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Inheritance of Resistance to Yellow Mosaic Virus Disease on Bambara Groundnut

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A B S T R A C T

Plant viral diseases inflict serious economic losses in major crops by reducing yield and compromising quality. The present study was conducted at K-block, University of Agricultural Sciences, Bengaluru. M_2 generation was raised during *summer* season of the year 2014-15.The inheritance pattern of YMV disease was studied in M_2 segregating populations of Bambara groundnut. In the M_2 segregating populations of SB-42 and S-165A studied, a good fit of 3: 1 (Susceptible: Tolerant) ratio was observed this indicates that single recessive gene controls tolerance to YMV disease in Bambara groundnut.

Introduction

Bambara groundnut (*Vigna subterranea* (L.) Verdc.), member of the family *Fabaceae* is a self-pollinating diploid annual legume crop with a chromosome number of 2n=22. It is an important food crop grown widely in semi-arid Africa and it is closely related to cowpea (*Vigna unguiculata*) with which it shares its origin of genetic diversity. In Africa, Bambara groundnut is the third most important legume after groundnut and cowpea (Sellschope, 1962). *Vigna subterranea* is an extreme inbreeder; an autogamous crop with flower that are cleistogamous in nature (Uguru and Agwatu, 2006), which gives rise to high percentage selfing since, the floral structure is perfect resulting in extreme inbreeding. For any effective selection programme genetic variation must exist. Radiation and other chemical mutagens have been used to induce variability in crop plants (Ahloowalia *et al.*, 2004).

Viruses are one of the major constraints in pulse production among the plant pathogens affecting pulse production worldwide. Plant viral diseases inflict serious economic losses in major crops by reducing yield and compromising quality (Kang *et al.*, 2005).

Among several viral diseases of pulse crops, yellow mosaic virus causes major loss in the yield of the crop. In 1955 yellow mosaic disease was first identified in India and it occurs in a number of leguminous plants, *i.e.*, mungbean, urdbean, cowpea, soybean, horse gram, lablab bean, french bean, moth bean and some other leguminous hosts; and some hosts of the family *Malvaceae* and *Solanceae* (Dhingra and Chenulu, 1985; Qazi *et al.*, 2007). This disease was first reported in Bambara groundnut by Muniyappa and Veeresh, (1984) at UAS, GKVK, Bengaluru and subsequently by Smita Veeraghanti, (2012). The disease is characterized by faint yellow discoloration of young leaves and bright yellowing of older leaves on *Voandzeia subterranea* (Bambara groundnut) (caused by horse gram yellow mosaic virus). The chemical management of the vector is costly since numerous sprays of insecticides are required to control whitefly. Recently recurrent spraying has led to health danger and ecological influence. On the contrary, use of virus resistant varieties, if available, is the best approach to alleviate occurrence of Yellow mosaic virus disease in areas where the infection is a major constraint to production. Use of disease resistant crop varieties is regarded as an economical and durable method of controlling viral diseases.

Materials and Methods

The study was carried out at K-block, University of Agricultural Sciences, Bengaluru. M_2 generation was raised during *summer* season of the year 2014-15. The experimental material for this study consist of two varieties of Bambara groundnut having good agronomic base belonging to different accessions *viz*., SB-42 (light brown, round shape and white hilum) and S165A (dark brownish, dark spotted surface and oval shape). These seeds were obtained from Directorate of Groundnut Research, Junagadh through National Bureau of Plant Genetic Resources.

Ethyl methane sulphonate (EMS) was used as a chemical mutagen to induce mutation in the seeds of Bambara groundnut varieties. EMS causes alkylation of guanine bases (G) leading to mispairing or mismatch pairing in the DNA of a treated organism as opposed to large deletions or rearrangements (Sharma and Sharma, 1986). Under these conditions, an alkylated G pairs with T in place of C, causing a G/C to A/T transition in the backbone of the DNA (Henikoff and Comai, 2003). It can cause allelic mutations, small deletions (Schreck, 2002) and other chromosomal rearrangements (Barratt *et al.*, 2001) depending on the position of the mutation.EMS was obtained from Spectrochem, Mumbai, India having a dosimetry/half-life period of 30 hours with a molecular weight of 124.16 and density of 1.20.

