CHARACTERIZATION OF BRINJAL (*Solanum melongena* L.) AND ITS WILD RELATIVES

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(2018-11-114)

DEPARTMENT OF PLANT BREEDING AND GENETICS

COLLEGE OF AGRICULTURE

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CHARACTERIZATION OF BRINJAL (*Solanum melongena* L.) AND ITS WILD RELATIVES

By

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(2018-11-114)

THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"Characterization of brinjal (*Solanum melongena* L.) and its wild relatives"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Place: Padannakkad
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CERTIFICATE

Certified that this thesis entitled **"Characterization of brinjal (*Solanum melongena* L.) and its wild relatives"** is a record of research work done independently by Ms. Lintu P. (2018-11-114) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

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LINTU P

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Percent
ANOVA	Analysis of variance
c.m	Centimetre
CV	Coefficient of variation
CD	Critical difference
DAS	Days after sowing
DAT	Days after transplanting
et al.	Co-workers/ Co-authors
etc.	So on
Fig.	Figure
g	Gram
ha	Hector
i.e.	That is
IPGRI	International Plant Genetic Resources Institute
KAU	Kerala Agricultural University
KNO_3	Potassium nitrate
MT	Metric ton
NBPGR	National Bureau of Plant Genetic Resources
NHB	National Horticulture Board
No. of	Number of
POP	Package of practices
RARS	Regional Agricultural Research Station
S.	Solanum
SE	Standard error
Vit.	Vitamin
viz.	Namely
IC	Indigenous Collection
cm	Centimeter
mm	Millimeter
DUS	Distinctness, Uniformity and Stability
Nos.	Numbers

INTRODUCTION

1. INTRODUCTION

Brinjal also known as eggplant (*Solanum melongena* L., 2n=2x=24) is a popular and widely cultivated warm-season self-fertilized perennial plant, which is normally grown as annual vegetable crop in Central, Southern and Southeast Asia. It belongs to the Solanaceae-Nightshade family and the crop has large diversity for fruit color, shape, size and other morphological traits.

It is a good source of vitamins (mainly Vit. B) and minerals (Calcium, Phosphorous and Iron) in the tropical healthy diet. It is known for its medicinal property and good for diabetic patients (Shukla and Naik, 1993). The fruits are rich source of total sugar, phenols, glycoalkaloids and amide proteins (Bajaj *et al*., 1979). The phenolic acid content has greater influence on fruit culinary quality and antioxidant content (Stommel *et al*., 2015). In addition to minerals essential for the human diet, some of the wild relatives possess high level of bioactive compound like chlorogenic acid which promote good human health (Mennella *et al*., 2010; Meyer *et al*., 2015).

Based on conventional preference the brinjal cultivars are grouped as 'Occidental', preferred in North Africa, Europe, and America and as 'Oriental' brinjal, grown in East and Southeast Asia (Cericola *et al*., 2013). Even though brinjal is considered as a vegetable of Asian origin, most of its wild relatives are from Africa (Weese and Bohs, 2010). At present India is the second largest leading producer of brinjal after China at the global level. In India, it has a greater increase in production (12660 MT) and area (728 ha) in the last years (NHB; 2018-2019). In India large number of high yielding varieties, as well as varieties based on consumer preference such as Pusa purple long, Pusa purple cluster, Azad Kranti, Arka Keshav, Surya, etc., were released by various public and private institutions. This has led to the replacement of local landraces leading to narrowing of genetic base of brinjal (Tanksley and McCouch, 1997).

At present majority of high yielding brinjal varieties are facing the problem of a wide range of pests and diseases, among which shoot and fruit borer (*Leucinodes*

arbonalis) considered as a key pest causing drastic crop loss up to 85-90% (Prasad *et al*., 2017). In spite of huge morphological variability the sources of resistance in *S. melongena* gene pool is limited thus, restricting their potential for resistance breeding against biotic and abiotic stresses especially in the face of climate change. Conventional method of controlling the pest using insecticides is also not a feasible option.

The modern biotechnological approach using genetic modification (GM) is the viable solution currently available for this pest menace. In India Bt (*Bacillus thuringiensis*) brinjal has been developed by both public and private institutes as early as 2000, reached commercial application in 2008 and technology has been shared with other countries like Bangladesh and Philippines (Choudhary and Gaur, 2009). However, this technology could not be adopted in India due to the general moratorium and stiff resistance against the use of GM in food crops. As a policy to restrict GM in food crops there is a ban on introduction of Bt brinjal in Kerala.

In this scenario, wild species represent an alternative as well as acceptable source for resistance breeding. Wild species are reservoirs of valuable genes for hardiness and phytonutrients. So, it could represent a good source of variation for developing crop varieties with improved nutritional quality and climate resilience.

Modern hybrids of several essential crops bear introgressions from wild species arising from breeding projects carried out over the last 100 years (Hajjar and Hodgkin, 2007). One of the examples is tomato, where current commercial hybrids bear various combinations of 15 different introgressions from different wild species (Diez and Nuez, 2008; Sabatini *et al*., 2013). However, till date no variety has been developed in brinjal using traits from wild sources.

India is the place of vast genetic diversity of cultivated as well as wild brinjal. However, the wild gene pools are underrepresented in ex situ collections (Mutegi *et al*., 2015). Conservation of wild species becoming a matter of concern today as several species are known to be extinct in their natural environment not only due to the popularity of high yielding varieties but also other factors such as deforestation,

urbanization, mining, pollution and other climate change (Jarvis *et al*., 2008; Brummitt *et al*., 2015). Hence there is an urgent need to augment the presently available gene pool for broadening the genetic base of brinjal through exploration and collection not only for breeding purposes but also for conservation. Characterization is the next rudimentary step for the systematic utilization of wild relatives in breeding, as it will help identify traits and materials of potential breeding interest. South India, especially the Western Ghats which includes Kerala, is known to have wide variability for brinjal landraces and its wild types (Sebastian, 2000). Even though lots of studies have been conducted in taxonomy and phylogeny of brinjal, the information regarding growth, reproduction and agronomic traits of importance in wild resources are lacking. It is in this background, the present study was conducted to explore and assess the genetic variability in brinjal in different geographical areas of Kerala. It will form a basic document for crop improvement. The present study was conducted based on the following objectives:

- ✓ To characterize the brinjal genotypes and its wild relatives based on morphological characters and analyse the genetic variability in collected accessions
- ✓ To develop selection index for cultivated types

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Brinjal, eggplant or aubergine (*Solanum melongena* L.) belonging to Solanaceae family is a widely cultivated species in America, Europe and Asia. Other cultivated eggplants related to *S. melongena*, such as the Scarlet eggplant (*S. aethiopicum* L.) and the Gboma eggplant (*S. macrocarpon* L.) are cultivated mainly in Africa (Daunay *et al*., 2001).

2.1 Geographic origin and distribution

The origin of brinjal is not yet clear as scientists have various opinion on the same. The crop is believed to be originated in Indo-Burma region (Vavilov, 1926) but Sampson (1936) argued that the origin of brinjal was from African countries.

The literatures in 1106 AD have mentioned brinjal (Amarkosh, Nattingan, varttaka, etc) in it, which provides powerful evidence for its domestication in India years ago (Bhaduri, 1951). There are records to prove the existence of brinjal since the third century BC in India (Swarup, 1995).

Zeven and Zhukovsky (1975) reported that India was the origin of brinjal, later it was carried over to China during the fifth century BC. Accordingly, Nonnecke (1989) opinioned that brinjal has two origins. Later India and Indo-China are reported as the primary center of origin and China as secondary center of brinjal diversity (Vavilov, 1951; Lester and Hasan, 1991; Karihaloo and Gottlieb, 1995; Swarup, 1995).

According to Lester (1998) and Daunay *et al.* (2001), wild taxas like *S. aethiopicum* and *S. macrocarpon* were commercially domesticated in Africa.

Various data indicate that the origin of cultivated brinjal is from the several wild species that evolved in Africa. For example, *S. incanum* gave rise to a distinct species which spread to South-East Asia as the wild ancestor of *S. melongena* (Lester 1998). Lawanda and Chavan (1998) reported that the cultivated vegetable brinjal originated in India-China zone**.** Wees and Bohs (2010) reported that it is a vegetable of Asian origin whereas the wild types were from Africa.

Eggplant (*S. melongena* L.) is an Old World species that was domesticated in the region of Asia encompassed by China, India and Thailand. During the seventh century, the crop was brought from Southeast Asia and distributed to western and northern Africa, the Mediterranean basin and Europe by the Arabs during their incursions into these regions (Daunay *et al.,* 2001; Doganlar *et al.,* 2002).

The exploration and characterization of eggplant in India revealed that Western Ghats are the source of native and naturalized exotic species (Velayudhan *et al.,* 1996). Later, Chattopadhyay *et al.* (2011) reported Eastern Ghats, north-east zone**,** eastern and central India as the areas for eggplant variation.

Knapp *et al*. (2004) noticed wide and well-distribution of members in the solanaceae family due to their good adaptation to the various agro-ecological zones and reported a greater level of morphological variation among them.

Studies over hundreds of years revealed that the brinjal has large diversity for its fruit color, shape, size and other morphological traits. Accordingly, they are conventionally grouped as "Occidental" (North Africa, Europe and America) and "Oriental" (East and South-East Asia) eggplants (Cericola *et al*., 2013).

2.2 Taxonomy and classification

Eggplant (*Solanum melongena* L.) belongs to Solanaceae (nightshade) family. Almost all species under *Solanum* have a diploid set of chromosomes with 2n=24 (where, n=12) (Doganlar *et al*., 2002).

The nightshade family has more than 2300 species of flowering plants with 75 genera. Even though the term nightshade is mainly associated with a group of toxic species, it also has some economically important food crops like tomato (*Solanum lycopersicum*), potato (*Solanum tuberosum*) and brinjal (*Solanum melongena*) (Weese and Bohs, 2007).

Dunal (1852) and Seithe (1962) mentioned that this genus (*Solanum*) was classified into two major groups during the 19^{th} and 20^{th} centuries as spiny (with prickles) and spineless groups. Within these groups, the genus was subdivided into a

number of clades/sections (D'Arcy, 1972). Brinjal belongs to the *Leptostemonum* clade informally known as spiny solanum (Stern *et al*., 2011).

Choudhary (1976) reported three major botanical groups of *melongena* species *viz*., *Solanum melongena* var. *esculentum* (cultivated brinjal with egg-shaped or round fruits), *S. melongena* var. *serpentinum* (long and slender fruit) and *S. melongena* var. *depressum* (dwarf and bushy plant); cultivated for their edible fruit.

A large number of wild relatives have been discovered. There is considerable taxonomic ambiguity in the identity of wild progenitor of brinjal. It is difficult to decide the boundary between the cultivated *Solanum* and wild relatives (*S. insanum* and *S. incanum* (ancestor of *S. insanum*). The *S. melongena* and *S. incanum* have been more confused with distant relatives like *Solanum aethiopicum* L. (scarlet eggplant), *Solanum macrocarpon* L. (gboma eggplant) and with some other wild types. Later they acquired an informal taxonomic scheme for the same (Lester and Hasan, 1990; Lester and Hasan, 1991). Daunay *et al*. (1991) reported a wide range of morphological variations in brinjal at genera, species and cultivar levels.

Karihaloo and Gottlieb (1995) reported India has a wide range of wild species having very close similarity with cultivated brinjal which makes confusion in the taxonomic studies. With the help of enzymatic electrophoretic studies, they noticed a genetic similarity between wild species (*S. incanum* and *S. insanum)* and *S. melongena.* Later Sakata and Lester (1997) reported that not only *S. incanum* but also *S. macrocarpon* has a close similarity with *S. melongena*. Later on Lester (1998) reported *S. anguivi* and *S. dasyphyllum* are the ancestors of *S. aethiopicum* and *S. macrocarpon* respectively.

Daunay *et al*. (2001) reported that cultivated brinjal was evolved from *S. incanum*. The studies of Knapp (2013) and Mayer *et al.* (2015) support *S. insanum* as the wild progenitor of eggplant and *S. incanum* is considered as sister group of *S.insanum*.

The common eggplants include three closely related species and they were grouped into two sections, where *S. melongena* and *S. macrocarpon* come under the

section '*melongena*' and *S. aethiopicum* comes under section '*oliganthes*' (Levin *et al*., 2005; Levin *et al*., 2006).

The genus *Solanum* have three main clades; *S. thelopodium* (the sister of other *Solanum*), Clade I (have Regmandra, African non-spiny species and the Potato, Archaesolanum, Normania, Morelloid and Dulcamaroid clades) and Clade II (have Cyphomandra, Geminata, Brevantherum, and Leptostemonum clades). The clades I and II are subdivided at least into 10 subclades (like abnormal clades recognized by Bohs, 2005) (Weese and Bohs, 2007). Frary *et al.* (2007) and Knapp *et al*. (2013) reported that the genus can be subdivided into 13 clades. Taher *et al*. (2017) reported that these clades are distributed under New World, Old World and Australian clades. Around 450 species are recognized in subgenus Leptostemonum. Under this subgenus more than 300 species had their origin in Old World few in the New World and Australia. The brinjal/eggplant complex consisting of *S. melongena* and its wild ancestor *S. insanum* among the Old World clades are included under Eggplant clade. The scarlet eggplant complex consisting of *S. atheopicum* and *S. anguivi* and gboma eggplant complex consisting of *S. macrocarpon* and *S. dasyphyllum* are classified under Anguivi clade.

Cericola *et al.* (2013) identified three main morphological groups through principal component and hierarchical principal component analyses. They noticed all the three groups constitute both Occidental (39%, 45% and 16% respectively from group 1, 2, and 3) and Oriental (35%, 30% and 35% from group 1, 2 and 3 respectively) group of germplasm.

Many authors (Furini and Wunder, 2003; Han *et al*., 2003; *et al.* and Knapp, 2013) reported the monophyletic origin of species under Leptostemonum clade through genetic level studies using markers. Furini and Wunder (2003) studied the genetic relationship between the eggplant complexes using molecular markers.

2.2.1 Wild relatives of *Solanum melongena*

The eggplant complex includes *Solanum melongena* (cultivated brinjal), *Solanum insanum* and *Solanum incanum* (Pearce and Lester, 1979). In addition to

cultivated eggplant, two more Old World species come under the brinjal group, *Solanum aethiopicum* L. (scarlet eggplant) and *Solanum macrocarpum* L. (gboma eggplant), which is the most frequently used classification of brinjal and they are cultivated for their edible fruits (Weese and Bohs, 2010).

Based on the phylogenetic association and crossability with *S. melongena*, the wild types are categorized into members of primary, secondary and tertiary gene pools (Harlan and de Wet, 1971).

The primary gene pool consist of cultivated brinjal and its wild ancestor *S. insanum* (Ranil *et al*., 2017), which produce normal fertile progeny on crossing with *S. melongena* (Plazas *et al.,* 2016). The secondary gene pool has large number of wild relatives like *S. aethiopicum*, *S. anguivi*, *S. macrocarpon*, *S. dasyphyllum*, *S. linnahanum S. tomentosum* (Rotino *et al.,* 2014; Kouassi *et al*., 2016). The interspecific hybrids derived from this gene pool will be partially fertile or weak due to their reproductive barriers. The tertiary gene pool includes distantly related species like *S. torvum, S. elaeagnifolium* and *S. sisymbriifolium* which are used in breeding programs for their resistance features, but crossing needs specific breeding techniques to succeed (Plazas *et al*., 2016; Syfert *et al*., 2016). Some of the important species are reviewed here

a) Solanum incanum

It is also known as bitter apple, thorn apple, sodom apple or snake apple. It is a weedy species with spines on stem, calyx and stalk and acts as an indicator of less fertile soil. Fruits are green and mottled and are used against microtic skin infections in Kenya (Mwaura *et al*., 2011). It shows resistance against shoot and fruit borer (*Leucinodes orbonalis*) (Anushma *et al*. (2018), fusarium wilt (*Fusarium oxysporum*) (Yamkawa and Mochizuki, 1979), Phomopsis blight (*Phomopsis vexans*) (Rao, 1980) and verticillium wilt (Prohens *et al*., 2013).

b) Solanum aethiopicum

Solanum aethiopicum is an important vegetable grown for its fruit and leaf.

The fruits are round or oval in shape with smooth or grooved surface, which is consumed by cooking or raw. The fruit is sweet to bitter in taste (it varies with the saponin content). Due to the high carotene content, on ripening the fruit becomes orange or red in colour(Macha, 2005). It has four cultivated groups namely Gilo, Shum, Kumba and Aculeatum (Plazas *et al*., 2014). Aculeatum is grown for ornamental purpose, whereas the remaining three for vegetable purpose. *Solanum gilo* is a major leaf and fruit vegetable indigenous to tropical Africa (Sunseri *et al*., 2010). It is used in traditional medicines against skin infections, asthma, constipation, swollen joint pains, dyspepsia and gastro-esophageal reflux disease (Bello *et al*., 2005).

They can be used in resistance breeding against shoot and fruit borer (Anushma *et al*., 2018), Phomopsis blight (Ahmad, 1987), Fusarium wilt (Yamkava and Mochizuki, 1979), bacterial wilt (Sheela *et al*., 1984; Collonier *et al*., 2001)

c) Solanum macrocarpon

Solanum macrocarpon is a green leafy vegetable commonly grown for its glabrous and large (50cm x 30cm) green leaves. It has creamy white, greenish-white or light green coloured fruits with long and persistent clasping calyx. On physiological ripening, the fruit surface will crack and turn yellow, orange or brown colour. Compared to *S. aethiopicum*, macrocarpon fruits are sweet in taste (Macha, 2005) and it shows resistance to shoot and fruit borer (Gowda *et al*., 1990).

d) Solanum insanum

It is a wild progenitor of cultivated brinjal (Knapp *et al.,* 2013; Vorontsova *et al.,* 2013; Aubriot *et al.,* 2016). Even though it is consumed as a vegetable, its consumption is mainly associated with medicinal value. It causes miscarriage in pregnant ladies and useful against cold (Meyer *et al*., 2014).

It is used against liver problems (in China), in India it is used in the treatment of toothache, cough, skin problems, cholesterol (fruit), cholera (leaf), fever, vomiting,

poisonous infections and ulcer. Seeds are used as sedatives (in Philippines***)*** (Meyer *et al*., 2014; Sivarajan and Balachandran, 1994; Elias *et al*., 2010; Brown, 1920).

e) Solanum viarum

It is a weedy and woody shrub. It is a good source of solasodine, which is present at higher concentration in the gelatinous layer covering the seeds (Saini, 1966). It is used against the treatment of cancer and rheumatic arthritis (Chandra and Srivastava, 1984). It also shows resistance against shoot and fruit borer (Ghosh *et al.,* 2007), Epilachna beetle (*Epilachna viginctioctopunctata*) (Sambandam *et al*., 1976), phomopsis blight (Kalda *et al*., 1977) and little leaf (Datar and Ashtaputre, 1984).

f) Solanum indicum

It exhibits resistance against diseases namely little leaf, phomopsis blight (Kalda *et al*., 1977) and pest *viz*., shoot and fruit borer (Behera *et al*., 1999; Behera *et al*., 2002). It has good medicinal properties and is used for curing various human ailments (Patel *et al*., 2001; Bahgat *et al*., 2008).

g) Solanum torvum

Solanum torvum is a prickly shrub of 1 to 3 m tall with a strong and deep woody taproot and numerous woody laterals. It shows resistance to *Epilachna* (Sambandam *et al*., 1976), little leaf (Rao,1980), bacterial wilt *Verticillium dahliae* and *Verticillium alboratum* (Daunay *et al*., 1991). Hence use of *S. torvum* as rootstock for *S. melongena* will enhance drought and flood tolerance along with improved growth and fruit quality (Tsay and Lin, 2005).

h) Solanum mammosum

S. mammosum fruits contain bio constituents toxic to human but it is rich source of solasodine which is used in pharmaceutical production. Despite its toxicity to human, recent studies says that it is used as vegetable of eating quality (AVRDC, 2003) and in Philippines, both leaves and fruits are consumed as vegetable. *S. mammosum* is a weedy shrub with dense thorns on stem and midribs of leaves. It is

commonly known as nipple fruit or cow's udder. It is resistant to bacterial wilt (Singh *et al.* 2017).

2.3 REPRODUCTIVE BIOLOGY

Studies related to flower biology of a crop have great significance in crop improvement programs and seed production. Flowering and fruit set are the most important factors which determine yield of cultivated brinjal.

Flowering in brinjal is highly influenced by environmental factors like humidity and temperature and it varies with varying climate. Quagliotti (1979) noticed that it takes 55-110 days for flowering after sowing depending on the species. Pandit *et al.* (2010) observed thermosensitive nature of cultivated brinjal and reported that a cooler climate will enhance early flowering in brinjal. Dhaka and Soni (2012) noticed that a minimum of 69.60 days is required for flowering in brinjal after transplanting. But Das *et al.* (2017) reported the juvenile phase in brinjal ends within 40.83 – 58.17 days after transplanting.

Heterostyly is a common feature in eggplant, which determines the mode of reproduction, succeeding fruit set and development. Even though it is a self-pollinated crop, the natural cross-pollination in brinjal leads to genetic variability to some extent. Length of style in flowers is one of the varietal characteristics in brinjal (Passam and Bolmatis, 1997). Das *et al*. (2017) reported that the yield of cultivated brinjal plants depends on the pattern of flowering. Brinjal exhibits extra-axillary flowering and there are three flowering patterns in brinjal *viz*., solitary, cyme and mixed.

The fruit set, size of fruit and presence of seeds are highly dependent on the position of mature stigma and anther pore during anthesis. Maximum fruit set with maximum number of seeds is observed in flowers where mature stigma is in close proximity to the anther pores (Passam and Bolmatis, 1997).

Based on position of stigma with respect to position of anther, brinjal has four types of flowers *viz.*, long-styled (has big ovary), medium-styled (medium ovary), pseudo-short-styled (bears rudimentary ovary) and true short-styled (have very rudimentary ovary) flowers. Das *et al*. (2017) noticed three times bigger ovaries in long-styled flowers than short-styled flowers.

Chen (2001) reported the long and medium styled flowers will show maximum fruit set whereas pseudo-styled and short-styled flowers fail to produce flowers even though they are not completely sterile. Pandit *et al*. (2010) reported that if the ratio of long-styled and medium-styled flowers to pseudo and short-styled flowers is high, then higher will be the fruit set.

Oyelana and Ogunwenmo (2012), observed stigma receptivity will reduce slowly after anthesis. In eggplant, anthesis occurs in early morning (6.14 am - 7.15 am), while anther dehiscence at or just before anthesis (7.00 am - 9.20 am) (Das *et al.*, 2017).

Bourua (1988) reported heterostyly in *S. mammosum* with short, medium and long style ranging from 1 mm to 12-15 mm. He observed that anthesis completes just prior to anther dehiscence.

Puthiamadom (2016) reported variation in flowering behaviour of *S. melongena* and its wild accessions (*S. viarum. S. incanum* and *S. gilo*). She reported colour in stigmatic surface of *S. gilo* become glossy green to deep yellow at the time of receptivity, which is a unique feature of Gilo, where as in other wild variants in solanum was observed to be most plumpy and glossy green. She also reported protandry in Gilo.

In recent years the literatures regarding plant breeding and genetics have made emphasis on brinjal. Here some of the selected reviews are presented under the titles:

2.4 Exploration and collection of brinjal genotypes and its wild relatives

2.5 Evaluation of diversity and genetic variability

2.4 EXPLORATION AND COLLECTION OF BRINJAL AND ITS WILD RELATIVES

Plant genetic resources (PGR) serves as the base material for any crop improvement program. It includes modern *cultivars*, breeding stocks, *obsolete cultivars, landraces*, wild forms and wild *species* of cultivated crops. National Bureau of Plant Genetic Resources (NBPGR), the nodal institute for genetic resource management holds more than 2500 accessions of brinjal (Kumar et al., 2008).

Exploration and collection serve as the source for collecting and conserving variability in the crop and its relatives. The cultivated brinjal has narrow genetic base. Collection of wild relatives helps in broadening the genetic base and crop improvement.

Velayudhan *et al*. (1996) analyzed morphological variability in plant and fruit characters of brinjal and the study revealed that the Western Ghats are the source of a large number of aboriginal and exotic species. In this study, several rare landraces of *Solanum melongena* and its wild relatives were collected by five survey trips conducted to the peninsular region. This includes 216 genotypes of *Solanum melongena*, one of *Solanum macrocarpon* and the remaining accessions belong to its 25 wild relatives.

Exploration and collection of landraces and wild relatives of brinjal were carried by Sebastian (2000), A total of 50 accessions of genus *Solanum* were collected which includes 47 local cultivars of brinjal belonging to *Solanum melongena* and 3 wild types which include *Solanum insanum*, *Solanum macrocarpon* and *Solanum xanthocarpum*. She reported wide variability for morphology, yield, yield attributes and reactions to various biotic stresses *viz*, fruit and shoot borer (*Leucinodes orbonalis*), bacterial wilt (*Ralstonia solanacearum*), phomopsis blight (*Phomopsis vexans*) and little leaf (mycoplasma).

Kumar *et al*. (2008) collected 622 accessions of brinjal from different agroecological regions of India of which 543 lines were collected from different farm

fields and 79 were of foreign origin. They recorded a wide range of variation for 31 descriptors.

Saito *et al*. (2014) collected 131 lines from 44 villages of 12 districts in northern Laos during the exploration of vegetable genetic resources. These accessions consisted 112 of *Solanum melongena*, five of *Solanum aethiopicum* L., three of *Solanum gilo*, three of *Solanum macrocarpon* L., two of *Solanum sanitwongsei*, one of *Solanum viarum* and five unknown *Solanum spp.*

Thirty five accessions of brinjal which representing the sample of different districts of Bangladesh were collected by Solaimana *et al.* (2015) from Horticulture Research Centre (HRC), Gazipur. Based on characterization studies, he concluded that lines SM-111, SM-84, EGN-27, SM-183, BARI begun-6 can be used as parents in hybridization programs.

2.5 EVALUATION OF DIVERSITY AND GENETIC VARIABILITY

Morphological characterization helps to identify duplicates in the collection and to develop a core collection for conservation as well as for varietal improvement.

Being the primary center of origin for brinjal, Indian flora provides a wide range of variable brinjal genotypes for its genetic progress (Ganabus, 1964). The morphological characterization help to distinguish between the accessions resembling each other.

2.5.1 Morphological characterization of brinjal genotype based on qualitative traits

Morphological characterization is important in order to provide details on the characteristics of genotypes assuring the maximum utilization of the germplasm to the final users.

Recording and compiling data on the essential characteristics that differentiate accessions within a species makes more easy and rapid discrimination between phenotypes. It allows for a clear grouping of accessions, the creation of core

collection, enable the identification of duplicates, detection of gaps and the retrieval of useful germplasm for breeding resulting in a clear understanding of the composition of collection and its genetic diversity.

Eggplant collections have been evaluated mostly for morphological and agronomic characters such as plant, flowering and fruiting characters (Karihaloo and Gottlieb, 1995), which display a wide diversity in plant morphology, physiology and biochemical properties (Daunay *et al*., 1991; Collonier *et al*, 2001).

Krishnamoorthy and Subramonian (1953) allocated brinjal flowers into four types *viz*., long, medium, pseudo short and short-styled flowers. They observed that under natural climatic condition, 27% of flowers will develop into fruit and 93% of fruit set is observed in long-styled flowers.

Based on shape of the fruit 325 brinjal genotypes were grouped into four *viz*., round (103), oval (20), oblong (97) and long (105) and further grouped into four *viz*., purple (245), green (54), white (6) and variegated (20) based on fruit colour (Singh *et al*., 1999). Kumar *et al*. (2008) reported that fruit colour, shape and size are the most distinct characters that vary between the cultivated brinjal and their wild types.

Naujeer (2009) studied 34 brinjal accessions including 27 *S. melongena*, two *S. macrocarpon*, one *S. nigrum*, one *S. torvum* and three *S. violaceum*. She reported shiny to very shiny fruit in cultivated *S. melongena* accessions with pendant fruit position and uniform colouration, whereas the *S. macrocarpon* had smaller round to spherical, erect fruits of pale green colour with dark green strips, *S. violaceum* had small oval to round fruits of dull pale green colour in a semi-pendent fruit position and *S. torvum* and *S. nigrum* had dark green fruits with uniform colour distribution.

Chattopadhyay *et al.* (2011) characterized 32 different eggplant accessions collected from different locations of Eastern India and observed the predominance of the mixed pattern of flowering (45.71%) over cluster type (42.86%).

Lagat (2016) examined seventy two African brinjal accessions, including four varieties of *Solanum aethiopicum* (54), *Solanum macrocarpon* (1), *Solanum sp* (15)

and *Solanum anguivi* (6). He registered accessions without prickles (68.1%) and with prickles (31.9%) including some *S. atheopicum* accessions with prickles as well as without prickles. He also reported that 87.5% of the total accessions had upright growth habit, 9.7% with intermediate and 2.8% with prostrate growth habit in both field and greenhouse conditions.

Dash *et al*. (2019) evaluated 110 genotypes of brinjal for 20 qualitative characters and noticed the accessions were showed variation in traits *viz*., plant branching, stem pigmentation, colour of leaf blade, lobing in leaf blade, tip angle of leaf, leaf hair, type of flowering (cyme, mixed and solitary) and corolla colour.

2.5.2 Mean performance of brinjal genotypes based on quantitative traits

Babu and Patil, (2008) evaluated 90 brinjal genotypes for 12 quantitative characters. Among them, four accessions showed higher yield potential namely DBC - 14-KA (3020g), DBC-75-KA (3280g), DBC-38-HA (3615g) and DBC-13-BA (3032g).

Chattopadhyay *et al.* (2011) characterized 32 different accessions for its 12 quantitative traits. All of them showed superior and significant variation especially in characters like days to 50% flowering, fruits per plant, weight, diameter and length of fruit and yield per plant. The length of marketable fruit showed a variation range of 8.70 cm to 23.9 cm. The lines Punjab Sadabahar showed early 50% flowering (47 days), whereas maximum time period of 79 days was observed in cultivar Deshi Makra. Accession BB-85 has produced more marketable fruits per plant (12).

The wild relatives generally takes more number of days for 50% flowering. Nyadanu *et al*. (2014) reported 87-100 days in *S. macrocarpon* landraces of Ghana. Lagatt (2016) and Sanga (2017) reported 61-78 days in *S. gilo.*

Kaushik *et al*. (2016) evaluated six *S. melongena* accessions, 21 accessions of 12 wild types and 45 interspecific hybrids of brinjal with wild types. They reported that the wild types were more variable than cultivated types and interspecific hybrids have intermediate ranges of variation and coefficient of variation. The wild

accessions and hybrids had larger plant size, greater leaf prickliness, maximum flowers per inflorescence, and small fruits than the cultivated species. The *S. melongena* accessions and hybrids had had more anthocyanin pigmentation than the wild species.

Sanga *et al*. (2017) collected 15 *Solanum gilo* accessions from different agro-climatic regions of India and recorded the variability in the accessions. Accession CHFG-12 (63.18) showed maximum height whereas CHFG-5 (45.91) showed minimum height. Genotype CHFG-2 and CHFG-11 took minimum days for first fruit set (69.84 and 71.66 respectively). CHFG-2 showed early harvest. A maximum fruit diameter of 4.53 cm and maximum fruit length of 2.97 cm was observed in the study.

Islam *et al*. (2018) observed desirable and drastic variation for 12 quantitative characters in 40 brinjal accessions. The lowest coefficient of variation was showed by days to initial edible fruit development (5.48 %), whereas height of plant, plant spread and number of primary branches showed highest values of coefficient of variation.

Dash *et al*., (2019) reported wide range of variability with plant height ranging from 29.8 cm to 105.56 cm.

2.5.3 Components of genetic variability for quantitative traits of brinjal (GCV, PCV, heritability and genetic advance)

The relative value of components of variance such genetic variability, heritability and genetic gain are important measures for making effective selection in crop improvement. The magnitude of variability is estimated with GCV and PCV, which gives an idea about the magnitude of variation present in a population. The heritability indicates the extent of variability transmitted to a progeny. The estimation of genetic advance along with heritability helps in understanding the type of gene action involved in the expression of various polygenic characters. Information about gene action helps in deciding breeding procedures for the improvement of the trait.

Kushwah and Badhyopadhya (2005) reported high GA for number of flowers per inflorescence and the characters days to 50% flowering, flowers per

inflorescence, days to initial harvest, number of fruit per picking, length, number of fruits per plant and yield recorded higher value of heritability. Chattopadhyay *et al*. (2011) reported the prevalence of additive gene expression for the character number of days to 50% flowering, which had highest heritability and GA.

Thangavel *et al*. (2011) recorded highest phenotypic and genotypic coefficient of variance along with high heritability coupled with high genetic advance for the attributes such as days to initial flowering and branches per plant characterizing the prevalent additive effect of genes during inheritance of these traits.

Kumar *et al*. (2013) reported high GCV and PCV for the traits such as fruit length, calyx length, number of fruits per plant and fruit yield per plant, which also recorded high heritability coupled with genetic advance.

Yadav *et al*. (2016) evaluated 40 genotypes and observed a significant difference between all the studied 13 quantitative traits indicating the existence of variability in all the traits. In this study, they observed a higher PCV compared to GCV for all traits.

Tasing (2019) observed high GCV, PCV, heritability and genetic advance for traits like number of fruits per cluster, weight of fruit, height of the plant, length and girth of fruit, level of reducing sugar, yield per plant, level of non-reducing sugar, number of main branches and total sugar.

2.5.4 Association analysis

Quantitative traits often display complex mutual relationships having huge implications in evolutionary processes and plant improvement. These relationships are the result of genetic correlations, which can be caused by pleiotropy or linkage disequilibrium (Lynch and Walsh 1998). The correlation analysis quantify the degree to which two variables are associated. This helps to identify how much the variation in a character will cause changes in other character.

In some cases, correlation coefficients are not enough to explain true relationship between two characters. It can be explained through path analysis in

which the correlation coefficients are split into direct and indirect effect and it explains the actual contribution of each traits and its impact through other characters. The correlation present between two characters may be due to their correlation with a common trait. In such cases path analysis explains the real cause and effect of association.

Mak and Vijayarungam (1980) observed the positive correlation of fruit yield per plant with number of main branches and number of seeds in fruit while studying the interrelationship between certain characters in 27 brinjal varieties.

Gautam and Srinivas (1992) noticed higher coheritability of plant canopy size and fruits per plant along with yield.

Sharma and Swaroop (2000) in their evaluation of 27 genotypes found superior correlation of yield with fruit per plant, weight and width of fruit, while an opposite correlation was observed in case of 50% flowering. The path analysis discloses fruits on a plant had highest direct effect at genotypic level. Therefore for modifying yield direct selection of these characters can be made, while fruits on a plant, diameter and weight of fruit show high direct effect at phenotypic level. Some characters show indirect effect on yield such as number of branches, height of plant and fruit length via number of fruits on the plant, hence selection of these traits will contribute for improvement of yield.

Yield of brinjal has a positive correlation with number of fruits per plant, diameter of fruit and number of harvest at phenotypic as well as at the genotypic level. Days to first harvest show an opposite association with yield at genotypic level (Kushwah and Bandhyopandhya, 2005).

Bansal and Mehta (2008) used 26 genotypes of brinjal for path and correlation analysis and showed a positive association of yield with plant canopy spread, tallness of plant, number of leaves, fruits and branches per plant at genotypic level. The direct effect of per plant fruit to yield followed by weight of fruit, days to 50% flower set, leaves per plant and fruit set percentage is analyzed through path analysis.

Twenty three green fruited brinjal accessions were used to study correlation and path analysis. From the study close relationship of yield with fruit index, fruits per bunch, fruit weight and per plant fruits. Fruits per plant, fruit weight, fruit index, days to initial picking, number of main branches and size of plant canopy exhibit direct effect on yield (Lohakare *et al*., 2008).

Jadhao *et al*. (2009) observed the characters like height of plant, number of main branches, days to final harvest, fruit weight and per plant fruits show significant and superior correlation with yield. Path analysis shows a direct effect on yield with tallness of plant, main branches per plant, days to initial flowering and harvest, length and weight of fruit.

Height of plant showed association with number of branches, fruit length, width and weight. Number of fruits on a plant and fruit weight showed direct effect on yield. Number of branches and diameter of fruit showed indirect effect on yield via fruit weight (Muniappan *et al*., 2010).

Thangamani and Jansirani (2012) conducted a study with 25 hybrids and observed yield per plant have positive association with branches per plant, percentage of long-styled flower, fruit width, ascorbic acid content and number of fruits on plant, whereas days to initial flowering will not show any correlation with yield. The path analysis revealed direct association of fruits per plant with yield and the indirect association of same along branches per plant and weight of fruit. So in order to improve the yield, emphasis should be done to the selection of traits showing positive and direct effect on yield.

Tasing (2019) reported positive and notable correlation of fruit yield per plant with fruit girth, length and weight of fruit, but it showed negative correlation with days to 50% flowering, days to initial harvest and per plant fruits. The traits like number of main branches, length of fruit, phenols concentration, days to 50% flower set, solasodine concentration, per plant fruits, reducing sugar and width and weight of fruit showed a direct effect towards yield, whereas negative effect was observed in case of the traits like height of the plant and days to initial harvest at genotypic level.

2.5.5 Genetic diversity analysis (D^2 analysis and cluster analysis)

Genetic diversity is the very basis of existence of plants in nature and for crop improvement. Information concerning the extent and nature of genetic diversity within a crop species is essential for an effective breeding program. It is particularly useful for characterizing individual accession and cultivar and as a general guide in the selection of the parents for hybridization (Furini and Wunder, 2004).

Genetic diversity can be assessed among strains/varieties/entries of a species using multivariate techniques. These techniques can be used in assessment of genetic divergence, classification of germplasm into different groups and selection of diverse parents to develop transgressive segregants or hybrids for exploiting heterosis.

Quamruzzaman *et al*. (2009) estimated the genetic divergence in 19 accessions of eggplant using Mahalanobis's D^2 statistics. They obtained five clusters, the first cluster comprised more (seven) genotypes, whereas the lowest number (two) in cluster IV and V each. The cluster V showed greater intra-cluster distance and cluster III showed the least value (1.067 and 0.916 respectively). The clusters IV and V had the maximum value of inter-cluster distance (10.748). The plant height, leaf length, and width, leaf pedicel length, calyx prickles showed maximum mean value and these characters appeared in the fifth cluster whereas, cluster II had maximum mean for the characters such as number of main branches per plant, width of fruit, single fruit weight, yield per hectare and fruit pedicel prickles.

Nandan and Mayuri (2009) analyzed genetic divergence in 14 accessions with help of Mahalanobis D^2 statistics. These accessions were grouped into five clusters ignoring the diversity in geographical locations, stipulating non-parallelism of both genetic and geographical diversity. The cluster I and II showed more inter-cluster distance followed by cluster III and IV, which emphasize the wider variation and diversity among these clusters.

Polignano *et al*. (2010) evaluated brinjal and its allied species (*S. gilo* and *S. macrocarpon*) for 16 morpho-agronomic and fruit attributes and noticed existence of diversity among the 98 genotypes. The total divergence majorly depended on height

of plant, time of flowering, number of flowers on inflorescence, fruit length and acidity. Each species were subjected to cluster analysis based on genetic status and grouped them into three clusters. The genetic status (sub-species, varietal or botanical group, cultivar and population) and genetic divergence did not show any relationship.

Das *et al*. (2010) analyzed 40 brinjal genotypes for their varying morpho-physiological attributes and genetic diversity by D^2 statistics. Nine traits were used for the study and all of them showed wide variation in the 40 accessions. The D^2 value showed a range of 8.13 to 8015.95 which depicts the highest variability within the accessions. On clustering the 40 genotypes were grouped into ten different clusters with maximum number of genotypes in cluster I. The cluster X had a maximum intra-cluster distance. The three characters *viz.*, yield per plant, fruits per plant and weight of fruit contributed more to the divergence. Such diverse parents can be picked out for hybridization in order to exploit heterosis at the maximum level and for efficient selection from the segregating progeny.

Islam *et al*. (2011) estimated the genetic divergence of 11 accessions of eggplant. The clustering resulted in four groups *viz*., cluster I, II, III and IV with four, three, two and two accessions respectively in each group. Cluster II showed maximum intra-cluster distance and cluster IV have the minimum value. Cluster I and III exhibited greatest inter-cluster distance of 2.203. The features like fruit weight, diameter and length, flower stock length, plant height and per plant yield have maximum contribution towards the overall divergence. The traits like flowers per bunch, plant canopy size (north-south), leaf blade and petiole length, fruits and branches per plant recorded maximum mean values in cluster III. Cluster IV recorded greatest mean values for the features like initial flowering nodes, plant canopy size (east-west), flower stock length, width of leaf petiole, length of fruit, height of plant and per plant yield whereas the cluster I had greatest mean values for features like width of flower stock, width of leaf, number of main branches, weight and width of fruit.

