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MUNGBEAN YELLOW MOSAIC DISEASE (YMD) A DESTRUCTIVE DISEASE OF COWPEA: ECONOMIC IMPACT AND MANAGEMENT PRACTICES

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ABSTRACT

Cowpea, a crucial pulse crop in India, suffers significant yield losses due to various diseases, with yellow mosaic disease (YMD) being one of the most devastating. This review comprehensively explores the literature on YMD, emphasizing the economic impact and management practices, particularly the role of germplasm in conferring resistance. Germplasm serves as a critical reservoir of resistance genes against biotic stresses, including viral diseases. The study investigates the Begomovirus genus, highlighting their distribution, economic impact, symptomatology, host range and molecular characteristics. Emphasis is placed on understanding the taxonomy, genome organization and physical properties of these viruses. Additionally, this review discusses the results of field surveys conducted across different regions in India to assess the incidence and severity of YMD in cowpea and other legumes. This synthesis provides valuable insights for future genome-wide association studies (GWAS) focused on enhancing YMD resistance in cowpea, thereby contributing to sustainable crop production and food security.

Key words : Cowpea, YMD, Germplasm, Host plant resistance, MYMIV, GWAS.

Introduction

Legumes provide the much-needed proteins to our predominantly vegetarian population. It represents the second largest family of higher plants, second only to grasses in agricultural importance (Doyle and Luckow, 2003). Resource poor farmers across the developing world depend on grain legumes to sustain the health of their families and livestock, and to enhance their economic well-being. Cowpea (*Vigna unguiculata* L. Walp., 2n=2x=22) is one of the most important and nutritious diploid minor pulse crops of India, belonging to the Fabaceae family. It is a multifaceted crop, with young pods used as a vegetable, dried grains as dal, and also serving as fodder and a cover crop. Cowpea cultivation enhances soil fertility by enriching nitrogen levels in the soil due to its nitrogen-fixing ability (Martey *et al*., 2021). Additionally, it has the advantage of being a short-duration crop, for vegetable purpose ready for harvest within 45 to 90 days. For grain production, the crop can be harvested approximately 90 to 125 days after sowing, once the pods are fully matured. It can also be grown as a fallow crop in rice fields after the rice harvest generating additional income and enriching the soil (Becker *et al*., 2024).

Cowpea is a highly nutritious and comparatively inexpensive source of quality protein, phosphorus, iron and vitamins making it an excellent substitute for meat, eggs and other protein-rich foods (Ferreira *et al*., 2022). The major cowpea-growing countries include Nigeria, Niger, Burkina Faso, Ghana, Kenya, Uganda, Malawi and Tanzania in Africa, as well as India, Sri Lanka, Myanmar, Bangladesh, the Philippines, Indonesia and

Thailand. Cowpea is a warm-weather legume, that is highly tolerant to drought and heat, making it well-adapted and crucial for achieving climate resilience (Carvalho *et al*., 2019).

Approximately 80% of yield loss in legumes, including cowpea, is attributed to viral diseases, the Mungbean Yellow Mosaic Virus (MYMV) alone accounts for 80 to 100% of this loss (Bhanu *et al*., 2017). Annually, more than US $ 300 million is lost in various leguminous crops due to MYMV infection (Varma and Malathi, 2003). Reshmi Raj *et al*. (2020) reported yield losses of about 75 to 100% in mungbean due to yellow mosaic disease (YMD). YMD was first reported in mungbean fields in India during the 1950's at the Indian Agricultural Research Institute, New Delhi (Nariani, 1960). Yellow mosaic disease (YMD) is caused by four viruses namely, mungbean yellow mosaic virus (MYMV), mungbean yellow mosaic India virus (MYMIV) and Horse gram yellow mosaic virus (HgYMV) and dolichos yellow mosaic virus (DoYMV). All these viruses belong to the genus *Begomovirus* and the family *Geminiviridae*. They are transmitted by the whitefly (*Bemisia tabaci* Genn.) vector in a persistent circulative manner (Nair *et al*., 2017; Reshmi Raj *et al*., 2020). MYMV, in particular is responsible for yield reductions in mungbean-growing countries across Asia, including India (Karthikeyan *et al*., 2014). Naimuddin and Singh (2016) reported that the Dolichos yellow mosaic virus (DoYMV) has a genome remarkably similar to the other three viruses, although it has only been found in Dolichos bean (*Lablab purpureus* L.).

As there are no effective formulations presently available in the market to control viral diseases like YMD, reducing the disease's impact and severity primarily involves supressing the vector (whitefly) with either synthetic or non-synthetic insecticides, as well as removing alternate or collateral hosts (Nalla *et al*., 2023). Although, this strategy is neither economically viable nor sustainable due to the environmental pollution caused by insecticides, their potential to increase host resistance in vectors and their serious effects on human and animal health. Consequently, using resistant varieties is the only economically feasible, environmentally safe and sustainable approach for increasing cowpea production in regions severely affected by YMD. Screening cowpea genotypes under both natural and controlled conditions through challenge inoculation will aid in identifying stable resistant sources that can be used utilized in breeding programs and directly as varieties to mitigate losses caused by YMD (Abhishek *et al*., 2024a).

