Vegetable Science (2023) 50(2): 261-273
doi: 10.61180/vegsci.2023.v50.i2.01
ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)
www.isvsvegsci.in

REVIEW PAPER

Okra: Breeding and Genomics

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Abstract

Okra is an important vegetable crop cultivated throughout the tropical and subtropical parts of the world and in the warmer regions of the temperate zones. Its commercial cultivation is distributed exclusively across the various developing countries in Asia and Africa. The commonly cultivated okra is reported to a tetraploid species and has a very large and complex genome which hampers its speedy genetic improvement utilizing modern omics technology. Breeding methodologies suitable for self-pollinated crops have been often utilized for the genetic improvement of okra such as plant introduction, pure line selection, hybridization followed by selection, mutation breeding and heterosis breeding. Pedigree selection and heterosis breeding has been used by okra breeders which resulted in the development of lots of varieties and hybrids in India. In modern-day okra breeding along with high yield potential, multiple tolerance to YVMV, OELCV, sucking pest and borer, easy to harvest, dark green fruit color and ideal plant type are the major target traits. During the last few decades, different public sector institutions has developed and released as many as 33 improved varieties/hybrids for the benefit of the farming community across the country. Few of these varieties/hybrids have already made a noteworthy impact in okra production in India. This article reviewed the current status of okra breeding including genetic resources, cytogenetic relationship, breeding objectives, varietal development, resistance breeding, biotechnological intervention and its future improvement strategies.

Keywords: Okra, Genetics, Breeding, Genetic resource, Biotechnology.

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Citation: Singh, B., Karmakar, P., Singh, P., Maurya, B.K., Singh, H., Sagar, V., Mishra, G.P. and Sanwal, S.K. (2023). Okra: Breeding and Genomics. Vegetable Science 50(2): 261-273.

Source of support: Nil

Conflict of interest: None.

Received: 27/08/2023 **Revised:** 25/12/2023 **Accepted:** 28/12/2023

Introduction

Okra (*Abelmoschus esculentus*) is a commercially important summer vegetable cultivated in tropical and sub-tropical areas in the world. Okra is also known as lady finger or *Bhindi* and is one of the major vegetables grown in the summer and rainy seasons in India. It belongs to the hibiscus family, Malvaceae and is characterized by its typical showy flower. Almost 99% of okra cultivation is distributed exclusively across the various developing countries of Asia and Africa. The world okra production is estimated to be around 9.96 million tons, India ranked 1st in the okra production in the world, with 6.35 million tonnes from 0.52 million ha and contributes more than 72% to the global production (FAOSTAT. 2020). Based on the FAO estimates around 75% of the okra market is in India and 12% is in Nigeria. Okra grown both as rain-fed and irrigated crop is the most valued and popular vegetable consumed in fresh, frozen and dried forms. Over the last few years, okra is gaining its popularity and ground as a global crop because of the appreciation of its nutritional values by the growing numbers of consumers. Besides, India exports okra seeds to more than 20 countries across the globe. This further indicates okra's growing popularity as a global crop. Over 80% of the okra seed market is in India and is covered through hybrid seeds.

Global seed requirement of okra is expected to reach 600 MT mark with a value of $ 300m by 2030.

Okra plays a significant role in human nutrition as it provides carbohydrates, protein, fat, minerals and vitamins. Okra mature seed is also has a superior nutritional quality which is rich in oil and protein and beneficial to human health. The crude fiber of okra fruit and stem is used for industrial purposes in the paper industry (Kochlar, 1986). Hemorrhoids and ulcer relief have both been attributed to its medicinal significance (Adams, 1975). Additionally, it is an excellent source of iodine, which is helpful in the treatment of simple goitre, as well as other compounds with medical applications. It is very helpful in treating chronic dysentery, spermatorrhoea, and genitourinary diseases (Nandkarni, 1927). Okra's roots and stalks are used to clean the cane juice used to make gur or brown sugar (Chauhan, 1972). Roughly ground and roasted, its mature seeds are roasted, ground, and used as a substitute for coffee in some countries. Tender pods of okra are used as a delicious vegetable. The edible immature fruits of okra are considered as highly nutritious and are rich in dietary fibers, carbohydrates, flavonoids, vitamins and minerals. Okra fruit also exhibits appreciable antioxidant activities, solely due to its richness for vitamin C, carotenoids and flavonoids (Gemede *et al*., 2016; Petropoulos *et al*., 2018). It helps to mitigate constipation when fresh pods are eaten regularly. Due to its high fiber content, it is used in weight control and reduces cholesterol. Moreover, it is rich source of protein, and minerals (calcium, potassium and iodine). The fresh pod contains around 88% water, 0.1% fat, 8% carbohydrate, 1.8% protein and 0.9% fiber. Okra mucilage has the potential for use as food, non-food products and medicine. The fruit color of okra varies from green to red and later is the most predominant in the market. Being a newer market segment and the potential health benefits due to anthocyanin content the demand of red okra is growing day by day in India (Karmakar *et al*., 2022).

Okra breeding is still developing globally with novel issues, strategies, and methods. The ultimate goal of okra breeding is to improve desired traits and productivity over the parent's use and the current standard commercial requirement of a specific area. Yellow vein mosaic disease affects the quality and yield of the crop is the main production barrier for okra. Small landholding farmers are being discouraged from growing the crop due to the severe incidence of the diseases the virus belongs to the, family Geminiviridae and genus Begomovirus (Fauquet & Stanley, 2005). Recently, the BYVMD complex was shown to be associated with the virus with a genomic component typical of monopartite begomoviruses, homologous DNA A and a single-stranded beta satellite (Jose & Usha, 2003). In okra one of the major problems is Yellow vein mosaic disease caused by BYVMV with an estimated yield loss of about 50-94 % which depends upon the growth stage of crop at infection time. Similarly, enation leaf curl disease due to OELCV is also emerging as a serious problem rendering yield penalties of about 30-100%. Further, several other factors are also responsible for reducing the production in India such as, loss of resistance to yellow vein mosaic in ruling varieties (Borah *et al*., 1992), emergence of new biotypes of whitefly vectors and development of moderate to strong resistance to commonly used insecticides by vectors (Rashida *et al*., 2005). Omics methodologies viz., genomics, transcriptomics, proteomics and metabolomics play an important role in crop improvement by simplifying the identification of genes, proteins and metabolites associated with drought tolerance (Singh *et al*., 2014). However, there is limited genome sequence information available for okra. This may be attributable to the complex and allopolyploid genome of the crop (Zhan *et al*., 2019). But now, on a global scale, the focus of okra improvement programs has shifted to develop high-yielding, multiple tolerance to biotic stresses F_1 hybrids with desirable market-driven traits.

Origin

Okra is referred as tindisha and gandhumula mentioned in ancient Sanskrit literature. It was known in Egypt in the 12th century. Okra was introduced into tropical and subtropical America perhaps through the African slaves in the time of early post-Columbian. The origin of okra remains controversial perhaps it is originated in Ethiopia and upper Nile region of Sudan, West Africa or Tropical Asia. A putative ancestor (*A. tuberculatus*, 2n = 58) being native to Uttar Pradesh in India, suggests the Indian origin whereas, another putative ancestor (*A. ficulneus*, 2n = 72) presence in East Africa, suggesting northern Egypt and Ethiopia as its geographical origin (Charrier, 1984). For *A. caillei* it is difficult to suggest an origin outside from West Africa which is only found in West Africa. Its origin by hybridization with *A. manihot* is difficult to accept even if its presence, mentioned in the Flora of West Africa (Hutchinson & Dalziel, 1958) was not recently confirmed in this area and herbarium samples are lacking. According to Zeven & Zhukovsky (1975), okra is believed to have originated in the Hindustani Centre of Origin, particularly in India, Pakistan and Burma and the genus *Abelmoschus* is considered to be of Asiatic origin. However, according to some other authors, *A. escculentus* originated in India (Masters, 1875), Ethiopia (de condolle, 1883; Vavilov, 1951), West Africa (Chevalier, 1940) and Tropical Asia (Grubben, 1977). Grubben (1977) considered the Mediterranean, Near East and southern USA to be secondary centers of diversity where introduction and selection enabled adaptation to the agro-climatic conditions of those regions. However, the genus *Abelmoschus* is polytypic with both polyploidy and hybridity, so the origin of cultivated okra may be polyphyletic rather than from a single species (Joshi & Hardas, 1976), a hypothesis supported by the variation in chromosome numbers (2n = 66-144) in *A. esculentus* (Datta & Naug, 1968).

