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Identification of Yellow Mosaic Virus (YMV) Resistant Black Gram *(VignamungoL.)* Genotypes for Cultivation in Northern India

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Abstract: *Black gram (Vignamungo L. Hepper) is a pulse crop and used as a protein rich food in human diet. India is the largest producer of black gram. A primary gene centre of black gram is found in India, thus many landraces of black gram is available in this region, which can be used as parental lines for improvement of black gram against YMV infection. In the present study 32 black gram genotypes was screened to identify the YMV infection resistant and susceptible genotypes through field experiment. The four genotypes of black gram i.e, UPU 8335, IPU 99-25, PGRU-95004 and SPS-43 were identified as highly YMV resistant, whereas the four genotypes i.e. IPU 2K-99-226, IPU 99-3, IPU 99-235 and NDU 94-10 were identified as highly susceptible genotypes. The present study will be helpful to suggest the YMV resistant genotypes for farmers in north India anduseful to select the parental lines for development of YMV resistant black gram varieties through crop improvement program.*

Keywords: *Black gram; Vignamungo; Yellow mosaic virus.*

1. INTRODUCTION

Black gram *(Vignamungo L. Hepper)* is commonly known as urd bean belongs to family *leguminoseae* and the subfamily *Papilionaceae.* It is an annual and important short duration pulse crop native to central Asia. The origin of Black gram has been reported in India [1] and requires a hot and humid growing season. The optimum temperature for better growth of Black gram ranges between 25^{o}C to 35^{o}C but it can tolerate up to 42^{o}C. Black gram is successfully grown as a summer and rainy season crop in India. Black gram is used for human food (dal, papad, bari, halwa and imarti), fooder and green manure. It contains about 24% protein, 60% carbohydrates, 1.3% fat and is the richest source of phosphoric acid among various pulses. India is the largest producer of urd bean which occupies about 14% of the total area under pulse crops in the country and ranks fourth in area and production after chickpea, pigeonpea and mungbean. There are various abiotic and biotic factors which affect the production of Urd bean. Till now there is very little exploitation is performed of various landraces for improvement of cultivated Black gram varieties [2]. There is reasonable possibility about presence of abiotic and biotic stress tolerant genotype of black gram in India, because it originated in India.

Yellow mosaic virus causes high amount of grain loss in case of black gram.Yellow Mosaic Virus (YMV) belongs to the genus *Begomovirus* and transmitted by the vector white fly, *Bemisiatabaci.* The yield loss due to this disease is *5-100%* depending upon disease severity, susceptibility of cultivars and population of white fly [3-5]. In Indian subcontinent Yellow Mosaic Disease (YMD) is caused by two virus species viz., Mungbean Yellow Mosaic India Virus (MYMIV) commonly occurring in northern part of India and Mungbean Yellow Mosaic Virus (MYMV) confined to southern India. The crop behavior for nature of resistance is due to existence of different species of Yellow Mosaic Viruses (YMVs). Thus effective screening for resistance towards YMV infection is a considerable criterion in varietal development program of black gram *(VignamungoL.)* varieties [6]. Morphological characterization is the first step in the classification and evaluation of germplasm[7,8]. Qualitative characters are important for plant description [8,9]and are influenced by consumer preference, socio-economic scenario and natural selection [8,10]. Present study was undertaken to identify the Yellow Mosaic Virus (YMV) resistant black gram *(VignamungoL.)* genotypes for successful cultivation in Northern India.

2. MATERIALS AND METHODS

The seeds of thirty two black gram *(VignamungoL.)* genotypes were procured from Indian Institute of Pulses Research (IIPR) Kanpur, Uttar Pradesh, India. All procured black gram genotypes were evaluated at Biotechnology experimental field of Motilal Nehru National Institute of Technology (MNNIT), Allahabad, Uttar Pradesh, India *duringKharif* season (July-September) 2014. The experiment was laid out in a randomized block design (RBD) with three replications of 3 meters length. Row to row and plant to plant spacing were

maintained at 45×15 cm. The genotypes UPU-8335 and IPU 99-115 were used as check genotypes for YMV infection. All the recommended agronomic practices were followed to raise a good crop. The screening of genotypes was performed in natural field conditions. The visual assessment by a single observation of a group of plants was performed after 45 days of sowing.

3. RESULTS AND DISCUSSION

Based upon the severity of infection by YMV, the black gram *(Vignamungo .L)* genotypes were divided into five categories, highly resistant (No plants showing any symptom for YMV infection), resistant (≤10% plants exhibiting symptom for YMV infection), moderately resistant (11-20% plants exhibiting symptom for YMV infection), susceptible (21-50% plants exhibiting symptom for YMV infection) and highly susceptible (≥ 51% plants exhibiting symptom for YMV infection). The YMV resistant property of thirty two different genotypes of black gram *(Vignamungo .L)* is presented in Table, 1. The four genotypes of black gram *(Vignamungo .L)* viz., UPU 8335, IPU 99-205, PGRU-95004, and SPS-43 was identified as highly YMV resistant, whereas the four genotypes viz., IPU *2K-99-226,* IPU 99-3, *IPU-99-235* and *NDU-94-10* was observed as highly susceptible genotypes for Yellow Mosaic Virus (YMV) infection.

Table 1: Grouping of thirty two black gram *(Vignamungo L.)* genotypes based on Yellow Mosaic Virus (YMV) resistance property.

Sl. No.	Genotype	Category
1	UPU 8335	Highly resistant
2	IPU 99-205	Highly resistant
3	PGRU 95004	Highly resistant
4	SPS 43	Highly resistant
5	PGRU 9598	Resistant
6	NG 2119	Resistant
7	GE 154	Resistant
8	KU 300 (Shekhar-2)	Resistant
9	IPU 99-243	Resistant
10	IPU 99-199	Resistant
11	IPU 99-115	Resistant
12	SPS 7	Resistant
13	IPU 557	Moderately resistant
14	IPU 25	Moderately resistant
15	UH 82-14	Moderately resistant
16	PDU 2	Moderately resistant
17	UH 82-51	Moderately resistant
18	IPU 2K-99-224	Moderately resistant
19	SPS 38	Moderately resistant
20	LBG-623	Moderately resistant
21	IPU 99-150	Moderately resistant
22	PU 31	Moderately resistant
23	T 9	Susceptible
24	IPU 99-204	Susceptible
25	2K-7	Susceptible
26	Sol No-2	Susceptible
27	IPU 99-24	Susceptible
28	IPU 99-176	Susceptible
29	IPU 2K-99-226	Highly Susceptible
30	IPU 99-235	Highly Susceptible
31	IPU 99-3	Highly Susceptible
32	NDU 94-10	Highly Susceptible

Several efforts have been made in the last decade to understand how plants defend themselves against viruses [11]and elucidate the mechanisms by which these pathogens invade cells to subvert sub cellular matching for their own survival [12]. Nevertheless, viruses continue to be a major global threat in in the production of crop plants and their control remains a challenge of this century [13, 14]. Results of this study indicate the extent of wide genetic variations present among the black gram *(VignamungoL.)* genotypes for resistance level of YMV infection and their potential for improvement against YMV infection. The present study is helpful to select the YMV resistant genotypes for cultivation in farmer's field of north India. Understanding about the resistance level of different genotypes will also be helpful for development of highly YMV resistant varieties through future crop improvement program.

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