Yellow Mosaic Virus: Taxonomy, Economic Impact, and Symptomatology

The Genus *Begomovirus*

Genus *Begomovirus* is the largest group of plant viruses, responsible for causing devastating crop diseases both in India and globally (Malathi *et al*., 2017). It includes more than 200 members, making it the largest genus within the family *Geminiviridae* (Fauquet *et al*., 2008). Begomoviruses infect both monocot and dicot crops, particularly those of significant economic value (Varsani *et al*., 2017). The Family *Geminiviridae* encompasses nine genera of plant viruses with single-stranded DNA genomes. These viruses are classified into genera based on their host, vector and genome arrangement. Among these nine genera, *Becurtovirus*, *Capulavirus*, *Curtovirus*, *Eragrovirus*, *Grablovirus*, *Mastrevirus*, *Topocuvirus* and *Turncurtovirus* possess monopartite genomes. In contrast, members of the genus Begomovirus have either mono- or bipartite genomes (Varsani *et al*., 2017 and Zerbini *et al*., 2017).

Four begomoviruses *viz*., mungbean yellow mosaic virus (MYMV) (Reshmi Raj *et al*., 2020), mungbean yellow mosaic India virus (MYMIV) and horsegram yellow mosaic virus (HgYMV), dolichos yellow mosaic virus (DoYMV) cause yellow mosaic disease (Malathi and John, 2008; Naimuddin and Singh, 2016). Thongmeearkom *et al*. (1981) were the first to observe virus particles, while Honda *et al*. (1983) were the first to purify these particles from the leaf cells of mungbean.

Begomovirus distribution

According to Lefeuvre *et al*. (2011), Begomovirus evolved around ten million years ago. MYMD was first documented by Nariani (1960) in fields at IARI, New Delhi, India. This disease is a major cause of loss in the production of mungbean in India, Sri Lanka, Pakistan, Bangladesh, Papua New Guinea and Thailand (Varma *et al*., 1992, Jones, 2003 and Haq *et al*., 2011). MYMV was found to be most devastating, especially in South Asian countries (Jyothi *et al*., 2020). Nariani (1960) observed that MYMV was one of the most prominent and economically devastating disease affecting pulse productivity throughout Asia. According to Nath and Saikia (1995), it was the most significant constraint to mungbean cultivation in Assam. Malathi *et al*. (2017) revealed that about 16 % of the globally recorded gemini viruses are prevalent in India. Generally, the major isolate of yellow mosaic virus infecting mungbean in Western and Southern India is MYMV whereas MYMIV isolate is predominantly found in India, Pakistan, Bangladesh, Nepal and Vietnam (Malathi and John, 2009). In India,

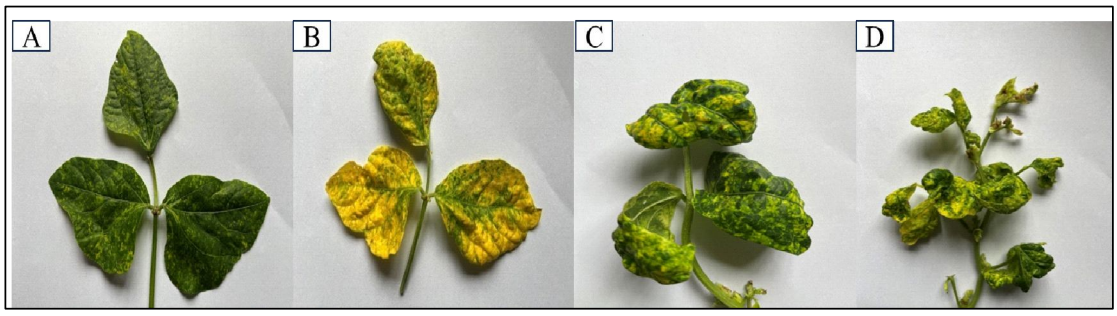

Fig. 1 : Close up view of characteristic yellow mosaic symptoms in cowpea.

yellow mosaic disease has been reported from Punjab, Haryana, Delhi, Uttar Pradesh, Uttarakhand, Madhya Pradesh, Rajasthan, Gujarat, Chhattisgarh, Andhra Pradesh, Tamil Nadu, West Bengal, Bihar, Karnataka and Meghalaya (Abhishek *et al*., 2024b). Ghuge *et al*. (2018) noted an increasing prevalence of MYMV in Maharashtra, indicating a growing threat to successful mungbean cultivation in the region.

