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Huirem Chandrajini Devi
Ph.D. (Agri.) Scholar,
Department of Plant Pathology,
Central Agricultural University,
Manipur, India

Dr. V Prasanna Kumari
Assistant Professor,
Department of Plant Pathology,
Acharya N.G. Ranga University
Hyderabad (Agricultural College,
Bapatla), Andhra Pradesh, India

Dr. Ph. Sobita Devi
Professor, Department of Plant
Pathology, Central Agricultural
University, Manipur, Manipur,
India

W Tampakleima Chanu
Ph.D. (Agri.) Scholar,
Department of Plant Pathology,
Central Agricultural University,
Manipur, Manipur, India

K Sarda Devi
Ph.D. (Agri.) Scholar,
Department of Plant Pathology,
Central Agricultural University,
Manipur, Manipur, India

Corresponding Author:
Huirem Chandrajini Devi
Ph.D. (Agri.) Scholar,
Department of Plant Pathology,
Central Agricultural University,
Manipur, Manipur, India

Response of different blackgram [*Vigna mungo* (L.) Hepper] genotypes against mungbean yellow mosaic virus and whitefly (*Bemisia tabaci* Genn.)

Huirem Chandrajini Devi, Dr. V Prasanna Kumari, Dr. Ph. Sobita Devi, W Tampakleima Chanu and K Sarda Devi

Abstract
Mungbean Yellow Mosaic Virus (MYMV), a whitefly transmitted Gemini virus, is one of the severe constraints that afflict blackgram crop in India and other countries. *Mungbean* yellow mosaic disease incidence ranged between 3.73 (DKU-87) and 96.15% (LBG-623). Based on disease reactions, nine genotypes *i.e.*, DKU-87, DKU-102, KPU-21, UG-281, KPU-6, KPU-29, KPU 12-1731, KPU 12-133 and PU 12-11 were categorized as resistant (0.85 to 1.50 score), while LBG-752 as moderately resistant (2.75) and genotypes OBG-32, KPU-1, KPU-22 and KPU-9 as susceptible whereas Co5 and LBG-623 as highly susceptible. Whitefly infestation was first noticed by 14 day after sowing and its population gradually increased till 70 DAS, which declined later with slight fluctuations in all genotypes. The highest whitefly population per plant was recorded in LBG-623 (7.55) which was followed by Co5 (7.34). A positive correlation (0.973) was observed between whitefly population and MYMV severity.

Keywords: Blackgram, mungbean yellow mosaic virus and whitefly

Introduction
Blackgram [*Vigna mungo* (L.) Hepper] is an excellent source of easily digestible protein with low flatulence. In addition to 26% protein, 57% carbohydrate and 1.2% fat, it is a good source of phosphoric acid, calcium, thiamine (B1), riboflavin (B2) and niacin (B3) (Singh and Awasthi, 2004) [20]. Blackgram suffers from biotic stress due to fungal, bacterial and viral diseases resulting in heavy yield losses (Nene, 1972; Varma and Malathi, 2003) [13, 22]. Among viral diseases, yellow mosaic disease caused by *Mungbean Yellow Mosaic Virus* (*MYMV*) is a serious constraint in blackgram cultivation that could result in 100% yield loss (Nene, 1972 and Biswas *et al*., 2009) [13, 4].

Due to significant positive correlation between yellow mosaic disease incidence and whitefly population (Kumar *et al.*, 2004) [11], management of *MYMV* through chemical control of vector was attempted by several workers (Ganapathy and Karuppiah, 2004; Konar and Paul, 2005; Salam *et al*., 2009) [5, 9, 18]. However, chemical control is always uneconomical compare to development of resistant varieties for reducing *MYMV* incidence and severity (Nariani, 1960; Singh and Awasthi, 2004) [12, 20].

Considering the potentiality of the spread of yellow mosaic disease of blackgram and its seasonal recurrence, it is essential to screen genotypes through forced feeding methods, which can ensure 100% infection rate, and a standardized inoculum pressure. In the present study, 16 genotypes of blackgram screened under natural conditions in order to identify the resistant sources to be used further in breeding programs.

