MAKERERE  **UNIVERISITY**

RICE YELLOW MOTTLE VIRUS DISEASE RESISTANCE AMONG DIVERSE RICE GENOTYPES

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A SPECIAL PROJECT REPORT SUBMITTED TO DEPARTMENT OF AGRICULTURAL PRODUCTION IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF THE BACHELOR OF SCIENCE IN AGRICULTURE DEGREE OF MAKERERE UNIVERSITY

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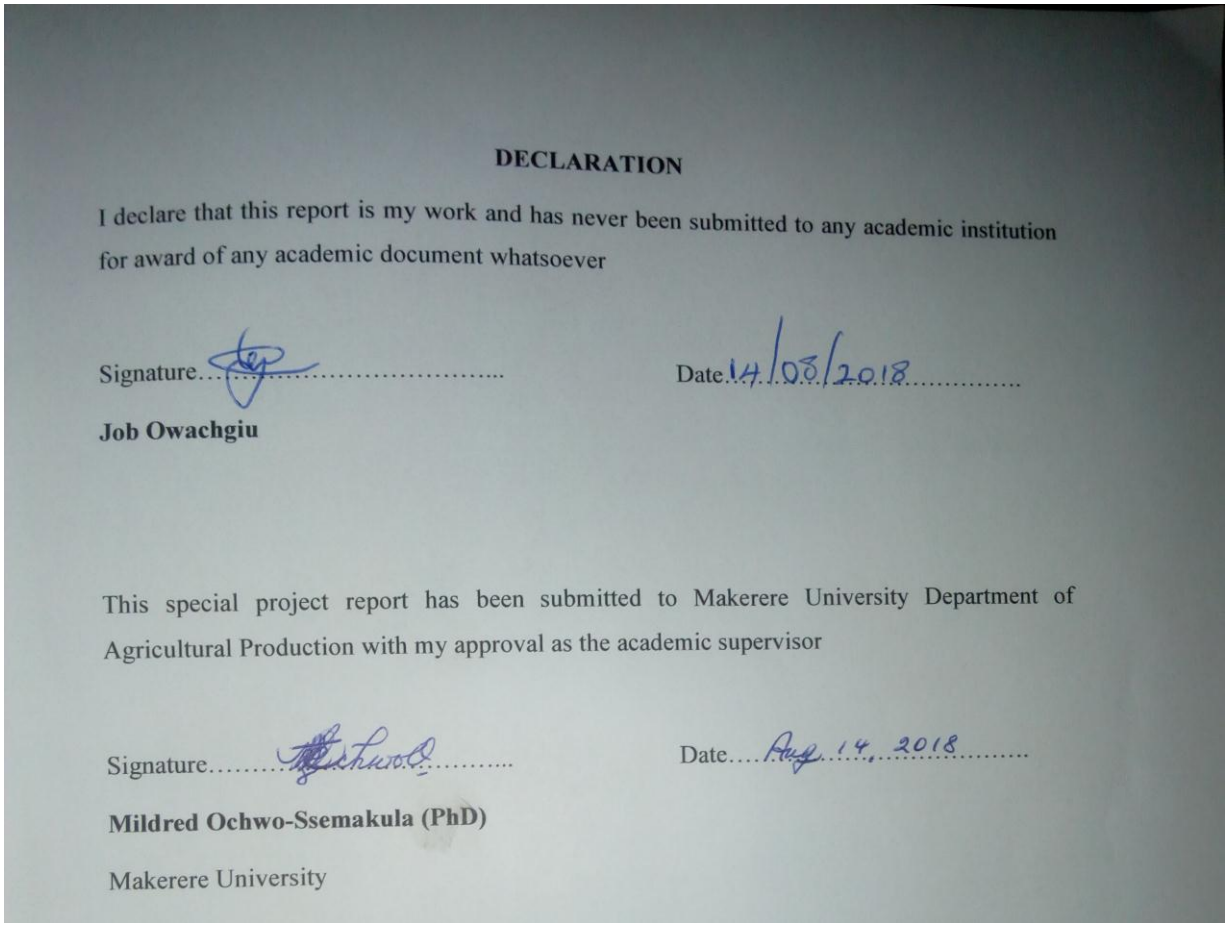
DECLARATION



DECLARATION

I declare that this report is my work and has never been submitted to any academic institution for award of any academic document whatsoever

Signature…….. Date 14/08/2018……

Job Owachgiu

This special project report has been submitted to Makerere University Department of Agricultural Production with my approval as the academic supervisor

Signature…….. Date…. Aug. 14, 2018……

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Makerere University

DEDICATION

I dedicate this report to my mother Mrs. Florence Jathim and my father Mr. John Jathim for their continued moral and financial support.

