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ANALYSIS OF RESISTANCE TO *YAM MOSAIC VIRUS,* GENUS *POTYVIRUS* IN WHITE GUINEA YAM (*DIOSCOREA ROTUNDATA* POIR.) GENOTYPES

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Abstract: Resistance to *Yam mosaic virus* (YMV), genus *Potyvirus* was studied in 10 populations of selected white Guinea yam (*Dioscorea rotundata*). Plants of resistant genotypes: TDr 35, TDr 1621, TDr 93-1, TDr 93-32, TDr 95-107, TDr 93-23, and susceptible ones: TDr 87/00211, TDr 87/00571 and TDr 95-127 were screened for their reaction to the pathogen by symptom severity scoring scale of 1-5, and by quantifying virus multiplication by triple antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA). Controlled crosses were made among the genotypes within and between the groups according to reactions to the pathogen. The resultant F_1 progenies were evaluated for the infection by disease symptom development and by TAS ELISA to detect a symptomless infection in an insect-proof screenhouse for the assessment of inheritance of resistance to YMV. A genetic analysis of the reactions of progenies derived from the *D. rotundata* genotypes to inoculation with YMV strongly suggests that resistance to the virus is a dominantly inherited trait. Segregation ratios obtained from the families indicate that at least two dominant genes are involved.

Key words: *Yam mosaic virus* (YMV), genus *Potyvirus*, *Dioscorea rotundata*, resistance, triple antibody sandwich enzyme-linked immunosorbent assay.

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Introduction

Yam mosaic virus (YMV) genus *Potyvirus*, family *Potyviridae* is the most important virus infecting both cultivated and wild yams especially *Dioscorea rotundata*, *D. alata*, *D. cayenensis* and *D. praehensilis* in the yam-growing areas of the world (Thouvenel and Fauquet, 1979; Porth et al., 1987). YMV is reported in the growing regions of Nigeria, Ghana, Cameroon, Benin, Côte d'Ivoire, Burkina Faso and Togo in West Africa (Thouvenel and Fauquet, 1979; Porth et al., 1987; Thottappilly, 1992; Brunt et al., 1996) and also in Guadeloupe and Guyana (Brunt et al., 1996). YMV is the most widespread among all the viruses infecting yams in Nigeria (Hughes et al., 1997) and in Ghana (Olatunde, 1999). YMV causes several symptoms including mottling, leaf and vein chlorosis, leaf mosaic, leaf distortion and malformation, shoestringing of leaf as well as plant stunting. YMV is reported to cause about 40% of yield reduction in *D. rotundata* (IITA, 1981). Among all the viruses identified to infect yams, YMV is the causal agent of the most important virus disease (Thouvenel and Dumont, 1988, 1990; Goudou-Urbino, 1995).

Protection of crops against pathogens may be realized by different means such as chemical application, phytosanitation, and use of biological control agents or resistant varieties. Breeding for resistance is usually preferred due to its cost-effectiveness and the minimal impact on the environment (Hogenboom, 1993). This is because once resistance to the causal agent of the disease is established it can be transferred from generation to generation.

For a higher level of food production, greater income and improved nutritional status of the poor people in sub-Saharan Africa, resistant landraces grown in the region must be identified and hybridized with other genotypes having desired qualities to bring about high level resistant offspring with improved and reliable yield.

Several studies by various authors identified inheritance of resistance. Legnani et al. (1995) identified a peculiar type of resistance in F_2 progenies of *Lycopersicon hirsutum* cv. PI247087 (a resistant line) to infection with isolates of Potato virus Y (PVY) genus *Potyvirus* which allows the virus to multiply in the inoculated leaves but could not establish a systemic infection, thus suggesting a mechanism which interferes with the long distance migration of the virus in infected plants. Numerous studies have been conducted to elucidate the mode of inheritance of resistance of several cultivars of soybeans (*Glycine max*) to isolates of *Soybean mosaic virus* (SMV) genus *Potyvirus* (Kiihl and Hartwig, 1979; Buzzell and Tu, 1984; Lim, 1985; Buss et al., 1989; Bowers et al., 1992).

