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Reactions and Resistance Status of Differential Rice Genotypes to Rice Yellow Mottle Virus, Genus *Sobemovirus* in Cote d'Ivoire

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Abstract: High yielding rice genotypes with good levels of resistance to RYMV were identified at Africa Rice Center-WARDA in Cote d'Ivoire. The yields and resistance stability of these genotypes, however, remain uncertain. The performance of 13 genotypes over 10 different RYMV isolates from 7 localities in Cote d'Ivoire was tested in the screenhouse. Chlorophyll (SPAD) and yield reductions due to RYMV disease were evaluated. Considerable diversity was observed in the reactions of these genotypes to all the RYMV isolates. Percentage yields and SPAD reduction were between 2.3-90.3 and 5.3-40%, respectively. Of 13 rice genotypes studied, IR 47686-15-1-1(P) had the lowest mean SPAD and yield reductions. The levels of resistance shown by japonicas were better than those of indicas. Six genotypes (FARO 11; GIGANTE (tete); H 232-44-1-1; IR 47686-15-1-1(P); IR 47686-15-1-1; ITA 235) could be described as possessing both stable and acceptable levels of resistance to RYMV. The high genotype by environment interactions in the reactions of the rice genotypes to RYMV suggests the possible existence of different strains of RYMV in Cote d'Ivoire. This information could be useful in rice breeding programs aiming at deployment of RYMV resistant genotypes to different rice ecologies and localities in Cote d'Ivoire.

Key words: RYMV, reaction, genotype, SPAD reduction, yield reduction, indica, japonica

INTRODUCTION

Rice Yellow Mottle Virus (RYMV), genus sobemovirus, is the only known virus disease of rice in Africa and it is indigenous to the continent. RYMV was first described in 1966 in Kenya[1] and has subsequently been reported throughout West Africa, Madagascar, Tanzania, Zanzibar and most recently Mozambique.

RYMV is highly infectious, environmentally stable and is transmitted both mechanically and by Chrysomelid beetle vectors in the field[2-4]. The spread of the disease has been facilitated by intensive agriculture husbandry practise[5] and this disease is limited to rainfed and irrigated lowlands and can be lethal to the infested plants if infection occurs early. The virus, depending on the genotype, causes yellowing, mottling and stunting of infected plants with narrowing of emerging leaves. Infection leads to incomplete emergence of the panicle with sterile or unfilled grains. When infection occurs early, the plant normally dies. RYMV is one of the most economically damaging diseases of rice in sub-Saharan Africa[6]. The estimated reduction in yield due to RYMV infection in susceptible lowland cultivars was up to 97%[7] and as high as 54% in a tolerant upland cultivars[8].

At present, varietal resistance seems the most promising control mechanism. However, immunity to the virus is only found in *Oryza glaberrima* landraces and good sources of tolerance have so far been identified only in tropical japonica *O. sativa* rices. But lowland farmers generally prefer the higher-yielding indica rices, among which no sources of strong resistance have been found to date[6]. In fact, all major rice varieties grown in West African lowlands, such as Bouaké 189, Jaya, BG 90-2 and IR 1529-680-3, are highly susceptible to RYMV[9].

The aim of this study was to investigate the reactions and resistance status of differential rice genotypes to Rice yellow mottle virus in Cote d'Ivoire. Besides, pathogen-varietal resistance mechanism will be used to identify and characterise rice genotypes for stable resistance to RYMV as such information is useful for developing rice varieties with durable resistant to RYMV in Cote d'Ivoire.

MATERIALS AND METHODS

Rice genotypes: Thirteen differential rice genotypes (Table 1) used in this study were obtained from WARDA and NARS partners in Mali and Niger.

