



Screening of rice genotypes for resistance to rice yellow mottle virus in Tanzania

Barnabas Justo Sitta*, John Joseph, Charles Chuwa, Victoria Bulegeya

Tanzania Agricultural Research Institute, Dakarwa Centre, Morogoro, Tanzania

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Abstract

Rice is the second major food crop in Tanzania contributing to food security and cash flow to poor resource farmers. However, Rice Yellow Mottle Virus (RYMV) is among the important disease devastating production in many rice growing regions in Tanzania. The reactions of 22 rice genotypes to an isolate of RYMV were studied. The appearance and development of symptoms in the various varieties were scored on a 1-9 scale. The observed reactions ranged from susceptible, moderately susceptible, moderately resistance, resistance to highly resistant. Nine per cent (9.09) of the varieties showed a high level of resistance while fifty per cent (50) were highly susceptible. The intermediate reactions were 27.27% resistant and 13.64% moderately resistant. This study was able to identify rice genotypes resistant to RYMV to be used in breeding program for introgression RYMV resistance into commercial released variety.

* **Corresponding Author:** Barnabas Justo Sitta ✉ barnabassitta@yahoo.com

Introduction

Rice is among the key crop in Tanzania contributing to the food security and cash flow to the poor farmers. The crop stand as the second most produced food crop where 20% of the production accounted by the small holder farmers under rain fed conditions (Mtaki, 2018). The crop is grown over ten regions of Tanzania however the production per unit area still down ranging from 1 to 1.5 tonnes per hectore (January *et al.*, 2018). The average production is less four times the average production in Asia countries such as Vietnam (5.3 - 6.0 t ha⁻¹), China (5.0 t ha⁻¹), Thailand (4.9 t ha⁻¹) and Pakistan (4.0 t ha⁻¹) (Kilimo-trust, 2012; FAO, 2015). The down fall of production in Tanzania is contributed by number of factors these includes biotic factor, abiotic factor, and poor mechanization , among which the insects and diseases are the most key constraints devastating rice production in Asia and Africa, Tanzania included (Kouassi *et al.*, 2005).

Rice Yellow Mottle Virus (RYMV) emerge as the most important disease devastating production in many rice growing countries in Africa (Hubert *et al.*, 2017). In Tanzania the disease was first reported in 1993 at Mkindo irrigation scheme located in Morogoro. Two years later after the first entry, the disease was spread over the major rice producing regions of the country including Morogoro, Mwanza and Shinyanga (Hubert *et al.*, 2017). The virus causing RYMV belongs to genus *Sobemoviridae*, transmitted mechanically by insect vector in contact with the plant sap (Tamm and Truve, 2000, Hubert *et al.*, 2017).

RYMV is characterized by mottle and yellowing symptoms that are sometimes confused with the deficiency in nitrogen and iron toxicity (Ochola and Tusiime, 2011). Necrosis of the susceptible cultivars leads to plant death (Ochola and Tusiime, 2011). Yield loss due to RYMV reaches up to 100% for the susceptible cultivars. The attributing effect caused by RYMV that leads to total yield loss are reduced tillering ability of the genotype, stunting, asynchronous flowering, poor panicle exertion, discoloration of spikelet, and seed sterility (Muhammadu *et al.*, 2010). Insecticide has been used

to control the insect vectors carrying the viral particles, however the efficiency of this method has no significant impact in control of the pest. Breeding for resistance is the most promising and economical friendly mechanism of limiting infection and yield losses caused by RYMV. The study was undertaken to know the genetic potential of these cultivars in order to be introgressed into the breeding programme for further study.

Material and method

Planting materials

Twenty two genotypes were used in the experiment to screen for resistance to RYMV, among which two genotypes namely Mwangaza and Gigante were used as checks. Details of the materials are presented in the table 1 below.

Table 1. List of Genotype material used for screening against RYMV.