Mignouna et al. (2001) reported that segregation into resistant and susceptible individuals in a three population's inheritance study indicated that resistance in *D. rotundata* is inherited differentially as a dominant and recessive character, thus

suggesting that two major genes control resistance to *Yam mosaic virus* (YMV), genus *Potyvirus* in white guinea yams.

The objectives of this study were to contribute to the knowledge of genetic control of resistance to YMV, in *D. rotundata* using landraces with a range of resistance/susceptibility to YMV under vector-controlled conditions, and to study the F_1 hybrids produced.

Materials and Methods

Selection of parental lines and hybridization

Following visual scoring of disease symptoms as described by Mignouna et al. (2001) and Odu et al. (2004) on a scale of 1-5, serological evaluation, and observation of flowering pattern to determine the sex, 10 *D. rotundata* genotypes were selected for use as parental lines from the 24 evaluated genotypes in four agro-ecological zones in Nigeria (Table 1).

Table 1. Accession numbers, names, sources and sexes of *Dioscorea rotundata* genotypes used in the resistance studies.

IITA Accession number	Local/source name	Original source	Sex
TDr 93-1	Akwoki	Abuja, Nigeria	Female
TDr 93-23	Obiaoturugo	Obinagu, Nigeria	Female
TDr 93-32	Amula	Zaki-biam, Nigeria	Female
TDr 95-107	Maria	Ndayako, Nigeria	Female
TDr 95-115	Nyagode	Abuja, Nigeria	Male
TDr 95-127	Dandiyo	Keffi, Nigeria	Male
TDr 35	Atoja	Ibadan, Nigeria	Female
TDr 1621	Lololo	Togo	Female
TDr 2269	-[a]	-	Female
TDr 87/00211	Breeder's line	IITA, Ibadan, Nigeria	Male

[a]No information is available; TDr = Tropical *Dioscorea rotundata*; IITA = International Institute of Tropical Agriculture.

The genotypes were planted at a density of one plant per square meter and each experimental plot (6 m x 5 m) was planted with 30 sets of each genotype and replicated four times. The experimental design was a randomized complete block (RCBD). Individual staking of each of the plant stands was done at emergence to increase the area of leaf exposure to sunlight and to facilitate controlled crossing of individual plants.

Intercrosses of two resistant male genotypes (TDr 1621, TDr 35) with two susceptible female genotypes (TDr 87/00211, TDr 95-127) and one moderately resistant female genotype (TDr 95-115) were performed. Similarly, five moderately resistant male genotypes (TDr 93-32, TDr 93-1, TDr 93-23, TDr 95-107, TDr 2269) were intercrossed with the two susceptible female genotypes (TDr 87/00211, TDr 95-127) (Table 2).

Table 2. *Dioscorea rotundata* parental genotypes and F_1 populations showing numbers of plants exhibiting symptoms of infection and numbers of plants that tested positive for *Yam mosaic virus* genus *Potyvirus* infection by TAS-ELISA after mechanical inoculation.

Parents		Total no. of F_1 plants tested	Total no. of plants showing symptoms	No. of plants positive by ELISA[a]
Male	Female			
TDr 1621 (R)	TDr 87/00211 (S)	87	22	22
TDr 35 (R)	TDr 87/00211 (S)	354	69	94
TDr 35 (R)	TDr 95-127 (S)	183	43	52
TDr 35 (R)	TDr 95-115 (MR)	43	12	21
TDr 93-32 (MR)	TDr 95-127 (S)	129	48	55
TDr 93-32 (MR)	TDr 87/00211 (S)	155	45	48
TDr 93-1 (MR)	TDr 95-127 (S)	64	28	25
TDr 93-1 (MR)	TDr 87/00211 (S)	112	26	30
TDr 95-107 (MR)	TDr 87/00211 (S)	170	29	44
TDr 93-23 (MR)	TDr 87/00211 (S)	140	28	37
TDr 93-23 (MR)	TDr 95-127 (S)	82	22	21
TDr 2269 (MR)	TDr 87/00211 (S)	45	8	11
Total		1,564	380	460

R = Resistant; MR = Moderately resistant; S = Susceptible; [a]Enzyme-linked immunosorbent assay.