Economic impact of YMVD

Singh *et al*. (1971) observed that the yield of soybean infected by MYMV, was reduced by 21-61% depending on the timing and intensity of the infection. Nair and Nene (1973) reported that urdbean plants infected with YMD produced no seeds. MYMV infection results in an annual loss of more than US $ 300 million in various leguminous crops (Varma and Malathi, 2003). Viral diseases account for approximately 80% of yield loss in pulses, with MYMV alone responsible for 80-100% yield loss (Bhanu *et al*., 2017). MYMV is a devastating disease, it deteriorates seed quality and reduces yield by up to 85%, leading to significant economic losses in legumes (Karthikeyan *et al*., 2014). Singh *et al*. (2020) highlighted that YMD is a major disease of mungbean, causing severe yield losses. YMD degrades seed quality, and early-stage infections can even kill the plants, resulting in yield losses up to 100% (Nainu and Murugan, 2020). YMD in India has resulted in yield reductions of 75-100% in mungbean, depending on disease incidence, virus strains, mungbean genotypes and interaction between these factors (Reshmi Raj *et al*., 2020; Jyothi *et al*., 2020). Marabi *et al*.(2021) reported that YMD causes 85-100% economic losses in soybean, influenced by crop susceptibility, vector population, infection duration, and favourable abiotic factors.

Symptomatology of YMD

Nariani (1960) reported that the first symptoms of YMD appeared as mild yellow specks or spots on the young leaves of the mungbean, with some apical leaves turning completely yellow as the yellow areas expanded. Older leaves possess irregular green and yellow patches while the younger leaves show complete yellowing due to the MYMV. The complete yellowing reduces photosynthetic efficiency of plant which ultimately affecting its yield (Malathi and John, 2009). The most noticeable symptoms appeared on the foliage as small, yellow specks along the veinlets, which later spread over the lamina and were followed by necrosis. These symptoms were accompanied by shortening of internodes, severe stunting of plants with little to no flowers and pods that, if formed, became thin, curled upwards and produced small, immature, shrivelled seeds (Nainu and Murugan, 2020). Abhishek *et al*. (2024b) studied the symptoms of YMD and found that they include yellowing and chlorosis, followed by necrosis, vein banding (yellow and green), shortening of internodes, stunting of plants and pod deformation with a few shrivelled seeds. Plants infected at an early-stage exhibit more severe mosaic symptom. The symptoms appear in the form of small irregular yellow specs and spots along the veins, which enlarge until leaves were completely yellowed (Fig. 1).

YMD Host Range

Qazi *et al*. (2007) reported that several legume crops, including soybean, mothbean, mungbean, cowpea and urdbean were infected with MYMV. *Ageratum conizoides*, *Vigna trilobata*, *Corchorus olitorius* and *Alternanthera sessilis* were found to possess MYMIV virus and were considered as true alternate weed hosts of MYMIV (Marabi *et al*., 2021). Among six crop hosts i.e., *Cajanus cajan*, *Glycine max*, *Phaseolus vulgaris*, *Vigna mungo*, *Vigna radiata* and *Vigna unguiculata* all exhibited yellow mosaic disease symptoms, harboured the MYMIV virus and were considered true hosts of the virus.

Deepa *et al*. (2017a) observed that the virus causing YMD was successfully transmitted from mungbean to mungbean, blackgram, *Nicotiana benthamiana*, horsegram, pigeonpea, soybean, cowpea, *Acalypha indica*, *Alternenthera sessile*, *Croton bonplandianum*, *Euphorbia geniculata*, *Malvestrunm coromandelium* and *Phyllanthus maderaspatensis* but not to *Parthenium*

hysterophorus. Alternate hosts of MYMV included *Nicotiana benthamiana*, *Vigna mungo* (blackgram), *Macrotyloma uniflorum* (horsegram), *Cajanus cajan* (pigeonpea), *Glycine max* (soybean), *Vigna ungiculata* (cowpea) and weed hosts *viz.*, *Acalypha indica*, *Malvestrunm coromandelium*, *Croton bonplandianum*, *Euphorbia geniculata*, *Alternenthera sessile* and *Phyllanthus madraspatensis*. These host plants served as potential alternate hosts and major source of virus inoculum for MYMV during the off season (Pandey, 2018). Ganesh *et al*. (2020) found that pigeonpea, blackgram, greengram, soybean, *Parthenium hysterophorus*, *Croton bonplandianum*, *Malvestrunm coromandelium* and *Alternenthera sessile* serves as hosts for YMD on horsegram, transmitted by whitefly (*B. tabaci*) in North Eastern Karnataka, India.

Incidence and distribution of Yellow Mosaic Virus (YMV) in various Crop Regions of India

Jayappa *et al*. (2017) reported that MYMV was present in all fields surveyed across four major mungbean-growing districts of Southern Karnataka *viz.*, Tumakuru, Chamarajanagar, Hassan and Chitradurga. Mungbean crops cultivated in South India were typically infected with MYMV, a whitefly-transmitted Gemini virus, and the highest incidence of YMD caused by MYMIV was prevalent in Central and Northeast India during studies on cowpea (Mantesh *et al*., 2020). Kumar *et al*. (2018) conducted surveys during 2011-12 and 2012-13 in five districts of Rajasthan such as Banswara, Bundi, Chittorgarh, Kota and Udaipur. They found that the highest mean disease severity was reported in Kota, while the highest whitefly population was observed Banswara. Conversely, the minimum disease severity and whitefly population were recorded in Bundi district. Chaithanya *et al*. (2020) revealed that both MYMIV-A and MYMV-A contribute to YMD IN black gram, with MYMIV-A being dominant over MYMV-A in samples collected from various regions in Andhra Pradesh with YMD infection.

