CHAPTER - II

REVIEW OF LITERATURE

The present review is an attempt at bringing together some of the findings on morphological, biochemical and molecular markers. To fill up the gap, wherever it was necessary, the reviews on other crops are also included. The morphological, biochemical and molecular aspects have been reviewed under following sub-headings.

2.1 Morphological Characterization
2.2 Biochemical Characterization
2.3 Molecular Characterization

2.1 MORPHOLOGICAL CHARACTERIZATION

Morphological markers can be an effective means to determine genetic relatedness among genotypes and among selections used in brinjal breeding programmes. Some of the findings related to morphological markers are summarized below.

There is great morphological diversity among brinjal varieties, cultivars, wild and weedy plants and between related species observed for several characters. Fruit color, size, shape and taste were the most noticeable traits that showed differences among individuals (Frary et al., 2007).

The color differences of fruits are basically due to two color pigments and their effects on appearance and are controlled by more than one genes. These pigments are chlorophyll a and b and anthocyanins which are in different amounts and in combination to determine the exact color of the fruits. As a result, brinjal fruits can be from white to black in color with a gradient of purple, yellow and green. In addition to the skin color, uniformity of plants, striped or spotted color configurations are possible (Daunay et al., 2001).

The size of brinjal fruits may vary from grams to a kilo and vary greatly in length. Another variable morphological character is the shape of the brinjal fruits. Round, egg shaped, oblong, pear shaped, long and curved are some examples of different forms of the fruits.
In addition to those features and morphological differences, there are also other important traits that exhibit a wide range of variety in brinjal. Flower color, hairiness, leaf shape, spines, resistance to pest and diseases are some more examples (Lawande and Chavan, 1998).

Karihaloo and Gottlieb (1995) studied the morphological characters in brinjal and established a closed phylogenetic relationship between cultivated *Solanum melongena* and superficially similar weedy (*Solanum insanum*) and wide (*Solanum incanum*) forms existing in South Asia. Total 29 accessions of *S. melongena* which included relatively advanced cultivars and land races representing wide diversity of morphological and agronomic attributes available in these species; have shown that polymorphism was actually confined to only seven accessions, the rest being monomorphic at all the loci. These results indicated the highly uniform genetic architecture of brinjal suggesting that the species have a very narrow genetic base and that the three taxa are conspecific even though they include extensive morphological diversity.

Analysis of eggplant (*Solanum melongena*) related germplasm at morphological level to contribute in phylogenetic interpretations and germplasm utilization studied by Furini and Wunder (2004). A total of 94 Solanum accessions, including eggplants and related species, were morphologically characterized based on greenhouse observations, Morphological parameters were helpful in assessing similarities or differences among accessions, and molecular data were used to support morphological conclusions. By considering the type of plant development and parameters such as leaf shape, presence or absence of spines, flower colour and habit, fruit colour and shape *etc.*, a dendrogram was computed based on the Dice genetic distances using the neighbour-joining method. The analysis was efficient in the assignment of a species name for eight out of nine accessions that were not previously classified, and revealed that 14 further accessions were misnamed in the collection originally received.

Pathmarajah and Eeswara (2005) studied the variability complement to the morphological characteristics in brinjal cultivar identification among 16 brinjal accessions and three cultivars available in Sri Lanka. Nine morphological characters (growth habit, leaf blade colour, leaf blade lobing, fruit curvature, fruit colour
distribution, % of type of flowers per plant, number of fruits per inflorescence and days to first harvest). Three cultivars and six accessions were differentiated by combining qualitative morphological characters and rest was categorized into four groups. All the cultivars and accessions were uniquely distinguished by combining the morphological characteristics with isozyme fingerprint. Results of the present study suggested that sufficient variability were present in brinjal to allow the use of isozyme analysis as a system for cultivar identification.

Prohens et al. (2005) studied the morphological and molecular diversity of a collection of 27 accessions of Spanish accessions of eggplant that were grown both in the open field (summer crop) and in greenhouse (winter crop). Results of the morphological characterization showed that Spanish accessions displayed an important variation for most of the traits studied. Most morphological traits were not greatly affected by the growing environment (open field or greenhouse). However, for other traits, such as those related to the pigmentation of plant and flowers, prickliness and fruit shape, there were differences among environments. The study of the molecular diversity showed that control accessions were not genetically differentiated from the Spanish accessions, indicating that the Spanish eggplants encompass an important part of the genetic diversity present in this crop.

Gunjeet et al. (2008) worked on morphological diversity in brinjal (Solanum melongena) in a set of 622 accessions, comprising 543 accessions from indigenous sources and 79 accessions of exotic origin, was assessed. Wide range of variations for 31 descriptors, 113 quantitative and 118 qualitative, were recorded. The wide regional variation for plant, flower and fruit descriptors revealed enough scope for improvement of yield characters by selection. The genetic differences among the landraces are potentially relevant to breeding programmes in that the variability created through hybridization of the contrasting forms could be exploited.

Significant accumulations of wide morphological diversity at both inter and intra specific levels were observed in eggplant landraces. Naugeer (2009) conducted study of morphological characterization of 27 S. melongena, two S. macrocarpon, one S. nigrum, three S. violaceum and one S. torvum accessions to assess and measure morphological diversity in eggplant genetic resources conserved at the National gene bank in Mauritius in order to promote their conservation, effective management,
sustainable use and legal protection. Nine quantitative and 14 qualitative traits were characterized based on (IBPGR 1990) eggplant descriptor list. Significant (P < 0.01) correlations were observed between several related traits of high agronomic importance and breeding potentials in selection of genetically divergent parents for hybridization. Yield was positively correlated with leaf area (r = 0.2), fruit length and width (r > 0.5) and fruit weight (r = 0.8) but inversely related with number of fruits per plant (r = -0.6) and plant height (r = -0.5). The phenogram constructed through UPGMA clustering method showed the phenetic relationship between *S. melongena* accessions, their related species and wild types. It classified the *S. melongena* accessions into Long, Semi long, Round and Oblong cultivar groups based on fruit shape, colour and size. Principal Component Analysis revealed that fruit characters were important marker traits with a large coefficient of variation (> 40 percent) that most effectively discriminated between eggplant accessions and hence useful in establishing a simple but effective eggplant classification system at the gene bank.

The genetic variability in indigenous brinjal land races of Dimapur district of Nagaland and their traditional cultivation practices were studied by Bhagowati and Changkija (2010). They obtained large variability of land races in high land of Nagaland. There were enormous potentials of semi-perennial races and the immature fruits also possess certain medicinal properties as per the traditional belief. Systematic documentation and preservation of these valuable germplasm resources need immediate attention of scientific communities of the country. In their investigation, the genetic variability with respect to certain economic traits in a few traditional land races of brinjal in Dimapur district of Nagaland was studied. In their investigation, variability with respect to fruit shape and other characters were recorded. Among their studied land races, the maximum average fruit length for purple long land race was recorded to be 17.27 cm with the minimum average fruit circumference of 2.23 cm. On the other hand, maximum average fruit circumference of 11.15 cm together with minimum fruit length of 6.12 cm was recorded for white egg type brinjal land race.

Study on the genetic divergence was carried out by Muniappan *et al.* (2010) to assess the genetic variability, association analysis, direct and indirect effects of eight morphological characters in thirty-four eggplant genotypes. High phenotypic coefficient variation and genotypic coefficient variation were recorded by number of
branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight, and fruit yield per plant. The characters were mostly controlled by additive gene action, hence it could be inferred that simple selection will be effective for these characters. The characters such as number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight exhibited significant and positive association with fruit yield per plant. Path analysis indicated that number of fruits per plant and average fruit weigh had high direct effects and were the major factors that determine fruit yield per plant in brinjal.

Mass grading of vegetables provide useful insight into designing of sizing machine and reducing the packaging and transportation costs. In this research, tomato mass was correlated to different physical attributes using linear and non-linear models into three different classifications: (1) single or multiple variable regressions of tomato dimensional characteristics, (2) single or multiple variable regression of tomato projected areas and (3) estimating tomato mass based on its volume. The results of Amin et al. (2011) showed that mass modeling of tomato based on intermediate diameter and first projected areas are the most appropriate factors in the first and the second classifications, respectively. In third classification, the best model was obtained on the basis of the actual volume as $M = 0.001 V + 1.498$ with $R^2 = 0.974$, whereas corresponding values were 0.91 and 0.93 for assumed tomato shapes (oblate spheroid and ellipsoid), respectively. The best model for prediction of mass base on dimension was $M = 0.206 b^2 - 19.61 b + 558.1$, $R^2 = 0.916$ and R.S.E. = 4.57 which in economical and agronomical point of view, is suitable for grading and sizing systems.

Santosh et al. (2012) studied morpho-physiological characterization of five cultivated species of chilies: 32 C. annuum, 5 C. baccatum, 27 C. chinense, 6 C. frutescens and 1 C. pubescens. The record of the descriptors of each plant was performed from seed to fruit maturity, aiming not only the identification of the species but also the determination of a narrower group of more useful characteristics that would allow that identification. Results of hierarchical cluster analysis showed that the most useful characteristics needed for the correct identification are: seed and corolla color, presence of spots on petals, and the presence or absence of ring constriction. Capsaicinoids were quantified by HPLC. Values between 88 and 14,814
mg kg$^{-1}$ were registered for capsaicin, and between 4 and 5860 mg kg$^{-1}$ for dihidrocapsaicin, resulting in a range of 1417 SHU for *C. annuum* ‘Padrón’ to 324,928 SHU for *C. chinense* ‘Scotch Bonnet’. No direct relationship between pungency and species was found, although *C. chinense* reached the highest levels.

Fabio and Leo (2013) characterized six eggplant ecotypes (G1 to G6) and three eggplant varieties (Birgah, Black bell and Viola di Firenze) from a morphological, phenological and production point of view, gathered from Sicily and the smaller islands. The genotypes G1 and G3 were found to be more productive than the varieties used in the test field. Ecotype G1 produced fruits which were dark violet and highly glossy, and produced the lowest percentage of discarded fruits; ecotype G2 had a high marketable fruit yield per plant, whereas populations G3, G5 and G6 were found to have a high average fruit weight. The six ecotypes were found to be highly non-uniform as regards both the plant and fruit morphological characteristics.

