Research Article

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Screening of watermelon genotypes for tolerance against mosaic disease in Western Rajasthan

S. K. Maheshwari, B. R. Choudhary, Hanuman Ram and D. Singh

ICAR-Central Institute for Arid Horticulture, Bikaner- 334 006 (Rajasthan)

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ABSTRACT

Mosaic disease, caused by the cucumber mosaic virus, is a significant threat to watermelon production in the arid and semi-arid regions of India. Screened 13 watermelon genotypes for tolerance to mosaic disease under open field conditions during the summer season of 2021 ICAR-Central Institute for Arid Horticulture, Bikaner. Among the 13 watermelon genotypes, none was found to be immune or highly resistant to mosaic disease. However, seven genotypes-AHW/BR-1, AHW/BR-13, AHW/BR-16, AHW/BR-37, AHW/BR-5, AHW/BR-7, and AHW/BR-11 were classified as moderately resistant, with disease indices (PDI) ranging from 12.36% to 21.38%.

Introduction

Watermelon [*Citrullus lanatus* (Thunb) Mansf.] is one of the most popular desert fruit grown all over world. In India, it is grown, mostly as riverbed side crop, in Uttar Pradesh, Rajasthan, Gujarat, Maharastra, Punjab and Haryana. China is the leading country in production of watermelon followed by Turkey, United States and Iran (Huh *et al.*, 2008). It is an excellent source of vitamin A and C and one cup of watermelon juice contain approximately 48.59 mg of vitamin C and 556.32 IU of vitamin A besides 48 calorie of energy. The fruit contains 92% water, 0.2% protein, 03% minerals and 7.0% carbohydrates (Thamburaj and Singh, 2000). It has sufficient variation in productivity and quality and is able to withstand damage from biotic and abiotic factors and caused great economic losses (Wehner *et al.*, 2001). The low productivity of watermelon is mainly due to many diseases incited by viruses, fungi, bacteria, nematodes and phytoplasma. A large number of viruses have been reported from time to time to infect this crop *viz.,* watermelon mosaic virus-1, watermelon mosaic virus-2, cucumber mosaic virus, watermelon chlorotic stunt virus, watermelon bud necrosis virus and watermelon curly mottle virus, which induced mild to severe mosaic, yellowing, chlorosis, necrosis, puckering, distortion, mottling, reduction of leaf size, development of vein clearing and stunting of the plants.

Systemic symptoms consist of downward leaf curling or rolling and mosaic. Severely infected plants did not bear flowers and could not produce fruits. In a very few cases, if flowers appeared, very small sized distorted fruits were produced. Mosaic disease caused by cucumber mosaic virus has become potential threat to the cultivation of watermelon. Cucumber mosaic virus (CMV) is the most destructive and economically important plant virus which drastically affects the crop quality and yield of the cucumber plants (Scholthof *et al.*, 2011). The first mosaic disease in cucurbits was caused by cucumber mosaic virus (Doolittle, 1916). Cucumber mosaic virus (CMV) has wider host range of 1200 different plant species and transmitted by 60 different species of aphids (Lecoq and Desbiez, 2012). Field screening is one of

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Corresponding author
Email: maheshwariskciah@gmail.com (Dr. S.K. Maheshwari)

the best method of integrated disease management against this disease. The cheapest and economical control of this disease can be achieved by resistant genetic stock. Keeping in view, this important component of integrated disease management, efforts were made to screen watermelon genotypes against mosaic disease and to identify tolerant genotypes in Western Rajasthan.

Material and Methods

Thirteen watermelon genotypes *viz*., AHW/BR-1, AHW/BR-5, AHW/BR-7, AHW/BR-11, AHW/BR-13, AHW/BR-14, AHW/BR-16, AHW/BR-17, AHW/BR-25, AHW/BR-28, AHW/BR-30, AHW/BR-31 and AHW/BR-37 were tested against mosaic disease at Vegetable Block of ICAR-Central Institute for Arid Horticulture, Bikaner with normal cultivation practices under field conditions. Seeds of 13 genotypes were sown in Randomized Block Design with a spacing of 50 cm x 100 cm in three replications during summer season of 2021. No plant protection measures were sprayed in the present study. Susceptible genotype 'AHW/BR-14' was sown after each five rows of the test genotypes as check. It was also grown around the border of the field to serve as infector rows. Data on disease severity of mosaic symptoms were recorded during growth period of the crop. The reactions for tolerance due to mosaic disease in watermelon were categorized by using 0-4 disease rating scale (Singh *et al*., 2007): immune (0) = 0% symptoms, resistant (1) = 0.1 to 10.0% leaf area infected, moderately resistant (2) = 10.1 to 25.0% leaf area infected, susceptible (3) = 25.1 to 50.0% and highly susceptible (4) = > 50.0% leaf area infected. The percent disease index (PDI) was calculated a formula suggested by McKinney, 1923.