Tasing (2019) conducted divergence analysis and concluded that the fruit yield showed maximum range of divergence followed by number of fruits per cluster,

height of plant and presence of flavonoids. From clustering cluster III and V showed high inter-cluster distance, hence those genotypes in these clusters showed maximum divergence.

Sulaiman *et al*. (2020) grouped 29 accessions into six clusters based on agro-morphological traits using UPGMA method. He reported the cross between cluster I with cluster VI and cluster V can be used to attain higher heterosis among accessions

2.6 SELECTION INDEX

Genetic diversity and selection procedure decides the progress in any breeding program. Smith (1936) first proposed the use of discriminant function in plants. He suggested the construction of an index called selection index for simultaneous selection of multiple traits. It is a linear combination of characters associated with yield. It involves discriminant function based on relative economic importance of various characters. Selection index assists to sort out or select plants for the improvement of a crop based on different characters having economic importance.

Vadivel and Bapu (1991) analyzed index score in exotic germplasm lines. A positive and maximum score of selection index was exhibited by lines Murena, Solara, Nagpur type and Annamalai, which are a good source for hybridization. A local accession from Maharashtra showed greatest score value for secondary branches and per plant fruit, whereas a USA line Black Beauty showed superiority for length, girth and weight of fruit. These types of accessions will act as the base source for hybridization and will produce greater variability which can be subjected to selection and improvement.

Sebastian (2000) constructed selection index in brinjal landraces using discriminant function technique. The characters plant height, days to flowering, fruit length, fruit breadth, branches per plant, fruit weight, fruits per plant, stem girth and harvest index along with yield per plant were used for constructing selection index. Based on the index score ten accessions namely S33, S22, S23, S47, S25, S55, S15, S42, S32 and S52 were identified as superior.

Hasan *et al*. (2016) constructed selection index in chilli using yield per plant and four yield component characters having positive correlation and positive direct effect on yield at genotypic level. They concluded that selection index with three characters (I_{345}) showed more genetic gain (2.46) and relative efficiency (215.51%), hence the selection of high-yielding chilli based on these three traits will be more effective.

Setyawan *et al.* (2016) reported selection index with four characters (pod diameter, fresh pod weight, number of cocoa beans per pod, and dry weight per cocoa bean) in cocoa is more efficient. Plants developed from the seeds having maximum index score were selected for further studies.

2.7 BRINJAL PEST AND DISEASES

2.7.1 Pests

The narrow genetic base of cultivated brinjal makes it prone to a number of pests and diseases, leading to a dramatic reduction in crop yield. It is therefore necessary to isolate and conserve genotypes that are highly resistant to these stresses.

Brinjal shoot and fruit borer (*Leucinodes orbonalis)* is the major pest in brinjal. Its first occurrence on brinjal plant was reported by Hampson (1896) in India. Kumar and Ram (1998) reported that fruit width, weight and volume have negative correlation with borer infestation and it is considered as indirect selection criteria for advancing its resistance.

Tejarathu *et al*. (1991) reported that the brinjal wild relative *S. gilo* showed resistance to this pest and this genotype is cross compatible with *S. melongena* hence the character can be incorporated into cultivating species of eggplant.

Grewal and Singh, (1992) noticed an association of borer infestation with thickness of shoot, area of leaf and juvenile period of crop. Number of seeds per fruit, yield per plant and thickness of fruit skin have significant negative correlation with borer infestation (Patil and Ajri, 1993). Pradhan (1994) reported the rate of infestation is less in varieties with long fruits than that with round fruits.

Gupta and Kauntey (2008) reported that dark purple and white fruited varieties are more susceptible to *Leucinodes orbonalis* than those with light purple or green coloured fruit. Higher the quantity of lignin, least will be the incidence of fruit and shoot borer, (Khorsheduzzaman *et al*., 2010).

Prasad *et al*., 2017 reported that shoot and fruit borer (*Leucinodes arbonalis*) cause drastic crop loss up to 85-90%, hence it is considered as a key pest of brinjal

2.7.2 Diseases

Bacterial wilt by *Ralstonia solanacearum* is one of the major disease in brinjal. Its presence in solanaceous crops was first reported by Smith (1896). Plants show symptoms such as stunted growth, wilting, yellowing and finally total collapse.

Sadashiva *et al*. (1993) noticed the resistance for bacterial wilt in cultivars IHR 180 and IHR 181 which survived without infection even after 125 days of transplanting. Sharma *et al.* (2005) screened the parental lines and first-generation progenies against bacterial wilt. The parental lines CH 249 and CH 309 showed resistance to this disease and the offsprings showed moderate resistance to this pathogen. Sharma and Kumar (2007) reported Swarna Shyamli, Swarna Pratibha, BB 64, JC 8, Arka Keshav and Arka Nidhi as the resistant genotypes of brinjal.

Siddique *et al*. (2000) reported the little leaf in brinjal is caused due to infection of phytoplasma with symptoms of little leaf, proliferation of axillary bud, phyllody, stunted and bushy growth. Kumar *et al.* (2012) reported first incidence of *Candidatus Phytoplasma asteris* on brinjal in India. The RFLP analysis results showed that in Bihar, BLL (brinjal little leaf) was closely related to group 16SrI and they are responsible for the disease.

Karmakar and Singh, (2017) screened interspecific hybrids and their parents (Pant Rituraj, Pant Samrat, *S. aethiopicum*, *Solanum gilo*, and *S. khasianum*) against phomopsis blight. He reported highest resistance in wild species like *S. gilo* and *S. khasianum*. The F_1 progenies from the cross *S. gilo* × *S. melongena*, *S. aethiopicum* × *S. gilo*, Pant Rituraj × *S. gilo*, *S. aethiopicum* × Pant Samrat and *S. gilo* × Pant Samrat

showed more resistance among the crosses. The gene from resistant wild species (*S. gilo)* can be incorporated into cultivated species through systemic backcross. But Kumar *et al*. (2020) reported less incidence of *Phomopsis vexans* in *Solanum gilo, Solanum aethiopicum* and cultivar Pant Samrat with disease index value of 0.00

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The detailed description of materials used and the methodology followed in the present study entitled "Characterization of brinjal (*Solanum melongena* L.) and its wild relatives" are outlined in this chapter. The study was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Padannakkad (2018-2020).

3.1 Experiment-1: Exploration and collection of brinjal genotypes

3.1.1 MATERIALS

Forty two accessions of brinjal including both cultivated and wild relatives collected from different localities of North Kerala as well as those indented from Regional station NBPGR, Thrissur.

3.1.2 METHODOLOGY

A detailed survey was directed in various brinjal growing belts of North Kerala in the five districts *viz*., Kasaragod, Kannur, Malappuram, Kozhikode and Wayanad for collecting the available brinjal landraces and its wild relatives. The information and contact details of various vegetable growing farmers were gathered from Krishi Bhavans of different panchayaths in these districts for effective collection of genotypes. The seeds and seedlings of 30 locally cultivated brinjal genotypes including two wild relatives were collected by visiting farmer's field. Twelve accessions comprising six *S. melongena* and six close wild relatives were obtained from the regional station of NBPGR, Thrissur. All the 42 genotypes were raised in protrays and observed for germination as well as proper establishment. Dormancy and delayed germination were observed in some genotypes especially the wild relatives. The seeds of wild types were soaked in one per cent KNO_3 solution for one hour and washed thoroughly in distilled water three to four times for breaking dormancy and enhancing germinability (Plate 1). Those accessions which were showing very low germination were eliminated from the study. A total of 30 genotypes comprising 25 local cultivars and 5 wild relatives were finally retained for field evaluation. The

seedlings of these accessions were maintained in protrays for one month for proper root and shoot development. The passport data (Table 1) consisting details of the collection such as date, source, location *etc*. was prepared.

3.2 Experiment-2: Evaluation of collected accessions of brinjal and its wild relatives for diversity and genetic variability in qualitative and quantitative traits

3.2.1 MATERIALS

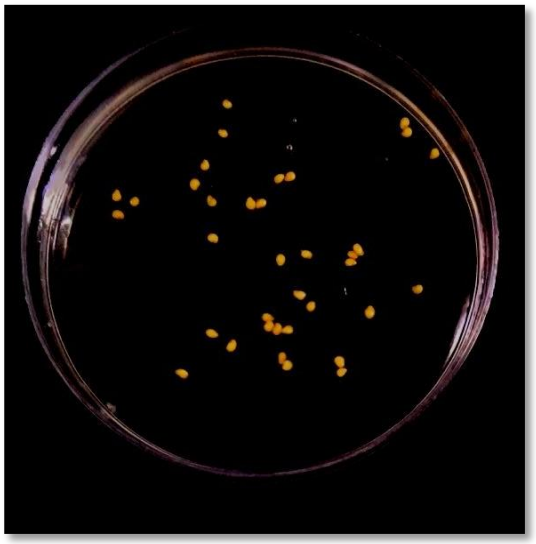
One-month-old seedlings of selected thirty accessions were carried forward for field evaluation from October to May (2019-2020).

3.2.2 METHODOLOGY

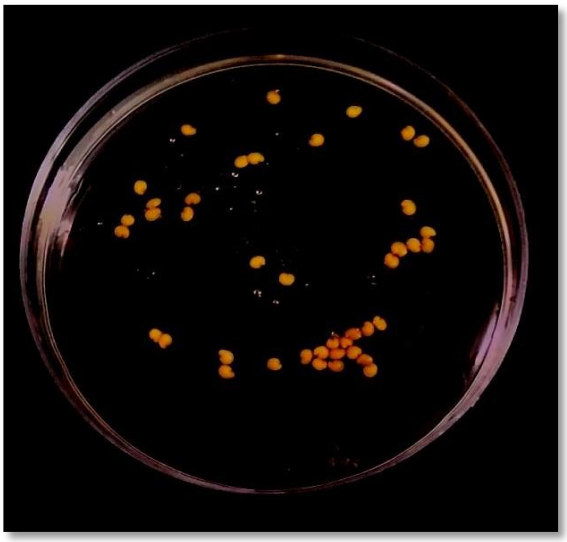
The experiment was laid out in Randomised Block Design with thirty treatments and three replications (Plate 2 and 3). One month old seedlings were transplanted to the main field at a spacing of 75cm x 60cm after one week of lime application followed by one week of FYM application. The fertilizer application and all other intercultural practices were carried out as per Kerala Agricultural University Package of Practices (POP, 2016). Plant protection measures were taken up as and when incidences of pests and diseases were noticed. Fruit and shoot borer incidence was observed 90 DAT and imidacloprid was applied to control the same. Chlorantraniliplore (coragen) was sprayed against jassids. Plants showing bacterial wilt symptoms were immediately removed and soil drenching with a solution containing a mixture of bleaching powder and benzimidazole (bavistin) was carried out in these plots. Observations on 17 qualitative and 22 quantitative attributes were recorded. The observations made in the field are listed below;

3.3 Observations

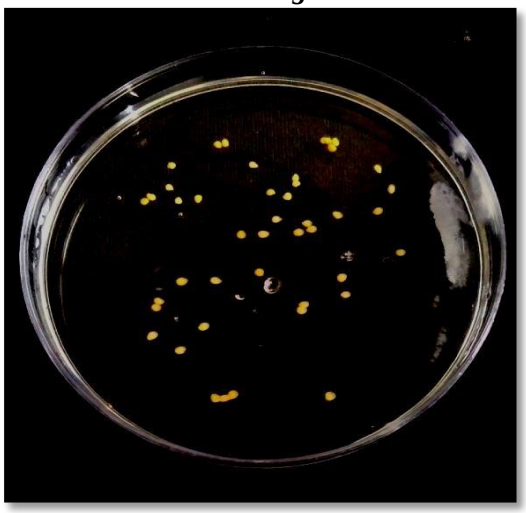
Five plants were randomly selected and tagged from each plot per accession for recording observations on 17 qualitative and 22 quantitative characters based on IPGRI (1990) descriptors and DUS (2009) .



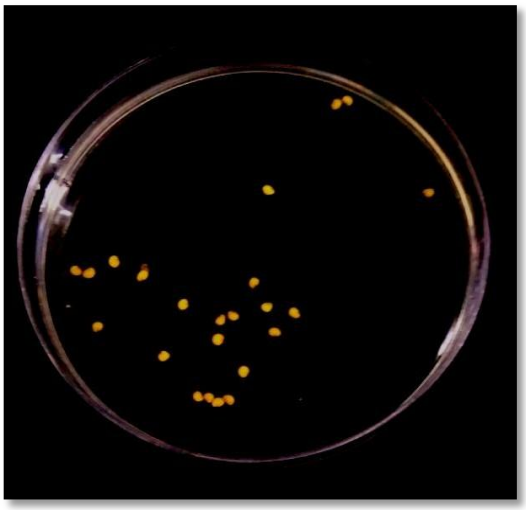
Solanum gilo



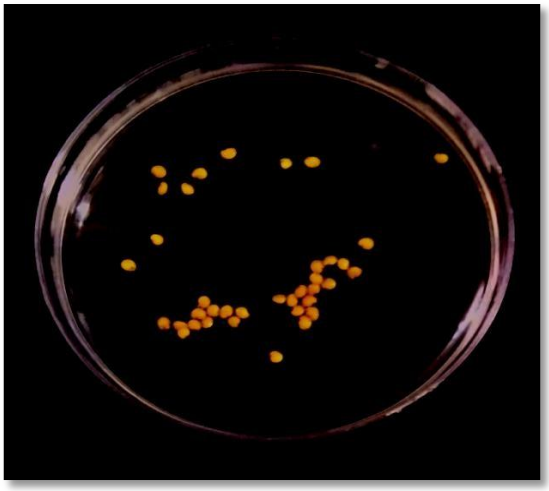
Solanum viarum



Solanum xanthocarpum



Solanum incanum



Solanum insanum

Plate 1. Wild brinjal seeds treated with $KNO_3$1% (1 hour) for breaking dormancy

Plate 2. Field preparation

Plate 3. Field overview of thirty brinjal accessions

Table 2. Passport data of 30 accessions of brinjal

Sl. No.	Collection number	Genus	Date of collection	Collection source	Village	District	Latitude (E)	Longitude (N)	Altitude (m) (AMSL)	Main characteristics
1	SM-1	*S. melongena*	28-5-2019	Farm field	Valanchery	Malappuram	76.0732	10.8878	47	Long slender green coloured fruit
2	SM-2	*S. macrocarpon*	1-6-2019	Farm field	Thillenkery	Kannur	75.6659	11.9274	12	Tomato like light green fruit. It has long(>75%) persistent calyx which looks like a leaf
3	SM-3	*S. melongena*	3-6-2019	Farm field	Kuttikunnu	Malappuram	76.2386	11.2855	400	Green coloured fruit
4	SM-4	*S. melongena*	3-7-2019	Farm field	Muthuvallur	Malappuram	75.965	11.1799	13	Purple coloured fruit
5	SM-5	*S. melongena*	5-7-2019	Farm field	Morayur	Malappuram	76.0189	11.1341	47	Milky white coloured fruit
6	SM-6	*S. melongena*	6-7-2019	Farm field	Karandoor	Kozhikode	75.8771	11.3049	15	Round light purple coloured fruit
7	SM-7	*S. melongena*	8-7-2019	Farm field	Perumanna	Kozhikode	75.8849	11.245	15	White coloured fruit
8	SM-8	*S. melongena*	8-7-2019	Farm field	Akode	Malappuram	75.8999	11.2173	13	Oval shaped purple coloured fruit
9	SM-9	*S. melongena*	8-7-2019	Farm field	Thrikkalayoor	Kozhikode	76.0218	11.2448	12	Blackish purple coloured round fruits
10	SM-10	*S. melongena*	9-7-2019	Farm field	Kandoth	Kannur	75.2179	12.1175	15	Long purple fruit

11	SM-11	*S. melongena*	9-7-2019	Farm field	Cherukunnu	Kannur	75.3004	12.0041	9	Long purple fruit
12	SM-12	*S. melongena*	9-7-2019	Farm field	Cherukunnu	Kannur	75.3004	12.0041	9	Green coloured fruits
13	SM-13	*S. melongena*	14-7-2019	Farm field	Vettilappara	Malappuram	76.0798	112,448	51	Light green coloured fruit
14	SM-14	*S. melongena*	25-7-2019	Farm field	Thondernadu	Wayanad	75.9376	11.7341	18	Purple coloured fruit
15	SM-15	*S. melongena*	8-8-2019	Farm field	Cheruvadi	Kozhikode	76.008	11.2711	15	Purple coloured oblong fruit
16	SM-16	*S. melongena*	8-8-2019	Krishibhavan	Edavannappara	Malappuram	75.9775	11.2448	13	Milky white coloured fruit
17	SM-17	*S. melongena*	10-9-2019	Farm field	Kizhisseri	Malappuram	76.0073	11.1833	51	Green coloured fruits
18	SM-18	*S. melongena*	10-9-2019	Krishibhavan	Vettukad	Malappuram	75.965	11.1799	13	Purple coloured fruit
19	SM-19	*S. melongena*	12-9-2019	Farm field	Cheekode	Malappuram	75.987	11.2293	51	Green coloured round fruit
20	SM-20	*S. melongena*	15-9-2019	Farm field	Thottumukkam	Kozhikode	75.9963	11.3212	15	Purple coloured fruit
21	SM-21	*S. melongena*	16-9-2019	Krishibhavan	Kondotty	Malappuram	75.9935	11.1337	13	Purple coloured fruit
22	SM-22	*S. mammosam*	24-9-2019	Farm	Padannakad	Kasaragod	75.11	12.2759	12	Yellow fruited ornamental plant with spines on all parts of plant except on the fruit
23	SM-23	*S. melongena*	24-9-2019	Farm	Padannakad	Kasaragod	75.1101	12.2759	12	Long purple fruit with small prickles on the calyx
24	SM-24	*S. melongena*	28-9-2019	Farm	Pilicode	Kasaragod	75.1633	12.1997	12	Long purple fruit

25	SM-25	*S. melongena* (IC 241675)	18-11-2019	NBPGR	-	-	-	-	-	All the plant part have light green coloured spines except on the fruits. Fruits are round in shape with green colour
26	SM-26	*S. melongena* (IC 545863)	18-11-2019	NBPGR	-	-	-	-	-	Purple fruit
27	SM-27	*S. Melongena* (IC 427008)	18-11-2019	NBPGR	-	-	-	-	-	Large green coloured fruits
28	SM-28	*S. incanum* (IC 620612)	18-11-2019	NBPGR	-	-	-	-	-	Dark green coloured fruits with thorns on the fruit calyx
29	SM-29	*S. gilo* (IC 618025)	18-11-2019	NBPGR	-	-	-	-	-	Green pumpkin-like small fruit
30	SM-30	*S. insanum* (IC 256161)	18-11-2019	NBPGR	-	-	-	-	-	Bushy plant with more number of spines on leaf, stem and calyx. Dark green coloured round fruit with a bitter taste

3.3.1 QUALITATIVE CHARACTERS

3.3.1.1 Plant growth habit

The growth habit of thirty genotypes were recorded and grouped into three as upright (3), intermediate (5) and prostrate (7).

3.3.1.2 Stem colour

The stem colour of different brinjal accessions was recorded as; those with and those without anthocyanin pigmentation. Based on intensity, accessions with stem anthocyanin pigmentation were grouped under weak, medium and strong.

3.3.1.3 Leaf blade lobing

The lobing pattern of leaf blade was studied and categorized into five groups *viz*., very weak (1), weak (3), intermediate (5), strong (7) and very strong (9) (Fig. 1).

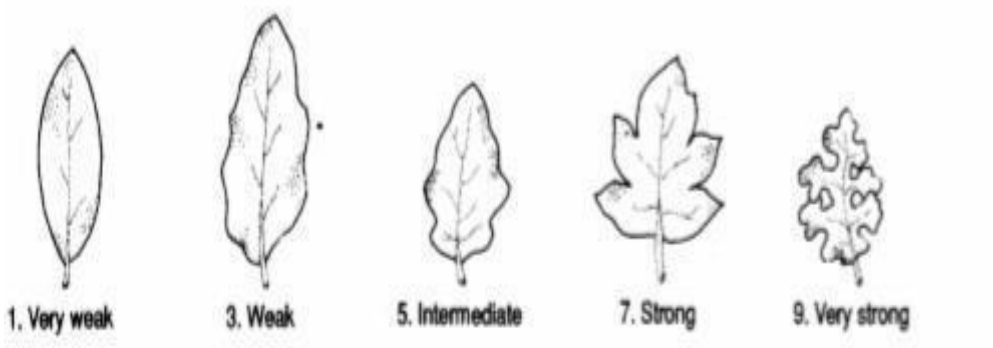


Figure 1. Leaf blade lobing

3.3.1.4 Leaf blade tip angle

The angles of leaf tip were observed and based on the variation observed it was grouped into very acute (1), acute (3), intermediate (5), obtuse (7) and very obtuse (9) (Fig.2).

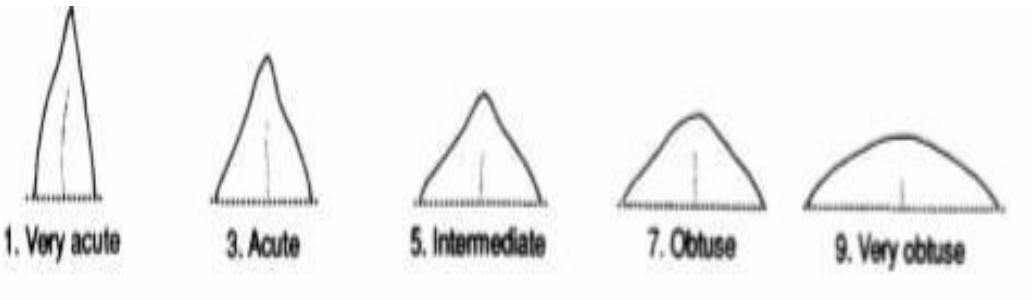


Figure 2. Leaf blade tip angle

3.3.1.5 Leaf blade colour

Leaf blade colour of thirty accessions was observed and grouped into following categories, *viz.*, light green (1), green (3), dark green (5), greenish violet (7) and violet (9).

3.3.1.6 Leaf prickles

The accessions were categorized into different groups based on the number of prickles present on the upper surface of leaf blade *viz.*, none, very few (1-2), few (3-5), intermediate (6- 10), many (11-20) and very many (>20).

3.3.1.7 Petiole colour

Colour of petiole was observed in different accessions and grouped as green (1), greenish violet (3), violet (5), dark violet (7) and dark brown (9).

3.3.1.8 Corolla colour

Based on variation in corolla colour, flowers were grouped as greenish-white (1), white (3), pale violet (5), light violet (7) and bluish violet (9).

3.3.1.9 Pollen colour

There is no classification for the colour of pollen as per IPGRI descriptor. All the accessions had light yellow coloured pollen.

3.3.1.10 Fruit curvature

Based on the curvature the fruits were grouped into six categories (Fig. 3)

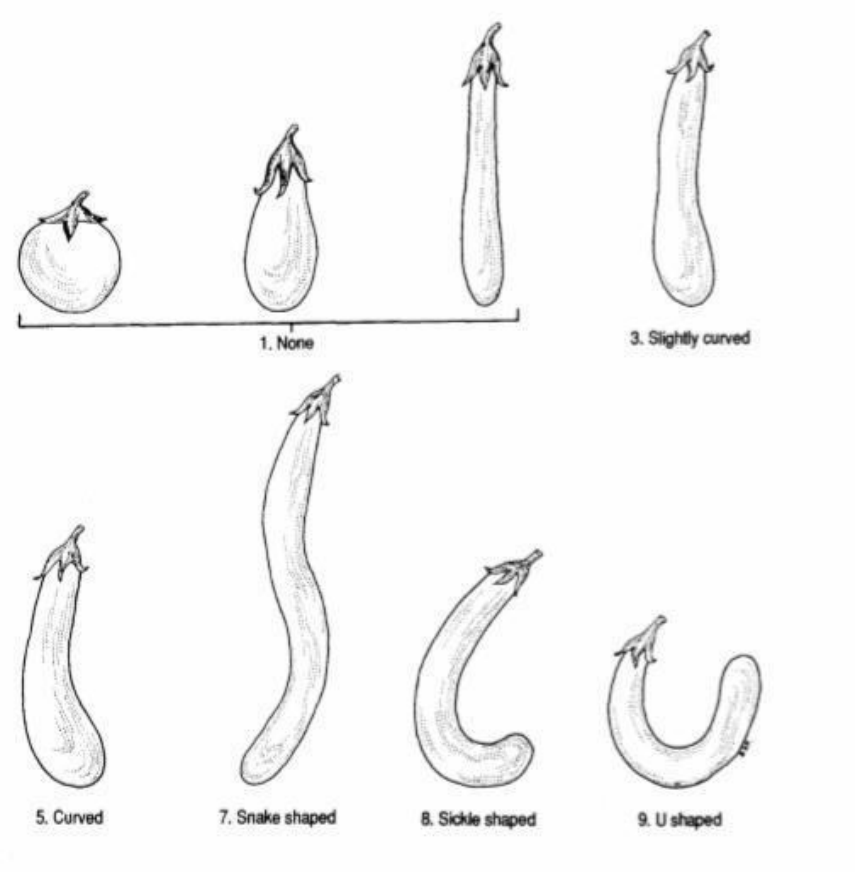


Figure 3. Fruit curvature

3.3.1.11 Fruit shape

The shape of fruit was recorded by observing the position of the widest portion of the fruit from base to tip and grouped as;

(i) About 1/4 away from the base to tip (3)

(ii) About 1/2 away from the base to tip (5)

(iii) About 3/4 away from the base to tip (7)

3.3.1.12 Fruit apex shape

Based on the shape of fruit apex the fruits were categorized into protruded (3), rounded (5) and depressed (7).

3.3.1.12 Fruit apex shape

Based on the shape of fruit apex the fruits were categorized into protruded (3), rounded (5) and depressed (7).

3.3.1.13 Fruit colour at physiological ripening

The colour of fruit at physiological ripening was recorded and grouped as green (1), deep yellow (2), yellow-orange (3), deep orange (4), fire red (5), poppy red (6), scarlet red(7), light brown (8) and black (9).

3.3.1.14 Fruit flesh density

The fruits were dissected and flesh density noted by feeling the texture with fingers. Based on the flesh density these were grouped as very loose (spongy) (1), loose (crumbly) (3), average density (5), dense (7) and very dense (9).

3.3.1.15 Fruit position

Fruit position was recorded and categorized as erect (1), semi-erect (3), horizontal (5), semi-pendant (7) and pendant (9).

3.3.2 QUANTITATIVE CHARACTERS

The thirty genotypes were evaluated for the 22 quantitative characters as follows and scoring for 13 characters as per IPGRI descriptors are given in Apendix I.

3.3.2.1 Plant height (cm)

Height of the plant was measured from the collar region to tip of the plant at the flowering stage (55 DAT) and the mean value calculated.

3.3.2.2 Plant breadth (cm)

The widest part of a plant was selected for measuring the plant breadth or plant spread at the flowering stage (55 DAT) and the mean was worked out.

3.3.2.3 Number of primary branches

The number of primary branches was counted at the flowering stage (55 DAT) and the mean value was calculated.

3.3.2.4 Leaf blade length (cm)

The third leaf from the tip of the shoot (fully developed leaf) was selected and the length from leaf base to tip was measured in cm for five leaves from randomly selected shoots of a plant and the mean worked out.

3.3.2.5 Leaf blade width (cm)

The widest part of the third leaf from the shoot tip was measured in cm for five leaves from randomly selected shoots of a plant and the mean was calculated.

3.3.2.6 Petiole length (mm)

The fully developed five leaves were selected from a plant and length from leaf axil to the base of the leaf blade was measured in mm and the average was worked out.

3.3.2.7 Days to first flowering

The total number of days from transplanting to first flowering was recorded in randomly selected five plants from each plot and the mean value calculated.

3.3.2.8 Days to 50 per cent flowering

The total number of days from transplanting to 50% plants in a plot showing at least one flower was recorded for each accession per plot.

3.3.2.9 Number of flowers per inflorescence

The average number of flowers per individual cluster on a plant was observed in randomly selected five plants from a plot and mean worked out.

3.3.2.10 Number of long-styled flowers per inflorescence

Based on the position of style with respect to anther cone in hermaphrodite flowers, the flowers having long style positioned above anther cone were counted per cluster for randomly selected clusters in five plants and mean worked out.

3.3.2.11 Number of medium styled flowers per inflorescence

Based on the position of style with respect to anther cone in hermaphrodite flowers, the flowers having medium style at the same level of anther cone were counted per cluster for randomly selected clusters in five plants and mean worked out.

3.3.2.12 Relative style length (mm)

The extent of style length from the tip of the anther cone in bisexual flowers was measured and categorized as short (~1 mm), intermediate (~3 mm) and Long (~5 mm).

3.3.2.13 Fruit length (cm)

Length of fruit was measured from calyx base to fruit tip in cm for five fruits per plant and the mean worked out.

3.3.2.14 Fruit diameter (cm)

The widest part of the fruit was selected and the diameter at that position was measured in centimeter. The mean was worked out for five fruits per plant

3.3.2.15 Fruit length/breadth ratio

The length-breadth ratio of fruit was observed and the fruits were grouped into six (Fig.4).

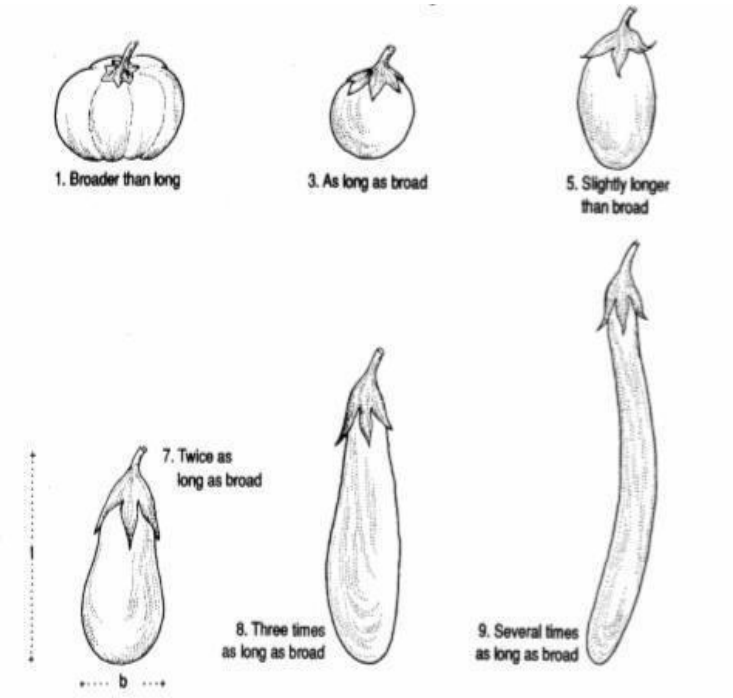


Figure 4. Fruit length/breadth ratio

3.3.2.16 Relative fruit calyx length

The calyx length is measured as percentage to fruit length and grouped as very short (<10%), short (~20%), intermediate (~50%), long (~70%) and very strong (>75%).

3.3.2.17 Fruit pedicel length (cm)

Length of fruit pedicel was measured in centimeter from fruit pedicel axis to calyx base.

3.3.2.18 Fruit weight (g)

Fruits harvested from five randomly selected plants were weighed individually in grams and the average worked out to calculate the weight per fruit.

3.3.2.19 Number of days from anthesis to fruit set

The number of days from anthesis to fruit set in five randomly selected plants from a plot was recorded and the mean value calculated.

3.3.2.20 Number of days from fruit set to maturity

The number of days from fruit set to its commercial maturity was recorded and the mean worked out for each accession.

3.3.2.21 Number of fruits/plant

The number of fruits from all pickings was counted and the mean value calculated.

3.3.2.22 Number of seeds per fruit

The number of seeds from three physiologically ripened fruits was counted from each of five randomly selected plants and calculated the mean value.

3.3.2.23 Fruit yield per plant (g)

The total fruit yield per plant in grams was calculated by taking the weight of harvested fruits per plant and the average worked out.

3.3.3 PEST AND DISEASES

The incidence of pest and disease were recorded in percentage by recording the number of plants showing the disease or pest symptoms per plot to the total number of plants per plot.

3.3.3.1 Fruit and shoot borer infestation

The number of plants showing shoot infestation and the number of damaged fruits was recorded for each genotype and it was represented in percentage.

$$\text{Percentage infestation} = \frac{\text{Number of affected plants}}{\text{Number of plants observed}} \times 100$$

Total number of plants

3.3.3.2 Phomopsis blight incidence

There was no incidence of phomopsis blight.

3.3.3.3 Bacterial wilt

The plants showing wilt symptom were recorded and subjected to ooze test.

$$\text{Percentage infestation} = \frac{\text{Number of affected plants}}{\text{Total number of plants}} \times 100$$

3.3.3.4 Little leaf incidence

None of the genotypes showed the incidence of little leaf

3.4 STATISTICAL ANALYSIS

The data on various observations studied during experiment were subjected to statistical analysis using Origin 2019b software. the data were subjected to following statistical analysis:

3.4.1 Analysis of Variance (ANOVA)

For quantitative data, analysis of variance (ANOVA) and covariance was performed.

Source	d.f	S.S	M.S	E.M.S	F ratio
Replication	(r-1)	Sr	Mr	$\sigma^2e + g\,\sigma^2r$	Mr /Me
Genotype	(g-1)	Sg	Mg	$\sigma^2e + r\,\sigma^2g$	Mg /Me
Error	(r-1) (g-1)	Se	Me	σ^2e	
Total					

Where,

r= Number of replications

g= Number of genotypes

Mr = Mean square due to replications

Mg= Mean square due to genotypes

Me = Mean square due to error

$\sigma^2 e$ = Expected environment variance

$\sigma^2 r$ = Expected variance due to replications

$\sigma^2 g$ = Expected variance due to genotypes

For the comparison purpose, Standard error (S.E), Critical difference (C.D) and Coefficient of variation (C.V) were worked out

$$S.E.(\pm) = \sqrt{\frac{Me}{r}}$$

$$C.D = \sqrt{2 x \frac{Me}{r}} \text{ x t } \text{(at error degrees of freedom)}$$

$$C.V (\%) = \frac{\sigma}{\bar{x}} \text{ x } 100$$

Where,

Me = Error mean sum of square

r = Number of replications.

t = Table value of t at error d. f. (at 5% and 1%level of significance)

3.4.1 Genetic variability parameters

The components of variation such as coefficients of variation, heritability, genetic advance, correlation and path coefficient were estimated as per Nadarajan and Gunasekaran (2005). The significance of genotypic and phenotypic correlation coefficients among the characters observed was assessed at 5 % and 1 % levels from the table value at (n-2) degrees of freedom.

3.4.1.1 Estimation of variance component

Genotypic and phenotypic components of variance were done with the help of following formulae.

$$\text{Genotypic variance } (\sigma 2g) = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma 2p) = \sigma 2g + \text{MSS (error)}$$

3.4.1.1 Coefficient of variation

Phenotypic and genotypic coefficient of variation was calculated using the following formula.

a) Phenotypic coefficient of variation (PCV %) $= \frac{\sigma p}{\text{Mean}} 100$

b) Genotypic coefficient of variance (GCV %) $= \frac{\sigma g}{\text{Mean}} 100$

Where,

σp and σg are phenotypic and genotypic standard deviations respectively.

The PCV and GCV were calculated in percentage and categorized into low (<10%), moderate (10-20%) and high (>20%) (Sivasubramanian and Menon, 1973).

3.4.1.2 Heritability (Broad sense)

The heritability in broad sense was calculated in percentage. It is the ratio of genotypic variance to phenotypic variance and can be estimated using the formula given by Burton (1952).

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p} 100$$

Where,

$\sigma^2 g$ and $\sigma^2 p$ are genotypic and phenotypic variance respectively

The value of heritability was grouped as low (<30%), moderate (30-60%) and high (>60%) (Johnson *et al*., 1955).

3.4.1.3 Genetic advance

The genetic advance was estimated using the formula proposed by Johnson *et al*. (1955).

$$GA = k \times h^2 \times \sigma p$$

Where,

k – Standardized selection differential at specific level selection intensity (k = 2.06 at 5% selection intensity) (Miller *et al.,* 1958)

h^2 – Heritability of selected character

σp – phenotypic standard deviation of the original population

3.4.1.4 Genetic gain

The genetic advance expressed in percentage of the mean will give genetic gain. Based on the value obtained they were grouped as low (<10%), moderate (10-20%) and high (>20%) (Johnson *et al*., 1955).

$$\text{GA (\%)} = \frac{\text{Genetic advance}}{\text{Mean}} 100$$

3.4.1.5 Phenotypic and genotypic correlations

The phenotypic and genotypic correlation was calculated from respective values of variances and covariances. Its significance was worked out from the table r-value at n-2 degrees of freedom (where n is the number of observations in pair). OPSTAT software was used for correlation analysis.

3.4.1.6 Path coefficient analysis

Using path analysis the association between fruit yield and other traits were split into direct and indirect effects. Based on the range of values obtained the direct and indirect effects were categorized as negligible (0.0-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-1.00) and very high (>1.00) (Lenka and Mishra, 1973).

3.1 GENETIC DIVERSITY ANALYSIS

3.1.1 Diversity analysis for qualitative characters

All qualitative data were converted to a nominal scale based on IPGRI descriptors. Cluster analysis of qualitative characters was performed using UPGMA (Unweighted Pair Group Method with Arithmetic mean) method and dendrogram was constructed.

3.1.2 Diversity analysis for quantitative characters

The cluster analysis for quantitative data was performed using Standardized Euclidean Square Distance method and thirty genotypes of brinjal were grouped into clusters based on 22 quantitative characters using Tocher's method. Inter and intra-cluster distance and cluster means were calculated for individual characters based on the performances of various genotypes in each cluster.

Multivariate analysis using Mahalanobis D^2 statistic was used for assessing of the genetic divergence between genotypes. The generalized distance between any two populations is defined as,

$D^2 = Y_{ij}\ \beta_i\ \beta_j$

Where,

Y_{ij} = The reciprocal matrix to the common dispersion matrix

β_i = The difference between the two mean values of the two populations for i^{th} character (μ_{i1}-μ_{i2})

β_j = The difference between the mean values of the two populations for the j^{th} character (μ_{j1}-μ_{j2})

μ = Vector mean values for all the characters

The formula for the estimation of distance, D^2 from

accessions $D^2 p = d_1 (S^{-1}) d$

Where,

$D^2 p$ = Square of the distance considering P

values. $d_1 = (X_{i1} - X_{i2})$

X = Vector for mean values of all the

characters S^{-1}= inverse of variance

covariance matrix

Formula for computation of D values, which requires inversion of the matrix, becomes complicated especially when the numbers of variables under consideration are large.

Therefore, the original correlated un-standardized variables (X_i) were transformed to standardized uncorrelated variables (Y_i) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two population i.e., D^2_i.

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula,

$$D^2 = (Y_{i1} - Y_{i2})^2$$

Where,

Y_{i1} = Vector of transformed mean values, for first genotype Y_{i2} = vector of transformed mean values, for second genotype

The square root of the D^2 values gives the generalized distance (D) between the two populations. The D^2 values were arranged in a matrix form. The significance of D^2 values between any populations was tested using the following formula.

$$F = \frac{(n_1 + n_2 - p - 1)}{(n_1 + n_2 - 2)\,P} \times \frac{(n_1 n_2)}{(n_1 + n_2)} D^2$$

This computed F values was compared with table F value at 5% and 1% levels of significance with P (number of characters) and $(n_1 + n_2 - p - 1)$ degrees of freedom.