Zaki *et al.* (2013) characterized eleven different morphological forms of Moroccan paprika grown under field conditions in Tadla-Azilal region; analysis of morphometric data of different morphotypes (variants) was performed. The 11 morphotypes were evaluated for their qualitative traits of ripe fruits. Statistically significant differences among these variants were found for all the fruit characters studied. The evaluated morphotypes differed also in vitamin C, capsaicin, ASTA value and coordinated chromatic of color. The morphotype fruits evaluated had high genetic diversity and potential to fulfill the industry requirements. Morphotype 1 had the most desired commercial trait such as high ASTA value, high DW/FW ratio and low pungency. The results obtained in this study can be used as accurate information to establish a program of breeding to develop new commercial hybrids with fruits enriched for more desired commercial traits.

Morphological variation of thirty-five brinjal genotypes was investigated by Solaiman *et al.* (2014) in order to screen efficient genotypes for a hybridization program in Bangladesh. The phenotypic coefficient of variation (PCV) was higher than that for genomic coefficient of variation (GCV). The PCV estimates were high for the number of branches, number of fruits per plant, and single fruit weight. Heritability estimates were high for the single fruit weight with high genetic advance. In spite of high heritability values for most traits, the expected genetic advance as a
percentage of the mean ranged from 19.92 to 121.51. Multivariate analysis was performed using Principal Component Analysis (PCA), principal coordinate analysis, cluster analysis and canonical variate analysis. With PCA, multivariate analysis of Mahalanobis’s distance ($D^2$), and cluster analysis, the genotypes were grouped into six clusters. The longest inter-cluster distance was between clusters II and III, and the shortest was between clusters V and VI. Cluster VI showed the longest intra-cluster distance but cluster II showed the shortest. Genotypes of cluster I were suitable for number of branches per plant; cluster II for the fruit length; cluster III for the number of fruits per plant and cluster IV for the single fruit weight and yield. Considering the performances, genotypes SM-111, SM-84, EGN-27, SM-183, and BARI begun-6 are suitable parents for the hybridization programme.

Dhruve et al. (2015) conducted research work in brinjal (Solanum melongena L.) local types to identify suitable varieties for cultivation with morphological and nutraceutical traits. Mean performance showed that AB-07-02 registered the highest fruit length followed by GBL-1. In case of fruit girth, fruit weight and fruit volume, data were recorded higher for GOB-1. From the nutrient point of view, Doli-5 for higher ascorbic acid and lower amount of glycoalkaloid, AB-09-01 for maximum acidity and total carbohydrates and AB-07-02 for higher anthocyanin were found. Therefore these genotypes/varieties could be better utilized for further breeding programme.

In order to protect biodiversity and preserve local germplasm, Zhani et al. (2015) collected five local accessions of chili pepper (Capsicum frutescens L.) for their morphological characterization. Results showed that the pepper accessions were significantly different in many characters studied. Souk Jedid accession produced plants with erect and short habit, small and lanceolate leaves and grouped flowers, whereas the rest of accessions have dichotomous branching with bushy secondary stems, large and oval leaves and solitary flowers. The fruits had enrobing calyx, narrow triangular shape, dark red color at maturity and a smooth to slightly wrinkled surface in addition they are pungent but difference was observed in attitude, sinuation of pericarp at basal part, surface texture and glossiness.
2.2 BIOCHEMICAL CHARACTERIZATION

In addition to morphological data, biochemical and other types of data are also being applied for characterization in the solanaceae family. These have been used classically in taxonomy and in other fields of science.

Experiment based on molecular investigations was started just three decades ago for this family (Daunay et al., 2001). In this view, some of the first studies were carried out at the protein level and examined differences in allozyme and isozyme patterns between individuals (Kaur et al., 2004).

Basically in these studies, Solanum melongena, commonly known as eggplant or brinjal was compared with its weedy and wild forms and close relatives (Karihaloo and Gottlieb, 1995). The purpose of these studies was to measure genetic diversity in those organisms and these types of markers were identified as being especially advantageous for cultivar studies.

The PAGE (polyacrylamide gel electrophoresis) is based on the separation of proteins and amino acids with different net charge and/or different molecular weight and/or conformation on the basis of their migration at different rates through matrix of starch or acrylamide gels. The analyzed protein types include storage proteins and isozymes are the different molecular forms of an enzyme that catalyze the same reaction, called as isozymes. Isozymes represent different genes whose products catalyses the same reaction.

Isshiki et al. (1994) investigated isozyme variation in seventy-three accessions of eggplant for elucidating intraspecific relationships of Solanum melongena. Of the nine enzymes examined, three enzymes viz., alcohol dehydrogenase at locus Adh-2, glucose-6-phosphate isomerase at locus Gpi-2 and phosphoglucomutase at loci Pgm-1 and Pgm-2 were polymorphic among the accessions, whereas the other enzymes (acid phosphatase and glutamine synthase) showed no detectable variations.

Barrera et al. (2005) evaluated two hundred and sixty-one accessions of the genus Capsicum with five polymorphic enzymatic systems, including esterase (EST), peroxidase (PRX), 6-phosphogluconate dehydrogenase (6-PGDH), aspartate amino transferase (GOT), and malic enzyme (ME). Using a cluster analysis (UPGMA) the
genetic variability of these accessions was characterized. Grouping of the species *C. baccatum* and *C. pubescens* were observed, while the species *C. annuum*, *C. chinense* and *C. frutescens* did not group independently. The five enzymatic systems showed a total of 83 bands, distributed in the whole set of samples as: PRX with 15 bands; 6-PGDH with 8 bands, GOT with 8 bands; ME with 17 bands and EST with 37 bands. The most polymorphic enzymes were EST and the ME, followed by PRX, 6-PGDH and GOT.

Toppino *et al.* (2008) evaluated the extent of genetic recombination between two species, *Solanum melongena* and *Solanum aethiopicum* by employing biochemical and molecular markers. A dihaploid population obtained through anther culture of the corresponding tetraploid somatic hybrids was genetically analyzed. The extent of disomic/tetrasomic inheritance and segregation ratios of three isozyme systems and inter simple sequence repeat (ISSR) markers were evaluated. The isozyme markers segregated in the dihaploids in a distorted manner, their segregations did not fit in with any of the expected segregation ratios. However, tetrasomic inheritance was suggested for G-6-PDH 2 and SKDH 1 loci.

### 2.2.1 Peroxidase

Kamel and Ghazy (1973) studied the peroxidases isozyme in *Solanum melongena* leaves. Three major peroxidases designated as A, B₂ and B₃ from eggplant leaves have been reported. Peroxidases A, B₂ and B₃ were considered to be true peroxidases on the basis of k₁:k₄ ratio. The pH optima for the three enzymes were found to be 7.0, 6.0 and 6.5 respectively.

Autar *et al.* (1976) worked on the sub cellular distributions of isoenzymes in fruits of a normal cultivar of tomato (*Lycopersicon esculentum* Mill). The enzymes studied were peroxidases and other isozymes. The activities in the supernatant fraction of all of these enzymes decreased during of normal fruit growth. In the particulate fractions, some enzymes decreased while others increased in activity.

Demetri and James (1978) found that major peroxidase has been present in the tomato peri carp of the ripe and green fruit. A purification scheme yielding this enzyme approximately 85% pure has been developed. The tomato enzyme resembles horse-radish peroxidase (HRP) in a standard peroxidase assay and in its ability to be reduced to ferroperoxidase, to be converted to oxyferroperoxidase (compound III),
and to form peroxidase complexes with hydrogen peroxide (compounds I and II). In contrast to the HRP, the tomato peroxidase fails to catalyze the aerobic oxidation of indole-3-acetic acid in the presence of 2, 4-dichlorophenol and manganese. The tomato peroxidase can be resolved into two non-identical subunits in the presence of dithiothreitol while HRP remains as a single polypeptide chain after such treatment. Dithiothreitol is oxidized in the presence of tomato or horseradish peroxidase with the enzymes accumulating in their oxyferroperoxidase forms during the oxidation reaction. Whereas HRP returns to its free ferric form at the end of the reaction, the tomato enzymes converted into a form that absorbs at 442 nanometers.

Espelie and Kolattukudy (1985) purified an anionic peroxidase (EC 1.11.1.7) in 110-fold from wound-healing slices of Solanum tuberosum by a combination of ammonium sulfate fractionation, Sephadex G-100 gel filtration, isoelectric focusing, and phenyl-Sepharose CL-4B chromatography in 24% yield. The purified enzyme was homogeneous as judged by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and horizontal thin-layer polyacrylamide gel electrophoresis. The molecular weight of the enzyme was estimated to be 47,000 by both Sephadex G-100 gel filtration and sodium dodecyl sulfate-polyacrylamide gel electrophoresis. This peroxidase was found to be a glycoprotein containing about 17% carbohydrate, approximately one-quarter of which was shown to be glucosamine residues. It was found to have an isoelectric point of 3.15. An anionic peroxidase was also isolated from abscisic acid-treated callus tissue culture of S. tuberosum by the above purification procedure. The two enzymes were shown to be immunologically similar, if not identical, based on their crossreactivity with rabbit antibody prepared against the peroxidase from wound-healing slices, whereas the major cationic peroxidase from wound-healing slices did not crossreact with this antibody. The anionic enzyme from both sources showed very similar specific activities when assayed with a range of substrates, whereas the specific activities found for the cationic isozyme isolated from wound-healing slices were quite different.

Panie et al. (1993) showed the techniques for varietal identification of vegetable crops (brinjal, tomato, capsicum) using isozymes electrophoresis. Several isozymes peroxidase and others were analysed to standardize in proper condition of plant ages, plant parts, sample extraction solution, gel concentration and staining solution. Isozymes extracted with phosphate buffer, pH 7.5-8.5 from leaves of seven day old seedling showed the best expression of banding.
Study of selected isozymes in *Capsicum baccatum*, *Capsicum eximium*, *Capsicum cardenasii* and two interspecific F<sub>1</sub> hybrids in *Capsicum* species were carried out by Onus (2000). The standard technique of horizontal gel electrophoresis was employed. The gel was cut into several slices and stained for different enzyme systems like peroxidase and others. After fixing the gel slices in 50% aqueous glycerol, the number and position of stained bands were recorded. Electrophoretic studies indicated that *C. eximium* and *C. cardenasii* had more alleles in common with each other than they had with *C. baccatum*. The results indicated that *C. baccatum* were electrophoretically distinct from *C. eximium* and *C. cardenasii*. These results also support the division which was based predominantly on corolla colour and morphological characters and showed that while *C. eximium* and *C. cardenasii* belong to the purple-flowered species group, *C. baccatum* belongs to the white-flowered species group.

