**Field-Based Disease Indexing of Soybean Genotypes Against Yellow Mosaic Virus**

**Abstract**

Yellow Mosaic Virus (YMV) is a major biotic constraint to soybean (Glycine max L. Merrill) production in India, significantly reducing yield and productivity. To identify resistant sources and characterize genetic variability for YMV resistance, a field experiment was conducted during the *Kharif* 2023 at the experimental field, Department of Genetics and Plant Breeding, College of Agriculture, RVSKVV, Gwalior, Madhya Pradesh, India. Ninety-two diverse soybean genotypes, including three checks *viz*., JS 20-98, JS20-34 and RVSM 2011-35, were evaluated under natural epiphytotic conditions using a Randomized Block Design with two replications. Spreader rows of the highly susceptible variety JS335 were also planted to ensure uniform YMV inoculum pressure. Disease severity was scored based on a standardized 0–5 scale, wherein lower scores indicated higher resistance. Substantial variability was evident in disease response, with genotypes categorized as highly resistant, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible. Genotypes such as RVS 23-1, RVS 23-8, JS20-98, PS1693 and PS1696 exhibited higher levels of resistance, remaining asymptomatic or showing negligible symptoms. In contrast, genotypes *viz*., JS335 and RVS2001-4 displayed high susceptibility, validating their role as spreader lines. The identification of genotypes with moderate to high resistance highlights their potential utility in breeding programmes. These findings provide a valuable foundation for the development of YMV-resistant soybean cultivars in future. Integration with molecular markers and gene expression studies may accelerate resistance breeding and contribute to sustainable soybean cultivation in YMV-endemic regions.

**Keywords:** Crop improvement, Disease indexing, Disease resistance, Soybean (*Glycine max*), Yellow Mosaic Virus (YMV)

**Introduction**

Soybean (*Glycine max* L. Merill), originated from East Asia, has become a globally important crop. It contributes around 25% of the world’s edible oil and nearly two-thirds of livestock protein concentrate (Mishra *et al*., 2024a). These have commonly gained the moniker “Golden bean” “Cow of the field”, and is a versatile oilseed and leguminous food crop valued for its high-quality protein, substantial oil content and presence of bio-active compounds beneficial to human health (Mishra *et al*., 2021a; Mishra *et al*., 2025a). Owing to its significant economic and nutritional value these play a crucial role in scientific research. Its seeds are rich in protein (40%), oil (20%) and health promoting phytonutrients. Additionally, soybeans are a valuable source of essential amino acids, vitamins and minerals such as isoflavones, tocopherol, linoleic acid, Vitamin B complex, Potassium, sodium, magnesium *etc*. (Mishra *et al*., 2025b). A diverse range of soybean-based products has been developed to enhance its culinary and nutritional applications. These include soymilk, roasted soybean, soy mayonnaise, boiled soybeans, miso, soy yoghurt, soy cheese, soy sauce, tempeh, tamari tofu, textured soy protein and textured vegetable protein (Mishra *et al*., 2020a; Sharma *et al*., 2021). Over the past century, soybean have emerged as a major global crop, with Brazil, US and Argentina leading production in 2021-22. India also contributed significantly, with Madhya Pradesh, Maharashtra and Rajasthan being the top producing states during *kharif* 2023. These states collectively reported high sowing areas and yields, highlighting soybean’s growing importance in Indian agriculture (Mishra *et al*., 2024b). Despite its agronomic and economic importance, soybean productivity is frequently constrained by an array of biotic stresses, among which Yellow Mosaic Virus (YMV) poses a major threat in tropical and subtropical regions, particularly in South and Southeast Asia (Mishra *et al*., 2024c).

