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Molecular and pathological identification of maize genotypes having *Wsm* gene governing resistance against MDMV and MCDV

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Abstract

Maize is seriously affected by different viruses like *Maize Dwarf Mosaic Virus* (MDMV) and *Maize Chlorotic Dwarf Virus* (MCDV) throughout the world. In Bangladesh, no genotype has been identified yet as a source of resistant gene against MDMV and MCDV. The study was carried out with the objective to screen nine maize genotypes carrying *Wsm* gene using three sets of Single Sequence Repeat (SSR) marker. Maize plants were inoculated with viruses. Symptoms were scored at 7, 10 and 14 dpi (days post inoculation) to calculate infection percentage and Area Under Disease Progress Curve (AUDPC). The molecular result indicated that BHM-7, BHM-5, V-92, Uttaran and Duranta carried *Wsm* gene, but according to pathological test, functional resistance was observed for only BHM-7, V-92 and Uttaran on the basis of infection percentage and AUDPC score. BHM-7 (BARI Hybrid Maize 7) was noticed as the best one for showing resistance against MDMV and carrying *Wsm* gene. No genotype was found to govern resistance against MCDV.

Introduction

Maize (*Zea mays*) is an important crop throughout the world including Bangladesh which occupies a large portion of world economy (Gong *et al.*, 2015; Ranum *et al.*, 2014; Ahmed, 2013; Roper, 2013; Moniruzzaman *et al.*, 2009; Paliwal *et al.*, 2000; Dowswell *et al.*, 1996). But each year yield decreases due to occurrence of different diseases. Maize dwarf mosaic disease is one of them which is caused by a series of viruses including *Maize dwarf mosaic virus* (MDMV), *Maize chlorotic dwarf virus* (MCDV), *Sugarcane mosaic virus* (SCMV), *Johnsongrass mosaic virus* (JGMV), *Sorghum mosaic virus* (SrMV), *Zea mosaic virus* (ZeMV) and *Pennisetum mosaic virus* (PenMV) (Zambrano *et al.*, 2014, Stewart *et al.*, 2012; Stewart *et al.*, 2013). All of them except MCDV are classified as the "sugarcane mosaic subgroup" of the virus genus *Potyvirus*, under the family *Potyviridae* (Balarabe *et al.*, 2014, Haider *et al.*, 2011, Mohammadi and Hajieghrari 2009, Shukla *et al.*, 1992). The genus *Potyvirus* is one of the largest virus genera which currently includes 111 confirmed species; a further 86 tentative species have been noted by the International Committee on Taxonomy of Viruses (ICTV) (Zheng *et al.*, 2010; Zheng *et al.*, 2008; Fauquet *et al.*, 2005). Potyviruses are economically important groups of plant viruses that pose a dangerous threat to crops around the world (Dujovny *et al.*, 2000; Moriones and Luis-Arteaga, 2000; Inoue-Nagata *et al.*, 2002; Larsen *et al.*, 2003).

MDMV is one of the most important plant pathogenic viruses for corn that is distributed throughout the southern USA (Pataky *et al.*, 1990), Europe (Tosic *et al.*, 1977), Asia (Klein *et al.*, 1973) and Australia (Penrose, 1974). The virus is transmitted mechanically by in a non-persistent manner by a broad range of aphids (Ford *et al.*, 2004). The diagnostic symptoms of MDMV are white mosaic, chlorosis and streak on young leaves which result reduced plant biomass (Lapierre and Signoret, 2004). *Maize chlorotic dwarf virus* (MCDV) is another destructive virus belongs to the genus *Waikavirus* of the family *Sequiviridae* which is an economically devastating maize disease throughout the world especially in the Southeastern United States. It is considered to be the second major corn virus disease in the USA (Knoke and Louie, 1981). The virus is transmitted by leafhopper in a semi-persistent manner (Reddick *et al.*, 1997; Gingery *et al.*, 1981).). Symptoms appeared on maize due to MCDV are chlorotic spots, stunting, severe stunting, leaf discoloration (reddening and yellowing) and leaf-tearing (Bradfute *et al.*, 1972).

