Vegetable Science (2023) Vol. 50 (Special Issue): 166-176

doi: 10.61180/vegsci.2023.v50.spl.04

ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)

www.isvsvegsci.in

REVIEW ARTICLE

Brinjal: Breeding and Genomics

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Abstract

Brinjal (*Solanum melongena* L.,) also known as eggplant is an important solanaceous vegetable crop grown across tropical and subtropical regions of the world. India is the centre of origin of the crop, large diversity in the morphology of fruit and plant type exists in the country. Also, a large number of wild relatives is being utilized in breeding programs as a source of biotic and abiotic stress tolerance. Conventional breeding programs have focused on improving plant type and yield through the development of high-yielding varieties and hybrids. More recently, breeding for stress tolerance and enhanced nutritional content has gained importance. Genetic inheritance studies, mapping, molecular tools are enriching the crop improvement work. Of late, the availability of high-quality genome sequences has spurred functional analysis at the genome level augmenting molecular tools for marker-assisted selection. In the present article, attempt has been made to highlight the improvement work carried out from relevance of the crop diversity to genomic-level knowledge advancement. Future prospective in brinjal improvement having relevance in Indian context is also highlighted.

Keywords: Brinjal, breeding, eggplant, genomics, improvement, molecular, Solanum melongena and transgenics.

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Citation: Akanksha, Tiwari, J.K., Bhuvneswari, S., Karkute, S.G., Tiwari, S.K. and Singh, M. (2023). Brinjal: Breeding and Genomics. Vegetable Science 50(spl): 166-176.

Source of support: Nil

Conflict of interest: None.

Received: 05/10/2023 **Accepted:** 28/12/2023

Introduction

Eggplant (*Solanum melongena* L.), known by various names such as brinjal or aubergine, is a prominent member of the diverse Solanaceae family, which encompasses around 3000 species across nearly 90 genera (Vorontsova and Knapp, 2012). Widely cultivated in tropical and subtropical regions, eggplant is a staple vegetable crop, contributing significantly to global agricultural production. In 2021, the cultivation of brinjal covered 1.96 million hectares, yielding approximately 58.64 million metric tonnes worldwide. Notably, eggplant holds a place among the top five essential vegetable crops in Asia and the Mediterranean region, with China, India, Egypt, Turkey, and Indonesia emerging as leading producers (www.fao.org/faostat).

In India, a major player in the global eggplant production landscape, the cultivation of brinjal is projected to reach 12.98 million metric tonnes in 2022 (Anonymous, 2022). While the crop is grown throughout the country, key brinjal-producing states include West Bengal, Orissa, Gujarat, Bihar, and Madhya Pradesh. India's brinjal, characterized by glossy, round-shaped fruits with purple skin and a green calyx, is exported to various countries, including Sri Lanka, Maldives, Singapore, Sudan, and Mali. Beyond its culinary significance, eggplant boasts nutritional value, being low in calories, high in fiber, and rich in bioactive compounds. Phenolic acids, particularly chlorogenic acid, constitute a significant portion of the total phenolics in the fruit flesh, while anthocyanin in

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the fruit skin adds to its health benefits (Plazas *et al.,* 2014; Braga *et al.,* 2016). Moreover, eggplant serves as a source of essential minerals such as phosphorus, potassium, calcium, and magnesium. The nutritional composition varies across cultivars and is influenced by environmental factors.

Recognized for its prolific nature, eggplant is often hailed as the "poor man's vegetable" (Som and Maity, 2002). Additionally, eggplant is acknowledged for its medicinal properties, historically used in treating conditions like toothache, liver complaints, and diabetes. Notably, different cultivars exhibit variations in nutritional content, with white cultivars containing double the crude fiber of purple and green cultivars (Flick *et al.,* 1978). Despite its nutritional benefits, eggplant cultivation faces challenges, including susceptibility to diseases, insect pests, and abiotic stresses such as heat and drought. Major diseases affecting eggplant include Fusarium wilt, Verticillium wilt, bacterial wilt, bacterial blight, little leaf (viral), and nematodes. Among insect-pests, the fruit and shoot borer (*Leucinodes orbonalis*) pose a significant threat, causing up to 70% yield loss.

In light of these challenges, there is a growing imperative for understanding and harnessing eggplant genetic resources through conventional and molecular breeding approaches. This involves the utilization of genomics tools to expedite the improvement of eggplant varieties, addressing both yield and quality considerations. In this context, this comprehensive exploration aims to delve into the genetic resources, characterization, and utilization of eggplant, providing insights into the challenges and opportunities for accelerated improvement in eggplant cultivation.