Genome, properties and molecular characterization of *Begomovirus*

Taxonomy of *Begomovirus*

Genome: ssDNA

Family: *Geminiviridae*

Genus/Group species: *Begomovirus*

Type member: Mungbean yellow mosaic virus and Mungbean yellow mosaic India virus (Kolte and Tiwari, 2011).

Physical properties of the virus

Like all other members of the Geminiviridae family, LYMV and the cotton leaf curl disease (CLCuD) causing geminiviruses posess geminate (twinned) particles measuring approximately 18-20 nm in diameter and 30 nm length. These particles are composed of Two incomplete T=1 icosahedra fused together, creating a structure that includes 22 pentameric capsomeres and 110 identical protein subunits (Qazi *et al*., 2007). The thermal inactivation point of these viruses is between 40 to 50p C for 10 minutes. Their longevity *in vitro* is 1-2 days at 20^0C and their dilution endpoint ranges from 10^{-2} to 10^{-3} (Honda and Ikegami, 1986).

Genome organization of *Begomovirus*

Malathi *et al*. (2017) observed that either monopartite or bipartite genome was present in begomoviruses while, remaining eight genera of *Geminiviridae* contains monopartite genome. Bisaro (2006) studied that in maximum cases viral genome was bipartite and consists of two separately encapsidated genome components i.e., DNA-A and DNA-B like in MYMV. In case of bipartite virus, they have two components *i.e.*, DNA-A and DNA-B, which were similar in size, but vary in sequence except for a common region (CR) of 200-250 bp that remains largely similar within the virus components but varies between viruses.

Monopartite Begomoviruses possess a ~2.7 kb DNA-A component, whereas bipartite begomoviruses contain both a ~2.7 kb DNA-A component and ~2.6 kb DNA-B component. Partly overlapping open reading frames (ORFs) are present in both genomic components, arranged bidirectionally. In DNA-A, six ORFs are present: AV1/V1 and AV2/V2 are oriented in the sense direction, while AC1/C1, AC2/C2, AC3/C3 and AC4/C4 are oriented in the antisense direction. Additionally, in some bipartite begomoviruses, the presence of an ORF AC5/C5 has also been reported (Fontenelle *et al*., 2007).

In bipartite begomoviruses, the DNA-A component encodes several proteins, including the replication-associated protein, coat protein, transcriptional activator protein, replication enhancer protein and a protein involved virus movement. These proteins are also associated with RNA silencing suppression, splicing and determining the pathogenicity of the virus. The DNA-B component encodes the movement protein and nuclear shuttle protein (Van Regenmortel, 2007). Monopartite begomoviruses, which contain only the DNA-A genomic component, have been reported exclusively in old world viruses (Yaqoob *et al*., 2020).

Molecular characterization of yellow mosaic disease (YMD)

A study to detect variations in YMD caused by

different isolates of YMV in southern India found that pulses in Tamil Nadu were infected with two different yellow mosaic viruses: MYMV and HgYMV (Maheshwari *et al*., 2014). Validation of geographical confinement by identifying yellow mosaic virus species showed MYMIV in soybean samples collected from Northern and Central India and MYMV in samples collected from Southern and Western India (Ramesh *et al*., 2016).

Abarshi *et al*. (2017) reported that the begomovirus infecting lima bean in India was a novel isolate of the previously described HgYMV. The study found approximately 97% nucleotide similarity between the DNA-A sequences of this virus and those of begomovirus species infecting legumes. Phylogenetic analysis clustered HgYMV-Lb with legume-infecting begomoviruses from the Indian subcontinent, particularly with MYMV. DNA-B sequences showed 70% nucleotide similarity with isolates of MYMV and MYMIV. Phylogenetic analysis of these sequences grouped HgYMV-Lb with MYMV infecting soybean in Madurai (MYMV-Sb:Mad) and MYMIV infecting soybean in Bangladesh (MYMIV-BD:Yb).

In a study conducted during the *Kharif* season of 2016, MYMIV was detected in nine out of ten soybean samples. PCR products of 750 bp and 541 bp were obtained using DNA-A (CP) and DNA-B specific molecular markers, respectively (Marabi *et al*., 2021). Between 2012 to 2014, leaf samples from mungbean, other legume plants and weeds showing virus-like symptoms were collected from mungbean-growing regions in India. The study found MYMV-Urdbean in the northern states (Punjab and Delhi), MYMIV in eastern India (Jharkhand) and MYMV-Vigna in the southern states (Tamil Nadu, Karnataka and Telangana) (Nair *et al*., 2017).

Prema and Rangaswamy (2018) conducted an experiment for detect and characterize the coat protein gene of MYMV from Karnataka. They found that the YMV infecting mungbean crop in Hebbal, Bangalore, is MYMV and not MYMIV; it was identified as a variant of MYMV. Recently, Banerjee *et al*. (2018) identified a new isolate (Mg-mungbean^{-1}) of MYMIV from Meghalaya, India, which contained a recombinant DNA-B component. The confirmation of this novel isolate as MYMIV was based on a DNA-A phylogenetic tree. Additionally, Marabi *et al*. (2018) identified the effective utilization of CP primers for the proper detection of MYMIV, which was found to be the most common cause of YMD in soybean crops.

