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Genetic variations of rice yellow mottle virus disease on selected rice (*Oryza sativa* L) genotypes and their effects on yield and yield-related traits

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Abstract

Rice yellow mottle virus (RYMV) is one of the most important disease affecting rice production in Africa. This research aimed to estimate the effect of RYMV disease on some yield-related traits in Korean rice germplasm recently introduced into Ghana and identify new sources of RYMV resistance for use in breeding. One hundred and seventy-six (176) rice genotypes including two highly resistant and a susceptible check, were used for this research. The experiment was laid in 4 × 44 lattice design with four replications in RYMV inoculated and non-RYMV inoculated environments in a screen house at CSIR-Crops Research Institute (CRI), Fumesua, Ghana, in 2019. The non-RYMV inoculated environment served as a control. Significant positive correlations were observed between disease severity and percentage grain yield reduction. RYMV reduced the culm length, tiller number, plant height, panicle number, biomass, and grain yield. The first five principal components explained 92.39% of the variation in the germplasm, with panicle number, tiller number, heading date, grain yield/plant and disease severity being the main discriminatory traits. The biplot indicated that genotypes 8261112 and 8261119, together with Gigante and Tog7291 (resistant checks), were the least impacted by the disease. We identified four main clusters from the hierarchical cluster analysis. Five highly resistant and 10 resistant genotypes were identified. The newly identified resistant genotypes will be used in breeding for resistance to RYMV disease in Africa.

Keywords: Disease severity; principal components; days to heading; hierarchical cluster analysis

Variations Génétiques de la Maladie Du Virus de la Panachure Jaune du Riz Sur des Génotypes Sélectionnés De Riz *(oryza Sativa* L) Et Leurs Effets Sur Le Rendement Et Les Caractères Liés Au Rendement

Résumé

Le virus de la panachure jaune du riz (RYMV) est l'une des maladies les plus importantes affectant la production de riz en Afrique. Cette recherche visait à estimer l'effet de la maladie du RYMV sur certaines caractéristiques liées au rendement dans le matériel génétique du riz coréen récemment introduit au Ghana et à identifier de nouvelles sources de résistance au RYMV à utiliser dans la sélection. Cent soixante-seize génotypes de riz, dont deux très résistants et un sensible, ont été utilisés pour cette recherche. L'expérience a été menée selon un plan en treillis 4 × 44 avec quatre répétitions dans des environnements inoculés par le RYMV et non inoculés par le RYMV dans une maison-écran au CSIR-Crops Research Institute (CRI), Fumesua, Ghana, en 2019. L'environnement non inoculé par le RYMV a servi de contrôle. Des corrélations positives significatives ont été observées entre la gravité de la maladie et le pourcentage de réduction du rendement en grains. Le RYMV a réduit la longueur des chaumes, le nombre de tiges, la hauteur des plantes, le nombre de panicules, la biomasse et le rendement en grains. Les cinq premières composantes principales expliquent 92,39 % de la variation dans le germoplasme, le nombre de panicules, le nombre de tiges, la date d'épiaison, le rendement en grains/plante et la gravité de la maladie étant les principaux caractères discriminatoires. Le biplot indique que les génotypes 8261112 et 8261119, ainsi que Gigante et Tog7291 (témoins résistants), ont été les moins touchés par la maladie. Nous avons identifié quatre groupes principaux à partir de l'analyse hiérarchique des groupes. Cinq génotypes hautement résistants et 10 génotypes résistants ont été identifiés. Les génotypes résistants nouvellement identifiés seront utilisés dans la sélection pour la résistance à la maladie RYMV en Afrique.

Mots Clés: Gravité de la maladie; composantes principales; jours jusqu'à l'épiaison; analyse hiérarchique en grappes.

Introduction

Rice production in Africa is challenged by many abiotic and biotic stresses of which diseases feature prominently (Séré *et al.,* 2013). Rice yellow mottle virus (RYMV) disease is one of the most damaging rice disease in Africa (Okioma & Sarkarung, 1983; Traore *et al.,* 2006; Traoré *et al.,* 2009; Suvi *et al.,* 2018; Agnoun *et al.,* 2019). It has been reported in all major rice growing ecologies in Africa at varying degrees of incidence and severity that appear to be dependent on the type of variety planted, the rice ecology (upland, lowland or irrigated), the climatic conditions under which the rice is cultivated, and age of the rice plant at infection (Awoderu, 1991). RYMV has a more devastating effect on rice plants infected at the seedling stage than a late-stage infection (Onwughalu *et al.,* 2010). Among the three major diseases of rice in Africa, RYMV was observed to be the most severe in rain-fed lowlands followed by rice blast, whereas, bacterial blight was more of a problem in irrigated rice fields (Traore *et al.,* 2015). Research conducted by Omiat *et al.* (2023) showed RYMV disease prevalence in nine out of eleven regions surveyed in Ghana in both improved and local rice varieties with 77% incidence. Studies in Uganda showed that the disease was present in all areas surveyed and at a high incidence of between 62% and 80% (Ochola & Tusiime, 2011). High incidence of RYMV has been observed in Ghana, Niger, Cote d'Ivoire and Burkina Faso (Kouass *et al.,* 2005; Omiat *et al.,* 2023).