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Table 1: Identity of differential rice genotype used

Codes	Genotypes	Varieties
V_1	ADNY 11	Indica
V_2	BOUAKE 189	Indica
V_3	CHIANUNG SEN YU	Japonica
V_4	FARO 11	Japonica
V_5	GIGANTE (tete)	Indica
V_6	H 232-44-1-1	Indica
V_7	IR 47686-15-1-1(P)	Japonica
V_8	IR 47686-15-1-1	Japonica
V_9	ITA 235	Japonica
V_{10}	LAC 23	Japonica
V_{11}	LEIZHUNG	Indica
V_{12}	MOROBEREKAN	Japonica
V_{13}	PNA 647F4-56	Japonica

Table 2: Identity of RYMV isolates used for pathological study

Codes	Isolates	Country of origin	Localities	Ecosystems
KA	KGO-1	Cote d'Ivoire	Korhogo	Irrigated
KC	KGO-34	Cote d'Ivoire	Korhogo	Irrigated
KB	KGO-24	Cote d'Ivoire	Korhogo	Irrigated
TG	TGL-5	Cote d'Ivoire	Tengrela	Lowland
BE	BDL-5	Cote d'Ivoire	Boundiali	Upland
BH	BDL-8	Cote d'Ivoire	Boundiali	Upland
BC	BFL-3	Cote d'Ivoire	Bouafle	Irrigated
AD	ADZP-11	Cote d'Ivoire	Adzope	Irrigated
TP	TLP-17	Cote d'Ivoire	Toulepleu	Irrigated
AR	ABGR-16	Cote d'Ivoire	Abengourou	Lowland

RYMV isolates: Ten atypical RYMV isolates (Table 2) used for this study were originated from 7 different localities in Cote d'Ivoire. They were obtained from plant pathology unit, WARDA. Before used, each isolate was first propagated in the susceptible rice variety Bouake189, following mechanical inoculation of 28 old plants in the screenhouse. Four weeks after inoculation, leaves from each RYMV isolate bearing typical yellow mottle symptoms were harvested and used for inoculating rice genotypes.

Inoculation of rice genotypes: The thirteen young differential rice genotypes were inoculated mechanically[10] with the 10 isolates in the screenhouse 20 days after direct seedling in 3 replicates. Another sets of same thirteen young differential rice genotypes in 3 replicates not inoculated were used as controls. Infected leaf samples of each RYMV isolate were ground with 0.01 M phosphate buffer pH 7.0 at the ratio of 1:10 (w/v) and the resulting homogenate filtered through cheesecloth. Carborundum powder (600 mesh) was added to the inoculum to aid the penetration of the virus into leaf tissues. Each rice plant was inoculated thrice same day.

SPAD and yield measurement: Chlorophyll (SPAD) and yield reductions due to RYMV disease were evaluated. Yields were measured at maturity for all the rice genotypes while SPAD was measured using SPAD 502 Chlorophyll Meter[11,12] at 42 days after inoculation. SPAD and yield measurement were obtained both for test and control genotypes.

Data analysis: Using SPAD and yield data from both test and control genotypes, percentage SPAD and yield reductions due to RYMV disease were determined for each genotype. IRRISTAT version 4.3 statistical software was used for all the analyses. Variance and mean comparison of percentage SPAD and yield reductions were analyzed. Genotype (cultivar) by environment (isolate) interaction effects on SPAD and yield reductions was carried out using Additive Main effect and Multiplicative Interaction (AMMI) analysis[13]. Cluster dendograms showing classification of genotype (cultivar) levels of resistance to environment (isolate) and classification of environment (isolate) pathogenic level to genotype (cultivar) were plotted using AMMI analysis.

RESULTS

Considerable diversity was observed in the reactions of 13 rice genotypes to 10 RYMV isolates from 7 different localities in Cote d'Ivoire in terms of SPAD and yield reductions (Table 3). Percentage yield and SPAD reductions, due to RYMV disease, were

