality, yield and yield attributing traits made easy for the success of any crop improvement programme. Recognition of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character in future generations.

Since, the selection is based on phenotypic observations in which the quantitative traits are taken into consideration. To analyzing the data involves some statistical modelling techniques *viz.*, mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean for different characters in aonla have been enumerated to drawn out the acceptable results from the 14 genotypes studied in the present experiment.

5. 4 Genetic variability, heritability and genetic advance as per cent of mean for growth, yield and quality parameters

Among the different characters studied, high GCV and PCV were observed for fruit weight, fruit volume, fruit length, fruit diameter, pulp weight, stone weight, pulp to stone ratio, yield per tree, TSS, acidity, vitamin C, TSS/Acid ratio, tannins, fat and flavonoid. It indicates the presence of a higher magnitude of variability for these characters, which would be helpful for further selection. Similar

results were observed by Patel *et al.* (2016), Rabha *et al.* (2013), Sridar *et al.* (2018), Verma *et al.* (2003), Marboh *et al.* (2018) and Lal *et al.* (2016), Raghava and Tiwari (2008), Rao *et al.* (2016) and Sindhe (2019).

Moderate GCV and PCV were observed for plant height, stem girth, total sugar, reducing sugar and non-reducing sugar. This indicates medium variability and traits have good scope for selection. These traits have good scope for selection. The similar findings observed by Patel *et al.* (2016), Verma *et al.* (2003), Rabha *et al.* (2013) and Sridar *et al.* (2018).

Low GCV and PCV values were observed for number of seeds per fruit, phenols and antioxidants. This indicates that low variability in these traits, for further selection induction of variability is needed.

5.4.2 Heritability

Heritability and genetic advance are important selection parameters. The ratio of genotypic variance to the phenotypic variance is known as heritability and expressed in percentage. Heritability is a better indicator of carrying the characters from parents to progenies.

A higher value of heritability in a broad sense indicates that the characters are less influenced by the environmental effects and selection is made based on the phenotypic performance. Often, heritability in a broad sense is not a genuine indicator of selection, since only additive components of variance is channeling from generation to generation. A Low value of heritability of a character reveals that trait is highly influenced by environmental effects and selection of trait may be difficult due to masking effects of the environment on the genotypic effects. Moderate heritability of a trait for selection is much reliable through phenotypic performance by eliminating the environmental effects.

The high estimates of heritability coupled with high genetic advance over per cent of mean were noticed for the traits such as plant height, stem girth, fruit weight, fruit volume, fruit length, fruit diameter, pulp weight, stone weight, pulp to stone ratio, yield per tree, TSS, acidity, vitamin C, TSS to acid ratio, total sugar, reducing sugar, non-reducing sugar, tannin, fat, flavonoid and fibre content. Higher heritability estimates indicated that character was less influenced by the environmental conditions, high capacity of the characters for transmission to subsequent generation and high heritability when coupled with high genetic advance as per cent mean may be attributed to the additive gene effect. Similar results observed by Patel *et al.* (2016) and Verma *et al.* (2003), Rabha *et al.* (2013), Sridar *et al.* (2018), Lal *et al.* (2016), Rao *et al.* (2016) and Sindhe (2019)

The high estimates of heritability coupled with moderate genetic advance over per cent of mean were noticed in traits such as number of seeds per stone, phenol and antioxidant content. Higher heritability estimates indicated that character was less influenced by the environmental conditions, and high heritability when coupled with moderate genetic advance as per cent mean may be attributed to the additive gene effect.

5.5 Correlation studies

Correlation co-efficient analysis measures the mutual relationship between various plant characters and determines the component characters on which, selection can be based for improvement in the yield. Correlation provides information on the nature and extent of relationship between all pairs of characters. Hence, when the breeder applies selection for a particular character, not only it improves that trait, but also other characters and it will provide a reliable measure of genetic association between them which is useful in breeding programmes.