Generally, viral diseases are controlled by removal of virus reservoirs and vector but that may reduce biodiversity. Again, chemical control of vectors is not possible due to non-persistent mode of virus transmission (Adams *et al.*, 2005; Ingvardsen *et al.*, 2010). So, cultivation of resistant maize varieties is the most effective way to control virus infections. A number of maize inbred lines and landraces have been identified showing resistance to MDMV, SCMV, JGMV and SrMV (Kuntze *et al.*, 1995, Redinbaugh and Pratt, 2008). The inbred line Pa405 is one of them which is resistant due to presence of three dominant genes referred as *Wsm1*, *Wsm2* and *Wsm3* that confer resistance to another member of the family *Potyviridae* and genus *Tritimovirus*, *Wheat streak mosaic virus*

(WSMV) (McMullen *et al.*, 1994; Mikel *et al.*, 1984, Redinbaugh and Pratt, 2008, Stewart *et al.*, 2013a). *Wsm1* is located on the short arm of chromosome 6, *Wsm2* near the centromere on chromosome 3 and *Wsm3* on the long arm of chromosome 10 (McMullen *et al.*, 1994; Redinbaugh and Pratt, 2008; Stewart *et al.*, 2012). *Wsm* loci govern resistance to MDMV and SCMV (Jones *et al.*, 2011) as well as JGMV and SrMV (Stewart *et al.*, 2013b) when introgressed into the susceptible maize inbred line Oh28.

In Bangladesh, no line or landrace has been identified yet as a resistant one. So, screening of maize genotypes as a source of virus resistance might be a potential need. This research program has been conducted to screen maize genotypes carrying *Wsm* gene and resistant gene against MDMV and MCDV using SSR marker. Additionally, virus was introduced into all maize genotypes artificially from which infection percentage and area under disease progress curve (AUDPC) were calculated. Both results were compared to identify best genotype carrying resistant gene and giving functional resistance.

Materials and Methods

Experimental site and plant materials

Experiment was conducted in the net house, Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU) and Biotechnology Laboratory of Biotechnology Division, Bangladesh Institute of Nuclear Agriculture (BINA). Nine maize genotypes (Uttaran, Duranta, BHM-5, BHM-7, BHM-9, V-92, H-981, pop corn and sweet corn) taken from Bangladesh Agricultural Research Institute (BARI) were selected as experimental materials.

Virus inoculation and scoring

Virus stocks were incorporated into seeds (developed from BC_1-F_1 progeny of a backcross between Pa405 and Oh28) through vascular puncture inoculation (VPI) method (Stewart *et al.*, 2013a). Seeds were received as a cordial gift from Stewart. Those seeds were planted and after growing, leaves with virus symptom were collected. The virus infected leaves were used to prepare inoculation sap which was artificially inoculated into experimental materials at 3-4 leaf stage by rubbing. Carborundum powder and buffer solution were added to the sap. Plants were inoculated at total of three times at two to three days intervals. Individual plants were scored as no symptoms (0), limited symptoms (1) and severe symptoms (2) at 7, 10 and 14 days post-inoculation (dpi) with day 0 being the first inoculation date.

Genomic DNA Isolation and Polymorphism Survey for Primer Selection

DNA was extracted from the young leaves from 25 days old seedlings of each genotype using the Cetyl Trimethyl Ammonium Bromide (CTAB) mini-prep (modified) method. The quality of the isolated DNA in the protocol was sufficient for PCR analysis. Three sets of primer (Table 1) were used for screening: umc1300 for detection of *Wsm* loci (Ingvardsen *et al.*, 2010), MDMVgen for detection of loci responsible against MDMV and MAHP35-MCDV-s for loci against MCDV (http://www.maizegbd.org). These markers were selected based on their potentiality for population discrimination which was determined by preliminary experiment with three sets of primers (data not shown).

