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GENETICS FOR YELLOW VIEN MOSAIC VIRUS RESISTANCE IN OKRA : A REVIEW

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ABSTRACT

Yellow vein mosaic disease (YVMD) is the most common disease affecting okra (*Abelmoschus esculentus* (L.) Moench), significantly lowering pod yields as well as quality. The condition is brought about through a combination of several different mono and bipartite begomoviruses and satellites of them. Because controlling the disease with treatments may be quite challenging, the most effective course to take is to create immune or tolerant okra cultivars. Several investigations have been done to identify different sources of resistance and the inheritance patterns of YVMV resistance in okra. Making better use of and enhancing the current genetic pool of okra demands understanding and accepting research on disagreement origins in wild and grown species, connected infectious agents, the connection between diseases and their vectors, areas vulnerable to virus epidemics, ideal circumstances for disease spread, methods for assessment and breeding techniques. This review aims to shed light on the genetic basis of YVMV resistance in okra and provide an detailed examination of the resistant sources that are presently readily available.

Key words : Begomoviruses, Epidemics, Okra, Resistant, Species.

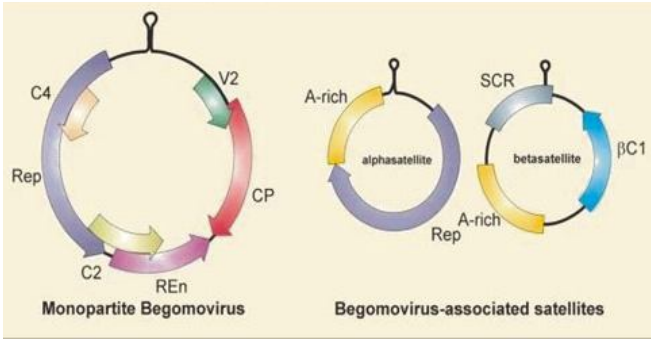
Introduction

Okra, also know as lady's finger or bhindi, is a significant vegetable crop cultivated in tropical and subtropical regions due to its simple process of cultivation, regular yield, and its capacity to deal with an extensive number of environmental conditions. Representing 60% of the country's fresh product exports, it is an important year-round vegetable crop produced in India and an important export (Patel *et al*., 2019). It has gained appeal as a fruit and vegetable in tropical and subtropical regions, such as India, Africa, Turkey and other nations nearby. In India, okra is grown in huge amounts all over the summer and rainy seasons due to its attractive green fruits. Okra belongings to the Malvaceae family and includes around 72 to 144 chromosomes. It often gets cross-pollinated; outcrossing, which occurs when pollination is facilitated by insects, may range from 4% to 19% and can reach 42.2%. Producing okra presents several difficulties due to both biotic and abiotic stress. One of the primary causes to be concerned is the fact that the majority of producing kinds and hybrids are vulnerable to the yellow vein mosaic virus (YVMV). This virus is semi-persistently transmitted through the whitefly species, and it can infect okra at any phenological stage (Khatun *et al*., 2020; Sanwal *et al*., 2014). It is prevalent in eastern India's Gangetic flat land (Das *et al*., 2012). The impact of YVMV disease on the production of crops can range from 50% to 94%, which is regarded as severe, depending on the stage of crop growth, when the virus first emerges in India (Venkataravanappa *et al*., 2013). Due to this, YVMV poses an important farming challenge for okra, which leads to quality and yield losses

everywhere the crop is cultivated. Plants exhibit stunted growth, with fewer leaves and deformed fruits, after 20 days of germination; loss of production may vary from 94% to 100%. Vein banding, vein-related chlorophyll breakdown, mosaic patterns and overall plant stunting are every indication of YVMV.

Yellow Vein Mosaic Disease of Okra

The virus generating the yellow vein mosaic disease of okra was initially identified in 1924 under the previous Bombay Presidency and is now referred to as the Bhendi yellow vein mosaic virus (BYVMV). This virus relates to the Begomovirus genus in the Geminiviridae group and is semi-persistently transferred by white flies. Green islands inside the leaf tissue linked by a web of yellow veins are typical indications of a BYVMV infection. In serious circumstances, leaves may become entirely yellow or creamy. Depending on the age of a plant, YVMD may result in yield losses that range from 30% to 100%. This severe disease, which may impact okra plants at all stages of growth and development, becomes particularly common in eastern India's Ganges region.