There are seven major serotypes of the RYMV based on coat protein variability: S1, S2 and S3 are the West African strains, while S4, S5, S6 and S7 are from East Africa (Séré *et al.,* 2013; Ndikumana *et al.,* 2017). In Ghana, the S2 strain has been found to cause RYMV disease *(Salaudeen et al., 2010).* RYMV is transmitted from plant to plant by invertebrate feeding. Many insects, about forty species (Coleoptera, Orthoptera, Homoptera, Diptera, etc), are vectors of RYMV (Bakker, 1970; Koudamiloro *et al.,* 2015; Koudamiloro *et al.,* 2019). Also, vertebrates such as cattle, donkeys and rats can transmit RYMV by feeding (Soungalo & Peters, 2003). RYMV can also be transmitted by wind due to abrasive contact between leaves of plants(Sarra *et al.,* 2004).

The main symptoms of RYMV disease are pale yellow mottled leaves, stunted growth, fewer tillers, asynchronous flower formation, and brown to dark brown discoloration of grains (Séré *et al.,* 2013). The average yield loss of RYMV ranges from 20% to as high as 100% in susceptible rice genotypes depending on growing conditions and time of infection (Kouass *et al.,* 2005; Sereme *et al.,* 2016). Tolerant genotypes are the most cost-effective, environment-friendly, and sustainable way of managing RYMV disease (Salaudeen, 2014).

Genes conditioning RYMV resistance have been reported by several researchers (Ndjiondjop *et al.,* 1999; Albar *et al.,* 2003; Thiémélé et al., 2010). Expression of RYMV resistance genes is subject to the rice genotype, environment and their interaction (Ventelon-Debout *et al.,* 2008). Complete and partial resistance to the disease has been reported (Salaudeen, 2014; Traore *et al.,* 2015). Partial resistance is conditioned by minor genes, and it is characterized by low virus titres (virus accumulation) at early stages of infection and delayed symptom development. Complete resistance is associated with a lack of symptom development, blockage of virus movement and an undetectable virus (Ndjiondjop *et al.,* 1999; Thiemele *et al.,* 2010). The resistance genes to RYMV are found in both *O. sativa* and *O. glaberrima* with most genes coming from the latter (Pinel-galzi *et al.,* 2016). The first RYMV resistance gene described in rice is *RYMV1* found on chromosome 4 (Ndjiondjop *et al.,* 1999; Pinel-galzi *et al.,* 2016). The *RYMV1* gene is responsible for the resistance present in O. *glaberrima* genotypes Tog5681, Tog5672 and Tog5674, with alleles *Rymv1-3*, *Rymv1-4* and *Rymv1- 5*, respectively (Thiemele *et al.,* 2010). Two other cultivars, cv Gigante and cv Bekarosaka of *O. sativa* subsp. *indica* were highly resistant to the virus (Coulibaly *et al.,* 1999). Gigante and Bekarosaka had allele 2 of the *RYMV1* gene, generally known as "*RYMV1-2*" (Ndjiondjop *et al.,* 1999; Traoré *et al.,* 2010). In addition, *RYMV2* and *RYMV3* resistance genes have been identified in O. *glaberrima* genotypes, Tog7291 and Tog5307, respectively (Thiemele *et al.,* 2010). The emergence of resistance-breaking RYMV isolates is a matter of concern in developing resistant rice varieties (Séré *et al.,* 2013). New strains emerge via mutation and recombination which can overcome the resistance of commercial rice varieties (Suvi *et al.,* 2018). Thus, commercial varieties must be improved continuously through breeding.

Successful breeding depends on heritability for the traits of interest and the genetic variability in available germplasm. Genetic variability can be increased by introducing and selecting germplasm from different regions. Under the Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI), rice germplasm from Korea has been introduced into many African countries, including Ghana. These germplasm can be useful sources of resistance to RYMV and other agronomic traits. Yield and yield-related traits of rice such as tiller number, panicle number, plant height, days to heading and biomass are known to be affected by RYMV (Bakka, 1970; Kouassi *et al.,* 2005). However, quantitative estimates of the effect of RYMV on yield-related traits are scanty (Kouassi *et al.,* 2005). Estimating the impact of RYMV on yield-related traits of various rice genotypes will indicate their level of resistance (or susceptibility) to the disease. Also, assessing the genetic variation in the Korean rice germplasm will provide information about its usefulness for breeding.

This research aimed to estimate the impact of RYMV disease on some yield-related traits, determine genotypic variation in the Korean rice germplasm, and identify new sources of RYMV resistance for breeding new cultivars.