3.2 SELECTION INDEX

The selection index (Smith, 1936) using discriminant function (Fisher, 1936) was used to discriminate the accessions with respect to all characters. It is described as,

Selection index (I) = $b_1 x_1 + b_2 x_2 + \ldots\ldots\ldots\ldots + bn\ xn$

Genetic worth of the plant (H) = $a_1 G_1 + a_2 G_2 + \ldots\ldots\ldots\ldots + bn\ Gn$

where,

$x_1, x_2 \ldots\ldots\ldots\ldots xn$ - phenotypic values

$G_1, G_2 \ldots\ldots\ldots\ldots Gn$ - genotypic values

With respect to characters $x_1, x_2 \ldots\ldots\ldots\ldots xn$

The economic weight assigned to all character is assumed to be uniform and it will be equal to unity; *ie*., $a_1, a_2 \; a_k = 1$

Determined the regression coefficient (when H and I exhibit maximum correlation between them)

$$\text{Regression coefficients (b)} = P^{-1} G a$$

Where, P - phenotypic variance-covariance matrix

G - genotypic variance-covariance matrix

A - coloum vector of economic traits

Expected genetic gain (GS1) or genetic advance for discriminant function was estimated for different indices involving various character combinations by using the formula,

$$GS_1 = Z/Q \; (b_1g_1y + b_2g_2y + ... + bngny)\; ½$$

Where,

Z/Q - selection intensity at 5%

b1,b2,.....bn - coefficient values of character 1, 2, and n respectively

g1y,g2y,--gny - are corresponding genotypic covariance of these characters with dependent character (fruit yield/plant)

Genetic advance for the dependent character (GS_2) was calculated using the formula,

$$GS_2 = VG/(VP)\; ½ \; x \; K$$

Where,

VG - genotypic variance

VP - phenotypic variance

K - selection differential (2.06)

Relative efficiency over direct selection (%) was worked out separately for different combinations of characters with the help of following formula,

Relative efficiency = GS_1/GS_2 X100

It measures the effectiveness of various selection indices constructed through different character combinations. The relative efficiency of direct selection for yield is considered as 100 percent.

RESULTS

4. RESULT

Brinjal is an important vegetable crop in the tropical and subtropical regions. It has a large number of wild relatives that are sources of variation for breeding program. However, these wild relatives remain largely unexploited. Hence the experiment entitled "Characterization of brinjal (*Solanum melongena* L.) and its wild relatives" was conducted at College of Agriculture, Padannakkad. Thirty genotypes of brinjal (*Solanum melongena* L.) including its wild relatives were collected from North Kerala and NBPGR Thrissur. The final collections included for the study consisted of maximum genotypes from Malappuram (11) followed by Kozhikode (5), Kannur (5), Kasargod (3), Wayanad (1) and six accessions from NBPGR, Thrissur (Table 2). These were evaluated in the field, the observations were recorded based on qualitative and quantitative characters. Statistical analysis of the data was conducted and the results of the study are presented in this chapter.

4.1 Morphological characterization of thirty brinjal genotypes based on qualitative characters

Thirty brinjal genotypes were evaluated for seventeen qualitative characters using IPGRI descriptors. The descriptor values of the characters of each genotype are given in Tables 3.1, 3.2, 3.3 and 3.4 respectively.

4.1.1 Plant growth habit

Majority of genotypes (22 Nos. including wild SM-2 (*S. macrocarpon*), SM-28 (*S. incanum*) and SM-29 (*S. gilo*)) had upright growth habit. Six genotypes *viz*., SM-11, SM- 14, SM-18, SM-22 (*S. mammosam*), SM-24 and SM-27 had intermediate type of growth habit and two genotypes (SM-25 and SM-30 (*S. insanum*)) had prostrate type of growth habit.

4.1.2 Stem colour

According to IPGRI, there was no descriptor for stem colour, so this observation was taken on the basis of DUS character. The accessions were grouped

Table 2. Thirty brinjal genotypes included in the study

Sl. No.	Accession number	Place of collection
1	SM-1	Malappuram
2	SM-2 (*S. macrocarpon*)	Kannur
3	SM-3	Malappuram
4	SM-4	Malappuram
5	SM-5	Malappuram
6	SM-6	Kozhikode
7	SM-7	Kozhikode
8	SM-8	Malappuram
9	SM-9	Kozhikode
10	SM-10	Kannur
11	SM-11	Kannur
12	SM-12	Kannur
13	SM-13	Malappuram
14	SM-14	Wayanad
15	SM-15	Kozhikode
16	SM-16	Malappuram
17	SM-17	Malappuram
18	SM-18	Malappuram
19	SM-19	Malappuram
20	SM-20	Kozhikode
21	SM-21	Malappuram
22	SM-22 (*S. mammosam*)	Kasaragod
23	SM-23	Kasaragod
24	SM-24	Kasaragod
25	SM-25	NBPGR
26	SM-26	NBPGR
27	SM-27	NBPGR
28	SM-28 (*S. incanum*)	NBPGR
29	SM-29 (*S. gilo*)	NBPGR
30	SM-30 (*S. insanum*)	NBPGR

into four based on the intensity of anthocyanin pigmentation. Majority of the accessions (26 Nos.) had green coloured stem, two (SM-7 and SM-9) had light green stem. Accession SM-15 had purple and SM-29 (*S. gilo*) had dark purple pigmentation on the stem.

4.1.3 Petiole colour

The result showed that based on the intensity of anthocyanin, leaf petiole showed various pigmentation. Accessions SM-22 (*S. mammosam*) and SM-1 showed unique petiole colour of dark purple and dark brown respectively. Thirteen genotypes had leaves with green petiole, eight had greenish violet petiole and seven had purple-coloured petiole.

4.1.4 Leaf blade colour

The plants had two types of leaves based on colour. Out of the thirty genotypes maximum had green leaves (26 accessions) and four *viz*., SM-11, SM-15, SM-22 (*S. mammosam*) and SM-29 (*S. gilo*) had dark green leaves.

4.1.5 Leaf prickles

Out of thirty genotypes, maximum number of accessions (20 Nos.) were without prickles and the remaining had prickles. These were grouped based on the number of prickles present on the upper surface of the leaf. Five accessions (SM-11, SM-12, SM-18, SM-23 and SM-24) had few (3-5 Nos.) prickles, four accessions (SM-22 (*S. mammosam),* SM-25, SM-26 and SM-30 (*S. insanum*)) had intermediate (6-10 Nos.) prickles and SM-10 had very few (1-2 Nos.) prickles.

4.1.6 Leaf blade lobing

Among thirty, nineteen accessions including SM-30 (*S. insanum*) had intermediate leaf lobing pattern which is followed by nine genotypes including wild types SM-22 (*S. mammosam*) and SM-29 (*S. gilo*) with strong leaf lobing. The wild accessions SM-2 (*S. macrocarpon*) and SM-28 (*S. incanum*) had weak leaf blade lobing.

4.1.7 Leaf blade tip angle

Based on the leaf tip angle the genotypes were classified into four as very acute, acute, intermediate and obtuse leaf tip angle. Sixteen accessions including wild types SM-2 (*S. macrocarpon*) and SM-22 (*S. mammosam*) had acute leaf tip angle. Six cultivated accessions along with two wild accessions (SM-28 (*S. incanum*) and SM-29 (*S. gilo*)) had intermediate leaf tip angle, four (SM-4, SM-5, SM-8 and SM-21) had very acute leaf tip angle and two (SM-9 and SM-30 (S. *insanum*)) had obtuse leaf tip angle.

4.1.8 Corolla colour

Based on variation observed in corolla colour, the thirty accessions were classified as genotypes with white (6 Nos.), pale violet (11 Nos.), light violet (12 Nos.) and bluish violet flowers. The wild accession SM-22 (*S. mammosam*) had bluish-violet flowers.

4.1.9 Pollen colour

The colour of pollen was observed and there was no variation. All the thirty genotypes had yellow coloured pollen.

4.1.10 Fruit curvature

Based on curvature, the fruits were grouped into four. Maximum accessions (20 Nos.) were without any curves, five (SM-1, SM-11, SM-13, SM-24 and SM-26) had slightly curved fruits, three accessions (SM-3, SM-17 and SM-21) had curved fruits and two (SM-23 and SM-10) had snake-shaped fruits. None of the wild accessions showed any curves on fruits.

4.1.11 Fruit shape

Based on the position of the widest portion of the fruit from base to tip, the thirty accessions were classified into three. Maximum genotypes (22 Nos.) including wild accessions namely SM-2 (*S. macrocarpon*), SM-28 (*S. incanum*), SM-29 (*S. gilo*) and SM- 30 (*S. insanum*) had widest portion ½ away from the base to tip of the fruit, seven had widest portion ¾ away from base to tip and two accessions *viz.*, SM-

15 and wild accession SM-22 (*S. mammosam*) had widest portion ¼ away from base to tip.

4.1.12 Fruit flesh density

Among thirty accessions, thirteen including wild accession SM-28 (*S. incanum*) had crumply flesh density, nine accessions had very loose flesh density which included the wild accessions SM-29 (*S. gilo*) and SM-30 (*S. insanum*). Three accessions (SM-8, SM-15 and wild SM-22 (*S. mammosam*)) had dense flesh. The accessions SM-3, SM-6 and SM-11 had very dense flesh and two accessions *viz*., SM-13 and wild SM-2 (*S. macrocarpon*) had average fruit flesh density.

4.1.13 Fruit apex shape

Based on fruit apex shape the thirty genotypes were categorized into three *viz*., depressed (12 accessions), round (9 accessions) and protruded (9 accessions) fruit apex. All the wild accessions had depressed fruit apex except *S. insanum* (SM-30), which had round fruit apex.

4.1.14 Fruit colour at commercial ripening

The maximum number of accessions (14 Nos.) had purple-coloured fruits, twelve accessions had green coloured fruits including all wild accessions except SM-22 (*S. mammosam*), which had yellow coloured fruit on commercial ripening and three accessions had milky white coloured fruits.

4.1.15 Fruit colour at physiological ripening

All the genotypes had yellow coloured fruit on physiological ripening except SM- 29 (*S. gilo*), which had red coloured fruit.

4.1.16 Fruit position

As per IPGRI descriptors, thirty genotypes were categorized as pendant, semi-pendant and horizontal based on the fruit bearing habit of the plant. All the *S. melongena* accessions (25 Nos.) as well as the wild accessions SM-28 (*S. incanum*) and SM-30 (*S. insanum*) had pendant fruit habit. The wild genotypes namely SM-2 (*S. macrocarpon*) and SM-29 (*S. gilo*) had semi-pendant and SM-22 (*S. mammosam*) had horizontal fruit bearing habit.

Table 3.1 Morphological characterization of 30 brinjal genotypes based on 17 qualitative characters

Sl. No.	Accessions	Growth habit	Stem colour	Petiole colour	Leaf blade colour
1	SM-1	Upright	Green	Brown	Green
2	SM-2	Upright	Green	Green	Green
3	SM-3	Upright	Green	Greenish violet	Green
4	SM-4	Upright	Green	Purple	Green
5	SM-5	Upright	Green	Green	Green
6	SM-6	Upright	Green	Greenish violet	Green
7	SM-7	Upright	Light green	Green	Green
8	SM-8	Upright	Green	Greenish violet	Green
9	SM-9	Upright	Light green	Green	Green
10	SM-10	Upright	Green	Purple	Green
11	SM-11	Intermediate	Green	Purple	Dark green
12	SM-12	Upright	Green	Green	Green
13	SM-13	Upright	Green	Green	Green
14	SM-14	Intermediate	Green	Purple	Green
15	SM-15	Upright	Purple	Purple	Dark green
16	SM-16	Upright	Green	Green	Green
17	SM-17	Upright	Green	Green	Green
18	SM-18	Intermediate	Green	Green	Green
19	SM-19	Upright	Green	Green	Green
20	SM-20	Upright	Green	Purple	Green
21	SM-21	Upright	Green	Green	Green
22	SM-22	Intermediate	Green	Dark Purple	Dark green
23	SM-23	Upright	Green	Greenish violet	Green
24	SM-24	Intermediate	Green	Greenish violet	Green
25	SM-25	Prostrate	Green	Green	Green
26	SM-26	Upright	Green	Green	Green
27	SM-27	Intermediate	Green	Greenish violet	Green
28	SM-28	Upright	Green	Greenish violet	Green
29	SM-29	Upright	Dark Purple	Purple	Dark green
30	SM-30	Prostrate	Green	Greenish violet	Green

Table 3.2 Morphological characterization of 30 brinjal genotypes based on 17 qualitative characters

Sl. No.	Accessions	Leaf prickles	Leaf blade lobing	Leaf tip angle	Corolla colour
1	SM-1	None	Intermediate	Acute	Pale violet
2	SM-2	None	Weak	Acute	Pale violet
3	SM-3	None	Intermediate	Intermediate	Pale violet
4	SM-4	None	Intermediate	Very acute	Pale violet
5	SM-5	None	Intermediate	Very acute	Pale violet
6	SM-6	None	Intermediate	Acute	Pale violet
7	SM-7	None	Strong	Intermediate	White
8	SM-8	None	Intermediate	Very acute	Pale violet
9	SM-9	None	Intermediate	Obtuse	Pale violet
10	SM-10	Very few(1-2)	Intermediate	Acute	Pale violet
11	SM-11	Few (3-5)	Strong	Acute	Pale violet
12	SM-12	Few (3-5)	Strong	Acute	White
13	SM-13	None	Intermediate	Acute	Pale violet
14	SM-14	None	Strong	Acute	Pale violet
15	SM-15	None	Strong	Acute	Pale violet
16	SM-16	None	Intermediate	Acute	White
17	SM-17	None	Intermediate	Intermediate	White
18	SM-18	Few (3-5)	Intermediate	Acute	Pale violet
19	SM-19	None	Intermediate	Intermediate	Pale violet
20	SM-20	None	Intermediate	Acute	Pale violet
21	SM-21	None	Intermediate	Very acute	White
22	SM-22	Intermediate (6-10)	Strong	Acute	Bluish violet
23	SM-23	Few (3-5)	Intermediate	Acute	Pale violet
24	SM-24	Few (3-5)	Strong	Acute	Pale violet
25	SM-25	Intermediate (6-10)	Intermediate	Intermediate	Pale violet
26	SM-26	Intermediate (6-10)	Intermediate	Intermediate	Pale violet
27	SM-27	None	Strong	Acute	Pale violet
28	SM-28	None	Weak	Intermediate	Pale violet
29	SM-29	None	Strong	Intermediate	White
30	SM-30	Intermediate (6-10)	Intermediate	Obtuse	Pale violet

Table 3.3 Morphological characterization of 30 brinjal genotypes based on 17 qualitative characters

Sl. No.	Accessions	Pollen colour	Fruit curvature	Fruit shape (wide part from base to tip)	Fruit flesh density	Fruit apex shape
1	SM-1	Yellow	Slightly curved	½ away	Crumply	Protruded
2	SM-2	Yellow	None	½ away	Avg. density	Depressed
3	SM-3	Yellow	Curved	¾ away	Very dense	Depressed
4	SM-4	Yellow	None	½ away	Very loose	Round
5	SM-5	Yellow	None	¾ away	Very loose	Protruded
6	SM-6	Yellow	None	½ away	Very dense	Depressed
7	SM-7	Yellow	None	½ away	Crumply	Round
8	SM-8	Yellow	None	½ away	Dense	Depressed
9	SM-9	Yellow	None	½ away	Crumply	Depressed
10	SM-10	Yellow	Snake shaped	½ away	Very loose	Protruded
11	SM-11	Yellow	Slightly curved	½ away	Very dense	Round
12	SM-12	Yellow	None	½ away	Crumply	Protruded
13	SM-13	Yellow	Slightly curved	½ away	Avg. density	Round
14	SM-14	Yellow	None	½ away	Very loose	Depressed
15	SM-15	Yellow	None	¼ away	Dense	Depressed
16	SM-16	Yellow	None	¾ away	Crumply	Round
17	SM-17	Yellow	Curved	½ away	Crumply	Protruded
18	SM-18	Yellow	None	½ away	Crumply	Depressed
19	SM-19	Yellow	None	¾ away	Crumply	Round
20	SM-20	Yellow	None	½ away	Crumply	Protruded
21	SM-21	Yellow	Curved	¾ away	Very loose	Protruded
22	SM-22	Yellow	None	¼ away	Dense	Depressed
23	SM-23	Yellow	Snake shaped	½ away	Crumply	Protruded
24	SM-24	Yellow	Slightly curved	½ away	Very loose	Protruded
25	SM-25	Yellow	None	½ away	Crumply	Round
26	SM-26	Yellow	Slightly curved	¾ away	Crumply	Round
27	SM-27	Yellow	None	¾ away	Very loose	Depressed
28	SM-28	Yellow	None	½ away	Crumply	Depressed
29	SM-29	Yellow	None	½ away	Very loose	Depressed
30	SM-30	Yellow	None	½ away	Very loose	Round

Table 3.4 Morphological characterization of 30 brinjal genotypes based on 17 qualitative characters

Sl. No.	Accessions	Fruit colour at commercial ripening	Fruit colour at physiological ripening	Fruit position	Fruit length/breadth ratio
1	SM-1	Green	Yellow	Pendant	Three times longer as broad
2	SM-2	Green	Yellow	Semi pendant	Broader than long
3	SM-3	Green	Yellow	Pendant	Slightly longer than broad
4	SM-4	Purple	Yellow	Pendant	Three times longer as broad
5	SM-5	Milky white	Yellow	Pendant	Three times longer as broad
6	SM-6	Purple	Yellow	Pendant	Broader than long
7	SM-7	Milky white	Yellow	Pendant	Three times longer as broad
8	SM-8	Purple	Yellow	Pendant	Slightly longer than broad
9	SM-9	Purple	Yellow	Pendant	As long as broad
10	SM-10	Purple	Yellow	Pendant	Several times as long as broad
11	SM-11	Purple	Yellow	Pendant	Three times longer as broad
12	SM-12	Green	Yellow	Pendant	Slightly longer than broad
13	SM-13	Green	Yellow	Pendant	Three times longer as broad
14	SM-14	Purple	Yellow	Pendant	Slightly longer than broad
15	SM-15	Purple	Yellow	Pendant	Slightly longer than broad
16	SM-16	Milky white	Yellow	Pendant	Twice as long as broad
17	SM-17	Green	Yellow	Pendant	Three times longer as broad
18	SM-18	Purple	Yellow	Pendant	Three times longer as broad
19	SM-19	Green	Yellow	Pendant	Slightly longer than broad
20	SM-20	Purple	Yellow	Pendant	Three times longer as broad
21	SM-21	Purple	Yellow	Pendant	Three times longer as broad
22	SM-22	Yellow	Yellow	Horizontal	Slightly longer than broad
23	SM-23	Purple	Yellow	Pendant	Several times as long as broad
24	SM-24	Purple	Yellow	Pendant	Three times longer as broad
25	SM-25	Green	Yellow	Pendant	Slightly longer than broad
26	SM-26	Purple	Yellow	Pendant	Three times longer as broad
27	SM-27	Green	Yellow	Pendant	Twice as long as broad
28	SM-28	Green	Yellow	Pendant	As long as broad
29	SM-29	Green	Red	Semi pendant	Slightly longer than broad
30	SM-30	Green	Yellow	Pendant	As long as broad

4.1.17 Fruit length-breadth ratio

Among *S. melongena*, maximum genotypes (12 Nos.) had fruit length-breadth ratio three times longer as broad. Nine genotypes were with fruits slightly longer than broad, three *viz*., SM-9, SM-28 and SM-30 (*S. insanum*) had fruits slightly longer than broad, fruits of SM-2 (*S. macrocarpon*) and SM-6 were broader than long, SM-16 and SM-27 had fruits twice as long as broad. Fruits several times as long as broad was noticed in accessions SM-23 and SM-10.

4.2 Morphological characterization of thirty brinjal genotypes based on quantitative characters

The thirty brinjal genotypes were evaluated for 22 quantitative characters as per IPGRI descriptor and subjected to statistical analysis. The results thus obtained are given below:

4.2.1 ANALYSIS OF VARIANCE AND MEAN PERFORMANCE OF THIRTY BRINJAL GENOTYPES

The results of analysis of variance in 22 characters of 30 genotypes are presented in Table 4. All the genotypes exhibited significant difference for all the characters under study. The mean performance of thirty brinjal genotypes for 22 characters studied are presented in Table 5.

4.2.1.1 Plant height (cm)

The genotypes differed significantly for plant height and the values ranged from 28.89 cm (SM-30 (*S. insanum*)) to 86.46 cm (SM-22 (*S. mammosam*)) with an average of 63.96 cm height. Eleven genotypes recorded height lower than the average value. Among *S. melongena* accessions, SM-4 was the tallest (77.22 cm) and SM-9 the shortest (46.01 cm).

4.2.1.2 Plant breadth (cm)

The plant breadth ranged from 58.37 cm to 96.75 cm with an average of 72.71 cm. Maximum number of genotypes (19 Nos.) had breadth less than the average

Table 4. Analysis of variance of 22 characters of 30 brinjal genotypes

Source of Variations	df	Mean Sum of Squares											
		1. Plant height (cm)	2. Plant breadth (cm)	3. Number of primary branches	4. Leaf blade length (cm)	5. Leaf blade width (cm)	6. Petiole length (mm)	7. Days to first flowering	8. Days to 50 % flowering	9. No. of flowers/ inflorescence	10. No. of long-styled flowers	11. No. of medium-styled flowers	12. Relative style length (mm)
Replicate	**2**	8.481	24.096	0.025	0.036	0.06	0.089	0.578	2.411	0.131	0.036	0.045	0.016
Treatments	**29**	341.875	347.792	8.566	29.937	25.701	8.895	46.885	82.632	5.171	2.249	0.623	0.597
Error	**58**	1.696	4.485	0.057	0.008	0.009	0.008	0.371	0.285	0.054	0.081	0.034	0.016

Source of Variations	df	Mean Sum of Squares									
		13. Fruit length (cm)	14. Fruit diameter (cm)	15. Relative fruit calyx length (%)	16. Fruit pedicel length (mm)	17. Fruit weight (g)	18. No. of days from anthesis to fruit set	19. No. of days from fruit set to maturity	20. No. of fruit/plant	21. Fruit yield/ plant (g)	22. Number of seeds/fruit
Replicate	**2**	0.02	0.005	0.025	0.026	9.377	1.211	5.7	0.184	1054.56	1196.98
Treatments	**29**	63.115	9.377	468.616	4.078	3714.184	85.580	121.963	45.348	518657.9	323313.5
Error	**58**	0.011	0.004	1.507	0.011	8.695	1.361	1.78	0.343	1405.82	1780.403

All the accessions were significant at 5% and 1% level of probability for all the characters

value. The wild SM-30 (*S. insanum*) recorded the minimum plant spread (58.37 cm) and *S. melongena* accession SM-14 had recorded maximum plant spread (96.75).

4.2.1.3 Number of primary branches

Among the thirty genotypes, *S. melongena* SM-26 had maximum number of primary branches (11.4) followed by SM-18 (10.27) and a minimum number of branches are observed in SM-24 (4.47). Among the wild relatives studied, maximum number of primary branches (8.67) are noticed in SM-29 (*S. gilo*).

4.2.1.4 Leaf blade length (cm)

Great variation for leaf blade length was observed, which ranging from 6.62 cm to 21.58 cm with a mean length of 17.05 cm. The wild genotype SM-30 had smallest leaf blade of 6.62 cm among all the genotypes. Among *S. melongena* accessions SM-25 had smallest leaf length of 13.54 cm and longest leaf blade (21.58 cm) was observed in SM-7 followed by SM-20 (20.68 cm) and SM-21 (20.14 cm).

4.2.1.5 Leaf blade width (cm)

The widest leaf blade was observed in wild accession *S. macrocarpon* (SM-2) (17.09 cm), whereas in case of *S. melongena* accessions SM-21 (16.78 cm) had widest leaf blade. The minimum leaf width (3.54 cm) was observed for wild *S. insanum* (SM-30).

4.2.1.6 Petiole length (mm)

The wild type showed highest variation for petiole length in which minimum length (16.1 mm) was observed in SM-30 and maximum (96.5 mm) in SM-22. In case of *S. melongena* accessions, length of petiole ranged from 33.4 mm (SM-25) to 81.6 mm (SM- 12).

4.2.1.7 Days to first flowering

The thirty genotypes showed significant difference for days to first flowering, which ranged from 42.67 to 60.33 days. The result showed that SM-11 required least number of days for first flowering (42.67) followed by SM-10 (43). Among the wild

types earliest flowering (43 days) was observed in *S. macrocarpon* (SM-2) and SM-29 (*S. gilo*) showed longest juvenile period (60.33 days).

4.2.1.8 Days to 50% flowering

Among all the accessions SM-23 required least number of days for 50% flowering(43.33 days) and the longest duration was observed in wild accession SM-29 (71.33 days). The accession SM-25 showed the longest duration of 53.67 days for 50% flowering among *S. melongena* accessions and wild *S. macrocarpon* showed least number of days for 50% flowering of 48.67 days among the wild accessions.

4.2.1.9 Number of flowers per inflorescence

A significant variation was observed in the number of flowers per inflorescence and its value ranged from 1 to 6.33 flowers per inflorescence. The wild type SM-29 (*S. gilo*) had maximum (6.33) number of flowers per inflorescence followed by *S. Melongena* accession SM-21 (5.33). The least number of flowers was recorded in SM-11 (1.00) and wild accessions SM-2 and SM-30 (2.00) among all the genotypes studied.

4.2.1.10 Number of long-styled flowers per inflorescence

The number of long-styled flowers per inflorescence ranged from 0.87 to 6.33 among *S. melongena* accessions. The maximum number of long-styled flowers per inflorescence (3.7) was noticed in SM-1 and minimum number of long-styled flowers per inflorescence (0.87) were recorded in SM-7 and SM-11. The wild accession SM-30 (*S. insanum*) had maximum number of long-styled flowers (6.33) among all the genotypes studied.

4.2.1.11 Number of medium-styled flowers per inflorescence

The highest number of medium-styled flowers per inflorescence (1.8) was recorded in SM-18 followed by *S. incanum* (SM-28; 1.73) and the accessions SM-25 and SM-22 showed complete absence of medium styled flowers.

4.2.1.12 Relative style length (mm)

The brinjal accessions showed significant difference for relative style length (style length in relation to anther cone). Maximum relative style length (2.77 mm)

was recorded in SM-4 and the minimum length (0.87 mm) in SM-25. In case of wild type, the maximum relative style length observed was 1.27 mm (SM-2; *S. macrocarpon*) and the least was 0.93 mm (SM-29; *S. gilo*).

4.2.1.13 Fruit length (cm)

The longest fruits were observed in *S. melongena* accession SM-11 (21.32 cm). All the wild accessions had shorter fruits with shortest (2.00 cm) recorded in *S. insanum* (SM- 30). Among *S. melongena* accessions the shortest fruit was recorded in SM-9 (4.99 cm) followed by SM-3 (5.47 cm).

4.2.1.14 Fruit diameter (cm)

Fruit diameter showed significant variation ranging from 2.01 cm to 10.46 cm with an average diameter of 4.47 cm. The majority (20 Nos.) of accessions have diameter less than the average value. Among all the accessions maximum fruit width was observed for SM-27 (10.46 cm) followed by SM-14 (8.01 cm) and wild accession SM-30 (*S. insanum*) had recorded minimum diameter (2.01 cm). Among *S. melongena* accessions SM-13 recorded minimum fruit diameter (2.71).

4.2.1.15 Relative fruit calyx length (%)

The maximum relative calyx length was observed in wild type SM-2 (*S. macrocarpon*) (77.67%) and among *S. melongena* accession in SM-20 (22.3%). Minimum relative calyx length was recorded for SM-21 (10.13%).

4.2.1.16 Fruit pedicel length (mm)

The accession SM-27 had maximum fruit pedicel length (59.4 mm) followed by SM-23 (54.2 mm) and SM-9 has least pedicel length of 19.4 mm. Among wild accessions, SM-2 (*S. macrocarpon*) has maximum pedicel length (40.8 mm) and SM-30 (*S. insanum*) has smallest pedicel (7.7 mm), which was smallest among all the accessions.

4.2.1.17 Fruit weight (g)

Among the 30 genotypes, maximum fruit weight was observed for *S. melongena* accession SM-27 (192.67 g) followed by SM-23 (108 g) and minimum in SM-12 (29.04 g). All the wild accessions showed comparatively low fruit weight except *S. macrocarpon* (SM-2), which recorded 67.89 g fruit weight and minimum (4.61g) in SM-30 (*S. insanum*).

4.2.1.18 Number of days from anthesis to fruit set

A significant difference was observed for the number of days from anthesis to fruit set and the value ranged from 11 days to 35.67 days. The wild relatives had longer duration from anthesis to fruit set with maximum (35.67 days) recorded by SM-29 (*S. gilo*) followed by SM-22 (*S. mammosam*) (31 days) and the minimum (11.67 days) was recorded for SM- 30 (*S. insanum*). In case of local cultivars least number of days (11) from anthesis to fruit set was recorded in SM-19 and SM-24 and the maximum number of days (18) was recorded for SM-25. *S. melongena* accessions had taken lesser number of days from anthesis to fruit set with majority (17 Nos.) less than the average value of 15.18 days.

4.2.1.19 Number of days from fruit set to maturity

Accession SM-3 recorded the minimum number of days (28.33) from fruit set to maturity followed by SM-4, SM-7, SM-9 and SM-24 (30.67 days) and the maximum number of days from fruit set to maturity (53.67 days) was recorded in the wild accessions SM-29 (*S. gilo*) followed by SM-30 (*S. insanum*) (49.33 days). Among the *S. melongena* accessions, SM-27 showed maximum duration from fruit set to maturity (46 days) followed by SM-26 (45.33 days).

4.2.1.20 Number of fruits per plant

Among local cultivars, SM-19 had maximum number of fruits per plant (15.11) followed by SM-1 (14) and least number of fruits were observed in SM-13 (7.67). In case of wild type maximum number of fruits per plant was observed in SM-22 (*S. mammosam*; 26.67) followed by SM-28 (*S. incanum*; 18.89) and minimum

number of fruits were recorded in SM-2 (*S. macrocarpon*; 7.11) followed by SM-30 (*S. insanum*; 8.22). Among the *S. melongena*, eight accessions had shown an above average value of 12.05 for this trait.

4.2.1.21 Fruit yield per plant (g)

Among all the accessions studied *S. melongena* accession SM-27 recorded the maximum fruit yield (2146.44 g) followed by SM-23 (1434.11 g) and minimum yield was recorded in SM-12 (292.67 g). Among the wild types, SM-28 (*S. incanum*) had maximum fruit yield (1072.89 g) and the minimum fruit yield (63.33 g) was recorded in SM-30 (*S. insanum*), which was the lowest among all the accessions studied.

4.2.1.22 Number of seeds per fruit

The maximum number of seeds (1591.33) were documented in *S. melongena* SM- 23 followed by the wild accession SM-28 (*S. incanum*; 1510.67) and the minimum number of seeds (174.67) were recorded in wild accessions SM-22 (*S. mammosam*) followed by SM-30 (*S. insanum*; 211).

4.2.2 INCIDENCE OF PESTS AND DISEASES

4.2.2.1 Brinjal fruit and shoot borer infestation

Brinjal shoot and fruit borer infestation in thirty genotypes was recorded and the percentage incidence was calculated. The findings are presented in Table 6. Most of the genotypes recorded high incidence of shoot and fruit borer infestation. The maximum incidence of 92.59% was recorded in SM-11 followed by 85.19% in three accessions *viz*., SM-3, SM-15 and SM-18. Accessions SM-25 showed comparatively lesser incidence (3.7%) of fruit and shoot borer followed by SM-12 (7.41%). Three wild relatives *viz*., SM-22 (*S. mammosam*), SM-29 (*S. gilo*) and SM-30 (*S. insanum*) recorded the complete absence of fruit and shoot borer during the entire period of study.

Table 5. Mean performance of 22 characters in 30 brinjal genotypes

	PH (cm)	PB (cm)	NPB	LL (cm)	LW (cm)	PL (mm)	DFF	D50 %F	NF/I	NLS	NMS	RSL (mm)	FL (cm)	FD (cm)	RCL [%]	FPL (mm)	FW [g]	NAF	NFM	NF/P	FY/P [g]	NS/P
SM-1	64.51	67.45	6.73	16.64	9.23	42.5	44.33	50.67	5.00	**3.70**	1.13	1.37	12.48	3.98	11.80 (0.12)	34.5	71.67	14.00	31.00	14.00	765.33	715
SM-2 (W)	67.24	63.87	**4.73**	**18.72**	**17.09**	77.5	43.00	48.67	**2.00**	**1.07**	**0.80**	**1.27**	**4.52**	**5.48**	**77.67 (0.89)**	**40.8**	**67.89**	16.00	32.00	**7.11**	458.67	486.33
SM-3	65.52	63.95	5.67	16.06	13.23	69.3	43.33	48.33	2.80	1.47	0.93	1.13	5.47	4.46	11.27 (0.11)	43.6	37.67	12.67	**28.33**	9.11	565.33	1019.3
SM-4	**77.22**	84.10	9.40	18.47	8.83	53.6	44.33	51.33	3.00	1.67	1.27	**2.77**	11.27	3.41	21.67 (0.22)	43.8	100.0	17.00	30.67	8.67	770.67	681
SM-5	71.67	85.15	7.73	19.71	12.38	67.0	45.33	50.67	1.67	1.07	0.80	1.17	15.48	5.58	10.20 (0.10)	44.3	84.44	11.33	31.00	9.33	770.33	656
SM-6	66.37	62.42	5.13	13.88	11.38	34.8	44.00	48.67	1.17	1.00	0.33	1.17	8.19	6.47	20.87 (0.21)	19.7	95.00	16.00	39.00	9.00	902	907.67
SM-7	67.84	66.79	8.13	**21.58**	13.31	65.8	44.00	49.67	2.00	**0.87**	1.33	1.07	8.01	2.99	10.23 (0.10)	30.2	69.67	15.00	30.67	10.67	668.22	878
SM-8	70.11	86.28	6.67	15.82	9.92	46.5	45.33	51.33	2.73	1.33	0.67	1.00	10.00	4.42	10.17 (0.10)	38.1	88.33	17.33	31.33	11.67	1019.33	686
SM-9	**46.01**	70.43	7.93	15.73	11.72	55.0	44.67	49.67	2.13	0.93	0.93	1.00	**4.99**	4.02	10.27 (0.10)	**19.4**	62.00	15.33	30.67	9.33	592.33	939.33
SM-10	66.80	67.92	5.47	19.15	13.95	72.1	43.00	48.67	1.60	1.00	0.80	1.07	10.53	4.99	10.70 (0.11)	34.0	73.33	13.00	31.33	12.11	1285.67	642
SM-11	60.42	60.27	**4.73**	19.74	12.76	53.0	**42.67**	48.00	**1.00**	**0.87**	0.89	1.13	21.32	4.42	20.60 (0.21)	34.7	88.67	12.00	34.00	11.33	983	843.67
SM-12	53.78	61.91	6.73	16.66	13.68	**81.6**	44.33	50.33	2.20	1.47	0.87	0.93	5.12	3.02	22.03 (0.22)	31.2	**29.04**	12.00	32.67	11.45	**292.67**	492.67
SM-13	53.78	62.55	6.87	14.14	9.66	44.3	44.33	50.67	2.60	2.07	0.87	1.10	9.49	**2.71**	10.33 (0.10)	23.7	62.33	14.00	31.67	**7.67**	442.44	776.67
SM-14	71.33	**96.75**	8.67	19.40	13.69	47.5	44.67	51.00	2.00	1.07	0.80	1.20	9.14	8.01	20.53 (0.21)	44.4	79.00	**11.00**	33.00	12.00	905.33	993.67
SM-15	68.02	87.05	7.67	15.31	10.97	61.5	44.67	51.00	4.00	2.47	1.60	1.07	9.38	5.34	15.33 (0.15)	29.1	102.3	14.00	32.00	12.00	1144	614
SM-16	68.15	71.75	6.00	17.66	16.44	68.7	43.33	47.67	2.40	1.07	0.60	0.90	12.73	3.12	11.67 (0.12)	24.3	56.26	12.67	32.33	11.22	576.67	728
SM-17	63.86	68.71	5.80	18.66	14.68	56.2	43.67	48.33	3.60	1.87	1.47	1.03	11.98	3.45	10.63 (0.11)	41.6	72.22	13.33	32.33	13.67	867	785
SM-18	63.02	80.67	10.3	18.62	12.42	75.8	44.33	50.00	4.27	2.67	**1.80**	1.00	15.17	3.90	10.90 (0.11)	40.8	97.48	13.33	31.33	12.89	1185.56	**477.67**
SM-19	56.97	**58.66**	7.60	18.42	13.37	67.6	44.67	50.00	4.53	3.00	1.67	0.90	7.96	6.90	20.63 (0.21)	44.3	68.67	**11.00**	34.33	**15.11**	996.78	1067.3
SM-20	68.44	92.41	8.80	20.68	12.23	65.1	43.33	48.67	2.53	0.93	0.80	1.03	7.99	3.42	**22.30 (0.22)**	35.0	92.67	14.67	34.00	13.00	1275.67	629.67

	PH (cm)	PB (cm)	NPB	LL (cm)	LW (cm)	PL (mm)	DFF	D50 %F	NF/I	NLS	NMS	RSL (mm)	FL (cm)	FD (cm)	RCL [%]	FPL (mm)	FW [g]	NAF	NFM	NF/P	FY/P [g]	NS/P
SM-21	71.60	68.30	6.07	20.14	**16.78**	47.9	44.33	49.33	**5.33**	2.83	1.53	1.07	11.47	2.78	**10.13 (0.10)**	38.6	62.00	15.00	32.00	12.67	799.55	996.67
SM-22 (W)	**86.46**	**74.45**	5.73	12.84	15.51	**96.5**	55.67	64.00	4.00	**3.67**	0.00	0.96	4.40	3.13	12.67 (0.13)	19.5	20.22	31.00	31.67	**26.67**	519.45	174.67
SM-23	59.81	85.57	9.13	16.72	11.51	66.1	43.33	**43.33**	2.80	1.13	1.27	1.10	14.96	4.82	10.60 (0.11)	54.2	108.0	16.67	33.33	12.67	1434.11	**1591.33**
SM-24	69.84	73.24	4.47	19.67	13.41	67.0	43.67	50.00	2.07	1.07	1.27	1.00	**18.03**	5.46	11.63 (0.12)	44.9	99.67	**11.00**	30.67	11.67	1233.67	890.67
SM-25	47.00	67.55	6.73	**13.54**	**8.34**	**33.4**	**49.33**	**53.67**	2.77	1.67	**0.00**	**0.87**	5.53	4.40	10.63 (0.11)	27.4	96.33	**18.00**	45.00	11.22	1041	1222
SM-26	57.93	78.23	**11.4**	17.74	11.34	64.3	45.00	50.33	2.93	1.87	0.87	1.00	8.36	4.59	11.10 (0.11)	20.8	67.33	13.67	45.33	8.22	614.11	591.67
SM-27	67.25	85.49	7.67	19.73	14.24	57.4	44.33	50.33	3.73	1.93	1.40	1.60	11.45	**10.5**	20.13 (0.20)	**59.4**	**192.7**	12.67	**46.00**	11.67	**2146.44**	1050
SM-28 (W)	64.49	65.09	7.27	11.61	9.29	25.1	46.33	54.33	5.07	2.70	**1.73**	1.23	4.17	3.66	21.10 (0.21)	31.9	56.85	14.33	**31.33**	18.89	**1072.89**	**1510.67**
SM-29 (W)	74.33	65.97	**8.67**	17.77	16.50	69.5	**60.33**	**71.33**	**6.33**	3.00	1.07	**0.93**	2.75	2.68	**11.67 (0.12)**	17.2	11.43	**35.67**	**53.67**	18.22	199.22	261
SM-30 (W)	**28.89**	**58.37**	8.13	**6.62**	**3.54**	**16.1**	52.67	59.67	**2.00**	**1.07**	**0.80**	1.10	**2.00**	**2.01**	21.50 (0.22)	**7.7**	**4.61**	**11.67**	49.33	8.22	**63.33**	**211**
Mean	63.96	72.71	7.2	17.05	12.38	58.29	45.54	51.32	3.01	1.75	1.01	1.14	9.48	4.47	16.7 (0.17)	33.97	73.93	15.18	34.73	12.05	853.03	783.96
CV (%)	2.04	2.91	3.32	0.51	0.75	1.55	1.34	1.04	7.75	16.3	18.2	11.7	1.12	1.45	7.36	3.12	3.99	7.69	3.84	4.86	4.4	5.38
CD	2.13	3.46	0.39	0.14	0.15	0.15	0.99	0.87	0.38	0.47	0.3	0.21	0.17	0.11	2.01	0.17	4.82	1.91	2.18	0.96	61.28	68.96

Transformed values are given in the parenthesis

PH = Plant height (cm), PB = Plant breadth (cm), NPB = Number of primary branches, LL = Leaf blade length (cm), LW = Leaf blade width (cm), PL = Petiole length (mm), DFF = Days to first flowering, D50%F = Days to 50 per cent flowering, NF/I = Number of flowers per inflorescence, NLS = Number of long styled flowers, NMS = Number of medium styled flowers, RSL = Relative style length (mm), FL= Fruit length (cm), FD = Fruit diameter (cm), RCL = Relative fruit calyx length (%), FPL = Fruit pedicel length (mm), FW = Fruit weight, NAF = Number of days from anthesis to fruit set, NFM = Number of days from fruit set to maturity, NF/P = Number of fruit/plant, FY/P = Fruit yield /plant, NS/P = Number of seeds/fruit, W-Wild relatives.