Genotypes	Pedigree	Origin
Komboka	IR 05N 221/IR 79253-55-1-4-6	TARI-Dakawa
ARU 1189	IR77454-22-B-20-2-2-B-7-	Uganda
ARU 1191	IR77454-22-B-20-2-2-B-7-	Uganda
TXD 306	TXD 306-5-B-1	TARI-Dakawa
NamChe 6	NM7-5-2-B-P-79-7	Uganda
ARU 1190	IR77454-22-B-20-2-2-B-7-	Uganda
NamChe 3	NM7-29-4-B-P-80-8	Uganda
NERICA 1	WAB450-1-B-38-HB	TARI-Dakawa
TXD 307	TXD307-1-3-3-2-5	TARI-Dakawa
SATO 1		TARI-Dakawa
TXD 85	TXD 40-85-35-2-3	TARI-Dakawa
TAI	IR 03A 262/IR 77032-47-2-3-3	IRRI-Dakawa
TXD 88	TXD 40-88-B5-1-2	TARI-Dakawa
E 20	NM7-22-11-B-P-1-1	Uganda
Mwangaza		TARI-Dakawa
E 22	NM7-20-4-B-P-1-1	Uganda
NERICA 2		TARI-Dakawa
NamChe5	NM7-27-1-B-P-77-6	Uganda
Gigante		TARI-Dakawa
SATO 9	TXMs44-1-7	TARI-Dakawa
NERICA 4	WAB450-1-B-P-91-HB	TARI-Dakawa
NamChe 1	WAB95-B-B-40-HB	Uganda

Site

The experiment was conducted in the screen house at Tanzania Agricultural Research Institute (TARI) Dakawa. TARI-Dakawa is located in Mvomero District in Morogoro about 45 km from Morogoro Municipaland 2km from Morogoro - Dodoma

highway. The site is located 6°5'S, 37°4'E of Equator and has an altitude of 360m a.s.l.

Experimental design and Layout

The experiment was set out by randomized complete block design in four replications, the genotypes were planted in double rows at spacing of 20 cm x20 cm. Four seeds were planted per hill then thinned into one plant per hill. The trial was set free from weeds by hand weeding, DAP fertilizer was used as basal dressing and Urea as a top dressing fertilizer at the late of 125kg/ha. Irrigation was well observed and at the age of 14 days the plants were inoculated by RYMV inoculum.

Inoculums preparation and Inoculation

The inoculums used for inoculation was collected from the prone affected hotspot area for RYMV in Mkindo, Mvomero-Morogoro. The collected inocula were stored in the refrigerator to ensure the viral particles remain active for inoculation. Thereafter the collected leaves were grinded by use of sterilized mortar and pestle. The grounded leaf tissues were diluted with the distilled water.

Inoculation exercises were done at 14 days old of the experimental genotypes from emergence. Artificial inoculation was conducted where by the inocula were rubbed on the leaves by hand assisted by Carborandum (Silcon Carbide) to ensure microscopic injury for easy penetration of the viral particles. At seven days interval the plants were re-inoculated to ensure no single plant escape from infection.

Data collection

Disease scoring

Disease scoring commenced one week after inoculation in weekly basis, the scale of 1 to 9 was used in scoring data.

According to Zouzou *et al.*, (2008), rated the disease severity score as highly resistant, resistant, moderately resistant, susceptible and highly susceptible as indicated here below.

Table 2. Scoring scale for disease severity (Rice Yellow Mottle Virus).

Scale	Symptom
1	Indicate no any symptom observed
3	Indicates the leaves green but with sparse dots or streak and less than 5% reduction of plant height.
5	Indicates leaves green or pale green with mottling, 6-25% height reduction, flowering slightly delayed.
7	Indicates leaves pale yellow or yellow, 26-75% height reduction, flowering delay.
9	Indicates leaves yellow or orange, more than 75% height reduction, no flowering or some plants dead

Table 3. Rice Yellow Mottle Virus (RYMV) Disease Severity Scoring Scale (Zouzou *et al.*, (2008).

Severity range	Score	Reaction
1-1.5	1	highly resistant
1.6-4.5	3	Resistant
4.6-6.5	5	moderately resistant
6.6-8.5	7	Susceptible
8.6-9.0	9	highly susceptible

Agronomic and Yield data

Agronomic data were collected as per growth stages, such data were tillering ability which was recorded per each hill and plant height which was measured from the ground up to the tip of the shoot in centimeter; other data collected were yield data.

Data analysis

Data were subjected to analysis of variance using Plant Breeding Tools (PB Tools 1.4) and STAR 2.0.1 to obtain the mean squares for both yield component data and disease severity. Area under disease progress curve (AUDPC) was used to calculate progression of disease across the four weeks.