Barrera et al. (2005) studied the isozyme characterization of *Capsicum* accessions from Amazonian Colombian collection in that, two hundred and sixty-one accessions of the genus *Capsicum* were studied and evaluated polymorphic enzymatic systems for peroxidase and other enzymes. Using the cluster analysis, the genetic variability of these accessions was characterized. In that, grouping of the species *C. baccatum* and *C. pubescens* were observed and concluded that these studies can be useful for future ecological and evolutive studies.

Bhattacharya et al. (2009) investigated shoot and fruit borer infestation to eggplant (*Solanum melongena* L.) and correlate it to specific biochemical characteristics. Seven cultivars of eggplant were sampled at 10, 15, 20, and 25 days after flowering (DAF) for peroxidase (PO) and polyphenoloxidase (PPO) activity and at 15, 20, and 25 DAF for phenol content. Stepwise multiple regression analysis revealed that there was a lack of correlation between fruit infestation and PO activity. However, a correlation between fruit infestation; PPO activity at 15, 20, and 25 DAF; and phenol content at 15 and 20 DAF was observed. Principal components analysis indicated that BCB-38 was the best performing cultivar and could be used as improved genetic material in future breeding programmes.

Gyanendra et al. (2011) studies the total phenol content, peroxidase and polyphenol oxidase enzyme activities and the total protein profile in tomato cultivars
(Lycopersicon esculentum Mill.), tolerant and susceptible to fusarium wilt disease was studied. The tolerant cultivars of tomato viz., Feb-2, Feb-4, Floradade and NF-31 had significantly higher phenol content as well as peroxidase and polyphenol oxidase activities than the susceptible ones (Sel-7, Sel-18 and Punjab Chhuhara). The maximum peroxidase activity was recorded in the resistant cultivar, Flora dade (0.073 unit/ml) and minimum in the susceptible cultivar, Sel-18 (0.241 unit/ml). Major differences in soluble protein banding pattern were observed in the susceptible and resistant cultivars. The hierarchical cluster analysis was performed using NTSYS-PC(v.1.8) software. The dendrogram using the average linkage between the groups, showed proximity of resistant cultivars viz., Feb-4, Feb-2, Flora dade and NF-31 to the wild species with respect to similarity of banding patterns. The three susceptible cultivars viz., Sel-7, Punjab Chhuhara and Sel-18 were grouped separately.

2.2.2 Esterase

Conicella et al. (1990) studied the activity of esterase isoenzymes of 15 wild and cultivated Capsicum accessions and found that all these accessions exhibited three main banding patterns. All accessions from Central Mexico, including the cultivated type, and some from the USA, had pattern A. Other accessions from the USA, Central America and Peru had pattern B. The Colombian accessions possessed pattern C, which was distinguished by having more bands, apparently identical with those in hybrids between A and B. F₁ plants between a Colombian accession used in hybridization and accessions with patterns A and B showed associations of 4 or 6 chromosomes at meiotic metaphase I. It is postulated that pattern C resulted from a process of gene duplication.

Pathmarajah and Eeswara (2005) detected isozymes variability complement by electrophoresis. They studied six enzymes including esterase in 16 brinjal accessions and three cultivars available in Sri Lanka. Starch gel electrophoresis was used to analyse extracts prepared from young leaf tissues of seven-day-old seedlings grown under greenhouse conditions. The result was consistent with brinjal and based on the location of the bands 16 accessions and three cultivars were categorized into three groups. Unique combinations of isozymes variants of all the enzymes assayed were able to differentiate thirteen accessions and two cultivars (79%). Results of their study
suggested that sufficient variability were present in brinjal to allow the use of isozyme analysis as a system for cultivar identification.

Barrera et al. (2005) studied isozyme characterization of Capsicum accessions from Amazonian Colombian collection in that, two hundred and sixty-one accessions of the genus capsicum were studied and evaluated polymorphic enzymetic systems for esterase and other enzymes. Using the cluster analysis, the genetic variability of these accessions was characterized. In that, grouping of the species C. baccatum and C. pubescens were observed and also showed a high variability, as no identical material was found in the phenogram so concluded that these studies can be useful for future ecological and evolutive studies and these variability can be used as a new source of genetic diversity for the improvement in commercial varieties of Capsicum.

Markova et al. (2006) studied expression of esterase isoenzymes in 1272 seeds which was used to estimate hybridity of tomato. Individual seeds (440) of the parental genotypes taken from different experimental stations. The banding patterns were obtained by means of vertical block electrophoresis in polyacrylamide gels. It was established that quantitative variation of locus Est-1 can be applied to prove hybridity of F₁ tomato seeds. This marker is related to the genetic nature of tomatoes and is not the result of the environmental influence.

2.2.3 Polyphenol oxidase (PPO)

Concellon et al. (2004) showed the characterization and changes in polyphenol oxidase from eggplant fruit (Solanum melongena L.) during storage at low temperature. Polyphenoloxidase (PPO) and its catecholase activity studied during storage of fruit. The high catecholase activity was observed using 4-methylcatechol. The soluble PPO fraction was the most thermostable, as well as the most active, form of the enzyme.

Kaur et al. (2004) studied the diversity of enzyme electrophoretic patterns in the eggplant complex. Studies on electrophoretic patterns of five enzymes like polyphenol oxidase and others that resulted in the identification of 10 isozyme loci represented by 20 alleles involved in the control of the above enzymes. It showed high number of phenotypes presented a single morph. The most frequent phenotypes were identified in S. melongena, S. insanum and S. incanum indicating close genetic
proximity of the three taxa. *S. melongena* accessions showed high degree of zymogram homogeneity, while the other two species were more diverse.

Studies on the biochemical basis of five selected brinjal genotypes viz., BL009, ISD006, TURBO, EG058, EG075 were carried out at Tamil Nadu Agricultural University, India. Khorsheduzzaman et al. (2010) showed that few genotypes had the higher amount of poly phenol oxidase (PPO). Significant and negative correlation was found between per cent infestation (shoot and fruit) with PPO content, whereas it was positively correlated with reducing sugar content.

Aldo et al. (2011) studied catecholase and cresolase activities of eggplant polyphenol oxidase (PPO). Enzyme activity was determined by measuring the increase in absorbance using catechol as substrate and 3-methyl-2-benzothiazolinone hydrazone (MBTH) as coupled reagent. The effects of substrate specificity, heat inactivation, temperature, pH, and inhibitors were investigated to understand the enzymatic alteration of ready-to-eat preparations. Browning of vegetables was determined through a colorimeter. Decrease of lightness and increase of color difference values were correlated with tissue browning. Anti-browning agents were tested on PPO under the same conditions. The enzyme activity was strongly inhibited by 0.4 M citric acid. Under natural pH conditions, the enzyme was also inhibited by tartaric acid and acetic acid. All of the results were used to understand the best conditions for food transformation (ready-to-eat and grilled eggplant slices).

Santoshkumar (2012) studied plant polyphenol oxidases (PPOs) from various plant sources for their ability to oxidize phenolic compounds to produce brown pigmentation upon tissue damage. Eggplant or brinjal (*Solanum melongena*), exhibits severe browning reaction upon tissue injury and has been manifested by PPOs. Using a combination of biochemical, molecular and immunological approaches, the present study aims at understanding the structural and functional aspects of eggplant PPOs. Chapter 1 provides a retrospective account on plant polyphenol oxidases: its distribution, physico-chemical properties, structural features in relation to enzymic action, functional roles and its applications. It also envisages the importance of molecular characterization of eggplant PPOs, the information conspicuously missing so far. Research on PPO in plants has been multi-dimensional as it strives to understand the in vivo roles, post-harvest losses of agricultural produce and its
potential biotechnological applications. The isolation of six eggplant PPO genes (SmePPO1–6) by RACE and genome walking as well as its comprehensive characterization is described in Chapter 2. These PPO genes (~1.8 kb) were found to be intronless similar to most of the dicotyledonary PPOs and correspond to eight eggplant PPO unigenes. Though SmePPO genes exhibit considerable variation in the transit peptide regions, copper-binding regions and UTRs, they can be clearly distinguished into two distinct structural classes (SmePPO1-3 and SmePPO4-6) based on predicted structural features. A deletion of 7 amino acids in copper binding region B of SmePPO4-6 is most likely responsible for their functional diversity.

A relatively new local type of eggplant, *Solanum melongena* L. ‘Kadife’ is widely consumed in Turkey because of its economic availability and good nutritional qualities. However, the high polyphenol content of eggplant renders it susceptible to unattractive oxidative browning catalyzed by polyphenol oxides (PPOs). Hulya et al. (2015) characterized PPO in eggplant cultivar at three stages of its development. They determined substrate specificity, optimum pH and temperature, and optimum substrate concentration of the partial purified eggplant fruits PPO during ripening. Results showed that L-DOPA was proved to be the preferred PPO substrate in all three stages of ripening. Optimum activity was observed at pH 7.0 for PPO in extracts of ripening and overly-ripe eggplant, while activity in extracts of immature eggplant exhibited a broad pH optimum between, pH 5.0 and 7.0. In general, at all ripening stages, PPO was most active at 30°C and was most sensitive to inhibition by sodium metabisulphite and ascorbic acid. The metal ions (Hg2+, Mn2+, Fe3+ and Co2+) mostly inhibited PPO activities.

Polyphenol oxidase (PPO) catalyzes the conversion of phenolic compounds into \( \alpha \)-quinones which will lead to food browning. This phenomenon causes huge implications on food industries, as it degrades food quality over time. Ng and Wong (2015) partially purified PPO up to 5.26-fold with 11.23% yield combining both ammonium sulphate precipitation and gel filtration chromatography. The enzyme activity was 5120 EU/mL using 4-methylcatechol as substrate. Maximal PPO activity was found at 30°C, pH 5.0 for 4-methylcatechol and 40°C, pH 6.0 for catechol. The PPO showed a higher affinity towards 4-methylcatechol but higher thermal stability when reacting with catechol. The \( K_m \) and \( V_{\text{max}} \) values were 5.00 mM, 2000 EU/ml for 4-methylcatechol and 10.79 mM, 526.32 EU/ml for catechol. Energy for
inactivation (Ea) obtained using 4-methylcatechol and catechol were 12.57 kJ/mol and 14.23 kJ/mol from respective substrates. Sodium disulfite was a better inhibitor where 79.17% of PPO inhibition was achieved. The isolation and characterization of round brinjal PPO serves as a guideline to predict the behavior of enzyme, leading to effective prevention of its browning during processing and storage.