4.2.2.2 Phomopsis blight incidence

No incidence of phomopsis blight was observed in any of the accessions during the entire period of study.

4.2.2.3 Bacterial wilt

Among the 30 accessions only two accessions showed incidence of bacterial wilt (SM-9 and SM-13).

4.2.2.4 Little leaf incidence

There was no incidence of little leaf in any of the thirty accessions studied.

4.2.2.5 Other pest and diseases

Incidence of damping-off was observed in all genotypes except in wild accession SM-22 (*S. mammosam*) at the seedling stage.

Severe infestation of leaf hopper was observed in seven accessions (SM-8, SM-10, SM-11, SM-23, SM-24, SM-26 and SM-28) in the field, as seen in Table 6. The maximum infestation of 96.29% was recorded in SM-24 followed by 88.89% in SM-11. The minimum incidence of 3.7% was recorded in SM-26.

4.2.3 GENETIC VARIABILITY PARAMETERS

Genetic parameters *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), genetic advance and genetic gain (genetic advance expressed as per cent of mean) estimated for 22 characters are presented in Table 7.

4.2.3.1 Genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV)

All the characters recorded slightly higher value of PCV than GCV. Maximum GCV and PCV were observed for relative fruit calyx length (84.07; 84.45) followed by fruit yield per plant (48.68; 48.88). Minimum GCV and PCV values were

Table 6. Percentage of incidence of pests and diseases in 30 genotypes

Accessions	Shoot and fruit borer infestation (%)	Bacterial wilt (%)	Leafhopper (%)
SM-1	70.37	0.00	0.00
SM-2	25.92	0.00	0.00
SM-3	85.19	0.00	0.00
SM-4	25.92	0.00	0.00
SM-5	51.85	0.00	0.00
SM-6	70.37	0.00	0.00
SM-7	40.74	0.00	0.00
SM-8	59.26	0.00	48.15
SM-9	48.15	18.52	0.00
SM-10	81.48	0.00	70.37
SM-11	92.59	0.00	88.89
SM-12	7.41	0.00	0.00
SM-13	81.48	62.97	0.00
SM-14	62.97	0.00	0.00
SM-15	85.19	0.00	0.00
SM-16	81.48	0.00	0.00
SM-17	37.04	0.00	0.00
SM-18	85.19	0.00	0.00
SM-19	48.15	0.00	0.00
SM-20	62.97	0.00	0.00
SM-21	51.85	0.00	0.00
SM-22	0.00	0.00	0.00
SM-23	70.37	0.00	40.74
SM-24	81.48	0.00	96.29
SM-25	3.70	0.00	0.00
SM-26	51.85	0.00	3.70
SM-27	48.14	0.00	0.00
SM-28	29.63	0.00	62.97
SM-29	0.00	0.00	0.00
SM-30	0.00	0.00	0.00

recorded for days to first flowering followed by days to 50% flowering. High GCV and PCV of above 20% were recorded for flower and fruit characters. Moderate (10-20%) GCV and PCV values were recorded for plant height, plant breadth, days to 50% flowering, leaf blade length and number of days from fruit set to maturity. The character days to first flowering recorded low GCV and PCV (8.65; 8.75).

4.1.1.1 Heritability and genetic advance

Broad sense heritability was estimated for all the 22 characters considered and the result is presented in Table 7. Almost all the characters showed more than 90% heritability. The broad-sense heritability ranged from 85.3% to 99.9%.

High (>20%) genetic gain that is genetic advance expressed as percentage of mean was recorded for plant characters such as plant height (34.05), plant breadth (29.73), number of primary branches (47.706), leaf blade length (38.154), leaf blade width (48.67) and petiole length (60.75).

The flower characters such as days to 50% flowering (20.92), number of flowers per inflorescence (88.02), number of long-styled flowers (94.911), number of medium- styled flowers (83.501) and relative style length (80.895) showed high genetic gain.

Similarly higher value of genetic gain was exhibited by fruit characters such as fruit length (99.65), fruit diameter (81.406), relative fruit calyx length (153.191), fruit pedicel length (70.32), fruit weight (97.591), number of days from anthesis to fruit set (70.231), number of days from fruit set to maturity (36.73), number of fruits per plant (65.479), fruit yield per plant (99.869) and number of seeds per fruit (85.32). Days to first flowering (17.601) recorded moderate genetic gain.

All characters recorded high heritability coupled with high genetic gain except days to 50% flowering (97.7; 17.60), which had high heritability along with moderate genetic gain.

Table 7. Genetic parameters of 22 quantitative characters in 30 brinjal genotypes

Sl. no	Characters	Mean	Coefficient of variation		Heritability (%)	Genetic advance	GA as per cent of mean
			PCV (%)	GCV (%)			
1	Plant height	64.51	16.77	16.65	98.5	21.77	34.05
2	Plant breadth	67.45	14.99	14.71	96.2	21.62	29.73
3	Number of primary branches	6.73	23.62	23.39	98	3.44	47.71
4	Leaf blade length	16.64	18.54	18.53	99.9	6.50	38.15
5	Leaf blade width	9.23	23.65	23.64	99.9	6.03	48.67
6	Petiole length	42.5	29.57	29.53	99.7	3.54	60.75
7	Days to first flowering	45.54	8.75	8.65	97.7	8.02	17.60
8	Days to 50 per cent flowering	51.32	10.26	10.21	99	10.74	20.92
9	Number of flowers per inflorescence	3.01	44.09	43.40	96.9	2.65	88.02
10	Number of long styled flowers	1.75	51.23	48.58	89.9	1.66	94.91
11	Number of medium styled flowers	1.01	47.5	43.88	85.3	0.84	83.50
12	Relative style length	1.08	42.46	40.84	92.5	0.87	80.9
13	Fruit length	9.48	48.4	48.39	99.9	9.45	99.65
14	Fruit diameter	4.47	39.57	39.54	99.9	3.64	81.41
15	Relative fruit calyx length	16.70	84.45	84.07	99	25.58	153.19
16	Fruit pedicel length	34.0	34.42	34.28	99.1	2.39	70.32
17	Fruit weight	73.93	47.71	47.54	99.3	72.15	97.59
18	Number of days from anthesis to fruit set	15.18	35.75	34.91	95	10.66	70.23
19	Number of days from fruit set to maturity	34.73	18.62	18.22	96	12.76	36.73
20	Number of fruit/plant	12.05	32.51	32.15	98	7.89	65.48
21	Fruit yield /plant	853.03	48.88	48.68	99	851.91	99.87
22	Number of seeds/fruit	783.96	42.11	41.76	98	668.87	85.32

4.1.2 CORRELATION ANALYSIS

Genotypic and phenotypic correlation study was conducted using 22 quantitative characters. The association between all these characters in all possible combinations was worked out and the result is presented in Table 8. Majority of characters showed higher value for genotypic correlation than phenotypic correlation.

The dependent variable fruit yield per plant showed significant positive genotypic and phenotypic association with plant height (rg 0.223, rp 0.222), plant width (rg 0.502, rp 0.492), leaf blade length (rg 0.371, rp 0.370), number of long-styled flowers per inflorescence (rg 0.326, rp 0.297), fruit length (rg 0.498, rp 0.495), fruit diameter (rg 0.665, rp 0.662), fruit pedicel length (rg 0.683, rp 0.679), fruit weight (rg 0.890, rp 0.883), number of seeds per fruit (rg 0.532, rp 0.526) and negative association with days to first flowering (rg -0.430, rp -0.422), days to 50% flowering (rg -0.443, rp -0.438) and number of days from anthesis to fruit set (rg -0.289, rp -0.284).

The association among all independent variables such as all vegetative, flowering and fruiting characters are examined in detail.

Among the vegetative characters, plant height had significant positive genotypic and phenotypic correlation with plant width (rg 0.424, rp 0.424), leaf blade length (rg 0.510, rp 0.506), leaf blade width (rg 0.6, rp 0.595), petiole length (rg 0.505, rp 0.502), number of flowers per inflorescence (rg 0.251, rp 0.247), number of medium-styled flowers per inflorescence (rg 0.266, rp 0.251), fruit length (rg 0.238, rp 0.236), fruit pedicel length (rg 0.354, rp 0.349), number of days from anthesis to fruit set (rg 0.4, rp 0.377) and number of fruits per plant (rg 0.458, rp 0.446). However, it showed negative genotypic and phenotypic correlation (rg -0.343, rp -0.331) with number of days from fruit set to maturity.

Plant breadth had significant positive genotypic and phenotypic association with number of primary branches (rg 0.489, rp 0.480), leaf blade length (rg 0.343, rp 0.336), fruit length (rg 0.279, rp 0.273), fruit diameter (rg 0.366, rp 0.359), fruit pedicel length (rg 0.438, rp 0.426) and fruit weight (rg 0.530, rp 0.516). However, it

showed significant positive correlation at genotypic level only (rg 0.215) with relative style length.

The characters such as number of flowers per inflorescence (rg 0.257, rp 0.246), number of long-styled flowers per inflorescence (rg 0.299, rp 0.274), relative style length (rg 0.233, rp 0.217) and number of days from fruit set to maturity (rg 0.311, rp 0.302) showed significant and positive genotypic and phenotypic correlation with the number of primary branches. Leaf blade width (rg -0.304, rp -0.302) and relative fruit calyx length (rg -0.246, rp -0.237) had negative correlation with number of primary branches.

Leaf blade length had significant positive association with leaf blade width (rg 0.644, rp 0.644), petiole length (rg 0.508, rp 0.507), number of long-styled flowers per inflorescence (rg 0.319, rp 0.292), relative style length (rg 0.263, rp 0.253), fruit length (rg 0.540, rp 0.540), fruit diameter (rg 0.301, rp 0.301), fruit pedicel length (rg 0.599, rp 0.597) and fruit weight (rg 0.432, rp 0.430). Days to first flowering (rg -0.458, rp -0.452), days to 50% flowering (rg -0.404, rp -0.402) and number of days from fruit set to maturity (rg - 0.296, rp -0.290) had negative significant association with leaf blade length.

Leaf blade width had positive significant correlation with petiole length (rg 0.708, rp 0.706), relative fruit calyx length (rg 0.213, rp 0.211), fruit pedicel length (rg 0.278, rp 0.276), number of days from anthesis to fruit set (rg 0.247, rp 0.242) and number of fruits per plant (rg 0.277, rp 0.274).

Leaf petiole length showed positive significant association with fruit pedicel length (rg 0.230, rp 0.229), number of days from anthesis to fruit set (rg 0.265, rp 0.259), number of fruits per plant (rg 0.286, rp 0.283). The number of seeds per fruit (rg -0.347, rp -0.345) and number of days from fruit set to maturity (rg -0.287, rp -0.281) showed negative correlation at genotypic and phenotypic level with leaf petiole length.

Number of days to first flowering showed significant positive correlation at genotypic and phenotypic level with number of days to 50% flowering (rg 0.975, rp 0.957), number of flowers per inflorescence (rg 0.447, rp 0.436), number of medium-

styled flowers per inflorescence (rg 0.445, rp 0.421), number of days from anthesis to fruit set (rg 0.824, rp 0.799), number of days from fruit set to maturity (rg 0.631, rp 0.609) and number of fruits per plant (rg 0.559, rp 0.545). It showed negative significant correlation at genotypic and phenotypic level with number of long-styled flowers per inflorescence (rg -0.304, rp - 0.277), relative style length (rg -0.392, rp - 0.369), fruit length (rg -0.532, rp -0.525), fruit diameter (rg -0.312, rp -0.309), fruit pedicel length (rg -0.539, rp -0.536), fruit weight (rg - 0.527, rp -0.521) and number of seeds per fruit (rg -0.457, rp -0.448).

Number of flowers per inflorescence (rg 0.476, rp 0.466), number of medium-styled flowers per inflorescence (rg 0.487, rp 0.456), number of days from anthesis to fruit set (rg 0.791, rp 0.766), number of days from fruit set to maturity (rg 0.571, rp 0.557) and number of fruits per plant (rg 0.557, rp 0.546) showed positive and significant association with days to 50% flowering. It showed significant negative association with relative style length (rg -0.279, rp -0.271), fruit length (rg -0.535, rp - 0.532), fruit diameter (rg -0.297, rp -0.295), fruit pedicel length (rg -0.537, rp -0.531), fruit weight (rg -0.529, rp -0.523) and number of seeds per fruit (rg -0.529, rp -0.519) at genotypic and phenotypic level and number of long-styled flowers per inflorescence showed negative significant association at genotypic (rg -0.228) level only.

Number of flowers per inflorescence had positive significant association with number of medium-styled flowers per inflorescence (rg 0.897, rp 0.851), number of long- styled flowers per inflorescence (rg 0.490, rp 0.459), number of days from anthesis to fruit set (rg 0.471, rp 0.451) and number of fruits per plant (rg 0.599, rp 0.582). It had negative significant association (rg -0.218, rp -0.215) with fruit length.

Number of long-styled flowers per inflorescence had positive significant association with number of medium-styled flowers per inflorescence (rg 0.280, rp 0.272), relative style length (rg 0.481, rp 0.423), fruit length (rg 0.274, rp 0.253), fruit pedicel length (rg 0.464, rp 0.420), fruit weight (rg 0.254, rp 0.237), number of fruits per plant (rg 0.682, rp 0.634) and number of seeds per fruit (rg 0.284, rp 0.259). It had negative significant correlation with number of days from anthesis to fruit set (rg - 0.310, rp -0.298) at genotypic and phenotypic level. The number of medium-styled

flowers per inflorescence showed significant positive genotypic and phenotypic correlation with number of days from anthesis to fruit set (rg 0.451, rp 0.425).

The characters like fruit length (rg 0.241, rp 0.234), fruit pedicel length (rg 0.387, rp 0.373) and fruit weight (rg 0.339, rp 0.323) showed positive significant association at genotypic and phenotypic level with relative style length. It had significant positive correlation with relative fruit calyx length (rg 0.211) at genotypic level only. Number of days from anthesis to fruit set (rg -0.302, rp -0.290) and number of fruits per plant (rg - 0.441, rp -0.418) had negative significant correlation with relative style length.

Fruit length had significant positive genotypic and phenotypic correlation with fruit diameter (rg 0.226, rp 0.226), fruit pedicel length (rg 0.533, rp 0.530), fruit weight (rg 0.551, rp 0.549) and number of seeds per fruit (rg 0.225, rp 0.223). It had significant negative genotypic and phenotypic association with relative fruit calyx length (rg -0.242, rp-0.238), number of days from anthesis to fruit set (rg -0.409, rp -0.399) and number of days from fruit set to maturity (rg -0.356, rp -0.348).

Fruit diameter had significant positive correlation with fruit pedicel length (rg 0.584, rp 0.582), fruit weight (rg 0.708, rp 0.705), fruit yield per plant (rg 0.665, rp 0.662) and number of seeds per fruit (rg 0.354, rp 0.350). Number of days from anthesis to fruit set (rg -0.308, rp -0.300) showed significant negative genotypic and phenotypic correlation with fruit diameter.

Relative fruit calyx length showed a negative significant association with number of fruits per plants (rg -0.246, rp -0.239). The fruit pedicel length had significant positive genotypic and phenotypic association with fruit weight (rg 0.668, rp 0.664) and number of seeds per fruit (rg 0.491, rp 0.484). Number of days from anthesis to fruit set (rg -0.374, rp-0.361) and number of days from fruit set to maturity (rg -0.379, rp -0.367) showed significant negative genotypic and phenotypic correlation with fruit pedicel length. Fruit weight had significant positive genotypic and phenotypic correlation with number of seeds per fruit (rg 0.454, rp 0.447). It had significant negative association with number of days from anthesis to fruit set (rg -0.360, rp -0.345) and number of fruits per plant (rg -0.246, rp-0.245) at both genotypic and phenotypic level.

Number of days from anthesis to fruit set had significant negative genotypic and phenotypic correlation with number of seeds per fruit (rg -0.355, rp -0.349). It had positive significant correlation with number of days from fruit set to maturity (rg 0.372, rp 0.354) and number of fruits per plant (rg 0.618, rp 0.596). Number of days from fruit set to maturity had significant negative genotypic correlation (rg -0.217) with number of seeds per fruit.

4.1.1 PATH ANALYSIS

The correlation analysis revealed that the dependent variable fruit yield per plant had significant genotypic correlation with majority of the independent variables such as growth, flowering and fruiting characters. Hence to get a clear picture of cause and effect relationship the genotypic correlation were partitioned into direct and indirect effect using path coefficient analysis. The results are presented in Table 9.

The diagonal values in genotypic path matrix gives the direct effect of 21 characters on fruit yield per plant. The residual effect of path analysis in thirty accessions of brinjal for 21 quantitative characters is 0.04747.

A detailed study of path coefficient analysis in brinjal showed that the highest positive direct effect on fruit yield per plant was exhibited by days to first flowering (1.919) followed by fruit weight (0.806). However, only fruit weight had positive significant genotypic correlation with yield, whereas days to first flowering had negative significant genotypic correlation with yield.

The characters like leaf length (0.414), number of long-styled flowers (0.366), fruit weight (0.806) and number of fruits per plant (0.493) showed high positive direct effect, of which only leaf length and fruit weight showed significant positive correlation indicating true association with yield. Number of primary branches (-0.531), leaf width (-0.42), fruit length (-0.301), fruit pedicel length (-0.36) and number of days from anthesis to fruit set (- 0.475) showed high negative direct effect. Among these characters, only number of days from anthesis to fruit set had shown significant negative correlation with yield (rg -0.289). The characters fruit length and

Table 8. Genotypic and phenotypic correlation of 22 quantitative characters in 30 brinjal genotypes

		A	B	C	D	E	F	G	H	I	J	K
A	Rg	1										
	Rp	1										
B	Rg	0.424**	1									
	Rp	0.424**	1									
C	Rg	-0.142	0.489**	1								
	Rp	-0.136	0.480**	1								
D	Rg	0.510**	0.343**	0.039	1							
	Rp	0.506**	0.336**	0.038	1							
E	Rg	0.600**	0.022	-0.304**	0.644**	1						
	Rp	0.595**	0.021	-0.302**	0.644**	1						
F	Rg	0.505**	0.165	-0.022	0.508**	0.708**	1					
	Rp	0.502**	0.162	-0.020	0.507**	0.706**	1					
G	Rg	0.029	-0.154	0.148	-0.458**	-0.051	0.000	1				
	Rp	0.030	-0.148	0.142	-0.452**	-0.050	0.000	1				
H	Rg	0.107	-0.161	0.116	-0.404**	-0.029	0.000	0.975**	1			
	Rp	0.107	-0.161	0.116	-0.402**	-0.029	0.000	0.957**	1			
I	Rg	0.251*	-0.016	0.257*	-0.051	0.154	0.023	0.447**	0.476**	1		
	Rp	0.247*	-0.016	0.246*	-0.050	0.151	0.023	0.436**	0.466**	1		
J	Rg	0.032	0.065	0.299**	0.319**	0.062	-0.016	-0.304**	-0.228*	0.490**	1	
	Rp	0.038	0.061	0.274**	0.292**	0.057	-0.017	-0.277**	-0.204	0.459**	1	
K	Rg	0.266*	-0.121	0.120	-0.178	0.081	0.090	0.445**	0.487**	0.897**	0.280**	1
	Rp	0.251*	-0.115	0.115	-0.168	0.075	0.090	0.421**	0.456**	0.851**	0.272**	1
L	Rg	0.153	0.215*	0.233*	0.263*	-0.168	-0.192	-0.392**	-0.279**	-0.042	0.481**	-0.169
	Rp	0.143	0.204	0.217*	0.253*	-0.161	-0.187	-0.369**	-0.271**	-0.052	0.423**	-0.166
M	Rg	0.238*	0.279**	-0.122	0.540**	0.127	0.110	-0.532**	-0.535**	-0.218*	0.274**	-0.176
	Rp	0.236*	0.273**	-0.121	0.540**	0.127	0.110	-0.525**	-0.532**	-0.215*	0.253*	-0.169
N	Rg	0.166	0.366**	-0.034	0.301**	0.175	0.032	-0.312**	-0.297**	-0.150	0.091	-0.130
	Rp	0.165	0.359**	-0.033	0.301**	0.175	0.032	-0.309**	-0.295**	-0.149	0.082	-0.127
O	Rg	0.016	-0.139	-0.246*	0.058	0.213*	0.101	-0.139	-0.086	-0.192	-0.053	-0.189
	Rp	0.013	-0.140	-0.237*	0.057	0.211*	0.099	-0.136	-0.089	-0.181	-0.063	-0.188
P	Rg	0.354**	0.438**	-0.020	0.599**	0.278**	0.230*	-0.539**	-0.537**	0.030	0.464**	-0.075
	Rp	0.349**	0.426**	-0.025	0.597**	0.276**	0.229*	-0.536**	-0.531**	0.030	0.420**	-0.074
Q	Rg	0.177	0.530**	0.089	0.432**	-0.005	-0.065	-0.527**	-0.529**	-0.135	0.254*	-0.190
	Rp	0.174	0.516**	0.086	0.430**	-0.004	-0.065	-0.521**	-0.523**	-0.132	0.237*	-0.180
R	Rg	0.400**	-0.031	0.059	-0.167	0.247*	0.265*	0.824**	0.791**	0.471**	-0.310**	0.451**
	Rp	0.377**	-0.033	0.052	-0.163	0.242*	0.259*	0.799**	0.766**	0.451**	-0.298**	0.425**
S	Rg	-0.343**	-0.130	0.311**	-0.296**	-0.186	-0.287**	0.631**	0.571**	0.196	-0.204	0.081
	Rp	-0.331**	-0.117	0.302**	-0.290**	-0.181	-0.281**	0.609**	0.557**	0.189	-0.187	0.073
T	Rg	0.458**	0.027	-0.065	-0.122	0.277**	0.286**	0.559**	0.557**	0.599**	0.682**	0.011
	Rp	0.446**	0.025	-0.065	-0.119	0.274**	0.283**	0.545**	0.546**	0.582**	0.634**	0.003
U	Rg	0.223*	0.502**	0.037	0.371**	0.054	-0.003	-0.430**	-0.443**	0.020	0.326**	-0.057
	Rp	0.222*	0.492**	0.036	0.370**	0.054	-0.005	-0.422**	-0.438**	0.022	0.297**	-0.054
V	Rg	-0.101	0.056	-0.040	0.093	-0.089	-0.347**	-0.457**	-0.529**	-0.000	0.284**	-0.141
	Rp	-0.100	0.055	-0.041	0.092	-0.088	-0.345**	-0.448**	-0.519**	0.002	0.259*	-0.137

		L	M	N	O	P	Q	R	S	T	U	V
L	Rg	1										
	Rp	1										
M	Rg	0.241*	1									
	Rp	0.234*	1									
N	Rg	0.167	0.226*	1								
	Rp	0.162	0.226*	1								
O	Rg	0.211*	-0.242*	0.202	1							
	Rp	0.199	-0.238*	0.199	1							
P	Rg	0.387**	0.533**	0.584**	0.127	1						
	Rp	0.373**	0.530**	0.582**	0.125	1						
Q	Rg	0.339**	0.551**	0.708**	0.021	0.668**	1					
	Rp	0.323**	0.549**	0.705**	0.021	0.664**	1					
R	Rg	-0.302**	-0.409**	-0.308**	-0.052	-0.374**	-0.360**	1				
	Rp	-0.290**	-0.399**	-0.300**	-0.045	-0.361**	-0.345**	1				
S	Rg	-0.153	-0.356**	0.083	-0.025	-0.379**	-0.060	0.372**	1			
	Rp	-0.149	-0.348**	0.079	-0.020	-0.367**	-0.059	0.354**	1			
T	Rg	-0.441**	-0.161	-0.125	-0.246*	-0.078	-0.246*	0.618**	-0.001	1		
	Rp	-0.418**	-0.160	-0.124	-0.239*	-0.076	-0.245*	0.596**	0.006	1		
U	Rg	0.143	0.498**	0.665**	-0.131	0.683**	0.890**	-0.289**	-0.099	0.072	1	
	Rp	0.134	0.495**	0.662**	-0.126	0.679**	0.883**	-0.284**	-0.092	0.070	1	
V	Rg	0.079	0.225*	0.354**	-0.151	0.491**	0.454**	-0.355**	-0.217*	-0.083	0.532**	1
	Rp	0.084	0.223*	0.350**	-0.148	0.484**	0.447**	-0.349**	-0.205	-0.077	0.526**	1

** Significance at 1% level
* significant at 5% level

A = Plant height (cm), B = Plant breadth (cm), C = Number of primary branches, D = Leaf blade length (cm), E = Leaf blade width (cm), F = Petiole length (mm), G = Days to first flowering, H = Days to 50 per cent flowering, I = Number of flowers per inflorescence, J = Number of long-styled flowers/ inflorescence, K = Number of medium styled flowers/ inflorescence, L = Relative style length (mm), M = Fruit length (cm), N = Fruit diameter (cm), O = Relative fruit calyx length (%), P = Fruit pedicel length (mm), Q = Fruit weight (g), R = Number of days from anthesis to fruit set, S = Number of days from fruit set to maturity, T = Number of fruit/ plant, U = Fruit yield/ plant (g), V = Number of seeds/ fruit.

fruit pedicel length had shown positive genotypic correlation with yield. Number of primary branches and leaf width had insignificant genotypic correlation. Even though plant width (0.252) and petiole length (0.222) have moderate and positive direct effect, only plant width showed significant correlation (0.502) with fruit yield.

The low positive direct effect over yield was noticed for traits like plant height (0.161), relative style length (0.155) and number of days from fruit set to maturity (0.181). All the remaining traits except number of seeds per fruit had shown negligible direct effect as well as insignificant genotypic correlation with yield. Number of seeds per fruit had shown significant genotypic correlation (0.532) with yield despite negligible direct effect (0.084) on yield.

The indirect effect of all the 21 characters on fruit yield per plant through other characters were assessed.

Plant height had shown moderate positive indirect effect through leaf blade length (0.211) and number of fruits per plant (0.226), this resulted in its significant genotypic correlation with yield. However, plant height had low indirect effect via some characters and negligible indirect effect via remaining characters.

Plant breadth had high positive indirect effect through fruit weight (0.428) and moderate positive indirect effect through days to 50% flowering (0.292) resulted in its significant positive genotypic correlation with yield, even though it had a moderate direct effect over yield.

Number of branches per plant had moderate positive indirect effect through days to first flowering (0.284) and negative indirect effect through days to 50% flowering (-0.211). It had negligible indirect effect through most of the traits resulting in insignificant genotypic correlation with yield.

Leaf length had high positive indirect effect through days to 50% flowering (0.73) followed by fruit weight (0.349). This resulted in significant positive genotypic correlation with yield. Leaf width had shown moderate indirect effect through leaf blade length (0.267) and low indirect effect through some characters and negligible indirect effect through remaining characters. Hence the genotypic correlation was insignificant.

Petiole length had shown moderate positive indirect effect through leaf length (0.21) and moderate negative indirect effect through leaf blade width (-0.298), resulting in an insignificant correlation.

Days to first flowering had exhibited very high negative indirect effect through days to 50% flowering (-1.763) as well as high negative indirect effect through fruit weight (- 0.425) and number of days from anthesis to fruit set (-0.392). Which resulted in its significant negative genotypic correlation with yield despite having high direct effect over yield.

Days to 50% flowering had very high positive indirect effect through days to first flowering (1.871). But it had very high negative direct effect over yield as well as high negative indirect effect through fruit weight (-0.427) and number of days from anthesis to fruit set (-0.376). These led to its negative genotypic correlation with yield.

Number of flowers per inflorescence had high positive indirect effect through days to 50% flowering (0.858) and moderate positive indirect effect through number of fruits per plant (0.295). But this trait had negative indirect direct effect through days to 50% flowering (-0.86) and negative moderate indirect effect through number of days from anthesis to fruit set as well as low and negligible indirect effect through all other characters. Which resulted in an insignificant genotypic correlation with yield.

The number of long-styled flowers had high positive indirect effect via days to 50% flowering (0.412) and moderate positive indirect effect through fruit weight (0.205) leading to a significant genotypic correlation with yield.

Number of medium-styled flowers had high positive indirect effect through days to first flowering (0.854) and number of fruits per plant (0.336). But it had negative high indirect effect through days to 50% flowering (-0.881) and moderate indirect effect through number of days from anthesis to fruit set (-0.214), this resulted in its negative insignificant genotypic correlation.

Relative style length had high positive indirect effect via days to 50% flowering (0.504) and moderate positive indirect effect through fruit weight (0.273). but it had high

negative indirect effect via days to first flowering (-0.753) and moderate negative indirect effect through number of fruits per plant (-0.218) resulting in its insignificant genotypic correlation with yield.

Fruit length had high positive indirect effect through days to 50% flowering (0.967) followed by fruit weight (0.444) and moderate indirect effect through leaf blade length (0.224) resulting in its positive significant correlation with yield even though it had negative direct effect over yield.

Fruit diameter had high indirect effect through fruit weight (0.571) followed by days to 50% flowering (0.537) resulting in high genotypic correlation with yield.

Relative calyx length had moderate negative indirect effect through days to first flowering (-0.266) and negative direct effect with yield.

Fruit pedicel length had high positive indirect effect via days to 50% flowering (0.971) followed by fruit weight (0.539). Thus contributing to its significant positive genotypic correlation with yield.

Fruit weight had significant positive indirect effect via days to 50% flowering (0.957) and high direct effect indicating significant genotypic correlation with yield.

Number of days from anthesis to fruit set had very high positive indirect effect via days to first flowering (1.582) and very high negative indirect effect via days to 50% flowering (-1.431) resulting in negative genotypic correlation with yield.

Number of days from fruit set to maturity had very high indirect effect via days to first flowering (1.211) and days to 50% flowering (-1.033). This mutually cancels the indirect effect resulting in insignificant genotypic correlation.

Number of fruits per plant had very high indirect effect via days to first flowering (1.073) and days to 50% flowering (-1.008) as well as moderate negative indirect effect through number of days from anthesis to fruit set (-0.294), resulting in its insignificant genotypic correlation despite having high positive direct effect over fruit yield.

Table 9. Genotypic path coefficient analysis using 12 quantitative characters in 30 brinjal genotypes

	PH	PB	NPB	LL	LW	PL	DFF	D50%F	NF/I	NLS	NMS	RSL
PH	**0.161**	0.068	-0.023	0.082	0.096	0.081	0.005	0.017	0.04	0.005	0.043	0.025
PB	0.107	**0.252**	0.123	0.086	0.006	0.042	-0.039	-0.041	-0.004	0.016	-0.03	0.054
NPB	0.075	-0.259	**-0.531**	-0.021	0.162	0.012	-0.079	-0.062	-0.137	-0.159	-0.064	-0.123
LL	0.211	0.142	0.016	**0.414**	0.267	0.21	-0.19	-0.167	-0.021	0.132	-0.074	0.109
LW	-0.252	-0.009	0.128	-0.271	**-0.42**	-0.298	0.021	0.012	-0.065	-0.026	-0.034	0.071
PL	0.112	0.037	-0.005	0.113	0.157	**0.222**	0	0	0.005	-0.004	0.02	-0.043
DFF	0.056	-0.296	0.284	-0.879	-0.097	0	**1.919**	1.871	0.858	-0.583	0.854	-0.753
D50 %F	-0.194	0.292	-0.211	0.73	0.053	0	-1.763	**-1.809**	-0.86	0.412	-0.881	0.504
NF/I	-0.007	0.0004	-0.007	0.001	-0.004	0	-0.012	-0.013	**-0.026**	-0.013	-0.024	0.001
NLS	0.012	0.024	0.11	0.117	0.023	-0.006	-0.111	-0.084	0.18	**0.366**	0.103	0.176
NMS	0.002	-0.001	0.001	-0.001	0.001	0.001	0.003	0.003	0.005	0.002	**0.006**	-0.001
RSL	0.024	0.033	0.036	0.041	-0.026	-0.03	-0.061	-0.043	-0.007	0.074	-0.026	**0.155**
FL	-0.072	-0.084	0.037	-0.163	-0.038	-0.033	0.16	0.161	0.066	-0.082	0.053	-0.073
FD	0.009	0.02	-0.002	0.017	0.01	0.002	-0.017	-0.017	-0.008	0.005	-0.007	0.009
RCL	-0.001	0.005	0.008	-0.002	-0.007	-0.003	0.005	0.003	0.007	0.002	0.006	-0.007
FPL	-0.128	-0.158	0.007	-0.216	-0.1	-0.083	0.194	0.194	-0.011	-0.167	0.027	-0.14
FW	0.143	0.428	0.072	0.349	-0.004	-0.052	-0.425	-0.427	-0.109	0.205	-0.154	0.273
NAF	-0.19	0.015	-0.028	0.08	-0.118	-0.126	-0.392	-0.376	-0.224	0.147	-0.214	0.144
NFM	-0.062	-0.024	0.056	-0.054	-0.034	-0.052	0.114	0.103	0.036	-0.037	0.015	-0.028
NF/P	0.226	0.013	-0.032	-0.06	0.137	0.141	0.276	0.275	0.295	0.006	0.336	-0.218
NS/P	-0.009	0.005	-0.003	0.008	-0.008	-0.029	-0.038	-0.045	0	0.024	-0.012	0.007
R(G)	**0.223**	**0.502**	**0.037**	**0.371**	**0.054**	**-0.003**	**-0.43**	**-0.443**	**0.02**	**0.326**	**-0.057**	**0.143**

PH = Plant height (cm), PB = Plant breadth (cm), NPB = Number of primary branches, LL = Leaf blade length (cm), LW = Leaf blade width (cm), PL = Petiole length (mm), DFF = Days to first flowering, D50%F = Days to 50 per cent flowering, NF/I = Number of flowers per inflorescence, NLS= Number of long-styled flowers/ inflorescence, NMS = Number of medium styled flowers/ inflorescence, RSL = Relative style length (mm), FL = Fruit length (cm), FD = Fruit diameter (cm), RCL = Relative fruit calyx length (%), FPL = Fruit pedicel length (mm), FW = Fruit weight (g), NAF = Number of days from anthesis to fruit set, NFM= Number of days from fruit set to maturity, NF/P= Number of fruit/ plant, NS/P
= Number of seeds/ fruit, R(G)= Genotypic correlation with yield per plant

Table 9. Genotypic path coefficient analysis using 12 quantitative characters in 30 brinjal genotypes

	FL	FD	RCL	FPL	FW	NAF	NFM	NF/P	NS/P
PH	0.038	0.027	0.003	0.057	0.028	0.064	-0.055	0.073	-0.016
PB	0.07	0.092	-0.035	0.11	0.133	-0.008	-0.033	0.007	0.014
NPB	0.065	0.018	0.131	0.011	-0.047	-0.031	-0.165	0.034	0.021
LL	0.224	0.125	0.024	0.248	0.179	-0.069	-0.123	-0.05	0.039
LW	-0.054	-0.074	-0.09	-0.117	0.002	-0.104	0.078	-0.116	0.037
PL	0.024	0.007	0.023	0.051	-0.014	0.059	-0.064	0.063	-0.077
DFF	-1.02	-0.599	-0.266	-1.035	-1.012	1.582	1.211	1.073	-0.878
D50%F	0.967	0.537	0.156	0.971	0.957	-1.431	-1.033	-1.008	0.957
NF/I	0.006	0.004	0.005	-0.001	0.004	-0.012	-0.005	-0.016	0
NLS	0.1	0.033	-0.02	0.17	0.093	-0.114	-0.075	0.004	0.104
NMS	-0.001	-0.001	-0.001	0	-0.001	0.003	0.001	0.004	-0.001
RSL	0.037	0.026	0.033	0.06	0.052	-0.047	-0.024	-0.068	0.012
FL	**-0.301**	-0.068	0.073	-0.161	-0.166	0.123	0.107	0.049	-0.068
FD	0.013	**0.056**	0.011	0.033	0.04	-0.017	0.005	-0.007	0.02
RCL	0.008	-0.007	**-0.034**	-0.004	-0.001	0.002	0.001	0.008	0.005
FPL	-0.192	-0.211	-0.046	**-0.36**	-0.241	0.135	0.137	0.028	-0.177
FW	0.444	0.571	0.017	0.539	**0.806**	-0.291	-0.048	-0.198	0.366
NAF	0.194	0.147	0.025	0.178	0.171	**-0.475**	-0.177	-0.294	0.169
NFM	-0.064	0.015	-0.005	-0.069	-0.011	0.067	**0.181**	0	-0.039
NF/P	-0.08	-0.062	-0.121	-0.039	-0.121	0.305	-0.001	**0.493**	-0.041
NS/P	0.019	0.03	-0.013	0.041	0.038	-0.03	-0.018	-0.007	**0.084**
R(G)	**0.497**	**0.665**	**-0.131**	**0.683**	**0.89**	**-0.289**	**-0.099**	**0.072**	**0.532**

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PH = Plant height (cm), PB = Plant breadth (cm), NPB = Number of primary branches, LL = Leaf blade length (cm), LW = Leaf blade width (cm), PL = Petiole length (mm), DFF = Days to first flowering, D50%F = Days to 50 per cent flowering, NF/I = Number of flowers per inflorescence, NLS= Number of long-styled flowers/ inflorescence, NMS = Number of medium styled flowers/ inflorescence, RSL = Relative style length (mm), FL = Fruit length (cm), FD = Fruit diameter (cm), RCL = Relative fruit calyx length (%), FPL = Fruit pedicel length (mm), FW = Fruit weight (g), NAF = Number of days from anthesis to fruit set, NFM= Number of days from fruit set to maturity, NF/P= Number of fruit/ plant, NS/P = Number of seeds/ fruit, R(G)= Genotypic correlation with yield per plant

Number of seeds per fruit had high positive indirect effect via days to 50% flowering (0.957) and fruit weight (0.366) resulting in high genotypic correlation with yield.

4.1.2 DIVERSITY ANALYSIS

The diversity of thirty brinjal accessions was examined on the basis of 17 qualitative and 22 quantitative characters. The findings are presented in this section:

4.1.2.1 Diversity analysis based on 17 qualitative characters

The diversity of thirty brinjal genotypes was studied based on 17 qualitative characters using UPGMA method and the dendrogram was prepared. The clustering pattern and the cluster similarity/dissimilarity are examined in detail.

4.1.2.1.1 Clustering pattern based on qualitative characters

The clustering pattern of thirty brinjal genotypes are given in Table 10. The dendrogram developed through UPGMA method shows that there are three main clusters at a similarity coefficient of 1.5 (Fig.22). The similarity coefficient ranged from 0 to 2.5. Maximum number of accessions (26) are grouped under cluster I, followed by cluster II (SM-22, SM-15 and SM-11) and cluster III (SM-29).

4.1.2.1.2 Cluster similarity/dissimilarity analysis

The similarity and dissimilarity between the three clusters were studied with the help of a dendrogram (Fig.22) constructed using qualitative data and scoring data of qualitative characters. The findings are presented in Table 11.

The dendrogram shows three main clusters and several sub-clusters. Cluster I has maximum number of genotypes (26) with similarity for leaf colour (green), which differ from cluster II and cluster III with dark green leaf. The cluster I is subdivided into two based on plant growth habit, sub-cluster A has genotypes with prostrate growth habit (SM-25 and SM-30) and sub-cluster B had genotypes with upright and intermediate grown habit.