Table 1. List of SSR primer used for screening maize lines carrying desired loci

Name of primer		Sequence	GC %	Melting temperature (Tmº)
umc1300	Forward	ACCACCAGGTGTCCTTCCTT	55	64.7
	Reverse	GTTGCAGCAGACGAAGAA	50	60.3
MDMVgen	Forward	CACCAATTAACCCTCACTAAAGGGAAA	40.7	68.1
	Reverse	TTTTTTGTCTCTCACCACGAAAC	39.1	64.1
MAHP35-MCDV-s	Forward	TGTTCCACGGAAGCGCCGA	63.1	74.6
	Reverse	CATTAAAACCGGACTGAGCGGTGGC	56	74.9

PCR amplification profile

PCR amplification reactions for each of the SSR markers were performed in a 10 µl reaction volume containing 2 µl genomic DNA, 1 µl of 10X buffer, 0.8 µl of $MgCl_2$, 2 µl 0f dNTPs, 0.5 µl of each forward and reverse primer, 0.2 µl of Taq polymerase and 3 µl of ddH_2O. PCR amplification was performed using a touchdown profile (Ingvardsen *et al.*, 2010) designed for the annealing temperature (T_a) of the primer pair: initial denaturation, followed by 12 cycles of 30 s at 94º C, 1 min at Ta+ 12 ºC and 1 min at 72 ºC with a reduction of the annealing temperature of 10C at each cycle, followed by 30 cycles of s at 94 ºC, 1 min at Ta and 1 min at 72 ºC, followed by a final extension.

Data Analysis

Scoring of virus symptoms had been used to calculate % infection and AUDPC (Area Under Disease Progress Curve). Percent infection is the mean for three independent replications of each line. AUDPC was calculated from means of disease ratings for each line in each replicate using trapezoid method from the time of first disease scoring. The trapezoid method is the most common way to calculate AUDPC. It is performed by using a formula devised by Campbell and Madden in 1990 or by plotting a graph of percentage of infection against time and summing the trapezoids between time intervals (http://www.ehow.com/how12033613calculate-audpc.btml). The genotype with 100% infection would posses 14 score in AUDPC.

Three types of primer evolved three different types of conclusion. The first primer, umc1300 was used to identify lines carrying *Wsm* loci. The lines responsible against MDMV and MCDV were screened using MDMVgen primer and MAHP35-MCDV-s primer, respectively. In all above cases only the presence and absence of band will be observed. Presence of band referred the genotype as resistant and absence of band indicated the genotype as susceptible.

Results

Responses of maize genotypes to viruses

In the experiment nine genotypes were inoculated with virus and scored for symptoms development at 7, 10 and 14 dpi (days post inoculation). The mean percentage infection and AUDPC for each line are shown in Table 2. A control was maintained for each genotype, but in Table 2 a representative one has been shown.

Table 2. Responses of different maize genotypes inoculated with virus

Sl. No.	Genotype Name	% Infection	AUDPC (Area Under Disease Progress Curve)
1	Pop corn	66.67	9.700
2	BHM-9	88.83	12.995
3	BHM-7	33.33	4.840
4	BHM-5	60.00	9.000
5	V-92	22.17	3.160
6	Uttaran	33.33	4.840
7	Duranta	50.00	7.335
8	H-981	66.67	9.600
9	Sweet corn	72.17	10.155
10	Control	11.00	1.815