2.2.4 Superoxide dismutase (SOD)

Baoli et al. (1998) investigated that the eggplant after grafting prevents disease, increase yield, and grafted on eggplant roots, stems, leaves and flowers of different organs of polyphenol oxidase (PPO), superoxide dismutase (SOD) and esterase (EST) isozymes. The results showed that the resistance of grafted eggplant and isoenzymes changes were closely related, showing characteristic bands for the emergence of some resistant and susceptible zone disappeared or diminished, which changed in PPO isoforms were significantly higher than SOD and EST.

Priscila et al. (2008) determined activity the isoforms of superoxide dismutase (SOD) from the organs of tomato cultivar after 104 days of development. The total activities were higher in the stem than in others tissues. Staining analysis following gel electrophoresis revealed the existence of four SOD isoforms in leaves, three in fruits, but only two isoforms in the roots and stems.

2.2.5 Glycoalkaloid

Kirsoy (2006) studied solamargine which is a known eggplant glycoalkaloid and has an important place for human health was characterized in eggplant. For characterization, two eggplant lines S.melongena MM738 and S.linnaeanum MM195 were used. Although for identification and detection of glycoalkaloid concentration, many different methods have been utilized, but high-performance liquid chromatography (HPLC) was used to analyze glycoalkaloid concentration in eggplant. In HPLC, spiking of samples was done using a solamargine standard and it was found that S. melongena had an undetectable level of solamargine, while S. linnaeanum had between 17.6 and 33.4 mg solamargine per gram of freeze dried powder. In addition to characterization of glycoalkaloids in S.melongena MM738 and S.linnaeanum MM195, different types of molecular markers were surveyed for polymorphism in S.melongena MM738 and S.linnaeanum MM195 for mapping.
total of 47 polymorphic markers were tested on the F₂ population and located on the eggplant molecular genetic map.

### 2.2.7 Sugar

Khorsheduzzaman *et al.* (2010) studied biochemical basis of resistance to *Leucinodes orbonalis* Guenee and their correlation with shoot and fruit borer damage in five selected brinjal genotypes and showed that both shoot and fruit of less susceptible genotypes had the higher amount of poly phenol oxidase (PPO), phenylalanine ammonium lyase (PAL) and lignin and lower amount of reducing sugar. Significant and negative correlation was found between percent infestation (shoot and fruit) with PPO, PAL and lignin content, whereas it was positively correlated with reducing sugar content. Among the biochemical constituents, PPO, PAL and lignin contents were negatively correlated with reducing sugar but PPO were positively correlated with PAL and lignin content and vice-versa.

### 2.2.8 Antioxidant Activity

Nasrabadi *et al.* (2011) examined effect of chlorpyrifos and malathion on antioxidant enzymes in tomato and brinjal. Both the vegetables are highly susceptible to insect attack. To enhance the yield and net economic return from these vegetables, growers apply heavy doses of chloropyrifos and malathion, which generate xenobiotic / pollution stress on these crops leading to creation of reactive oxygen species (ROS) in them which culminate the plants into death through cellular damages. Scavenging of ROS through stimulation of antioxidant enzymes such as SOD, POD and PPO is the most adaptive mechanism for the tolerance of pollution. The results of the present investigation revealed that both the pesticides have caused highly significant stimulation in the activities of SOD, POD and PPO, and it increased with the increasing dose of chloropyrifos and malathion.

Goswami *et al.* (2013) studied carbaryl mediated biochemical alterations in eggplant. In this study the effect of three different concentrations (0.125% w/v, 0.25% w/v and 1.25%w/v) of carbaryl solutions on germination and on biochemical parameters like free amino acid, protein, soluble insoluble sugar content and amylase activity of Eggplant seeds was studied. Additionally, the activity of antioxidative enzymes in leaf tissues was determined. A significant dose dependent decrease
(p<0.01) in germination percentage and early seedling growth in terms of root length was observed in seeds treated with different concentrations of carbaryl. An increase in percent phytotoxicity and percent inhibition of germination was observed in seeds carbaryl treated seed. Interestingly reduction in soluble sugar content, free amino acid content and amylase activity was found in the cotyledons of seeds treated with carbaryl, while the total protein and insoluble sugar content increased significantly. Foliar application of carbaryl showed dose dependent increase in peroxidase (POD) activity in leaf tissues. But the activity of catalase (CAT) enzyme in both treated and control were not distinct. Leaf protein analysis showed alterations of certain protein bands in carbaryl treated samples than control. The change in activity of peroxidase in leaf tissues of carbaryl treated samples could be due to carbaryl induced oxidative stress response.

Sultana et al. (2013) studied methanolic (80%) extracts of various parts (green crown, peel and flesh) of selected varieties of round and long brinjal and explored for total phenolic content (TPC) and antioxidant activity using a number of colorimetric assays. The results showed that TPC methanolic extracts, of different parts of selected varieties of brinjal, ranged from 16.72-25.00 mg GAE/100g DW. The highest amount (22.05-25.00 mg GAE/100g DW) was obtained in round brinjal extracts and the lowest in long brinjal extracts (16.72-20.43 mg GAE/100g mg GAE/100g DW). Similarly, the methanolic extracts of round brinjal exhibited better inhibition of oxidation of linoleic acid (59.34-64.00 %) as compared to that of long brinjal (56.91-60.56 %). The analysis of variance data showed that the difference in peroxide inhibition capacity and reducing power of different parts of brinjal was significant (p<0.05). The highest DPPH scavenging activity (70.01%) was achieved with methanolic extracts of peels of round brinjal. The present study suggested that round brinjal contained higher antioxidant components and potential as compared to the long variety. A positive correlation was observed between the phenolic component and free radical scavenging potential of methanolic extracts of different parts of brinjal suggesting its use as a bioactive functional food.

The research work was carried out by Talukder et al. (2015) to determine the physico-chemical characteristics and antioxidant assay of 13 selected tomato germplasm collected from the south-western region of Bangladesh. A significant variation among the germplasm in relation to fruit characteristics was observed. The
highest values found in germplasm No. 6 in respect of total weight of fruit, length of fruit, width of fruit and depth of fruit among the 13 selected germplasm. The highest seed weight of fruits was observed in germplasm No. 2. The highest titrable acidity (0.953%) was observed in germplasm No. 12. The highest vitamin C (24.33 mg/100 g) content of fruit pulp was determined from germplasm No. 3, while germplasm No. 13 was best in respect of pH (4.833); germplasm No. 3 in total soluble solids (6.033%) content; germplasm No. 5 in carotenoids (0.848 mg/100 g) content, germplasm No. 2 in anthocyanin (0.125 mg/100 g) content and germplasm No. 11 in flavonoids (5.270 g/100 g) content of fruit pulp. The highest antioxidant was found in germplasm No. 7 and that was lowest in germplasm No. 9. The IC50 values and antioxidant content is opposite each other. It was revealed from the study that germplasm No. 7 had comparatively lower IC50 values. Thus, germplasm No. 7 contain comparatively higher antioxidant content. On the other hand, germplasm No. 9 had comparatively higher IC50 values, hence germplasm No. 9 contain comparatively lower antioxidant content.

2.2.9 Chlorophyll/Carotenoids

Saxena and Diwaker (2012) Take leaves of brinjal plant treated with five concentrations of the leaves’ extract of Ricinus communis along with normal and infected leaves’ were taken after 72 hrs for the estimation of chlorophyll content. Highest chlorophyll ‘a’ was recorded 0.656 mg/g. with 3.0% concentration, while chlorophyll ‘b’ was 0.409 mg/g. and total chlorophyll content was 1.065 mg/g. In comparison to normal 0.269, 0.356 & 0.625 mg/g. and infected leaves i.e. 0.220, 0.322 and 0.541 mg/g chlorophyll, respectively.

Biochemical characteristics and fruit yield of brinjal was studied by Rajan et al. (2013) for a period of 90 days. The experimental plants were supplied with different quantities of dyeing industry residue such as 0, 200, 400, 600, 800, 1000, and 1200mg for treatment T1 (control) T2, T3, T4, T5, T6 and T7, respectively. Germination of brinjal (Solanum melongena L.) was higher (96%) in treatment T2 with 200 mg of dyeing industry effluent residue and lower (85%) in T7 with 1000 mg of residue. Chlorophyll a,b, total chlorophyll and Carotenoids of brinjal were higher in T3. Total soluble sugar and protein of brinjal were higher in T2. Free amino acids and
L-Proline of brinjal was higher in T₆. Leaf nitrate of brinjal was higher in T₃ and lower in T₆. Nitrate reductase was higher in T₀ and lower in T₆. Catalase was higher in T₆.

2.2.10 Protein

Waseem et al. (2008) studied xerophytic herb found in Karachi and B. acanthoides was used against root-knot nematode invivoto and greenhouse experiments. Its effect on root-knot infection, growth, chlorophylls and protein contents in leaves of okra (Arka anamika) and brinjal (Black beauty) plants were observed. Aqueous extracts of B. acanthoides significantly inhibited egg hatching of root-knot nematode and caused appreciable mortality of second stage juveniles of M. javanica in vitro. Soil amendment with shoot material of B. Acanthoides at 1% and 2% (w/w) significantly suppressed nematode galling in okra and brinjal roots. B. acanthoides amendment resulted in enhanced growth, chlorophyll and total protein contents in okra and brinjal compared to unamended M. javanica inoculated plants.