Materials and Methods

Plant material

A set of 176 rice genotypes (Supplementary Material Table S1), including 172 Korean rice breeding genotypes, two highly resistant, a moderately resistant (Amankwatia) (Amadu, 2019), and a susceptible (Jasmine 85) (Traore *et al.,* 2015) check, were evaluated for their level of resistance to RYMV infection. The resistant checks, Gigante and Tog7291, had *rymv1-2* (resistant gene1-allele2) (Ndjiondjop *et al.,* 1999) and *rymv2* (resistant gene2) (Coulibaly *et al.,* 1999), respectively.

The experiment was laid in 4 x 44 α-lattices with four replications in RYMV inoculated and non-inoculated environments in a screen house at CSIR - Crops Research Institute (CRI), Fumesua, Ghana, in 2019. The non-inoculated RYMV environment served as the control. Each entry consisted of one row with three plants at a spacing of 20 cm × 20 cm. Weeds were manually removed as soon as they were observed on the field. Fertilizer was applied at a rate of 90 kg N: 60 kg P: 60 kg K/ha.

Plant inoculation

Virus isolates (S2) from the field were cultured and multiplied in a two-week-old susceptible rice variety (Jasmine 85) and tested on known resistant genotypes, Tog7291 and Gigante. Leaves were first collected from infected plants (Jasmine 85) 14 days after inoculation and used as an inoculum source for the experiment. Mechanical inoculation was carried out 14 days after planting by rubbing the leaves of the plants for inoculation from the leaf base to the tip using fingers dipped in the sap extracted from infected plants (containing Carborundum 600 mesh for easier plant tissue penetration). Inoculation was carried out again a week later to avoid the escape of plants.

Serological assay

Using the protocol developed by DSMZ (QC-SOP-0087 Anl.002 double antibody sandwich ELISA (DAS-ELISA, Ver2.0), Double Antibody Sandwich Enzyme-linked Immunosorbent Assays (DAS-ELISA) was conducted to compare visual evaluation on symptoms following the procedure of Asante *et al.* (2020). A polyclonal antibody homologous to RYMV sourced from DSMZ^{TM}, Germany, was used as the coating antibody. The same antibody from DSMZ^{TM} was used as conjugate after being coupled with alkaline phosphatase.

Data collection

The symptoms of the disease were assessed every four days after the first inoculation for the first 20 days and, after that, weekly for the next 40 days. Disease severity was assessed using a standard evaluation system (SES) for rice (IRRI, 2002). Scoring was carried out on an individual plant basis and averaged for each genotype (John & Thottappilly, 1987).

Each genotype in inoculated and non-inoculated environments was assessed daily from the booting stage until heading. The average number of days to heading for each genotype was then determined on three randomly selected plants. Similarly, at maturity, average plant height (PH), culm length (CL), panicle length (PL), and biomass yield for each genotype were determined on three randomly selected plants. The biomass yield (BM/plt) was estimated for each genotype using the whole fresh plant (including the grains) of the three randomly selected plants, weighed using a digital scale, and the average recorded. We weighed grains separated from the whole plants used for biomass yield determination using a Constant digital scale (Model 14192-466F) to determine the average grain yield at 14% moisture content for each genotype. Percentage reductions in the various traits studied were determined using the data from inoculated and non-inoculated plants according to Zouzou *et al.* (2008).

Data analysis

The variations among inoculated and non-inoculated plants were used to measure the effect of RYMV on plant traits. Plant traits, disease severity and ELISA assay for each genotype were used to classify the genotypes as resistance or susceptible. The mean score recorded was used to evaluate disease severity. Average severity ranges of 1-1.5, 1.6-3.5, 3.6-5.5, 5.6-7.5, and 7.6-9 were recorded as 1, 3, 5, 7 and 9, respectively. Genotypes with scores of 1, 3, 5, 7, and 9 were considered highly resistant (HR), resistant (R), moderately resistant (MR), susceptible (S) and highly susceptible (HS), respectively and used to separate means of the genotypes (Zouzou *et al.,* 2008). The impact of RYMV on growth and yield-related components of each genotype was determined according to the formula of Zouzou *et al.* (2008):

Impact (%) = (100 × (Ni-I))/Ni
Where mean values of the:
Non-inoculated plants = Ni,
Inoculated plants = I.

Data on the impact of RYMV was normalized using Log (+1) transformation before analysis using analysis of variance (ANOVA). ANOVA, cluster analysis, correlation analysis, biplot and principal component analysis (PCA) were performed using R statistical software, version 4.0.2. Analysis of variance was conducted on mainly two factors, the genotypes and their interaction with the disease on the one hand and the impact caused by the disease on the other hand. Kendall rank correlation analysis was used to determine the relationships between RYMV disease severity, and the traits studied. In contrast, Pearson's product- moment correlation was used to determine the relationships among the traits.