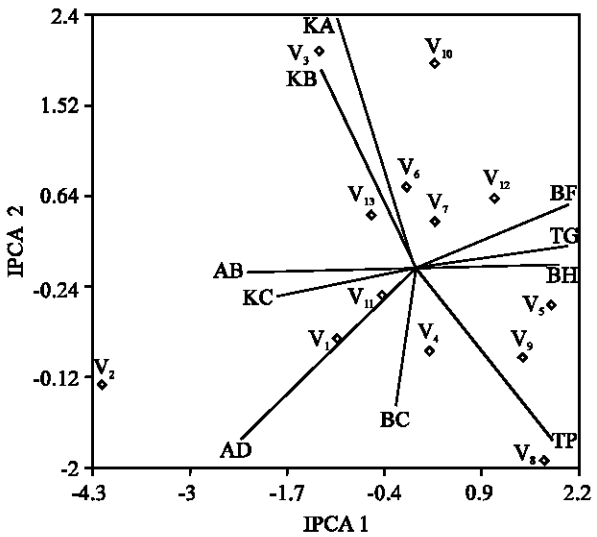

Fig. 1: Genotype (cultivar) by environment (isolate) interaction effects on SPAD reduction using additive main effects and multiplicate interaction (AMMI) analysis. Genotype: V_1= ADNY 11; V_2 = BOUAKE 189; V_3= CHIANUNG SEN YU; V_4= FARO 11; V_5= GIGANTE; V_6= H 232-44-1-1; V_7 = IR 47686-15-1-1(P); V_8= IR 47686-15-1-1; V_9 = ITA 235; V_{10}= LAC 23; V_{11}= LEIZHUNG; V_{12} = MOROBEREKAN; V_{13} = PNA 647F4-56. Environment: KA = KGO-1; KC = KGO-34; KB = KGO-24; TG = TGL-5; BE = BDL-5; BH = BDL-8; BC= BFL-3; AD= ADZP-11; TP= TLP-1; AR= ABGR-16

Table 3: Analysis of variance for percentage SPAD reduction (% Spadr) and yields reduction (% Yieldr)

	% Spadr				% Yieldr		
Sources	DF	SS	MS	F	SS	MS	F
Treatment	129	18868	146	2.28**	129091	1001	3.46**
Variety (V)	12	4545	379	5.92**	45115	3760	12.99**
Isolate (I)	9	5225	581	9.07**	4658	518	1.79ns
VxI	108	9098	84	1.32*	79319	734	2.54**
Error	260	16644	64		75229	289	
Total	389	35512			204321		

** = significant at 1% level, * = significant at 5% level, ns = not significant

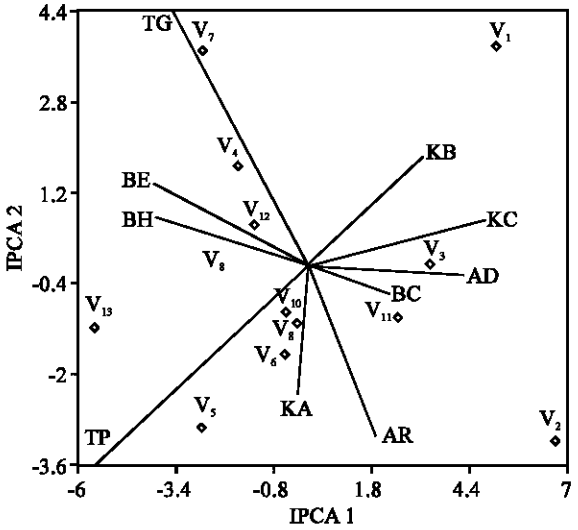

Fig. 2: Genotype (cultivar) by environment (isolate) interaction effects on yield reduction using Additive Main effects and Multiplicate Interaction (AMMI) analysis. Genotype: V_1 = ADNY 11; V_2 = BOUAKE 189; V_3 = CHIANUNG SEN YU; V_4 = FARO 11; V_5 = GIGANTE; V_6 = H 232-44-1-1; V_7 = IR 47686-15-1-1(P); V_8 = IR 47686-15-1-1; V_9 = ITA 235; V_{10} = LAC 23; V_{11} = LEIZHUNG; V_{12} = MOROBEREKAN; V_{13} = PNA 647F4-56. Environment: KA = KGO-1; KC = KGO-34; KB = KGO-24; TG = TGL-5; BE = BDL-5; BH = BDL-8; BC = BFL-3; AD = ADZP-11; TP= TLP-1; AR= ABGR-16

between 2.3-90.3 and 5.3-40%, respectively (Table 4 and 5). Of 13 rice genotypes studied, IR 47686-15-1-1(P) had the lowest mean SPAD and yield reduction. According to AMMI analysis, KA, KB and TG isolates were responsible mainly for unfavourable interactive conditions leading to significant yield and SPAD reduction in all the rice cultivars (Fig. 1 and 2). Based on cluster dendrogram classification for isolates pathogenic and genotypes viral resistance levels, 6 isolates (KA, KB, AD, AR, KC) were highly pathogenic and 4 isolates