Results and Discussion

Data presented in Table 1 indicated that variation in percent disease index (PDI) of mosaic disease was found in all the genotypes of watermelon crop. Among 13 genotypes of watermelon, range of average percent disease index (PDI) of mosaic disease caused by cucumber mosaic virus was 12.36 to 30.24%. Minimum disease index (12.36%) was recorded in genotype AHW/BR-5, followed by AHW/BR-37 (14.29% disease index) which were not statistically at par with each other. Maximum disease incidence (30.24% PDI) was recorded in genotype 'AHW/BR-14', followed by AHW/BR-30 (28.72%) which were also not statistically at par with each other.

The results presented in Table 2 reveal that out of 13 watermelon genotypes, none was found immune and tolerant against mosaic disease. Seven genotypes (AHMM/BR-5, AHMM/BR-37, AHMM/BR-7, AHMM/BR-1, AHMM/BR-13, AHMM/BR-11 and AHMM/BR-16) were categorized as moderately resistant and 06 genotypes *viz*., AHW/BR-31, AHW/BR-28, AHW/BR-17, AHW/BR-25, AHW/BR-30 and AHW/BR-14 were found as susceptible. Cucumber mosaic virus (CMV) poses a significant threat to various cucurbits, including watermelon and cucumber, causing substantial yield losses. Identifying and utilizing host resistance is widely regarded as the most effective strategy for managing this virus and mitigating its impact on crop production. In a similar study by Sugiyama *et al.* (2006) screened 152 melon accessions for resistance to Cucumber green mottle mosaic virus (CGMMV) and identified only *Chang Bougi* (*Cucumis melo var. makuwa*) as resistant. In contrast, Sharma *et al.* (2011) reported that none of the 20 watermelon varieties tested were resistant or immune to natural viral infections. While only two varieties *i.e.* Arka Jyoti and MHW-6 were found moderately resistant against viruses and 05 varieties viz., Nath-102, Nath-202, Special Number-1, NS-246 and NS-295 were rated as moderately susceptible. Crespo *et al.* (2018) evaluated germplasm of *C. sativus, C. anguria* as well as *C. metuliferus* using CGMMV. Only two *C. sativus* accessions showed mild symptoms while rest had severe infections. Guner *et al*., (2019) found resistant germplasm *viz*., PI 595203, PI 386016, PI 386024, PI 386026, PI 244018, PI 244019, PI 485583, PI 494528, and PI 494529 against Zucchini yellow mosaic virus in the watermelon.

Table 1. Screening of watermelon genotypes for tolerance against mosaic disease

S. No.	Name of genotypes	PDI	Disease reaction
1	AHW/BR-1	17.82 (24.42)*	Moderately Resistant
2	AHW/BR-5	12.36 (20.54)	Moderately Resistant
3	AHW/BR-7	16.67 (24.02)	Moderately Resistant
4	AHW/BR-11	20.53 (26.83)	Moderately Resistant
5	AHW/BR-13	20.34 (26.72)	Moderately Resistant
6	AHW/BR-14	30.24 (33.22)	Susceptible
7	AHW/BR-16	21.38 (25.28)	Moderately Resistant
8	AHW/BR-17	26.73 (31.09)	Susceptible
9	AHW/BR-25	27.22 (31.66)	Susceptible
10	AHW/BR-28	25.57 (30.10)	Susceptible
11	AHW/BR-30	28.72 (32.18)	Susceptible
12	AHW/BR-31	25.36 (30.17)	Susceptible
13	AHW/BR-37	14.29 (22.11)	Moderately Resistant
		CD (5%) = 7.703 CV =16.485	

*Figures in parenthesis are angular transformed value

Table 2. Disease reaction of different watermelon genotypes against mosaic disease

Disease reaction	Genotypes
Immune (I) (0.0%)	Nil
Resistant (R) (0.1 to 10%)	Nil
Moderately resistant (MR) (10.1 to 25%)	AHMM/BR-5, AHMM/BR-37, AHMM/BR-7, AHMM/BR-1, AHMM/BR-13, AHMM/BR-11 and AHMM/BR-16
Susceptible (S) (25.1 to 50%)	AHW/BR-31, AHW/BR-28, AHW/BR-17, AHW/BR-25, AHW/BR-30 and AHW/BR-14
Highly susceptible (HS) (> 50%)	Nil

Conclusion

The study demonstrated that watermelon genotypes in Western Rajasthan exhibited low mosaic disease severity due to dry atmospheric conditions and erratic rainfall, which limited disease development. However, this disease has the potential to become a significant threat to watermelon cultivation if not addressed in a timely manner. It is concluded that moderately resistant watermelon genotypes, such as AHW/BR-5, AHW/BR-37, AHW/BR-7, AHW/BR-1, AHW/BR-13, AHW/BR-11, and AHW/BR-16, are effective in combating mosaic disease.

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Conflict of Interest

The authors have no conflict of interest.

Data Sharing

All relevant data are within the manuscript.

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