Table 10. Clustering pattern of seventeen qualitative characters of 30 brinjal genotypes (UPGMA method)

Clusters	Number of genotypes	Genotypes and place of collection
Cluster I	26	SM-1 (Malappuram)
		SM-4 (Malappuram)
		SM-10 (Kannur)
		SM-20 (Kozhikode)
		SM-23 (Kasaragod)
		SM-24 (Kasaragod)
		SM-14 (Wayanad)
		SM-27 (NBPGR)
		SM-18 (Malappuram)
		SM-5 (Malappuram)
		SM-16 (Malappuram)
		SM-21 (Malappuram)
		SM-13 (Malappuram)
		SM-17 (Malappuram)
		SM-7 (Kozhikode)
		SM-12 (Kannur)
		SM-26 (NBPGR)
		SM-2 (Kannur) **.w**
		SM-19 (Malappuram)
		SM-28 (NBPGR) **.w**
		SM-6 (Kozhikode)
		SM-8 (Malappuram)
		SM-9 (Kozhikode)
		SM-3 (Malappuram)
		SM-25 (NBPGR)
		SM-30 (NBPGR) **.w**
Cluster II	3	SM-11(Kannur)
		SM-15 (Kozhikode)
		SM-22 (Kasaragod) **.w**
Cluster III	1	SM-29 (NBPGR) **.w**

Cluster II has three genotypes *viz.*, SM-11, SM-15 and SM-22. The three genotypes shared similarity with respect to leaf blade colour (dark green), leaf blade lobing (strong), leaf blade tip angle (acute) and fruit colour at physiological ripening (yellow); hence they grouped under the same cluster. These three accessions were subdivided into two sub-cluster *viz.*, cluster A (SM-11 and SM-15) and cluster B (SM-22). SM-22 differs from all other accessions with respect to petiole colour (dark purple), corolla colour (blush violet), fruit colour at commercial ripening (yellow) and fruit position (horizontal).

The genotype *S. gilo* (SM-29) is placed singly in cluster III since it differs from other 29 accessions in terms of stem colour (dark purple) and fruit colour at physiological ripening (red).

4.2.6.1.2 Genetic diversity analysis based on 22 quantitative characters

The diversity of thirty brinjal genotypes was studied based on 22 quantitative characters using Mahalanobis D^2 statistics and the genotypes were grouped into eight clusters. The study also reveals the percentage of contribution of these characters towards total divergence, clustering pattern and intra-cluster and inter-cluster distance. The dendrogram and cluster diagram were prepared through the Tocher's method and Mahalanobis euclidean distance method respectively.

4.2.6.1.4 Clustering pattern based on quantitative character

The Mahalanobis D^2 statistics conducted in the morphological data of 30 brinjal accessions collected from five districts as well gene bank grouped them into 8 clusters (Table 12). Genotypes from different districts of North Kerala grouped into the same cluster, which indicates their close affinity.

Maximum number of accessions (22) were grouped under cluster I, followed by two accessions in cluster III (SM-25 and SM-28) and the remaining accessions grouped singly in cluster II, IV, V, VI, VII and VIII respectively.

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Table 11. Scoring data of qualitative characters in 30 brinjal genotypes

Treatment	PGH	SC	PC	LBC	LBL	LBTA	LP	CC	FC	FS	FFD	FAS	FCCR	FCPR	FP	L/B
SM-1	3	5	9	3	5	3	0	7	3	5	3	3	1	2	9	8
SM-2 *W	3	5	1	3	3	3	0	5	1	5	5	7	1	2	7	1
SM-3	3	5	3	3	5	5	0	7	5	3	9	7	1	2	9	5
SM-4	3	5	5	3	5	1	0	7	1	5	1	5	7	2	9	8
SM-5	3	5	1	3	5	1	0	5	1	3	1	3	2	2	9	8
SM-6	3	5	3	3	5	3	0	5	1	5	9	7	7	2	9	1
SM-7	3	3	1	3	7	5	0	3	1	5	3	5	2	2	9	8
SM-8	3	5	3	3	5	1	0	5	1	5	7	7	7	2	9	5
SM-9	3	3	1	3	5	7	0	5	1	5	3	7	7	2	9	3
SM-10	3	5	5	3	5	3	1	7	1	5	1	3	7	2	9	8
SM-11	5	5	5	5	7	3	3	5	3	5	9	5	7	2	9	8
SM-12	3	5	1	3	7	3	5	3	1	5	3	3	1	2	9	5
SM-13	3	5	1	3	5	3	0	7	3	5	5	5	1	2	9	8
SM-14	5	5	5	3	7	3	0	7	1	5	1	7	7	2	9	5
SM-15	3	7	5	5	7	3	0	5	1	7	7	7	7	2	9	5
SM-16	3	5	1	3	5	3	0	3	1	3	3	5	2	2	9	7
SM-17	3	5	1	3	5	5	0	3	5	5	3	3	1	2	9	8
SM-18	5	5	1	3	5	3	3	7	1	5	3	7	7	2	9	8
SM-19	3	5	1	3	5	5	0	7	1	3	3	5	1	2	9	5
SM-20	3	5	5	3	5	3	0	7	1	5	3	3	7	2	9	8

SM-21	3	5	1	3	5	1	0	3	5	3	1	3	7	2	9	8
SM-22*W	5	5	7	5	7	3	5	9	1	7	7	7	3	2	5	5
SM-23	3	5	3	3	5	3	3	5	1	5	3	3	7	2	9	8
SM-24	5	5	3	3	7	3	3	5	3	5	1	3	7	2	9	8
SM-25	7	5	1	3	5	5	5	7	1	5	3	5	1	2	9	5
SM-26	3	5	1	3	5	5	5	5	3	3	3	5	7	2	9	8
SM-27	5	5	3	3	7	3	0	7	1	3	1	7	1	2	9	7
SM-28*W	3	5	3	3	3	5	0	7	1	5	3	7	1	2	9	3
SM-29*W	3	9	5	5	7	5	0	3	1	5	1	7	1	3	7	5
SM-30*W	7	5	3	3	5	7	5	5	1	5	1	5	1	2	9	3

PGH = Plant growth habit, SC = Stem colour, PC = Leaf petiole colour, LBC = Leaf blade colour, LBL = Leaf blade lobing, LBTA= Leaf blade tip angle, LP = Leaf prickles, CC = Corolla colour, FC = Fruit curvature, FS = Fruit shape, FFD = Fruit flesh density, FAS = Fruit apex shape, FCCR = Fruit colour at commercial ripening, FCPR = Fruit colour at physiological ripening, FP = Fruit position, L/B = Fruit length/breadth ratio, *W = Wild type

All accessions from Malappuram *viz.*, SM-1, SM-3, SM-4, SM-5, SM-8, SM-13, SM-16, SM-17, SM-18, SM-19 and SM-21, accession from Wayanad (SM-14) and all accessions from Kozhikode *viz.*, SM-6, SM-7 SM-9, SM-15 and SM-20 were included in cluster I.

Out of three accessions collected from Kasargod, two *viz.*, SM-23 and SM-24 were grouped into cluster I and one into cluster VII (SM-22). Out of four accessions collected from Kannur two were included in cluster I, one in cluster II (SM-11) and one in cluster IV (SM-2). The *S. melongena* accessions collected from NBPGR fell in cluster I (SM-26), II (SM-25) and V (SM-27).

Detailed examination of the eight clusters revealed that all the five wild types *viz.*, SM-2 (*S. macrocarpon*), SM-22 (*S. mammosam*), SM-28 (*S. incanum*), SM-29 (*S. gilo*) and SM-30 (*S. insanum*) were placed in different clusters *viz.*, cluster IV, cluster VII, cluster III, cluster VI and cluster VIII respectively.

4.2.6.1.4 Intra-cluster and inter-cluster distance of thirty brinjal genotypes

The intra-cluster and inter-cluster distance of 30 genotypes are presented in Table 13. The diagonal value shows the intra-cluster distance which ranges from 0 to 3784.88. cluster I recorded maximum intra-cluster distance (3784.88) pointing out greater heterogeneity of genotypes within the cluster which was followed by cluster III (1643.19). The clusters II, IV, V, VI, VII and VIII are solitary clusters hence they had zero intra- cluster distance.

Inter-cluster distance recorded higher value than intra-cluster distances, which indicates the homogenous or heterogeneous nature of the accessions within the cluster and between the cluster.

The inter-cluster distance ranged from 4651.88 to 44564.7. The highest inter-cluster distance was recorded between cluster VIII and V (44564.7) followed by clusters VIII and II (41962), indicating a wide range of diversity between these clusters.

Table 12. Clustering pattern of quantitative characters of 30 brinjal genotypes

Clusters	Number of genotypes	Genotypes with their place of collection
Cluster 1	22	SM-3 (Malappuram)
		SM-12 (Kannur)
		SM-9 (Kozhikode)
		SM-26 (NBPGR)
		SM-20 (Kozhikode)
		SM-19 (Malappuram)
		SM-10 (Kannur)
		SM-15 (Kozhikode)
		SM-8 (Malappuram)
		SM-4 (Malappuram)
		SM-17 (Malappuram)
		SM-14 (Wayanad)
		SM-7 (Kozhikode)
		SM-18 (Malappuram)
		SM-5 (Malappuram)
		SM-16 (Malappuram)
		SM-23 (Kasaragod)
		SM-1 (Malappuram)
		SM-13 (Malappuram)
		SM-6 (Kozhikode)
		SM-21 (Malappuram)
		SM-24 (Kasaragod)
Cluster 2	1	SM-11 (Kannur)
Cluster 3	2	SM-25 (NBPGR)
		SM-28 (NBPGR) .W
Cluster 4	1	SM-2(Kannur) .W
Cluster 5	1	SM-27 (NBPGR)
Cluster 6	1	SM-29 (NBPGR) .W
Cluster 7	1	SM-22 (Kasaragod) .W
Cluster 8	1	SM-30 (NBPGR) .W

4.2.6.1.5 Cluster mean

The cluster mean values of 22 quantitative characters are presented in Table 14. Cluster VII with single genotype SM-22 (*S. mammosam*) had maximum mean value for plant height (86.46) and the minimum for the same was observed in cluster VIII with single genotype SM-30. In the case of plant width, maximum mean value was noted in cluster V (85.49) and least in VIII (58.37).

Cluster VI recorded highest number of primary branches (8.67) and cluster IV and II recorded minimum (4.73) for the same.

Cluster VIII (SM-30) recorded minimum value for leaf length (6.62), width (3.54) and petiole length (16.1). Maximum values for leaf blade length (19.74), leaf blade width (17.09) and petiole length (96.5) were recorded in cluster II, IV and VII respectively.

Early flowering as well as least number of flowers per inflorescence was recorded in cluster II (SM-11). The genotype SM-29 in cluster VI had shown maximum mean for days to first flowering, days to 50% flowering and number of flowers per inflorescence.

The maximum mean value for number of long-styled flowers was recorded in solitary cluster VII (3.67) having genotype SM-22 and that for medium-styled flowers was recorded in cluster V (1.4) with genotype SM-27. The mean value of relative style length ranged from 0.93 (cluster VI) to 1.6 (cluster V).

The maximum mean fruit length and fruit diameter were recorded in cluster II (21.32) and cluster V (10.5) respectively. The cluster VIII with genotype SM-30 recorded minimum fruit length (2) and diameter (2.01).

The single wild genotype SM-2 (*S. macrocarpon*) in Cluster IV recorded maximum mean value for relative calyx length (0.89) and the minimum for the same was recorded in cluster VI (0.12) having single wild accession SM-29 (*S. gilo*).

Cluster V with genotype SM-27 recorded maximum mean value for fruit pedicel length (59.4) and fruit weight (192.67). The minimum value for these characters were recorded in cluster VIII (7.7 and 4.61).

The highest cluster mean values for number of days from anthesis to fruit set (35.67) and from fruit set to maturity (53.67) were recorded in cluster VI with

Table 13. Intra and inter-cluster distance in 30 brinjal genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	**3784.88**	7792.36	8400.57	5740.69	9127.76	6658.72	7388.82	27419.6
Cluster 2		**0**	19333.07	14200.8	14143.1	15017.1	15475.5	**41962**
Cluster 3			**1643.19**	11709.7	17094.1	11594.6	7080.64	8671.7
Cluster 4				**0**	10500.3	4651.88	7265.34	33117.8
Cluster 5					**0**	15246.8	16289.4	**44564.7**
Cluster 6						**0**	5723.43	29839.5
Cluster 7							**0**	20382.2
Cluster 8								**0**

Where Diagonal value indicates intra-cluster distance

Table 14. Cluster mean values of 22 characters in 30 brinjal genotypes

	PH	PB	NPB	LL	LW	PL	DFF	D50%F	NF/I	NLS	NMS	RSL	FL	FD	RCL [%]	FPL	FW [g]	NAF	NFM	NF/P	FY/P [g]	NS/P
Cluster 1.	64.66	74.56	7.38	17.77	12.46	60.01	44.18	49.53	2.88	1.66	1.07	1.14	10.37	4.45	0.14	35.48	76.32	13.82	32.68	11.28	868.5	807.24
Cluster 2.	60.42	60.27	**4.73**	**19.74**	12.76	53	**42.67**	**48**	**1**	**0.87**	0.89	1.13	**21.32**	4.42	0.21	34.7	88.67	12	34	11.33	983	843.67
Cluster 3	55.75	66.32	7	12.58	8.815	29.25	47.83	54	3.92	2.19	0.87	1.05	4.85	4.03	0.16	29.65	76.59	16.17	38.17	15.06	1057	**1366.3**
Cluster 4	67.24	63.87	**4.73**	18.72	**17.09**	77.5	43	48.67	2	1.07	0.8	1.27	4.52	5.48	**0.89**	40.8	67.89	16	**32**	**7.11**	458.7	486.33
Cluster 5.	67.25	**85.49**	7.67	19.73	14.24	57.4	44.33	50.33	3.73	1.93	**1.4**	**1.6**	11.45	**10.5**	0.2	**59.4**	**192.7**	12.67	46	11.67	**2146**	1050
Cluster 6	74.33	65.97	**8.67**	17.77	16.5	69.5	**60.33**	**71.33**	**6.33**	3	1.07	**0.93**	2.75	2.68	**0.12**	17.2	11.43	**35.67**	**53.67**	18.22	199.2	261
Cluster 7	**86.46**	74.45	5.73	12.84	15.51	**96.5**	55.67	64	4	**3.67**	**0**	0.96	4.4	3.13	0.13	19.5	20.22	31	**31.67**	**26.67**	519.5	**174.67**
Cluster 8	**28.89**	**58.37**	8.13	**6.62**	**3.54**	**16.1**	52.67	59.67	2	1.07	0.8	1.1	**2**	**2.01**	0.22	**7.7**	**4.61**	**11.67**	49.33	8.22	**63.33**	211

PH = Plant height (cm), PB = Plant breadth (cm), NPB = Number of primary branches, LL = Leaf blade length (cm), LW = Leaf blade width (cm), PL = Petiole length (mm), DFF = Days to first flowering, D50%F = Days to 50 per cent flowering, NF/I = Number of flowers per inflorescence, NLS= Number of long-styled flowers/ inflorescence, NMS = Number of medium styled flowers/ inflorescence, RSL = Relative style length (mm), FL = Fruit length (cm), FD = Fruit diameter (cm), RCL = Relative fruit calyx length (%), FPL = Fruit pedicel length (mm), FW = Fruit weight (g), NAF = Number of days from anthesis to fruit set, NFM= Number of days from fruit set to maturity, NF/P= Number of fruit/ plant, NS/P = Number of seeds/ fruit, R(G)= Genotypic correlation with yield per plant

accession SM-29 (*S. gilo*). Cluster VIII with *S. insanum* recorded minimum cluster mean for number of days from anthesis to fruit set (11.67) and cluster VII with *S. mammosum* recorded minimum (31.67) number of days from fruit set to maturity.

The highest mean value for number of fruits per plant was recorded in cluster VII (26.67) with single wild accession SM-22 and minimum mean value for the same character in cluster IV (7.11).

Cluster V with single *S. melongena* (SM-27) accession recorded maximum fruit yield (2146) and cluster VIII with single wild accession *S. insanum* (SM-30) had minimum fruit yield (63.33).

The highest mean value for number of seeds per fruit was recorded in cluster III (1366.3) followed by cluster V (1050) and minimum mean value for the same character was recorded in cluster VII (174.67).

4.2.6.1.6 Percentage contribution of quantitative characters towards divergence

The percentage contribution of each characters towards genetic divergence are presented Table 15. Among 22 characters studied, fruit yield per plant contributed the maximum towards the diversity (39.77%) followed by leaf blade width (20.92%) and number of fruits per plant (16.09%). Number of days from anthesis to fruit set showed least contribution towards diversity (0.46%) followed by fruit pedicel length (0.69%). All remaining characters except leaf blade length, fruit length and diameter, petiole length, relative calyx length and number of seeds per fruit did not showed any contribution towards diversity.

Table 15. Percentage contribution of characters towards genetic divergence in 30 brinjal genotypes

Source	Contribution %
Fruit yield / plant	39.77
LB width	20.92
Number of fruits /plant	16.09
LB length	10.8
Fruit length	3.22
petiole length	2.76
Fruit diameter	2.76
Relative fruit calyx length	1.38
Number of seeds/fruit	1.15
Fruit pedicel length	0.69
Days to anthesis to fruit set	0.46

4.2.6.1.7 Ranking of genotypes in clusters

Based on association analysis and divergence analysis three yield attributes viz., fruit weight, number of fruits per plant and fruit yield per plant were used for ranking the genotypes in each cluster and the result are presented in table 16. The genotypes were sorted in descending order and ranked accordingly. Mean rank was calculated to identify the best genotype.

Cluster I was largest with maximum genotypes. Based on overall ranking in this cluster the genotypes namely SM-23, SM-20, SM-15, SM-18, SM-10, and SM-24 had superior ranks. In cluster III, the wild accession SM-28 (*S. incanum*) ranked superior followed by *S. melongena* accession SM-25.

The remaining cluster not ranked as these were solitary. Even if cluster V had single genotype (SM-27), it showed superiority for two major characters *viz.*, fruit weight and fruit yield per plant. Based on this SM-27 in cluster V is considered as overall superior best ranking genotype.

4.1.1 SELECTION INDEX

Selection index was constructed through discriminant function analysis. Five characters (yield per plant (X1; as independent variable), number of long-styled

Table 16. Ranking of 30 brinjal genotypes for quantitative characters in clusters

Cluster 1	Fruit weight (g)	Fruit weight rank	Number of fruits/plant	Number of fruits/plant rank	Fruit yield/plant (g)	Fruit yield/plant rank	Overall ranking
SM-3	37.67	21	9.110	18	565.33	20	19.67
SM-12	29.04	22	7.670	22	292.67	22	22
SM-9	62.00	18	9.330	16	592.33	18	17.33
SM-26	67.33	16	8.220	21	614.11	17	18
SM-20	92.67	7	13.000	4	1275.67	3	**4.66**
SM-19	68.67	15	15.110	1	996.78	8	8
SM-10	73.33	11	12.110	8	1285.67	2	7
SM-15	102.33	2	12.000	9	1144	6	**5.67**
SM-8	88.33	8	11.670	12	1019.33	7	9
SM-4	100.00	3	8.670	20	770.67	14	12.33
SM-17	72.220	12	13.670	3	867	11	8.67
SM-14	79.000	10	12.000	10	905.33	9	9.67
SM-7	69.670	14	10.670	15	668.22	16	15

Cluster 1	Fruit weight (g)	Fruit weight rank	Number of fruits/ plant	Number of fruits/plant rank	Fruit yield/plant (g)	Fruit yield/plant rank	Overall ranking
SM-18	97.480	5	12.890	5	1185.56	5	**5**
SM-5	84.440	9	9.330	17	770.33	15	13.67
SM-16	56.260	20	11.22	14	576.67	19	17.67
SM-23	108.00	1	12.67	6	1434.1	1	**2.67**
SM-1	71.670	13	14.00	2	765.33	13	9.33
SM-13	62.330	17	12.00	11	442.44	21	16.33
SM-6	95.000	6	9.000	19	902	10	11.67
SM-21	62.000	19	12.67	7	799.55	12	12.67
SM-24	99.670	4	11.67	13	1233.7	4	**7**
Cluster II							
SM-11	88.670	1	11.330	1	983	1	1
Cluster III							
SM-25	96.330	1	11.22	2	1041	2	1.67
SM-28	56.850	2	18.89	1	1072.89	1	1.33

Cluster IV	Fruit weight (g)	Fruit weight rank	Number of fruits/plant	Number of fruits/plant rank	Fruit yield/plant (g)	Fruit yield/plant rank	Overall ranking
SM-2	67.890	1	7.11	1	458.67	1	1
Cluster V							
SM-27	192.670	1	11.67	1	2146.44	1	1
Cluster VI							
SM-29	11.430	1	18.22	1	199.22	1	1
Cluster VII							
SM-22	20.220	1	26.67	1	519.45	1	1
Cluster VIII							
SM-30	4.610	1	8.22	1	63.33	1	1

flowers (X2), fruit diameter (X3), fruit weight (X4) and number of seeds per fruit (X5)) having significant correlation and positive direct effect on fruit yield per plant at genotypic level were selected for construction of selection index. The expected genetic gain and relative efficiency were calculated separately for each character as well as character combinations (Table 17).

Selection indices for individual characters revealed comparatively high genetic gain for number of long-styled flowers (723.58) and yield per plant (706.96). These also showed maximum relative efficiency of 86.14% and 84.16% respectively. Minimum genetic gain (354.36) and relative efficiency (42.18%) was shown by number of seeds per fruit. The inclusion of this character with other characters combination lowered the relative efficiency.

In selection index based on two characters, the maximum relative efficiency was observed in combination of fruit yield per plant and number of long-styled flowers (86.08%) followed by the combination of fruit yield per plant and fruit diameter (85.09%). Minimum relative efficiency (42.27%) was recorded in character combination of long- styled flowers and number of seeds per fruit.

In combinations including three characters, relative efficiency was recorded maximum (87.57%) in the combination of fruit yield per plant, number of long-styled flowers and fruit diameter. Minimum relative efficiency was recorded in combination of number of long-styled flowers, fruit diameter and number of seeds per fruit (55.23%)

The four trait combination of fruit yield per plant, number of long-styled flowers, fruit diameter and fruit weight showed maximum expected genetic gain (738.35) and relative efficiency (87.9%) which followed by the four trait combination of fruit yield per plant, number of long-styled flowers, fruit diameter and number of seeds per fruit (735.77 and 87.59% respectively.

The selection index constructed for the combination of five characters recorded maximum genetic gain (738.69) and relative efficiency (87.94%).

Identification of genotypes with the best character combination plays major role in crop improvement. This helps in selection of parents for hybridization program.

Based on the above result four character combination of fruit yield per plant, number of long-styled flowers, fruit diameter and fruit weight was identified as the best selection index. Using this selection index (I_{1234}), scoring was carried out for *S. melongena* accessions and the results are presented in Table 18. By considering the high index score, the genotypes SM-27 (1422.03), SM-20 (1024.7), SM-10 (1015.4), SM-23 (995.43), SM-25 (812.19), SM-24 (768.8), SM-8 (699) and SM-18 (697.65) were identified as superior.

Table 17. Construction of selection indices in 30 brinjal genotypes

Selection index	Expected genetic gain	Relative efficiency over direct selection (%)
I1 = 0.837 X1	706.959	84.158
I2= 74.332 X2	723.58	86.14
I3 = 113.601 X3	406.949	48.444
I4 = 8.51 X4	607.936	72.37
I5 = 0.53 X5	354.36	42.184
I12 = 0.895 X1 + (-163.804 X2)	723.066	86.076
I13 = 0.955 X1 + (-40.425) X3	714.801	85.092
I14 = 1.079 X1 + (-3.136) X4	712.855	84.86
I15 = 0.865 X1 + (-0.064) X5	707.862	84.266
I23 = 39.224 X2 + 112.699 X3	408.723	48.655
I24 = (-83.225) X2 + 8.787 X4	612.991	72.972
I25 = (-24.667) X2 + 0.539 X5	355.115	42.274
I34 = (-21.539) X3 + 9.297 X4	610.227	72.643
I35 = 89.509 X3 + 0.356 X5	463.556	55.183
I45 = 7.906 X4 + 0.14 X5	613.556	73.039
I123 = 1.057 X1 +(-190.595) X2 + (-52.644) X3	735.601	87.568
I124 = 1.18 X1 + (-174.31) X2 + (-3.643) X4	730.772	86.993
I125 = 0.907 X1 + (161.51) X2 + (-0.03) X5	723.262	86.099
I134 = 1.095 X1 + (-32.112) X3 + (-2.131) X4	717.172	85.374
I135 = 0.984 X1 + (-40.664) X3 + (0.067) X5	715.781	85.208
I145 = 1.126 X1 + (-3.291) X4 + (-0.081) X5	714.281	85.03
I234 = (-92.943) X2 + (-26.574) X3 + 9.791 X4	616.378	73.375
I235 = (-20.37) X2 + 89.431 X3 + 0.364 X5	463.95	55.23
I245 = (-102.26) X2 + 8.12 X4 + 0.169 X5	620.862	73.909
I345 = (-23.005) X3 + 8.729 X4 + 0.144 X5	616.14	73.347
I1234 = 1.212 X1 + (-192.757) X2 + (-43.684) X3 + (-2.33) X4	738.351	87.895
I1235 = 1.069 X1 + (-188.402) X2 + (-52.602) X3 + (-0.029) X5	735.773	87.588
I1245 = 1.206 X1 + (-170.926) X2 + (-3.725) X4 + (-0.048) X5	731.248	87.05
I1345 = 1.14 X1 + (-31.751) X3 + (-2.293) X4 + (0.078) X5	718.492	85.531
I2345 = (-114.015) X2 + (29.524) X3 + 9.201 X4 + 0.177 X5	624.967	74.398
I12345 = 1.233 X1 + (-189.75) X2 + (-43.318) X3 + (-2.41) X4 + (-0.04) X5	738.685	87.935

Table 18. Scoring in 30 brinjal genotypes based on best selection index

Sl. No.	Treatment	Index score
1	SM-1	354.962
2	SM-3	195.479
3	SM-4	294.304
4	SM-5	326.786
5	SM-6	503.507
6	SM-7	238.414
7	SM-8	**699.007**
8	SM-9	192.406
9	SM-10	**1015.4**
10	SM-11	604.408
11	SM-12	-24.028
12	SM-13	82.6533
13	SM-14	387.469
14	SM-15	511.56
15	SM-16	297.331
16	SM-17	435.921
17	SM-18	**697.645**
18	SM-19	405.834
19	SM-20	**1024.7**
20	SM-21	385.547
21	SM-23	**995.431**
22	SM-24	**768.795**
23	SM-25	**812.194**
24	SM-26	208.158
25	SM-27	**1422.03**

DISCUSSION

5. DISCUSSION

Brinjal (*Solanum melongena* L.) is the most important *Solanum* crop native to the Old World. At the global level, it has been one of the crops with the greatest increase in production in the last few years mainly due to development and adoption of improved varieties and hybrids. This has also led to replacement of innumerable landraces and local crops/cultivars resulting in a narrow genetic base of the *Solanum melongena.* In contrast, the innumerable wild relatives of brinjal remain untapped as a potential source of wide variation.

Exploration and collection were carried out to capture the existing variation in brinjal including its wild relatives and the available variability in collection broadened by germplasm acquisition from gene bank. The evaluation of brinjal genotypes and their wild relatives was carried out using morphological descriptors through variability, character association, genetic diversity analyses and constructing selection index to identify the best genotypes for further crop improvement. The findings from the present study are discussed below:

5.1 Exploration and collection of brinjal genotypes

The detailed survey before the actual collection of brinjal genotypes was mainly confined to North Kerala due to limited exploration studies conducted previously in these regions. The survey showed that the cultivation of local cultivars of brinjal was confined to small pockets and that too mainly as homestead cultivation. Hence, the survey was focused only on homesteads and small scale vegetable growers. The seeds of 42 accessions were obtained which consisted of 30 (28 *S. melongena* and two wild relatives) from field visits and 12 (five *S. melongena* and seven wild accessions) from Regional station NBPGR, Thrissur. Poor viability and limited quantity of seeds resulted in the elimination of seven *S. melongena* accessions from the study. The wild species of brinjal have germination issues related to dormancy. In the present study the wild relatives *S. indicum, S. xanthocarpum, S. macrocarpon* and *S. viarum* obtained from NBPGR were eliminated due to poor germinability even after dormancy breaking treatments. Similar poor germination was

observed by Gisbert *et al*. (2011) in *S. incanum*, *S. macrocarpon* and *S. melongena* and they reported the presence of dormancy in wild species and the loss of viability in orthodox seeds in general as the reasons for poor germination. Due to the problems associated with seed germination and lack of required agroclimatic conditions necessary for multiplication, the germplasm of wild relatives are often lost during the process of seed multiplication. Seed dormancy and asynchronous maturity are some of the problems encountered in their maintenance and multiplication (Pandey *et al.*, 2005).

Out of total accessions collected, twenty five local cultivars of *S. melongena* and five wild relatives (*S. macrocarpon*, *S. mammosum*, *S. incanum*, *S. gilo* and *S. insanum*) of brinjal were taken for further detailed evaluation using morphological descriptors. Among the related species , *S. gilo* and the *S. macrocarpon* belong to the cultivated groups of Scarlet and Gboma African eggplant complexes respectively. The final collections included for the study consisted of maximum genotypes from Malappuram (11) followed by Kozhikode (5), Kannur (5), Kasargod (3), Wayanad (1) and six accessions from NBPGR, Thrissur. The passport data information for each of the thirty accessions is presented in Table 1.

5.2 Morphological characterization of brinjal accessions based on 17 qualitative traits

The morphological characterization of available plant genetic resource makes essential information for the breeders, which help them in pre-breeding as well as in breeding programs for crop improvement. The wide variability in *S. melongena* for plant and fruit characters and the essentiality of DUS characterization in varietal registration makes morphological characterization an indispensable tool for effective management and sustainable utilization of brinjal genetic resources. Besides, it is a preliminary step in taxonomic delineation and classification of eggplant complex especially with the presence of the wide morphological diversity in wild and weedy forms.

The primary characterization involves qualitative characters such as growth habit, stem colour, fruit colour, fruit shape, hairiness and prickliness. The secondary characterization based on quantitative characters involves more complex characters of agronomic importance such as yield components, disease and pest resistance and biochemical content. The present study involves morphological characterization based on both qualitative and quantitative characters using descriptors of IPGRI. All the vegetative, flowering and fruiting characters except pollen colour showed wide range of variability and the findings are discussed below:

5.2.1 Vegetative characters

The findings of the present study in general reveals a wider range of variation in wild relatives than cultivated types of *S. melongena* for the descriptors studied under vegetative characters such as plant growth habit, anthocyanin pigmentation in vegetative parts, prickliness and leaf characters. This contemplates the fact that one single *S. melongena* species has been compared with a combination of wild and related species (Kaushik *et al*., 2016). All three forms of plant growth habits were observed in *S. melongena* as shown in Plate 4 but majority of them were upright which is in line with the findings of Islam *et al.* (2018) and Parida *et al*. (2020). The wild relatives *S. macrocarpon*,

S. incanum and S. gilo were having upright growth habit, intermediate growth habit was seen in few S. melongena and S. mammosum and prostrate growth habit in S .insanum (Plate 5)and in one S. melongena genotype (SM 25) [Fig. 5] . However, Naujeer (2009) had reported intermediate growth habit in majority of S. melongena, upright growth habit in S. macrocarpon and prostrate habit in other related species in the study on characterization of *S. melongena* and related wild species. Lagat (2016) reported upright growth habit in the African eggplant accessions consisting of *S. aethiopicum* and *S. macrocarpon*. Ranil *et al*. (2017) are of the view that both erect as well as prostrate habit are seen in *S. insanum* considered to be wild progenitor of brinjal but essentially erect habit in *S. incanum.* According to Choudhury *et al.* (2010), the upright habit is an important trait in *S. melongena* for good vigor

facilitating intercultural operations, harvesting and allows free air circulation in the plant thus checking pest and disease attack.

Brinjal shows the presence or absence of anthocyanin pigmentation in various plant parts such as anther tip, leaf vein, stem, petiole, pedicel, fruit, corolla and leaf margin. In the present study wide variation for the pattern and tissue specificity of anthocyanin pigmentation was observed in the vegetative parts such as stem and petiole, between cultivated and wild types. This variation and tissue-specificity of anthocyanin pigmentation in brinjal is the result of anthocyanin biosynthetic pathway, regulatory gene duplication and further sequence divergence (Purugganan and Wessler, 1994). In the present study, most of the accessions had green (87 %) coloured stem followed by light green (7 %), purple (3 %) and dark purple (3 %) as seen from Fig.6. There was absence of anthocyanin in stem of all *S. melongena* accessions except SM 15 which had purple stem and in all wild relatives except *S. gilo* with dark purple stem (Plate 6). Sifau *et al.* (2014) observed both green and greenish-purple stem in *S. gilo* genotypes. The genotypes showed wide range of variation with respect to leaf petiole colour ranging from green to dark brown colour [Fig.7]. Few *S. melongena* genotypes and *S. macrocarpon* were lacking anthocyanin in petiole. The *S. incanum* and *S. insanum* considered as wild ancestors of brinjal had greenish-purple petiole. Prohens (2013) had reported absence of anthocyanin in stem and leaf in *S. incanum* genotype used as parent for interspecific hybridization, Ranil *et al*. (2017) reported moderate anthocyanin in leaf petiole for *S. insanum* collected from wild habitat in Srilanka. The *S. melongena* accession (SM 15) with purple stem and the *S. gilo* with dark purple stem had purple petiole this is in line with the findings of Page *et al.* (2019) who reported purple petiole colour in *S. gilo* . *S.mammosum* had dark purple *and S. melongena* (SM1) had dark brown petiole (Plate 7*).* Leaf blade showed two types of colouration [Fig. 8] with most of the cultivated genotypes and the wild ancestors *S. macrocarpon*, *S. incanum* and *S. insanum* having green, whereas the *S. mammosum* and *S. gilo* having dark green as shown in Plate 8 A.

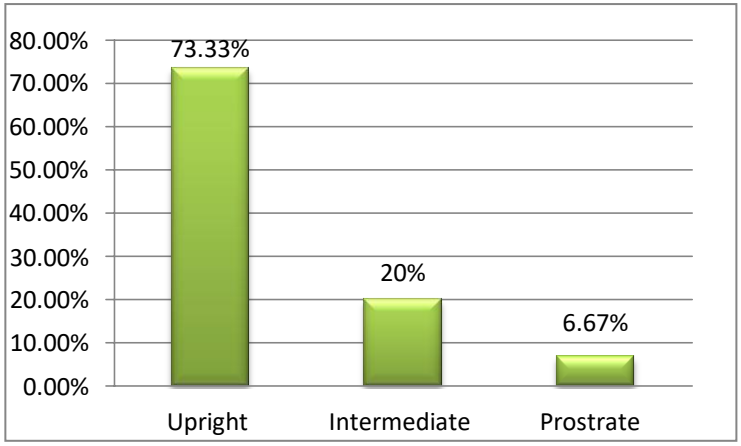


Figure 5. Plant growth habit in 30 brinjal genotypes

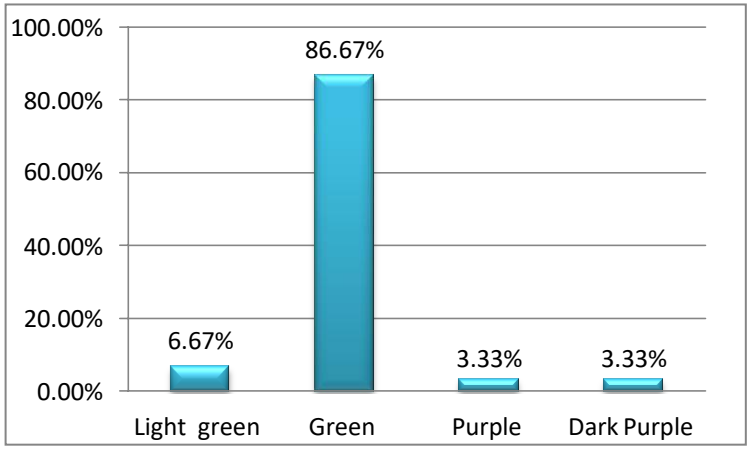


Figure 6. Stem colour of 30 brinjal genotypes

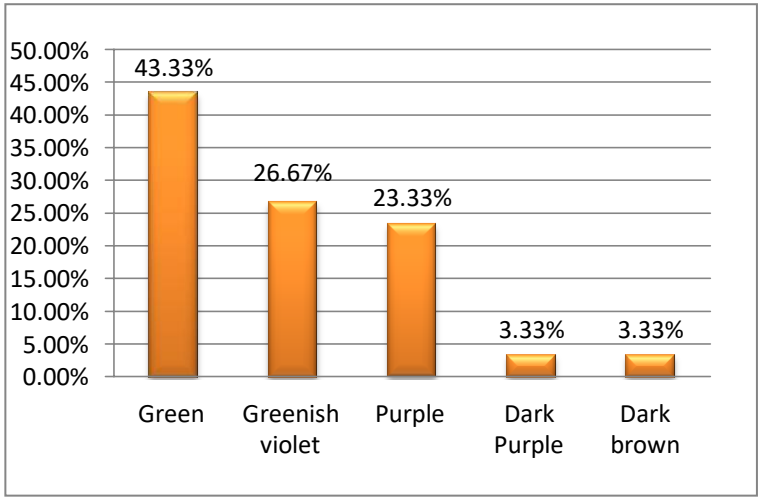


Figure 7. Leaf petiole colour of 30 brinjal genotypes

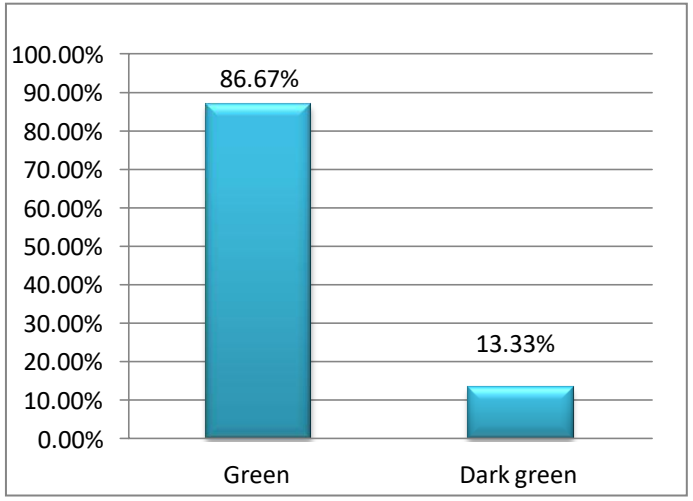
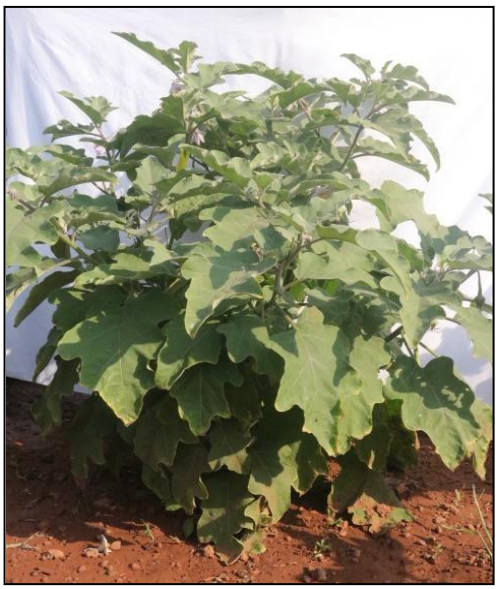


Figure 8. Leaf bale colour of 30 brinjal genotypes

Upright (SM-12)



Intermediate (SM-18)

Prostrate (SM-25)

Plate 4. Variation in plant growth habit of *S. melongena* accessions

Upright (*S. gilo*)

Intermediate (*S. mammosum*)

Prostrate (*S. insanum*)

Plate 5. Variation in plant growth habit of wild relatives

Light green (SM-9) **Purple (SM-15)**

Green (SM-23) **Dark Purple (*S. gilo*)**

Plate 6 Variability in plant stem colour

Green (SM-9) | Greenish violet (SM-6) | Purple (SM-4)

Dark purple (***S. gilo***) | Brown **(SM-1)**

Plate 7 Variation in leaf petiole colour

Prickliness is a character in brinjal and wide variation has been noticed for the density, size and shape of prickles and their presence on leaf, stem and calyx. Leaf prickles and hairs are important marker traits for characterization of wild and cultivated types. In the present study based on number of prickles on adaxial surface of leaf the genotypes were grouped into those without any prickles and those having prickles based on number as very few (1-2), few (3-5) and intermediate (6-10) [Fig. 9]. Majority of accessions (67 %) *S. melongena* including wild relatives *S. macrocarpon, S. gilo* and *S. incanum* were without prickles. The drastic reduction in prickliness in *S. melongena* has been the result of domestication and selection for ease of harvesting (Page *et al*., 2019). Plazas *et al*. (2014) observed absence of prickles in Gilo group one of the four cultivated groups belonging to *S. aethiopicum* others being Shum, Kumba, and Aculeatum of Africa and reported presence of prickles in *S. aethiopicum.* Lagat (2016) reported strong presence of leaf prickles in few *S. aethiopicum* accessions characterized for drought tolerance In this study, two *S.melongena* accessions (SM-25 ; SM -26), *S. mammosum* and *S. insanum* had intermediate prickles (Plate 8 B). However, considerable variation has been reported in *S. insanum* the wild progenitor of brinjal with regards to prickliness as both prickly and non prickly types are present in *S. insanum* (Plazas *et al*., 2016; Ranil *et al*., 2017). Slight prickliness (0-2) has been reported in *S. incanum* (Prohens *et al*., 2012). Presence of prickles and leaf hairs will irritate insect pests while feeding, which in turn will prevent insect attack to some extent (Chandra et al., 2014). Prohens *et al*. (2007) and Gisbert *et al.* (2011) reported parallelism in prickliness with biotic and abiotic stress tolerance.