Rai et al (2011) studied peroxidase and polyphenol oxidase enzyme activities and the total protein profile in tomato cultivars (Lycopersicon esculentum Mill.), tolerant and susceptible to Fusarium wilt disease. The tolerant cultivars of tomato viz., FEB-2, FEB-4, Flora Dade and NF-31 had significantly higher phenol content as well as peroxidase and polyphenol oxidase activities than the susceptible ones (Sel-7, Sel-18 and Punjab Chhuhara). The maximum peroxidase activity was recorded in the resistant cultivar, Flora Dade (2.073 unit/ml) and minimum in the susceptible cultivar, Sel-18 (0.241 unit/ml). Major differences in soluble protein banding pattern were observed in the susceptible and resistant cultivars. The hierarchical cluster analysis was performed using NTSYS-pc (V.1.8) software. The dendrogram using the average linkage between the groups, showed proximity of resistant cultivars viz., FEB-4,FEB-2, Flora Dade and NF-31 to the wild species with respect to similarity of banding patterns. The three susceptible cultivars viz., Sel-7, Punjab Chhuhara and Sel-18 were grouped separately.

2.2.11 Phenol

Mitra and Majumdar (1977) reported changes in phenol and polyphenol oxidase activity in four brinjal varieties infected with little leaf disease at different stages of disease development. Both phenol content and polyphenol oxidase activity
decreased in the three varieties (Pusa Purple Round, Arka Navneet, T-2) at all stages of disease. However, the variety Pusa Purple Long reacted in different way.

Prabhu et al (2009) investigated biochemical basis of host plant resistance for shoot and fruit borer of brinjal using selected genotypes from the back crosses involving cultivated brinjal varieties and Solanum viarum. The different levels of biochemical constituents namely peroxidase, poly phenol oxidase, total phenols, and solasodine contents were observed in genotypes derived from inter-specific crosses and their parents. A higher level of polyphenol oxidase activity was observed in interspecific cross F6 EP65 x S. viarum. There was a clear correlation between the levels of biochemical constituents and shoot and fruit borer incidence. This study showed the biochemical parameters responsible for the resistance and could be used for the development of superior genotypes with resistance to shoot and fruit borer.

Shahhin et al. (2013) estimated total phenol content (TPC) of different varieties of Solanum melongena L. varied from 3.16 ± 0.04 to 7.86 ± 0.33 mg GAE/g of fresh weight (FW). It also revealed that all varieties of Solanum tuberosum L. with peel contained higher TPC than without peel. Comparison between mean TPC of different varieties Solanum tuberosum L. with and without peel on FW basis by independent sample the t-test showed a significant difference (p = 0.003) in TPC. Findings of present study indicated that BARI Begun-8, high yielding varieties of Solanum melongena and Solanum tuberosum with peel are good sources of polyphenols and therefore may contribute as a source of dietary antioxidant.
2.3 MOLECULAR CHARACTERIZATION

Molecular markers have acted as versatile tools and have been effectively employed in diverse fields like taxonomy, physiology, embryology and genetic engineering. Molecular markers like RAPD, ISSR and SSR can be used in breeding, MAS, mapping, fingerprinting, population genetics and phylogenetic studies (Nunome et al., 2002). A challenge for eggplant research is that, despite the fact that the use of molecular markers for phylogenetic studies is well-established; very few studies have described the development of new markers for eggplant. Some of the findings related to molecular markers are reviewed as listed.

2.3.1 Randomly Amplified Polymorphic DNA (RAPD)

A new DNA polymorphism assay was developed in 1990 that is based on the amplification by the polymerase chain reaction (PCR) of random DNA segments, using single primer of arbitrary nucleotide sequence. The amplified DNA fragment is referred as RAPD markers.

Karihaloo et al. (1995) carried out RAPD analysis on 52 accessions of S. melongena and related weedy forms known as “S. insanum” established that even though S. melongena and S. Insanum were highly diverse morphologically, it has no longer appropriate to distinguish them taxonomically.

Rodriguez et al (1999) studied variation among and within capsicum species revealed by RAPD markers. A total of 134 accessions from six Capsicum species maintained at the Asian Vegetable Research and Development Center were characterized using 110 randomly amplified polymorphic DNA (RAPD) markers. Ten pairs of potentially duplicated accessions were identified. Multidimensional scaling analysis of the genetic distances among accessions resulted in clustering corresponding to a previous species assignment except for six accessions. Diagnostic RAPDs were identified which discriminate among the Capsicum species. The diagnostic markers were employed for improved taxonomic identification of accessions since many morphological traits used in the identification of Capsicum are difficult to score. Three Capsicum accessions, misclassified based on morphological traits, were reassigned species status based on diagnostic RAPDs. Three accessions, not previously classified, were assigned to a species based on diagnostic RAPDs.
Definitive conclusions about the species assignment of three other accessions were not possible. The level of diversity between *Capsicum annuum* accessions from the gene bank and the breeding program were compared and no differences were observed either for RAPD variation or diversity. The utilization of genetic resources as a source of variance for useful traits in the breeding program may be the reason for the similarity of these two groups.

Nunome *et al.* (2001) mapped the fruit shape and colour development traits in eggplant (*Solanum melongena* L.) based on RAPD. They constructed a linkage map of eggplant using F$_2$ population derived from a cross between a breeding line, EPL-1 and an introduced line, WCGR112-8, from India. The two parental lines showed contrasting responses to several pathological traits. Parental lines were screened with 1,232 random primers for RAPD. The linkage map showed 88 RAPD loci.

Archak *et al.* (2002) analysed genetic diversity of 27 tomato cultivars using RAPD markers, generated by 42 random primers. The overall high levels of pairwise similarity (Jaccard’s mean = 0.825) and low levels of marker diversity (mean = 0.165) implied the existence of limited genetic variation in the investigated materials. Interestingly, old introductions and locally developed cultivars of the 1970s exhibited significantly greater genetic variation than the ones released during the 1990s. Reduction in the genetic diversity among modern tomato cultivars may be attributed to the recent trend towards breeding for similar plant and fruit characteristics.

Klein-Lankhorst *et al.* (2004) used a set of 11 oligonucleotide decamer primers, each primer directed the amplification of a genome-specific “fingerprint” of DNA fragments. By comparing ‘fingerprints’ of *L. esculentum*, *L. Pennelli* and *L. esculentum* chromosome 6 substitution line LA1641, which carries chromosome 6 from *L. pennelli*, three chromosome 6-specific RAPD markers could be directly identified among the set of amplified DNA fragments. One of the RAPD markers was found to be tightly linked to the nematode resistance gene.

Kochieva *et al.* (2004) used RAPD marker system to determine genetic variation and phylogenetic relationships within the genus *Capsicum*. In total, 1921 bands were used in the genome analysis of 61 accessions representing 11 species of the *Capsicum* genus. The genetic data confirmed the recognition of *C. frutescens* and *C. chinense* as separate species with high bootstrap values. Molecular markers
revealed high genetic similarities of *C. pubescens* with *C. eximium* and *C. cardenasii*. *C. tovarii* was found to be genetically rather closer to *C. baccatum* (RAPD data). Molecular data also supported the close relationships of *C. galapagoense* with *C. frutescens* (RAPD analysis) and this species could, therefore, be considered to be a member of the *C. annuum* complex.

Saraye (2005) carried out survey of genetic diversity among Mauritian eggplant (*Solanum melongena L.*) varieties and two wild species *Solanum torvum* and *Solanum violaceum* using random amplified polymorphic DNA (RAPD) markers. Among total of 31 arbitrary primers screened, only seven primers were found to be highly informative and they produced distinct and polymorphic bands. A total of 67 amplified products were obtained which exhibited 54.7% polymorphism. The dendrogram obtained from the RAPD markers showed the genetic variation exists between the cultivated varieties and the wild types.

Behra *et al.* (2006) used 23 STMS primers for the assessment of genetic diversity from 96 accessions including 92 of *Solanum melongena* and four related non-tuberous species (*Solanum insanum, S. incanum, S. integrifolium* and *S. sysimbriifolium*). Eleven of the 23 primers tested showed polymorphism. Molecular markers can be employed to identify the hybrids and also to monitor introgression of the useful genes.

Chen and Wang (2006) worked on the genetic variation in the graft union of eggplant. RAPD analysis of calluses in the homo- and hetero-graft union revealed the presence of graft union specific bands, while donor specific bands were found absent in the hetero-graft union. This suggested that genetic variation occurred in the graft union and grafting might have the potential as a breeding approach.

Koundal *et al.* (2006) evaluated RAPD based genetic diversity in brinjal (*Solanum melongena*). A total of 38 brinjal accessions including one wild species, *Solanum sisymbriifolium* were characterized. Out of 45 primers employed to generate RAPD profiles, reproducible patterns were obtained with 32 primers and 30 (93.7%) of these detected polymorphism. A total of 149 bands were obtained, out of which 108 (72.4%) were polymorphic.
Oyama et al. (2006) studied levels of genetic variation and genetic structure of 15 wild populations and three domesticated populations of *Capsicum annuum* by RAPD markers. A total of 166 band (all of them polymorphic) and 126 bands (125 of them polymorphic) were amplified in wild and domesticated populations, respectively. Mean percentage of polymorphism was 34.2% in wild populations and 34.7% in domesticated populations. Mean and total genetic diversity were 0.069 and 0.165 for wild populations and 0.081 and 0.131 for domesticated populations. AMOVA indicated that total genetic diversity was equally distributed within (48.9 and 50.0%) and among (50.0 and 51.1%) populations in both wild and domesticated samples.

Singh et al. (2006) identified the genetic diversity within the genus *Solanum* (*Solanaceae*) as revealed by RAPD markers. Among 28 accessions of eggplant which represents total five species. Twenty-eight samples of eggplants were collected from different parts of the country. A total of 144 polymorphic amplified products were obtained from 14 decamer primers which discriminated all the accessions. The similarity result indicated presence of high level of genetic diversity in eggplant and a dendrogram constructed by UPGMA method showed that *S. incanum* was closest to *S. melongena* followed by *S. nigrum*.

Singh et al. (2007) studied RAPD markers for hybrid seed purity testing in tomato (*Solanum lycopersicum*). Two potential hybrids of tomato, *viz.*, NTH-1 (DVRT-Flora Dade) and NTH-7 (DVRT-297/754) were used in this study. Reproducibility of the OPB161193 marker was confirmed in the five independent PCR reactions. The OPB161193 marker was absent in all the 20 female plants (DVRT-1) and present in all the 20 male plants (Flora Dade) and hybrids (NTH-1). Hence, this marker could be commercially used to detect selfed-seeds in the hybrid seed lot of NTH-1.