Causal organism of yellow vein mosaic disease of okra

Begomovirus, with 132 species, is the most extensive and most significant genus within the Geminiviridae family. It is named after the Bean Golden Mosaic Virus, which just so happens to be its type species. These viruses have concentrated on a vast majority of dicotyledonous plants, which include either a bipartite genome with two DNA components (DNA-A and DNA-B) or a monopartite genome resembling DNA-A (Brown *et al.*, 2012). The BYVMD complex, whose has been connected to the virus, was found to contain homologous DNA-A and a single-stranded betasatellite, two genomic characteristics similar to monopartite begomoviruses (Jose and Usha, 2003).

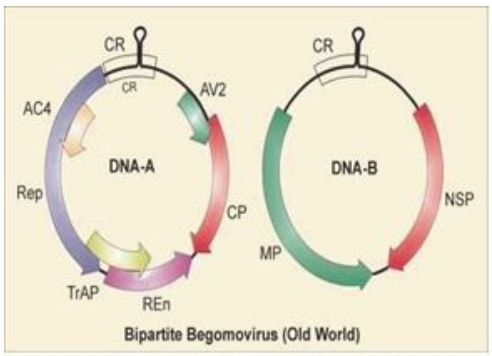
Okra is prone to at least ten different viruses in India (Venkataravanappa, 2008) and YVMD has been linked to a significant reduction in okra production.

Vector Transmissibility of Begomo viruses

Only the whitefly *Bemisia tabaci* (Gennadius) is the means through which begomo viruses spread between plants. Depending on what they prefer as plant hosts and ways of transmission, these whiteflies can be divided into numerous biotypes, marked A though T (Seal *et al.*, 2006). The most prevalent biotype in India and across the rest of the entire world is B. The specialization of 15 begomoviruses belonging to the "B" biotype in the vector, as described by Chattopadhyay *et al.* (2011), shows that this specific biotype of *B. tabaci* is more efficient in transmitting begomoviruses compared to other biotypes. The population dynamics of the whiteflies in Kalyani, West Bengal have been observed on an ongoing basis. Based on reports, there had been a significant drop in whiteflies from Feb to the start of April, followed by an increase in August month.

Genetics of YVMV Resistance

In 2017 study findings of Seth *et al.* (2017) analyzed the genetic control of the yellow vein mosaic virus (YVMV) disease in okra and its association to biochemical indications. They observed that resistance to YVMV diseases was established by two complementary dominant genes in the Tolerant X Susceptible (T X S) crossing, however resistance was determined with two duplicate dominant genes inside the Tolerant X Tolerant (T XT) cross. Furthermore, the investigation showed a significant non-allelic interaction among the percent disease index (PDI) for YVMV



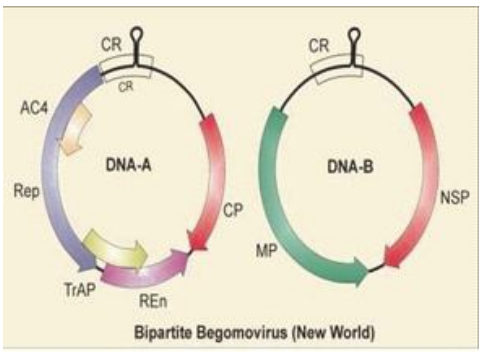


Fig. 1 : Monopartite and Bipartite Begomo viruses with their associated satellites.

Table 1 : List of different Begomo viruses infecting okra.

Viruses	Genome	Distribution	References
Bhendi yellow vein mosaic virus	Monopartite	India	Kulkarni (1924)
Bhendi yellow vein Bhubhaneshwar virus	Monopartite	India	Venkataravanappa *et al.* (2013a)
Bhendi yellow vein Haryana virus	Monopartite	India	Venkataravanappa (2008)
Bhendi yellow vein Maharashtra virus	Monopartite	India	Venkataravanappa (2008)
Cotton leaf curl Bangalore virus	Monopartite	India	Venkataravanappa *et al.* (2013a)
Cotton leaf curl Allahabad virus	Monopartite	India	Venkataravanappa *et al.* (2012a)
Bhendi yellow vein Delhi virus	Bipartite	India	Venkataravanappa *et al.* (2012a)
Tomato leaf curl New Delhi virus	Bipartite	India	Venkataravanappa (2008)
Radish leaf curl virus	Monopartite	India	Kumar *et al.* (2012)
Okra yellow vein mosaic virus	Monopartite	Pakistan	Zhou *et al.* (1998)
Bhendi yellow vein mosaic virus	Monopartite	Pakistan	Zhou *et al.* (1998

Table 2 : Okra germplasm tolerant or resistant to yellow vein mosaic virus.