Sivakumar *et al*. (2020) conducted an experiment in which F_2 progenies were subjected to PCR amplification using tobacco N gene primers. Parental polymorphisms revealed a single band of 500 bp, which was present in wild *Vigna* sp. (MYMV resistant), but absent in CO 5 mungbean variety (MYMV susceptible). The 500 bp DNA band was found in all the F_2 resistant individuals using the same tobacco N gene primers. Chaithanya et al., (2020) reported the presence of both begomovirus species (MYMIV-A and MYMV-A) in samples collected from seven districts in Andhra Pradesh during the *Rabi* and *Kharif* seasons of 2016-17. PCR amplification using specific primers resulted in products of 700 bp for MYMV-A and 500 bp of MYMIV-A.

Management of yellow mosaic disease (YMD)

The eradication of primary hosts of YMV, such as perennial weeds and summer whiteflies has been found to facilitate the management of YMD (Malathi and John, 2009; Karthikeyan *et al*., 2014). An experiment found that the application of systemic insecticide combinations at the early growth stage was effective for whitefly management, as it killed the vector and simultaneously protected the plant against further attacks. It was also recommended that field sanitation, plucking infested leaves, using water sprays, and avoiding excess nitrogen fertilizer can help curb the whitefly population (Karthikeyan *et al*., 2014).

YMD management using insecticides to control whiteflies has been considered effective, but the development of insecticide resistance in vectors has led to a rise in the disease. Additionally, the excessive use of chemicals has had detrimental impacts on both the environment and human health (Mishra *et al*., 2020). An experiment found that the application of the systemic insecticide imidacloprid contributed to higher seed yields. The results showed that seeds treated with imidacloprid at 5 ml/kg, followed by two sprays of imidacloprid at 0.5 ml/l, could be effectively used to manage YMD and its vector in black gram (Archana *et al*., 2018). Furthermore, the mean disease incidence was lowest with the application of imidacloprid insecticide compared to other treatments (Younas *et al*., 2021).

Host plant resistance

Germplasm serves as a principal reservoir of genes for resistance

Plant genetic resources, as key components of agro-biodiversity, serves as a reservoir of genes and form the foundational units for crop enhancement programs that contribute to national food security. These resources provide genes for resistance against various biotic and

abiotic stresses. Genes sources from germplasm have been instrumental in breeding the modern cultivars and hybrids we have today. With their broad genetic bases, they act as a buffer against various viral diseases (Bohra *et al*., 2022). For instance, a single resistant gene from the wild rice germplasm *Oryza nivara* protected millions of hectares of rice fields from tungro virus. Similarly, resistance to the *Bhendi yellow vein mosaic virus* in okra was achieved using *Abelmoschus tuberculatus*.

Characterization and evaluation of germplasm at ICAR-NBPGR have identified promising virus-resistant germplasm lines in various pulses. Notably, pigeon pea germplasm accessions IC245198, IC45768, IC73313, IC73332 and IC73336 have been identified as highly resistant to the Pigeon pea sterility mosaic virus, while urdbean germplasm accessions IC144901, IC001572, IC011613 and IC485638 have shown high resistance to the Mungbean yellow mosaic virus (Rana *et al*., 2016). Additionally, several mungbean accessions, including IC0418452, IC0418454, IC0418469, IC0418510, IC0539814, IC0148392, IC0610380, and IC0394728, have been found resistant to the Bean common mosaic virus (BCMV) (Deepika *et al*., 2023). Cowpea accessions IC199699, IC201097, IC214751, IC353315 and IC259072 have been identified as resistant to BCMV and are considered promising donors (Abhishek *et al*., 2024a). Furthermore, Cowpea accessions EC98661, IC412901, EC107128 and IC426824 have also demonstrated resistance against yellow mosaic disease (Abhishek *et al*., 2024b). The evaluation of germplasm opens up the possibility of discovering cowpea accessions resistant to YMD.

Screening of genotypes under natural conditions

Subedi *et al*. (2016) conducted an experiment at the Grain Legume Research Program, Rampur, Chitwan, screening 48 mungbean genotypes against yellow mosaic disease over two consecutive years (2013-2014). Most of the entries exhibited a susceptible reaction, but some genotypes, including IPM-01-03, IMB 37, MEHA, / SUKUMAR, V0 6008 (B-G), HUM-16, V0 2023 (A-B), 5248 Chitwan, Kalyan and VC 6173 C showed resistant reactions.