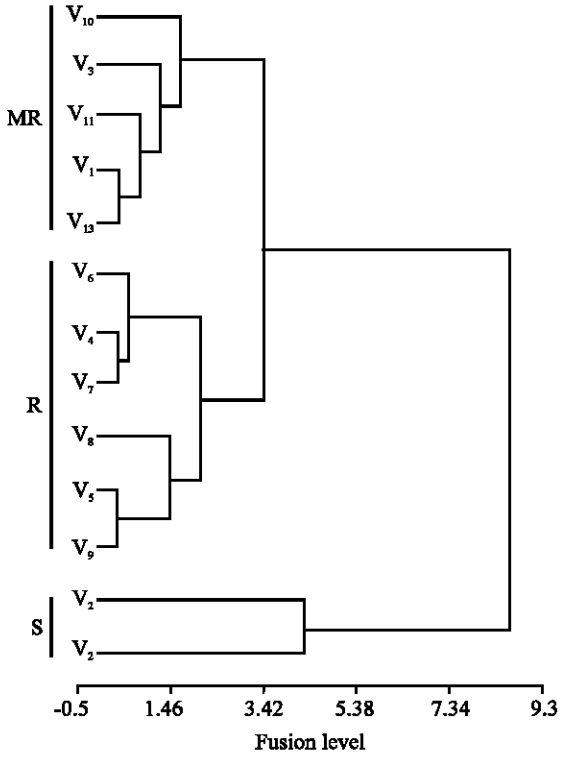

Fig. 3: Cluster dendrogram showing classification of genotype (cultivar) level of resistance to environment (isolate) using Additive Main effects and Multiplicate Interaction (AMMI) analysis. Genotype: V_1 = ADNY 11; V_2 = BOUAKE 189; V_3 = CHIANUNG SEN YU; V_4 = FARO 11; V_5 = GIGANTE; V_6 = H 232-44-1-1; V_7 = IR 47686-15-1-1(P); V_8 = IR 47686-15-1-1; V_9 = ITA 235; V_{10} = LAC 23; V_{11} = LEIZHUNG; V_{12} = MOROBEREKAN; V_{13} = PNA 647F4-56. R = Resistant; MR = Moderately resistant; S = Susceptible

(BE, BH, TG, TP) were mildly pathogenic, while 6 genotypes (V_4, V_5, V_6, V_7, V_8, V_9) were highly resistant, 5 genotypes (V_1, V_3, V_{10}, V_{11}, V_{13}) were moderately resistant and 2 genotypes (V_2, V_{12}) were susceptible (Fig. 3 and 4).

DISCUSSION

The Additive Main effect and Multiplicative Interaction (AMMI) analysis has been shown to be effective in understanding complex Genotype by Environment (GE) interactions typical of National Turfgrass Evaluation Program (NTEP) variety trials[14]. Interactions in such complex data sets are difficult to understand with ordinary analysis of variance (ANOVA). Genotype by environment interaction can be defined as the differential response of

Table 4: Analysis of means comparison for percentage SPAD reduction due to RYMV disease