Yellow Mosaic Virus, primarily transmitted by the whitefly (*Bemisia tabaci*), is one of the most devastating viral diseases affecting soybean (Amrate *et al*., 2023). The disease is characterised by the appearance of yellow patches or mosaics on leaves, reduced photosynthetic efficiency, stunted growth and ultimately significant yield losses (Mishra *et al*., 2020 b; Mishra *et al*., 2021b; Rahman *et al.*, 2023). The growing challenges posed by YMV are further exacerbated by climate change, which influences the epidemiology of vector-borne diseases through increased temperatures, erratic rainfall patterns and extended growing seasons (Caminade *et al*., 2019; Amrate *et al*., 2020; Swathi *et al*., 2021). Such environmental changes are known to enhance the population dynamics and geographical distribution of insect vectors, thereby intensifying disease incidence and severity in previously less-affected regions (Rocklöv *&* Dubrow; 2020; Abbasi, 2025). The absence of effective chemical control measures for viral pathogens further highlights the need for identifying and utilizing host-plant resistance as a sustainable management strategy (Subedi *et al*., 2023; Krenz *et al*., 2024).

Field based evaluation under natural epiphytotic conditions remains a reliable approach for screening and characterizing genotypic resistance to YMV. Such assessment facilitates the identification of resistant germplasm line(s), which can serve as a critical resource for resistance breeding programmes to develop YMV-tolerant/resistant cultivars. The present investigation was undertaken to evaluate a diverse set of soybean genotypes for their reaction to YMV under natural field conditions and to categorize them based on disease severity. This study aimed to contribute to the ongoing efforts in enhancing YMV resistance through genetic improvement, thereby supporting stable soybean production in endemic regions.

**2. Materials & Method**

**2.1 Experimental Site**

The present investigation was conducted during the *Kharif* season of 2023 at the experimental field, Department of Genetics and Plant Breeding, College of Agriculture, RVSKVV, Gwalior, Madhya Pradesh, India. The experimental site was characterized by a semi-arid climate with extreme temperature variations. June is typically the hottest month, with maximum temperatures rising up to 48°C, while the winter season records minimum temperatures as low as 4°C. During the crop growth period (July to October 2023), normal weather conditions prevailed, with an average maximum and minimum temperature of 35.2°C and 24.5°C, respectively. A total of 907.7 mm of rainfall was received during this period, although its distribution was scanty and uneven. The region receives an average annual rainfall of 750–800 mm, primarily between late June and the end of September.

**2.2 Experimental Material and Design**

A total of 92 diverse soybean [*Glycine max* (L.) Merrill] genotypes, including three check varieties *viz.,* JS20-98, JS20-34 and RVSM2011-35 were evaluated in this investigation. The genotypes were acquired from RAK College of Agriculture, Sehore, under the jurisdiction of Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya (RVSKVV), Gwalior, Madhya Pradesh. The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each genotype was sown in three-meter-long rows, maintaining a spacing of 30 cm between rows and 5–7 cm between plants. Standard agronomic practices were followed throughout the crop season to ensure proper crop establishment and growth.

**2.3 Screening of Genotypes against Yellow Mosaic Virus (YMV) Disease**

To evaluate the putative resistance of genotypes against Yellow Mosaic Virus (YMV) under natural field conditions, the experiment incorporated spreader rows of the highly susceptible varietyJS335 along the borders of the experimental plots. This was done to facilitate uniform disease pressure across the experimental area. The scoring for disease incidence was conducted only after the border spreader genotype JS335 exhibited full-blown YMV symptoms. Visual observations of symptoms on leaves and overall plant growth were recorded (Figure 1), and disease reactions were scored based on the 0–5 scale as suggested by Lal *et al*. (2005) and presented in Table 1.

**Table 1 Yellow Vein Mosaic Virus Disease severity rating scale (0-5)**

|  |  |  |
| --- | --- | --- |
|  **Scale** |  **Description** |  **Disease Reaction** |
|  0 | No symptoms on plant | Highly resistant (HR) |
|  1 | 1-5 % plants exhibiting mottling of leaves symptom | Resistant (R) |
|  2 | 5-15 % plants exhibiting mottling and yellow discolouration symptoms | Moderately resistant (MR) |
|  3 | 15-25 % plants exhibiting mottling and yellow discolouration symptoms | Moderately Susceptible (MS) |
|  4 | 25-50 % plants exhibiting mottling and yellow discolouration symptoms | Susceptible (S) |
|  5 | >50 % plants exhibiting mottling and yellow discolouration reduced flowers and pods | Highly Susceptible (HS) |

For the purpose of this study, genotypes with scores of 0, 1, and 2 were categorized as resistant, while those scoring 3 to 5 were considered susceptible.