Species	Name of germplasm
A.esculentus (germplasm showing field tolerance toYVMV)	Bulk, F-3, M-31, L-1, Parbhani Kranti,
	AS12, AE 7, KS30, KS322, KS323,
	S-1-1, P-7, 3(I), IC 9273, Baunia
	IC 006485, IC 23592, IC 282230,
	These include IC 469548, IC 541224, IC 028883, IC 128894, IC 043742, IC 045815, IC 043735, IC 045802, IC 045814, IC 541224, IC 218887, IC 069286, and EC 305619.
A. caillei (Resistant or symptom less carriers of YVMV)	18 accessions from Ivory Coast, 5 from Ghana, 1 from Liberia, Susthira, EC 031830 (Asuntemkolo) from Ghana and African and a Japanese variety of *A. manihot* subsp. *manihot* (2n = 194) from Ghana
Wild species	A. *tetraphyllus* var. *penns, A. manihot.*
	A. enbeepeegearenses

conditions and the additive X additive type, showing little opportunity for development with standard selection techniques. Over the period of the Punjab Padmini variety's evolution, it has been discovered that even though *A. caillei's* resistance to YVMV had been controlled by two beneficial dominant genes exhibiting additive effects, *A. manihot's* resistance had been affected by a single dominant gene. Segregating generations deviate from the simple Mendelian inheritance pattern, indicating suggesting okra's YVMV resistance is mostly an involved genetic characteristic. The study suggests deferring selection for better features for as long as future generations of segregating populations since additive and crucial elements have the capacity to be effectively mistreated. It involves selfing following a few decades of delay selection, or inter-mating between chosen segregates, in an attempt to break unfavourable linkages and promote the accumulation of beneficial genes for trait advancement.

Biochemical basis of resistance to virus disease

Many investigations have shown the significance of biochemical components such as phenols, ascorbic acid, and related enzymes in determining a host plant's resistance or susceptibility to diseases in a variety of crops. In this environment, phenolic compoundswidely spread secondary products in plantshave an important effect. High amounts of peroxidase (POD), phenylalanine ammonialyase (PAL) and polyphenol oxidase (PPO) have been observed in plants treated to multiple both abiotic and biotic resistance stimulants (Seth *et al*., 2017). Plant disease resistance is often linked to increased activity of peroxidase or the oxidation of phenol compounds in diseased tissues, however peroxidase alone is not directly linked to resistance against diseases. Peroxidase activity in leaves of tobacco has been found to be correlated positively to resistance to TMV in many studies. The production of lignin and the decomposition of hydrogen peroxide at harmful amounts, which build up in plant tissues as the consequence of pathogen diseases are additional roles of peroxidase. Since, it can oxidize vital compounds like phenolics throughout the plant or the pathogen, it is

believed that it plays a role in plant defense mechanisms. It seems that polyphenol oxidase (PPO) exists separately within plant cells; yet, pathogenic attacks or tissue senescence might lead to rupture of the membrane, which could start the production of quinone through rendering PPO easier to access to its substrate. Since resistant genotypes show bigger activity, antioxidant enzymes are important for preserving non-toxic quantities of H_2O_2 in cells while regulating signal movement. Peroxidase and PPO activity levels have been shown to be bigger in resistance pearl millet genotypes against downy mildew as compared to susceptible ones, as reported by Sapre *et al.* (2014).

Conventional Breeding for resistance to YVMV

Pedigree method of breeding

Certain plants from the F_2 generation are selected, and their progeny in subsequent generations are examined and tested, all using the pedigree technique. Comprehensive records of parent-progeny relationships are kept in the form of pedigree records. These records provide a connection between each progeny and the original F_2 plant that produced it. This method is applied to segregate populations of crosses in self-pollinated crops in order to select for combination or transgressive breeding.

Varieties developed by pedigree method of breeding are

- Pusa Makhmali (1955)

  Pusa Sawani: IC1542×Pusa Makhmali–Tolerant toYVMV
- Varsha Uphar: Lam selection1×Parbhani Kranti
- Hisar Unnat: Sel 2-2× Parbhani Kranti
- VRO-6 (Kashi Pragati)
- IIVR-10 (Kashi Satdhari)

Inter specific hybridization and Backcrossing

Interspecific hybridization involves crossing two species within the same genus, enabling the transfer of beneficial genes from wild, less-developed species to cultivated ones.

Schematic representation of Interspecific hybridization and Backcrossing.