5.5.1 Phenotypic correlation and genotypic correlation

Fruit weight (g)

Fruit weight showed highly significant and positive association with fruit volume, fruit length, fruit diameter, pulp weight, and yield per plant at both phenotypic and genotypic level. Whereas, significant positive correlation of fruit weight was noticed with acidity and vitamin C at genotypic level. Similar results were observed by Parmar *et al.* (2020), Gupta and Kour (2019), Perveen *et al.* (2019), Pooja *et al.* (2018), Reeta (2017), Lal *et al.* (2016), Patel *et al.* (2016), Jana *et al.* (2015), Rabha *et al.* (2013) and Majumder *et al.* (2012).

Fruit volume (cc)

Fruit volume had found highly significant and positive association with fruit length, fruit diameter, pulp weight and yield at both phenotypic and genotypic level. Whereas, significant positive correlation of fruit diameter was noticed in acidity and vitamin C at genotypic level. Similar records were observed by Parmar *et al.* (2020), Perveen *et al.* (2019), Reeta (2017), Patel *et al.* (2016), Jana *et al.* (2015) and Rabha *et al.* (2013).

Fruit length (cm)

The trait fruit length had showed highly significant and positive association with fruit diameter, pulp weight, and yield at both genotypic and phenotypic level and also fruit length has highly significant positive correlation with TSS, total sugar, reducing sugar, non-reducing sugar, acidity and vitamin C at genotypic level only. Similar records were observed by Parmar *et al.* (2020) and Gupta and Kour (2019), Perveen *et al.* (2019), Pooja *et al.* (2018), Lal *et al.* (2016), Patel *et al.* (2016), Rabha *et al.* (2013) and Majumder *et al.* (2012).

Fruit diameter (cm)

Fruit diameter showed highly significant association with pulp weight and yield at both genotypic and phenotypic level while, for TSS, total sugar, reducing sugar, non-reducing sugar, acidity and vitamin C and yield at genotypic level only. Similar findings observed by Parmar *et al.* (2020), Gupta and Kour (2019), Perveen *et al.* (2019), Pooja *et al.* (2018), Lal *et al.* (2016), Rabha *et al.* (2013) and Patel *et al.* (2016).

Pulp weight (g)

During this study Pulp weight showed highly significant and positive association with yield per tree at both phenotypic and genotypic level. whereas, significant positive correlation with acidity was at genotypic level only. Similar records were in accordance with Pooja *et al.* (2018) and Patel *et al.* (2016).

Total soluble solids (^oBrix)

The trait TSS showed highly significant positive correlation with total sugar, reducing sugar and non- reducing sugar at both phenotypic and genotypic level and also with yield per tree at genotypic level. Similar records observed by Lal Nag *et al.* (2020), Parmar *et al.* (2020), Gupta and Kour (2019), Perveen *et al.* (2019), Pooja *et al.* (2018), Lal *et al.* (2016), Patel *et al.* (2016), Jana *et al.* (2015) and Rabha *et al.* (2013).

Acidity (%)

Acidity showed highly significant positive correlation with vitamin C at both genotypic and phenotypic level. At genotypic level, total sugar, reducing sugar, non-reducing sugar and yield per tree had highly significant positive correlation with acidity. Similar findings were observed by Lal Nag *et al.* (2020), Parmar *et al.* (2020), Gupta and Kour (2019), Perveen *et al.* (2019), Pooja *et al.* (2018), Lal *et al.* (2016), Patel *et al.* (2016), Jana *et al.* (2015) and Rabha *et al.* (2013).

Vitamin C (mg/100g)

Vitamin C showed highly significant positive correlation with total sugar, reducing sugar, non- reducing sugar, and yield at genotypic level. At phenotypic level, Vitamin C showed non - significant positive correlation with total sugar, reducing sugar, non- reducing sugar. while non- significant negative correlation for yield per tree. Similar records were observed by Perveen *et al.* (2019), Pooja *et al.* (2018), Patel *et al.* (2016), Rabha *et al.* (2013) and Srinivas *et al.* (2010).