Distribution of *Abelmoschus* sp.

Abelmoschus is a well familiar genus in the family Malvaceae, acknowledged due its economically significant cultivated species *A. esculentus* (okra) grown in many parts of the world, especially in tropical and subtropical countries. Indian sub-continent is considered as centre of diversity of this genus, due to the presence of extensive morphological diversity. In India, various species of *Abelmoschus* are widely distributed in different phytogeographical regions from the Himalayas to the Southern peninsular parts of India. On the other hand, the presence and occurrence of another cultivated species *A.caillei* is restricted to West and Central Africa (Yadav *et al*., 2014). Various species of *Abelmoschus* are well recognized including the common/cultivated okra (*A. esculentus*), West African okra (*A. caillei*), *A. ficulneus*, *A. manihot*, *A. manihot* var. *tetraphyllus*, *A. moschatus* and *A. tuberculatus* (Kumar *et al*., 2010). Recently, a few new wild okra species such as *Abelmoschus angulosus* var. *mahendragiriensis, A. pungens* var. *mizoramensis, Abelmoschus enbeepeegearense* and *A. palianus* has been identified in India (Misra *et al*., 2018; John *et al*., 2020; John *et al*., 2013; Sutar *et al*., 2013). These genetic resources provide opportunities for okra breeding targeting various economic traits. Within India, eight crop-specific explorations for *Abelmoschus* have already been organized, exploring and collecting in parts of northern, northwestern plains in Punjab, Haryana. Rajasthan, Gujarat and Uttar Pradesh; adjoining foothills in Himachal Pradesh; central and western parts mainly in Madhya Pradesh and Maharashtra; the southern peninsular tract in Karnataka, Tamil Nadu and Kerala, eastwards in Andhra Pradesh and Orissa and the Assam plains and adjoining hilly tracts of the northeastern region. Distribution of Wild *Abelmoschus* Species in different Phyto-geographical Regions is presented in Table 1. Misra *et al*. (2022) reported new distribution of three taxonomic varieties of wild okra *viz*., *Abelmoschus angulosus* var. *grandiforus*, *A. tuberculatus* var. *deltoidefolius* and *A. tuberculatus* var. *tuberculatus* from Eastern India.

Genetic Resources and Diversity

Crop plant evolution either natural or human-directed, is primarily based on existing genetic diversity in the population. Diversity can be described as the degree of differentiation between or within species. The base of any crop improvement is majorly dependent upon differences between existing inter and intra-specific species. As much as diversity or dissimilarity present within species give more scope for improvement in plant performances for different traits. The presence of genetic diversity within and between crop plant species permits the breeders to select superior genotypes either to be directly used as new varieties or to be used as parent in a hybridization programme. To achieve heterosis and produce transgressive segregates, diversity between two progenitors is necessary. Consequently, finding an appropriate donor parent among cultivated species of okra is a prerequisite for the development of tolerant recombinant line(s) to YVMV & OELCV diseases. Traditionally, a combination of morphological, molecular marker and agronomic traits has been used to measure genetic diversity. Okra germplasm holding of different countries is presented in Table 2.

Agro-morphological Characterization

Morphological and genetic diversity in okra, has been evaluated by phenotypic markers (Bisht *et al*., 1995; Duzyaman, 2005), but these are influenced by environmental

Table 1: Occurrence of wild *Abelmoschus* species in different phyto-geographical regions

S. No.	*Species*	*Distribution*
1.	*A. angulosus*	Kerala, Tamil Nadu
2.	*A. criniturs*	Himanchal Pradesh, Orrisa, Uttarakhand and Uttar Pradesh
3.	*A. ficulneus*	Uttarakhand, Orrisa and Madhya Pradesh
4.	*A. manihot* ssp. *tetraphyllus* var. *tetraphyllus*	Jammu & Kashmir, Rajasthan, Madhya Pradesh, Chattisgarh, Maharashtra, Tamil Nadu, Andhra Pradesh, Uttar Pradesh
5.	*A. manihot* ssp. *tetraphyllus* var. *pungens*	Chattishgarh, Madhya Pradesh, Rajsthan, Maharshtra and Uttar Pradesh
6.	*A. moschatus* ssp. *moschatus*	South China, South East Asia, Andman & Nicobar Islands, Jammu & Kashmir and Uttrakhand
7.	*A. moschatus* ssp. *tuberosus*	Tamil Nadu, Kerala and Parts of western ghats
8.	*A. tuberculatus*	Rajasthan, Uttar Pradesh, Madhya Pradesh and Maharashta
9.	*A. manihot*	China, India and Nepal
10.	*A. caillei*	West Africa
11.	*A. sagittifolius*	Eastern India, South China, South East Asia, and Northern Australia
12.	*A. enbeepeegearensis*	Western Ghat of Viz., Kerala, Karnataka and Tamil Nadu

Source: Bisht & Bhat (2006)

Table 2: Okra germplasm in all over the world in different countries

S. No.	*Institute*	*Accession*
1	National Bureau of Plant Genetic Resources, New Delhi-110 012, India	4000
2	Southern Regional Plant Introduction Station, USDA-ARS-SAA, Griffin, USA	3379
3	World Vegetable Center, Tiwan	122
4	Institut Int. de la Recherche Scientifique pour Dev en Afrique, BP V 51, Abidjan, Cote d'Ivoire	1430
5	Lab. Ress. Genetiques et Amelior. des Plantes Tropicales, ORSTOM F-34032 Montpellier Cedex, France	965
6	National Plant Genetic Resources Laboratory, IPB/UPLB College 4031 Laguna, Philippines	905
7	Institute of Plant Breeding, College of Agriculture UPLB, 4031, Laguna, Philippines	477
8	National Centre for Genetic Resources and Biotechnology, Ibadan, Nigeria	374
9	Jericho Reservation Area, National Horticultural Research Inst., Ibadan, Nigeria	258
10	Crop Research Institute Plant Genetic Resources Unit, P. O. Box 7, Bunso- East Akim, Ghana	198
11	Plant Genet. Resources Centre, Gannoruwa, Peradeniya, Sri Lanka	193
12	Departamento de Fitotecnia - Universidad Federal de Vicosa, 36571-000 Vicosa, Minas Gerais, Brazil	192
13	Horticultural Research Section Agricultural Research Corporation Wad Medani, Sudan	173
14	Institut Togolais de Recherches Agronomique, Lome, Togo	170
15	Lab. de Recursos Geneticos (CCTA), Universidade Estadual do Norte Fluminense, Av.Alberto Lamego, Brazil	159
16	Miglior. Genetico e Prod. Sementi DIVRAPA, Universita di Torino Via Pietro Giuria 15,10126 Torino, Italy	131
17	Agril. Rehabilitation Programme, Dept. of Agric. & Livestock, Konedobu, Papua New Guinea	112
18	Mount Makulu Agric. Research Sta., Chilanga, Zambia	106

Source: From IPGRI database (http://www.ipgri.org).

factors and show continuous variation. The cultivated and wild okra genetic resources are phenotypically diverse and they can be useful for developing okra hybrids with desired agronomic, horticultural, physiological and nutritional traits for drought tolerance breeding (Aladele *et al*., 2008; Muleken *et al*., 2016; Munir *et al*., 2016). A total of 585 accessions and 314 varieties of okra were characterized by (Martin *et al*., 1981) and Siemonsma (1982a), respectively for yield contributing attributes. For YVMV disease reaction, two sets of germplasm consisting of 94 and 74 accessions were screened by (Sandhu *et al*., 1974) and Sharma & Sharma (1984), respectively. Hamon & Charrier (1983) evaluated 718 samples of cultivated okra for fruit traits and reported considerable variation for this trait. Genetic and morphological diversity of 50 accessions of okra germplasm studied by (Kyriakopoulou *et al*., 2014) and also established the relationship with the Greek landrace. A total of 21 okra genotypes were evaluated for 25 morpho-agronomic traits in Ethiopia and reported appreciable diversity among them (Kenaw *et al*., 2023). A total 241 accessions of wild relatives of okra comprised of *A. ficulneus*, *A. manihot* ssp. *tetraphyllus*, *A. moschatus*, and *A. tuberculatus* at ICAR-NBPGR and reported considerable diversity for morphological characters such as epicalyx segments, shape, size and persistence, petal color and petal blotch, stem and fruit pubescence, pigmentation of various plant parts, days to flowering etc (Bisht *et al*., 1995). The genetic resources of *Abelmoschus* have been identified as a potential source of desirable genes that can be useful for the genetic improvement program (Table 3).