Material and Methods
The experiment was conducted during *kharif* 2014-15 at the Regional Agricultural Research Station (RARS), Lam, Guntur using 16 blackgram genotypes namely KPU-1, KPU-9, KPU-6, KPU-29, KPU-21, KPU-22, KPU 12-133, KPU 12-1731, OBG-32, LBG-752, DKU-87, DKU-102, UG-281, PU 12-11, Co5 and LBG-623 (susceptible check) obtained from RARS, Lam. A Randomised Block Design with two replications in a microplot of 5 x 4 m with spacing of 30 x 10 cm was followed and percent disease incidence was recorded weekly using the formula

$$\text{Per cent MYMV incidence} = \frac{\text{Number of plants infected in a micro plot}}{\text{Total number of plants in a micro plot}} \text{x } 100$$

By using 0-9 modified scale of All India Coordinated Research Project on MULLaRP (Alice and Nadarajan, 2007) [1], *MYMV* severity was recorded weekly

Table 1: Modified MULLaRP scale (0-9)

Scale	Description
0	No visible symptoms on leaves
1	Very minute yellow specks on leaves
2	Small yellow specks with restricted spread covering 0.1-5% leaf area of plant
3	Yellow mottling of leaves covering 5.1-10% leaf area of plant
4	Yellow mottling of leaves covering 10.1-15% leaf area of plant
5	Yellow mottling and discolouration of 15.1-30% leaf area of plant
6	Yellow discolouration of 30.1 to 50% leaf area of plant
7	Pronounced yellow mottling and discolouration of leaves and pods, reduction in leaf size and stunting of plants covering 50.1-75% foliage of plant
8	Severe yellow discolouration of leaves covering 75.1 to 90% of foliage, stunting of plants and reduction in pod size
9	Severe yellow discolouration of leaves covering above 90.1% of foliage of plant, stunting of plants and no pod formation

The per cent disease index (PDI) was computed from above (0-9) scale by using the formula of Wheeler (1969) [23].

$$\text{PDI} = \frac{\text{Sum of all the numerical ratings}}{\text{Number of observations} \times \text{Maximum disease rating}} \text{x } 100$$

The genotypes were assigned different disease reactions based on the categorization given by Gantait and Kantidas (2009) [6] (Table-2).

Table 2: Categorization of blackgram genotypes based on MYMV disease severity

PDI	Rating	Reaction
0.1-5	1.0 to 2.0	Resistant (R)
5.1-15	2.1 to 4	Moderately resistant (MR)
15.1-30	4.1 to 5	Moderately susceptible (MS)
30.1-75	5.1 to 7	Susceptible (S)
75.1-100	7.1 to 9	Highly susceptible (HS)

Population of whitefly was enumerated by using the magnifying lens (Salam *et al*., 2009) [18] during the early hour of the day. The data was recorded from the top three trifoliate leaves of plant of five randomly selected plants of each genotype at weekly interval.

Results and Discussion

Yellow mosaic virus disease incidence ranged from 3.73 (DKU-87) to 96.15% (LBG-623) in the genotypes screened for *MYMV* incidence after 91 DAS. Significantly low *MYMV* incidence was recorded in nine genotypes *viz.*, DKU-87 (3.73%), DKU-102 (4.19%), KPU-29 (5.57%), KPU-21 (5.79%), KPU-6 (5.97%), PU 12-11 (6.63%), KPU 12-133 (6.78%), KPU 12-1731 (6.97%) and UG-218 (7.01%) while 14.47% incidence was observed in LBG-752 genotype. Significantly high *MYMV* incidence was recorded in genotypes Co5 (93.53%) and LBG-623 (96.15%) and in other four genotypes *viz*., OBG-32, KPU-1, KPU-22 and KPU-9 disease incidence was 67.38, 64.37, 56.68 and 49.21% respectively (Table 3). Yellow mosaic disease incidence in genotype Co5 was reported as 68% (Khattak *et al*., 2004) [8] and 100% (Sahoo and Sahu, 1991) [17]. Obaiah *et al*. (2013) [14] and Prasanthi *et al*. (2013) [16] reported LBG-752 as moderately resistant and LBG-623 as highly susceptible genotypes to *MYMV* infection. Sowmini and Palaniappan (2014) [21] reported Co5 as *MYMV* susceptible genotype.