Akbar *et al*. (2017) screened eighty-three mungbean genotypes against MYMD during the summer seasons of 2014 and 2015. They found that only one genotype (NM 6-68-2) was comparatively tolerant with a disease incidence of 10%, while the accession NM 1-32-1 was highly susceptible in both years. Parihar *et al*. (2017) screened two hundred and twenty genotypes during 2010 and 2011 at 17 different locations. From these, a set of twenty-five genotypes was further selected for evaluate them at six locations over two years to identify more stable resistant genotypes. Only three genotypes showed a high degree of resistance and stability across locations. Similarly, Bhanu *et al*. (2017) conducted a screening of twenty-five mungbean genotypes against MYMV, which were sown during the summer season of 2015. The results revealed that only seven mungbean genotypes exhibited resistant reaction, most of the genotypes were characterized as moderately susceptible to highly susceptible.

Similarly, Ghuge *et al*. (2018) screened seventy-four genotypes against YMD in mungbean and identified only eight as resistant, with the average incidence of YMD across various genotypes ranging from 0 to 68.42%. Nainu and Murugan (2020), screened eighty-one mungbean genotypes against MYMV and found that none were highly resistant, though seven genotypes were categorized as resistant.

Sivakumar *et al*. (2020) evaluated MYMV incidence by growing crossed seeds under field conditions. The F_1 generation exhibited a dominant resistant reaction, while the F_2 populations displayed a wide range of segregants, including susceptible, parental, and intermediate types, in response to MYMV disease incidence. Similarly, Jyothi *et al*. (2020) screened 107 mungbean genotypes under field conditions during the summer season at UAS, Dharwad (Karnataka). They observed that 16 genotypes were resistant and 14 genotypes showed a moderately resistant reaction to MYMV disease.

Kumari *et al*. (2020) screened 128 urdbean genotypes for resistance to MYMV over two consecutive years, during the Summer and Kharif season of 2015-2016. Among these, five genotypes were found to be disease-free, 19 genotypes were highly resistant, and 22 consistently showed resistant reaction in both seasons. Kumar *et al*. (2018) conducted an experiment on mungbean to assess the impact of meteorological factors on MsYMV disease incidence and vector population during *Summer*, *Kharif*, *Rabi* 2017 as well as *Summer* 2018. The corelation analysis revealed that, across all seasons, maximum temperature was positively correlated with the whitefly population.

Patil *et al*. (2021) observed that maximum and minimum temperature, along with relative humidity at 7 hrs had a positive, but non-significant impact on the whitefly population. In contrast, relative humidity at 14 hrs and rainfall (mm) had a negative non-significant impact on the whitefly population. The minimum temperature significantly and positively influenced

MYMV disease progression and transmission. Maximum temperature, relative humidity at both 7 and 14 hrs, and rainfall also positively influenced MYMV disease progression and transmission, although the impact was non-significant. Meteorological factors contributed 42.7% to the whitefly population and 97.75% to MYMV disease development overall.

Abhishek *et al*. (2024b) evaluated 1,127 cowpea germplasm accessions for yellow mosaic disease (YMD) at two disease hotspots (Hyderabad and Delhi), identifying 181 as putatively resistant. Of these, 100 were selected for further testing and whitefly-mediated screening confirmed MYMIV resistance in 20 accessions. Further, the YMD-associated Begomovirus was characterized using rolling circle amplification coupled with sequencing of the full DNA-A genome of MYMIV, which shared an identity of 99.02% with the MYMIV isolate infecting cowpea in Pakistan (Fig. 2). These 20 accessions are considered valuable for mapping resistance genes and breeding for YMD resistant cultivars.

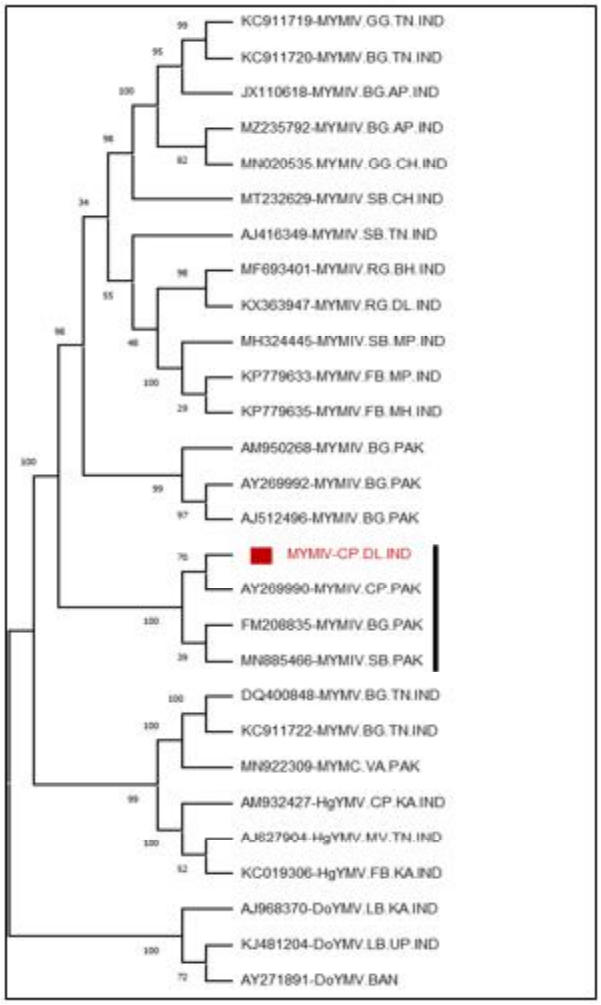

Fig. 2 : Phylogenetic analysis of MYMIV DNA-A sequences with other MYMIV isolates, as reported by Abhishek *et al*. (2024).