The highest infection percentage (88.88%) was observed for BHM-9 having AUDPC value around 13 out of 14, followed by Sweet corn (72.17%) with 10.155 AUDPC value (Table 2). In BHM-9, severe curling of leaves and disease progress curve indicated high susceptibility to potyvirus (Fig.1: i.a and ii.a). Followed by Pop corn and H-981 both had same infection rate (66.67%) but value of AUDPC were slightly different (9.7 and 9.6 respectively) (Table 2). Pop corn and H-981 had common mosaic symptoms and mild curling (Figure not shown). BHM-5 had lower infection and symptom severity than BHM-9, BHM-7, Pop corn and Sweet Corn. Its recorded infection was 60% and AUDPC value was 9 (Table 2). Transparent long streak beside mid rib, mild curling and limited mosaic had been also scored for BHM-5 which gave a clear idea of disease progression (Figure and graph not shown). So, it might be moderately susceptible to virus. Duranta had almost similar type of symptoms of BHM-5 but disease severity was lower than that. A 50% infection was observed in 7.335 for AUDPC (Table 2). Though it was less severe, the disease progress curve showed gradual increase in disease symptom (Graph not shown). Observing infection percentage Duranta might be considered as moderately resistant to virus. The disease severity is almost similar for Uttaran and BHM-7. Both had same infection rate (33.33%) and same value for AUDPC (4.84) which indicated that their symptom severity was lower than other genotypes except V-92 (Table 2). Only light mosaic symptom was observed for BHM-7 which ultimately showed less disease severity (Fig1: i.b and ii.b).

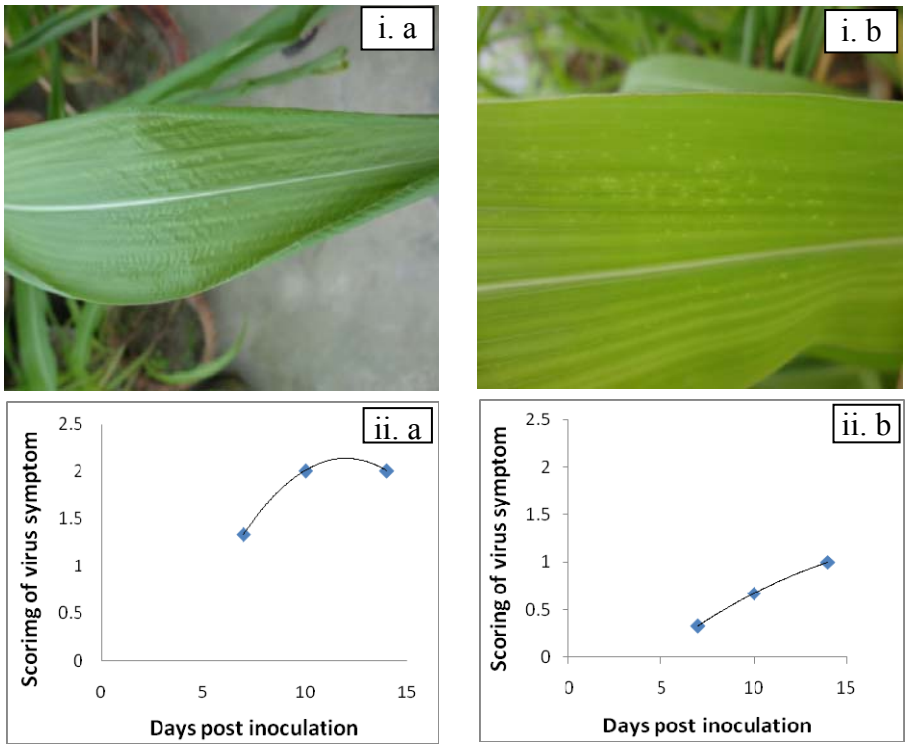

Fig. 1. Virus symptoms observed during scoring (i) and disease progress curve (ii) for genotype BHM-9 (a) and BHM-7 (b)

V-92 showed least disease severity than any other inoculated genotype. Only slight mosaic symptom was observed during scoring which results in lowest infection rate (22.17%) with the lowest AUDPC value of 3.16 (Table 2). Control (without virus inoculation) was maintained for each genotype, only one representative one is shown here. Theoretically, control (without virus inoculation) should not express any symptoms as there was no inoculation. But in this experiment, difference had been observed i.e. very slight curling was present (Figure not shown). This might be due to insect vector which transmitted virus from inoculated plant to control. As a result instead of 0% infection, 11% infection was observed with 1.815 value of AUDPC (Table 2).