Planting and germination of yam seeds

A layer of coco-peat was placed at the bottom of a 0.9 x 0.6 m metal tray and Jiffy 7 peat pellets (Forestry Supplies Inc. U.S.A.) were arranged side by side on the coco-peat with each tray having 240 pellets. The pellets were then sprayed with water to the saturation point. After about 3-5 minutes, more water was added and this was repeated until the pellets were fully expanded. Each of the pellets at this time was about $1^5/_8$ inches high.

The expanded pellets were then sprayed with fungicide (5 g litre^{-1} of benlate in water containing 50% benomyl (w/w)), water-soaked and drilled in the middle. The seeds were planted in the holes with one seed per pellet, labeled with plastic pegs to differentiate between the crosses and watered when necessary to ensure the germination of the seeds and uptake of nutrients from the pellets and the coconut

peat. Germination counts were done at 2-day interval for each of the crosses, using pushpins of assorted colors (one color per day) to distinguish already counted seedlings.

Germinated seedlings were transplanted into 7 or 8-inch Stewart's pots which were previously filled with a mixture of heat sterilized top-soil and coconut peat (1:3). Individual plants from each of the crosses were labeled and randomized within the screenhouse. There were 15 blocks of parent plants and progenies arranged in 20 rows of 6 plants per block.

YMV detection in F_1 and their parents

Three leaf samples were collected from all plants (both F_1 and parents) in the screenhouse and indexed serologically to detect YMV infection prior to mechanical inoculation. Triple antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA) described by Thottappilly et al. (1998) was used for the detection of YMV in leaf samples collected from F_1 plants and the parents as reported by Odu et al. (2004). The monoclonal antibody used was YMV-M24, produced against YMV at the IITA, which was found to detect YMV isolates from other countries including Cameroon, Nigeria, Benin, Togo, Côte d'Ivoire, Burkina Faso and Guinea (Njukeng, 1998).

Mechanical inoculation of progenies (F_1 population) and their parents with YMV

Plants of *Nicotiana benthamiana* infected with standard isolate of YMV (Mignouna et al., 2001) were used as source of inoculums 10 days after inoculation with the virus antigen. All F_1 progenies and parents planted in the screenhouse were mechanically inoculated with the inoculum after being dusted with carborundum (600 mesh). Inoculation buffer was 0.03M sodium phosphate buffer pH 8.3, containing 0.2% DIECA, while sterilized mortars and pestles were used and disposable gloves were worn during inoculation. All plants were inoculated twice, with the second inoculation taking place three weeks after the first. Ten plants of each genotype were inoculated with the buffer as healthy controls.

Symptom evaluation and serological virus detection for YMV

All the inoculated plants were scored for the presence/absence of virus symptoms and severity 5, and 10 weeks after the second inoculation as previously reported by Mignouna et al. (2001) and Odu et al. (2004). Plants with score of 1 (no symptom) were considered as resistant while those scoring between 2 and 5 (2: moderate or mild symptoms, 3: severe symptoms, 4: very severe symptoms, 5: distortion, malformation of leaf or stem) were evaluated as susceptible.

Leaf samples were collected from all inoculated F_1 progenies and parent plants in the screenhouse, and tested for the presence of YMV by TAS-ELISA. Plants having leaf samples with mean absorbance value twice or more than that of the healthy sample were considered susceptible. A DYNEX MRX ELISA plate reader (DYNATECH, USA) was used to determine the absorbance value for each of the samples.