The frequency distribution for lobing in leaf [Fig. 10] showed intermediate lobing in maximum genotypes (63%) consisting of *S. melongena* and its wild progenitor *S. insanum* followed by strong lobing (30%) in few *S. melongena* (Plate 9 A) .Wild relatives *S. gilo* and *S. mammosum* showed intermediate lobing and weak lobing (7%) was observed only in *S. macrocarpon* and *S. incanum* (Plate 9 B). However, in case of wild relatives, such as *S. macrocarpon* strong lobing (Naujeer, 2009) and weak to intermediate lobing (Plazas *et al.,* 2016) have been reported. Ranil *et al*. (2017) observed intermediate lobing in *S. insanum* and intermediate to strong

lobing in *S. incanum*. Most of the *S. melongena* genotypes and *S. macrocarpon* were showing acute leaf tip angle followed by few *S. melongena* including *S. incanum* and *S. gilo* with intermediate and *S. insanum* showing obtuse leaf tip as shown in Fig.11 (Plate10). Rounded to acute leaf tip has been reported in *S. insanum* and *S. incanum* (Ranil *et al*., 2017), intermediate in *S. aethiopicum* (Page *et al*., 2019) and *S. macrocarpon* (Naujeer, 2009). The observation made in *S. melongena* accessions for lobing and leaf tip angle in this study are consistent with those made by Shekar (2011), Islam *et al*. (2018), Dash *et al*. (2019) and Parida *et al*. (2020).

5.2.2 Flower characters

In the present study based on corolla colour of the flower the genotypes are grouped into four *viz*., white, pale violet, light violet and bluish violet (Fig.12). Pigments and biochemical compounds such as anthocyanin and acyl glycosides play a major role in imparting flower colour which in turn aid in insect pollination and subsequent fruit production (Dasgupta and De, 2007). The present study showed prominence of purple- flowered accessions in the *S. melongena* genotypes. Similar observations were also made by Chattopadhyay *et al*. (2011), Khan and Singh (2014) and Islam *et al*. (2018) in their studies on *S. melongena*. In the present study, *S. insanum* and *S. macrocarpon* had pale violet and *S. incanum* had light violet flowers as also documented in the studies of Ranil *et al.* (2017) and Plazas *et al.* (2016). The wild relatives *S. gilo* and *S. mammosum* were distinct with the former showing white and the latter bluish violet-colored flower (Plate 11). However, Lagat (2016) in his study on African eggplant observed white-flowered *S. macrocarpon* and flower colour ranging from white to bluish violet (1-9) in *S. aethiopicum* accessions.

5.2.3 Fruit characters

Fruit characters such as color, flavor, flesh density/firmness and shape in cultivated brinjal are profoundly influenced by consumer preference. The present investigation indicated much higher variation for fruit shape in the cultivated *S. melongena* accessions than its wild relatives. This corroborates the general observation in the domestication of crop plants where a marked morphological

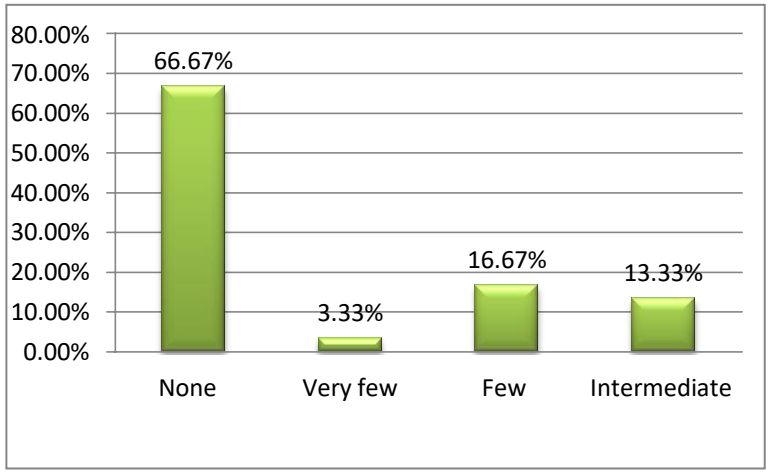


Figure 9. Leaf prickles on 30 brinjal genotypes

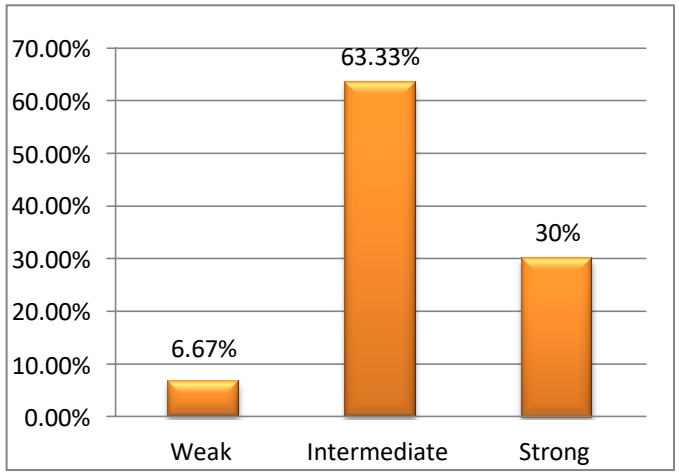


Figure 10. Leaf blade lobing of 30 brinjal genotypes

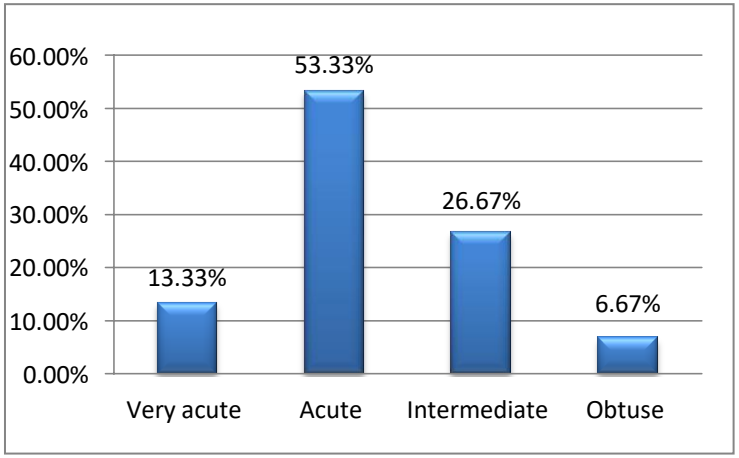


Figure 11. Leaf blade tip angle in 30 brinjal genotype

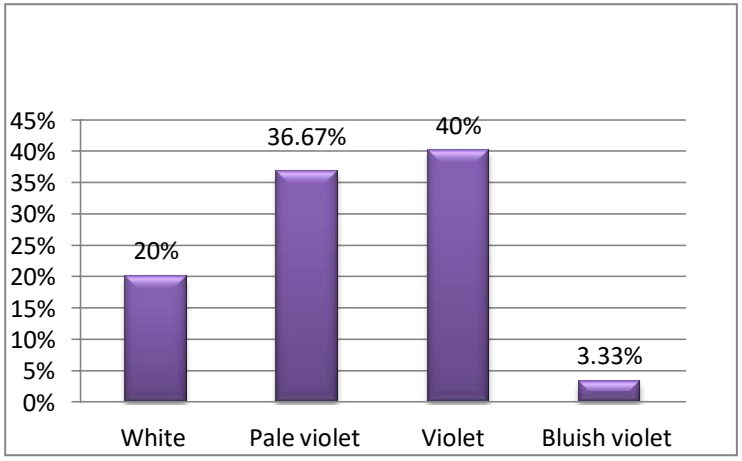


Figure 12 Corolla colour of 30 brinjal genotypes

Dark green (SM-11) **Green (SM-10)**

A. **Leaf blade colour in *S. melongena***

Leaf without prickles

SM-4

Leaf with prickles

SM-10
Very few

SM-18
Few

S. mammosum
Intermediate

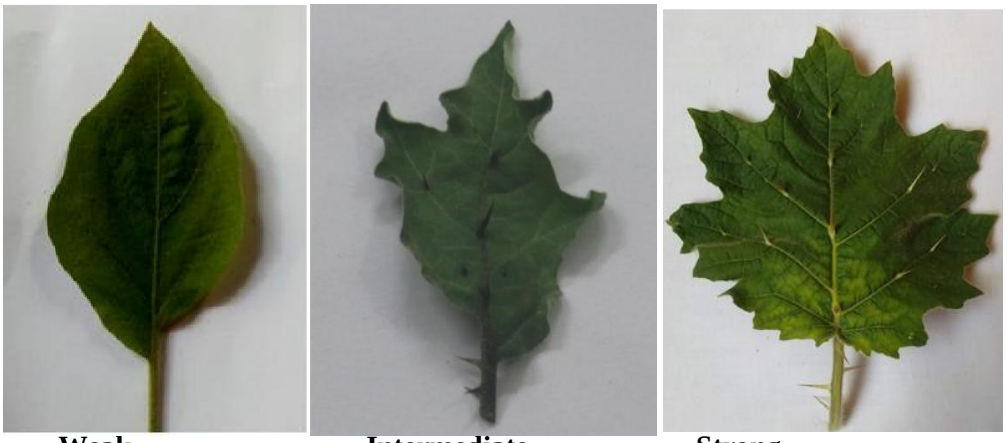
B. variation in number of leaf prickles

Plate 8. Variation with respect to leaf colour and number of prickles

A. **Leaf blade loabing in *S. melongena***

Intermediate (SM-5) **Strong (SM-15)**

B. Leaf blade loabing in wild relatives



Weak (*S. incanum*) **Intermediate (*S. insanum*)** **Strong (*S. mammosum*)**

Plate 9. Variation in leaf blade loabing

Leaf blade tip angle

Very cute

Acute

Intermediate

Obtuse

Plate 10. Variation in leaf blade tip angle

White (SM-21)

Pale violet (SM-5)

Violet (SM-25)

Bluish violet (*S. mammosum*)

Plate 11. Variation in corolla colour

variation is seen in the functional part (in present case fruit) for which the crop is domesticated (Meyer and Purugganan, 2014).

Four descriptors defining the fruit shape *viz*., fruit curvature, fruit shape based on position of widest portion from base to tip, fruit apex shape and fruit length breadth ratio have been used for the present study. Majority of the accessions (66.67 %) which included all the wild and maximum the cultivated types had fruits without any curvature [Fig.13]. Among the local cultivars of *S. melongena*, fruits with weak, medium and strong curvature (snake-shaped fruits) were also observed as seen in Plate 12. Various researchers have reported most of the studied *S. melongena* genotypes have fruits without any curves (Parida *et al*., 2020; Solaimana *et al.*, 2014; Islam *et al*., 2018).

In present study majority of *S. melongena* accessions and all wild accessions except *S. mammosum* (70 %) had fruits with widest portion ½ away from base to tip (Fig.14) and few cultivated brinjal including white fruited SM -16 had widest part of the fruit ¾ away from base to tip and *S. melongena* accessions SM 15 (Plate13) and *S. mammosum* had widest portion ¼ away from base to tip of fruit. All three fruit apex shapes were observed in both *S. melongena* and wild accessions (Plate 14) with a frequency distribution of 30% genotypes for rounded, 30 % for flattened and 40% showing depressed apex (Fig. 15). The wild relatives in this study had round to oval fruits. *S. incanum* had spherical fruits with round apex and *S. insanum* had oval fruits with flattened apex which is also documented by Ranil *et al*. (2017). *S. macrocarpon* had round fruits with flattened apex. But Naujeer (2009) reported *S. macrocarpon* having round fruits with round apex. *S. mammosum* had unique fruits with protuberances at the base and protruded fruit tip with depressed apex commonly referred to as nipple fruit nightshade and also as cow's udder (Singh *et al*., 2017).

Based on fruit length breadth ratio maximum variation was observed in *S. melongena* genotypes with the descriptor state values ranging from 1-9 and the majority showing 5-9 values. The frequency distribution for this character as seen in Fig.16 shows maximum genotypes (40 %) three times as long as broad (descriptor value 8 observed only in *S. melongena* accessions) and remaining for wild and

cultivated accessions. The wild relatives showed very low range from 1-5. *S. macrocarpon* with the lowest value (1) followed by S. *insanum*, S. *incanum* (3) and *S. mammosum* and *S. gilo* (5). In the present study the fruit size of *S. melongena* based on length breadth ratio is from medium to very large and that of wild relatives is from small to medium which are almost matching the observations made by Page *et al*. (2019). *S. melongena* genotypes showed wide variation in fruit flesh density ranging from very loose to very dense (1-9). However, majority of the S. *melongena* genotypes including the wild relatives S. *insanum*, *S. gilo* and *S. incanum* (Fig.17) were having very loose to crumply flesh. *S. macrocarpon* and *S. mammosum* had average to dense flesh and none of the wild relatives in the present study show very dense flesh. Ranil *et al*. (2017) had reported gelatinous mesocarp in *S. insanum* and *S. incanum*. Observations similar to the present study were made by Polignano *et al*. (2010) for fruit flesh consistency in *S. macrocarpon* but they reported higher values for the same in *S. gilo* in a study consisting of *S. melongena*, *S. macrocarpon* and *S. aethiopicum* accessions. This is contrary to the findings of Kaushik *et al*. (2016) who reported wide variation for this character in wild species while characterizing a population consisting of *S. melongena*, twelve wild species from all the three gene pools and their interspecific hybrids. Solaimana *et al*. (2015) reported fruits with average dense and dense fruit flesh in *S. melongena*.

The *S. melongena* genotypes are having pendant fruits and it is the general characteristic of *S. melongena*. In the present study, more than 90% of genotypes had pendant fruit (Fig.18). *S. macrocarpon* and *S. gilo* had semi pendant fruits and *S. mammosam* had unique horizontal fruit [Plate 15]. In the wild relatives *S. aethiopicum* and *S. macrocarpon* three types of fruit position *viz*., erect, semi-erect and pendant fruit position have been reported (Page *et al*., 2019).

Fruit color is another important marker-trait differentiating cultivated and wild types. The wide variation exhibited in general by *S. melongena* for fruit colour at commercial ripening stage is the consequence of continuous selection based on local and regional preferences which is also reflected in the present study. The role of anthocyanins for purple to black colour skin in brinjal is of common knowledge but recent reports emphasize the significant role of both anthocyanins and chlorophylls

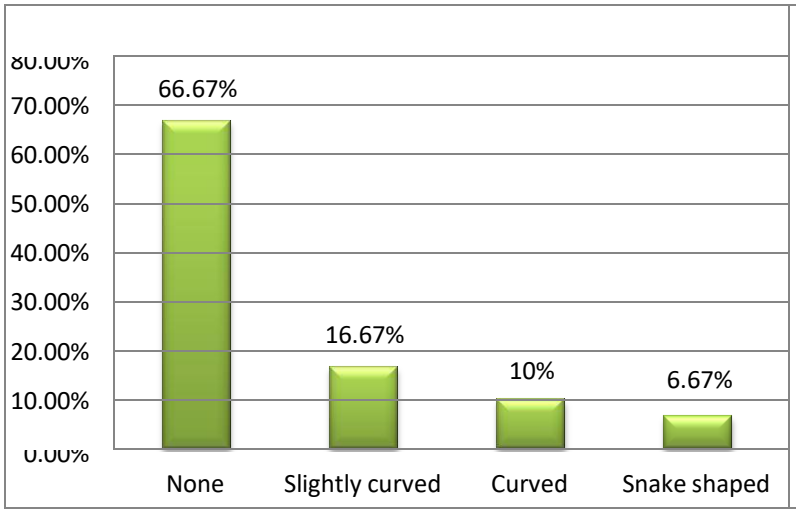


Figure 13. Fruit curvature of 30 brinjal genotypes

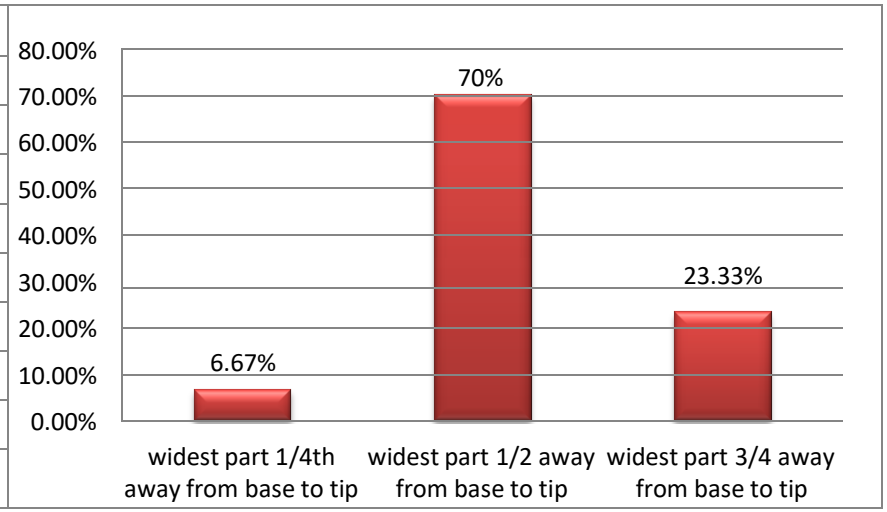


Figure 14. Fruit shape of 30 brinjal genotypes

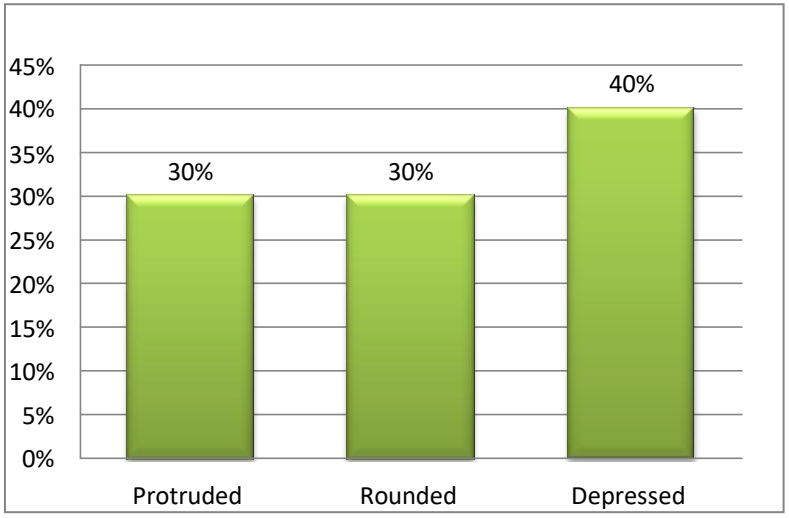


Figure 15. Fruit apex shape of 30 brinjal genotypes

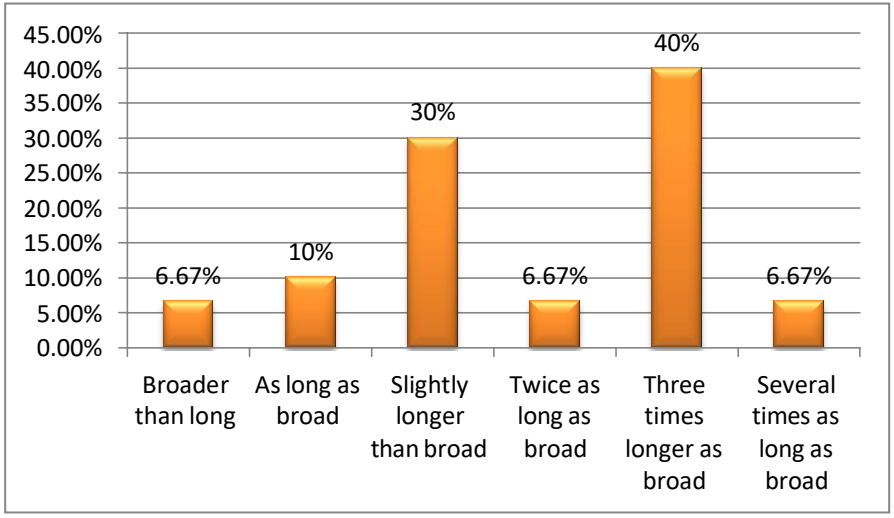


Figure 16. Fruit length/breadth ratio of 30 brinjal brinjal genotypes

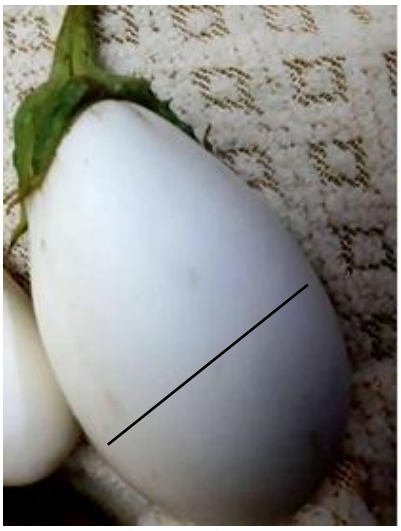
None (without any curves)

Slightly curved

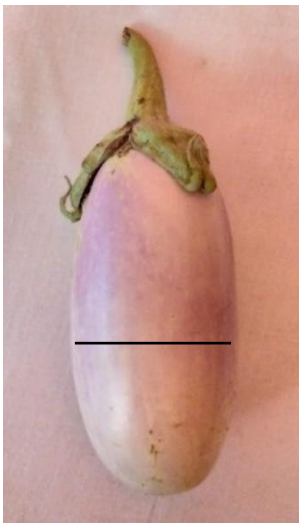
Curved

Snake shaped

Plate 12. variation in fruit curvature



(SM-16)
¾ away from base



(SM-17)
½ away from base

(*S. mammosum*)
¼ away from base

Plate 13. Variation in fruit shape in brinjal accessions

Round (SM-8)

Protruded (SM-17)

Depressed (SM-27)

Plate 14 variation in fruit apex shape in *S. melongena*

SM-17

SM-14

Pendant

S. mammosum
Horizontal

S. macrocarpon
Semi-pendant

Plate 15. Variation in fruit position

for dark violet to black pigmentation attribute of many eggplant varieties. Thus suggesting that fruits are green fruited if anthocyanins are absent or present at very low concentration and in case chlorophyll concentration is also low fruits are white (Stommel and Dumm, 2015; Gisbert *et al.*, 2011). In the present study, there were *S. melongena* accessions exhibiting three respective fruit colours *viz.*, white,

green and purple on commercial ripening with almost 50 % of them exhibiting purple followed by green (36.6 %) and three of them milky white coloured fruits (Fig.19). All the wild relatives were green fruited on commercial ripening except S. *mammosum* which were yellow fruited (Plate 16 A). All the accessions had yellow colour pigmentation (96.6 %) during its physiological ripening [Fig. 20] except *S. gilo* where its fruit turn to red on physiological ripening (Plate 16 B) and it may be due to the deposition of carotenoids (Dhar *et al*., 2014).

5.3 Morphological characterization of brinjal based on 22 quantitative characters

A further detailed evaluation of cultivated and wild accessions of brinjal for quantitative traits pertaining to agronomic, breeding and economic importance was carried out. The quantitative data were subjected to variability analysis, (analysis of variance, coefficient of variation (GCV, PCV, heritability and genetic advance), association analysis (correlation and path analysis), genetic diversity analysis and discriminant function analysis (selection index). Analysis of variance revealed significant variation among the 30 genotypes for all the 22 characters, indicating presence of high genetic variability. The results of the 22 quantitative traits subjected to statistical analysis are discussed below:

5.3.1 Analysis of variability parameters

The mean performance and range of 30 genotypes for 22 quantitative characters revealed distinct variation between cultivated and wild genotypes for the plant, flowering and fruiting characters. The study also showed that flower and fruit

characters had a major contribution in the variation observed with the maximum contribution observed for flower characters. Four flowering characters *viz*., number of flowers per inflorescence, number of medium styled flowers, long-styled flowers per inflorescence and relative style length accounted for maximum values for coefficient of variation.

All the genotypes are classified from short (20-60 cm) to intermediate (60-100 cm) for height. The wild relatives had shown a wider variation for plant height ranging from short in *S. insanum* (28.89 cm) to intermediate in *S. mammosum* (86.46 cm) when compared with cultivated *S. melongena* (46.01-77.2 cm). However, Ranil *et al*. (2017) have reported short to tall plants (40-150 cm) in field-grown accessions of both *S. incanum* and *S. insanum*. As *S. melongena* and *S. insanum* its wild progenitor are interfertile, many intermediate individuals can be observed (Knapp *et al*., 2013). Considerable variation has also been described both between and within *S. insanum* populations in central and Southern India (Davidar *et al*., 2015; Mutegi *et al*., 2015). The *S. insanum* accession in the present study may be the intermediate form. *S. mammosum* a herb or shrub growing up to 1.5 m in height, is considered as a wild invasive species introduced as an ornamental to India (Singh *et al*., 2017). In this study *S. macrocarpon* and *S. gilo* are medium in height. *S. macrocarpon* belonging to Gboma eggplant complex consists of both cultivated forms with a plant height of 40-52 cm and semi-cultivated forms of 65-85 cm (Page *et al*., 2010). Plazas *et al*. (2014) observed very tall plants (150 cm) in the Gilo group the most diverse group of *S. aethiopicum* belonging to Scarlet eggplant complex. Lagat (2016) observed very wide range of variation for plant height (12.5-81.5 cm) in landraces of *S. aethiopicum*.

In case of plant canopy spread the cultivated *S. melongena* had shown wider range of variation compared to wild relatives. The *S. melongena* accessions were showing narrow (40-60 cm) to broad canopy spread (90-150 cm) whereas the wild relatives showed narrow to intermediate (60-90 cm) canopy spread. The majority of *S. melongena* accessions are having intermediate height and spread. Ahmed *et al.*

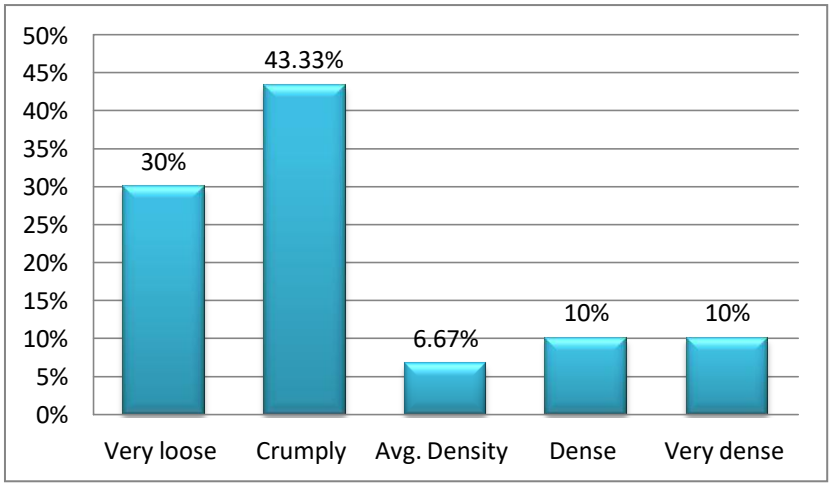


Figure 17. Fruit flesh density of 30 brinjal genotypes

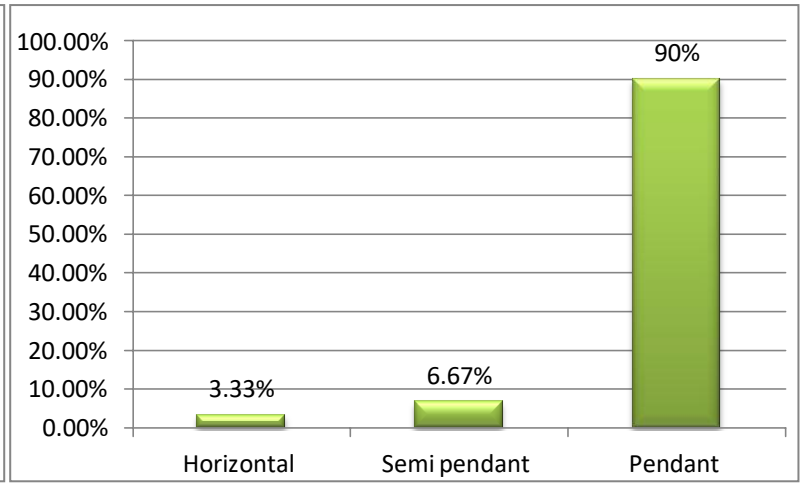


Figure 18. Fruit position of 30 brinjal genotypes genotypes

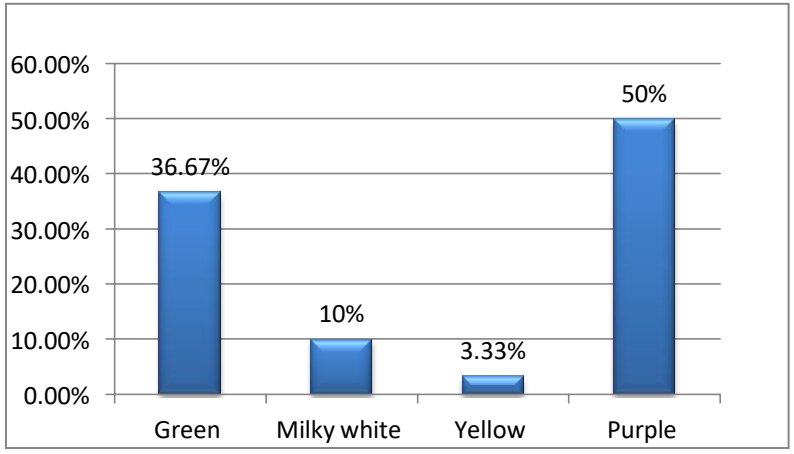


Figure 19. Fruit colour at commercial ripening of 30 brinjal genotypes

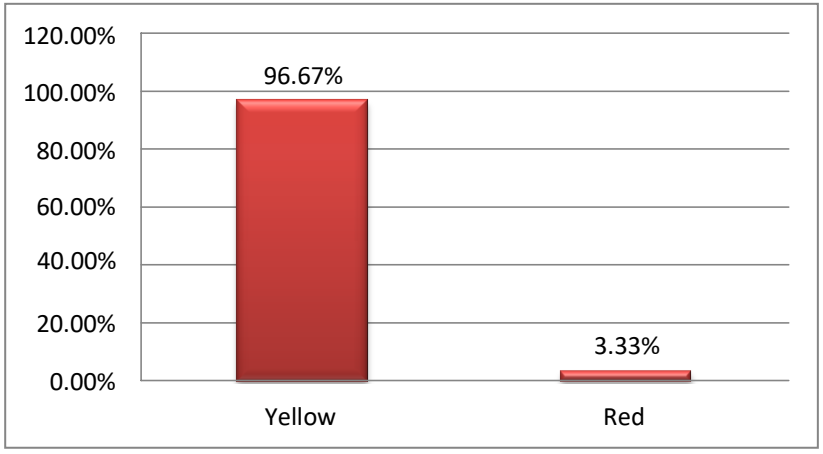


Figure 20. Fruit colour at physiological ripening of 30 brinjal genotypes

Green (SM-27)

Milky white(SM-16)

Purple (SM-23)

Yellow (S. mammosum)

A. Fruit colour at commercial ripening

Yellow (SM-20)

Red (*S. gilo*)

B. Fruit colour at physiological ripening

Plate 16. Variation in fruit colour

(2014) and Das *et al*. (2017) have reported occurrence of variation in canopy spread in their respective studies.

The choice of spreading/non-spreading varieties in brinjal is influenced by the pattern of cropping and the scale of cultivation with respect to spacing and intercultural operations. Optimal plant canopy and height are considered important not only for yield as it improves photosynthesis but also for stress tolerance (Jiang *et al*., 2016).

Based on the number of primary branches, the *S. melongena* genotypes showed weak (5-10) to intermediate branching (10-20) whereas among wild relatives only weak branching was observed with the *S. macrocarpon* having the least number of primary branches. Optimal number of main branches helps to regulate equilibrium between sources and sink to increase the brinjal production (Maghfoer *et al.*, 2014). There were notable differences between the cultivated *S. melongena* genotypes and the wild relatives for leaf characters. The *S. melongena* genotypes had intermediate leaf length (10-20 cm), intermediate (5-10 cm) to wide leaf (10-15 cm and above) and intermediate (30-50 mm) to long petiole (50-100 mm). The wild relatives had short (up to 10 cm) to intermediate (10- 20 cm) leaf length, narrow (up to 5 cm) to wide leaf and short (10-20 mm) to long (50- 100 mm) petiole. Among the wild relatives, *S. insanum* and *S. incanum* had short, narrow leaves with short petiole and the former exhibiting lowest values for leaf parameters in this germplasm collection. Similar observations have been made by Ranil *et al*. (2017) in field grown accessions of *S. insanum* and *S. incanum*. In this study, *S. macrocarpon* had intermediate leaf length and long petiole with widest leaf (17.09 cm) among all accessions which is consistent with observations of Page *et al*. (2019) and Naujeer (2009) who had observed more much wider leaves in the same species. *S. mammosum* had intermediate leaf length, wide leaf and the longest petiole (96.5 cm) among all accessions.

Flowering characters in brinjal have immense implications from breeding perspective. Even though brinjal is a perennial, it is commonly cultivated as an annual crop. Based on favorable agro-climatic condition brinjal can take 45 to 90 days for initial flowering after emergence (Kowlaska, 2008). Majority of the current varieties

in brinjal have been developed through selective breeding for early harvesting. The flowering duration parameters such as days to first flowering and 50 % flowering are indicators of earliness as it allows for early harvest in brinjal. The present study revealed distinct variation for the two parameters between the cultivated and the wild relatives with the wild relatives showing wider range than the cultivated *S. melongena*. In *S. melongena* accessions days to first flowering ranged from 43 to 49 days and days to 50% flowering ranged from 43 to 53 days. Early first flowering was recorded in SM 11 (42.67 DAT) and SM 23 (43.33 DAT) which also recorded early 50% flowering (43.3 DAT). Similar observations were made by Pandit *et al.* (2010) who attributed it to the thermo sensitive nature of *S. melongena* with cooler temperature hastening the first flowering.

The wild relatives required more days for first flowering (43-60 days) and days to 50% flowering (49-71 days). *S. macrocarpon* had shown the least number days for first flowering (43 days) and 50% flowering (48.67 days) which is contrary to the observations made by Nyadanu *et al*. (2014) who reported 87-100 days for days to 50% flowering in *S. macrocarpon* landraces of Ghana. The contrasting results in case of *S. macrocarpon* may be due to the different agroclimatic zones of study and also due to cultivar differences depending on the purpose of cultivation either for fruit or leaf purpose as this species is used for both leaf and fruits. Among wild relatives, *S. gilo* recorded maximum number of days for first flowering (60.33 days) and days to 50% flowering (71 days) which is in agreement with the observations of Lagat (2016) and Sanga (2017).

Flowering in brinjal is extra axillary and rather a complex phenomenon wherein genotypes having flowers borne solitary, in clusters or mixed (both solitary and cluster together) also occur (Karapanos *et al*., 2008). In the present study, the mixed flowering habit was noted in general except for a few accessions showing solitary habit alone. This is in agreement with the findings of Pradeepa (2002) who reported that the flowering habit can vary between the cultivated brinjal genotypes. They also report that a mixed flowering habit is more common in brinjal and that solitary alone or clustering habit alone is rare. But wide variation is noticed between the cultivated and the wild relatives. The wild relatives had produced flowers in

cluster except for *S. macrocarpon* and *S. insanum* which had 1-2 flowers per inflorescence. The wild relative *S. gilo* had maximum flowers per inflorescence. This is in confirmation with the findings of Page *et al.* (2019) who documented multiple or single flowers per inflorescence in *S. insanum*, *S. aethiopicum* and *S. macrocarpon*. Ranil *et al*. (2017) also reported 1-2 flowers per inflorescence in *S. insanum* and 5-10 flowers per inflorescence in *S. incanum*. The number of flowers per inflorescence has great implications in brinjal breeding as a lower value of this trait helps in maintaining uniformity in fruit size (Sekara and Bieniasz, 2008).

Based on the position of stigma relative to the anther cone four types of flowers *viz*., long-styled with large ovary, medium-styled with medium size ovary, pseudo-short- styled with rudimentary ovary and true short-styled with very rudimentary ovary are found in brinjal (Thamburaj and Singh, 2001). In the present study, only the long-styled and medium-styled flowers per inflorescence (Plate 17 A) were counted as these are considered as functionally fertile flowers (Hazra *et al*., 2003). The study showed that the number of long-styled flowers was more than the medium-styled flowers per inflorescence in all *S. melongena* accessions with few exceptions. It has been reported that in brinjal about 60% of the flowers are constituted by long-styled flowers and remaining by medium-styled (20%) and short-styled (10%) flowers (Kowlaska, 2006; Karapanos *et al*., 2008). The accession SM-7 and SM-24 had more number of medium-styled flowers compared to long- styled ones; SM-11 had almost equal number of medium-styled and long-styled flowers and the accession SM-25 had shown only long-styled flowers with complete absence of medium-styled flowers per inflorescence. Many previous studies suggest that not only the frequency of occurrence of different flower types but also the percentage of long-styled and medium-styled flowers is a genotype dependent characteristic in brinjal (Karapanos *et al*., 2008). All the wild relatives had shown a trend similar to *S. melongena* with *S. mammosum* being distinct from all the genotypes showing maximum number of only long-styled flowers and complete absence of medium-styled flowers per inflorescence. The long-styled flowers are considered responsible for more effective fruit set in brinjal (Passam and Bolmatis, 1997; Kowalska, 2003; Kowalska, 2006; Sujin *et al*., 2017; Das *et al*., 2017).

According to researchers, however, more than the length of style it is the relative position of stigma from the anther pore that influences the fruitset in brinjal. They also observed that flowers in which the stigmata is in close proximity to the anther pores maximum fruit weight and seed set occur. In the present study, the relative style length was recorded only in long-styled flowers (Plate 17 B). All the accessions had short relative style length (~1 mm) ranging from 0.87 mm (SM-25) to 1.6 mm (SM-27) except SM-4 which had an intermediate (~3 mm) relative style length. The wild relatives also had short relative style (<1 mm) in *S. mammosum* and *S. gilo* whereas in *S. incanum*, *S. insanum* and *S. macrocarpon* it was >1 mm.

Fruiting characters are the next set of characters after flowering characters, contributing not only to overall variation but also to fruit yield. A distinct variation was noted between the cultivated and wild accessions of brinjal for all the fruiting characters. The cultivated accessions had shown wider range of variation for fruit size i.e length and breadth ranging from intermediate (~5 cm) to very long (>20 cm) in terms of length and from intermediate (~3 cm) to very large (>10 cm) in terms of diameter. The accession SM- 11 had longest fruits in terms of length and SM-27 had the largest fruits in terms of diameter (Plate 18 A). The wild relatives had small sized fruits in general with a size range varying from short and small (~2 cm) in *S. insanum* to intermediate and large (~5 cm) in *S. macrocarpon* (Plate 18 B) which is in agreement with the observation of Naujeer (2009) and Page *et al*. (2019) who reported small to medium fruit size *in S. aethiopicum* and *S. macrocarpon*. Ranil *et al*. (2017) reported small spherical fruits in both *S. insanum* and *S. incanum*. All accessions had short relative calyx length (~20%) measured as percentage of total fruit length except *S. macrocarpon,* which had very long relative calyx length (>75%). *S. macrocarpon* belonging to the cultivated African Gboma eggplant complex consists of both leafy and fruity cultivars of which leafy types have inedible hard fruits and fruity types have large soft fruits with long edible calyx (Page *et al*., 2019).