	RYMV Isolates										
Varieties (V)	KGO-1	KGO-34	KGO-24	TGL-5	BDL-5	BDL-8	BFL-3	ADZP-11	TLP-1	ABGR-16	V-Mean
ADNY 11	15.0ab	12.3a	23.7b-d	4.0c	9.0a	8.3a	18.3bc	25.3bc	7.3b	27.3ab	15.1
BOUAKE 189	25.7a	20.0a	38.7a	14.0a-c	15.0a	10.0a	28.0ab	40.0a	8.7ab	33.0a	23.3
CHIANUNG SEN YU	14.3ab	19.7a	26.3a-c	10.0a-c	9.0a	14.3a	21.0a-c	20.3b-d	6.0b	19.0a-d	16.0
FARO 11	10.7ab	8.3a	12.3c-e	9.0bc	5.3a	11.0a	19.0a-c	10.7cd	11.0ab	6.0d	10.3
Gigante(tete)	17.0ab	12.3a	22.7b-d	16.7a-c	18.0a	17.3a	19.7a-c	14.7b-d	19.0ab	12.3b-d	17.0
H 232-44-1-1	12.3ab	18.3a	28.3ab	11.3a-c	19.0a	9.0a	14.3bc	18.7b-d	10.7ab	15.7b-d	15.8
IR 47686-15-1-1(P)	9.7b	15.0a	7.7e	6.7bc	7.0a	6.0a	10.0c	7.3d	10.7ab	17.7b-d	9.8
IR 47686-15-1-1	24.7ab	18.0a	11.3de	24.7a	20.7a	11.3a	17.7bc	16.7b-d	20.3ab	10.0cd	17.5
ITA 235	18.3ab	12.0a	19.3b-e	14.0a-c	13.7a	11.0a	15.7bc	16.3b-d	23.3a	12.3b-d	15.6
LAC 23	15.7ab	16.3a	29.3ab	10.3a-c	16.0a	15.3a	19.0a-c	15.3b-d	12.7ab	25.3ab	17.5
LEIZHUNG	16.7ab	16.7a	27.0a-c	9.0bc	15.0a	10.0a	33.3a	29.0ab	11.7ab	24.0a-c	19.2
MOROBEREKAN	20.7ab	12.0a	22.3b-d	19.3ab	20.0a	15.0a	18.0bc	23.3bc	18.0ab	25.7ab	19.4
PNA 647F4-56	11.0ab	20.7a	24.3a-d	7.7bc	15.3a	10.0a	26.7ab	24.3bc	7.3b	16.7b-d	16.4
I-MEAN	16.3	15.5	22.6	12.1	14.1	11.4	20.1	20.2	12.8	18.8	16.4

Table 5: Analysis of means comparison for percentage yields reduction due to RYMV disease

	RYMV Isolates										
Varieties (V)	KGO-1	KGO-34	KGO-24	TGL-5	BDL-5	BDL-8	BFL-3	ADZP-11	TLP-1	ABGR-16	V-Mean
ADNY 11	32.7ab	71.7abc	69.7ab	47.0ab	26.3abc	23.0b	59.3a-c	69.7ab	12.7c	45.0b -d	45.7
BOUAKE 189	61.7a	79.7a	90.3a	10.0c	21.3c	31.0b	75.3a	89.3a	35.3bc	77.7a	57.2
CHIANUNG SEN YU	53.0a	77.0ab	66.7a-c	53.7ab	38.0a-c	42.7b	77.3a	78.7a	46.0b	74.0ab	60.7
FARO 11	37.3ab	24.0de	41.7b-e	37.0abc	46.3a-c	41.0b	54.0a-c	24.7de	38.0bc	20.0de	36.4
GIGANTE(tete)	36.3ab	11.3e	17.7e	26.3bc	28.3a-c	21.0b	43.3b-d	14.3de	61.7b	24.3de	28.5
H 232-44-1-1	40.3a	48.7bcd	35.0de	33.0abc	29.3a-c	36.3b	33.3cd	34.7de	55.0b	45.3b-d	39.1
IR 47686-15-1-1(P)	9.3b	11.3e	33.0de	41.0abc	28.3a-c	31.3b	12.3d	12.0e	32.0bc	2.3e	21.3
IR 47686-15-1-1	41.0a	23.3de	25.7e	36.0abc	23.7bc	50.7ab	30.7cd	34.0de	33.3bc	33.3cd	33.2
ITA 235	37.3ab	30.0de	29.0e	22.0bc	35.7a-c	35.0b	32.0cd	45.7b-d	35.7bc	34.0cd	33.6
LAC 23	42.3a	45.3cd	29.7e	35.3abc	53.7a-c	21.7b	37.7b-d	33.7de	42.3bc	49.0a-d	39.1
LEIZHUNG	42.7a	44.3cd	61.7a-d	35.3abc	40.0a-c	39.3b	68.3ab	66.3a-c	41.3bc	59.3a -c	49.9
MOROBEREKAN	46.7a	31.7de	39.3b-e	41.3abc	56.0ab	33.7b	47.7abc	35.7de	39.0bc	42.0cd	41.3
PNA 647F4-56	32.3ab	10.0e	37.7c-e	61.0a	58.3a	73.3a	38.0bcd	39.7c-e	89.3a	50.7a-d	49.0
I-MEAN	39.5	39.1	44.4	36.8	37.3	36.9	46.9	44.5	43.2	42.8	41.1