Analysis of inheritance

The Chi-square statistical test (Little and Hills, 1978) was performed to determine if the observed ratios of resistant to susceptible plants deviated from expected ratios. The observed ratio was considered to fit the expected ratio if the appropriate chi-square (χ^2) value had a corresponding probability of >0.05 (Gomez and Gomez, 1984).

Analysis of inheritance of resistance to YMV was carried out using the data from the virus symptom severity rating of the hybrids and their parents, as well as from the data from the serological indexing.

Results and Discussion

Pre-inoculation indexing of the F_1 progenies by TAS-ELISA did not detect any YMV infection. Although seed transmission of many viruses has been reported in several studies (Sekar and Sulochana, 1988; Thottappilly, 1992; Ndiaye et al., 1993; Brunt et al., 1996), it was not detected among the 1,564 seedlings screened during the course of this study. This included the use of TAS-ELISA serological detection method to detect any masked/latent infection by YMV in the *D. rotundata* progenies. This result concurs with the findings of Thouvenel and Fauquet (1979), when they screened progenies of crosses among several *D. cayenensis* genotypes for YMV infection by symptomatology alone.

Inoculation of transplanted seedlings growing in the screenhouse with YMV induced various YMV-associated symptoms such as mosaic, green vein-banding and chlorosis in some of the inoculated plants. Symptoms appeared on newly formed leaves 3 weeks after the first inoculation.

Of all the 1,564 F_1 plants that were established in the screenhouse for resistance study, a total of 380 seedlings showed symptoms while 460 tested positive for the presence of YMV by TAS-ELISA (Table 2), suggesting that 80 plants were also infected but symptomless. These symptomless infections could result from a tolerance mechanism operating in the particular genotypes. This confirms the findings of Mignouna et al. (2001), when they observed asymptomatic F_1 progenies which were ELISA-positive. The cross between TDr 35 and TDr 87/00211 had the highest number of plants that expressed symptoms and also those that were positive for YMV by TAS-ELISA. Resistance to viruses is often

evaluated by the expression of disease symptoms without necessarily quantifying virus multiplication (Fraser, 1990). Plants can be classified as resistant when no symptoms or necrotic lesions develop and as susceptible when symptoms appear (Scholten et al., 1996). Observation of symptom expression complemented with the use of ELISA serological technique for the detection of virus infection in this study has shown that TAS-ELISA is both sensitive and consistent. TAS-ELISA was able to detect symptomless infection in genotypes that would have been taken as resistant if symptom observation had been employed as the sole method of indexing.

Although the variations in symptom severity may be due to differences in virus concentration, some genotypes could express symptoms independently of the rate of virus concentrations (Kuhn et al., 1981).

There was an approximately 50% correlation between the average symptom severity score of the crossed parents and the average severity ratings of the F_1 population (Figure 1). This shows that there is the relationship between the crossed parents and the resultant offspring with relation to symptom expression. Correlation analysis was carried out between ELISA reading (A_{405}) and the symptom severity scores in the F_1 generation of the hybrids for YMV infection. There was a highly significant positive correlation ($p<0.0001$) in the correlation matrix between symptom score and the ELISA reading of all plants.

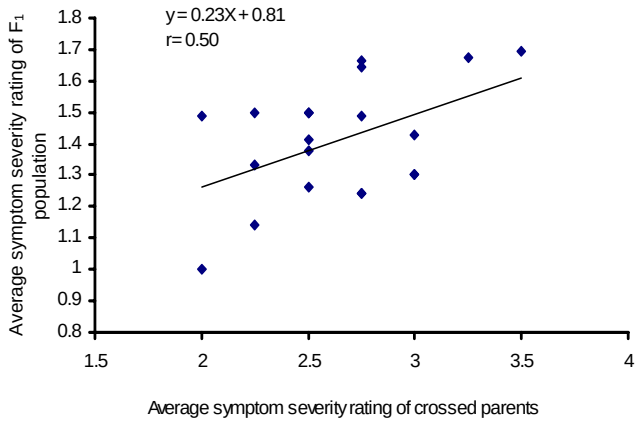

Figure 1. Relationship between parents and F_1 population in virus symptom severity score.