Based on 0-9 score and their corresponding disease reactions, nine genotypes *i.e.*, DKU-87, DKU-102, KPU-21, UG-281, KPU-6, KPU-29, KPU 12-1731, KPU 12-133, and PU 12-11 were categorized as resistant and disease score ranged from 0.85 to 1.50. In LBG-752 disease score of 2.75 was recorded and was categorized as moderately resistant. The genotypes KPU-1, KPU-22, KPU-9 and OBG-32 were recorded as susceptible whereas Co5 and LBG-623 were regarded as highly susceptible with more than 7.0 disease score (Table 4.1).

Gupta (2003) [7] evaluated 38 *urdbean* genotypes and reported two genotypes as immune to *MYMV*, 11 genotypes as resistant and nine genotypes as moderately resistant. Obaiah *et al*. (2013) [14] evaluated 56 blackgram genotypes for *YMV* infection and reported 22 genotypes as resistant, 11 as moderately resistant and the remaining 23 as susceptible. Kumar *et al*. (2014) [10] recorded genotypes of blackgram *i.e.*, Azad U-2, KU 96-3, LBG-645, IPU 2-43 and NDU 5-7 as *MYMV* resistant. Genotype evaluation was documented by several workers earlier (Asthana *et al*., 1998; Basandrai *et al*., 1999; Pathak and Jhamaria, 2004) [2, 3, 15]. It was observed that genotypes with *MYMV* infection at early age of the crop were found to be susceptible with high PDI than resistant genotypes and the present results are in accordance with the earlier reports (Shad *et al*., 2006; Prasanthi *et al*., 2013) [19, 16].

Table 3: Disease incidence of *mungbean* yellow mosaic disease and final disease score in blackgram genotypes during *kharif* 2014-15

S. No.	Genotypes	Disease incidence	Final Disease Score	Disease reaction
1	KPU-1	64.37	5.65	S
2	KPU-6	5.97	1.13	R
3	KPU-29	5.57	1.30	R
4	KPU-9	49.21	5.90	S
5	KPU-21	5.79	1.05	R
6	KPU-22	56.68	5.70	S
7	KPU 12-133	6.78	0.90	R
8	KPU 12-1731	6.97	1.30	R
9	OBG-32	67.38	6.65	S
10	LBG-752	14.47	2.75	MR
11	DKU-87	3.73	0.85	R
12	DKU-102	4.19	0.95	R
13	UG-218	7.01	1.00	R
14	PU 12-11	6.63	1.50	R
15	Co5	93.53	7.60	HS
16	LBG-623	96.15	7.85	HS
SEm±		1.58	0.19	
CD (P ≤ 0.05%)		4.76	0.58	
CV%		10.01	11.91	

Whitefly Population in blackgram genotypes

Whitefly population was first recorded at 14 DAS and gradually increased up to 70 DAS, later declined with slight fluctuations in all the genotypes *i.e.*, between 1.68 (KPU 12-1731) and 7.55 (LBG-623) per plant. Number of whiteflies per plant was 7.55 in LBG-623 and 7.34 in Co5. The lowest whitefly population was recorded in KPU 12-1731 (1.68) which was on a par with DKU-87 (1.70), KPU 12-133 (1.83), DKU-102 (1.87) and KPU-29 (1.95) (Table 4 and Fig.1). A

positive correlation (0.973) was observed between whitefly population and *MYMV* severity.

The present study was in agreement with the reports of Sahoo and Sahu (1991) [17] who reported the highest whitefly population in susceptible blackgram genotype Co5 with 90% *MYMV* incidence. Similar reports on whitefly population in *mungbean* were documented (Khattak *et al*., 2004; Kumar *et al*., 2006; Lakshminarayan *et al*., 2007; Mishra *et al*., 2012) [8]. Viruliferous *B. tabaci* play significant role in transmitting yellow mosaic disease (Nene, 1972) [13]. Some genotypes are least preferred by whitefly due to heavy pubescence (Inbar and Gerling, 2008; Taggar and Gill, 2012) or antioxidant compounds particularly phenols in the leaves that act as the physical and chemical defences against the microbes, insects and herbivores (Metraux and Raskin, 1993; Taggar *et al*., 2014).