Origin and Domestication of Eggplant

Eggplant (*Solanum melongena* L.) finds its roots in India or Indo-China, with over 42 Solanum species thriving in the region. Historical evidence indicates its cultivation in China from the 4th century, and its introduction to the Mediterranean by Arabs in the 7th century. Believed to be native to the Old World, eggplant's journey involves its domestication from S. insanum, evolving from the Middle Eastern/African species *S. incanum. S. melongena* L. is the primary Asian eggplant, extensively cultivated in India. Notably, two semi-cultivated or wild relatives, *S. aethiopicum* and *S. macrocarpon*, are found in sub-Saharan Africa. These species, originating in West Africa, contribute to the genetic diversity of cultivated eggplant through cross-breeding. The domestication process of eggplant in Asia, particularly in the Indo-Burma area, is supported by archaeological findings in Rakhigarhi, India, dating back to 4000 BCE. Phylogenetic studies position cultivated eggplant close to its wild ancestor, Solanum incanum, within the "*S. incanum-S. melongena* complex."

Eggplant Gene pool

The eggplant gene pool, shaped by the intricate interplay of domestication and crossing behaviors, is characterized by a diverse set of wild species. These species, typically bitter, spiny, and small-fruited, fall into the "eggplant complex," classified into three gene pools. The primary gene pool (GP1) encompasses the cultivated *S. melongena* and its immediate wild ancestor, S. insanum, known for their ease of crossability and fertility in hybrids. Moving to the secondary gene pool (GP2), scarlet eggplant (*S. aethiopicum*) and gboma eggplant (*S. macrocarpon*) take center stage, along with their progenitors and over 40 challenging-to-cross wild species. Examples include partial sterile hybrids obtained from *S. tomentosum, S. linnaeanum, and S. dasyphyllum* due to inherent hybridization barriers. The tertiary genepool (GP3) introduces distantly related wild species like *S. sisymbriifolium, S. elaeagnifolium*, and *S. torvum,* necessitating special pre-breeding techniques for successful hybridization. India recognized as the center of eggplant diversity, hosts about 28 Solanum species, with maximum diversity observed in the western and eastern peninsular regions and the northeastern region.

In terms of genetic resources and diversity, eggplant's richness is evident with over 5,665 accessions of *S. melongena,* 798 accessions of *S. aethiopicum,* and 196 accessions of *S. macrocarpon* conserved globally. India's National Bureau of Plant Genetic Resources (NBPGR) alone holds more than 1,900 accessions. The World Vegetable Center leads in collections, with over 2,200 accessions spanning 90 countries. Wild eggplant relatives, distributed across Africa and Asia, emerge as valuable sources of genes for stress tolerance in breeding programs, despite their often prickly exteriors and bitter fruits. In the diverse landscape of India, regional preferences for eggplant characteristics vary, giving rise to a multitude of landraces still in cultivation. Noteworthy varieties like Udupi MattuGulla, AgsechiVayingim, and RamnagarBhanta, some even registered as Geographical Indications, reflect the cultural nuances and richness embedded in eggplant cultivation across the country.

Eggplant Gene Banks

Collection and conservation of germplasm is done in gene banks. Eggplant germplasm is conserved at various national/international gene banks. The World Vegetable Centre (earlier AVRDC), Taiwan holds the largest number over 3000 accessions belonging to 90 different countries. Other international gene banks maintaining germplasm collections are the Plant Genetic Resources Conservation Unit, USDAARS, USA; the Center for Genetic Resources at the Wageningen University & Research, The Netherlands; the Vavilov Research Institute of Plant Genetic Resource in Russia; the ICAR-National Bureau of Plant Genetic Resources in India; the Institute of Vegetables and Flowers in China and the French National Institute for Agricultural Research (INRA) in Avignon, France etc. (GENESYS, 2020).

S. melongena is maximum recorded in India with over 5000 accessions and 21000 globally. *S. macrocarpon* and S.

aethiopicum were found maximum in West Africa with a total of 1365 and 4230, respectively. The Asian Vegetable Research and Development Center (AVRDC) Shanhua, Taiwan, is also one of the largest genebank holders of the three cultivated eggplants with 2256 of *S. melongena*, 60 of *S. aethiopicum*, and 42 accessions of *S. macrocarpon*. In India, it is estimated that 1800 eggplant landraces, cultivars, and wild species were collected by the National Bureau of Plant Genetic Resources, NBPGR, New Delhi. Likewise, a large number of eggplant collections are maintained worldwide (Table 1).