Two hundred well matured healthy and uniform sized non-dormant seeds of each variety of Bambara groundnut were used for the chemical treatment. Five different concentrations of EMS 0.1, 0.2, 0.3, 0.4 and 0.5 per cent were used to treat the seeds. The solution of EMS was prepared corresponding to the required concentrations using double distilled water. The pH of aqueous solution was adjusted at 8.5 by using 0.2M solution of sodium tetra borate (Borax). The volume of solution prepared was about three times of volume of seeds. The seeds were pre-soaked in double distilled water for five hours at room temperature (28 ± 2ºC) prior to treatment. After pre-soaking the excess of moisture in the seeds was then removed by filter paper. Seeds were then soaked in freshly prepared aqueous solution of different doses EMS for six hours at room temperature (28 ± 2ºC) with intermittent shaking after every hour. After the treatment, the seeds were

washed thoroughly with double distilled water for eight to ten times and sown in the field along with control (untreated seeds). Pre-soaked seeds in only double distilled water for six hours were used as control.

Screening M2 genotypes for YMV under natural field condition

The M_2 populations were subjected for disease screening under natural infection at 50 days after sowing (Selvi*et al.,* 2006). The M_2 plants were classified based on per cent disease incidence of YMV for parents and individual plants of each M_2 population as per procedure given by Selvi *et al.,* (2006) and scales were depicted in the Table 1.

$$\text{Per cent disease incidence} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

The inheritance pattern of YMV disease was studied in M_2 segregating populations of Bambara groundnut. The disease resistance was classified into two groups, those with no apparent symptoms as resistant and those with visual expression of symptoms as susceptible. The reaction for the diseases was recorded as resistant and susceptible on all individual plants of M_2 generation. The recorded observations were subjected to Chi-square test based on expected ratios. The goodness of fit between expected and observed segregation ratios were worked out. The Chi-square was calculated by using the following formula. Where, O = Observed frequency, E = Expected frequency. The significance of Chi-square value was tested by comparing the calculated Chi square value with table value at 5 Per cent and 1 Per cent level of significance at appropriate degrees of freedom (n-1), where, n = number of classes of trait under consideration.

Results and Discussion

In the present study, the M_2 populations of SB-42 and S-165A were screened during *summer* 2014 under natural field condition for YMV. All M_2 populations were scored for YMV reaction under natural condition as per scale given by Selvi *et al.,* (2006). In the M_2 segregating populations of SB-42 and S-165A studied, a good fit of 3: 1 (Susceptible: Tolerant) ratio was observed and Table 2 and 3 suggests that single recessive gene controls tolerance to YMV disease in Bambara groundnut and these results are in agreement with the previous work of Shakoor *et al.,* (1977), Anand Kumar *et al.,* (2008) and Reddy (2009) (Fig. 1 and 2).

Table.1 YMV disease reaction scale

Scale	Percent Disease Incidence	Disease reaction
0	No infection	Highly resistant (HR)
1	1-5% mottling of leaves	Resistant (R)
3	5-10 % mottling of leaves	Moderately resistant (MR)
5	10-25% mottling and yellow discoloration leaves	Moderately susceptible (MS)
7	25-50% mottling and yellow discoloration leaves	Susceptible (S)
9	> 50% severe yellow mottling leaves, reduced flower and fruits	Highly Susceptible (HS)

Table.2 Inheritance of YMV disease resistance in M_2 populations of SB-42 variety

Concentration of EMS in per cent	Number of plants in M_2 population		Total Plants	Expected Ration	χ^2 Calculated value(3:1)	χ^2 Table value
	Tolerant	Susceptible				
0.1	82	247	329	3:1	0.0010	3.841
0.2	106	317	423	3:1	0.0008	3.841
0.3	165	493	658	3:1	0.0020	3.841
0.4	52	155	207	3:1	0.0016	3.841
0.5	73	220	293	3:1	0.0011	3.841

Table.3 Inheritance of YMV disease resistance in M_2 populations of S-165A variety

Concentration of EMS in per cent	Number of plants in M_2 population		Total Plants	Expected Ration	χ^2 Calculated value(3:1)	χ^2 Table value
	Tolerant	Susceptible				
0.1	80	241	321	3:1	0.0010	3.841
0.2	56	170	226	3:1	0.0059	3.841
0.3	140	421	561	3:1	0.0006	3.841
0.4	55	160	215	3:1	0.0432	3.841
0.5	39	121	160	3:1	0.0333	3.841

Fig.1 Field view of bambara groundnut

Fig.2 YMV infected plants in M2 generation

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