Ecofarming
e-Magazine for Agriculture and Allied Sciences
http://www.ecofarming.rdagriculture.in
e-ISSN: 2583-0791

# Biotechnology approach

## for yellow mosaic disease resistance in pulses

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***Received: November, 2024; Accepted: December, 2024; Published: January, 2025***

### Introduction

Pulses are the universal crops rated as one among the important crops in the world. Because they possessed the biological nitrogen-fixing mechanism. They inherited the in situ high protein contribution. There are many factors responsible for low productivity ranging from plant ideotype to biotic and abiotic stresses.

Most emerging infectious diseases of plants are caused by viruses. Plant viral diseases cause serious economic losses in many pulse crops by reducing seed yield and quality. Among the various diseases, the yellow mosaic disease was given special attention because of its severity and ability to cause yield loss of up to 100 percent.

At present mainly four distinct viruses *viz.,* Mungbean yellow mosaic India virus (MYMIV), Mungbean yellow mosaic virus (MYMV), Horsegram yellow mosaic virus (HgYMV), Dolichos yellow mosaic virus (DoYM). It is mainly transmitted through the insect. Nariani (1960) first report the occurrence of yellow mosaic disease of mungbean and its transmission by the whitefly *Bemisia tabaci* predominantly. It is having bipartite genomes (DNA-A and DNA-B). The virus has single stranded DNA genome of approximately 2.8 Kb. Various biotechnology approaches are used to develop a resistant variety against the yellow mosaic virus. YMD is transmitted through Mechanical transmission, Graft transmission, Seed transmission, Insect transmission.

Conventional breeding approaches are more time consuming for crop improvement. The biotechnological approach assists it to fasten crop improvement. i.e., Marker assisted backcross and recurrent selection.

Different biotechnological approaches such as molecular markers, marker-assistance selection (MAS), QTL mapping, genome editing, gene silencing, transgenic approach play the most important role to identify disease resistant genes and their mechanism against YMD. SSR (simple sequence repeats) markers, SNPs (single nucleotide polymorphism) are most widely used. QTL analysis is used to identify genes for resistance, their location on chromosomes, gene action etc. Novel genome editing tools such as TALEN, ZFN, CRISPR/Cas9open new windows in the field of biotechnology and have high accuracy/ precision to edit genome as per requirement.

### Review of research work

**Kabi*et al.* (2017)** analyzed twenty-six different greengram genotypes for YMVby using a resistant gene analogous (RGA) marker named CYR1 which produced amplicon at 90 bp in seven genotypes (OBGG-2013-8, OBGG-2013-21, OBGG-2013-16, OBGG-2013-11, OBGG-2013-20, OBGG-2013-39 and OBGG-2013-12) which concluded that these seven

genotypes have yellow mosaic virus resistance gene and this marker is efficient and ubiquitous for genotyping of YMV reaction. OBGG 2013-20 was an YMV resistance and high yielding line which can be used as YMV donor or can be released as a variety. OBGG 2013-34 have 23.88% higher yield potential than best check but moderately susceptible to YMD thus needs further improvement by hybridization with suitable YMV resistant varieties.

**Rambabu*et al.* (2018)** experimented on blackgram to find out the markers linked to yellow mosaic virus resistance gene, MYMV resistant parent T9, and MYMV susceptible parent LBG 759 were crossed to produce a mapping population. A total of 50 SSR primers were used to study parental polymorphism. Of these 14 SSR markers were found polymorphic showing 28% of polymorphism between the parents. These fourteen markers were used to screen the $F_2$ populations to find the markers linked to the resistance gene by bulk segregant analysis. The marker CEDG185 present on linkage group 8 clearly distinguished resistant and susceptible parents, bulks, and ten $F_2$ resistant and susceptible plants indicating that this marker is tightly linked to the yellow mosaic virus resistance gene.

**Kumari*et al.* (2018)** performed inoculation on T1 seedlings of transgenic and non-transgenic plants where the viral replicative DNA level was assessed for ten plants and a quality concentration of viral replicative form was seen in the transgenic lines. Northern blot analysis detects siRNA in the transgenic line 2 of event A, line 5 and 6 of event B, as well as line 9 and 10 from event C, inoculated with viruliferous whiteflies, and a high level of siRNA (21–22 nt) was observed in the transgenic line 2 and line 10 which corroborated by the non-detectable level of viral replicative DNA and low concentration of viral transcript for replication as estimated in qRT-PCR. Results obtained in this study confirmed the transgene construct can be used to develop resistance against begomoviruses in soybean and other crops, as it targets the most conserved domain governing whitefly transmission.

**Vadivel *et al.* (2020)** worked on the blackgram for identification as well as validation of quantitative trait loci (QTL) for MYMV disease resistance in blackgram. A total of 112 $F_{2:3}$ lines were evaluated for MYMV disease resistance along with parents *viz.*, MDU 1 (MYMV disease susceptible), and Mash 1008 (MYMV disease resistant). A total of 525 SSR primers were used to test polymorphism between parents MDU 1 and Mash 1008. Genotyping was carried out for 112 $F_{2:3}$ RILs of the cross MDU 1 x Mash 1008 with 35 polymorphic SSR markers. QTL study indicated the presence of two major QTLs for MYMV disease score in LG 2 and LG 10 at 60 DAS with 20.90 and24.90% of phenotypic variation respectively. Validation of these QTLs in two other mapping populations indicated that QTL on LG 10was validated with the high phenotypic variation of 45.40-46.00%. Hence it may conclude that *qmymv10_60* may be utilized for MAS/MABC with assured improvement on MYMV disease resistance in blackgram.

## Conclusion

- Mosaic disease caused by YMD is a major production constraint limiting pulses yield.
- Plant manifest resistance through a mechanism such as morphological, biochemical and genetic.
- Different marker was identified for the detection of YMD genes. e.g., RAPD, SCAR, SSR.
- At present, Marker assisted selection and QTL mapping are the most widely used biotech. approaches.
- The transgene construct can be used to develop resistance against begomoviruses in soybean and other crops, as it targets the most conserved domain governing whitefly transmission.

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