Screening of genotypes under glasshouse conditions

Whitefly (*Bemisia tabaci* Genn.) is a polyphagous pest of Indian origin and a vector of many viral diseases. It has the capability to transmit approximately 300 virus species from various genera, including Begomovirus (~90 per cent), Carlavirus, Crinivirus, Closterovirus and Ipomovirus (4%). The virus moves in a persistent circulative manner after entering the vector. Although, the virus circulates within the whitefly, it does not replicate before transmitted (Castillo *et al*., 2011). Among these, only *Bemisia tabaci* Genn. is known to transmit Begomovirus (Malathi *et al*., 2017).

Nariani (1960) was the first to record the outbreak of MYMD and its transmission by whitefly (*Bemisia tabaci*) (Jyothi *et al*., 2020). Czosnek (2008) reported that time duration of 15 to 60 minutes for acquisition and 15 to 30 minutes for inoculation through phloem sap was essential for the virus transmission. A latent period of about 8 hours was required for successful transmission. The transmission ability of the whitefly was directly proportional to its acquisition access period (AAP), with age and gender also influencing the transmission efficiency of virus (Czosnek, 2008). The persistence of transmission depends on the minimum AAP and the maximum retention duration of the virions in the whiteflies, typically 10 days for female and 3 days for males (Mishra *et al*., 2020).

Whitefly thrive best under hot and humid conditions. The virus cannot be transmitted to their eggs, neither male nor female whiteflies retain the infectivity throughout their entire lifetime (Karthikeyan *et al*., 2014). To enhance transmission, begomoviruses negatively impact the longevity and fecundity of whiteflies (Varun and Saxena, 2017). Female whiteflies are three times more effective in transmission than male whiteflies (Karthikeyan *et al*., 2014). The greatest diversity of whitefly was observed in Asia, with Asia-I and AsiaII-1 being the predominant groups among the 11 genetic groups identified in India. Notably, the Asia-I group exhibited significantly higher transmission efficiency (Anokhe *et al*., 2018).

Shankarappa *et al*. (2008) evaluated twenty tomato (*Solanum lycopersicum*) hybrids for resistance to tomato leaf curl virus disease (ToLCVD) using whitefly-mediated inoculation in a glasshouse. Of these, only three hybrids exhibited a resistant reaction. Bag *et al*. (2014) evaluated eight field-resistant urdbean accessions under glasshouse conditions by artificial inoculation with viruliferous whiteflies to test for resistance to yellow mosaic disease.

Among these accessions two were categorized as highly resistance and two as resistant. Nagaraj *et al*. (2019) evaluated fourteen mungbean genotypes, including a susceptible check, for their resistance to YMD under challenged inoculation conditions for one season. They identified five genotypes *i.e*., AVMU 1698, AVMU 1699, AVMU 16100, AVMU 16101 and KPS 2 as resistant to YMD, as indicated by their lower Percent Disease Incidence. However, none of the genotypes was found to be immune to the disease.

Naveesh *et al*. (2020) assessed forty-three soybean genotypes for resistance to Soybean yellow mosaic virus (SYMV) using viruliferous whiteflies (*Bemisia tabaci*) via artificial inoculation under glasshouse conditions. The study found that none of the genotypes exhibited a highly resistant reaction, however 11 genotypes were classified as moderately resistant. Srivastava *et al*. (2021) screened *Solanum pseudocapsicum*, against chilli leaf curl disease (ChiLCD) using challenge inoculation with viruliferous whiteflies. Although, *S. pseudocapsicum* appeared asymptomatic to chilli leaf curl virus (ChiLCV) infection under these conditions, PCR analysis revealed the presence of the virus, designating the plant as a symptomless carrier of the disease.

Genome wide association studies

The primary goal with regard to YMD, is to achieve a comprehensive understanding of the genetic complexity of traits in bold-seeded sub-tropical leguminous crop such as cowpea. Historically, bi-parental QTL (Quantitative Trait Locus) linkage mapping has been an effective technique for identifying genetic regions that co-segregate with the trait of interest within experimental populations. However, the recent emergence of association or linkage disequilibrium (LD) mapping has become a powerful tool for elucidating the genetic and molecular basis responsible for natural phenotypic variation through genome-wide association study (GWAS) (Alqudah *et al*., 2020).

Uncovering the genetic factors responsible for environmentally controlled traits requires a fundamental understanding of the relationship between genetic polymorphism and phenotypic variation among individuals. To decipher the genetic mechanisms influencing complex characteristics, including disease resistance, it is vital to comprehend the allelic variation at specific loci that impacts the phenotype, as well as the genetic structures associated with particular attributes. Mapping techniques link the variance observed in plant phenotypes directly to the underlying causal loci. There are generally two types of mapping techniques used to understand the relationship between genotypic and phenotypic variants: bi-parental QTL mapping populations and association mapping (LD-based) involving many individuals (Alqudah *et al*., 2020). Both approaches aim to identify molecular markers associated with QTL. Recent advancements in genome sequencing and high-quality, dense SNP arrays have increased the appeal of these techniques for numerous crops, including wheat.