Results

Effect of RYMV on rice genotypes and their interactions

The mean grain yield and yield-related traits of rice genotypes assessed under RYMV inoculated and non-inoculated RYMV environments are presented in Tables S2 and S3, respectively. Significant ($P \leq 0.01$) differences were observed between the inoculated and non-inoculated environments for all the agronomic traits studied (Table S4). Genotype × inoculation environment interaction was significant for all traits (Table 1).

RYMV severity on rice genotypes

Significant differences in disease severity were observed within the genotypes (Table

Table 1. Mean squares of yield and yield related traits across inoculated and non-inoculated environments

Source of variance	DF	Plant height (cm)	Culm height (cm)	No of tiller per plant	Biomass per plant (g)	Days to heading	Panicle length (cm)	No of panicles per plant (cm)	Grain yield per plant (g)
Replicate	3	2299**	2168**	78**	2815**	4443**	7^{ns}	55**	288**
Block	43	565**	368**	12**	1564**	128**	49**	15**	43**
Genotype (G)	175	1292**	1032**	20**	1944**	495**	71**	17**	79**
Environment(E)	1	349700**	314139**	3446**	946345**	118062**	10530**	5368**	13668**
G × E	175	409**	272**	9**	1157**	104**	55**	9*	55**
Residual	1010	193	124	5	560	67	27	7	14

^{ns}Non-significant at $P > 0.05$; *Significant at $P \leq 0.05$; **Significant at $P \leq 0.01$.

S4). Five genotypes namely, 8261112, 8261119, 8210016, 8210079, and 8261475, had significantly lower levels of disease severity relative to the two resistant genotypes. Two genotypes (8261069 and 8230008) did not significantly (P>0.05) differ in disease severity from the susceptible check (Jasmine 85) (Tables S4 and S5).

Kendall Rank Correlation between DAS-ELISA test and RYMV severity of rice genotypes

The correlation (r) between the ELISA test and RYMV severity scores was 0.74. All the genotypes showed presence of the virus except genotypes 8261112, 8261119, and the two highly resistant checks (Gigante and Tog7291) (Table S4).

Impact of RYMV on yield traits of rice

Significant differences were observed among the inoculated and non-inoculated genotypes for plant height, culm length, tiller number per plant, biomass/plant, days to heading, panicle number/plant, panicle length and grain yield/plant (Table 2).

The impact of RYMV on yield and yield-related traits varied significantly among the genotypes (Table S4). RYMV caused significant reductions in plant height and culm length among the genotypes.The highest percentage reductions in culm length due to RYMV occurred in 8260195 (73.9%), followed by 8230034 (69.7%) and 8260198 (69.6%). The disease caused up to 72.4% reduction in tiller number of susceptible genotypes. In contrast, the disease did not impact the tiller numbers of four test genotypes (8210016, 8220022, 8261112, and 8261133) and the resistant checks (Tog7291 and Gigante). The disease also caused more than an 80.0% reduction in the biomass of 33 genotypes, similar to the susceptible check. The reduction in biomass of the two resistant checks was not significantly different from

Table 2. Mean squares of the impact of Rice yellow mottle virus disease on yield and yield related traits

Source of variance	*Df	Plant height (cm)	Culm length (cm)	Tiller number/ plant	Days to heading	Panicle length (cm)	Panicle number/ plant	Biomass/ plant (g)	Grain yield/plant (g)
Replicate	3	13.892**	11.538**	28.31**	9.039**	26.067**	5454.8**	21.615**	0.461^{ns}
Genotype	175	1.983**	1.856**	4.607**	2.447**	1.784**	2153.0**	4.54**	3.265**
Block/Rep	172	0.708^{nss}	0.716^{ns}	2.39*	0.99^{ns}	0.871^{ns}	1237.8*	1.996*	1.325^{ns}
Residual	353	0.658	0.695	1.827	0.877	0.80	988.3	1.535	1.258^{ns}

^{ns}Non-significant at $P > 0.05$; *Significant at $P \leq 0.05$; **Significant at $P \leq 0.01$.

genotypes 8261112, 8261119 and 8261293. The disease did not affect the number of days to heading of 12 genotypes (8261119, 8210065, 8261551, 8260641, 8220045, 8260715, 8261492, 8260599, 8260505, 8230033, 8260585, and 8230024) and the two resistant checks. Heading was delayed significantly in 8220056 and 8261620. RYMV infected genotypes 8220056 and 8261620 attained heading at 115.3 and 124.8 days after planting compared to their non-inoculated (74.0 days for 8220056; 80.8 days for 8261620) counterparts. The disease significantly impacted the panicle lengths of the two genotypes (8220056 and 8261620). The disease caused more than an 80% reduction on eight genotypes. The disease, however, did not significantly affect the number of panicles/plant in seven genotypes (8261112, 8220022, 8210016, 8261133, 8210004, 8261119, and 8210087) and the resistant checks (Tog7291 and Gigante). Reduction in grain yield in 41 of the genotypes was not significantly different from the susceptible and moderately resistant checks. Two genotypes 8210016 (4.2%) and 8261119 (0.5%), had the least reduction in yield due to RYMV and were comparable to the resistant checks. Six genotypes (8220045, 8230028, 8260019, 8260782, 8260347 and 8261620) recorded yield losses of 100%.