The fruit pedicel length ranged from short (~10 mm) to long (~50mm) in the present study. Among the wild relatives, *S. insanum* had shortest fruit pedicel and *S. macrocarpon* the longest fruit pedicel. The cultivated accession SM-27 had longest

A. Long and medium styled flowers

SM-21 **SM-20** ***S. gilo***

Medium-styled flower **long-styled flower**

B. Relative style length

Plate 17. Variation in style length

Longest fruit (SM-11) **Widest fruit (SM-27)**

S. macrocarpon *S. gilo* *S. mammosam* *S. insanum*

Fruit shape in wild relatives

Plate 18. Variation in fruit size in S. melongena and wild accessions

pedicel among all accessions. Some of the earlier studies have suggested that fruit pedicel length and calyx length (Wagh *et al*., 2013) have strong association with the susceptibility to fruit borer and shoot borer. Fruit weight and number of fruits per plant are the component characters making major contribution towards yield in brinjal. The cultivated genotypes showed wide range of variability for fruit weight, with a maximum value of 192.7 g (SM-27) followed by 108 g (SM-23) and minimum weight of 29.04 g (SM-12). Similar findings were reported by Kumar *et al.* (2013) in the *S. melongena* collection of Tamil Nadu. In wild relatives, the fruit weight was comparatively less due to its small fruit size. According to Banik *et al*., (2018), fruit weight in brinjal is highly dependent on the flowering habit, fruits produced from solitary flower being heavier than fruits produced from flower in clusters.

Solanum melongena sets fruit one week after anthesis which reaches commercial ripeness in another three to six weeks, depending on climatic conditions (*Solanum melongena*, PROTA 2015). In the present study, the duration from flowering to fruit set was in general two weeks for both *S. melongena* and wild relatives with exceptions *viz*., *S. gilo* recording maximum duration (35.67 DAF). Early fruit set from anthesis was recorded in *S. melongena* accessions SM-14, SM-19 and SM-24 (11 DAF). The wild relatives and the cultivated accessions showed difference in the maturity duration. The maturity duration in *S. melongena* ranged from 4 to 6 weeks and was seen to be more related to the fruit size. The accession SM-27 with largest fruit size and fruit weight took maximum days for maturity and early maturation (28.33 days) was noticed in the accession SM-3 having low fruit weight and size. In case of the wild relatives, maturity duration did not seem to be related to fruit weight and size as *S. gilo* having small fruit size and weight recorded maximum duration for maturity which was followed by *S. insanum*. Puthiamadom (2018) reported absence of flowering and fruiting in *S. gilo* accession endemic to North East region evaluated in Kerala. The duration of fruit development from anthesis to maturity is a trait showing high variability between species and is strongly related to biomass composition at various stages of fruit development (Roche, 2020).

The wild relatives showed wide range of variability for number of fruits per plant with maximum number of fruits recorded in *S. mammosam* (26.67) and

minimum in *S. macrocarpon* (7.11). The *S. gilo* and *S. incanum* recorded higher number of fruits (18) than *S. melongena*. Similar results were reported by Nyanadu *et al.* (2014) in a collection of *S. macrocarpon*. But Lagat (2016) reported higher number of fruits in *S. macrocarpon* and *S. aethiopicum* ranging from 50 to 100. Since both these species belong to cultivated groups of African eggplant complex a wide variability is noted in them in Africa. In the present study, *S. melongena* cultivars did not show much variability with a range from 7 (SM-7) to 15 (SM-19). However, Solaimana *et al*. (2015) reported number of fruits per plant ranging from 7.63 to 52.98. According to Karapanos *et al*. (2008), fruit setting is efficient in cultivars with high number of long-styled flowers per inflorescence which is reflected in the present study where *S. mammosum* and *S. melongena* accession SM-25 had high number of long-styled flowers per inflorescence and complete absence of medium-styled flowers per inflorescence and had produced high number of fruits per plant.

Fruit yield per plant in brinjal is a complex quantitative character dependent on various other fruit component characters, flowering characters and their mutual interrelationships. The cultivated *S. melongena* genotypes showed wide range of variation for this character ranging from low (500 g) to high (2500 g). Maximum fruit yield of 2146.44 g was observed in SM-27 which also recorded maximum fruit weight (192.7g) and minimum fruit yield was recorded in SM-12 (292.67 g) which also recorded least fruit weight (29.04 g). Seven accessions had shown intermediate fruit yield (>1000 g) i.e. accessions SM-23 (1434.11 g), SM-10 (1285.67 g), SM-20 (1275.67 g), SM-24 (1233.67 g), SM-18 (118.56 g), SM-25 (1041 g) and SM-7 (1019.33 g). These findings are in confirmation with those reported by Dhaka and Soni (2012), Vandana *et al*. (2014) and Gavade and Ghadage (2015). However, Ahmed *et al*. (2014) reported a very high fruit yield of 5320 g per plant in a study. The wild relatives recorded fruit yield ranging from very low (<250 g) in *S. gilo* to low (250-500 g) in *S. macrocarpon* with the exception of *S. incanum* which recorded intermediate fruit yield (500-1000 g). The wild relatives had small sized and lighter fruits which resulted in low fruit yield.

In brinjal, normal fruit set and development not only requires proper pollination and fertilization but also presence of mature seeds especially to fulfill the

breeding objective of hybridization and seed production. However, seeds reduce the fruit quality for fresh consumption and processing. In the present study, the seeds were counted only on physiological ripening of fruits. Among the *S. melongena* largest number of seeds were observed in SM-23 (1591.33) and the least number in SM-18 (477.67). Das *et al*. (2017) reported variation in number of seeds ranging from 269.75 to 2114.89.

5.3.2 Incidence of pest and disease

The perennial nature of brinjal makes it vulnerable to a number of biotic stresses, especially shoot and fruit borer infestation causing drastic reduction in crop yield. So it is necessary to isolate and conserve those genotypes which are highly resistant to these stresses. In the present study both the cultivated as well as wild genotypes were only observed for the incidence of major pest and diseases such as shoot and fruit borer, phomopsis blight, bacterial wilt and little leaf incidence (Plate 19).

The preliminary observation showed high incidence of shoot and fruit borer in majority of the cultivated genotypes. Based on the percentage of infested plants, 17 out of the 25 *S. melongena* genotypes showed more than 50% plant infestation, six of the remaining accessions showed less than 50% plant infestation and less than 10% plant infestation in two genotypes *viz*., the green fruited SM-25 (3.7%) and SM-12 (7.41%). In addition to this, severe incidence of leafhopper was recorded in five *S. melongena* accessions ranging from 3.7% (SM-26) to 96.29% (SM-24). No incidence of fruit and shoot borer was observed in the three wild genotypes *viz*., *S. mammosum*, *S. gilo* and *S. insanum.* The previous studies by Hazra *et al*. (2004) and Khorsheduzzaman *et al*. (2010) reported different responses of accessions for percentage of shoot and fruit borer incidence. The green fruited accessions of *S. melongena* showed comparatively lesser incidence of fruit and shoot borer which is supported by findings of Wagh *et al*. (2012), Dar *et al*. (2014) and Prasad *et al*. (2014).

Out of 30 accessions, only SM-9 and SM-13 showed the symptoms of bacterial wilt. There was no incidence of phomopsis blight and little leaf incidence. The above results need confirmation by further detailed examination through scoring for disease and pest in field screening studies. The preliminary observations give scope for utilization of the genotypes SM-25, SM-12, SM-22 (*S. mammosam*), SM-29 (*S. gilo)* and SM-30 *S. insanum* in resistance breeding programs.

5.3.4 Analysis of variance components

The relative value of components of variance such as genotypic and phenotypic coefficient of variation gives an idea about the magnitude of variation present in a population which in turn helps to choose traits for effective selection of desirable genotypes. Heritability indicates the extent of variability transmitted to a progeny which when coupled with the estimation of genetic advance helps in understanding the type of gene action involved in the expression of various polygenic characters. Information about gene action helps in deciding breeding procedures for the improvement of the trait. In this study, the variability components were worked out and the results of analysis are discussed below:

5.3.4.1 Genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance

Genetic variability, heritability and genetic gain are important measures for making effective selection in crop improvement. The magnitude of variability is estimated with GCV and PCV. In the present study, the PCV was higher than GCV for all the characters as seen in Fig.21. However, the difference between their values is negligible for all traits except for number of long-styled flowers per inflorescence indicating low susceptibility of these traits to environmental influence. Sivasubramanian and Menon (1973) categorized GCV and PCV as low (<10%), medium (10-20%) and high (>20%). In the present study, the vegetative characters plant height and plant breadth showed moderate GCV and PCV. All the floral and fruit traits except days to first flowering, days to 50% flowering and days from fruit

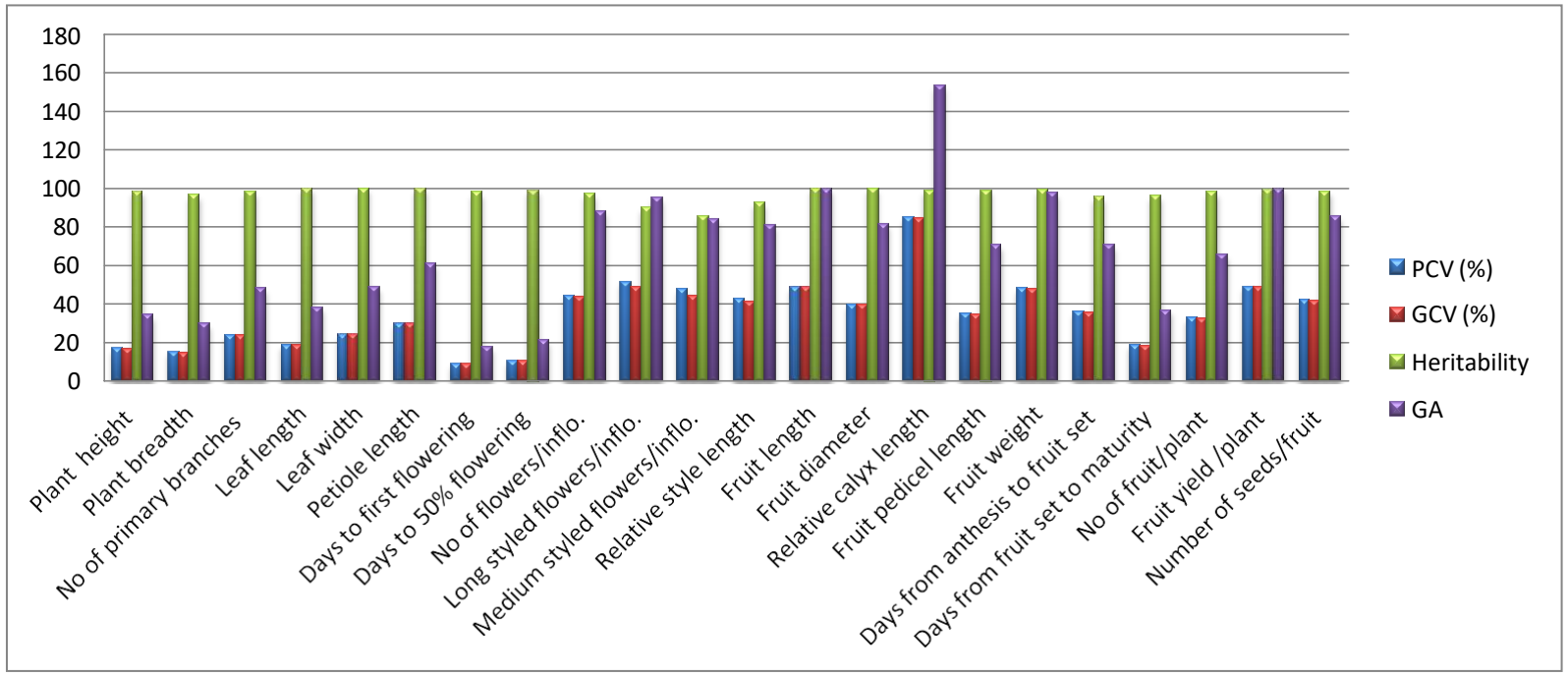


Figure 21. GCV, PCV, Heritability and Genetic advance as percentage of mean for quantitative characters

Larva

Adult

Infested fruit

Infested plant

Shoot and fruit borer infestation

Bacterial wilt in brinjal

Leaf hopper infested plant

Plate 19. Pests and diseases observed in the field

set to maturity had recorded high GCV and PCV. This indicates the presence of sufficient variability in the germplasm and there is scope for improvement of these traits through direct selection since they are less influenced by environment. Similar results were reported by Das *et al.* (2010), Muniappan *et al*. (2010), Prabakaran (2010), Kumar *et al.* (2012), Kumar *et al.* (2013), Arunkumar *et al.* (2013), Lokesh *et al*. (2013) and Nayak and Nagre (2013). The result of Sharma and Swaroop (2000) and Kumar *et al.* (2013) supported low GCV and PCV recorded for days to first flowering.

Heritability and genetic advance are two parameters which reveal gene action present in a population. Heritability is the index of extent of variability transmitted to progeny. In present study, very high heritability (>90%) was recorded for all the characters studied. Heritability estimate is relative to a population and only when it is considered along with genetic advance is more useful (Singh and Narayana, 1993). The genetic advance is the actual measure of genetic gain under selection and expressed in percentage of mean. The traits showing high heritability coupled with high genetic advance as percentage mean indicate additive gene action making selection effective for such characters in crop improvement.

High heritability along with high genetic advance as percentage mean was recorded in brinjal plant characters like plant height, plant breadth, number of primary branches, leaf length, leaf width and petiole length. Muniappan *et al.* (2010), Kumar *et al.* (2012), Arunkumar *et al*. (2013), Lokesh *et al*. (2013), Vandana *et al*. (2014) and Jirankali *et al*. (2019) reported similar result.

The flowering characters like days to 50% flowering, number of flowers/inflorescence, relative style length, number of long-styled and medium styled flowers/inflorescence also showed high heritability along with high genetic advance as per cent of mean. This is supported by findings of Sharma *et al*. (2000), Das *et al.* (2010), Chattopadhyay *et al*., (2011) and Sujin *et al*., (2017).

The fruit characters like fruit length, fruit diameter, relative calyx length, fruit pedicel length, fruit weight, number of days from anthesis to fruit set, number

of days from fruit set to maturity, number of fruits per plant, fruit yield per plant and number of seeds per fruit exhibited high heritability and genetic advance as percent mean indicating additive gene action, which is in agreement with the findings of Pathania *et al*. (2002), Das *et al*. (2010), Muniappan *et al*. (2010), Kumar *et al*. (2012), Lokesh *et al.* (2013), Vandana *et al*. (2014) and Jirankali *et al*. (2019).

5.3.5 Correlation analysis

Quantitative traits often display complex mutual relationships having huge implications in evolutionary processes and plant improvement. These relationships are the result of genetic correlations, which can be caused by pleiotropy (a phenomenon due to shared genetic influence) or linkage disequilibrium (non-random association of alleles) (Lynch and Walsh, 1998). However, genetic correlations can complicate progress of selection especially when there is unfavorable combination of traits. Fruit yield in brinjal is such a complex character resulting from various genetic as well as environmental factors, which are interrelated at different phases of plant growth. Hence, correlation analysis was carried out among 22 quantitative characters of 30 brinjal accessions to assesses the mutual association between various plant characters and determine the component characters based on which selection can be envisaged for genetic improvement of fruit yield. The results of the analysis are discussed in detail below.

In the present study value of genotypic correlation coefficient are higher than that of phenotypic correlation coefficient which indicates the apparent association of characters are largely due to genetic factors and lesser influence of environment. Similar findings were reported by Gogula (2011), Ahmed *et al*. (2012), Kumar *et al*. (2013) and Sujin *et al*. (2017).

The dependent variable fruit yield per plant showed significant and high positive genotypic and phenotypic correlation with eight characters *viz*., plant spread, leaf length, number of long-styled flowers, fruit length, fruit diameter, fruit pedicel length, fruit weight and number of seeds per fruit of the twenty-one quantitative characters. Thus indicating that selection for increased value of these characters can

bring about concomitant increase in fruit yield. Similar observations were made for fruit length (Rajyalakshmi *et al*. (2014), fruit diameter and fruit weight (Chattopadhyay *et al*., 2011; Kumar *et al*. 2013; Konyak *et al*., 2020). Negative significant correlation was observed between fruit yield and three characters related to flowering and fruit set duration *viz*., days to first flowering, days to 50% flowering and number of days from anthesis to fruit set. Similar observation was made by Kumar *et al.,* (2013) for days to first flowering but Konyak *et al.* (2020) reported positive correlation of fruit yield with days to 50 % flowering and days from anthesis to fruit set. Early flowering and fruit set increase the span of fruiting period and number of harvests consequently increasing fruit yield.

Among the vegetative characters, plant height, plant spread and leaf length had significant positive correlation with fruiting parameters such as fruit length and fruit pedicel length. Plant spread and leaf width had significant positive correlation with fruit diameter and fruit weight. Tall plants with broader canopy and leaf manifest increased level of chlorophyll status, the source which is responsible for increasing the sink i.e. fruit size and weight which in turn is reflected in high fruit yield. Plant height, leaf width and leaf petiole length had significant positive correlation with number of fruits per plant. Taller plants with wide leaf and longleaf axil can accommodate more number of fruits. The flowering duration characters v*iz*., days to first flowering, days to 50% flowering had significant negative correlation with fruiting parameters such as fruit pedicel length, fruit length, fruit diameter and fruit weight indicating early flowering and fruit set increased fruit size and fruit weight which is also reflected in the increased fruit yield. Early or first formed flowers called basal flowers are the ones that develop into fruits. The basal fruits are strong sinks and attain better size and weight by efficient utilization of carbohydrate assimilates from leaf (Karapanos *et al*., 2008).

Among the floral traits, the number of flowers per inflorescence had significant positive correlation with floral traits such as number of long-styled flowers and medium- styled flowers. Kowalska (2003) observed that the highest number of flowers with a long pistil and much fewer flowers with medium and short pistils are formed in eggplant. The flowering habit (solitary and cluster) and type of flower

based on style length are genotype dependent characters. The population in the present study consisted of both cultivated and wild species resulting in high variability for flowering habit and type of flowers. The number of flowers per inflorescence also had significant positive correlation with number of fruits per plant. Similar observations were made by Rajyalakshmi *et al*. (2014). The number of long-styled flowers per inflorescence had significant positive correlation with fruit parameters like fruit length, fruit diameter and number of fruits per plant. According to Kowalska (2006) and Sekara and Bieniasz (2008), the long and medium-styled flowers set fruits under normal field conditions with more efficient fruit set being observed in long- styled flowers. Thus, suggesting that although fruit yield relates to profuse flowering the fruit setting ability of flowers also has to be taken into consideration in brinjal (Karapanos *et al*., 2008).

The relative style length showed significant positive correlation with fruit length, fruit diameter, fruit pedicel length and fruit weight and negative association with number of fruits per plant. According to Karapanos *et al*. (2008) fruit load in brinjal is found to have negative effect on style length. Auxins control both stamen and pistil length, so auxins derived from developing fruits may inhibit the pistil length.

The fruit set and maturity duration are the traits showing strong and complex association with other fruiting and flowering traits. Number of days from anthesis to fruit set had significant negative correlation with the fruit parameters such as fruit length, fruit diameter, fruit pedicel length and fruit weight suggesting that early fruit set results in larger fruit size and fruit weight which in turn increases fruit yield. However, it was having significant positive correlation with days to first flowering, fifty percent flowering, number of long-styled flowers, days from fruit set to maturity and number of fruits per plant. Karapanos *et al.* (2008) reviewed earlier studies made by many researchers regarding fruit set in eggplant. These studies suggest that late formed solitary flowers or additional flowers in a cluster compete for carbohydrates with early formed fruits which are stronger sinks and also the hormones in such early formed fruits suppress the development of late formed fruits which are weaker sinks. Thus, ultimately resulting in large number of small sized fruits. These necessities the

desirability to have lower values for number of flowers per inflorescence as well as fruit set duration for maintaining proper and uniform fruit size in brinjal. Fruit set and development in brinjal is a highly complex process strongly influenced by flowering habit, heterostyly, hormones, environmental factors and their interaction. This is also further complicated by genetic factors such as linkage and pleiotropy having great implications in breeding programs.

Among the fruit characters, fruit length, fruit diameter and fruit pedicel length had significant correlation with fruit weight and number of seeds per fruit. All these characters were also having significant positive correlation with yield. Similar observations were also made by Rajyalekshmi *et al.* (2014), in their study of brinjal germplasm accessions. They went on to suggest that the association of characters manifest due to correlated response, a phenomenon in consequence of pleiotropy and linkage. They went on to further suggest that when two characters showing mutual correlation also show correlation with yield then such an association of characters is mainly due to pleiotropy. And that out of such mutually correlated characters when some show no correlation with yield then such an association is mostly due to linkage and not due to pleiotropy. In the present study, the significant association of fruit characters such as fruit size with fruit weight and with yield gives an indication of pleiotropy. There was significant negative correlation between fruit weight and number of fruits per plant but insignificant negative correlation between number of fruits and fruit yield. Such an association may be due to linkage. Thus, suggesting the mutual trade-off between the two traits in determining yield improvement.

In the present study, the correlation analysis reveals that the selection of genotypes based on traits like plant height, plant width, leaf blade length, number of long-styled flowers, fruit length, fruit diameter, fruit pedicel length, fruit weight, number of seeds per fruit, days to first flowering, days to 50% flowering and number of days from anthesis to fruit set can be considered for yield improvement.

5.3.6 Genotypic path coefficient analysis

The correlation coefficients are not enough to explain true relationship between two characters. It can be explained through path analysis in which the correlation coefficients are split into direct and indirect effect and it explains the actual contribution of each traits and its impact through other characters. The correlation present between two characters may be due to their correlation with a common trait. In such cases path analysis explains the real cause and effect of association.

In present study, highest positive and direct effect was shown by traits such as plant height, plant breadth, leaf blade length, number of long-styled flowers, fruit diameter, fruit weight, number of fruits per plant and number of seeds per fruit. But of these, leaf blade length, number of long-styled flowers and fruit weight had high direct effect and plant spread had moderate direct effect along with significant genotypic correlation with yield revealing the true association of these characters with fruit yield. This is in agreement with findings of Chattopadhyay *et al*. (2011) and Rajyalakshmi *et al*. (2014) for fruit weight and Ahmed *et al*. (2012) for plant width.

Among all the traits, days to first flowering had exhibited very high positive and maximum direct effect over yield effect but it had negative genotypic correlation with fruit yield. The negative correlation with fruit yield may be due to the very high negative indirect effect of the character through characters such as days to 50% flowering, fruit weight and days from anthesis to fruit set. As discussed earlier, in the correlation section of this chapter, the early flowering and fruit set is desirable for uniform and higher fruit weight. Hence, selection based on such characters showing indirect effects is desirable as their indirect effects are determining the significant genotypic correlation with yield.

The very high negative direct effect of days to 50% flowering and high negative direct effect of days from anthesis to fruit set and their significant negative genotypic correlation with yield indicate true association of these characters which in line with results of Gogula (2011).

The character fruit length had high negative direct effect but significant positive genotypic correlation with yield. The positive genotypic correlation of this character may be due to its high indirect effect via fruit weight. Similarly the characters *viz.*, plant breath and leaf width showing high positive direct effect over yield also show positive indirect effect via fruit weight over yield.

The character number of fruits per plant had high direct effect over yield but insignificant genotypic correlation with yield. The very high positive indirect effect *via* days to first flowering and very high negative indirect effect *via* days to 50% flowering had a mutual cancellation effect resulting in insignificant correlation of this trait with yield.

In the present investigation, a very low value of residual effect (0.047) was observed, indicating the sufficiency of the characters included in this study, as supported by findings of Sujin *et al.,* (2017).

The results of association analysis, thus reveal the importance of vegetative characters such as plant spread and leaf width, floral traits such as days to 50% flowering and number of long-styled flowers and component fruit trait *viz*., fruit weight on the basis

of their true relationship with yield. The trait number of fruits per plant since it had significant direct effect and also positive genotypic correlation with yield can also be taken into consideration for selection of genotypes.

5.3.7 Genetic diversity analysis

Genetic diversity is the very basis of existence of plants in nature and for crop improvement. Diversity in plant genetic resources facilitates plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (high yield potential, large seed, etc.) and breeder-preferred traits (pest and disease resistance and photosensitivity, etc.). It is also important with respect to adaptability of crop plants to varied environments with special reference to changing climatic conditions (Bhandari *et al.,* 2017). Genetic diversity can be assessed among

strains/varieties/entries of a species using multivariate techniques. These techniques can be used in assessment of genetic divergence, classification of germplasm into different groups and selection of diverse parents to develop transgressive segregants or hybrids for exploiting heterosis. In the present investigation genetic divergence was quantified in brinjal genetic resources based on 39 morphological descriptors (17 qualitative traits and 22 quantitative traits) using multivariate techniques. Cluster analysis was carried for qualitative data where similarities are considered and for quantitative data D^2 analysis was carried out where distance rather than similarities are considered (Anderson, 1984).

5.3.7.1 Clustering analysis based on qualitative characters

The cluster analysis is a multivariate method used for grouping similar lines/genotypes in one group and differentiate other groups. In present investigation, clustering was done by considering the similarity and dissimilarity in nominal values of 17 qualitative traits using UPGMA (Unweighted Pair Group Method with Arithmetic Mean). It is a hierarchical clustering based on average linkage, a robust method of handling clusters of different sizes (Fang *et al*., 2020).

The clustering of 30 eggplant accessions as revealed by the dendrogram (Fig.22) shows three main groups based on similarity within clusters and dissimilarity between clusters for anthocyanin pigmentation of plant parts, leaf prickliness, growth habit and colour at fruit ripening (commercial and physiological). Twenty six genotypes including wild accessions *S. macrocarpon* (SM-2) *S. incanum* (SM-28), *S. insanum* (SM-29) are grouped into cluster I based on green leaf colour differentiated from other groups consisting of genotypes with dark green colour which included wild relatives *S. mammosum* (SM-22) and *S. gilo* (SM-29). Cluster I is subdivided into sub-cluster A (SM- 25 and SM-30 (*S.insanum*)) with prostrate growth habit and leaf prickliness and sub-cluster B genotypes with upright to intermediate growth habit and leaf with none to very few prickles. The sub clustering of cluster I showed sub-cluster A falls into a separate cluster may be due to dark purple stem and red colored fruit on its physiological ripening. Genotypes in cluster II (SM-11, SM-15 and SM-22) show similarity with respect to dark green coloured leaf blade, strong leaf lobing

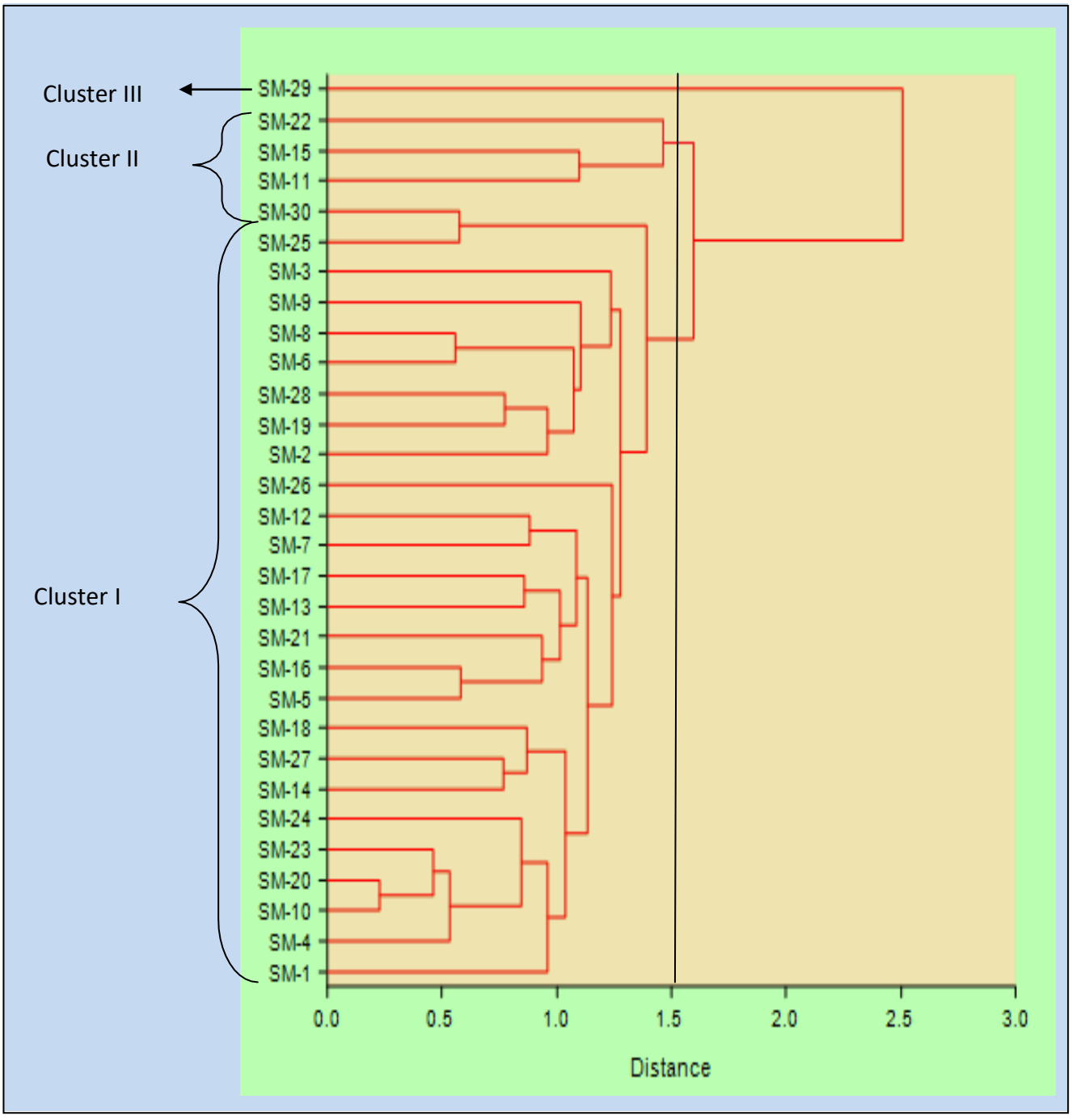


Figure 22. Cluster diagram showing relationship among 30 brinjal genotypesby UPGMA cluster analysis based on qualitative characters

and acute leaf tip angle. Cluster II on subdivision shows sub-cluster A with two genotypes (SM-11 and SM-15) having purple petiole, purple flower, purple and pendant fruits and sub-cluster B with SM-22 (*S. mammosum*) having some unique characters dark purple petiole, blush violet flower, yellow-coloured fruit on commercial ripening and horizontally positioned unique udder shaped fruits. Cluster III had one genotype SM-29 (*S. gilo*) African cultivated type unique with dark purple stem and scarlet red fruit color at physiological ripening.

Clustering pattern based on qualitative characters indicated that both wild and cultivated types comes under same cluster as seen in dendrogram. Thus it is observed cluster I had S. *insanum* grouped along with *S. melongena* for similarity in majority of the characters such as green leaf blade colour, intermediate lobing, pale violet corolla, fruits without curvature and fruits with widest part halfway from base to tip (ovoid shape). This may be due to close affinity of *S. insanum* with *S. melongena* as it is considered as the wild ancestor of brinjal (Syfert, 2016). *S. mammosum* and *S. gilo* were distinct from the cultivated species for their unique fruits and anthocyanin pigmentation in plant parts. The wild relatives were distinct from cultivated species for presence of prickles and anthocyanin pigmentation traits considered important for stress tolerance. This may be the reason for their adaptation in wide range of environmental conditions, including desertic and semi-desertic areas, environment with extreme temperatures (Knapp *et al*., 2013).

5.3.7.2 D^2 statistics based on quantitative characters

Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. Mahalanobis D^2 statistic is one such multivariate technique that helps in quantifying the degree of divergence between biological populations (Genetic distance) and to assess the relative contribution of different components to the total divergence. Hence, in the present study genetic divergence in brinjal genetic resources consisting of cultivated species and wild relatives for quantitative traits was assessed using Mahalanobis D^2 statistics, which measures the force of differentiation at the intra- and inter-cluster level and thus provides reasonable selection of genetically divergent

parents. The dendrogram was constructed through Tocher's method (Fig.23) which grouped the 30 brinjal genotypes into eight clusters. The clustering pattern of 30 genotypes revealed a clear separation of wild relatives and cultivated types. All the wild accessions were grouped in five different clusters (III, IV, VI, VII and VIII). All *S. melongena* genotypes were grouped into cluster I (22 Nos.), cluster II (SM-11), cluster III (SM-25) and cluster V (SM-27).

The grouping pattern of the 30 accessions showed all the genotypes collected from North Kerala grouped into one single cluster suggesting the parallelism between geographical diversity and genetic diversity. This is maybe due to the fact that maximum accessions (11 Nos.) were collected from Malappuram district and its neighboring district Kozhikode (4) and the remaining from Kannur, Kazharagod and Wayanad. Even though all the wild accessions in the present study were obtained from gene bank (NBPGR) except *S. macrocarpon* (SM-2) collected from Kannur, all of them had grouped into separate clusters. The *S. incanum* had grouped into cluster III along with cultivated accession SM- 25 obtained from NBPGR. Similar observations were made by Mutegi *et al*. (2015) in the diversity analysis consisting of natural populations of wild/weedy eggplant and cultivated populations in Southern India where the wild brinjal populations appeared to cluster according to their geographic origin. The closest wild relatives of brinjal are S. *insanum* and *S. incanum*. *S. insanum* is of Asian origin and is used medicinally in Southern China and is considered distinct from the cultivated *S. melongena* by local people. *S. incanum* is considered to be of African origin occurring widely in dry regions from Northern Kenya to Pakistan and in general occurs in drier areas (Knapp *et al.,* 2013).

Gboma eggplant *S. macrocarpon* and scarlet eggplant *S. gilo* belong to the cultivated brinjal domesticated in Africa conventionally grouped as 'Occidental" and differ from *S. melongena* grouped as 'Oriental' grown in East and Southeast Asia (Cericola *et al*., 2013). Hence, in the present study, two accessions SM-2 and SM-29 belonging to these species were grouped into separate clusters Cluster IV and Cluster VI respectively.

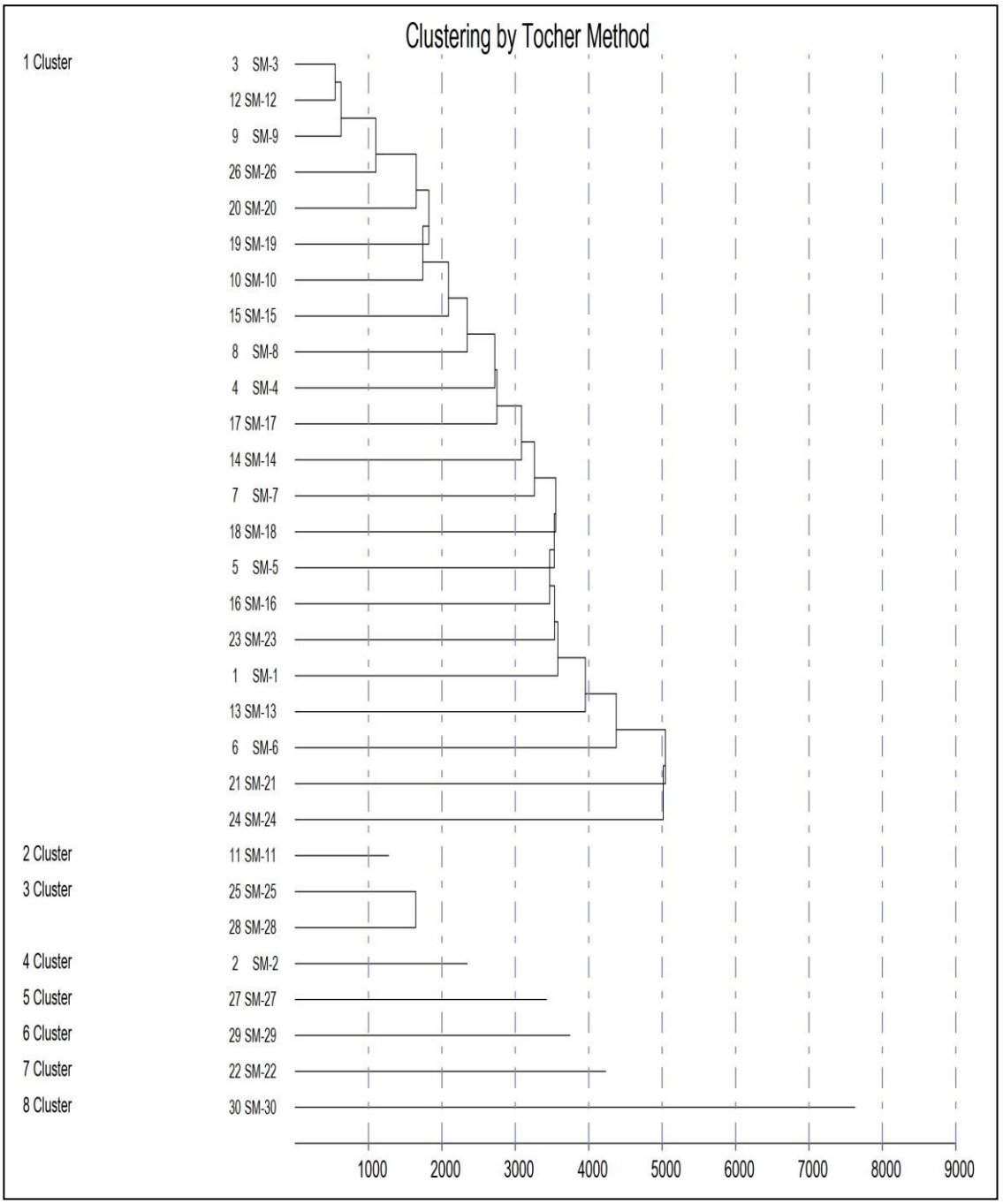


Figure 23. Dendrogram (cluster diagram) showing the relationship among 30 brinjal genotypes developed by Tocher method based on 22 quantitative characters

Solanum mammosum the wild relative collected from Kasaragod was placed in cluster VII. This species is considered as an invasive weedy species introduced into India as an ornamental for its fancy udder-shaped fruits (Singh *et al*., 2017).

The *S. melongena* accession SM-27 obtained from NBPGR was placed separately as a solitary constellation (cluster V) mainly for its morphological and genetic differentiation based on fruit characters.

5.3.7.2.1 Intra- cluster and inter-cluster distance

The maximum intra-cluster distance was reported in cluster I, followed by cluster III. The remaining clusters have zero intracluster distance since these clusters have single genotypes each (Fig.24). Banerjee *et al*., (2018) reported similar clustering in their respective studies. The intra-cluster distance is lower than inter-cluster distance as Tocher's method (Rao, 1952) allows establishing mutually exclusive clusters of objects adopting the criterion of optimization, which minimizes the average intra-cluster distance and maximizes the average inter-cluster distance (Silva and Dias, 2013).

The highest inter-cluster distance (44564.7) was recorded between solitary clusters VIII having *S. insanum* (SM-30) and V having SM-27 followed by cluster II (SM-11) and VIII indicating maximum divergence between these clusters. Hence the accessions in these clusters can be selected for interspecific hybridization. The accession belonging to cluster II and V and cluster I and V can be used for intraspecific hybridization.

5.3.7.2.2 Percent contribution of different characters and cluster means of brinjal

The clusters have been formed based on the contribution of different characters towards divergence. The contribution of each character towards genetic divergence was obtained through Wilk's test (Table 3). Among the characters, fruit yield/plant exhibited the maximum contribution (39.77%) towards diversity followed by leaf blade width (20.92%), number of fruits per plant (16.09%), leaf blade length

(10.8%), fruit length (3.22%), fruit diameter (2.76% and petiole length (2.76%). Other characters showed negligible or no contribution towards divergence. Banerjee *et al*., (2018) reported genetic divergence in brinjal was mainly contributed by number of fruits per plant in his study on brinjal.

Cluster means of eight clusters indicated variation in the magnitude of mean values for all 22 characters. The maximum cluster mean was in cluster V with genotype SM-27 for fruit diameter, fruit weight and fruit yield per plant. This cluster could be functional sources of genes for yield component attributes. The lowest cluster mean was in cluster II for days to first flowering and days to 50% flowering and in cluster VIII for number of days from anthesis to fruit set. Such early flowering

and fruit set could be helpful for developing an early plant type. A high yielding, early flowering and fruit setting brinjal breeds could be developed through utilizing the genotypes from these clusters as parents which is in line with findings of Ravali *et al*. (2017) and Kumar *et al*. (2013).