Mutlu et al. (2008) reported the tagging of the gene for resistance to fusarium wilt (FOM) in eggplant using SRAP, SRAP-RGA and RAPD markers. Analysis of segregation data confirmed the monogenic inheritance of resistance. DNA from F₂ and BC₁ populations of eggplant segregating for fusarium wilt resistance was screened with 2,316 primer combinations to detect polymorphism. Three markers were linked within 2.6 cM of the gene. RAPD marker H12 mapped 2.6 cM from the gene and on the same side as the other two markers.
Poczai et al. (2008) examined phylogenetic relationships and genetic variation in the genus *Solanum* based on the Random Amplified Polymorphic DNA (RAPD) technique. Genetic distances were estimated for 42 accessions from five subgenera (*Archaesolanum*, *Minon* (Syn. *Brevantherum*), *Leptostemonum*, *Potatoe*, and *Solanum*). This investigation provided new information and reinforced to phylogenetic studies.

Poczai et al. (2008) examined phylogenetic relationships and genetic variation was examined in the genus *Solanum* based on the random amplified polymorphic DNA (RAPD) technique. Genetic distances were estimated for 42 accessions from five subgenera. This investigation provided new information and reinforced some suggestions from previous phylogenetic studies. Analysis with random markers from the total genome clearly separated *Solanum* sect. *Dulcamara*, from the other members of *Solanum* subg. *Potatoe*, and indicated that among the analysed *Solanum* subgenera subg. *Solanum* is most closely related to it. The results suggested that *Solanum* sect. *Dulcamara* could be excluded from *Solanum* subg. *Potatoe*. The subclusters formed by *S. rostratum* and *S. citrullifolium* appear to be distinct from the subcluster formed by the two accessions of *S. sisymbriifolium*. This topology indicated that *Solanum* sect., *Androceras* and *Solanum* sect., *Crypyocarpum* were fairly closely related, although the data suggested that the two sections could not be maintained.

Sadder et al. (2008) studied genetic, morphological and agronomical variations by assessing Jordanian eggplant landraces. To assess genetic variation, the non-transcribed spacer of the 5S rDNA yielded invariant banding profiles for all the genotypes. However, nine RAPD primers showed polymorphisms in 81 out of 85 bands amplified.

Biswa et al. (2009) investigated the genetic relationship among ten promising eggplant varieties using RAPD markers. a total of 21 primers were screened out of which four were selected. With these primers, 76 clear and bright fragments were obtained, of which 44 fragments were considered polymorphic. The proportion of polymorphic loci and gene diversity values across all loci were 57.89% and 0.23, respectively. The UPGMA dendrogram based on genetic distance segregated the ten varieties of eggplant into two main clusters.
Multi-locus analysis using PCR based marker, Random Amplified Polymorphic DNA (RAPD) was used by Ansari and Singh (2013) to assess genetic diversity of 14 germplasm of Solanum species. It was observed that random primers (RAPD) showed polymorphism revealing genetic polymorphism in S. melongena and S. aethiopicum. Hence, it may be considered as an efficient marker technique for genetic diversity study among Solanum species. Furthermore, genetic similarity reveals variability within the S. melongena, whereas wide range of dissimilarity between S. melongena and S. aethiopicum.

Khalil et al. (2013) evaluated the F4 lines of eggplant derived from the crosses of Dohazari G x BAU Begun-1 and Laffa S x BAU Begun-1 for resistance to phomopsis blight and fruit rot under confined field conditions. The inoculated plants exhibited differential disease reactions. Among the parents, BAU Begun-1 was resistant whereas Dohazari G and Laffa S were susceptible. All the phenotypes of F4 progenies showed resistant reaction to the disease. Significant differences were observed among the phenotypes in all the yield components. High genotypic and phenotypic coefficient of variation, heritability and per cent genetic advance were estimated for number of fruits per plant, number of secondary branch per plant, fruit length and fruit breadth. Significant and positive correlation was observed between yield contributing characters. Random amplified polymorphic DNA technique was used for assessing genetic variation and relationship among parent cultivars and their F4 progenies of eggplant. Amplification with five decamer primers generated 69.0% polymorphic bands. Comparatively higher genetic distance was observed between Laffa S vs. green globose (Dohazari G x BAU Begun-1). The dendogram produced two main clusters, the parent cultivars and six F4 lines formed cluster I and one line in cluster II. F4 lines of the tested phenotypes showed similar disease reaction and divided into same sub-cluster. The parent cultivars were different in case of disease reaction and finally divided into two groups, susceptible cultivars Laffa S and Dohazari G belonged to group-I and the resistant parent BAU Begun-1 formed another group-II.

Khan et al. (2013) used Random Amplified Polymorphic DNA (RAPD) to brinjal genotypes in order to assess the degree of polymorphism among genotypes. Three RAPD primers were used to estimate genetic diversity in five brinjal cultivars.
A total of 30 bands were scored corresponding to an average of 10 bands per primer with 10 bands showing polymorphism (33.33%). One out of three primers (OPB-07) gave 50% polymorphism. A dendogram constructed based on UPGMA clustering method revealed two major clusters. The cluster-1 comprised of Swarna Mamian and Punjab-70 and cluster-2 comprised of Arka Kranti and Swarna Abhilamb, while Arka Shree occupies a distinct place in dendogram.

Siddiqua et al (2014) investigated genetic diversity in brinjal (Solanum melongena L.) using random amplified polymorphic DNA (RAPD). Fifteen brinjal germplasm and three decamer primers were used for random polymorphic DNA assay. A total of 17 fragments were obtained, out of which 12 (70.59%) were polymorphic. Each primer generated 4 to 8 amplified fragments with an average of 5.67 fragments per primer. The highest genetic distance (0.8873) and the lowest genetic identity (0.4118) were observed in Laffa (Elongated) versus Jessore L and Dharola combinations. The lowest genetic distance (0.1525) was observed in several cultivars. The unweighted pair-group method of arithmetic means (UPGMA) dendrogram was constructed from genetic distance and all brinjal cultivars were grouped into five clusters.

Sifau et al. (2014) used five highly polymorphic Random Amplified Polymorphic DNA (RAPD) primers to describe both the genetic relatedness and variability among 25 accessions of eggplant from Southwestern, Nigeria. At a truncated line of 65%, five clusters and two ungrouped samples are distinguishable from the dendrogram. The data revealed that Solanum dasyphyllum Schum. & Thonn was more closely related to Solanum macrocarpon L than to Solanum melongena L. The relatedness between Solanum incanum L and Solanum melongena, a probability of being progenitors from a common ancestral lineage was also shown. Occurrence of Solanum scabrum L and Solanum nigrum L in the same cluster different from S. melongena, is an indication of distant relatedness to S. melongena but close relatedness between them. High level of polymorphism was observed by the coefficient of variation which exhibited a good separation from a conserved region of the genome.

Boyaci et al. (2015) studied 38 eggplant genotypes, of which 32 were heirloom accessions collected from different regions of Burdur province five were
different local genotypes from other provinces, and one was a cultivar. The phylogenetic relationships among these heirlooms were evaluated using 40 morphologic descriptors and five randomly amplified polymorphic RAPD markers. The horizontal dendrograms were created by using UPGMA with both morphologic and molecular data. Burdur heirloom accessions showed high genetic diversity based on morphological and molecular data. The genetic similarity rates ranged from 0.29 to 0.91 according to the morphological data, and ranged from 0.84 to 0.98 according to the molecular data. Molecular data generated by RAPD method, compared to morphological data, were insufficient to reveal genetic diversity. Therefore, in order to confirm genetic variations, studies based on other molecular methods are necessary. The regional genetic populations include a wide eggplant genetic diversity which can be good source for the breeding studies performed in the future.

2.3.2 Inter simple sequence repeat (ISSR)

ISSR primers (Zietkiewicz et al., 1994) were an efficient tool for the genetic analysis. ISSR markers have been employed in many species for fingerprinting and phylogenetic studies, gene tagging, and mapping (Trojanowska and Bolibok, 2004). ISSRs appear to be quite evenly dispersed in the plant genome, although they were supposed to display a higher frequency in specific regions (simple sequence repeat hot spot).

Kochieva et al. (2002) analyzed ISSR markers for the study of genetic diversity and phylogenetic relationships in 54 wild accessions and cultivars of the genus Lycopersicon. Analysis involved 14 ISSR primers homologous to microsatellite repeats and containing additional selective anchor nucleotides. In total, 318 ISSR fragments were amplified for the wild and cultivated tomato genomes. The inter specific polymorphism revealed with the ISSR primers was 95.6%. Species-specific ISSR fragments were detected for each tomato species. The highest number (more than 20) of species-specific fragments was obtained for L. esculentum, although the intraspecific variation of ISSR patterns was low.

Isshiki et al. (2008) observed ISSR variations in eggplant (Solanum melongena L.) and related Solanum species. They studied eight cultivars and 12 accessions. A total of 552 polymorphic amplified bands were obtained from 34 of the 100 primers tested, and the percentage of polymorphisms was 99.1%. The cluster
analysis based on the ISSR markers classified the *Solanum* species into specific groups. The ISSR markers obtained by a few of the 34 primers were enough for distinguishing of the eight cultivars of eggplant.

Toppino *et al.* (2008) studied the ISSR of androgenetic dihaploids reveals tetrasomic inheritance in tetraploid somatic hybrids between *Solanum melongena* and *Solanum aethiopicum* group Gilo. The segregation of 280 ISSR markers (110 *aethiopicum*-specific, 104 *melongena*-specific, and 66 monomorphic) were evaluated in 71 dihaploids. According to the genetic constitution (simplex/duplex/triplex), almost 64% of the fragments revealed the tetrasomic and/or disomic inheritance. With regard to the assigned species-specific fragments, 68% and 4% were unambiguously the result of tetrasomic and disomic inheritance, respectively.

Tiwari *et al.* (2009) worked on the molecular characterization of brinjal (*Solanum melongena* L.) cultivars using ISSR markers. Molecular characterization of 19 advanced cultivars and landraces of brinjal was carried out using ISSR markers. Total 23 anchored and non-anchored ISSR primers produced 299 fragments. Of these, 56 (18.73%) ISSR fragments were polymorphic. All the cultivars could be distinguished based on ISSR profiles.