Total sugar (%)

Total sugar had a highly significant and positive correlation with reducing sugar, non- reducing sugar, at both phenotypic and genotypic level and highly

significant positive correlation with yield at genotypic level. Similar records were observed in Lal Nag *et al.* (2020), Pooja *et al.* (2018), Patel *et al.* (2016), Jana *et al.* (2015) and Rabha *et al.* (2013).

Reducing sugar (%)

Reducing sugar showed highly significant and positive correlation with non-reducing sugar at both phenotypic and genotypic level and highly significant positive correlation with yield per tree at genotypic level. Similar results were accordance with Lal Nag *et al.* (2020), Patel *et al.* (2016), Jana *et al.* (2015) and Rabha *et al.* (2013).

Non-reducing sugar (%)

Non-reducing sugar showed highly significant positive correlation with yield at genotypic level. Similar findings were observed by Lal Nag *et al.* (2020), Patel *et al.* (2016) and Rabha *et al.* (2013).

5.6 Phenotypic path co-efficient analysis

Path co-efficient studies fruit yield has been associated with a number of component characters and these characters themselves are inter-related. Every component trait will have a direct and indirect effect on yield. Path co-efficient analysis offered a much more realistic interpretation of the factors involved. Based on these effects exerted by the characters on the yield, one can consider that particular trait for improvement of the crop.

Fruit weight (g)

Fruit weight showed negative and direct effect on fruit yield per tree. Whereas, positive and indirect effect was exhibited by fruit length, pulp weight, TSS, acidity, vitamin C, total sugar, reducing sugar and non-reducing sugar. Similar studies were observed by Majumder *et al.* (2012) and Lal *et al.* (2016).

Fruit volume (cc)

Fruit volume showed negative and direct effect on fruit yield per tree. Whereas, positive and indirect effect was exhibited by TSS, acidity, vitamin C, total sugar, reducing sugar and non-reducing sugar. Similar findings were observed by Majumder *et al.* (2012).

Fruit length (g)

Fruit length showed negative and direct effect on fruit yield per tree. Whereas, positive and indirect effect was exhibited by TSS, acidity, vitamin C, total sugar, reducing sugar, non-reducing sugar. Similar findings observed by Parmar *et al.* (2020) Majumder *et al.* (2012) and Lal *et al.* (2016).

Fruit diameter (cm)

Fruit diameter showed positive and direct effect on fruit yield per tree. Whereas, positive and indirect effect was exhibited by pulp weight, Similar findings were observed by Parmar *et al.* (2020), Majumder *et al.* (2012) and Lal *et al.* (2016).

Pulp weight (g)

During this study, Pulp weight showed positive and direct effect on fruit yield per tree. Similar records were observed by Lal *et al.* (2016).

Total soluble solids (^oBrix)

Fruit volume showed negative and direct effect on fruit yield per tree. Similar studies were observed by Lal nag *et al.* (2020), Parmar *et al.* (2020), Majumder *et al.* (2012) and Lal *et al.* (2016).

Acidity (%)

Acidity showed positive and direct effect on fruit yield per tree. While, positive and indirect effect on total sugar, reducing sugar, and non- reducing sugar. Similar studies were observed by Lal nag *et al.* (2020 a), Parmar *et al.* (2020), Majumder *et al.* (2012) and Lal *et al.* (2016).

Vitamin C (mg/100g)

Vitamin C showed negative and direct effect on fruit yield per tree. Similar studies were observed by Lal *et al.* (2016).

Total sugar (%)

Total sugar showed positive and direct effect on fruit yield per tree. While, positive and indirect effect on reducing sugar and non- reducing sugar. Similar results were observed by Lal Nag *et al.* (2020 a).