Conventional Breeding

Eggplant, a self-pollinated crop, sees the preference for F1 hybrids in commercial cultivation, offering diverse fruit shapes and peel colors ranging from white to various shades of purple and green. Genetic diversity in cultivated eggplants is a result of extensive human selection, hybridization, and natural inter-crossing, with studies pointing to *S. ovigerum* as the initial domesticated landrace. Conventional breeding aims to address challenges like insect pests, diseases, and abiotic stresses such as salinity, heat, cold, and drought. Key breeding objectives include enhancing fruit yield, quality traits, and resistance to stresses. Manual emasculation and pollination, though effective, are labor-intensive, prompting the pursuit of cytoplasmic male sterility for breeding efficiency. Grafting technology has also proven beneficial, particularly in regions with serious soil-borne pathogens, where successful grafting has been demonstrated between *S. melongena* and various rootstocks.

Table 1: Eggplant germplasm in the world gene banks

Species	*GBIF*	*GENSYS*	*AVGRIS*
Cultivated eggplant			
Solanum melongena	21,852	4056	2256
Solanum aethiopicum	4230	590	60
Solanum macrocarpon	1365	95	42
Wild relatives of eggplant			
Solanum nigrum	211,385	44	20
Solanum americanum	27,624	43	189
Solanum torvum	12,775	115	39
Solanum villosum	11,590	48	17
Solanum sisymbriifolium	7054	4	10
Solanum nigrescens	4794	1	2
Solanum anguivi	4098	23	39
Solanum seaforthianum	3713	3	5
Solanum linnaeanum	3327	4	3
Solanum capsicoides	2638	1	1
Solanum viarum	2237	3	17
Solanum incanum	2008	28	3
Solanum aculeatissimum	1873	46	19
Solanum violaceum	1606	1	59
Solanum scabrum	1400	148	55
Solanum lasiocarpum	1076	31	34
Solanum virginianum	1032	3	3
Solanum trilobatum	207	10	7
Solanum ferox	150	11	8
Solanum insanum	110	11	16

Wild relatives of eggplant, including *S. aethiopicum, S. linnaeanum, S. sisymbriifolium, S. aculeatissimum,* and *S. torvum,* serve as valuable sources of disease resistance. The breeding efforts involve inter-specific hybridization, producing hybrids with resistance to bacterial wilt, Fusarium/Verticillium wilt, leafhopper, aphids, and fruit and shoot borer. Floral morphology in eggplant encourages both self and cross-pollination, with selfing undertaken to maintain purity. Breeding for improvement encompasses a wide array of traits, including high yield, earliness, better quality, plant architecture, fruit characteristics, low seed content, glossiness, slow browning of cut fruits, nutritional value, and resistance to various pests and diseases. Pure-line selection, pedigree, and backcross methods are commonly employed, with F1 hybrids gaining popularity due to their vigor, uniformity, and higher yield. Different fruit shapes, such as small round, long, oblong, and round, are bred for commercial cultivation (Table 2).

Crop wild relatives (CWR) are vital sources of resistance genes, and interspecific hybridization with CWR is a significant strategy for resistance breeding. Mapping populations are developed to identify resistant genes/alleles for biotic and abiotic stresses. The utilization of diverse wild relatives faces challenges in conventional sexual reproduction, leading to the use of CWR as rootstocks with susceptible cultivated varieties/hybrids as scions to create commercial grafts. These grafts exhibit tolerance to various stresses and demonstrate improved growth and yield traits.

Molecular Breeding

Conventional breeding efforts in eggplant have yielded various cultivars, but Marker-Assisted Selection (MAS) has not yet contributed to the development of varieties. The vast collection of eggplant germplasm globally necessitates characterization for utilization in breeding and genomics research, evaluating traits like phenotype, yield, and disease resistance. Molecular markers, including RAPD, SSR, ISSR, and AFLP, have been employed for characterizing genetic diversity. The first genetic map was established using RFLP markers in an F2 population of *S. melongena* × *S. linneanum*, subsequently improved with 110 COSII markers. QTLs were identified for morphological traits in later studies.