Assessment of Genetic Diversity through Molecular Breeding

To avoid effects of environmental factors on the true variation, molecular techniques have been used, including sequence-related amplified polymorphism (SRAP) (Gulsen *et al*., 2007), random amplified polymorphic DNA (RAPD) markers (Martinello *et al*., 2003; Aladele *et al*., 2008), and simple sequence repeats (SSRs) developed from okra transcriptome sequences (Schafleitner *et al*., 2013). Ravishankar *et al*. (2018) used Roche 454 Titanium pyrosequencing to sequence the genomic DNA in order to develop the microsatellite markers in okra. 61,722 reads were obtained out of a total output of 979,806 bp. A total of 2708 contigs had microsatellites out of the 3735 contigs derived from combined reads. In the end, 50 SSR primers were chosen using 402 microsatellites for okra amplification. Using next-generation sequencing technology, this is the first study on the emergence of genomic SSR markers in okra. Using morpho-agronomic descriptors and AFLP markers, Massucato *et al*. (2019) assessed the genetic variation among 30 Brazilian landrace accessions of okra. Five different AFLP primer pairs were used alo with 17 morpho-

Table 3: Germplasm sources for various important traits in okra

S. No.	*Traits*	*Sources*	*Reference*
1	Yellow vein mosaic virus (YVMV) resistance/tolerance	*A. angulosus, A. caillei*, *A. tetraphyllus, A. manihot* ssp. *manihot*, *A. moschatus, A. pungens, A. crinitus*, *A. manihot*	Singh *et al*. (2007) Dhankhar *et al*. (2005)
2	Okra Enation Leaf Curl (OELCV) resistance/tolerance	*A. pungens*, *A. manihot*, *A. crinitus*, *A. ficulneus* and *A. angulosus. A. crinitus*	Singh *et al*. (2007) Manjua *et al*. (2018) Dhaliwal & Sharma (2016) Mishra *et al*. (2017)
3	Powdery mildew resistant tolerant	*A. tetraphyllus, A. manihot, A. manihot ssp. manihot, A. moschatus*, *A. angulosus*	Dhankhar *et al*. (2005)
4	Red Spider Mite	EC 305656, EC 305664, EC 305696	Dhankhar *et al*. (2005)
5	Jassids	IC 7194, IC 8889 (*A. esculentus*); *A. manihot* ssp. *manihot* var. Ghana, *A. moschatus*, *A. crinitus*, EC 305656, 305694, 305695, 305714, 306731	Dhankhar *et al*. (2005)
6	Shoot and fruit Borer	*A. tuberculatus*, *A. caillei*, cv. Narnaul Special	Dhankhar *et al*. (2005)
7	Low temperature and frost	*A. angulosus*	Dhankhar *et al*. (2005)
8	Branches/plant	*A. tetraphyllus*	Dhankhar *et al*. (2005)
9	Fruits/plant	*A. tetraphyllus*, *A. manihot* ssp. *manihot*, *A. caillei*	Dhankhar *et al*. (2005)

agronomic descriptors. For all qualitative characteristics, polymorphisms were seen, while the quantitative traits were significant by deviance analysis. The genetic parameters established the existence of variability among accessions, and high precision and heritability indices were found for the traits related to fruit and plant height. Comprehensive reports on molecular diversity in okra are depicted in Table 4.

Cytogenetic Relationship in Okra

Cytological studies demonstrated that there are noteworthy differences for chromosome numbers and ploidy levels exist among the different species of *Abelmoschus*. The lowest chromosome number of 2n=56 was observed in *A. angulosus* (Ford, 1938), while the highest chromosome number close to 200 reported for *A. manihot* var. *caillei* or *A caillei* (Singh & Bhatnagar, 1975; Siemonsma, 1982a, 1982b). Cross ability relation and affinities between cultivated species *A. esculentus* and wild relatives established by various researchers on the basis of cytogenetic evidence. Joshi & Hardas (1956) and Joshi *et al*. (1974) observed that 29 of the 65 gametic chromosomes of *A. esculentus* had comprehensive homology with that of the *A. tuberculatus* (n=29). The other set of 36 chromosomes of *A. esculentus* revealed greater homology with *A. ficulneus* (n = 36) when compared with *A. moschatus* (n=36). These studies recognized the amphidiploid (29 T+36 Y) nature of the *A. esculentus*. Additional cluster of polyploidy species presenting genetic kinship includes *A. esculentus, A. tetraphyllus*, and *A. pungens* (Table 5).

Okra Breeding and Target Traits

Breeding objectives in okra typically focus on improving traits such as yield, viral disease resistance, and nutritional and fruit quality. As we know okra is susceptible to a number of diseases including fungal and viral infections. Breeding for disease resistance can help to reduce the impact of these diseases on the crop; leading to higher yield and better-quality produce. Okra breeders may also focus on improving the quality of the fruit itself, by selecting for traits such as size, color, texture and flavor this can help to increase the market value of the crop and make it more appealing to consumers varietal development in okra typically involves a combination of traditional breeding techniques such as selection and hybridization and modern biotechnology approaches, such as genetic engineering and molecular marker-assisted breeding. The principal breeding objectives for any breeding programme for genetic enhancement of okra usually based on the following breeding objectives:

- To develop high-yield potential varieties/hybrids with wider adaptabilities, ideal plant types and desirable market-driven traits.
- To develop varieties/hybrids for different maturity segments suitable to specific growing environments.
- Development of multiple diseases and pest-resistant/ tolerant varieties/hybrids, with special importance to yellow vein mosaic virus (YVMV), okra Enation leaf curl virus (OELCV), shoot and fruit borer, jassids, leafhoppers, red spider mites and root-knot nematodes.
- To breed varieties/hybrids capable of tolerating abiotic stresses, such as low temperature, drought, excessive moisture/water logging due to heavy rain, low fertility and soil salinity & alkalinity.
- To develop varieties and hybrids with dark green, tender, thin, medium long, smooth, 4 to 5 ridged pods at the marketable stage, faster fruit growth, easy to harvest and free from conspicuous hair, seed bulging and yellow ring at base for both fresh markets.

Table 4: Genetic diversity and molecular marker related studies in okra

Species	*No. of genotypes evaluated*	*DNA markers used*	*No. of Primers used*	*PIC*	*References*
A. escullentus	48	ISSRS	-	54.55%	Yuan *et al.* (2015)
A. escullentus	24	ISSRS	22	0.531929	Yuan *et al*. (2014)
A. escullentus	66	iPBS, SSRs	83 iPBS, 9 SSRs	0.66 iPBS 0.62 SSRs	Yıldız *et al*. (2015)
A. caillei, A. esculentus	93	RAPD	13	-	Aladele *et al*. (2008)
Abelmoschus	39	RAPD	31	-	Martinello *et al*. (2001)
A. esculentus	50	AFLP	33	12	Kyriakopoulou *et al*. (2014)
A. esculentus	22	AFLP	8	0.26	Akash *et al*. (2013)
A. esculentus	23	SRAP	39	-	Gulsen *et al*. (2007)
A. esculentus A. moschatus A. manihot	65	SSR	19	0.49	
A. esculentus A. tuberculatus A. moschatus A. manihot	24	SSR	18	0.53	Fougat *et al*. (2015)
A. esculentus A. tuberculatus *A.moschatus, A. moschatus ssp tuberosus A. manihot*	96	SSR	40	0.52	Schafleitner *et al*. (2013)

Table 5: Variation in the chromosome number of *Abelmoschus* spp

S. No.	*Species*	*Chromosome No.*	*Gene Pool*	*Sources*
1.	*A. tuberculatus*	58	GP-2	Joshi & Hardas (1953); Kuwada (1974); Joshi *et al*. (1974)
2.	*A. caillei*	194	GP-3	Singh & Bhatnagar (1975)
3.	*A. pungens*	138	GP-3	Joshi & Hardas (1976)
4.	*A. moschatus*	72	GP-3	Joshi *et al*. (1974)
5.	*A. ficulneus*	72, 78	GP-2	Joshi *et al*. (1974)
6.	*A. esculentus*	66, 72,108, 118, 120, 122, 124, 126-134, 130, 131-143, 132, 144	GP-1	Joshi & Hardas (1953); Gadwal at al. (196)8), Ford (1938); Teshima (1933), (1976); Kamalova (1977); Datta & Naug (1968); Kuwada (1966)
7.	*A. tatraphyllus*	130, 138	GP-3	Joshi & Hardas (1976); Ugale at al. (1976)
10.	*A. manihot*	60, 66, 68	GP-3	Teshima (1933); Chizaki (1934); Skovsted (1935); Kamalova (1977)

- To create cultivars with enhanced nutritive attributes that are also suitable for export, dehydration, canning, and freezing.