Kendall rank correlation coefficients among the variables

Except for panicle length, there were significant positive correlations between disease severity and percentage reduction in grain yield and yield-related traits (Table 3).

Principal components and biplot for the evaluated genotypes

In our study, five principal axes exhibited eigenvalues of >0.5, accounting for a cumulative variation of 92.39%. The first four PCAs accounted for 86.58% of the total variation. PC1, PC2, PC3 and PC4 explained

Table 3. Kendall rank correlation coefficients among disease severity and the impact of RYMV on rice traits

Trait	Plant height	Culm length	Tiller number	Days to heading	Panicle length	Panicle number	Bio-mass	Grain yield
Culm length	0.98**							
Tiller number	0.71**	0.68**						
Days to heading	0.59**	0.61**	0.41**					
Panicle Length	0.65**	0.52**	0.5**	0.35**				
Panicle number	0.76**	0.72**	0.95**	0.42**	0.54**			
Biomass	0.85**	0.85**	0.7**	0.57**	0.46**	0.74**		
Grain yield	0.78**	0.77**	0.69**	0.53**	0.45**	0.76**	0.84**	
Disease severity	0.62**	0.68**	0.67**	0.34**	0.11^{ns}	0.70**	0.75**	0.72**

Df = 174; **Significant at $P \leq 0.01$; ^{ns} Non-significant at $P > 0.05$; Df = degree of freedom

59.02%, 10.7%, 9.61% and 7.25% of the total variation, respectively (Table 4). The highest sources of variation under PC1, PC2, PC3, PC4 and PC5 were plant height, RYMV severity, days to heading and grain yield per plant, respectively (Table 4).

One of the most informative graphical representations of a multivariate dataset is via a biplot. Figure 1 shows how the traits and genotypes were distributed based on the biplot analysis. Genotypes 8261112, 8261119, Gigante and Tog7291, which were the least impacted by the disease, clustered together. Genotypes 8261069, 8260325 and Jasmine 85 showed the highest disease severity. The biplot result is similar to that of the correlation analysis (Table 3; Figure 1).

Genetic similarity among rice genotypes evaluated

Figure 2 shows hierarchical cluster analysis of the RYMV effect on the 176 genotypes. Four main clusters (1, 2, 3, 4) were identified: Cluster 1 had four genotypes, including two known resistant genotypes (Gigante and Tog7291); Cluster 2, 48 genotypes; Cluster 3, 120 genotypes, which includes the susceptible check (Jasmine 85); Cluster 4, is made up of four genotypes.

Host status of the genotypes inoculated with RYMV

Based on the effect of RYMV, which considered disease severity and results of the ELISA test, the genotypes were grouped into five categories: highly resistant, resistant, moderately resistant, susceptible and highly susceptible. Seven genotypes made up of five genotypes from the Korean germplasm (8261112, 8261119, 8210016, 8210079 and 8261475), and two resistant checks (Gigante and Tog7291) were highly resistant to RYMV. The study also identified 10 resistant, 84 moderately resistant, 72 susceptible and 3 highly susceptible genotypes to RYMV (Table S5).

Discussion

Rice productivity in sub-Saharan Africa is seriously threatened by RYMV disease (Salaudeen, 2014). Following inoculation, distinctive symptoms of RYMV disease were observed, with the intensity of symptoms varying among the tested genotypes. Susceptible genotypes were characterized by premature death, and significantly reduced grain yield, plant height, biomass, culm length, tiller number, panicle number, panicle length and delayed heading. These typical effects of RYMV on susceptible genotypes have also been reported by other researchers (Onwughalu *et al.,* 2010; Sitta *et al.,* 2019).

Plant height is one of the important components in evaluating the susceptibility or resistance of rice genotypes to RYMV (Onwughalu *et al.,* 2010; Mogga *et al.,* 2012; Salaudeen, 2014; Kam *et al.,* 2018). In this study, the reduction in plant height and culm length was as high as 71.7% and 73.9%, respectively, in the susceptible genotype. This finding supports earlier reports that plant height of susceptible rice genotypes are highly affected when infected at earlier growth stage of the plant (Onwughalu *et al.,* 2011). The small percentage reductions in plant height partially resistant genotypes found in this study are also consistent with the findings of Salaudeen (2014) and Kam *et al.* (2018), who reported that partly resistant plants, even with mild symptoms, may show stunted growth after RYMV infection. These findings suggest the importance of plant height in evaluating rice genotypes infected with RYMV.