Varieties developed through inter-specific hybridization are

- Punjab7– *A. esculentus* (Pusa Sawani) × *A.caillei*
- Punjab Padmini –*A. esculentus* (Reshmi)× *A.caillei*

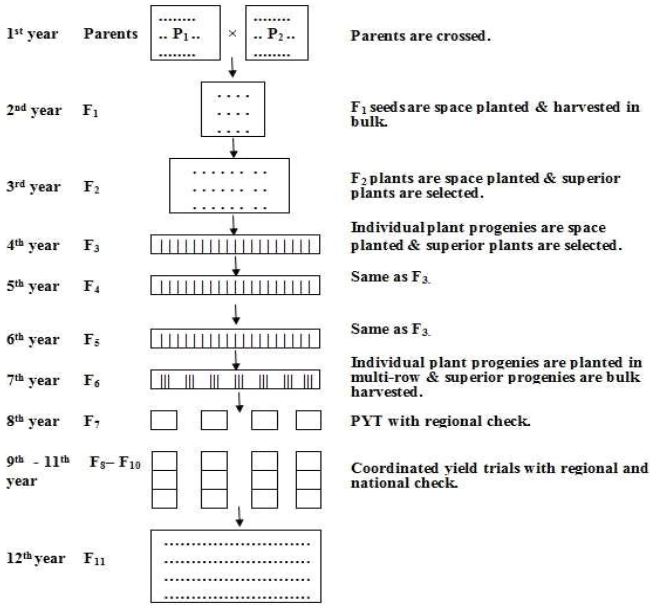


Fig 2 : Schematic representation of pedigree method of breeding.

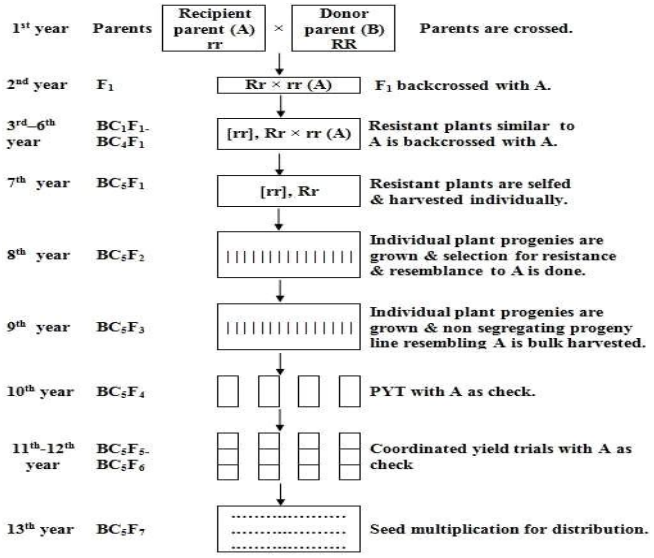


Fig. 3 : Schematic representation of Interspecific hybridization and Backcrossing.

- Parbhani Kranti -*A. esculentus* (Pusa Sawani)× *A. manihot*
- Arka Anamika and Arka Abhay–*A. esculentus* (IIHR20-21) × *A. tetraphyllus* var. *tetraphyllus*

Hybrids in okra

Hybrid vigour for yield and yield components has been exploited from the available germplasm of okra. Few private and public sector released F_1 hybrids are listed below.

- 'Deb-401'×'Parbhani Kranti','Barsha Laxmi'×'Parbhani Kranti',
- 'VNRGreen'×'Shagun'and 'Barsha Laxmi'×'Shagun'had lower PDI values and are

considered resistant (Das *et al*., 2013).

- BCO-1×Arka Anamika having high tolerance both under field and artificial conditions (Seth *et al*., 2017).

F_1 hybrids resistant to YVMV by other institutes

- Hyb-7 & 8, COBTH (TNAU)
- GOH-3 & 4 (Gujarat AU)
- DOH-2, DOH– 6, IARI

Recently IIHR, Bangalore has released a F_1 hybrid, which is the first genic male sterility-based hybrid in okra in the world, Arka Nikita.

Hybrids from Private sector with YVMV resistance

- Shakthi, Sonal, Sarika,Singham (Nunhems)
- No.10&64 (MAHYCO)
- Syngenta–152 (Syngenta)
- Hyb– (Krishidhan)
- Hyb –7315 (JK seedsAgri genetics)
- Avanthika (Bio-seed)
- Sahibha and Sahan (Rasi seeds)
- Janni,Navya and Radhika (Advanta seeds)
- NS811, NS862, NS7772 and NS7778 (Namdhari)

Mutation breeding

Chemical Mutagen- Punjab-8 (EMS-8)- a Pusa Sawani variant that was produced by treatment it using 1% ethyl methane sulfonate (EMS). This mutant showed a 99 percent decrease in YVMV disease, a 16% greater fruit number and a 107% increase in yield. (Arora and Sharma, 1990).