Molecular detection using SSR primer

Three sets of primers were used to detect desired gene in the genotype. Detection of *Wsm* gene was carried out using umc1300 primer. Umc1300 is a universal primer which screened five genotypes out of nine showing clear bands at around 485bp which indicated presence of *Wsm* gene (Fig. 2). Genotype having *Wsm* gene were considered as resistant to potyviruses and genotype without *Wsm* loci were considered as susceptible. According to this BHM-7, BHM-5, Duranta, Uttaran and V-92 were found as resistant (Table 3).

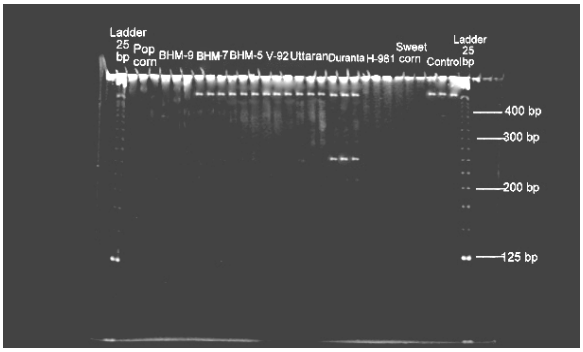

Fig. 2. Banding pattern of nine maize genotypes each with three replication using umc1300 primer confirming the presence of *Wsm* gene

Table 3. Resistance pattern of nine maize genotypes using three sets of markers

Genotypes	Banding pattern confirming *Wsm* gene against *Potyvirus* using umc1300 primer		Banding pattern against MDMV using MDMVgen primer		Banding pattern against MCDV using MAHP01-MCDV-s primer	
	Presence (P)	Absence (A)	Presence (P)	Absence (A)	Presence (P)	Absence (A)
Popcorn	-	A	-	A	-	A
BHM-9	-	A	-	A	-	A
BHM-7	P	-	P	-	-	A
BHM-5	P	-	-	A	-	A
V-92	P	-	-	A	-	A
Uttaran	P	-	-	A	-	A
Duranta	P	-	-	A	-	A
H-981	-	A	-	A	-	A
Sweet corn	-	A	-	A	-	A

MDMVgen primer was used for detection of genotype carrying loci responsible against MDMV which results in screening of a genotype showing clear band at around 125bp. As MDMV is a potyvirus, so the genotypes carrying *Wsm* gene should also govern resistance to this virus. But in molecular level, only one genotype (BHM-7) out of five genotype carrying *Wsm* gene showed the desired band (Fig. 3) i.e. showing resistance against MDMV. So, remaining eight genotypes were considered as susceptible and only BHM-7 was as resistant.

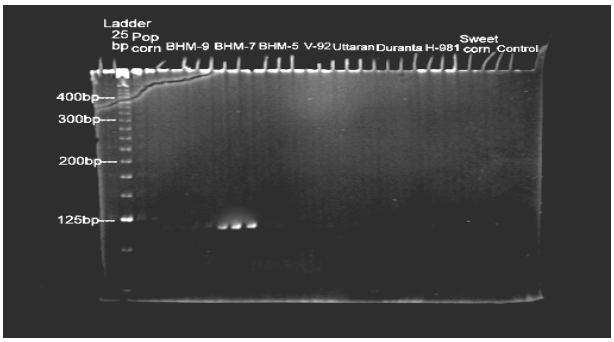

Fig. 3. Banding pattern of nine maize genotypes against MDMV using MDMVgen primer

No band was observed while MAHP01-MCDV-s primer was used to detect loci responsible against MCDV (Fig. 4). Many reasons could be responsible for failure in detection of gene responsible against MCDV. Further investigation is needed to find out cause or the way to detect the desired gene. From this finding, nine genotypes were considered as susceptible due to absence of band (Table 3).