The recent publication of a high-quality, chromosome-level whole genome sequence for eggplant has accelerated genomics-assisted breeding. While no varieties have been developed through MAS, recent studies have focused on mapping important economic traits using genome-wide

Table 2: Biotic/abiotic stresses and resistance source of eggplant species

Biotic/abiotic stress	*Resistance source (Solanum spp.)*	*References*
Diseases		
Bacterial wilt (*Ralstonia solanacearum*)	*S. hispidum*, *S. torvum*, *S. nigrum*, *S. xanthocarpum*, *S. sisymbrifolium*, *S. mammosum*, *S. integrifolium*, *S. melongena*	AVRDC (1998), Wang et al. (1998)
Phomopsis blight (*Phomopsis vexans*)	*S. aethiopicum*, *S. incanum*, *S. indicum*, *S. xanthocarpum*, *S. indicum*, *S. gilo*, *S. khasianum*, *S. nigrum*, *S. sisymbrifolium*, *S. nigrum*, *S. viarum*, *S. violaceum*	Pandey et al. (2002)
Fusarium wilt (*Fusarium oxysporum*)	*S. mammosum*, *S. incanum*, *S. aethiopicum*, *S. integrifolium*, *S. violaceum*	Yamakawa (1982)
Verticillium wilt (Verticillium spp.)	*S. aethiopicum*, *S. hispidum*, S. *linnaeanum*, *S. sisymbrifolium*, *S. torvum*	Tani et al. (2018)
Powdery mildew (*Leveillula taurica*)	*S. pseudocapsicum*, *S. aviculare*, *S. aculeatissimum*, *S. linnaeanum*	Bubici and Cirulli (2008)
Little leaf (viral)	*S. viarum*, *S. integrifolium*, *S. gilo*, *S. hispidum*, *S. melongena*	Sidhu and Dhatt (2007)
Insect-pest		
Fruit and shoot borer (*Leucinodes orbonalis*)	*S. aethiopicum*, *S. indicum*, *S. mammosum*, *S. macrocarpon*, *S. viarum*, *S. sisymbrifolium*, *S. integrifolium*, S. *xanthocarpum*, *S. nigrum*, *S. khasianum*, *S incanum*, *S. hispidum*	95-98 Ramasamy (2009), Lal et al. (1976), Rao (1980), Sharma et al. (1980)
Red spider mite (*Tetranychus urticae*)	*S. sisymbrifolium*, *S. pseudocapsium*, *S. mamosum*, *S. integrifolium*, *S. macrocarpon*	Schaff et al. (1982)
Root knot nematode (*Meloidogyne javanica*)	*S. hispidum*, *S. sisymbrifolium*, *S. melongena*, *S. torvum*, *S. violaceum*	Boiteux et al. (1996)
Leafhopper (*Amrasca devastans*)	*S. melongena*	AVRDC (1998)
Spotted or Epilachna beetle (*Epilachna vigintioctopunctata*)	*S. melongena*, *S. mammosuml*, *S. torvum*, *S. viarum*	Parker et al. (1995)
Aphid (*Aphis gossypii*)	*S. mammosum*¸*S. hispidum*	Rao (1980)
Gall midge	*S. macrocarpon*	Rao (1980)
Abiotic stress		
Salinity	*S. aethiopicum*, *S. sisymbriifolium*, *S. torvum*, *S. linnaeanum*	Anushma et al. (2018)
Drought	*S. khasianum*, *S. torvum*	Anushma et al. (2018)
Flood	*S. torvum*	Anushma et al. (2018)
Frost	*S. mammosum*, *S. viarum*, *S. grandiflorum*	Anushma et al. (2018)
High antioxidant activity	*S. aethiopicum*	Hanson et al. (2006)

markers. SSR markers have been linked to the dark purple skin color of eggplant, and candidate genes, such as Smechr0301963, have been identified for regulating fruit length. Genome-wide markers have been associated with various traits, including fruit size, color, leaf morphology, and nutrient components. Bacterial wilt resistance, a polygenic trait, has been explored using QTL mapping, identifying major QTLs for broad-spectrum resistance. Fusarium wilt resistance loci have also been mapped to specific chromosomes (Table 3).

Transgenic approaches, such as Bt brinjal, have been developed for resistance against brinjal shoot and fruit borer. Despite biosafety data, commercial release in India is pending, but it has been approved in Bangladesh and the Philippines. Transgenic events have also been attempted to reduce browning of cut fruits, induce parthenocarpy, and enhance stress tolerance. The recent exemption of genome-edited plants from stringent biosafety assessments in India opens up new possibilities for stress tolerance studies and potential commercial release.