To achieve the above-mentioned breeding objectives following are the major traits of genetic improvement of the okra.

- High yield with better fruit quality
- Dark green, tender, thin, medium long, smooth, 4 to 5 ridged pods at marketable stage
- Pods free from conspicuous hair seed bulging and yellow ring at base
- Early and prolonged harvest
- Shorter plant height with a greater number of nodes, short intermodal length
- Single stem or with branching habit in narrow-angle
- Optimum seed setting ability
- Easy to harvest
- Export and processing traits
- Resistance to disease (yellow vein mosaic virus, OELCV, fusarium wilt, cercosposra leaf spot)
- Resistance/tolerance to insect (fruit and shoot borer, jassids and whitefly)
- Tolerance to abiotic stresses (low temperature, excessive rains, saline and alkaline soils)

Varietal Wealth of Okra

Several varieties and hybrids were released and notified from different public sector institutions including ICAR institutes and SAUs in India covering all the agro-climatic zones for the benefit of farming communities. These released varieties/ hybrids were cultivated in different parts of the Indian Subcontinent. Apart from the number of varieties and hybrids identified and released by the SVRC of different states in India, a total 33 varieties and hybrids has been identified through AICRP(VC) in okra across the 8 Agro-climatic zones. The number of varieties released and notified from Indian Public Sector Institutions in okra is listed in Table 6.

Genetic Improvement through Traditional Breeding

The flower structure of okra favors self-pollination and still there is a chance of outcrossing up to an extent of 10-15%, which makes it an often- cross-pollinated crop. As the autogamous breeding system is a predominant breeding system in okra, therefore breeding methods commonly utilized for self-pollinated crops can be utilized for the genetic improvement of this crop. The breeding methodologies universally employed for okra improvement are plant introduction, pure line selection, intraspecific and interspecific hybridization using backcross techniques, heterosis breeding, mutation, and polyploidy breeding (Bisht & Bhat, 2006). With respect to plant introduction, Perkin's Long Green and Clemson Spineless Louisiana developed in the USA and was introduced to India during the early 1950s for commercial cultivation. Pure line selection was employed to bred the first improved variety of okra Pusa Makhmali from germplasm material collected from West Bengal (Singh & Sikka, 1955). The cultivars CO- 1 and Gujarat Bhinda 1 also developed through pure line selection (Singh *et al*., 2023). First YVMV-tolerant cultivar 'Pusa Sawani' in India is resulted from inter-varietal hybridization using the genotype IC-1542 followed by pedigree selection (Singh *et al*., 1962). India lots public sector varieties have bred through pedigree method of selection either from inter-varietal crosses or interspecific crosses includes Selection-2 (Thomas & Prashad 1985), Punjab Padmini (Sharma, 1982), Parbhani Kranti (Jambhale & Nerkar, 1986), Punjab-7 (Thakur & Arora, 1988), Arka Anamika, and Arka Abhay (Dutta, 1991). Variability can also be generated through artificial mutagenesis utilizing physical mutagens (gamma rays) or chemical mutagens (EMS). A mutant EMS-8 (Punjab-8) resistance to YVMV and tolerance to fruit borer has been developed through induced mutation from Pusa Sawani treated with 1% EMS (Singh *et al*., 2023). Numerous research findings indicated substantial yield improvement in okra ranging from 50 to 70% through the exploitation of heterosis (Jagan *et al*., 2013). Heterosis breeding is extensively used for yield gain in okra improvement. Heterosis breeding in okra is intended not only for yield improvement but also for sustainable protection against YVMV and OELCV diseases by incorporating the resistant gene(s). Considerable heterosis has been reported for yield and its contributing traits (Singh *et al*., 1977; Singh and Singh, 1979).

Breeding for Viral Disease Resistance

The okra crop is generally damaged by various biotic stresses, such as insects, fungi, nematodes and viruses. But the prominent threat to its cultivation in India is severe incidence of two viral diseases, viz. Yellow Vein Mosaic Virus (YVMV) disease and Okra Enation Leaf Curl Virus (OELCuV) disease, are transmitted through whitefly. The magnitude of yield loss caused by YVMV infestation in okra, drops with delay in infection of the plants, although a yield loss of 49 to 84% has been reported when crop is infected 50 to 65 days after sowing. While OELCuV in certain instances may be more damaging disease as compared to the earlier one and capable of causing 30 to 100% yield loss depending upon the age of the plant at the time of infection (Sanwal *et al*., 2014). Resistance breeding will be a feasible proposition to manage these viral diseases, but resistance attributes to these diseases is not stable and durable in the cultivated gene pool; and resistance may breakdown after 5-8 years

Table 6: Varietal wealth of okra in India from different Public Sector institutions

S. No.	*Public sector institution*	*Variety/hybrid*
1.	ICAR-IIVR, Varanasi	Kashi Mohini, Kashi Chaman, Kashi Kranti, Kashi Vardan, Kashi Vibhuti, Kashi Pragati, Kashi Satdhari, Shitla Jyoti, Kashi Mangali, Kashi Bhairav (F_1), Kashi Lila, Kashi Shristi (F_1), Kashi Lalima, Kashi Mahima, Kashi Utkarsh, Kashi Sahishnu, Kashi Parakram
2.	ICAR-IARI, Pusa, New Delhi	Pusa Makhmali, Pusa Sawani, Pusa A 4, Pusa Bhindi-5
3.	ICAR-IIHR, Bengaluru	Arka Abhay, Arka Anamika, Arka Nikita (F_1)
4.	PAU, Ludhiana	Punjab Padmini, Punjab-7, Punjab-8, Punjab no. 13
5.	CCSHAU, Hisar	Varsha Uphar, Hisar Unnat
6.	JAU, Junagadh	JOH-05-9 (F1 hybrid), JOL-2K-19 (GJO-3), JOH-0819 (F1 hybrids)
7.	KAU, Thrissur	Salkeerthi, Aruna, Kiran
8.	TNAU, Coimbatore	COBh H 1, CO.1, CO.2, CO.3

Source: https://iivr.icar.gov.in/; https://www.iari.res.in/en/index.php; https://nhb.gov.in/

of their development which lead the cultivars to become susceptible (Mishra *et al*., 2021). Pusa Sawani is the very first resistant variety against YVMV bred at IARI, New Delhi utilizing the genotype IC-1542 from West Bengal which is supposed to have contributed the genes for YVMV resistance in this variety; is regarded as the most widely cultivated symptomless carrier cultivar in India. Two recessive alleles at two loci were found to confer the resistance in this variety (Singh *et al*., 1962). Crops Wild Relatives (CWRs) of okra such as *Abelmoschus manihot* ssp. *manihot*, *Abelmoschus caillei* and *A. tetraphyllus* have been utilized to introgress the resistance gene into cultivated background in India, despite the occurrence of unilateral incompatibility (set fruits and seed only when cultivated okra used as female parent and sterility problem in interspecific hybrids). Okra varieties such as Parbhani Kranti, Arka Anamika, Punjab Padmini and Punjab-7 were the resultant of this type of breeding programme (Mishra *et al*. 2021). With respect to OELCV, the absence of characterized resistance sources in the cultivated background has forced the plant breeders to look beyond the cultivated gene pool into the wild relatives like *A. crinitus, A. ficulneus, A. angulosus* and *A. manihot* as stable and reliable sources of resistance to OELCV (Singh *et al*., 2007).

Mode of inheritance of the resistance gene(s) generally decides the durability and stability of the resistance against particular pathogens including viruses in plant. Specific resistance is characteristically inherited monogenically and is not durable. Horizontal resistance is supposed to have controlled through polygenically and is complex & durable (Walton, 1997). Several categories of mode of inheritance for YVMV disease resistance have been described in cultivated and wild gene pool. A number of research findings showed that YVMV resistance is governed by two dominant complementary genes (Bharathkumar *et al*., 2019; Dhankhar *et al*., 2005; Sharma *et al*., 1981); on the contrary to these reports, others have also been documented that there is a single dominant gene (Bharathkumar *et al*., 2019; Jambhale & Nerker 1981) accountable for the YVMV resistance in okra. YVMV resistance is also controlled by both additive genes (Das *et al*., 2013); both additive and non-additive gene (Seth *et al*., 2016) and duplicate gene action (Arora *et al*., 2008). Nonetheless, a single dominant gene reported to control YVMV resistance in interspecificc crosses between *Abelmoschus manihot* and *A. tetraphyllus* (Jambhale & Nerker, 1981). As resistance to YVMV is a complex trait, thus, it should be studied comprehensively utilizing an integrated approach like transcriptomics, proteomics and metabolomics (Mishra *et al*., 2017). With respect to the genetics of OELCV resistance, pattern of segregation in the F_2 generation of two cross combinations showed that the resistance to OELCV disease was controlled by two duplicate recessive genes, while generation mean analysis shown the involvement of both additive and non-additive effects for the inheritance of this disease in okra.

