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 greenhouse. 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 232-441-1; 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[2,3]. The spread of the disease has been facilitated by intensive agriculture husbandry practices[3] 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 infested 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%[4] and as high as 54% in a tolerant upland cultivars[5].

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 rice. But lowland farmers generally prefer the higher-yielding indica rice, 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[6].

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.
Table 1: Identity of differential rice genotype used

<table>
<thead>
<tr>
<th>Codes</th>
<th>Genotypes</th>
<th>Varieties</th>
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</thead>
<tbody>
<tr>
<td>V1</td>
<td>ADNY 11</td>
<td>Indica</td>
</tr>
<tr>
<td>V2</td>
<td>BOUAKE 189</td>
<td>Indica</td>
</tr>
<tr>
<td>V3</td>
<td>CHANUNG SEN YU</td>
<td>Japonica</td>
</tr>
<tr>
<td>V4</td>
<td>FARO 11</td>
<td>Japonica</td>
</tr>
<tr>
<td>V5</td>
<td>GIGANTE (tet)</td>
<td>Indica</td>
</tr>
<tr>
<td>V6</td>
<td>H 232-44-1-1</td>
<td>Indica</td>
</tr>
<tr>
<td>V7</td>
<td>IR 47686-15-1-1(P)</td>
<td>Japonica</td>
</tr>
<tr>
<td>V8</td>
<td>IR 47686-15-1-1</td>
<td>Japonica</td>
</tr>
<tr>
<td>V9</td>
<td>ITA 235</td>
<td>Japonica</td>
</tr>
<tr>
<td>V10</td>
<td>LAC 23</td>
<td>Japonica</td>
</tr>
<tr>
<td>V11</td>
<td>LEIZHUNG</td>
<td>Indica</td>
</tr>
<tr>
<td>V12</td>
<td>MOROBEREKAN</td>
<td>Japonica</td>
</tr>
<tr>
<td>V13</td>
<td>PNA 647F4-56</td>
<td>Japonica</td>
</tr>
</tbody>
</table>

Table 2: Identity of RYMV isolates used for pathological study

<table>
<thead>
<tr>
<th>Codes</th>
<th>Isolates</th>
<th>Country of origin</th>
<th>Localities</th>
<th>Ecosystems</th>
</tr>
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<tbody>
<tr>
<td>KA</td>
<td>KGO-1</td>
<td>Cote d'Ivoire</td>
<td>Korhogo</td>
<td>Irrigated</td>
</tr>
<tr>
<td>KC</td>
<td>KGO-34</td>
<td>Cote d'Ivoire</td>
<td>Korhogo</td>
<td>Irrigated</td>
</tr>
<tr>
<td>KB</td>
<td>KGO-24</td>
<td>Cote d'Ivoire</td>
<td>Korhogo</td>
<td>Irrigated</td>
</tr>
<tr>
<td>TG</td>
<td>TGL-5</td>
<td>Cote d'Ivoire</td>
<td>Tangrela</td>
<td>Lowland</td>
</tr>
<tr>
<td>BE</td>
<td>BDL-5</td>
<td>Cote d'Ivoire</td>
<td>Boundiali</td>
<td>Upland</td>
</tr>
<tr>
<td>BH</td>
<td>BDL-8</td>
<td>Cote d'Ivoire</td>
<td>Boundiali</td>
<td>Upland</td>
</tr>
<tr>
<td>BC</td>
<td>BFL-3</td>
<td>Cote d'Ivoire</td>
<td>Boualle</td>
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<tr>
<td>AD</td>
<td>ADZP-11</td>
<td>Cote d'Ivoire</td>
<td>Adzope</td>
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</tr>
<tr>
<td>TP</td>
<td>TLP-17</td>
<td>Cote d'Ivoire</td>
<td>Toulepleu</td>
<td>Irrigated</td>
</tr>
<tr>
<td>AR</td>
<td>ABGR-16</td>
<td>Cote d'Ivoire</td>
<td>Abengourou</td>
<td>Lowland</td>
</tr>
</tbody>
</table>

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, WARDIA. Before used, each isolate was first propagated in the susceptible rice variety Bouake189, following mechanical inoculation of 28 old plants in the greenhouse. 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[20] with the 10 isolates in the greenhouse 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[21,22] 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[19]. 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 multiplicative interaction (AMMI) analysis. Genotype: V1 = ADNY 11; V2 = BOUAKE 189; V3 = CHANUNG SEN YU; V4 = FARO 11; V5 = GIGANTE; V6 = H 232-44-1-1; V7 = IR 47686-15-1-1(P); V8 = IR 47686-15-1-1; V9 = ITA 235; V10 = LAC 23; V11 = LEIZHUNG; V12 = MOROBEREKAN; V13 = 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-16; AR = ABGR-16.](image-url)
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 (BE, BH, TG, TP) were mildly pathogenic, while 6 genotypes (V_1, V_2, V_3, V_4, V_5, V_6) were highly resistant, 5 genotypes (V_7, V_8, V_9, V_10, V_11) were moderately resistant and 2 genotypes (V_12, V_13) 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 trials⁴⁴. 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
varying genotypes under changes in the environment\textsuperscript{[20]}. 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\textsuperscript{[19]} 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\textsuperscript{[21,22]}. Six genotypes (Vs, Vg, Vm, Vc, Vm, Vm), 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\textsuperscript{[23]}.\textsuperscript{[24]}

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\textsuperscript{[25,26]}. Population resistance is enhanced by genes polymorphism that may result in short-term selection of more tolerant genotypes in stressful viral environments\textsuperscript{[27,28]}. 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 multiplicative 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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REFERENCES