Classification of plants in the segregating families into susceptible or resistant genotypes was possible due to the presence of symptoms and also due to the reliability of TAS-ELISA for the detection of YMV in infected symptomless F_1

plants. The segregation for resistance to YMV based on the virus symptom severity scores shows that most of the crosses conform to ratio 3:1 proposed for the ratio of the resistant to susceptible in the populations derived in the inheritance studies (Table 3). On the other hand, considering the serological indexing (Table 4), most of the crosses conform to the ratios 3:1 (assuming random chromosome assortment) and 2.48:1 (assuming random chromatid assortment) proposed for the ratio of the resistant to susceptible plants in the populations derived in the inheritance studies (Mignouna et al., 2001).

Table 3. Segregation for resistance to *Yam mosaic virus* (YMV), genus *Potyvirus* based on symptom severity scores of 20 F_1 families in a nursery obtained by crossing resistant and susceptible *Dioscorea rotundata* genotypes.

Family	Resistance levels of F_1[a]					Σ	χ^2(P%)[b] (R:S)
	1	2	3	4	5		
TDr 35 (R) x TDr 87/00211 (S)	289	44	21	0	0	354	0.0039
TDr 1621 (R) x TDr 87/00211 (S)	65	11	11	0	0	87	0.9506
TDr 93-23 (MR) x TDr 87/00211 (S)	111	16	12	1	0	140	0.2416
TDr 95-107 (MR) x TDr 87/00211 (S)	141	19	7	3	0	170	0.0168
TDr 93-32 (MR) x TDr 87/00211 (S)	110	25	18	2	0	155	0.2463
TDr 93-1 (MR) x TDr 87/00211 (S)	87	17	7	1	0	112	0.5127
TDr 2269 (MR) x TDr 87/00211 (S)	37	5	3	0	0	45	0.2632
TDr 35 (R) x TDr 95-127 (S)	140	25	18	0	0	183	0.6387
TDr 93-32 (MR) x TDr 95-127 (S)	79	20	26	4	0	129	0.0107
TDr 93-23 (MR) x TDr 95-127 (S)	55	14	13	0	0	82	0.0974
TDr 93-1 (MR) x TDr 95-127 (S)	36	15	11	2	0	64	0.3173
TDr 35 (R) x TDr 95-115 (MR)	31	4	7	1	0	43	0.6598

R = Resistant, MR = Moderately resistant, S = Susceptible; ∑ = Total of the plants evaluated for each cross; [a]Virus symptom severity score on a scale of 1-5, where 1 = symptomless and 5 = very severe symptoms; [b]χ^2(P<0.05; 1 degree of freedom) = 3.84; [c]Resistant:Susceptible based on a ratio of 3:1, resistance level 1 = Resistant, and 2-5 = Susceptible.

The segregation ratio obtained in the cross between TDr 1621, a resistant genotype and TDr 87/00211, a susceptible genotype, fits both the 3:1 (χ^2 = 0.004; P = 0.951) and 2.48:1 (χ^2 = 0.505; P=0.477). A better fit is obtained with a 3:1 ratio, which is expected in a cross between two different heterozygotes with two dominant genes in a simplex condition. The same segregation ratio is obtained in a cross between TDr 35, a resistant genotype and TDr 87/00211, a susceptible line, where a better fit is obtained with a 3:1 (χ^2 = 0.544; P = 0.461).