The higher number of tillers observed in healthy control plants compared to those infected with RYMV shows the considerable adverse effects of RYMV infection on rice productivity. This finding agrees well with the findings of other researchers (Bakker, 1970; Séré *et al.,* 2013), who reported significant reductions in tiller number of susceptible rice genotypes. The direct association of tillers with yield makes tiller production very relevant to rice production. The delayed

Table 4. Principal component analysis of RYMV severity and eight agronomic traits of rice

Trait	PC 1	PC 2	PC 3	PC 4	PC 5
Biomass	0.36	0.21	0.13	0.21	0.40
Culm length	0.37	-0.05	-0.20	-0.37	0.25
Grain yield/plant	0.35	0.09	0.10	0.33	0.52
Days to heading	0.21	-0.09	-0.84	0.44	-0.20
Plant height	0.40	-0.18	-0.12	-0.38	0.11
Panicle length	0.32	-0.43	0.03	-0.37	0.24
Panicle number per plant	0.38	-0.08	0.31	0.22	-0.36
RYMV severity	0.18	0.84	-0.14	-0.33	-0.26
Tiller number per plant	0.37	0.05	0.30	0.28	-0.44
Eigenvalue	5.31	0.96	0.86	0.65	0.52
Standard deviation	2.30	0.98	0.93	0.81	0.72
Proportion of variance %	59.02	10.70	9.61	7.25	5.81
Cumulative proportion %	59.02	69.72	79.33	86.58	92.39

PC = Principal component

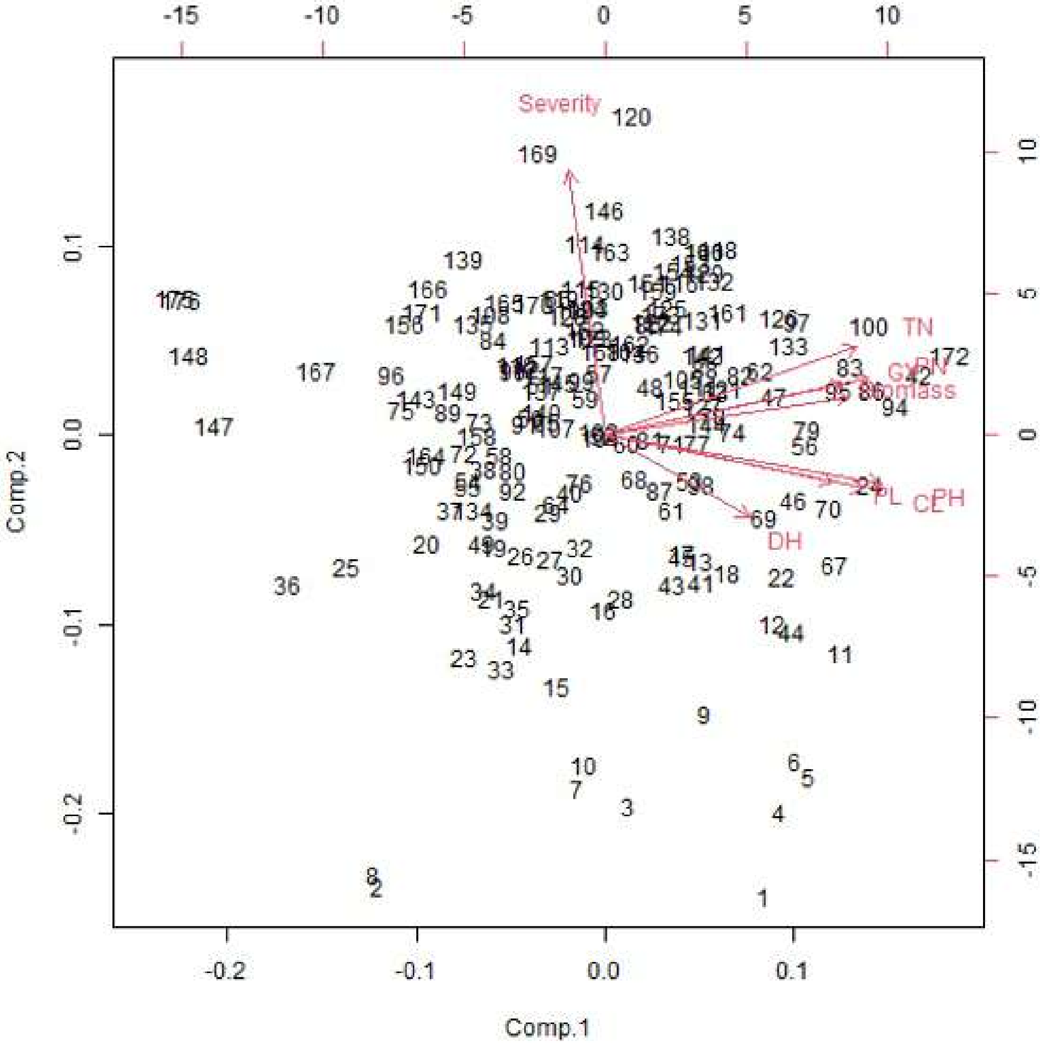

Figure 1. Biplot graphical display of RYMV severity and eight traits in 176 rice genotypes: TN= Tiller number; GY= Grain yield per plat; PN= Panicle number; PL= Panicle length; PH= Plant height; CL= Culm length; DH= Days to heading.