Reducing sugar (%)

Reducing sugar showed positive and direct effect on fruit yield per tree. While, positive indirect effect on non- reducing sugar. Similar studies were noticed by Lal Nag *et al.* (2020 a).

Non -reducing sugar (%)

Non -reducing sugar showed negative and direct effect on fruit yield per tree. Similar studies were observed by Lal Nag *et al.* (2020 a).

5.7 Genetic Divergence

The success of a breeding program depends upon the selection of parents. It has been found that the progenies derived from crossing divergent parents give divergent and useful progenies. The multivariate analysis based on Mahalanobis D² statistics is

employed as a powerful tool for measuring genetic divergence among the tested genotypes.

5.7.1 Mahalanobis generalized distance

The material used for the present study includes 14 genotypes of aonla were grouped into seven clusters using Tocher's method (Fig. 1). Among the seven clusters studied, Cluster II was the largest having five genotypes followed by cluster I having four genotypes and cluster III, IV, V, VI and VII were the least with one genotype each. The findings are similar to the results of Sharma *et al.* (2013), Singh *et al.* (2015 b), Kumar *et al.* (2020), Lal Nag *et al.* (2020 b) Rekha *et al.* (2011) and Baswal *et al.* (2017).

The intra-cluster distance revealed that cluster II with five genotypes showed maximum intra-cluster diversity depicting the presence of wide genetic divergence among the constituent genotypes. The higher degree of divergence among the genotypes, cluster would produce more segregating breeding material. Selection within such a cluster might be executed based on the maximum mean value for the desirable characters.

Based on the distance between clusters, *i.e.*, inter-cluster distances, the maximum divergence was observed between cluster VI and cluster IV indicating that the genotypes present in these clusters can be used as parents in hybridization programme to obtain superior segregants. Tannin content had contributed the maximum to the genetic divergence followed by vitamin C.

5.7.2 Cluster mean analysis

Cluster VI had the highest cluster mean value for TSS content followed by cluster VII, cluster III, cluster V, cluster II and cluster IV. The minimum cluster mean was observed in cluster I. Therefore, crosses between these respective clusters may be used to improve the TSS content so it ultimately improves the quality of aonla fruit.

The highest cluster mean for acidity was observed in cluster VII followed by cluster III, cluster I, cluster VI, cluster II, cluster IV and least cluster mean was observed in cluster V. Hence, crosses between genotypes belonging to these respective clusters would be helpful for achieving improvement in acidity content.

Cluster VII had the highest cluster mean value for vitamin C content followed by cluster III, cluster I, cluster VI, cluster II, cluster IV and least cluster mean was observed in cluster V. This indicates that the crosses between the genotypes belonging to this cluster may be tried to number vitamin C content.

Total sugar was found highest in VI, followed by cluster VII, cluster III, cluster V, cluster II, cluster IV and least was observed in cluster I. Therefore the crosses among the genotypes belonging to these clusters may be tried to improve total sugar.

Reducing sugar was found highest in cluster VI, followed by cluster VII, cluster III, cluster V, cluster II, cluster IV and least was observed in cluster I. This indicates that the crosses between the genotypes belonging to this cluster may be tried to improve reducing sugar.

The cluster mean value for fat content was highest in cluster IV, followed by cluster V, cluster I, cluster VII, cluster III, cluster II and least cluster mean was observed in cluster VI. This indicates crosses between these respective clusters may be tried to improve the fat content.

Fibre content was found highest in cluster V, followed by cluster VII, cluster II, cluster I, cluster III, cluster IV and least was observed in cluster VI. Crosses between genotypes belonging to these respective clusters may be tried to improve this character which ultimately contributes to quality.

Flavonoid content was found highest in cluster VII, followed by cluster IV, cluster III, cluster I, cluster II, cluster VI and least was observed in cluster V. Therefore, the crosses among the genotypes belonging to these clusters may be tried to improve this trait which ultimately contributes to quality.