Physical Mutagen- MDU-1, a Pusa Sawani mutant was generated in 1978 by Tamil Nadu Agricultural University in Coimbatore by the application of gamma rays (Kulkarni and Nerkar, 1992).

Prabhani Tillu- Additionally a processing-ready produced mutant (Kulkarni and Nerkar, 1992).

Biotechnological interventions

Due to a lack of molecular markers, a molecular genetic map and other genomic tools, the utilization of genotypes in okra breeding can frequently be limited. Okra's large chromosomal number (ranging from 56 to 196) as well as its polyploid nature makes it hard to construct chromosome linkage groups. Okra has a 16,000 Mb genome composed up of 65 linkage groups. Okra marker development research is scarce and primarily focused on cultivar traits. In *Abelmoschus* species, Mortinello *et al.* (2001) revealed an association between molecular markers and categorizing patterns using morphological features. In addition, Aladele *et al*. (2008) differentiated 93 accessions of West African (*A. caillei*) and common (*A. esculentus*) okra utilizing RAPD (random amplified polymorphic DNA) markers. Gulsen *et al.* (2007) suggested using sequence-related amplified polymorphism (SRAP) in marker-assisted selection (MAS) for several characteristics in Turkish genotypes.

Recently, 16 primers designed to amplify SSR regions of Medicago truncatula were used to study 20 okra accessions from Burkina Faso. Due to the presence of a distinct 440 bp fragment generated by primer MT-27, hairs on the fruits and late maturity in these two accessions, it was found that these two accessions were distinct from the other eighteen. For the purpose of to enhance viral resistance, efforts have been done to include certain genes, such as the antisense RNA gene and the coat protein (CP) gene.By introducing the cry1Ac gene from the bacterium Bacillus thuringiensis, efforts have been done to develop insect-resistant okra variations against the most destroying pest, the shoot and fruit borer (*Earias* sp.). It resulted in what is commonly referred to as Bt okra. Bt okra with the cry1Ac gene (Event OE-17A) is currently going through regulated field trials and safety evaluation. Whenever, it comes to viral diseases, okra is especially susceptible to Yellow Vein Mosaic Virus (YVMV). In an attempt to mitigate this, attempts have started to incorporate certain genes, such as the antisense RNA gene and the coat protein (CP) gene, to improve viral resistance.

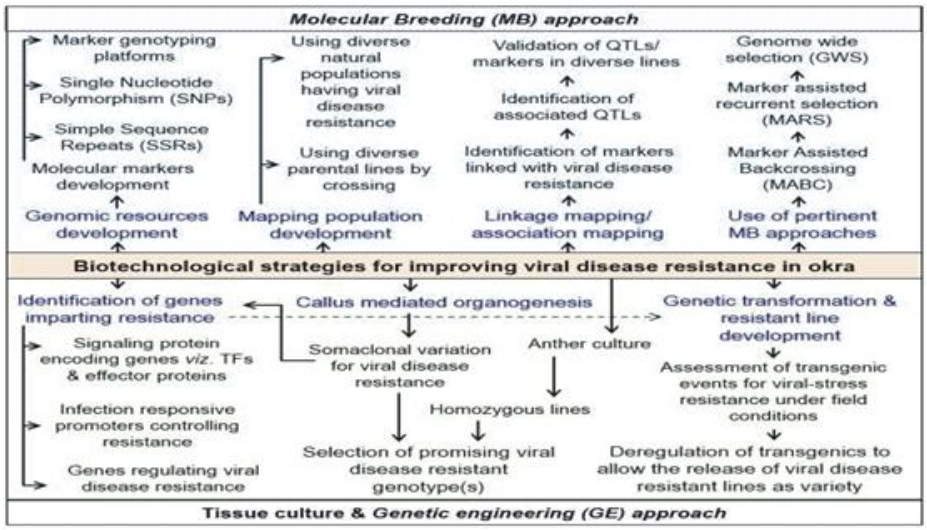


Fig. 4 : Schematic representation of biotechnological strategies.

Conclusion and Future Strategies

One of the most destructive begomviruses and related satellite groups, yellow vein mosaic virus, greatly decrease the yield of crops wherever it is grown. The outstanding adaptability associated with these begomoviruses has led to multiple genotypes which were resistant or tolerant to lose their resistance. Consequently, to create strains for non-specific resistant / tolerant types, a collaborative effort including plant breeders, entomologists, virologists, and plant biotechnologists will be needed to deal with this disease. Discovering reliable and consistent sources of viral disease resistance is an essential initial phase in any future breeding activity. Any advancement in the transgenic or strongly connected marker(s) with QTLs for viral disease resistance might open up novel possibilities for okra's capacity to resist viral disease.

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