**3. Result**

Screening of soybean genotypes under natural field conditions during *Kharif*, 2023 revealed considerable variability in resistance responses to Yellow Mosaic Virus (YMV) and presented in Table 2. Disease severity was assessed based on a standardized 0–5 scale, wherein lower scores indicated greater levels of resistance. A wide spectrum of reactions was observed among the genotypes, ranging from highly resistant to highly susceptible.

|  |  |  |
| --- | --- | --- |
|  |  |  |
| **Highly** **Resistant** | **Resistant** | **Moderately Resistant** |
|  |  |  |
| **Moderately Susceptible** | **Susceptible** | **Highly Susceptible** |

**Figure 1:** **Pictorial representation of the Yellow Vein Mosaic Virus (YVMV) disease severity rating scale utilized for disease screening under field conditions.**

The genotypes JS335 and RVS2001-4 exhibited the highest level of disease susceptibility, characterized by pronounced symptom expression and poor plant vigour. In addition, genotypes such as RVS 23-13, RVS23-15, NRC253, TS-156, NRC254, VLS105, and AS34 showed susceptible reactions, indicating a lack of effective resistance mechanisms against YMV. A moderate level of susceptibility was recorded in several genotypes including RVS 23-10, RVS 23-14, RVS 23-16, RVS 23-17, JS 20-34, JS 93-05, MACS 1756 and others, which displayed intermediate symptom expression and reduced growth parameters.

Conversely, a substantial number of genotypes exhibited moderate resistance, showing limited symptom development and relatively better plant health under field conditions. These included genotypes such as RVS23-4, RVS23-7, RVS23-12, RVSM35, VLS104 and Pusa SipaniBS-9 among others. Further, a notable proportion of genotypes demonstrated resistant responses, characterized by mild or no visible symptoms and normal growth, suggesting effective inherent resistance. Genotypes such as JS 20-116, Raj Soya24, Lok Soya 2 and RVSM 2011-35 consistently maintained resistance under natural infection pressure.

Remarkably, the minimum level of disease incidence was recorded in genotypes RVS 23-1, RVS23-8, RVS23-24, JS20-98, Raj Soya 18, PS1693 and PS 1696, which were classified as highly resistant. These genotypes remained asymptomatic or exhibited only negligible signs of infection, indicating strong resistance potential and making them promising candidates for incorporation into YMV-resistance breeding programmes.