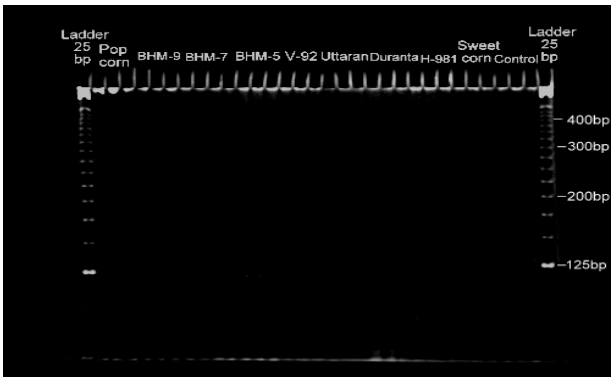

Fig. 4. Banding pattern of nine maize genotypes against MCDV using MAHP01-MCDV-s primer

Discussion

Performance of maize genotypes after virus inoculation

Scoring on viral symptoms was performed at 7, 10 and 14 days after inoculation of virus. Based on this value, infection (%) and AUDPC (Area Under Disease Progress Curve) were calculated (Table 2). High value of infection (%) and AUDPC indicated susceptibility and low value indicated resistance. So, V-92 might be considered as highly resistant; Uttaran and BHM-7 as moderately resistant; Pop corn, H-981, Duranta and BHM-5 as moderately susceptible; Sweet corn and BHM-9 as highly susceptible.

Stewart *et al.* (2013a) inoculated virus to a number of genotypes and calculated % infection and AUDPC at 0–14 dpi and 0–28 dpi. They found that the resistant genotype showed no infection (0%) and the susceptible one showed 100% infection. Molecular work was also performed to assure the scoring results. Jones *et al.* (2011) also got almost similar results while calculating % infection and AUDPC from scoring after inoculation. The susceptible genotype showed 100% and 80% infection in field condition and green house, respectively; whereas the resistant one showed 0% infection in both environments. *Wsm* confer resistance in dosage dependent manner.

In current study, the identified resistant genotypes were expected to carry *Wsm* gene, whether it might be *Wsm1* or *Wsm2* or *Wsm3*. But this assumption is made only based on virus symptom expressed in genotypes which were artificially inoculated with virus. To make sure about resistance or presence of *Wsm* gene, study was extended to molecular level.

Response of maize genotypes carrying *Wsm* gene

Wsm is a novel QTL (Quantitative Trait Loci) governing resistance to almost all members of the genus *Potyvirus*. The resistance was governed by either *Wsm1* or *Wsm2* or *Wsm3* or any interaction of these three loci. *Wsm1* provides resistance to both MDMV and SCMV but *Wsm2* and *Wsm3* cannot confer resistance by themselves to either MDMV or SCMV, but enhance resistance to both (Jones *et al.*, 2011). Again, in case of JGMV and SrMV, *Wsm1* confers resistance in a dose dependent manner and *Wsm2* and *Wsm3* confer more resistance in combination with *Wsm2* (Stewart *et al.*, 2013b). In general, *Wsm* loci are mainly responsible for resistance against different potyviruses following different mechanisms.

Here, only five genotypes among eight i.e. BHM-7, BHM-5, Uttaran, Duranta and V-92 were found to carry *Wsm* gene (Fig. 2). That's why these five genotypes having *Wsm* gene should govern resistance to potyviruses. But, infection percentage and AUDPC value indicated that, only BHM-7, V-92 and Uttaran were performed as resistant against potyvirus (Table 2) and BHM-5 and Duranta were not actively resistant although they possessed the desired gene. The reason behind this might be the non functional role of *Wsm1* rather *Wsm2* and/or *Wsm3* (Stewart *et al.*, 2013a). Pop corn, BHM-9, H-981 and Sweet corn were lack of that locus as a result they performed as susceptible genotype according to infection % and AUDPC value.

