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Screening of watermelon genotypes for resistance to mosaic disease under hot arid conditions of Rajasthan

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Abstract

Mosaic disease is one of the most important diseases in the production of watermelon under arid and semi-arid regions of India. Field trials were conducted to screen 13 watermelon/*mateera* genotypes *viz.*, RW-177-3, RW-187-2, GP-20, GP-35, GP-42, Thar Manak, AHW-19, AHW-65, Asahi Yamato, Sugar Baby, Arka Manik, Bikaner Local-1 and Barmer Local-1 for resistance against mosaic disease with normal cultivation practices during summer 2011 and 2012 at Plant Pathology Block of Central Institute For Arid Horticulture, Bikaner under field conditions. Resistant genotypes were categorized on the basis of disease incidence. Among 13 watermelon/*mateera* genotypes, none was found immune against disease. One variety 'Asahi Yamato' showed resistance with less than 10.0% disease incidence, ten genotypes were categorized as moderately resistant ranging from 10.1 to 25.0% disease incidence and two genotypes such as RW-177-3 and GP-20 having more than 25.0% disease incidence proved susceptible against mosaic disease.

Key words: Watermelon, genotypes, mosaic disease, resistance

Introduction

Watermelon [Citrullus lanatus (Thunb) Mansf.] is one of the most widely cultivated crop in the world. China is the leading country in production of watermelon followed by Turkey, United States and Iran (Huh et al., 2008). Watermelon is also known as Tarbooj, Kalinda and Mateera in some parts of India. This crop accounts for 6.8 per cent of the world area devoted to vegetable production (Goreta et al., 2005). In Rajasthan, mateera is an important landrace of Citrullus lanatus crop grown by farmers using their own saved seeds. It has sufficient variation in productivity and quality and is able to withstand damage from biotic and abiotic factors (Wehner et al., 2001). It is subjected to suffer various fungal and viral diseases, which inflict heavy damage on yield of the crop every year. Mosaic disease has become potential threat to the cultivation of watermelon in Western Rajasthan. This disease caused by cucumber mosaic virus (CMV). It is an important disease of Rajasthan as well as major watermelon growing states of India. Infected plants showed characteristic symptoms of dry, necrotic lesions along the veins of leaves, mottling, development of vein clearing and stunting of the plants. Field screening is one of 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 (Jadhav & Sharma, 1983). Keeping in view, this important component of integrated disease management, efforts were

made to screen watermelon genotypes against mosaic disease and to identify resistant/tolerant genotypes under hot arid conditions of Western Rajasthan.

Materials and Methods

Experimental trials were conducted during summer 2011 and 2012. Thirteen watermelon/mateera genotypes viz., RW-177-3, RW-187-2, GP- 20, GP- 35, GP- 42, Thar Manak, AHW- 19, AHW- 65, Asahi Yamato, Sugar Baby, Arka Manik, Bikaner Local-1 and Barmer Local-1 were tested against mosaic disease of watermelon at Plant Pathology Block of Central Institute For Arid Horticulture, Bikaner with normal cultivation practices under field conditions. Thirteen genotypes seeds were sown in Randomized Block Design with a spacing 50 x 100 cm in three replications during both seasons (summer 2011 and 2012). No plant protection measures were sprayed in the present study. Susceptible genotype 'Bikaner Local-1' 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 incidence of mosaic symptoms were recorded during growth period of the crop. The reactions for resistance due to mosaic disease in watermelon/mateera were categorized by using 0-4 scale (Singh *et al.*, 2007): immune (0) = 0% symptoms, resistant (1) = 0.1 to 10.0% symptoms, moderately resistant (2) =10.1 to 25.0% symptoms, susceptible (3) = 25.1 to 50.0% and highly susceptible (4) = >50.0% symptoms.

Results and Discussion

Pooled data of both the years (2011 & 2012) presented in Table 1 indicated that variation in disease

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Genotypes	Disease incidence (%)
RW-177-3	27.86* (31.82)
RW-187-2	17.14 (24.33)
GP- 20	30.50 (33.50)
GP- 35	22.50 (28.26)
GP- 42	16.25 (23.75)
Thar Manak	19.82 (26.42)
AHW- 19	17.14 (24.43)
AHW- 65	12.99 (21.10)
Asahi Yamato	05.83 (13.93)
Sugar Baby	13.80 (21.75)
Arka Manik	10.82 (19.18)
Bikaner Local-1	18.33 (25.34)
Barmer Local-1	21.87 (27.87)
CD at 5%=	2.77

Table 1. In vivo screening of watermelon genotypesagainst mosaic disease (pooled data 2011 & 2012).

*Figures in parenthesis are angular transformed

Table 2. Disease reaction of different watermenlon/mateera genotypes to mosaic disease

Disease reaction	Cultivars/genotypes
Immune (I)	Nil
(0.0%)	
Resistant (R)	Asahi Yamato
(0.1 to 10%)	
Moderately resistant (MR)	Arka Manik, RW-187-2,
(10.1 to 25%)	GP- 35, GP- 42,
	Thar Manak, AHW- 19,
	AHW- 65, Sugar Baby,
	Bikaner Local-1 and
	Barmer Local-1
Susceptible (S)	GP- 20 and RW-177-3
(25.1 to 50%)	
Highly susceptible (HS)	Nil
(> 50%)	

incidence of mosaic was found in all the genotypes of this crop. Among thirteen genotypes of watermelon/*mateera*, range of average disease incidence of mosaic was 5.83 to 30.50%. Minimum disease incidence (5.83%) was recorded in one variety 'Asahi Yamato', followed by variety 'Arka Manik' which were not statistically at par with each other. Maximum disease incidence (30.50%) was recorded in genotype 'GP-20', followed by RW-177-3 (27.86%) which were statistically at par with each other. These results are in consonance with the finding of earlier worker (Shah *et al.*, 2012) who reported that variation in disease incidence of different chilli germplasm against *mosaic* disease.

The results presented in Table 2 reveal that there was some variation in all the genotypes evaluated against mosaic disease. Out of thirteen watermelon/mateera genotypes, none was found immune (I) against mosaic disease. Among them, one variety 'Asami Yamato' showed resistant (R) with minimum disease incidence (5.83%), ten genotypes/varieties were categorized as moderately resistant (MR, 10.82 to 22.50%) and two genotypes viz., GP-20 and RW-177-3 were susceptible (S) having 27.86% and 30.50% disease incidence. The results supports the earlier findings of Singh et al. (2007) who reported that out of 146 genotypes of pigeon pea, 37 genotypes were caregorized as resistant (incidence up to 10%), 45 genotypes showed moderately resistant and rest were noted as susceptible and highly susceptible against sterility mosaic. Shah et al. (2012) screened 28 germplasm of chilli against mosaic disease and found minimum disease incidence in Jawahar, BC-21-2, LCA- 305 and Pant C-2 germplasm.

Conclusion

It is concluded that only one variety 'Asahi Yamato' of watermelon was found tolerance/resistant against mosaic disease with minimum disease incidence. The source of genotypes/varieties identified in present investigation under various categories could be utilized in breeding programme.

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