**Table 2 Response of soybean genotypes for yellow mosaic disease screening during *Kharif,* 2023**

| **S. No.** | **Genotypes** | **Disease Score** | **Disease Response** |
| --- | --- | --- | --- |
| 1 | RVS 23-1 | 0 | HR |
| 2 | RVS 23-2 | 1 | R |
| 3 | RVS 23-3 | 1 | R |
| 4 | RVS 23-4 | 2 | MR |
| 5 | RVS 23-5 | 1 | R |
| 6 | RVS 23-6 | 1 | R |
| 7 | RVS 23-7 | 2 | MR |
| 8 | RVS 23-8 | 0 | HR |
| 9 | RVS 23-9 | 1 | R |
| 10 | RVS 23-10 | 3 | MS |
| 11 | RVS 23-11 | 1 | R |
| 12 | RVS 23-12 | 2 | MR |
| 13 | RVS 23-13 | 4 | S |
| 14 | RVS 23-14 | 3 | MS |
| 15 | RVS 23-15 | 4 | S |
| 16 | RVS 23-16 | 3 | MS |
| 17 | RVS 23-17 | 3 | MS |
| 18 | RVS 23-18 | 2 | MR |
| 19 | RVS 23-19 | 2 | MR |
| 20 | RVS 23-20 | 1 | R |
| 21 | RVS 23-21 | 2 | MR |
| 22 | RVS 23-22 | 2 | MR |
| 23 | RVS 23-23 | 1 | R |
| 24 | RVS 23-24 | 0 | HR |
| 25 | RVS 23-25 | 2 | MR |
| 26 | RVS 23-26 | 1 | R |
| 27 | RVSM 35 | 2 | MR |
| 28 | JS 20-34 | 3 | MS |
| 29 | JS 93-05 | 3 | MS |
| 30 | JS 95-60 | 1 | R |
| 31 | JS 335 | 5 | HS |
| 32 | JS 20-116 | 1 | R |
| 33 | JS 20-69 | 1 | R |
| 34 | JS 20-98 | 0 | HR |
| 35 | RVS 76 | 1 | R |
| 36 | RVS 2001-4 | 5 | HS |
| 37 | Raj Soya 24 | 1 | R |
| 38 | Raj Soya 18 | 0 | HR |
| 39 | JS 20-29 | 1 | R |
| 40 | VLS 104 | 2 | MR |
| 41 | NRCSL 5 | 2 | MR |
| 42 | JS 24-26 | 1 | R |
| 43 | NRCSL 7 | 1 | R |
| 44 | SKAUS 3 | 1 | R |
| 45 | RVS 12-8 | 1 | R |
| 46 | KDS 1203 | 1 | R |
| 47 | NRC 253 | 4 | S |
| 48 | MACS 1756 | 3 | MS |
| 49 | Lok Soya 2 | 1 | R |
| 50 | AMS 2021-3 | 2 | MR |
| 51 | Himso 1695 | 2 | MR |
| 52 | TS-156 | 4 | S |
| 53 | NRCSL-8 | 1 | R |
| 54 | JS 24-34 | 1 | R |
| 55 | RSC 10-52 | 3 | MS |
| 56 | DS 1510 | 2 | MR |
| 57 | KSS 213 | 1 | R |
| 58 | MAUS 824 | 2 | MR |
| 59 | NRC 254 | 4 | S |
| 60 | AMS 2021-4  | 3 | MS |
| 61 | Himso 1696 | 2 | MR |
| 62 | DS 1529 | 2 | MR |
| 63 | KDS 1188 | 1 | R |
| 64 | MACS 1745 | 2 | MR |
| 65 | NRC 255 | 2 | MR |
| 66 | Asb 93 | 3 | MS |
| 67 | VLS 105 | 4 | S |
| 68 | NRCSL 4 | 2 | MR |
| 69 | NRC 257  | 1 | R |
| 70 | MAUS 814 | 2 | MR |
| 71 | SL 1311 | 1 | R |
| 72 | Asb 85 | 3 | MS |
| 73 | PS 1693 | 0 | HR |
| 74 | NRC 256 | 1 | R |
| 75 | RSC 1165 | 2 | MR |
| 76 | BAUS 124 | 2 | MR |
| 77 | DLSB 40 | 2 | MR |
| 78 | NRC 258 | 1 | R |
| 79 | Pusa Sipani BS-9 | 2 | MR |
| 80 | PS 1696 | 0 | HR |
| 81 | CAUMS 3 | 3 | MS |
| 82 | AUKS 212 | 2 | MR |
| 83 | RVSM 12-21 | 1 | R |
| 84 | NRC 259 | 2 | MR |
| 85 | AS 34 | 4 | S |
| 86 | RVSM 2011-35 | 1 | R |
| 87 | RSC 1172 | 3 | MS |
| 88 | AS 55 | 2 | MR |
| 89 | TS-208 | 3 | MS |
| 90 | NRC-260 | 2 | MR |
| 91 | NRC-196 | 3 | MS |
| 92 | Pusa Sipani SPS-433 | 2 | MR |

**4. Discussion**

The differential response of soybean genotypes to Yellow Mosaic Virus (YMV) infection observed in the present investigations highlights the existence of substantial genetic variability for disease resistance within the evaluated material. The identification of genotypes exhibiting varying degrees of resistance from highly susceptible to highly resistant-under natural field conditions provide critical insights for breeding programmes to enhance YMV resistance. Similar studies have also been conducted by Naveesh *et al*. (2020), Magar *et al*. (2024) and Amrate *et al*. (2020).