Biotechnological Interventions

Being a nutritional-rich crop, in okra not much focus has been placed on utilizing modern biotechnological technologies for genetic enhancement. Because there is lack of sufficient information related to molecular markers, genetics and other molecular tools for okra breeding (Saini *et al*., 2020). Okra faces many challenges such as pests, disease, and environmental stressors that can affect its yield and quality (Naveed *et al*., 2012). A quick method for improving okra is to use high throughput biotechnological methods such as chromosomal engineering, RNA interference (RNAi), genome-wide selection (GWS), chromosome engineering, targeted gene replacement, next-generation sequencing (NGS), and nano-biotechnology (Mishra *et al*., 2017). For the genetic improvement of okra several modern biotechnological tools have been utilized across the globe.

Marker-assisted breeding

Marker-assisted breeding is a biotechnological technique that enables the selection of plants with desired traits more efficiently and precisely. This method involves the identification and use of molecular markers linked to specific genes associated with desirable traits. In okra improvement, marker-assisted breeding has been applied to accelerate the development of new varieties with improved characteristics. For example, researchers have used molecular markers to facilitate the breeding of okra varieties with enhanced resistance to diseases such as Fusarium wilt, OELCV and YVMV. By identifying markers linked to disease-resistance genes, breeders can screen plants at the molecular level, allowing for the selection of individuals with the desired traits at an early stage of development. This expedites the breeding process, reducing the time and resources required to develop new disease-resistant okra varieties.

Genetic engineering

Genetic engineering has been employed to enhance the nutritional profile of okra. Researchers have successfully modified okra to increase the levels of essential nutrients, such as vitamins and minerals. For instance, efforts have been made to elevate the levels of vitamin A and iron, addressing nutritional deficiencies prevalent in certain regions where okra is a staple food. nonconventional breeding methods along with biotechnological techniques as an integrated approach to reduce the incidence of YVMV and OELCV in cultivated lines of okra (Sanwal *et al*., 2014; Kumari *et al*., 2017). Advancement in biotechnology needs to be properly incorporated and utilized at the grassroots level in okra (Chowdhury & Kumar, 2019).

Role of NGS and transcriptomics

The NGS technology is the discipline of molecular breeding, mainly for the identification and development of SSR markers. This method is a massively parallel sequencing (MPS) technology, are rapid, low cost and need less amount

of template preparation and with very high throughput (Singh & Singh, 2015). In okra crop very, less study has been done in relation to genomic approaches. The transcriptome technique is a potential approach to identify the genome sequences in crops in which very limited or no genome sequence information is available (Schafleitner *et al*., 2013). For the rapid and low-cost obtaining of the SNPs and avoids highly repetitive genomic regions, transcriptome sequencing is highly favorable. The NGS, RNA Sequencing, and direct RNA sequencing technologies might be applicable for transcriptome sequencing. Leaves and pod tissues of okra used for RNA sequencing. In okra, 150,000 unigenes and 935 SSRs from unigenes identified. Ravishankar *et al*. (2018) first reported the development of genomic SSR markers in okra using Roche 454 Titanium pyrosequencing technology. Approximately 61,722 reads were developed from 979,806 bp data. All of them assembled into 3735 contigs of which 2708 had microsatellites

Gene annotation and chromosome-scale genome assembly

Genome annotation is the plotting of genes onto genome assemblies and indexing their genomic coordinate (Aken *et al*., 2016). In the perspective of genome annotation, okra genome sub-group into two group, in which designated subgenome A consists 30 chromosomes and subgenome B contains 35 chromosomes. In *A. esculentus* almost 55.59% genome sequence was recognized as transposable elements (TEs). In which, most abundant class of repetitive sequences was exhibited by long terminal repeat retrotransposons (LTR-RTs) i.e. 32.26% of the *A. esculentus* genome. The majority of the LTR-RTs consist by Gypsy elements (20.98%) and thereafter Copia elements (4.41%). In total, 113364 protein-coding genes (A: 57374; B: 55879) were anticipated with high confidence, of which 95.89% could be functionally annotated by homologous sequences (Wang *et al*., 2023) and also represented a chromosome-scale genome of okra having a size of 1.19 Gb. Comparative genome analysis discovered the phylogenetic position of *A. esculentus*, besides whole-genome duplication events which happened extensively in all the species of the Malvaceae species.

Role of proteomics in okra improvement

In the recent past, genome sequencing data have suddenly racked up for okra crop, including *Theobroma cacao* (Argout *et al*., 2011), four species of cotton (Paterson *et al*., 2012), *Durio zibethinus* (Hu *et al*., 2019), and *Bombax ceiba* (Gao *et al*., 2018). Information about the genomic sequencing of okra is rare. Numerous proteomic investigations have revealed the genetic characteristics and gene expression patterns of distinct species. Unfortunately, the Malvaceae lack an integrative functional genomic database of various species that would allow users to collaboratively review and make use of pertinent data. This is likely because collecting, analyzing, storing, and displaying huge amounts of data is a difficult process. Proteomics analysis is a method that makes it easier to investigate how proteins are expressed globally and offers a wealth of knowledge on how individual proteins function in different biological processes. An MS/MS-based tandem mass tags (TMT) label analysis was developed recently for extensive protein quantification (Xu *et al*., 2017). Application of TMT-based proteomic technique analyzed the differentially expressed proteins between the NaCl-treated seedlings and check used in okra. Zhan *et al*. (2019) have identified a total of 7179 proteins, there were 317 differentially expressed proteins (DEPs), of which 165 proteins were up-regulated and with NaCl treated about 152 proteins down-regulated.

CRISPR/Cas9 technology

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated protein 9 (Cas9) technologies have revolutionized genetic engineering by providing a precise and efficient tool for targeted gene editing. In okra improvement, CRISPR/Cas9 technology has been employed to introduce specific genetic modifications with unprecedented accuracy. Researchers have used CRISPR/Cas9 to create okra varieties with improved traits, such as increased resistance to specific pathogens or enhanced drought tolerance. The precision of CRISPR/Cas9 allows for the modification of individual genes without introducing foreign DNA, addressing concerns related to genetically modified organisms (GMOs). This technology opens up new possibilities for tailoring okra varieties to meet the specific needs of different environmental conditions.

Future Prospective

The future thrust areas for research and development in relation to okra in India would be principally focused in improving okra productivity and sustaining India's position as a Global leader. To achieve the targeted productivity, it is essential to bred okra varieties/hybrids with very high yield potential and durable and stable resistance to YVMV and OELCV diseases. Future okra varieties/hybrids would be of wider adaptability, multiple tolerances to biotic and abiotic stresses, superior nutritional and keeping quality focusing on domestic as well as foreign markets for export. Special breeding efforts are essential to develop varieties/hybrids suitable to fulfil export standards. Future line of works for the sustainable breeding efforts in okra must cover the development of okra mini core set constituting a world diversity panel; identification and utilization of new sources of resistance to YVMV & OLCV diseases; development of MAGIC or bi-parental populations for early generation trait mapping through QTL-seq approach; creation of OkraTIL, a reverse genetics-based & functional genomics platform; genomics-assisted pre-breeding and shuttle-breeding platforms for new trait discovery; DH and speed breeding platforms for faster development of parental lines; infectious

clones based artificial screening protocol and search for CGMS system for cost-effective hybrid seed production.

References

Adams, C. F. (1975). Nutritive value of American foods in common units, U.S. Department of Agriculture. Agriculture Handbook, 425, 29.

Akash, M. W., Shiyab, S. M., & Saleh, M. I. (2013). Yield and AFLP analyses of inter-landrace variability in okra (*Abelmoschus esculentus* L.). Life Science Journal. 10(2), 2771-2779.

Aken, B. L., Ayling, S., Barrell, D., Clarke, L., Curwen, V., Fairley, S., & Searle, S. M. (2016). The Ensembl gene annotation system. Database, 093.

Aladele, S. E., Ariyo, O. J., & De Lapena, R. (2008). Genetic relationships among West African okra (*Abelmoschus caillei*) and Asian genotypes (*Abelmoschus esculentus*) using RAPD. African Journal of Biotechnology, 7, 1426–1431.