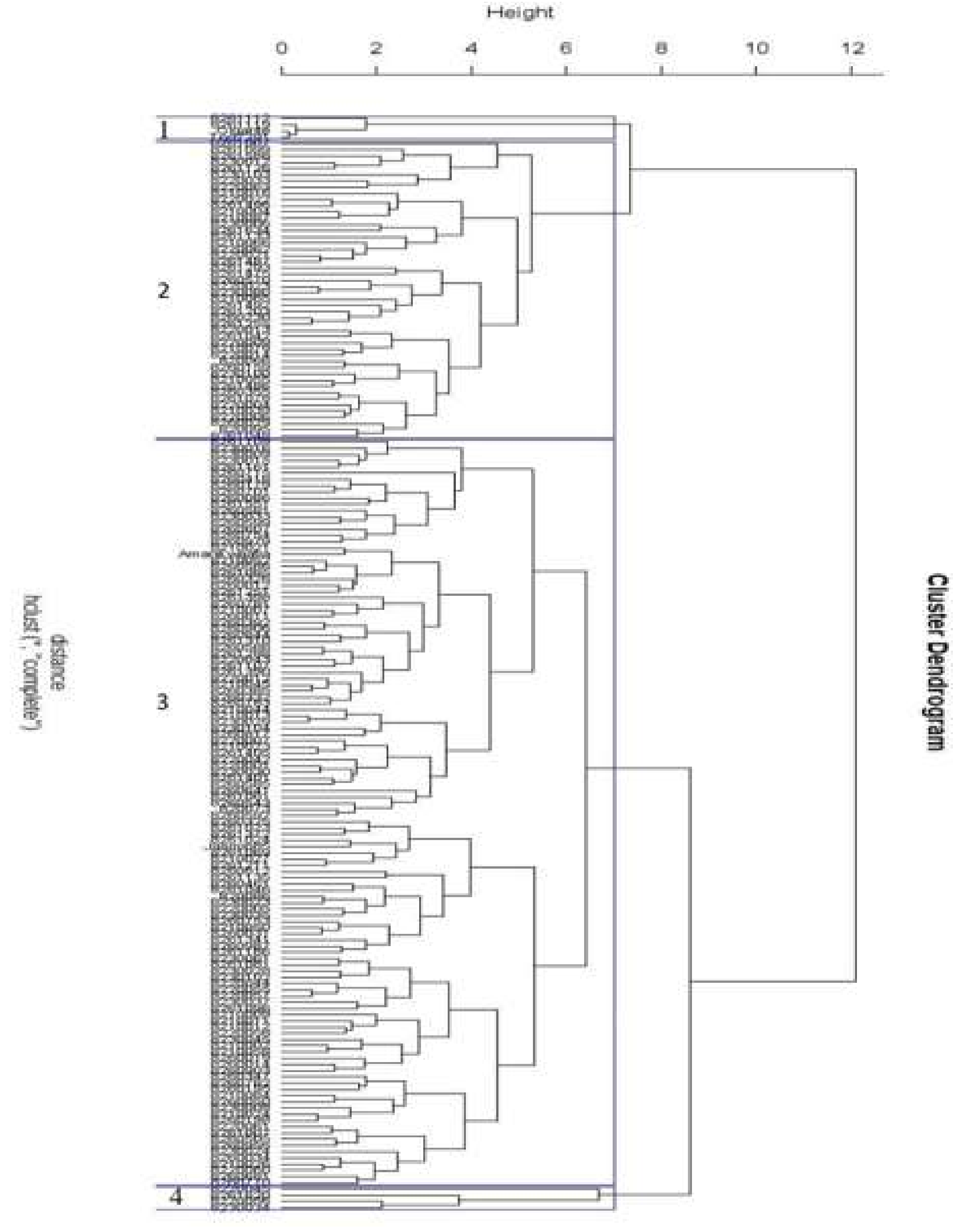

Figure 2. Cluster Dendogram representing distribution of 176 rice genotypes based on RYMV severity and morphological traits of rice.

heading due to RYMV infection in our study agrees with earlier reports by Kam *et al.* (2018) and Bakker (1970), who reported that RYMV infection resulted in late heading of susceptible rice genotypes. Delay in heading of rice leads to asynchronous maturity, thereby preventing mechanical harvesting and increasing cost of production.