Patel *et al.* (2011) assessed the genetic relation by screening DNA from thirteen *Capsicum* cultivars using inter simple sequence repeat (ISSR). Five ISSR primers amplified 204 reproducible bands of which 139 were polymorphic. The percentage of polymorphic bands detected by ISSR was 100%. The highest polymorphic bands obtained by the use of primers UBC-809 (34) and UBC-66 (53). This study revealed the great importance of guaranteeing the differentiation of chilli cultivars and its application for certification purposes.

More *et al.* (2013) determined the genetic diversity between brinjal varieties. For this purpose, eleven primers were used to characterize five brinjal varieties under cultivation in different state of India as contrasting genotypes. Sixty-nine scorable bands were generated among 44 comprised polymorphic markers, with an average of five polymorphic bands per primer. In the generated dendrogram, the accessions were placed in cluster, where cluster A include only one genotype from IARI, India (Pusa Purple Long) and clusterB is the biggest cluster which include three genotypes (Pragati, Vaishali, Krishna). This molecular marker tools are widely used in plant
research such asphylogenic studies as well as in cultivar identification and germplasm management. The selected primers were used for the first time in brinjal, representing valuable tools for future evaluations, with emphasis to diversity characterization and genetic mapping in brinjal.

2.3.3 Simple sequence repeats (SSR)

The first study about SSRs in eggplant concentrated on their suitability as a marker system for molecular analysis of this plant (Nunome et al., 2002). In the study, a linkage map of eggplant using SSR, AFLP and RAPD markers were built up. In another study, Nunome et al. (2009) specifically examined trinucleotide repeats in eggplant. The reason to use trinucleotide was due to their greater suitability for allele differentiation.

Nunome et al. (2002) showed characterization of trinucleotide microsatellites in eggplant. A small insert genomic library of brinjal (Solanum melongena L.) was screened with eight trinucleotide probes. In which two trinucleotide repeats, (AAC/TTG)n and (ACC/TGG)n, predominated, accounting for 84.5% of the isolated trinucleotide microsatellites. A total of 83.5% of the identified trinucleotide repeats contained seven repeat units or less. Inserts of the positive clones were sequenced and 85 PCR primer sequences bordering the microsatellite repeats were designed. In order to assess the polymorphism, 11 S. melongena lines and 11 Solanum relatives were used. Most of the markers that detected polymorphism between S. melongena lines contained eight or more repeat units. The motif most frequently found in Solanum was (AAC/TTG)n in this study. All the primer sets which detected PCR products in S. melongena yielded PCR products in S. incanum, which was in agreement with its very close relationship with S. melongena.

Samuel et al. (2002) used Simple Sequence Repeat (SSR) markers for the genetic analysis of tomato. Genetic similarities among the genotypes were calculated and a cluster analysis performed using NTSYS software. A high degree of diversity was observed in the Eritrean genotypes. Thirteen out of the 15 SSRs were polymorphic, with 2-5 alleles per marker. The average number of alleles per SSR locus was between 1.0 and 1.4. The dendrogram showed two major groups of genotypes, distinguishing the San Marzano and Marglob types. It showed the genetic relationships between Old Italian genotypes and the Eritrean genotypes in both types.
Saskia et al. (2002) generated SSR markers from two sources: (1) size-selected genomic libraries screened with (AT)n, (AT)n, (GT)n, (ATT)n and (CTT)n probes. (2) Gene Bank database. Primers were designed for 114 loci and used for genotyping 13 tomato varieties and three *Lycopersicon* species. Eighteen markers were used to evaluate the polymorphism among the commercial genotypes and were found to be a useful tool for cultivar identification.

Benor et al. (2008) determined the genetic diversity of 39 determinate and indeterminate tomato inbred lines collected from China, Japan, South Korea, and USA. Using 35 SSR polymorphic markers, a total of 150 alleles were found with moderate levels of diversity and a high number of unique alleles existing in these tomato lines. The mean number of alleles per locus was 4.3 and the average polymorphism information content (PIC) was 0.31. Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering at genetic similarity value of 0.85 grouped the inbred lines into four groups, where one USA cultivar formed a separate and more distant cluster. Clustering was consistent with the known information regarding geographical location and growth habit. The genetic distance information reported in this study might be used by the plant breeders when planning future crosses among these inbred lines.

Dimitrova et al. (2008) isolated seven clones containing (CTG)n/(CAG)n repeats (n ≥ 4) by screening *Lycopersicon esculentum* genomic DNA. Four of the clones contained more than one simple sequence repeat (SSR). The SSRs were analyzed in several *L. esculentum* cultivars after polymerase chain reaction (PCR) amplification. No length variations were observed, suggesting considerable locus stability. Five clones were from transcribed regions, which might explain the lack of cultivar variations. However, the conservation of CTG repeats was limited as differences in some transcribed loci were registered between *L. pennellii* and other *Lycopersicon* species. It was noted that in *Lycopersicon* trinucleotide repeat variation might be used for species identification.

Falcon et al. (2008) studied the diversity of Almagro eggplant and Andalusian accessions with morphological traits and molecular markers SSRs with the aim of obtaining a characteristic fingerprint of the Almagro eggplant. They found two SSRs alleles exclusive of Almagro eggplant and universal to all Almagro accessions by
using selected morphological descriptors and specific molecular markers also have been able to distinguish the PGI Almagro eggplant from closely related varieties. The SSRs have proved useful for detecting differences between the closely related Almagro and Andalusian accessions.

Khorsheduzzaman et al. (2008) studied molecular characterization of five brinjal (Solanum melongena L.) using Simple Sequence Repeats (SSR) markers. All the genotypes showed considerable variation in respect of morphological, anatomical and biochemical aspects. For study of relatedness, plant genomic DNA was extracted by CTAB based method using 11 randomly selected primers produced from Calgene Inc. USA. The primers developed 22 bands through PCR amplification out of which 15 from3 primers and were polymorphic. Genetic similarities of SSR profiles were estimated based on Jaccard’s coefficient value. The dendrogram generated two clusters and they were clearly distinct and separated from each other. Cluster-I consisted of genotypes TURBO and BL009; and cluster-II comprised of genotypes EG058, EG075 and ISD006. Genotype TURBO and BL009 were identified as the diverse genotype and showed a maximum of 17% dissimilarity from EG058, EG075 and ISD006. The similarity value ranged from 0.83 to 1.00 which indicated the presence of narrow range of genetic diversity at molecular level but have still a possibility of crossing among the genotypes of two clusters. The banding pattern of different genotypes could be utilized as reference for further comparisons.

Stagel et al. (2008) studied the gene-based microsatellite development for mapping and phylogeny studied in eggplant. From >3,300 genomic DNA sequences, 50 SSR-containing candidates suitable for primer design were recovered. Of these, 39 were functional, and were then applied to a panel of 44 accessions, of which 38 were cultivated eggplant varieties, and six were from related Solanum species. The usefulness of the SSR assays for diversity analysis and taxonomic discrimination was demonstrated by constructing a phylogeny based on SSR polymorphisms.

Asgedom et al. (2009) analyzed diversity among and heterogeneity within 25 local tomato cultivars from Eritrea; two South African; two Zairian and twelve old Italian cultivars, obtained from the Centre for Genetic Resources of The Netherlands (CGN). Tomato cultivars Isola, Aranka, Nunhems 6328 and VNT cherry were used as genotyping references. They found most of the tomato varieties heterogeneous having
13 polymorphic SSR loci with 2 to 5 alleles, which is unusual for true-to-type cultivars, while the cultivars obtained from the CGN were more or less homogeneous with monomorphic microsatellite loci. The average number of alleles for Eritrean varieties was 1.3; for the varieties from the CGN it was 1.04; and for the control cultivars it was 1.4. The results clearly confirmed that there was a high heterogeneity among the Eritrean varieties compared with the samples from the CGN suggesting genetic contamination among the Eritrean varieties.

Chen et al. (2009) investigated genetic variation in 216 different populations of tomato (*Solanum lycopersicum* L.) cultivars, hybrids, and elite breeding lines using single nucleotide polymorphism and simple sequence repeat markers. They analyzed 47 markers, 72.3% were polymorphic in the whole collection of 216 genotypes and 51.06–59.57% showed polymorphisms in individual populations. However, genetic variation was narrow in all the four populations. Nei’s genetic distance varied from 0.0422 to 0.1135 between populations and from 0.0085 to 0.3187 between lines in individual populations.

Nunome et al., (2009) constructed simple sequence repeat (SSR) enriched genomic libraries in order to develop SSR markers, and sequenced more than 14,000 clones. From these sequences, 2,265 primer pairs were designed to Xank SSR motifs. From amplification of 1,399 randomly selected primer pairs 1,054 SSR markers was identified. The markers had an average polymorphic information content of 0.27 among eight lines of *S. melongena*. The markers could be a useful resource for qualitative and quantitative trait mapping and for marker-assisted selection in eggplant breeding.

Genic microsatellite (SSR) markers were identified by Tumblen et al. (2009) from an expressed sequence tag library of *S. melongena* and used for analysis of 47 accessions of eggplant and closely related species. The markers had very good polymorphism in the 18 species tested including eight *S. melongena* accessions. Moreover, genetic analysis performed with these markers showed concordance with previous research and knowledge of eggplant domestication. These markers are expected to be a valuable resource for studies of genetic relationships, fingerprinting, and gene mapping in eggplant.
Feng et al. (2009) employed SSR markers for analysis on fingerprinting and genetic diversity of 88 potato cultivars. Ten of 138 pairs of SSR primers were screened out based on 16 distinct accessions. Ten primer pairs amplified a total of 135 alleles (including 133 polymorphic alleles) among the 88 cultivars, and the ratio of polymorphism was as high as 98.52%. Alleles amplified by each pair of primers ranged from 7 (primer S7) to 22 (primer S189), with a mean of 13.5. The polymorphic information content values (PIC) ranged from 0.7604 (primer S192) to 0.9375 (primer S189), with a mean of 0.8501. The fragment size varied from 80 to 380 bp. The DNA fingerprinting of 88 cultivars was constructed by six pairs of primers of S180, S25, S7, S151, S184, and S192. Eighty-seven out of 88 cultivars were univocally identified using only five SSR primers (S 180, S25, S7, S151, and S184). UPGMA cluster analysis of genetic similarity showed that all the materials were clustered into one group at the genetic similarity of 0.620, and 81.8% of the cultivars were still clustered together at the genetic similarity of 0.652. The genetic relationships of cultivars were identical to the family tree basically.