Somatic Hybridization

Protoplast fusion is advantageous in overcoming the pre- and post-fertilization barriers. This technique has enabled transfer of desirable agronomic traits from wild species into cultivated eggplants. A number of successful examples are available in eggplants (Table 4).

Genomics

Genomics research in eggplant has historically lagged behind other Solanaceous vegetables like tomato, potato, and pepper. Initial efforts to sequence the eggplant genome resulted in an incomplete and highly fragmented assembly. Recently, there have been significant advancements in eggplant genomics with the publication of a high-quality

Table 3: Molecular mapping of major genes/QTLs in eggplant

Trait/map	*Mapping population*	*Markers*	*Salient findings*	*References*
1st interspecific linkage map	*S. melongena* × *S. incanum* (91 BC_1)	242 markers (COSII, SSRs, AFLPs, CAPS, and SNPs)	Constructed genetic map (1,085 cM) and candidate genes involved in the biosynthesis of chlorogenic acid, polyphenol oxidase, fruit shape and prickliness.	Gramazio *et al.,* 2014
Verticillium wilt resistance	*S. melongena* × *S. linneanum* (48 F_2)	RAPD, AFLP	QTL mapping	Sunseri *et al.,* 2003
1st intraspecific linkage map	168 F2 individuals	181 RAPD and AFLP	QTLs for fruit shape, fruit stem and calyx pigmentation	Nunome *et al.,* 2001
Fusarium wilt resistance	305E40 × 67/3 (141 F2)	238 molecular markers	305E40 has resistant gene *Rfo-sa1* from *S. aethiopicum*	Barchi *et al.,* 2010
Bacterial wilt resistance	AG91-25 × MM738 (F6 RIL Population)	SNPs	Identified genes *ERs1* and *2* QTLs	Lebeau *et al.,* 2013; Salgon *et al.,* 2017
Parthenocarpy	LS1934/Nakate-Shinkuro (non-parthenocarpy) × AE-P03 (parthenocarpy)	326 common markers	Identified QTLs for parthenocarpy. Two QTLs *Cop3.1* and *Cop8.1* were mapped onto chromosomes 3 and 8, respectively. QTL *Cop8.1* was confirmed in a RIL population and useful for MAS.	Fukuoka *et al.,* 2012 Miyatake *et al.,* 2012
Prickliness	Togenashi-senryo-nigo (no-prickliness) × LS1934 (prickliness) (F2 population)		Identified a semi-dominant Prickle (*Pl*) gene locus on chromosome 6, causing the absence of prickles. Developed markers for MAS	Miyatake *et al.,* 2020
Peel colour		AFLP, SCAR		Liao *et al.,* 2009
Fusarium wilt resistance	*S. aethiopicum* (*Rfo-sa1*)	CAPS	Indentified gene *Rfo-sa1* on chromosome 2 for MAS application	Toppino *et al.,* 2008
Fusarium wilt	Gene *Fm1*	SSR	Mapped on chromosome 2	Miyatake *et al.,* 2016
Male sterility	*Rf*	SCAR	Mapped the gene *Rf*	Khan and Isshiki, 2016

genome assembly using Illumina, Nanopore, 10X genomics sequencing, and Hi-C technologies. This assembly, based on the inbred line HQ-1315, provides a valuable resource for understanding the genetic makeup of eggplant. The availability of a high-quality genome has facilitated the identification of linked markers associated with various traits and the mapping of quantitative trait loci (QTLs). The eggplant genome, spanning 12 chromosomes, has been extensively characterized, revealing millions of single nucleotide polymorphisms (SNPs) within and between different species. Resequencing studies have been conducted on diverse accessions, such as *S. melongena* and *S. incanum,* to explore genetic diversity and identify markers for breeding.

In addition to the cultivated eggplant (*S. melongena*), efforts have been made to sequence the genomes of related species, such as the scarlet eggplant (*S. aethiopicum*). These genomic resources have led to the identification of thousands of protein-coding genes and millions of SNPs, contributing to a deeper understanding of genetic diversity within the Solanaceae family. Genomics applications extend beyond basic sequencing, involving the development of databases, such as the Eggplant Microsatellite DataBase (EgMiDB), which cataloged perfect SSRs in the eggplant genome. High-quality genome sequence data has been utilized for SNP discovery, leading to the construction of high-density SNP-based genetic maps used for QTL mapping.