Argout, X., Salse, J., Aury, J. M., Guiltinan, M. J., Droc, G., Gouzy, J., Allegre, M., Chaparro, C., Legavre, T., & Maximova, S. N. (2011). The genome of *Theobroma cacao*. Nature Genetics, 43, 101–108.

Arora, D., Jindal, S. K., & Singh, K. (2008). Genetics of resistance to yellow vein mosaic virus in inter-varietal crosses of okra (*Abelmoschus esculentus* L. Moench). SABRAO J Breeding and Genetics, 40(2), 93–103.

Bharathkumar, M. V., Dhankhar, S. K., Dahiya, M. S., & Srikanth, M. (2019). Genetic architecture of resistance to yellow vein mosaic virus disease in advance lines of okra (*Abelmoschus esculentus*). Indian Journal of Agricultural Sciences, 89(4), 640-645.

Bisht, I. S., & Bhat, K. V. (2006). Genetic Resources, Chromosome Engineering and Crop improvement in Okra (*Abelmoschus sp.*). Chapter, 5, 149-185.

Bisht, I. S., Mahajan, R. K., & Rana, R. S., (1995). Genetic diversity in South Asian okra (*Abelmoschus esculentus*) germplasm collection. Annals of Applied Biology, 126, 539–550.

Borah, G. C., Saikia, A. K., & Shadeque, A. (1992). Screening of okra genotypes for resistance to yellow vein mosaic virus disease. Indian Journal of Virology, 8, 55–57.

Charrier, A. (1984). Genetic resources of the genus *Abelmoschus Med*. (Okra). International Board for Plant Genetic Resources, (No. IBPGR/84/194).

Chaudhari, S., & Kumar, S. (2019). Okra Breeding: Recent Approaches and Constraints. Annals of Biology, 35(1), 55-60.

Chauhan, D. V. S. (1972). Vegetable Production in India, 3rd ed., Ram Prasad & Sons (Agra).

Chevalier, A. (1940). L'origine, la culture et les usages de cinq Hibiscus de la section Abelmoschus. Revue Botanique Appliquée, 20, 319–328. Current Science, 106, 1470-1471.

Chizaki, Y. (1934). Breeding of a new interspecific hybrid between *Hibiscus esculentus* L. and *H. manihot* L. Japanese Journal of Crop Science, 6, 164–172,

Das, S., Chattopadhyay, A., Dutta, S, Chattopadhyay, S. B., & Hazra, P. (2013). Breeding okra for higher productivity and yellow vein mosaic tolerance. International journal Vegetable Science, 19, 58–77.

Datta, P. C., & Naug, A., (1968). A few strains of *Abelmoschus esculentus* (L) Moench their karyological in relation to phylogeny and organ development. Beiträge zur Biologie der Pflanzen, 45, 113–126.

De Candolle, A. (1883). Origine des plantes cultivées. G. Baillière et cie.

Dhaliwal, M. S., & Sharma, A. (2016). Breeding for resistance to virus diseases in vegetable crops. Innovations in horticultural sciences. New India Publishing Agency, New Delhi, 303-327.

Dhankhar, B. S., Mishra, J. P., & Bisht, I. S. (2005). Okra, In Plant Genetic Resources: Horticultural Crops, Dhillon, B. S., Tyagi, R. K., Saxena, S., & Randhawa, G. J., Eds., New Delhi: Narosa Publishing House, pp. 59–74.

Dutta, O. P. (1991). Okra germplasm utilization at IIHR, Bangalore, In International Crop Network Series, Report of an International Workshop on Okra Genetic Resources. Rome: International Board for Plant Genetic Resources, 5, 114–116.

Düzyaman, E. (2005). Phenotypic diversity within a collection of distinct okra (*Abelmoschus esculentus*) cultivars derived from Turkish landraces. Genetic Resources and Crop Evolution, 52, 1019–1030.

FAOSTAT. (2021). http://www.fao.org

Fauquet, C. M., & Stanley, J. (2005). Revising the way we conceive and name viruses below the species level: a review of geminivirus taxonomy calls for new standardized isolate descriptors. Archives of Virology, 150, 2151–2179.

Ford, C. E. (1938). A contribution to a cytogenetical survey of the Malvaceae, Genetica, 20, 431–452.

Fougat, R. S., Purohit, A. R., Kumar, S., Parekh, M. J., & Kumar, M. (2015). SSR based genetic diversity in *Abelmoschus* species. Indian Journal of Agriculture Science, 85, 1223-1228.

Gadwal, V. R., Joshi, A. B., & Iyer, R. D. (1968). Interspecific hybrids in *Abelmoschus* through ovule and embryo culture. Indian Journal of Genetics and Plant Breeding, 28, 269–274,

Gao, Y., Wang, H., Liu, C., Chu, H., Dai, D., Song, S., Yu, L., Han, L., Fu, Y., & Tian, B. (2018). De novo genome assembly of the red silk cotton tree (*Bombax ceiba*). Giga Science, 7, 051.

Gemede, H. F., Haki, G.D., Beyene, F., Woldegiorgis, A. Z., and Rakshit SK (2016) Proximate, mineral, and antinutrient compositions of indigenous Okra (*Abelmoschus esculentus*) pod accessions: Implications for mineral bioavailability. Food Science and Nutrition, 4(2), 223–233.

Grubben, G. J. H., (1977). Tropical Vegetables and their Genetic Resources. International Board for Plant Genetic Resources, FAO, Rome.

Gulsen, O., Karagul, S., & Abak, K., (2007). Diversity and relationships among Turkish okra germplasm by SRAP and phenotypic marker polymorphism. Biologia Bratislava, 62, 41-45.

Hamon, S. and Charrier, A. (1983). Large variation of okra in Benin & Togo (Ivory Coast), Plant Genetic Resources Newsletter, 56, 52–58.

Hu, Y., Chen, J., Fang, L., Zhang, Z., Ma, W., Niu, Y., Ju, L., Deng, J., Zhao, T., & Lian, J. (2019). *Gossypium barbadense* and *Gossypium hirsutum* genomes provide insights into the origin and evolution of allotetraploid cotton. Nature Genetics, 51, 739–748.

Hutchinson, J., & Dalzid, J. M. (1958). International Board for Plant Genetic Resources IBPGR. (1990). Report on International Workshop on Okra Genetic Resources held at the National bureau for Plant Genetic Resources, New Delhi, India. Flora of west tropical Africa 2nd edition, 1, 343-348.

ICAR-IARI. (2022). https://www.iari.res.in/en/index.php

ICAR-IIVR. (2022). https://iivr.icar.gov.in/

Jagan, K., Reddy, R. K., Sujatha, M., Sravanthi, V., & Reddy, M.

(2013). Heterosis for yield and yield components in okra (*Abelmoschus esculentus* L.). Journal of Pharmacy and Biological Sciences, 7, 69-70.

Jambhale, N. D. and Nerkar, Y. S. (1986). Parbhani Kranti, a yellow vein mosaic resistant okra, Horticulture Science, 21, 1470–1471.

Jambhale, N. D., & Nerkar, Y. S. (1981). Inheritance of resistance to okra yellow vein mosaic disease in inter-specifc crosses of *Abelmoschus*. Theoretical and Applied Genetics, 60, 313–316.

John, J. K., Krishnaraj, M. V., Pradheep, K., Patil, P., Harish, G. D. and K. V., B., (2020). A new variety of *Abelmoschus pungens* (Malvaceae) from Indo-Burma Biodiversity Hotspot. Journal of the Indian Association for Angiosperm Taxonomy, 30(2), pp.270-277.

John, K.J., Scariah, S., Nissar, V. M., Bhat, K.V. and Yadav, S. R. (2013). *Abelmoschus enbeepeegearense* sp. nov.(Malvaceae), an endemic species of okra from Western Ghats, India. Nordic Journal of Botany, 31(2), pp.170-175.

Jose, J., & Usha, R. (2003). Bhendi yellow vein mosaic disease in India is caused by association of a DNAb satellite with a begomovirus. Virology, 305, 310–317.

Joshi, A. B., & Hardas, M. W. (1956). Alloploid nature of Okra, *Abelmoschus esculentus* (L.) Moench. Nature, 178, 1190.

Joshi, A. B., & Hardas, M. W. (1976). Evolution of Crop Plants Longman, London. Okra In: Simmonds, NW (Ed.), pp 194–195.