McMullen and Louie (1991) used to rub-inoculate greenhouse-grown maize plants with an isolate of WSMV and suggested the presence of multiple genes controlling resistance to WSMV using RFLP (Restriction fragment length polymorphism) marker which also demonstrated that one specific gene for resistance in Pa405 was also located on chromosome 6 of maize. Zhang *et al.* (2016) conducted an experiment on wheat to identify germplasm that might carry resistance gene different from Wsm2. Eight newly reported resistant lines were examined by allelic tests and five of them were further analyzed for the inheritance of WSMV resistance. A Wsm2 linked marker was also genotyped on populations developed which suggested that WSMV resistance in six lines among them was controlled by either Wsm2 or a gene very closely linked to Wsm2. Resistance in rest two lines was controlled by a gene different form, but linked to Wsm2.

In this experiment, specific loci (*Wsm1* or *Wsm2* or *Wsm3*) responsible for resistance could not be identified. But the clear band of 485bp for each replication of those five genotypes confirmed presence of desired *Wsm* gene. An additional band was observed for Duranta at around 250bp, so author cannot exclude the possibility of presence of another allele/gene near or very closely linked to *Wsm* allele/gene. Further investigation is needed to find out the identity of that allele.

Response of maize genotypes against MDMV and MCDV

The performances of genotypes specifically against MDMV were also studied using separate primer sets. Similar type of experiment was also conducted by Jones *et al.* (2007) where 115 maize inbred lines were evaluated for resistance to MDMV and SCMV. F_2 populations were developed through crossing between resistant and susceptible lines which were scored for infection and symptom type. RFLP and SSR analyses were carried out using marker and data suggested that *Mdm1* or closely linked genes on chromosome 6S are associated with MDMV resistance in most germplasm, but that other loci also may affect resistance. In this case only one genotype out of nine (BHM-7) responded clearly (Fig. 3). But as MDMV is a member of genus *Potyvirus*, five genotypes carrying *Wsm* gene should also respond against MDMV. Presence of antagonistic relation might be the reason for which BHM-5, V-92, Uttaran and Duranta did not carry specific band responsible against MDMV. BHM-7 performed as resistant against MDMV (Table 3) due to presence of synergistic relation.

In case of MCDV, no genotype showed band for resistance against this virus (Fig.4), that's why all genotypes were considered as susceptible (Table 3) to MCDV. Jones *et al*. (2004) conducted an experiment to identify quantitative trait loci (QTL) controlling resistance to MCDV. Progeny from a cross between resistant and susceptible inbred line subjected to virus inoculation and AUDPC scoring was done according to MCDV symptoms. In addition to that genotypic (using SSR marker) and phenotypic analyses were also done which identified two QTL on chromosome 3 and 10 governing equal resistance. One thing should be addressed in this study that MCDV is a member of the genus *Waikavirus* under the family *Sequiviridae* and *Wsm* gene is responsible for resistance against potyviruses. This may be one reason for non responding behavior of maize genotypes. Critical review is needed to get a clear idea on fact.

Conclusion

The experiment was conducted to screen locally available maize genotypes carrying *Wsm* gene using SSR marker and successfully identified five genotypes: BHM-7, BHM-5, V-92, Uttaran and Duranta among which BHM-7, V-92 and Uttaran showed functional resistance and BHM-5 and Duranta showed non-functional resistance considering % infection and AUDPC value. BHM-9, H-981, Sweet corn and Popcorn were considered as susceptible genotype due to not having *Wsm* gene and high % infection and AUDPC value. Only one genotype BHM-7 (BARI hybrid maize 7) also showed resistance specifically against MDMV as expected. No genotypes were found to govern resistance against MCDV. Further investigation is needed to find out the resistance mechanism of maize genotypes carrying *Wsm* gene.

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