Parmar et al. (2010) screened a collection of twenty-five determinate and indeterminate cultivars of tomato from different geographical locations of India with twenty-three SSR (simple sequence repeat) primers in order to determine genetic identities, genetic diversity and genetic relationships among these cultivars. On an average, 40 alleles were amplified using SSR primers with scorable fragment sizes ranging from approximately 150 to 1000 bp. Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering grouped the cultivars into five groups with the USA cultivars forming a distinct group.

Jin et al. (2010) analyzed genetic variation of eighty-eight accessions including eighty-six of Solanum melongena and two wild related species (Solanum integrifolium and Solanum torvum) with 23 SSR primers. Twenty primers were successfully amplified, of which 19 showed polymorphism with a total of 68 detected alleles. The number of alleles per primer ranged from 2 to 6, with a mean of 3.6. Among 19 polymorphism primers, four primer pairs (EM117, EM155, EM126, EM127) gave rise to multiple polymorphic bands, two of which could be used for varieties certification in eggplant. The average genetic diversity of all the accessions measured by the Nie's genetic diversity, Shannon's Information index and effective
number of alleles were 0.41 (range 0.12~0.80), 0.7443 (range from 0.2617~1.6958) and 2.0151 (ranged from 1.1307~5.310), respectively. Genetic similarity among all the accessions ranged from 0.09 to 1 with an average of 0.69. The high diversity was displayed. Additionally, S. melongena had high average similarity with the wild species S. integrifolium (0.61) and low average similarity with S. torvum (0.26). UPGMA clustering at genetic similarity value of 0.60 grouped all the eggplant accessions into four groups, where S.torvum formed a separate and more distant cluster. Moreover, the fourth group can be further classified into two sub-groups, and the wild species S. integrifolium can be clearly separated from the other cultivated eggplants. However, majority of the cultivated eggplants were not clustered in ways concordant with taxonomic information.

Patel et al. (2011) assessed the genetic relation by screening DNA from thirteen Capsicum cultivars using microsatellite (SSR) markers. A total of one to five alleles were detected by six SSR primers, with an average of two alleles per primer. The number of alleles per locus ranged one (ssrCAMS-811) to five (ssrCAMS-142). The polymorphism information content (PIC) values ranged from 0.27 (ssrCAMS-405) to 0.67 (ssrCAMS - 142). This study revealed the importance of guaranteeing the differentiation of chilli cultivars and its application for certification purposes.

2.3.4 Comparison among Molecular Markers

Kochieva et al. (2004) used AFLP, RAPD and ISSR marker systems to determine genetic variation and phylogenetic relationships within the genus Capsicum. In total, 1921 bands were used in the genome analysis of 61 accessions representing 11 species of the Capsicum genus. AFLP, RAPD and ISSR dendrograms were congruent but not identical in the clustering of the analysed Capsicum accessions. The genetic data confirmed the recognition of C. frutescens and C. chinense as separate species with high bootstrap values. Molecular markers revealed high genetic similarities of C. pubescens with C. praetermissum (ISSR data). Molecular data supported the close relationships of C. galapagoense with C. annuum (ISSR analysis) and this species could therefore be considered to be a member of the C. annuum complex. Combining the results based on molecular data obtained in this
study and results obtained by other researchers an informal classification of *Capsicum* can also be proposed.

Tam *et al.* (2005) assessed genetic diversity in collections of tomato and pepper industrial lines by retro-transposon-based sequence-specific amplification polymorphism (SSAP) marker system. The utility of SSAP markers was compared to that of amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) markers. Among all results, SSAP was most informative of the three systems for studying genetic diversity in tomato and pepper, with a significant correlation of genetic relationships between different SSAP data sets and between SSAP, AFLP and SSR markers. For tomato, SSAP was more suitable for inferring overall genetic variation and relationships, while SSR has the ability to detect specific genetic relationships.

Rajput *et al.* (2006) studied PCR-based techniques to detect polymorphisms in brinjal. They used 60 RAPD primers and confirm the reproducibility. Every experiment was performed 50 times in which the reproducibility of two popular molecular marker techniques (RAPD and SSR) was examined. For each technique, an optimal system was chosen, which had been standardized and routinely used. The results obtained were compared with those of the original generator. RAPDs proved difficult to reproduce. While SSR alleles were amplified, but small differences in their size were obtained.

Tumbilen (2007) analyzed genetic diversity of Turkish eggplants and wild relatives with different molecular tools. To reveal genetic diversity among eggplant cultivars, AFLP marker system was applied to the sample genotypes and for the investigation of genetic variation between *S. melongena* and its wild relatives, SSR marker system was used. For the AFLP data for Turkish eggplants, and “r” value of 0.97 was obtained which was in the best scale. These results showed that 64.34% of the variation was observed between samples. According to the statistical results of SSR analysis, the “r” value of *Solanum* species genotypic data was found to be 0.88. This indicated the correlation between sample genotypic data and dendrogram was found to be high. The results of AFLP studies showed that although a high similarity value was observed, diversity was detectable among the accessions.
Falcon et al., (2009) studied morphological and molecular (AFLP and SSR) diversity in a collection of 38 black eggplant accessions, including commercial varieties and landraces as well as in six non-black control eggplants, from different origins. The results showed that black eggplants contained a considerable morphological and molecular diversity, but commercial varieties, and in particular F	extsubscript{1} hybrids, displayed a reduced morphological and molecular diversity when compared with landraces.

Demir et al. (2010) carried out molecular characterization of eggplant genotypes collected from different geographical regions of Turkey using SSR and RAPD markers. With amplification of five SSR loci, the number of alleles per microsatellite locus ranged from 2 to 10, with a total of 24 alleles. The average number of alleles per locus was 4.8. Using 11 decamer RAPD primers, 100 bands were amplified, among which 29 were polymorphic. The number of bands per primer ranged from seven (OPH10, OPH19, OPH20, OPH03) to 14 (OPB07). Primer OPB07 was the most polymorphic, generating 64% polymorphic bands; the rest of the primers gave less than 50% polymorphism. UPGMA dendrograms were used to examine the genetic relatedness of the genotypes.

Sunseri et al. (2010) assessed genetic diversity among 70 “scarlet eggplant” (*Solanum aethiopicum*) entries from different geographical origins. Entries were firstly evaluated for main morphological traits and chlorogenic acid content. In addition, amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) analyses were used to evaluate genetic relationships among entries. Matrices of genetic similarity from AFLP and SSR data were utilized in order to obtain a dendrogram. A large cluster included several entries from South America with limited rate of genetic variation was observed. On the contrary, higher amount of variation was observed in the cluster with entries from Africa and Italy. These entries appeared always morphologically and genetically distinguishable from the others. These results provided additional information for the conservation, improvement and legal protection of the ecoype “melanzanarossa di Rotonda”, cultivated in Italy.

Ali et al. (2011) analyzed genetic diversity of eggplant using inter-simple sequence repeat (ISSR) and RAPD procedures to subdivide 143 cultivated eggplants based on coefficient of parentage, genetic diversity index (GDI) and canonical
ISSR markers were more effective than RAPD markers for detecting genetic diversity. Their ISSR/RAPD data provide molecular evidence that coincides with morphological-based classification into three varieties and further subdivision into eight groups, except for two groups. Intensive use of elite parents and extensive crossing within groups have resulted in increased coefficient of parentage and proportional contribution but decreased GDI during the past decades. The recent introduction of alien genotypes into eggplant breeding programmes may broaden the genetic base.

Verma et al. (2012) used eleven RAPD and six SSR primers to analyze the genetic variation in 29 popular Indian brinjal varieties. The 11 RAPD primers generated 64 polymorphic markers with average of 5.81 polymorphic bands per primer. Genetic distance based on RAPD markers among all the varieties ranged from 0.07 to 0.78 with an average of 0.33. All the six SSR primer pairs were polymorphic with a total of 25 detected alleles. The number of alleles per primer ranged from 2 to 10, with a mean of 4.67. UPGMA clustering for RAPD and SSR markers grouped all the brinjal varieties into two clusters, but grouping patterns were different for each of the marker system. However, majority of the cultivated varieties did not cluster concordant to the collection site information or phenotypic data such as fruit shape or any other known traits. The genetic diversity of brinjal varieties reported in this study could be useful when planning future crosses amongst these varieties.

Das and Borah (2015) used random amplified polymorphic DNA (RAPD) and inter-simple sequence repeat (ISSR) markers for assessing genetic diversity and species relationships among eight species of Solanum. Both random and SSR primers revealed 90.9 and 96.1 % polymorphism, respectively. ISSR markers were found to be more efficient than the RAPD assay. The marker index and polymorphic information content varied from 40.8 to 47.0, 40.9 to 49.0 and 0.41 to 0.49, 0.43 to 0.49, respectively for both the RAPD and ISSR markers. Mean value of number of observed alleles, number of effective alleles, Nei’s gene diversity and Shannon’s index were 1.95-1.99, 1.47-1.75, 0.26-0.37 and 0.45-0.43 respectively for both the markers. Both UPGMA and PCA analyses of the data revealed clear groupings among the species. Genetically distinct genotypes identified by using RAPD and ISSR markers could be potential sources of germplasm for conservation and further improvement of the genus Solanum.
Thakkar et al. (2015) analyzed ten brinjal genotypes for their genetic diversity study through nineteen RAPD and ten ISSR primers among which ten RAPD and six ISSR primers gave good polymorphism with 83.43 and 81.03 per cent average polymorphism, respectively. The RAPD primers produce 480 amplified products with 71 bands among which 57 were polymorphic, giving average PIC and resolving power value of 0.837 and 3.48, respectively. The ISSR primers produced 52.17 average numbers of amplified products with 6.33 and 7.83 average numbers of polymorphic and total numbers of bands. The ISSR primers gave average PIC and resolving power value of 8.44 and 2.83, respectively. The RAPD primers produced band size range from 150 to 2659 while ISSR produced 113 to 3744. Jaccard's similarity range for RAPD, ISSR and pooled data were 0.50 to 0.77, 0.55 to 0.86 and 0.52 to 0.75, respectively. Different combinations of similarity matrix and cophectic values of RAPD, ISSR and pooled data showed good correction through Mantel's test (r=0.799 to 0.881) except for ISSR (r=0.486 to 0.463). Results indicated RAPD as a better marker and helped to study relatedness of different genotypes for future developments.