Joshi, A. B., & Hardas, M. W., (1953). Chromosome number in *Abelmoschus tuberculatus* Pal & Singh—a species related to cultivated bhindi. Current Science, Bangalore, 22, 384–385.

Joshi, A. B., Gadwal, V. R., & Hardas, M. W. (1974). Evolutionary studies in world crops, In Diversity and Change in the Indian Sub-Continent, Hutchinson, J. B., Ed., London: Cambridge Univ. Press, pp. 99–105.

Kamalova, G. V. (1977). Cytological studies of some species of the Malvaceae. Uzbekistan Biologija Zurnali, 3, 66–69.

Karmakar, P., Sagar, V., and Singh, P. M. (2022). Dynamics of anthocyanin and chlorophyll content in red fruited okra var. Kashi Lalima. Vegetable Science, 49(2), 197-203

Kenaw, W., Mohammed, W., Woldetsadik, K. (2023). Morpho-agronomic variability of okra [*Abelmoschus esculentus* (L.) Moench] genotypes in Dire Dawa, eastern Ethiopia. PLoS One, 18(7), e0288534.

Kochlar, S. I. (1986). okra (lady finger) in tropical crops, a text book of economic botany, 1, 263-264

Kumar, S., Dagnoko, S., Haougui, A., Ratnadass, A., Pasternak, N., & Kouame, C. (2010). Okra (*Abelmoschus spp.)* in West and Central Africa: Potential and progress on its improvement.

Kumari, P., Singh, S. P. and Gangopadhyay, K. K. (2017). Biotechnological strategies for improving viral disease resistance in okra.

Kuwada, H. (1966). The new amphidiploid plant named "*Abelmoschus tubercular-esculentus*," obtained from the progeny of the reciprocal crossing between *A. tuberculatus* and *A. esculentus*. Japanese Journal of Breeding, 16, 21–30.

Kuwada, H., (1974). F_1 hybrids of *Abelmoschus tuberculatus* x *A. manihot* with reference to the genome relationship. Japanese Journal of Breeding, 24, 207–210.

Kyriakopoulou, O. G., Arens, P., Pelgrom, K. T., Karapanos, I., Bebeli, P., & Passam, H.C. (2014). Genetic and morphological diversity of okra (*Abelmoschus esculentus* [L] Moench) genotypes and their possible relationships, with particular reference to Greek landraces. Scientia Horticulturae, 171(1), 58-70.

Manjua, K. P., Lakshmia, K. V., Babub, B. S., & Anithab, K. (2018). Evaluation of okra germplasm for their reaction to whitefly, *Bemisia tabaci* and okra yellow vein mosaic virus (OYVMV). Journal of Entomology and Zoology Studies, 6(2), 2491- 2496.

Martin, F.W., Rhodes, A.M., Perez, M., and Diaz, F. (1981). Variation in okra. Euphytica, 30, 697-715.

Martinello, G. E., Leal, N. R., Amaral Jr, A. T. D., Pereira, M. G., & Daher, R. F. (2003). Genetic diversity in okra using RAPD markers. Horticultura Brasileira, 21(1), 20-25.

Martinello, G. E., Leal, N. R., Amaral Jr., A. T., Pereira, M. G., & Daher, R. F., (2001). Comparison of morphological characteristics and RAPD for estimating genetic diversity in *Abelmoschus* spp. Acta Horticulturae, 546, 101-104.

Massucato, L. R., Nakamura, K. K., Ruas, P. M., Zeffa, D. M., Silva, D.J.H.D., & Gonçalves, L. S. A. (2019). Genetic diversity among Brazilian okra landraces detected by morphoagro-nomic and molecular descriptors. Acta Scientiarum Agronomy, 42.

Masters, M. T. (1875). Flora of British India Ashford Kent, J. D. Hooker, Ed., 1, 320–348.

Mishra, G. P., Seth, T., Karmakar, P., Sanwal, S. K., Sagar, V., Priti, Singh, P. M., & Singh, B. (2021). Breeding strategies for yield gains in okra (*Abelmoschus esculentus* L.). In Advances in Plant Breeding Strategies: Vegetable Crops: Volume 9- Fruits and Young Shoots. Cham: Springer International Publishing, (pp. 205-233).

Mishra, G. P., Singh, B., Seth, T., Singh, A. K., Halder, J., Krishnan, N., Tiwari, S. K., & Singh, P. M. (2017). Biotechnological advancements and begomovirus management in okra (*Abelmoschus esculentus* L.): status and perspectives. Frontiers in Plant Science, 8(360).

Misra, R. C., Karmakar, P., Dehury, S., Dash, S. K., & Ahlawat, S. P. (2022). New record of three taxonomic varieties of wild okra (*Abelmoschus* Medik.) for Eastern India. Vegetos, 36(3), 1058-1069.

Misra, R. C., Pani, D. R., Bharathi, L. K., & Ahlawat, S. P. (2018). *Abelmoschus angulosus* var. *mahendragiriensis* (Malvaceae): a new taxonomic variety of wild okra from Eastern Ghats of India. Genetic Resources and Crop Evolution, 65(3), 993–1002. doi:10.1007/s10722-017-0590-510

Muluken, D., Wassu, M., & Endale, G. (2016). Variability, heritability and genetic advance in Ethiopian okra [*Abelmoschus esculentus* (L) Monech] collections for tender fruit yield and other agro-morphological traits. Journal of Applied Life Sciences International, 4, 1–12.

Munir, M., Amjad, M., Ziaf, K., & Ahmad, A. (2016). Improving okra productivity by mitigating drought through foliar application of salicylic acid. Pakistan Journal of Agricultural Sciences, 53, 879– 884.

Nandkarni, K. M. (1927). Indian Meteria Medica Nadkarni and Co Bombay,

Nandkarni, K.M., (1927). Indian *Meteria Medica* Nadkarni and Co Bombay.

Naveed, A., Khan, A. A., & Rauf, S. (2012). The potential of breeding okra (*Abelmoschus esculentus* L.) for water stress tolerance. Crop Production for Agricultural Improvement, 217-235.

NHB. (2022). https://nhb.gov.in/

Paterson, A. H., Wendel, J. F., Gundlach, H., Guo, H., Jenkins, J., Jin, D., Llewellyn, D., Showmaker, K. C., Shu, S., & Udall, J. (2012). Repeated polyploidization of *Gossypium* genomes and the