5.3.4 Selection Index

Identification and selection of parents with desirable character combinations for the improvement of yield in segregating generation plays a major role in crop improvement and hybridization programs.

According to Smith (1936), selection of parents through index is one among the fundamental method of improvement of traits in crop plants at genetic level. Selection of plants with index providing proper weightage to each trait is more effective than selection with single traits or several traits independently.

In present study characters *viz*., fruit yield per plant (X_1), number of long-styled flowers per inflorescence (X_2), fruit diameter(X_3), fruit weight (X_4) and number of seeds per fruit (X_5) were considered to estimate selection index based on significant genotypic correlation with yield and high positive direct effect on fruit yield per plant. This is in line with work of Chattopadhyay *et al.* (2011) in construction of selection index for brinjal.

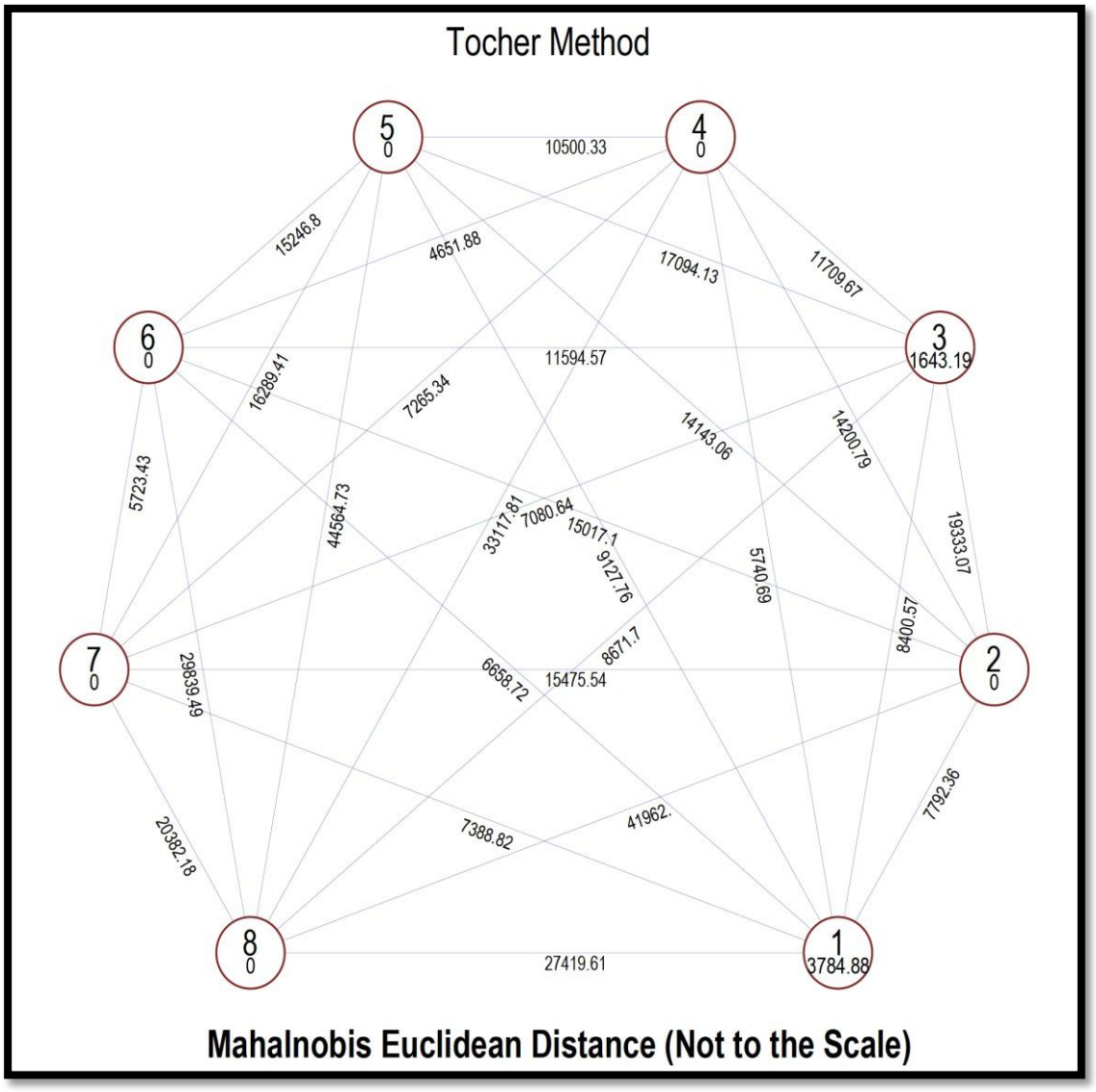


Figure 24. Cluster diagram prepared through Mahalnobis Euclidean Distance (Not to the Scale) method for 8 clusters

Selection of individual trait index I_2 (number of long-styled flowers per inflorescence) showing highest relative efficiency (86.14%) and expected genetic gain (723.58) will be more efficient over direct selection for yield. Relative efficiency of fruit weight (72.37%) was close to the relative efficiency of fruit yield per plant (84.158%) which indicates these trits can be utilized effectively over direct selection for brinjal crop improvement. Similarly, a higher relative efficiency over direct selection for fruit yield in brinjal was observed by Bashar *et al*. (2015) for individual characters like weight per fruit, number of fruits in solitary cluster and number of fruits in inflorescence per plant. For breeding purpose constructing selection index using combination of at least three characters is generally preferred as this makes selection more effective.

In the present study the index value for three (I_{123}; 87.568%), four (I_{1234}; 87.895%) and five (I_{12345}; 87.935%) have shown more relative efficiency over direct selection. The five character combination of fruit yield per plant, number of long-styled flowers per inflorescence, fruit diameter, fruit weight and number of seeds per fruit have maximum relative efficiency coupled with high expected genetic gain (738.685). However inclusion of trait, number of seeds per fruit in two traits, three traits, four traits combinations and considered individually reduce the selection efficiency. Hence in this study, the most efficient and effective index is the four trait combination (fruit yield per plant + number of long-styled flowers/inflorescence + fruit diameter + fruit weight).

5.4 Selection of parents suitable for breeding program in brinjal

Selection of appropriate parents for hybridization is one of the challenging task in the production of superior recombinant progeny. In present study, an attempt is made to utilize index score along with genetic diversity analysis for selection of superior genotypes as parents for hybridization program in future.

The crosses between genotypes belonging to clusters having high inter-cluster distance are considered to yield better segregates. The accessions SM-11, SM-27 and *S. insanum* of highly divergent clusters II, V and VIII respectively are identified as

potential parents for developing introgression line (ILs) an important step towards broadening of eggplant genetic base. The wild species *S. insanum* is classified under primary gene pool (GP1) based on its crossability with cultivated *S. melongena* species as reported by Plazas *et al.* (2016) who could obtain large amount of seeds per fruit when using *S. melongena* as a female parent in hybridization with *S. insanum*. The ILs will thus allow an expeditious use of genes from the wild species in present and future breeding programs in particular for traits related to climate change adaptation.

Compatible crosses are obtained when *S. melongena* accession is used as female parent in interspecific hybridization. Crosses involving *S.incanum* gives partially fertile hybrid progeny as it belongs to secondary gene pool and *S. mammosum* may lead to high incompatibility as it belongs to tertiary gene pool.

The *S. melongena* genotypes of highly divergent clusters like cluster I (SM 20, SM 10, SM 23, SM 24, SM 8 and SM 18), cluster III (SM 25) and Cluster V (SM 27) with highest index score are identified as potential parents for future breeding.

In brinjal breeding fruit colour plays a major role in selection of cross combination. In general the purple fruited genotypes are preferred to cross with purple fruited genotypes, and it is true with respect to green fruited and white fruited accessions also.

Based on above consideration cross combinations of genotypes belonging to highly divergent clusters and those with high index score are presented in descending order of inter-cluster distance in Table 19 and the following crosses can be taken for the future breeding program.

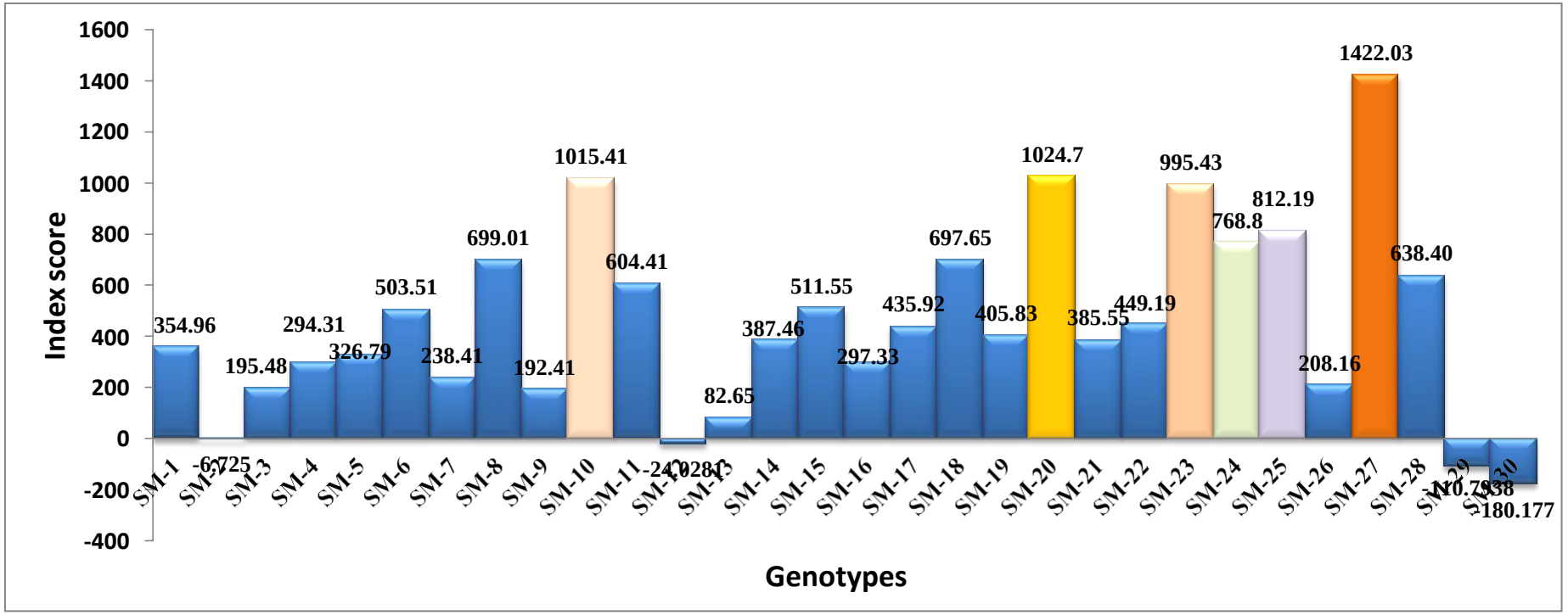


Figure 25. Index core developed for each genotypes by using best selection index (I_{1234})

SM -27

SM-23

SM-10

SM-20

Plate 20. Superior genotypes

Cont.

SM-24

SM-8

SM-18

SM-25

Table 19. Possible cross combinations of brinjal genotypes based on fruit colour and average cluster distance

Sl. No.	Cluster combination	Average cluster distance	Cross combination	Colour combination	Intra/Interspecific cross
1	V X VIII	44564.7	SM-27 x SM-30 (*S. insanum*)	Green x Green	Inter-specific cross
2	I X VIII (SM-30)	27419.6	SM-8 x SM-30	Purple x Green	Inter-specific cross
			SM-10 x SM-30		
			SM-18 x SM-30		
			SM-20 x SM-30		
			SM-23 x SM-30		
			SM-24 x SM-30		
3	V X III	17094.1	SM-27 x SM-25	Green x Green	Intra- specific cross
5	V X VI	15246.8	SM-27 x SM-29 (*S. gilo*)	Green x Green	Inter-specific cross
6	III X IV	11709.7	SM-25 x SM-2 (*S. macrocarpon*)	Green x Green	Inter-specific cross
7	III X VI	11594.6	SM-25 x SM-29	Green x Green	Inter-specific cross
8	IV X V	10500.3	SM-27 x SM-2	Green x Green	Inter-specific cross
9	III X VIII	8671.7	SM-25 x SM-30	Green x Green	Inter-specific cross
13	I X VI (SM-29)	6658.72	SM-8 x SM-29	Purple x Green	Inter-specific cross
			SM-10 x SM-29		
			SM-18 x SM-29		
			SM-20 x SM-29		
			SM-23 x SM-29		
			SM-24 x SM-29		
14	I X IV (SM-2)	5740.69	SM-8 x SM-2	Purple x Green	Inter-specific cross
			SM-10 x SM-2		
			SM-18 x SM-2		
			SM-20 x SM-2		
			SM-23 x SM-2		
			SM-24 x SM-2		
			SM-10 x SM-8		
			SM-18 x SM-8		

15	I X I	3784.88	SM-20 x SM-8	Purple x Purple	Intra- specific cross
			SM-23 x SM-8		
			SM-24 x SM-8		
			SM-10 x SM-18		
			SM-10 x SM-20		
			SM-23 x SM-10		
			SM-10 x SM-24		
			SM-20 x SM-18		
			SM-23 x SM-18		
			SM-24 x SM-18		
			SM-23 x SM-20		
			SM-20 x SM-24		
			SM-23 x SM-24		

Selection of superior parents become incomplete without some practical considerations such as earliness (days to first flowering, days to 50% flowering and number of days from anthesis to fruit set), fruit yield per plant, fruit weight, number of fruit per plant, number of long-styled flowers, etc., since we are concerned with more heterotic and adaptive segregating population.

The present investigation concludes that the green fruited SM-27 with high fruit yield and comparatively lesser incidence of shoot and fruit borer can be considered as one of the promising parent in future crop development programs. Similarly, the genotypes SM 20, SM 10, SM 23, SM 24, SM 8, SM 25 and SM 18 are identified as superior genotypes with respect to yield characters (Plate 20). The wild relatives from highly divergent clusters like cluster III (SM-28), cluster IV (SM-2), and cluster VIII (SM-30) can be exploited for their shoot and fruit borer resistance. The cross between SM 27 and green fruited SM 25 with prickles may help in development of potential F1 progeny with respect to yield and resistance to shoot and fruit borer.

5.4 Future line of work

- ✓ The fruit quality characters such as protein, phenol and vitamins can be estimated
- ✓ The study was entirely based on morphological characterization. It can be further validated with molecular markers
- ✓ The accessions have to be further evaluated for yield components characters, physiological parameters and nutritional quality in more seasons and locations

SUMMARY

6. SUMMARY

The study entitled "Characterization of brinjal (*Solanum melongena* L.) and its wild relatives" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Padannakkad during 2018-2020. The main objectives of the study was to characterize the brinjal genotypes and its wild relatives based on morphological characters; analyze the genetic variability in collected accessions and to develop selection index for cultivated types.

The experiment was laid out in randomized block design with 30 genotypes in three replications. The mean performance, variability parameters (GCV, PCV, heritability and GA), association studies based on correlation and path analysis, divergence analysis and selection index using discriminant function were studied. The important findings are presented below:

1. Forty two brinjal genotypes including both cultivated and wild relatives collected through detailed survey directed in various brinjal growing belts of North Kerala in the five districts *viz*., Kasaragod, Kannur, Malappuram, Kozhikode and Wayanad as well as those indented from regional station NBPGR, Thrissur, of which thirty genotypes were chosen for present study.

2. Passport data for thirty accessions were prepared and assigned collectors number.

3. The analysis of variance revealed significant variation among all the characters studied at 5% and 1% level of probability.

4. The mean performance of 30 genotypes for 22 quantitative characters revealed distinct variation between cultivated and wild genotypes for vegetative, flowering and fruiting characters.

5. Accessions SM-25 and SM-12 showed lesser incidence and wild accessions like

S. mammosum, *S. gilo* and *S. insanum* showed absence of shoot and fruit borer incidence. Out of thirty accessions, SM-9 and SM-13 showed symptoms of bacterial wilt. Among seven accessions which showed incidence of leafhopper, SM-26 showed lesser percentage of incidence and SM-24 showed the maximum.

6. High heritability coupled with high genetic advance as percent of mean was observed in vegetative characters (like plant height, plant breadth, number of primary branches, leaf blade length, leaf blade width and leaf petiole length), flowering characters (like days to 50% flowering, number of flowers/ inflorescence, number of long-styled flowers, number of medium styled flowers and relative style length) and fruit characters (like fruit length, fruit diameter, relative calyx length, fruit pedicel length, fruit weight, number of days from anthesis to fruit set, number of days from fruit set to maturity, number of fruits per plant, fruit yield per plant and number of seeds per fruit) indicating that the heritability is due to additive gene action, hence selection based on these characters are effective.
7. Correlation analysis revealed a positive significant correlation of yield with characters plant height, number of primary branches, leaf blade length, number of medium styled flowers, fruit pedicel length, fruit length, fruit diameter, fruit weight and number of seeds per fruit. The characters contributing for earliness (days to first flowering, days to 50% flowering and number of days from anthesis to fruitset) showed negative correlation with yield

8. Path analysis revealed that days to first flowering, plant height, number of medium styled flowers, fruit diameter, fruit weight and number of seeds per fruit had high positive direct effect, hence selection based on these characters help in improving yield

9. The cluster analysis of 30 genotypes based on 17 qualitative characters using UPGMA method grouped these genotypes into three clusters.

10. Genetic diversity analysis using Mahalanobis D^2 analysis grouped 30 genotypes into

eight clusters based on 22 quantitative characters.

11. Based on association analysis and divergence analysis three yield attributes *viz*., fruit weight, number of fruits per plant and fruit yield per plant were used for ranking the genotypes in each cluster.

12. Among 22 characters fruit yield per plant exhibited the maximum contribution towards diversity followed by leaf blade width, number of fruits per plant, leaf blade length, fruit length, fruit diameter and petiole length. Other characters showed negligible contribution towards divergence.

13. The maximum intra-cluster distance was reported in cluster I, followed by cluster III. The remaining are solitary clusters. The highest inter-cluster distance was recorded between solitary clusters VIII having *S. insanum* (SM-30) and V having S. melongena accession SM-27.

14. Selection index involving discriminant functions based on relative economic importance of various characters showed a combination of four characters (Fruit yield per plant + Number of medium styled flowers + Fruit diameter + Fruit weight) with maximum relative efficiency.

15. Based on high selection index score involving four-character combination and overall cluster ranking based on three yield attributes, two green fruited accessions SM 27, SM 25 and six purple fruited accessions SM-8, SM-10, SM-18, SM-20, SM-23 and SM 24 are identified as promising one.

16. Even though *S. incanum* (SM-28) and *S. mammosum* (SM-22) and are cross compatible with *S. melongena* the crosses involving *S. incanum* gives partially fertile hybrid progeny as it belongs to secondary gene pool and *S. mammosum* may lead to high incompatibility as it belongs to tertiary gene pool.

17. Based on selection index score and cluster divergence (high inter-cluster distance) the

SM-27 is identified as promising parent in intra-specific hybrid involving of SM-27 x SM-25 and inter-specific hybrids involving SM-27 x *S. insanum* and SM-27 x *S. macrocrpon*. This crosses may be attempted in future breeding program for obtaining progenies superior for yield as well as shoot and fruit borer resistant.

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APPENDIX

Apendix I

1. Plant height

   At flowering stage

1	Very short	(<20 cm)
3	Short	(~30 cm)
5	Intermediate	(~60 cm)
7	Tall	(~100 cm)
9	Very tall	(>150 cm)

2. Plant breadth

   At floewering stage

1	Very narrow	(<30 cm)
3	Narrow	(~40cm)
5	Intermediate	(~60 cm)
7	Broad	(~90 cm)
9	Very broad	(>150 cm)

3. Plant branching

   Number of primary branches per plant

1	Very weak	(~2)
3	Weak	(~5)
5	Intermediate	(~10)
7	Strong	(~20)
9	Very strong	(>30)

4. Leaf blade length

3	Short	(~10 cm)
5	Intermediate	(~20 cm)
7	Long	(~30 cm)

5. Leaf blade width

3	Narrow	(~5 cm)
5	Intermediate	(~10 cm)
7	Wide	(~15 cm)

6. Petiole length

0	None	
1	Very short	(<5 mm)
3	Short	(~10 mm)
5	Intermediate	(~30 mm)
7	Long	(~50 mm)
9	Very long	(>100 mm)

7. Relative style length

3	Short	(~1 mm)
5	Intermediate	(~3mm)

7	Long	(~5 mm)

8. Fruit length

From base of calyx to tip of fruit

1	Very short	(<1 cm)
3	Short	(~2 cm)
5	Intermediate	(~5 cm)
7	Long	(~10 cm)
9	Very long	(>20 cm)

9. Fruit breadth

Diameter at broadest part

1	Very small	(<1 cm)
3	Small	(~2 cm)
5	Intermediate	(~3 cm)
7	Large	(~5 cm)
9	Very large	(>10 cm)

10. Fruit pedicel length

1	Very short	(<5 mm)
3	Short	(~10 mm)
5	Intermediate	(~25 mm)
7	Long	(~50 mm)
9	Very long	(>75 mm)

11. Relative fruit calyx length

Measured as percentage of total fruit length

1	Very short	(<10%)
3	Short	(~20%)
5	Intermediate	(~50%)
7	Long	(~70%)
9	Very long	(>75%)

12. Fruit yield per plant

1	Very low	(<250 g)
3	Low	(~500 g)
5	Intermediate	(~1000 g)
7	High	(~2500 g)
9	Very high	(>5000 g)

13. Number of seeds per fruit

0	None	
1	Very few	(<10)
3	Few	(~50%)
5	Intermediate	(~100)
7	Many	(~300)
9	Very many	(>500)

CHARACTERIZATION OF BRINJAL (*Solanum melongena* L.) AND ITS WILD RELATIVES

By

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Abstract of the Thesis

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ABSTRACT

The study entitled "Characterization of brinjal (*Solanum melongena* L.) and its wild relatives" was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Padannakkad during 2018-2020. The main objectives of the study was to characterize the brinjal genotypes and its wild relatives based on morphological characters; analyze the genetic variability in collected accessions and to develop selection index for cultivated types. The experimental meterial consisted of 25 *S. melongena* accessions and five wild relatives (*S. mammosum*, *S. macrocarpon*, *S. insanum*, *S. incanum* and *S. gilo*) collected from North Kerala (Malappuram-11, Kozhikode-5, Kannur-4, Kasaragod-3, Wayanad-1) and Regional station, NBPGR, Thrissur (6).

The passport data of thirty accessions were prepared and these were evaluated for 17 qualitative and 22 quantitative characters based on IPGRI descriptor in field experiment laid out in Randomized Block Design with three replications. The morphological characterization based on qualitative characters showed wide variation for stem colour, leaf lobing, fruit shape and fruit colour. The results of analysis of variance indicated significant differences for all the quantitative characters indicating presence of high genetic variability. The mean performance of genotypes revealed distinct variation between cultivated and wild accessions for most of the characters. The wild accessions recorded lower values for fruit yield and fruit weight but longer duration for floweringand fruit set. Eight *S. melongena* accessions (SM 27, SM 25, SM 23, SM 20, SM 10, SM 23, SM 24 and SM 8) had high fruit yield per plant (more than 1000 g). The accession SM 27 had shown superiority for important yield component traits like fruit yield, fruit diameter and fruit weight. Among all accessions, the green fruited *S. melongena* accession SM-25 showed lesser incidence of shoot and fruit borer. Three wild accessions *S. mammosum* (SM 22), S. gilo (SM 29) and S. insanum (SM 30) showed no incidence offruit and shoot borer.

The variance component analysis revealed high heritability coupled with high genetic advance as per cent of mean for all flowering and fruit characters indicating

that most likely the heritability is due to additive effects making selection effective based on these characters. Association analysis revealed that plant height, days to first flowering, number of long styled flowers, fruit diameter, fruit weight and number of fruits per plant shown significant genotypic correlation and direct effect showing true association of these characters with fruit yield. Selection based on all these characters will help to achieve efficient improvement in fruit yield.

The UPGMA clustering of 30 eggplant accessions for qualitative traits revealed three groups based on anthocyanin pigmentation of plant parts and leaf prickliness, traits important for stress tolerance.

The genetic diversity analysis based on Mahalanobis D^2 statistics for 22 quantitative characters grouped 30 accessions into eight clusters. The clustering patern showed the *S. melongena* accessions collected from North Kerala grouped under cluster I (22) and cluster III (2). All the five wild accessions were grouped in five different clusters (III, IV, VI, VII and VIII). The green fruited accessions SM 25 and SM 27 collected from NBPGR were placed in cluster III and cluster V indicating their distinctness. The character fruit yield per plant, leaf blade width, number of fruits per plant and leaf blade length hade made major contribution towards genetic divergence with maximum by fruit yield per plant. The maximum intra-cluster distance was reported in cluster I, followed by cluster III. The remaining are solitary clusters. The highest inter- cluster distance was recorded between solitary clusters V and VIII, V and IV and V and III providing scope for hybridization between genotypes of these highly divergent cluster especially involving wild accession SM 30 for fruit and shoot borer resistance.

Selection index involving discriminant functions based on relative economic importance of various characters showed a combination of four characters (Fruit yield per plant + Number of long styled flowers + Fruit diameter + Fruit weight) with maximum relative efficiency. Based on high selection index score involving four character combination and overall cluster ranking for three yield attributes two green fruited accessions SM 25 and SM 27 and six purple fruited accessions SM-8, SM-10, SM-18, SM-20, SM-23 and SM 24 are identified as promising. Among these,

the green fruited accession SM 25 had shown very low incidence of fruit and shoot borer.

Based on selection index score and cluster divergence (high inter-cluster distance) the SM-27 is identified as promising parent in intra-specific hybrid involving of SM-27 x SM-25 and inter-specific hybrids involving SM-27 x *S. insanum* and SM-27 x *S. macrocrpon*. These crosses may be attempted in future breeding program for obtaining progenies superior for yield as well as shoot and fruit borer and bacterial wilt resistance.

സംക്ഷിപ്തം

പടന്നക്കാട് കാർഷിക കോളേജിന്റെ, സസ്യ പ്രജനന ജനിതക വിഭാഗത്തിന് കീഴിലായി 2018-2020 കാലയളവിൽ "വഴുതനയുടെയും അതിന്റെ കാട്ടിനങ്ങളുടെ പ്രതീകവൽക്കരണം" എന്ന തലക്കെട്ടിൽ പഠനം നടത്തുകയുണ്ടായി. വഴുതന ജനിതക രൂപങ്ങളുടെയും അതിന്റെ കാട്ടിനങ്ങളുടെയും രൂപാന്തര സ്വഭാവത്തെ കുറിച്ച് പഠിക്കുക തുടർന്ന് ശേഖരിച്ച ഇനങ്ങളുടെ ജനിതക വ്യതിയാനം വിശകലനം ചെയ്യുക കൃഷിചെയ്യുന്ന ഇനങ്ങൾക്കായി തിരഞ്ഞെടുക്കൽ സൂചിക വികസിപ്പിക്കുക എന്നിവയായിരുന്നു പഠനത്തിന്റെ പ്രധാന ലക്ഷ്യങ്ങൾ.

വടക്കൻ കേരളത്തിലെ അഞ്ചു ജില്ലകളായ കാസർകോഡ്, കണ്ണൂർ, കോഴിക്കോട്, മലപ്പുറം, വയനാട് എന്നിവിടങ്ങളിൽ നിന്നും കൂടാതെ എൻ. ബി. പി. ജി. ആർ. തൃശൂർ പ്രാദേശിക കേന്ദ്രത്തിൽ നിന്നും ശേഖരിച്ച വഴുതന ഇനങ്ങൾ ആണ് (25 നാടൻ വഴുതന ഇനങ്ങളും അതിന്റെ അഞ്ചു കാട്ടിനങ്ങളുമാണ്) പഠനത്തിനായി ഉപയോഗിച്ചത്. ശേഖരിച്ച വഴുതന ഈണങ്ങളുടെ പാസ്പോർട്ട് ഡാറ്റ തയ്യാറാക്കുകയും തുടർന്ന് കേരളം സർവകലാശാല ശുപാർശപ്രകാരമുള്ള പരിപാലന മുറയോട് കൂടി 30 വഴുതന ഇനങ്ങളെ റാൻഡ്മൈസ്ഡ് ബ്ലോക്ക് ഡിസൈനിൽ മുന്ന് അവർത്തനങ്ങളോട് കൂടി പരീക്ഷണം നടത്തുകയും ചെയ്തു.

വഴുതനയിലെ രൂപശാസ്ത്രപരമായ മൂല്യനിർണയത്തിൽ നിന്നും തണ്ടിന്റെ നിറത്തിലും ഇലയുടെ രൂപത്തിലും പഴങ്ങളുടെ നിറത്തിലും ആകാരത്തിലും 30 വഴുതനയുടെ ഇനങ്ങൾ വലിയ തോതിൽ വ്യത്യാസങ്ങൾ കാണിക്കുന്നതായി കണ്ടു. ക്വാണ്ടിറ്റേറ്റീവ് സ്വഭാവങ്ങളുടെ വേരിയൻസ് വിശകലനത്തിൻറെ ഫലങ്ങൾ ഇവയ്ക്കിടയിൽ ഉയർന്ന ജനിതക വ്യത്യാസത്തിൻറെ സാനിധ്യത്തെയാണ് സൂചിപ്പിച്ചത്. അതോടൊപ്പം ശരാശരി പ്രേകടനത്തിന്റെ അടിസ്ഥാനത്തിൽ വഴുതനയിലെ നാടൻ ഇനങ്ങളും കാട്ടുകുടുംബങ്ങളും തമ്മിൽ മിക്ക സ്വഭാവങ്ങളിലും വ്യക്തമായ വ്യത്യാസങ്ങൾ കാണികുന്നതായും കണ്ടു.

കാട്ടുവഴുതനകൾക്കു പൂവിടുന്നതിനും കായ്ക്കുന്നതിനും കൂടുതൽ ദൈർഘ്യം ഉള്ളതായി കണ്ടു കൂടാതെ അവ ഫലവിളവിലും ഫലഭാരത്തിലും കുറഞ്ഞ മൂല്യങ്ങൾ രേഖപെടുത്തിയതായും കണ്ടു. എസ്. എം -27, എസ്. എം.-25, എസ്. എം.-23, എസ്. എം.-20, എസ്. എം.-10, എസ്. എം.-18, എസ്. എം.-24 എസ്.

എം.-8 എന്നി എട്ടു നാടൻ ഇനങ്ങൾ ഫല വിളവിൽ മികവ് കാണിച്ചു (1000 ഗ്രാമിൽ കൂടുതൽ) . എസ്. എം.-27 എന്ന ഇനം ഫലം വിളവ്, പഴത്തിന്റെ വ്യാസം, പഴങ്ങളുടെ ഭാരം എന്നിവ പോലുള്ള പ്രധാന വിളവ് ഘടക സവിശേഷതകളിൽ മികവ് പുലർത്തി. പച്ച നിറമുള്ള വഴുതന ഇനങ്ങളിൽ (എസ്. എം. - 25) വഴുതന തണ്ടു തുരപ്പൻറെ സാന്നിദ്യം വളരെ കുറവായി കാണപ്പെട്ടു മാത്രമല്ല ഈ പരീക്ഷണ കാലയളവിൽ ഒരു കാട്ടുവഴുതനകളിലും ഇവയുടെ സാന്നിദ്യം രേഖപെടുത്തിയിട്ടില്ല.

വേരിയൻസ് ഘടക വിശകനാളത്തിലുടെ പൂക്കളും പഴങ്ങളും സംബന്ധിച്ചുള്ള എല്ലാ ഘടകങ്ങളും ഉയർന്ന പാരമ്പര്യവും ജനിതക മുന്നേറ്റവും പ്രേകടിപ്പിക്കുന്നതായി കണ്ടു ഇതിനു കാരണം ഈ ഘടകങ്ങൾ തമ്മിലുള്ള സങ്കലന പ്രഭാവമാണ്. അതുകൊണ്ടുതന്നെ ഇത്തരം ഘടകങ്ങളെ അടിസ്ഥാനമാക്കിയുള്ള തിരഞ്ഞെടുക്കലുകൾ എപ്പോഴും ഫലപ്രദമായിരിക്കും. സസ്യങ്ങളുടെ ഉയരം, ആദ്യമായി പൂവിടുന്ന ദിവസം, നീളമുള്ള ശൈലിയിലുള്ള പൂക്കളുടെ എണ്ണം, പഴങ്ങളുടെ വ്യാസം, പഴങ്ങളുടെ ഭാരം, ഒരു ചെടിയിലെ പഴങ്ങളുടെ എണ്ണം എന്നിവയുടെ ഗണ്യമായ ജനിതക പരസ്പര ബന്ധവും നേരിട്ടുള്ള പ്രഭാവവും ഈ ഘടകങ്ങൾക്ക് ചെടിയിലെ വിളവുമായുള്ള യഥാർത്ഥ ബന്ധത്തെയാണ് കാണിക്കുന്നതെന്ന് അസോസിയേഷൻ വിശകലനം വെളിപ്പെടുത്തി. ഇത്തരത്തിലുള്ള ഘടകങ്ങളെ അടിസ്ഥാനമാക്കിയുള്ള തിരഞ്ഞെടുപ്പ് ഫലം വിളവിൽ കാര്യക്ഷമമായ പുരോഗതി കൈവരിക്കാൻ സഹായിക്കും.

സസ്യ ഭാഗങ്ങളുടെ ആന്തോസയാനിൻ പിഗ്മെന്റേഷൻ, ഇലയിലെ മുള്ളുകളുടെ എണ്ണം എന്നിങ്ങനെയുള്ള ഒരു ചെടിയുടെ സമ്മർദ്ദ സഹിഷ്ണുതക് കാരണമാകുന്ന ഘടകങ്ങളെ ഉൾപ്പെടുത്തി യൂ .പി .ജി .എ .എം . ക്ലസ്റ്റർസ് 3 ഇനം വഴുതനകളെ 30 ക്ലസ്റ്ററിങ്ങിൻറെ സഹായത്തോടെ ആയി തിരിക്കുകയുണ്ടായി. അതേസമയം മഹലനോബിസ് ഡി സ്കയർ സ്ഥിതിവിവരക്കണക്കുകളെ അടിസ്ഥാനമാക്കിയുള്ള ജനിതക വൈവിധ്യ വിശകലനത്തിലൂടെ ഇവയെ എട്ട് ക്ലസ്റ്ററുകളായും തിരിച്ചുവടക്കൻ . കേരളത്തിൽനിന്നും ശേഖരിച്ച മിക്ക ഇനങ്ങളും I, II എന്നി ക്ലസ്റ്ററുകളിലായാണ് കാണപ്പെട്ടത് കൂടാതെ അഞ്ചു കാട്ടുബന്ധുക്കളെയും അഞ്ചു വ്യത്യസ്തങ്ങളായ ക്ലസ്റ്ററുകളിലാണ് കാണാന്കഴിഞ്ഞത് .

എൻനിന്നും ശേഖരിച്ച പച്ചനിറത്തിലുള്ള ൽ .ആർ .ജി .പി .ബി .

-.എം .പ്രവേശനങ്ങളായ എസ്25, എസ്-.എം .27 എന്നിവയെ III, V എന്നി ക്ലസ്റ്ററുകളിലായി സ്ഥിതി ചെയ്യുന്നതിൽ നിന്നും ഇവ തമ്മിലുള്ള വൈവിദ്ധ്യം മനസിലാക്കാൻ സഹായിക്കുന്നുചെടിയുടെ ഫല വിളവ് ., ഇലയുടെ വീതി, ഒരു ചെടിയിലെ പഴങ്ങളുടെ എണ്ണം, ഇലയുടെ നീളം എന്നി ഘടകങ്ങളാണ് ജനിതക വ്യതിചലനത്തിന് വലിയ സംഭാവന നൽകിയത് . കൂടുതൽ ഇൻട്രാ ക്ലസ്റ്റർ ദൂരം കാണിച്ചത് ക്ലസ്റ്റർ ഒന്നും തുടർന്ന് ക്ലസ്റ്റർ മൂന്നും ബാക്കിയുള്ളവ)V, VIII, V, IV, V, III) ഏകാന്ത ക്ലസ്റ്ററുകളാണ്ഏകാന്തമായ . ക്ലസ്റ്ററുകളായ ക്ലസ്റ്റർ V- നും VIII- നും,ക്ലസ്റ്റർ V- നും IV- നും പിന്നെ ക്ലസ്റ്റർ V- നും III- നും ഇടയിലാണ് ഏറ്റവും ഉയർന്ന ഇന്റർ ക്ലസ്റ്റർ ദൂരം- .രേഖപ്പെടുത്തിയിരിക്കുന്നത് ഇത്തരത്തിൽ ഉയർന്ന ഇന്റർ ക്ലസ്റ്റർ ദൂരം കാണിക്കുന്ന ക്ലസ്റ്ററുകളിൽ ഉൾപ്പെടുന്ന ഇനങ്ങൾ ഭാവിയിൽ ഹൈബ്രിഡിസഷനു വേണ്ടി ഉപയോഗിക്കാവുന്നതാണ് .കാട്ടുവർഗ്ഗത്തിൽ പെട്ട എസ്. എം.-30 യെ പ്രത്യേകിച്ചും തണ്ടിലും പഴത്തിലും കണ്ടുവരുന്ന തുരപ്പന്മാർക് എതിരെയുള്ള പ്രധിരോധം വർധിപ്പിക്കുന്നതിനായി ഉപയോഗിക്കാവുന്നതാണ്.

ആപേക്ഷിക സാമ്പത്തിക പ്രാധാന്യത്തെ അടിസ്ഥാനമാക്കി വിവിധ കോമ്പിനേഷനുകളിൽ തിരഞ്ഞെടുപ്പ് സൂചിക തയ്യാറാകുകയുണ്ടായി അവയിൽ നാലു ഘടകങ്ങളുടെ കോമ്പിനേഷനാണ്)ചെടിയുടെ ഫലം വിളവ് + പഴ വ്യാസം + നീളമുള്ള ശൈലിയിലുള്ള പൂക്കളുടെ എണ്ണം + .പരമാവധി ആപേക്ഷിക കാര്യക്ഷമത കാണിച്ചത് (പഴങ്ങളുടെ ഭാരം ഉയർന്ന സെലക്ഷൻ സൂചിക സ്കോറിന്റെയും മൊത്തത്തിലുള്ള ക്ലസ്റ്റർ റാങ്കിങ്ങിന്റെയും സഹായത്തോടെ രണ്ടു പച്ച വഴുതന ഇനങ്ങളെയും എസ്). എം.-27 നും, എസ്. എം.-25 ഉം ആറു പർപ്പിൾ വഴുതന ഇനങ്ങളെയും (എസ്). എം.-8, എസ്. എം.-10, എസ്. എം.-18, എസ്. എം.-20, എസ്. എം.-23, എസ്. എം.-24) ശ്രേഷ്ഠമായ ഇനമായി തിരഞ്ഞെടുത്തു.

സെലക്ഷൻ സൂചിക സ്കോറിന്റെയും ക്ലസ്റ്റർ വിഭജനത്തിന്റെയും (ഉയർന്ന ഇന്റർ(ക്ലസ്റ്റർ ദൂരം- അടിസ്ഥാനത്തിൽ തിരഞ്ഞെടുക്കപ്പെട്ട എസ്. എം.-27 എന്ന വഴുതന ഇനത്തെ ഭാവിയിൽ എസ്. എം -25 ഉൾപ്പെടുന്ന ഇൻട്രാ- - പെസിക് ഹൈബ്രിഡിസേഷനിലും എസ്എംസ്27 നെ ഉൾപ്പെടുന്ന ഇൻട്രാ- സ്പെസിക് ഹൈബ്രിഡിസേഷനിലും -എസ്എം)27 x സോളനം ഇന്സാനേം, എസ്എം-27 x സോളനം മാക്രോകർപോണ്ഇത്തരം .ഉപയോഗിക്കാവുന്നതാണ് (ബ്രീഡിംഗ് പ്രോഗ്രാമിലൂടെ മികച്ച വിളവ് നൽകുന്ന ഇനങ്ങളെ

ഉല്പാദിപ്പിക്കുന്നതോടൊപ്പം അവയിൽ തുരപ്പൻ കീടങ്ങളുടെയും ബാക്ടീരിയ വിൽറ്റ് രോഗത്തിന്റെയും പ്രതിരോധം വർധിപ്പിക്കാനും സഹായകമാകുന്നതാണ്.