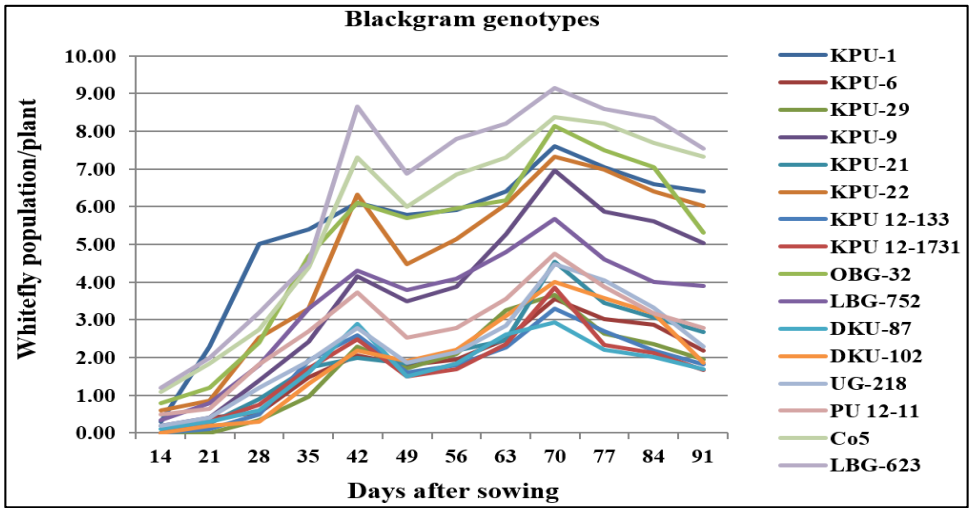

Fig 1: Whitefly population/plant in blackgram genotypes at weekly interval during *kharif* 2014-15

Table 4: Mean whitefly population/plant at weekly interval in blackgram genotypes during *kharif* 2014-15