Tannin content was found highest in cluster, followed by cluster III, cluster VII, cluster II, cluster I, cluster V and least was observed in cluster VI. Hence, the crosses between genotypes belonging to this cluster may be tried to improve tannin content.

The cluster mean values for phenol content was highest in cluster VII followed by cluster IV, cluster I, cluster III, cluster II, cluster VI and least cluster mean was observed in cluster V. Therefore, the crosses among the genotypes belonging to these clusters may be tried to improve this trait.

Antioxidant content was found highest in cluster VII, followed by cluster II, cluster I, cluster IV, cluster VI, cluster III and least was observed in cluster V. Therefore, the crosses among the genotypes belonging to these clusters may be tried to improve this trait which ultimately contributes to quality.

The cluster mean values for TSS to acid ratio was highest in cluster V, followed by cluster VI, cluster III, cluster II, cluster VII, cluster IV and least cluster mean was observed in cluster I. Therefore, the crosses among the genotypes belonging to these clusters may be tried to improve this trait.

Conclusion

From the present study, it is concluded that the analysis of variance revealed the existence of considerable variation among the genotypes for the traits studied. The genotype NA-7 was found superior compared to all other genotypes with respect to fruit and yield parameters followed by NA-6. Whereas, genotype K-23 is superior with respect to acidity, vitamin C, phenols, flavonoid and antioxidants so it would be the promising genotype while selecting superior genotypes.

In general, phenotypic coefficients of variation (PCV) were higher in magnitude than genotypic coefficients of variation (GCV) and narrow difference between them indicates the less environmental influence on expression of trait. High heritability coupled with high genetic advance was observed for all the characters except number of seeds per fruit, phenols and antioxidant.

Correlation studies revealed that all fruit parameters exhibited highly significant and positive association with yield at both phenotypic and genotypic level. Whereas, biochemical parameters showed significant and positive association with yield at genotypic level only. Path analysis for yield per tree showed direct and positive association with fruit diameter, pulp weight, acidity, total sugar and reducing sugar.

Tannin content contributed the maximum to the genetic divergence among the parameters studied followed by vitamin C, antioxidant, acidity, TSS, fibre, flavonoid, total sugar and TSS to acid ratio. Hence, these traits may be given high attention while selecting lines for hybridization programme to generate large variability.

Future line of work

- Desirable characters identified can be combined through introgression breeding
- Estimation of genetic diversity among the genotypes using molecular markers.

SUMMARY

VI SUMMARY

The present investigation entitled “Evaluation of aonla genotypes for yield and quality traits” was carried out during 2020-21 at Forest Research Station, near Govinakovi, Honnali taluk, Davangere district. The experiment was laid out in randomized complete block design with three replications and 14 genotypes *viz.*, NA-6, NA-7, S-2, S-4, S-5, S-7, S-9, K-16, K-17, K-19, K-18, K-23, V-11 and K-7. The salient findings of the present investigation are summarized below.

Among 14 genotypes studied, the longest tree height was recorded in K-18 (6.46 m). While, the shortest tree height was recorded in V-11 (3.55 m) and the maximum stem girth was recorded in S-4 (86.53 cm). Whereas, the minimum was recorded in V-11 (54.01 cm). Two different shapes of tree were observed in the aonla population *viz.*, spreading and erect type, 11 genotypes shows spreading type and three genotypes were erect in shape.

All genotypes had whitish grey trunk colour. The leaf colour varied from dark yellowish green to moderate yellow green and some genotypes have moderate olive green leaves. However, three types of leaf shape observed in the genotypes *i.e.*, oblong, elliptical and oval shape. The different leaf apex recorded were acute and obtuse.

Among 14 genotypes, the maximum fruit length was recorded in NA-7 (4.15 cm) and minimum was recorded in V-11 (1.90 cm). The highest fruit diameter was recorded in NA-7 (4.55 cm). Whereas, lowest was observed in V-11 (2.09 cm). The maximum fruit weight was recorded in NA-7 (50.84 g). While, the minimum was recorded in V-11 (6.03 g). The highest fruit volume was observed in NA-7 (47.33 cc) and the lowest was recorded in V-11 (5.90 cc).