Progeny of the cross between TDr 93-1, a moderately resistant genotype and TDr 87/00211 had good fits with 3:1 ($\chi^2 = 0.191$; P = 0.663) and 2.48:1 ($\chi^2 = 0.207$; P = 0.648), while the progeny between TDr 93-1 and TDr 95-127, another susceptible genotype, had good fits with ratios 1:1 ($\chi^2 = 3.063$; P = 0.080), and 2.48:1 ($\chi^2 = 3.333$; P = 0.0.068). The segregation of progeny of the cross between TDr 35, a resistant genotype, and TDr 95-115, a moderately resistant genotype, fits neither a 3:1 ($\chi^2 = 0.004$; P = 0.951) nor a 2.48:1 ($\chi^2 = 0.004$; P = 0.951) ratio. A good fit is obtained with a 1:1 ratio, which can be expected when a simplex heterozygote resistance plant is crossed to a nulliplex homozygote susceptible plant (Allard, 1960).

Table 4. Segregation ratios of F_1 populations obtained in crosses between resistant and susceptible *Dioscorea rotundata* genotypes based on serological indexing to detect *Yam mosaic virus* (YMV), genus *Potyvirus* after mechanical inoculation with the virus.

Cross	No. F_1 plants observed			Exp.[a] Ratio	χ^{2b}	Prob[c].
	Total	R	S			
TDr 35 x TDr 87/00211	354	260	94	3:1	0.544	0.461*
				2.48:1	0.823	0.364*
TDr 1621 x TDr 87/00211	87	65	22	3:1	0.004	0.951*
				2.48:1	0.505	0.477*
TDr 93-23 x TDr 87/00211	140	103	37	3:1	0.152	0.696*
				2.48:1	0.364	0.546*
TDr 95-107 x TDr 87/00211	170	126	44	3:1	0.071	0.791*
				2.48:1	0.676	0.411*
TDr 93-32 x TDr 87/00211	155	107	48	3:1	2.994	0.086*
				2.48:1	0.377	0.539*
TDr 93-1 x TDr 87/00211	112	82	30	3:1	0.191	0.663*
				2.48:1	0.207	0.648*
TDr 2269 x TDr 87/00211	45	34	11	3:1	0.007	0.931*
				2.48:1	0.404	0.525*
TDr 35 x TDr 95-127	183	131	52	3:1	1.138	0.286*
				2.48:1	0.009	0.924*
TDr 93-32 x TDr 95-127	129	74	55	1:1	2.799	0.094*
				3:1	21.398	<0.001
TDr 93-23 x TDr 95-127	82	61	21	3:1	0.016	0.899*
				2.48:1	0.391	0.532*
TDr 93-1 x TDr 95-127	64	39	25	1:1	3.063	0.080*
				2.48:1	3.333	0.068*
TDr 35 x TDr 95-115	43	22	21	1:1	0.023	0.879*
				2.48:1	8.485	0.004

R = Number of resistant F_1 plants based on enzyme-linked immunosorbent assay; S = Number of susceptible F_1 plants based on enzyme-linked immunosorbent assay; [a]Expected segregation ratio assuming Mendelian inheritance of dominant resistance genes; [b]Chisquare values; [c]Probability level associated with the calculated chi square value for each cross; 1:1 = 1 dominant resistant gene in simplex assuming chromosome (chromatid) segregation; 2.48:1 = 1 dominant resistant gene in duplex assuming chromatid segregation; 3:1 = 2 dominant resistant genes in simplex assuming chromosome segregation.

Assuming Mendelian inheritance of dominant genes in autotetraploids, tetrasomic inheritance is implicated in *D. rotundata* (Allard, 1960; Mignouna et al., 2001). From all the families studied, it is strongly suggested that resistance is dominantly inherited. Segregation of the progenies from crosses of TDr 1621, TDr 93-23, TDr 95-107 and TDr 2269 with susceptible genotype TDr 87/00211 fitted a ratio of 3:1 (Table 4) indicating control by two dominant genes in a simplex condition assuming random chromosome assortment (Vallejo et al., 1995; Mignouna et al., 2001).