		Whitefly population/plant											
S. No.	**Genotypes**	**14 DAS**	**21 DAS**	**28 DAS**	**35 DAS**	**42 DAS**	**49 DAS**	**56 DAS**	**63 DAS**	**70 DAS**	**77 DAS**	**84 DAS**	**91 DAS**
1	KPU-1	0.30 *(0.88)	2.30 (1.65)	5.01 (2.34)	5.40 (2.42)	6.10 (2.56)	5.78 (2.50)	5.92 (2.94)	6.40 (2.63)	7.62 (2.85)	7.04 (2.74)	6.60 (2.64)	6.40 (2.62)
2	KPU-6	0.00 (0.71)	0.40 (0.95)	0.53 (1.00)	1.48 (1.41)	2.07 (1.58)	1.80 (1.51)	1.95 (2.14)	2.48 (1.72)	3.55 (2.01)	3.02 (1.86)	2.87 (1.83)	2.19 (1.64)
3	KPU-29	0.00 (0.71)	0.00 (0.71)	0.35 (0.90)	0.96 (1.21)	2.30 (1.67)	1.71 (1.47)	2.10 (2.13)	3.26 (1.94)	3.67 (2.04)	2.64 (1.75)	2.37 (1.65)	1.95 (1.54)
4	KPU-9	0.20 (0.83)	0.40 (0.92)	1.40 (1.36)	2.42 (1.70)	4.16 (2.12)	3.50 (2.00)	3.89 (2.54)	5.28 (2.40)	6.97 (2.73)	5.87 (2.52)	5.62 (2.46)	5.04 (2.35)
5	KPU-21	0.00 (0.71)	0.25 (0.86)	0.90 (1.18)	1.74 (1.50)	2.00 (1.58)	1.85 (1.53)	2.19 (2.20)	2.47 (1.72)	4.54 (2.24)	3.46 (1.97)	3.06 (1.87)	2.68 (1.78)
6	KPU-22	0.60 (1.04)	0.85 (1.16)	2.53 (1.74)	3.30 (1.94)	6.32 (2.16)	4.47 (2.23)	5.14 (2.80)	6.07 (2.51)	7.33 (2.76)	6.98 (2.72)	6.41 (2.61)	6.02 (2.55)
7	KPU 12-133	0.00 (0.71)	0.10 (0.77)	0.50 (1.00)	1.94 (1.56)	2.60 (1.76)	1.61 (1.44)	1.80 (2.09)	2.26 (1.66)	3.30 (1.95)	2.69 (1.79)	2.18 (1.62)	1.83 (1.51)
8	KPU 12-1731	0.00 (0.71)	0.30 (0.88)	0.75 (1.12)	1.71 (1.48)	2.49 (1.73)	1.50 (1.41)	1.70 (2.02)	2.35 (1.69)	3.86 (2.09)	2.34 (1.68)	2.11 (1.61)	1.68 (1.47)
9	OBG-32	0.80 (1.14)	1.20 (1.30)	2.40 (1.70)	4.70 (2.28)	6.10 (2.57)	5.70 (2.49)	5.96 (2.94)	6.17 (2.56)	8.13 (2.94)	7.50 (2.82)	7.06 (2.74)	5.31 (2.41)
10	LBG-752	0.35 (0.92)	0.80 (1.13)	1.80 (1.52)	3.30 (1.95)	4.30 (2.19)	3.80 (2.07)	4.09 (2.57)	4.80 (2.30)	5.68 (2.49)	4.60 (2.26)	4.02 (2.09)	3.89 (2.09)
11	DKU-87	0.10 (0.77)	0.30 (0.89)	0.60 (1.04)	1.60 (1.45)	2.89 (1.84)	1.50 (1.41)	1.85 (2.07)	2.61 (1.76)	2.94 (1.85)	2.21 (1.64)	2.01 (1.58)	1.70 (1.46)
12	DKU-102	0.00 (0.71)	0.20 (0.83)	0.30 (0.89)	1.30 (1.34)	2.19 (1.64)	1.92 (1.55)	2.20 (2.14)	3.11 (1.90)	4.01 (2.11)	3.58 (2.02)	3.18 (1.89)	1.87 (1.54)
13	UG-218	0.20 (0.83)	0.40 (0.92)	1.20 (1.27)	1.91 (1.52)	2.78 (1.81)	1.87 (1.54)	2.15 (2.12)	2.86 (1.81)	4.49 (2.23)	4.04 (2.12)	3.32 (1.95)	2.30 (1.67)
14	PU 12-11	0.50 (1.00)	0.65 (1.07)	1.83 (1.52)	2.70 (1.77)	3.74 (2.06)	2.54 (1.74)	2.78 (2.29)	3.55 (2.01)	4.75 (2.29)	3.88 (2.09)	3.17 (1.91)	2.79 (1.81)
15	Co5	1.10 (1.26)	1.85 (1.53)	2.74 (1.80)	4.40 (2.19)	7.30 (2.79)	6.00 (2.55)	6.87 (3.09)	7.30 (2.79)	8.39 (2.94)	8.20 (2.94)	7.70 (2.85)	7.34 (2.80)
16	LBG-623	1.20 (1.30)	2.00 (1.58)	3.20 (1.92)	4.53 (2.24)	8.66 (3.00)	6.88 (2.72)	7.80 (3.24)	8.22 (2.95)	9.16 (3.07)	8.60 (2.98)	8.37 (2.98)	7.55 (2.84)
SEm ±		0.05	0.09	0.09	0.10	0.11	0.04	0.13	0.13	0.14	0.10	0.13	0.11
CD ($P \leq 0.05\%$)		0.16	0.28	0.28	0.29	0.35	0.13	0.39	0.39	0.42	0.30	0.39	0.32
CV%		12.20	17.25	13.45	11.05	10.98	20.85	10.56	12.19	11.56	8.83	12.21	10.70

Values in parentheses are square root transformed values

*Mean of two replications

Conclusions

Mungbean yellow mosaic disease incidence ranged between 3.73 (DKU-87) and 96.15% (LBG-623) and disease severity (PDI) ranged from 5.0 (DKU-87) to 79.98 (LBG-623). Area under Disease Progress Curve during the crop period ranged between 105.09 (DKU-87) and 2130.64 (LBG-623). Based on disease reactions, nine genotypes *i.e.*, DKU-87, DKU-102, KPU-21, UG-281, KPU-6, KPU-29, KPU 12-1731, KPU 12-133 and PU 12-11 were categorized as resistant (0.85 to 1.50 score), while LBG-752 as moderately resistant (2.75) and genotypes OBG-32, KPU-1, KPU-22 and KPU-9 as susceptible whereas Co5 and LBG-623 as highly susceptible.

Whitefly infestation was first noticed by 14 DAS and its population gradually increased till 70 DAS, which declined later with slight fluctuations in all genotypes. The highest whitefly population per plant was recorded in LBG-623 (7.55) which was followed by Co5 (7.34). Variation in whitefly population among the different genotypes may be due to leaf morphological characters and presence of antioxidant compound that acts as chemical defenses which could limit the infestation of whitefly on certain blackgram plants.

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