Results

Reaction of genotypes to RYMV

Results showed that there was significant variation among the accessions ($P \leq 0.05$) in reaction to RYMV, indicating that materials tested had diverse genetic backgrounds.

Table 4. Mean square for Rice Yellow Mottle Virus (RYMV) severity scores of 22 rice genotypes over four weeks after artificial inoculation.

Source of Variation	degree of freedom	Week 4	AUDPC	Disease Incidence	Number of Tillers	Plant height	Yield(T)/Ha
Replication	3	35.08	5220.53	1911.65	56.03	338.62	27.08
Genotype	21	24.71*	9394.11*	2680.63	34.28*	347.99*	8.52*
Residual	63	7.298	2451.3	2476.16	20.93	162.86	1.93
Total	87						

Generally, tested materials showed reactions to RYMV across four weeks at different levels. The symptoms varied starting from no symptoms, green leaves with sparse dots or streaks and less than 5% of height reduction, pale green with mottling and 6 to 25% of height reduction, flowering slightly delayed, yellowing and 26-75% of height reduction and lastly more than 75% of height reduction, no flowering and some plants dead. Reactions of the tested materials ranged from highly susceptible to highly resistance.

Namche3 indicated high resistance to RYMV scoring between 1-1.5 above one of the check used. Genotypes E20, E22, Namche 1, Namche 6, Namche 5, and NERICA 4 showed resistance to RYMV scoring between 1.6-6.5, TXD 88 and TXD 306 indicated as moderately susceptible with score ranged from 4.6-6.5. The genotypes TXD 85, TXD 307, TAI, SATO 9, SATO 1, NERICA 2, NERICA 1, Komboka, ARU 1191, ARU 1190, and ARU 1189 reacted as susceptible to RYMV scoring between 6.6-8.5.

Table 5. Reaction of twenty two rice genotypes to RYMV inoculation over four weeks.

Genotype	Disease severity				Reaction to RYMV	AUDPC	r AUDPC
	Week 1	Week 2	Week 3	Week 4			
ARU 1189	2.50	8.50	8.00	8.00	S	170.50	82.37
ARU 1190	2.00	6.00	7.00	7.00	S	132.00	63.77
ARU 1191	3.00	5.50	6.50	7.00	S	125.75	60.75
E 20	3.00	1.00	1.50	2.50	R	34.00	16.43
E 22	1.50	1.50	1.50	2.00	R	34.50	16.66
Gigante	1.00	5.00	5.00	5.00	MR	101.00	48.79
Komboka	3.50	7.00	7.00	8.00	S	148.75	71.86
Mwangaza	1.00	1.00	1.00	1.00	HR	23.00	11.11
Namche1	3.00	3.50	3.50	3.50	R	78.75	38.04
Namche3	1.00	1.00	1.00	1.00	HR	23.00	11.11
Namche6	1.00	1.00	3.50	4.00	R	43.00	20.77
Namche5	1.00	1.00	3.00	3.00	R	39.00	18.84
NERICA 1	1.00	3.00	7.00	7.00	S	94.00	45.41
NERICA 2	1.50	3.00	7.00	7.00	S	95.75	46.26
NERICA 4	1.00	1.50	3.50	3.50	R	48.75	23.55
SATO 1	5.00	6.00	6.50	7.50	S	138.50	66.91
SATO 9	2.50	6.00	6.00	7.00	S	125.75	60.75
TAI	1.00	6.00	8.00	8.00	S	136.50	65.94
TXD 306	1.50	7.00	6.00	6.50	MR	133.75	64.61
TXD 307	2.00	4.50	7.00	8.00	S	114.75	55.43
TXD 85	4.50	8.00	7.50	8.50	S	167.75	81.04
TXD 88	3.00	5.50	6.00	6.50	MR	121.75	58.81
Grand mean	2.11	4.20	5.14	5.52		35.01	46.78
%cv	89.17	59.97	54.24	48.92		51.13	51.13
Sed	1.33	1.78	1.97	1.91		96.84	16.91

Effect of RYMV in yield components by artificial inoculation at TARI-Dakawa

The results presented in table 6 revealed RYMV affected the genotypes performance in yield and yield components. The genotypes grouped as HR, R, and MR indicated less reduction in both plant height, number of tillers and 1000 grain weight as compared to the susceptible ones. The genotypes ARU 1190, SATO 1, TXD 307 and TXD 85 showed clearly the yield

performance were affected by the viral infections, the effect was observed on reduction in 1000 grain weight, number of tillers and the plant height. The genotypes TAI and Komboka behaved differently from the rest of the genotypes, the two genotypes indicated as susceptible to RYMV however the yield performance were not affected. This requires further studies through subjecting them into different RYMV strains and molecular studies to confirm their tolerance.