Segregation ratios of progenies from crosses involving TDr 35, TDr 32, and TDr 93-1 were more complicated. Progenies from their crosses to TDr 87/00211 fitted the 3:1 ratio as for the previous genotypes. Segregation of progenies from the crosses of TDr 35 to TDr 95-115 and TDr 95-127 fitted 1:1 and 2.48:1 ratios respectively although the latter combination could also fit a 3:1 ratio. Progenies from crosses of TDr 93-32 and TDr 93-1 to TDr 95-127 segregated in a 1:1 ratio. These segregation ratios are more consistent with the actions of a single dominant gene in each situation. Mignouna et al. (2001) attributed this apparent complexity to the possibility of genotypic mixtures among the parental lines.

The cross between TDr 93-32, a moderately resistant genotype and TDr 95-127, a susceptible genotype produced a ratio that had tendency to fit to a ratio of 1:1. The same goes for the cross between TDr 93-1, a moderately resistant genotype and TDr 95-127. It should be noted that all genotypes designated moderately resistant were actually infected, as they permit the multiplication and spread of YMV, but they only had mild symptoms arising from infection. Mignouna et al. (2001) reported that ELISA detected the presence of YMV in parental resistant genotypes, though at a level far below those obtained in susceptible genotypes. The segregation ratios obtained in the cross between TDr 93-1 and TDr 87/00211 on one hand, and TDr 93-1 and TDr 95-127 on the other hand corroborated the findings of resistance in TDr 93-1 by Mignouna et al. (2001). This may also be true for some of the other genotypes designated as moderately resistant (MR).

Regression of average YMV symptom severity ratings of F_1 population on mid-parent values was significant, and the heritability estimate calculated was 0.23 (Figure 1).

Conclusion

On the basis of the results obtained in this study, tetrasomic inheritance of resistance to YMV is implicated in *D. rotundata* genotypes. It is also strongly suggested that resistance is dominantly inherited. Segregation of the progenies derived from some resistant genotypes and the susceptible genotype TDr 87/00211 showed that resistance is controlled by two dominant genes in a simplex condition assuming random chromosome assortment.

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ANALIZA OTPORNOSTI NA *VIRUS MOZAIKA JAMA*, RODA *POTYVIRUS* KOD GENOTIPOVA BELOG GVINEJSKOG JAMA (*DIOSCOREA ROTUNDATA* POIR.)

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R e z i m e

Otpornost na virus mozaika jama (YMV), roda *Potyvirus* je proučavana kod 10 populacija odabranog belog gvinejskog jama (*Dioscorea rotundata*). Biljke otpornih genotipova, kao što su TDr 35, TDr 1621, TDr 93-1, TDr 93-32, TDr 95-107, TDr 93-23, i osetljivih, kao što su TDr 87/00211, TDr 87/00571 i TDr 95-127 su testirane kako bi se utvrdila njihova reakcija na patogene pomoću skale za ocenjivanje na osnovu intenziteta simptoma od 1 do 5, i kvantifikovanjem umnožavanja virusa trostrukom imunoenzimskom metodom na ploči (TAS-ELISA). Kontrolisana ukrštanja su sprovedena među genotipovima u okviru i između grupa prema reakcijama na patogen. Dobijeni F_1 potomci su vrednovani radi utvrđivanja infekcije pomoću razvoja simptoma bolesti i korišćenjem TAS ELISA kako bi se otkrila infekcija bez simptoma u mrežaniku otpornom na insekte radi procene nasleđivanja otpornosti na YMV. Genetička analiza reakcija potomaka koji potiču od genotipova *D. rotundata* na inokluaciju sa YMV snažno implicira da je otpornost na viruse dominantno nasledna osobina. Odnosi segregacije koji su dobijeni od porodica ukazuju da su najmanje dva dominantna gena uključena.

Ključne reči: virus mozaika jama (YMV), rod *Potyvirus*, *Dioscorea rotundata*, otpornost, trostruka imunoenzimska metoda na ploči.

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