Functional applications of genomics in eggplant include the identification and characterization of various gene families. Transcriptome and genome data have been employed to study transcription factors, such as WRKY and APETALA2/ETHYLENE RESPONSIVE FACTOR, associated with stress responses. Bioinformatics tools have enabled the identification of putative loci for allergens in eggplant fruits and the analysis of GRAS transcription factors involved in growth, development, and stress responses.

The recent advancements in eggplant genomics, facilitated by high-quality genome sequences and associated tools, provide a solid foundation for further research and applications in breeding, trait mapping, and functional genomics (Table 5).

Table 4: Successful examples of somatic hybridization in eggplant species

Fusion parents		*Fusion method*	*Salient findings*	*References*
S. melongena	*S. aethiopicum* gr. Aculeatum	Electrical	Fertile hybrids and fusarium wilt resistant	Rotino et al. (1995)
S. melongena	*S. aethiopicum* gr. Aculeatum	Electrical	Bacterial wilt resistant and high yield	Daunay et al. (1993)
S. melongena	*S. khasianum*	Electrical	Sterile and fruit and shoot borer resistant	Sihachakr et al. (1988)
S. melongena	*S. integrifolium*	-	Fertile and bacterial wilt resistant	Kameya et al. (1990)
S. melongena	*S. nigrum*	Electrical	Sterile and atrazine herbicide resistant	Sihachakr et al. (1989)
S. melongena	*S. nigrum*	polyethylene glycol	Sterile and herbicide atrazine resistant	Guri and Sink (1988)
S. melongena	*S. sanitwongsei*	polyethylene glycol	Fertile and bacterial wilt resistant	Asao et al. (1994)
S. melongena	*S. sisymbrifolium*	polyethylene glycol	Sterile hybrid resistant to mites and nematodes	Gleddie et al. (1986)
S. melongena	*S. torvum*	Electrical	Sterile hybrid resistance to nematodes and *Verticillium dahlia*	Sihachakr et al. (1989)
S. melongena	*S. torvum*	Polyethylene glycol	Sterile hybrid partial resistance to mites and resistance to Verticillium wilt	Guri and Sink (1988)
S. melongena	*S. torvum*	Electrical	Bacterial (*Ralstonia solanacearum*) and *Verticillium* wilt resistant	Collonnier et al. (2003)
S. melongena	*S. tuberosum*	Electrical	Bacterial wilt resistance	Yu et al. (2013)
S. integrifolium	*S. sanitwongsei*	UV	Bacterial wilt resistance	Iwamoto et al. (2007)

Table 5: Summary of recent research on eggplant genomics

Genotype	*Genomics technology*	*Salient findings*	*References*
305E40 (Fusarium wilt resistant) x 67/3 (susceptible)	RAD sequencing	Identified about 10,000 SNPs and 1,000 InDels, of which >2,000 SNPs were found useful for GoldenGate assay genotyping	Barchi *et al.,* 2011
First post-NGS genetic map of eggplant	415 SNP markers	Located QTLs for seven traits associated with anthocyanin content	Barchi *et al.,* 2012
191 eggplant accessions	GWAS	Identified 384 SNPs in a collection comprising of mixture of breeding lines, old varieties, and landraces from Asia and the Mediterranean basin	Cericola *et al.,* 2014, Portis *et al.,* 2015
377 eggplant accessions	GWAS	Identified 219 SNPs, of which five SNPs the SUN and OVATE homologs of tomato encoding for proteins promoting fruit elongation and negative role in the growth and elongation of fruit, respectively.	Liu *et al.,* 2019b
123 DH lines (MM738) (susceptible) × EG203 (resistant to *Ralstonia pseudosolanacearum*)	GBS	1,370 SNPs applied and identified two most stable QTLs located on chromosomes 3 and 6	Salgon *et al.,* 2017
121 F_2 population 1836 (eggplant) × *S. linnaeanum*	SLAF-seq	Applied 2,122 SNPs, of which identified 19 QTLs associated with plant and fruit traits	Wei *et al.,* 2020
163 F_7 RIL (305E40 × 67/3) intraspecific RIL population		High-quality genome sequence of male parent (67/3) and resequencing of female parent (305E40) led to the identification of 7,249 SNPs distributed on 12 eggplant chromosomes	Barchi *et al.,* 2019a
163 F_7 RIL (305E40 × 67/3)		Constructed eggplant genetic map of 2169.23 cM with an average marker distance of 0.4 cM, and determined genes related to anthocyanin content and seed vigor.	Toppino *et al.,* 2020
163 F_7 RIL (305E40 × 67/3)		Identified of several metabolomic QTLs (mQTLs) associated metabolites belonging glycoalkaloid, anthocyanin, and polyamines.	Sulli *et al.,* 2021