The highest pulp content was observed in NA-7 (48.43 g) and lowest was recorded in V-11 (5.28 g). The maximum stone weight was observed in NA-6 (2.51 g) and the minimum was recorded in V-11 (0.75 g). The number of seeds per stone were ranged from 5 to 6 among different genotypes. The maximum stone to pulp ratio was observed in K-23 (0.15) and the minimum was recorded in NA-6, NA-7 and S-5 (0.05). The highest pulp to stone ratio was observed in NA-7 (20.9) and lowest was recorded in K-23 (6.76).

Among 14 genotypes studied, the highest yield per tree was recorded in NA-7 (54.11 kg) while, the lowest was recorded in V-11 (25.22 kg) and maximum yield per hectare was recorded in NA-7 (14.98 t/ha) whereas, the minimum was recorded in V-11 (6.98 t/ha).

The higher total soluble solids of the pulp were recorded in K-7 (16.76 °Brix) and the least was observed in NA-6 (8 °Brix). The higher acidity content was recorded in K-23 (2.39 %) and the minimum was observed in S-4 (1.06 %). The highest ascorbic

acid content of the pulp was recorded in K-23 (403.65 mg/100g) and the lowest was recorded in S-4 (179 mg/100g). The maximum TSS to acid ratio of the pulp was observed in S-4 (10.08) and the minimum was recorded in NA-7 (4.23).

The higher total sugars of the pulp were recorded in K-7 (6.80 %) and the least was observed in NA-7 (4.55 %). The higher reducing sugar content was recorded in K-7 (4.46 %) and the lowest was observed in NA-7 (1.53 %). The highest non reducing sugar content of the pulp was recorded in K-7 (2.34 %) and the lowest was recorded in NA-7 (1.53 %).

The maximum fat content was observed in K-17 (1.64 %) and the minimum was recorded in NA-6 (0.39 %). The maximum fibre content was observed in S-4 (16.65 %) and the minimum was recorded in K-7 (10.25%). The maximum flavanoid was observed in K-23 (1.73 mg/g) and the minimum was recorded in S-4 (0.81 mg/g). The maximum tannin content was observed in K-17 (9.62 %) and the minimum was recorded in S-5 (5.23 %).

The higher phenol content of the pulp was recorded in K-23 (1.62 %) and the least was observed in S-4 (1.11%). The maximum antioxidant content was observed in K-23 (92.18 %) and the minimum was recorded in K-23 (83.20 %).

The results of genetic variability confess that the phenotypic coefficient of variation was higher than relative genotypic coefficient of variation for all the traits, However, the differences between GCV and PCV was narrow, indicating the relative resistance to environmental conditions. The higher estimates of GCV and PCV was observed for fruit weight, fruit volume, fruit length, fruit diameter, pulp weight, stone weight, pulp to stone ratio, yield per tree, TSS, acidity, vitamin C, TSS to acid ratio, tannins, fat and flavonoids.

The estimates of moderate GCV and PCV was observed for parameters plant height, stem girth and fibre content. Low values of GCV and PCV were observed for parameters like, number of seeds per stone, phenol and antioxidant content.

The higher values of heritability estimates were observed in parameters like, plant height, stem girth, fruit weight, fruit volume, fruit length, fruit diameter, pulp weight, stone weight, pulp to stone ratio, number of seeds per stone, yield per tree and also for biochemical parameters like TSS, acidity, vitamin C, TSS to acid ratio, total sugar, reducing sugar and non- reducing sugar, tannins, fat, fibre, flavonoid, phenols and antioxidant content.