Table 6. Response of twenty two rice genotype on artificial inoculation of RYMV and its effect on yield and yield components at TARI Dakawa.

Genotype	Week 4	Disease Incidence	Reaction to RYMV	Number of tillers	Plant Height	YIELD(t)/ha
ARU 1189	8.00	86.36	S	8.75	105.00	3.15
ARU 1190	7.00	53.37	S	10.25	108.75	1.13
ARU 1191	7.00	37.11	S	10.75	93.88	3.21
E 20	2.50	41.00	R	4.50	107.50	3.36
E 22	2.00	62.10	R	5.00	105.25	3.85
Gigante	5.00	54.97	MR	11.75	113.88	6.77
Komboka	8.00	35.85	S	12.75	100.12	5.32
Mwangaza	1.00	30.84	HR	9.75	116.62	3.10
Namche1	3.50	17.68	R	6.00	118.75	4.98
Namche3	1.00	19.68	HR	8.75	112.75	4.50
Namche6	4.00	12.05	R	5.25	111.25	4.13
Namche5	3.00	15.04	R	4.50	112.62	4.88
NERICA 1	7.00	40.24	S	10.75	93.75	3.45
NERICA 2	7.00	44.40	S	9.75	95.25	3.21
NERICA 4	3.50	21.13	R	6.00	97.50	4.49
SATO 1	7.50	58.16	S	10.75	89.00	1.95
SATO 9	7.00	14.23	S	11.75	96.25	3.51
TAI	8.00	51.22	S	10.00	98.88	5.38
TXD 306	6.50	69.81	MR	12.75	90.00	4.20
TXD 307	8.00	92.68	S	14.50	91.25	1.40
TXD 85	8.50	61.02	S	11.50	92.62	0.92
TXD 88	6.50	102.59	MR	10.25	97.50	2.61
Grand mean	5.52	46.43		9.36	102.20	3.61
%cv	48.92	107.17		48.86	12.49	38.47
Sed	1.91	35.19		3.23	9.02	0.98

Discussion

Rice productivity in Sub-Saharan Africa is seriously threatened by Rice Yellow Mottle Virus (RYMV) (Salaudeen M.T., 2014). Among the tested genotypes (upland and lowland) the disease indicated slow progression on the upland varieties as compared to the lowland varieties. This agrees with the previous study by Zouzou *et al.*, 2008 who observed the same

phenomenon implying that the aggressiveness of the isolates used were more active in lowland rice genotypes as compared to the uplands.

Losses caused by RYMV have raised attention to screen several rice genotypes to identify the source of resistance genes for introgression into farmers' preferred varieties. Study results indicated variations

among the 22 genotypes tested in reaction to RYMV inoculation, implying that the materials tested have different genetic backgrounds. None of the varieties tested were immune to RYMV but few varieties were highly resistant to RYMV as observed in other studies (Mogga *et al.* 2012; Munganyinka *et al.*, 2016). Distinctive RYMV symptoms were observed one week post inoculation and clear symptoms development was observed two weeks post inoculation. Most genotypes displayed maximum disease symptoms three to four weeks post inoculation as observed in other studies (Zouzou *et al.*, 2008).

The current study on rice yellow mottle virus pathogenicity indicated the tested genotypes falls into four groups which are highly resistance (HR), resistance (R), moderately resistance (MR) and susceptible (S). The genotype Namche 3 was grouped in the same group with the local check Mwangaza as highly resistance. The genotypes E20, E22, Namche5 and NERICA 4 were grouped as resistance while TXD 306, TXD 88 and Gigante grouped as the moderately resistance genotypes. This result agrees with the study conducted in Uganda by Munganyinka *et al.*, 2016 which identified NERICA 4 and Gigante as moderately resistance to RYMV and a study by Traure *et al.*, 2015 in Burkina Faso and Ghana which pointed Gigante as a moderate resistant variety. However most of the tested genotypes were grouped as susceptible to rice yellow mottle virus.

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