Eggplant genome (incomplete)	Covered 833.1 Mb spanning 74% of the eggplant genome, it was highly fragmented and not anchored to the eggplant chromosomes	Hirakawa *et al.,* 2014

Concluding Remarks and Future Prospects

Knowledge about available germplasm is crucial for crop breeding programs, and for eggplant, this involves the collection, conservation, and utilization of genetic diversity. While wild eggplant species harbor various stress resistances, their potential in breeding is limited due to crossing barriers, genetic studies' constraints, and lack of genomics resources. Despite India's rich genetic variability in eggplant species, especially in its center of origin, only a few have been utilized in breeding, mainly in genepools 1 and 2. Genepool 3 remains underrepresented, urging a focus on crossability and heterotic ability for traits like disease resistance and yield.

Eggplant breeding traditionally involves heterosis, backcrossing, pedigree, bulk, and pure-line selection methods. Recent priorities include parthenocarpy for seedless fruit development, anthocyanin pigmentation for quality, and rootstock breeding for disease resistance. Hybrid eggplant development, reliant on male sterile lines, is crucial for high yields. Genomic advancements enable marker discovery through synteny with tomato and pepper genomes, and re-sequencing coupled with SNP markers accelerates breeding. Nutritional profiling and exploring potential wild relatives for new genes and markers are contemporary focuses.

With the availability of the eggplant genome, researchers can leverage DNA methylation profiling, CRISPR/Cas9 technology for trait induction, and omics tools for comprehensive analysis. Collaborative pre-breeding projects at regional and national levels are recommended, addressing quality, biotic and abiotic stresses. Male sterile system exploitation, selection for quality fruit traits, and in vitro regeneration for doubled haploid line development are essential. Genome editing tools offer opportunities for climate-resilient, resource-efficient, and environmentally friendly eggplant improvement. In summary, harnessing eggplant genetic resources and applying genomics tools present vast prospects for future breeding advancements.

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सारांश

बैंगन (सोलनम मेलोंजेना एल.) जिसे बैंगन के नाम से भी जाना जाता है, दुनिया के उष्णकटिबंधीय और उपोष्णकटिबंधीय क्षेत्रों में उगाई जाने वाली एक महत्वपूर्ण सोलनसियस सब्जी है। भारत इस फसल की उत्पत्ति का केंद्र होने के कारण, यहां इसके फल और पौधों के प्रकार की आकृति में बड़ी विविधता मौजूद है। इसके अलावा, बड़ी संख्या में जंगली किस्मों का उपयोग जैविक और अजैविक तनाव सहिष्णुता के स्रोत के रूप में प्रजनन कार्यों में किया जा रहा है। पारंपरिक प्रजनन तकनीकी ने उच्च उपज देने वाली किस्मों और संकरों के विकास के माध्यम से पौधों के प्रकार और उपज में सुधार पर ध्यान केंद्रित किया है। हाल ही में, तनाव सहनशीलता और पोषक गुणवत्ता में सुधार के लिए प्रजनन अधिक जोर दिया गया है। आनुवंशिक वंशानुक्रम अध्ययन, मैपिंग, आणविक तकनीकी फसल सुधार कार्य को बढ़ावा दिया जा रहा है। हाल ही में, उच्च-गुणवत्ता वाले जीनोम अनुक्रम की उपलब्धता ने मार्कर-सहायता चयन के लिए आणविक उपकरणों को बढ़ाने वाले जीनोम स्तर पर कार्यात्मक विश्लेषण को प्रेरित किया है। प्रस्तुत लेख में फसल विविधता की प्रासंगिकता से लेकर जीनोमिक स्तर की ज्ञान उन्नति तक किये गये सुधार कार्यों पर प्रकाश डालने का प्रयास किया गया है। भारतीय संदर्भ में प्रासंगिकता रखने वाले बैंगन के सुधार में भविष्य की संभावनाओं पर भी प्रकाश डाला गया है।