High heritability coupled with high genetic advance as per cent of mean was observed for traits like plant height, stem girth fruit weight, fruit volume, fruit length, fruit diameter, pulp weight, stone weight, yield per tree, TSS, acidity, vitamin C, TSS to acid ratio, total sugar, reducing sugar, non- reducing sugar, tannins, fat, fibre, flavonoid content.

In the present study, the estimates of correlation coefficient revealed that association of yield per tree showed highly significant and positive correlation with fruit weight, fruit volume, fruit length, fruit diameter and pulp weight at both phenotypic and genotypic level. Whereas, biochemical parameters like TSS, acidity, vitamin C, total sugar, reducing sugar and non - reducing sugar showed highly significant and positive correlation with yield per tree at genotypic level only.

During this investigation, the path coefficient analysis revealed that the highest positive direct effects towards fruit yield per tree were contributed by fruit diameter, pulp weight, acidity, total sugar and non- reducing sugar. Whereas, negative direct effect towards yield per tree was contributed by fruit weight, fruit length, TSS, vitamin C and non- reducing sugar.

For diversity study 14 genotypes were grouped seven clusters using Tocher's method. Out of seven clusters, the cluster II was the largest comprising of five genotypes followed by cluster I having four genotypes and cluster III, IV, V, VI and VII were the least with one genotype each.

The intra-cluster distance revealed that cluster II with five genotypes showed maximum intra-cluster diversity depicting the presence of wide genetic divergence among the constituent genotypes. The higher degree of divergence among the genotypes within a cluster would produce more segregating breeding material. Selection within such a cluster might be executed based on the maximum mean value for the desirable characters.

Based on the distance between clusters *i.e.*, inter-cluster distances, the maximum divergence was observed between cluster VI and cluster IV indicating that the genotypes present in these clusters can be used as parents in hybridization programme.

Tannin content contributed the maximum to the genetic divergence among the characters studied followed by vitamin C, antioxidant, acidity, TSS, fibre, flavonoid, total sugar and TSS to acid ratio. Hence, these traits may be given high attention while selecting lines for hybridization programme to generate large variability.

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VII REFERENCES

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APPENDICES

VIII APPENDICES

Appendix -I: Weather data recorded at forest research station Govinakovi, Honnali (tq), Davanagere (dist)

Months	Rainfall (mm)	No. Rainy days	Temperature Maximum (°C)	Temperature Minimum (°C)	Relative Humidity (%)
January	0	0	31.8	16.3	67.3
February	0	0	32.7	16.6	59.1
March	13.4	1	35.0	19.4	56.5
April	49.4	4	35.7	21.1	58.3
May	88	6	34.7	21.9	63.9
June	116.6	11	29.8	20.9	80.9
July	154.4	17	28.5	20.5	83.5
August	265.8	16	27.4	20.1	85.9
September	191.6	14	29.1	20.2	88.0
October	148	8	29.8	19.3	85.2
November	0	0	30.7	17.4	77.7
December	16.2	1	30.2	15.7	75.9
Total/Mean	1043.4	78	31.8	16.3	73.5

Appendix -II: LIST OF SYMBOLS AND ABBREVIATIONS

Symbols	Abbreviations
%	Per cent
°C	Degree centigrade
°B	Degree brix
C.D	Critical difference
S. Em.	Standard error of mean
wt	Weight
cm	Centimeter
cm ²	Centimeter square
m	Meter
<i>et al.</i>	and others
<i>i.e.,</i>	That is
<i>viz.,</i>	Namely
cc	Cubic centimeter
mg	Milligram
ml	Milliliter
mm	Millimeter
g	Gram
kg	Kilogram
µg	microgram
g/l	Gram per litre
NaOH	Sodium hydroxide
H ₂ SO ₄	Sulphuric acid
GAE	Gallic acid equivalent
QE	Quercetin equivalent
HCA	Hydroxycitric acid
DPPH	2,2 –Diphenyl-1-picrylhydrazyl
Cv.	Cultivar