In a column, means followed by a common letter(s) are not significantly different at the 5% level by Duncan's Multiple Range Test

varying genotypes under changes in the environment[15]. When populations are not confined to one area, individuals must have the genetic make-up to survive in the environment they live in. In the current study, 10 RYMV isolates used covered major rice ecologies from seven different localities in Cote d'Ivoire leading to very high RYMV interactions among rice genotypes. The existence of different RYMV isolates or strains[16] have led to differential interactions with heavy implications on the genotype resistance and yield stability.

As revealed by this study, genotypes pathogenic resistance to different RYMV isolates first occurs at the level of the individual and involves physiological or behavioral tolerance or adaptability. Subsequent response to increasing viral pathogenicity may involve survival only of the better-adapted genotypes[13,17]. Six genotypes (V_4, V_5, V_6, V_7, V_8, V_9), out of 13 (Fig. 3), could be described as possessing both stable and acceptable levels of resistance to RYMV. Under different rice ecologies in Cote d'Ivoire, these 6 genotypes possessed heterogenous viral resistance characteristics making them to be more stable, adaptable and more resistant to stress induced by different isolates or strains originated from different localities. Genotypes that have adapted to endure variable isolates or strains infestations are more likely to tolerate an independent stress compared to those genotypes that are only adapted to a fixed isolate or strain[17,18].

As RYMV isolates population increases, there is probability that each of the 6 resistance genotypes obtained in this study will survive and evolve through combinations of genes present in the population[17,19]. Population resistance is enhanced by genes polymorphism that may result in short-term selection of more tolerant genotypes in stressful viral environments[14,17]. This possibly explained why the levels of resistance shown by japonicas were better than those of indicas.

Conclusively, the high genotypes by environment interactions in the reactions of the rice genotypes to

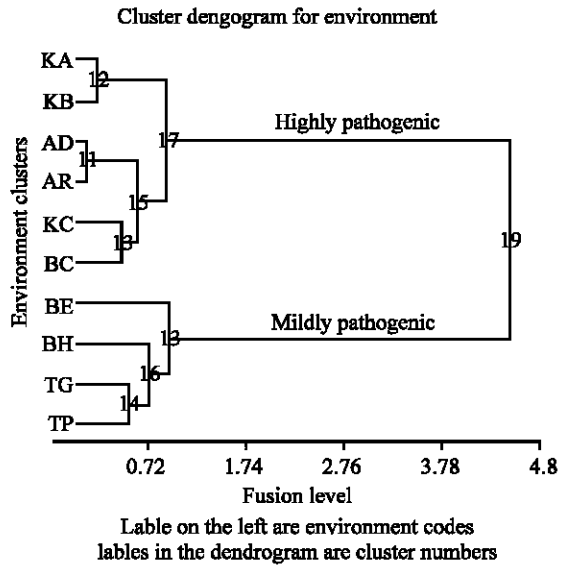

Fig. 4: Cluster dendrogram showing classification of environment (isolate) pathogenic level to genotype (cultivar) using additive main effects and multiplicate interaction (AMMI) analysis. Environment: KA = KGO-1; KC = KGO-34; KB = KGO-24; TG = TGL-5; BE = BDL-5; BH = BDL-8; BC = BFL-3; AD = ADZP-11; TP = TLP-1; AR= ABGR-16

RYMV suggest the possible existence of different strains of RYMV in Cote d'Ivoire. This information could be useful in the rice breeding programs aiming at deployment of RYMV resistant genotypes to different rice ecologies and localities in Cote d'Ivoire.

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