evolution of spinnable cotton fibres. Nature, 492, 423–427.
Petropoulos, S., Fernandes, A., Barros, L., and Ferreira, I. C. F. R. (2018). Chemical composition, nutritional value and antioxidant properties of Mediterranean okra genotypes in relation to harvest stage. Food Chemistry, 242, 466–474.
Rashida, P., Sultan, M. K., Khan, M. A., & Islam, N.U. (2005). Screening of cotton germplasm against cotton leaf curl Begomovirus (CLCuV). Journal of Agriculture and Social Sciences, 3, 35–238.
Ravishankar, K. V., Muthaiah, G., Mottaiyan, P., & Gundale, S. K. (2018). Identification of novel microsatellite markers in okra (*Abelmoschus esculentus* (L.) Moench) through next-generation sequencing and their utilization in analysis of genetic relatedness studies and cross-species transferability. Journal of Genetics, 97(1), 39-47.
Saini, P., Saini, P., Kaur, J. J., Francies, R. M., Gani, M., Rajendra, A. A., & Chauhan, S. S. (2020). Molecular approaches for harvesting natural diversity for crop improvement. Rediscovery of Genetic and Genomic Resources for Future Food Security, 67-169.
Sandhu, G. S. (1974). Sources of resistance to jassid and whitefly in okra germplasm. Crop Improvement, 1, 77–81
Sanwal, S. K., Singh, M., Singh, B., & Naik, P. S. (2014). Resistance to Yellow Vein Mosaic Virus and Okra Enation Leaf Curl Virus: challenges and future strategies. Current Science, 106(11), 1470-1.
Schafleitner, R., Kumar, S., Lin, C. Y., Hegde, S. G., & Ebert. (2013). The okra transcriptome as a source for gene sequence information and molecular markers for diversity analysis. Gene, 517(1), 27-36.
Seth, T., Chattopadhyay, A., Dutta, S., Hazra, P., & Singh, B. (2016). Evidence of economic heterosis and genetic control of fruit yield and yellow vein mosaic virus disease severity traits of okra. Vegetos, 29, 3. 10.5958/2229-4473.2016; 2016.
Sharma, B. R. (1982). "Punjab Padmini"-a new variety of okra, Progressive Farming, 18, 15–18.
Sharma, B. R., and Sharma, O. P. (1984). Field evaluation of okra germplasm against yellow vein mosaic virus, The Punjab horticultural journal, 24, 131–133
Sharma, B. R., Kumar, V., & Bajaj, K. L. (1981). Biochemical basis of resistance to yellow vein mosaic virus in okra, Genetica Agraria, 35, 121–130.
Siemonsma, J. S. (1982a). La culture du gombo (*Abelmoschus spp*) legume fruit. Thesis University Wageningen, the Netherlands.
Siemonsmo, J. S. (1982b). West African okra morphological and cytological indications for the existence of a natural amphiploid of *A esculentus* (L.) Moench and *A. manihot* (L.) Medikus. Euphytica, 31(1), 241-52.
Singh, B. D., & Singh, A. K. (2015). Marker-assisted plant breeding: principles and practices.
Singh, B., Rai, M., Kalloo, G., Satpathy, S., & Pandey, K. K. (2007). Wild taxa of okra (*Abelmoschus* species) reservoir of genes for resistance to biotic stresses. Acta Horticulturae, 752, 323–328.
Singh, H. B. & Sikka, S. M. (1955). "Pusa Makhmali"- a new find in lady's finger, Indian Farming, 4, 27.
Singh, H. B., & Bhatnagar, A. (1975). Chromosome number in an okra from Ghana. Indian Journal of Genetics and Plant Breeding, 36, 26–27.
Singh, H. B., Joshi, B. S., Khanna, P.O., & Gupta, P.S. (1962). Breeding for field resistance to YVMV in Bhindi. Indian Journal of Genetics and Plant Breeding, 22:137–144.
Singh, P., Chauhana,V., Tiwaria, B. K., Chauhan, S.S., Simon, S., Bilal, S. & Abidi, A. B. (2014). An overview on okra (*Abelmoschus esculentus*) and its importance as a nutritive vegetable in the world. International Journal of Pharmacy and Biological Sciences, 2230–7605.
Singh, S. B. (1979). Genetical studies in okra (*Abelmoschus esculentus* (L.) Moench). Ph.D. thesis, Punjab Agricultural University, Ludhiana.
Singh, S. P. (1977). Genetic divergence and nature of heterosis in okra, Indian journal of agricultural sciences, 47, 546–551.
Skovsted, A. (1935). Chromosome numbers in the family Malvaceae. Journal of Genetics, 31, 263–296.
Sutar, S., Patil, P., Aitawade, M., John, J., Malik, S., Rao, S., Yadav, S. and Bhat, K.V., (2013). A new species of *Abelmoschus* medik. (Malvaceae) from Chhattisgarh, India. Genetic resources and crop evolution, 60, pp.1953-1958.
Teshima, T. (1933). Genetical and cytological studies in an interspecific hybrid of *Hibiscus esculentus* and *H. manihot*. Journal of the Graduate School of Agriculture, Hokkaido University, 34, 1–155.
Thakur, M. R. & Arora, S. K. (1988). "Punjab-7" a virus resistant variety of okra, Progressive Farmimg, 24, 13.
Thomas, T. A., & Prashad, R. (1985). New okra selections, Indian Horticulture, 29, 19–21.
Ugale, S. D., Patil, R. C., & Khupse, S. S. (1976). Cytogenetic studies in the cross between *Abelmoschus esculentus* and *A. tetraphyllus*. Journal of Maharashtra Agricultural Universities, 1(2–6), 106–110.
Vavilov, N. I. (1951). Phytogeographic basis of plant breeding. The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica, 13, 1-366.
Walton, J. D. (1997). Biochemical Plant Pathology. Plant biochemistry, 487.
Wang, R., Li, W., He, Q., Zhang, H., Wang, M., Zheng, X., & Xing, L. (2023). The genome of okra (*Abelmoschus esculentus*) provides insights into its genome evolution and high nutrient content. Horticulture Research, uhad120.
Xu, D. B., Yuan, H. W., Tong, Y. F., Zhao, L., Qiu, L. L., Guo, W. B., Shen, C. J., Liu, H. J., Yan, D. L., & Zheng, B.S. (2017). Comparative proteomic analysis of the graft unions in hickory (*Carya cathayensis*) provides insights into response mechanisms to grafting process. Frontier Plant Science, 8, 676.
Yadav, S.R., Sutar, S., Bhat, K.V., John, K.J., Latha, M., Scariah, S., Nissar, V. A. M., Krishna, G., Malik, S. K., Rama, R. S., Merita, (2014). Genus *Abelmoschus* Medik. India- an illustrated guide for species identifcation. Indian Council of Agricultural Research, New Delhi, pp 4–13
Yıldız, M., Koçak, M., & Baloch, F. S. (2015). Genetic bottlenecks in Turkish okra germplasm and utility of iPBS retrotransposon markers for genetic diversity assessment. Genetics & Molecular Research, 14(3), 10588-10602.
Yuan, C. Y., Wang, P., Chen, P. P., Xiao, W. J., Zhang, C., Hu, S., & Guo, X. H. (2015). Genetic diversity revealed by morphological traits and ISSR markers in 48 Okras (*Abelmoschus escullentus* L.). Physiology and Molecular Biology of Plants, 21(3), 359-364.
Yuan, C. Y., Zhang, C., Wang, P., Hu, S., Chang, H. P., Xiao, & W. J. *et al*. (2014). Genetic diversity analysis of okra by intersimple sequence repeat (ISSR) markers. Genetics and Molecular Research, 13, 3165-3175.
Zeven, A.C. & Zhukovsky, P.M. (1975). Dictionary of cultivated plants and their Centres of Diversity: excluding ornamentals,

forests trees and lower plants. Centre for Agric. Pub. And Doc. (PUDOC), Wageningen, The Netherlands, 219.

Zhan, Y., Wu, O., Chen, Y., Tang, M., Sun, C., Sun, J., & Yu, C. (2019). Comparative proteomic analysis of okra (*Abelmoschus esculentus* L.) seedlings under salt stress. BMC Genomics, 20, 381.

सारांश

भिंडी एक महत्वपूर्ण सब्जी फसल है, जिसकी खेती दुनिया के उष्णकटिबंधीय, उपोष्णकटिबंधीय और समशीतोष्ण क्षेत्रों के गर्म भागों में आसानी से की जाती है। इसकी व्यावसायिक खेती मुख्य रूप से एशिया और अफ्रीका के विभिन्न विकासशील देशों में बडे पैमाने पर की जाती है। आम तौर पर खेती की जाने वाली भिंडी एक टेट्राप्लोइड प्रजाति है, और इसमें बहुत बड़े और जटिल जीनोम होने के कारण आधुनिक ओमिक्स तकनीक द्वारा त्वरित आनुवंशिक सुधार करने में बाधा डालते हैं। स्व-परागण वाली फसल के लिए उपयुक्त प्रजनन पद्धति का उपयोग अक्सर भिंडी के आनुवंशिक सुधार के लिए किया जाता है, जिसमे संकरण, उत्परिवर्तन प्रजनन और हेटेरोसिस प्रजनन आदि शामिल हैं। पिछले कई अनुसंधानों में प्रजनक द्वारा भिंडी वंशावली चयन और हेटेरोसिस प्रजनन का उपयोग किया गया जिसके परिणामस्वरूप भारत में कई किस्मों और संकरों का विकास हुआ है। आधुनिक युग में भिंडी प्रजनन के साथ-साथ उच्च उपज क्षमता, भिंडी पित्त शिरा मोजैक विषाणु, भिंडी पर्ण कुन्चन विषाणु तथा चूसने वाले कीट और छेदक के प्रति बहु-सहिष्णुता, तुडाई में आसान, फलों का गहरा हरा रंग तथा आदर्श पौधे का प्रकार प्रमुख लक्ष्य हैं। पिछले कुछ दशकों के दौरान, विभिन्न सार्वजनिक क्षेत्र के संस्थानों ने देश भर में कृषक समुदाय को लाभ पहुँचाने के लिए 33 उन्नत तथा संकर किस्मों को विकसित किया है। इनमें से कुछ किस्मे या संकर प्रजातियों ने भारत में भिंडी उत्पादन में उल्लेखनीय प्रभाव डाला है। इस लेख में आनुवंशिक संसाधनों, साइटोजेनेटिक संबंध, प्रजनन उद्देश्यों, विविधता विकास, प्रतिरोध प्रजनन, जैव प्रौद्योगिकी हस्तक्षेप और इसकी भविष्य की सुधार रणनीतियों सहित भिंडी प्रजनन की वर्तमान स्थिति की समीक्षा की गई है।