Association mapping in GWAS

Association mapping (AM), often referred to as linkage disequilibrium (LD) mapping, offers an alternative approach to QTL mapping. By relying on non-random associations among alleles at nearby loci (LD), this method seeks to establish connections between genotypes and phenotypes within a collection of unrelated individuals (Zondervan and Cardon, 2004). In this natural experiment, a large cohort of unrelated individuals, displaying significant allelic diversity is employed to capture all inherent QTLs governing the trait. To enhance mapping precision, AM leverages historical recombination events within the population (Nordborg and Weigel, 2008).

LD mapping was initially applied in human genetic studies and has gained increasing popularity in plant research (Nordborg and Weigel, 2008). The primary advantage of AM lies in its ability to utilize all recombination events that occurred throughout the evolutionary history of the sample, thereby improving mapping precision. Additionally, the diverse panel employed in AM effectively captures the range of actual QTLs associated with the trait.

Given its straightforwardness and cost-effectiveness compared to the resource-intensive process of generating mapping populations, AM is particularly advantageous for species that cannot be easily crossed, cloned, or have extended generation cycles (Nordborg and Weigel, 2008). However, AM does have certain limitations. One significant challenge is the need of phenotype a large sample size, which can be burdensome. Furthermore, the selection of specific germplasm may be constrained due to the difficulties in obtaining precise phenotypic data from plants that have adapted to diverse environmental conditions.

Candidate gene identification

Two primary strategies are employed in AM techniques: 1) the resequencing of selected candidate genes and 2) genome-wide association studies (GWAS), which leverage marker polymorphisms across all chromosomes (Hirschhorn and Daly, 2005).

In candidate gene studies, genetic markers are genotyped at loci believed to be significant for specific

Table 1 : Previously detected QTLs/QTNs in different traits in cowpea through GWAS.

S. no.	Traits	CandidateGenes/QTLs/SNP	Method of Detection	Reference
1.	Pod Length	Qpl.zaas-3 Qpl.zaas-5	GWAS	Xu *et al*. (2017)
2.	Aphid Resistance	C35011941_894 Scaf-fold30061_3363	GWAS	Qin et al. (2017)
3.	Seed Size	Vigun05g036000 Vigun05g039600 Vigun05g204200 Vigun08g217000 Vigun11g187000 Vigun11g191300	GWAS & meta-analysis	Lo *et al*. (2019)
4.	Days to flowering (DTF)	Vigun01g084000 Vigun01g227200 Vigun02g062600 Vigun03g296800	GWAS	Seo *et al*. (2020)
5.	Days to flowering (DTF)	FT, GI, CRY2, LSH3, UGT8, 7A2, LIF2 and HTA9	GWAS	Paudel *et al*. (2021)
6.	Fusarium Wilt Resistance	Vigun05g179900 Vigun04g003100 Vigun03g084000 Vigun06g089000 Vigun03g027900	GWAS	Dong *et al*. (2022)
7.	Bruchid Resistance	Vigun01g176500 Vigun01g176500 Vigun01g091500	ML-GWAS	Kpoviessi *et al*. (2022)
8.	Protein	Vigun01g091500	GWAS	Chen *et al*. (2023)

phenotypes. This approach requires the identification of SNPs both between lines and within specific genes. It has proven successful in plants, particularly for candidate genes associated with relatively simple pathways, such as starch synthesis in maize and for candidate genes associated with relatively simple pathways such as flowering time in Arabidopsis. Recently, there has been an increase in association studies focusing on candidate genes. Examples include the phytoene synthase locus in maize, the dwarf-8 gene in maize, the PsyI-AI locus in wheat and the rhg-1 gene in soybean (Abhishek *et al*., 2024b).

However, the candidate gene strategy has the potential to overlook functional variations in genes not specifically chosen as candidates. The GWAS, on the other hand, involves genotyping markers across the entire genome to uncover potential associations with multiple complex traits. This approach requires the rapid identification of high-density SNPs that accurately reflect the genome's linkage disequilibrium (LD) structure, using advanced DNA sequencing technology or high-density oligonucleotide arrays (Zhu *et al*., 2008). The required quantity and density of markers for a comprehensive genome scan depend on the genome size and the rate of LD decay in a particular species.

Compared to candidate gene strategies, GWAS is superior because modern advancements in sequencing technology, which allow for cost-effective acquisition of complete sequence data through next-generation sequencing. Recently, a variety of crops, including cowpea, have been the subject of GWAS investigations. These studies have identified multiple QTLs for various traits in cowpea, such as pod length, seed size, and responses to biotic stress. However, there has been a limited number of GWAS studies specifically on quality traits in cowpea. Table 1 provides an overview of the previous GWAS studies was conducted in cowpea.

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