The yield losses of 80 to 100% observed in the susceptible genotypes due to RYMV infection were similar to that reported from a survey conducted in Tanzania, where farmers experienced 100% yield loss in spite of heavy investment on management measures (Hubert *et al.,* 2016). The differences observed in performance of the different genotypes indicate that genetic background is a critical factor influencing yield loss caused by RYMV. Genes for RYMV resistance could be tightly linked to low yield (Salaudeen, 2014) probably because many sources of resistance have originated from *O. glaberrima,* which is less productive (Albar *et al.,* 2003; Thiemele *et al.,* 2010). Breaking this linkage through successive backcrossing with commercial varieties is crucial to breeding highly productive rice genotypes resistant to RYMV. Identifying elite genotypes that are resistant to RYMV in this study provides a good opportunity to use these genotypes directly in breeding programs to breed for resistance to RYMV.

The significant correlations observed between disease severity and grain yield and yield-related traits were confirmed by the output of the biplot analysis and suggest that these traits are very important in evaluating the effect of RYMV resistance, confirming the findings of Mogga *et al.* (2012). The strong positive correlation observed between RYMV severity and percentage reduction in biomass and grain yield in the biplot indicates that RYMV affects biomass and grain yield more than the remaining traits. The severity of RYMV and its effect on grain yield indicate the negative impact of RYMV disease on rice cultivation. The positive significant correlation observed in this study between grain yield and tiller number per plant agrees with the findings of Bakker (1970) and Séré *et al.* (2013).

The biplot revealed that genotypes 8261112, 8261119, 8210079, 8261475, 8261133, 8230016, 8261096, 8261634, 8210016, 8260029 together with the resistant checks (Gigante and Tog7291) were less affected by RYMV, while genotypes 8261069, 8260325, 8260612, 8210024, 8220063, 8261024 and the susceptible check (Jasmine 85) were grouped together as the most RYMV affected genotypes. It could, therefore, be deduced from the biplot result of our research that, the genotypes grouped with the resistant checks are resistant and those grouped with the susceptible check susceptible to RYMV as reported by Leite & Oliveira (2015).

Differences between genotypes and their interaction with the RYMV inoculation for the variables studied agree with earlier reports by Oludare *et al.* (2016) and Agnoun *et al.* (2019), who observed a strong interaction between the severity of RYMV and yield-related traits of rice genotypes. Thus, the genotypes varied in their response patterns to the inoculation environments, suggesting that the performance of non-inoculated genotypes cannot be used to predict responses of the genotypes under inoculation.

The results of this study showed considerable variation in the response of the rice genotypes evaluated for their reaction to RYMV in Ghana. The number of moderately resistant genotypes reported in our study confirms that there may be interesting sources of partial resistance in the rice germplasm, as earlier suggested by Thiemele *et al.* (2010). Thus, our findings will benefit breeding programmes to develop rice varieties with durable resistance to RYMV disease in West Africa. Partial resistance is generally more durable because it is controlled by multiple genes.

The five principal components that exhibited eigenvalues greater than 0.5, cumulatively explained 92.39% of the total variation among the genotypes studied. The highest source of variation were disease severity, panicle number per plant, tiller number per plant, days to heading and grain yield per plant, suggesting that these traits must be considered the most important for classifying variation in rice germplasm. Therefore, breeding towards RYMV resistance must be concentrated on these traits during selection and advancement in the germplasm, as supported by Jolliffe & Cadima (2016).

The clustering of genotypes 8261112 and 8261119 together with the resistant checks (Gigante and Tog7291) confirms the resistance of these genotypes to RYMV. These two genotypes will be very useful sources of potential genes for breeding for resistance to RYMV disease (Asante *et al.,* 2019).

Conclusion

The 176 rice genotypes, including three checks, varied in their responses to RYMV. The traits most severely affected by RYMV were biomass per plant, grain yield/plant, panicle number per plant, and culm length with reductions of up to 92.3%, 100%, 100% and 73.9%, respectively, for susceptible genotypes. The PCA suggested that, the number of panicles per plant, tiller number per plant, grain yield/plant and disease severity are the most important traits to be targeted in breeding for RYMV resistance. Genotypes 8261112 and 8261119 clustered together with the resistant checks. Five highly resistant genotypes (8261112, 8261119, 8210016, 8210079 and 8261475) and 10 resistant genotypes were identified. Further studies should be done to validate the resistance of the 15 genotypes identified and determine whether the genes controlling resistance are different from those already known.

Authors' contribution

BA: Performed the experiments; contributed to data analysis, wrote the paper.
MDA: Conceived and designed the experiments; supervised the experiments; wrote the paper.
AO: Contributed reagents and supervised laboratory experiments; wrote the paper.
IT: Helped in performance of experiment and data analysis.
DG: Helped in performance of experiment and data analysis.
KK: Contributed plant material
VOA: Helped to refine concept and experimental design, supervised the experiments; wrote the paper.
All authors read and approved the final manuscript.

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Conflict of Interest

The authors declare no conflict of interest in the publication of this article.

Supplementary Material

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