The highly susceptible reaction recorded in genotypes such as JS335 and RVS2001-4, which are known for their vulnerability to YMV, confirms their utility as effective spreader and indicator lines. These genotypes facilitate uniform disease pressure across the experimental field, ensuring the reliability of resistance screening. Similarly, the susceptible and moderately susceptible genotypes identified in this study are likely to possess either incomplete or no genetic resistance, rendering them unsuitable for cultivation in YMV-prone regions (Mishra *et al*., 2020a; Amrate *et al*., 2024; Kumari *et al*., 2024).

Moderately resistant genotypes demonstrated partial resistance, which may be attributed to the presence of quantitative trait loci (QTLs) governing disease tolerance. These lines, although not entirely free from symptom expression, demonstrated significantly lower disease incidence and could serve as valuable sources of polygenic resistance. Their inclusion in breeding programmes may enhance the durability of resistance by reducing the selection pressure on the virus, thereby delaying the emergence of virulent strains (Mishra *et al*., 2021c; Hoque & Haque, 2024; Gai *et al*., 2025).

In respect to importance, the genotypes were categorized as resistant or highly resistant. The consistent resistant performance of genotypes such as JS20-98, PS1693, PS1696, and Raj Soya 18 under natural YMV inoculum pressure suggests the presence of strong genetic resistance, possibly governed by resistance genes. These genotypes exhibited either negligible or no visible disease symptoms, indicating their potential for direct use in YMV-endemic areas and their suitability as parental lines in resistance breeding efforts. Their resistance may be attributed to restricted virus replication or movement, enhanced expression of defense-related genes, or a combination of both (Bag *et al*., 2014; Usovsky *et al*., 2022; Roy *et al*., 2025).

The observed resistance among diverse genotypes also highlights the importance of maintaining genetic diversity in soybean germplasm collections (Mishra *et al.*, 2024 d). Such variability not only facilitates the identification of resistance sources but also supports long-term resistance management strategies. Furthermore, the integration of these findings with molecular marker analysis and gene expression studies could enhance our understanding of the underlying resistance mechanisms and enable marker-assisted selection for durable YMV resistance (Deng *et al*., 2020; Upadhyay *et al*., 2020; Michaelis & Grohmann, 2023; Sharma *et al*., 2023; Yamin *et al*., 2023).

**Conclusion**

The present investigation effectively elucidated the variability in resistance responses of soybean genotypes to Yellow Mosaic Virus (YMV) under natural field conditions during the *Kharif* 2023 season. A diverse range of reactions-ranging from high susceptibility to complete resistance was observed, reflecting the rich genetic diversity within the tested material. The identification of genotypes exhibiting high levels of resistance, such as JS 20-98, Raj Soya 18, PS1693, and PS1696, is particularly noteworthy, as these lines consistently displayed negligible or no disease symptoms and maintained robust plant health. These highly resistant genotypes offer promising potential as parents in breeding programmes focused on enhancing YMV resistance.These lines can be further used as one of the parent in crossing programmes for introgression of disease resistance gene in the modern cultivars. In addition, moderately resistant genotypes may serve as valuable sources of quantitative resistance, contributing to durable resistance through polygenic inheritance. Conversely, the identification of highly susceptible genotypes emphasizes the need to avoid their deployment in YMV-endemic areas unless used strategically in resistance introgression efforts. The outcomes of this study underscore the importance of field-based screening under natural disease pressure as a reliable and efficient approach for identifying resistant genotypes. Continued evaluation and validation of resistant lines across diverse environments, coupled with molecular characterization, may proof instrumental in accelerating the development of YMV resistant cultivars, thereby contributing to sustainable soybean production and improved crop resilience against viral threats.

**Disclaimer (artificial intelligence)**

Author (s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, *etc*.) and text-to-image generators have been used during the writing or editing of this manuscript.

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