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I pray to the Almighty God to bless you all abundantly.

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LIST OF ACRONYMS

ADB	African Development Bank
AGRA	Alliance for a Green Revolution in Africa
ANOVA	Analysis of Variance
CABI	Centre for Agriculture and Bioscience International
D.F	Degrees of Freedom
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Food and Agriculture Organization of the United Nations Statistical database
FARA	Forum for Agricultural Research in Africa
HR	Highly Resistant
HS	Highly Susceptible
IRRI	International Rice Research Institute
JICA	Japan International Cooperation Agency
LEE	Lattice Error Effect
MR	Moderately Resistant
M.S	Mean sum of squares
MAFAP	Monitoring African Food and Agricultural Policies
MoFPED	Ministry of Finance Planning and Economic Development
NaCRRI	National Crop Resources Research Institute
NERICA	New Rice for Africa
ORF	Open Reading Frame
RB	Resistance Breaking
ReML	Restricted Maximum Likelihood
RNA	ribonucleic Acid
RYMV	*Rice yellow mottle virus*
R	Resistant
S	Susceptible
S. S	sum of square
SES	Standard Evaluation Scale
UniProtKB	Universal Protein Knowledge Base
UNRDS	Uganda National Rice Development Strategy
USDA	United States Department of Agriculture
VPg	Viral Protein genome-linked
WARDA	West Africa Rice Development Association

ABSTRACT

A diverse collection of 112 genotypes that had been introduced at NaCCRI to improve farmer grown rice genotypes were evaluated against three RYMV isolates from rice fields in Iganga (Eastern Uganda), Lira (Northern Uganda) and Kabanyolo (Central Uganda) which are areas considered to be RYMV "hotspots" in Uganda. The Iganga RYMV isolate was found to be the most virulent isolate and subsequently used to evaluate resistance level of the genotypes by using foliar symptom severity score and percentage grain weight reduction. The response to RYMV highly varied amongst the genotypes. Very few genotypes, however were found to be Highly resistant or Resistant. Genotypes Gigante, ARC36-2-P-2 (2), ARC39-145-P-3 (4), ARC39-145-P-2 (5), ARS126-3-B-1-2 (11) and IRL 53 (GP 54) were found to be Highly resistant while genotypes ARC36-2-1-2 (1), ARC36-4-EP-2 (3), IRL 2 (GP 54), IRL 4 (69 GP 54) and IRL 5 (GP 54) were Resistant when evaluated basing on symptom severity score. Percentage grain weight reduction varied between 0 and 100%. Gigante genotype was had a net gain in grain weight when infected with RYMV while 48.2% of the genotypes lost 100% grain weight and over 80% of the genotypes lost more than 60% grain weight. By coupling grain weight reduction and severity score, only genotypes Gigante, ARC36-2-P-2 (2), ARC39-145-P-3 (4), ARC39-145-P-2 (5), ARS126-3-B-1-2 (11), IRL 53 (GP 54), ARC36-2-1-2 (1), ARC36-4-EP-2 (3), IRL 2 (GP 54), IRL 5 (GP 54) and MET P44 were recommended for further breeding to improve rice genotypes in Uganda.

CHAPTER ONE

INTRODUCTION

1.1 Background

1.1.1 Origin, description and uses of rice

Rice is the world's most consumed cereal crop and the single leading provider of calories in the human diet (Awika, 2011). *Oryza sativa*, one of the two most widely grown species of rice, is believed to have been domesticated from wild grass *Oryza rufipogon* about 12,000 years ago in China while *Oryza glaberrima* was domesticated from *Oryza barthii* later in West Africa over 3500 years ago (Sweeney and McCouch, 2007).

Rice is a member of the Poaceae family with *Oryza sativa* and *Oryza glaberrima* as the most popularly grown species. It is an annual crop that grows to about 3-4 feet in height and matures in 110-136 days, depending on variety and environment (IRRI, 2018). Rice leaves are flattened and elongated with inflorescence made up of spikelets bearing flowers which are largely self-pollinating and produce monocotyledonous seeds.

Rice seeds are the most important part of the plant. The seeds are eaten or used for brewing. The husks can be used as substrate for mushroom growing, mulching, fuel, animal feeds and animal beddings. The seeds are high in carbohydrates and low in proteins and fats though the relative percentages of the nutrients vary according to variety (Kenedy & Burlingame, 2003).

1.1.2 Agronomic requirements of rice

Rice has several varieties which require a wide range of environmental growth requirements ranging from rain fed to irrigated agro ecological systems. Generally, late maturing varieties may need irrigation while the early maturing varieties may not. Additionally, tall varieties are suitable for flood-prone and unleveled fields while short varieties are suitable for leveled fields not prone to flooding (IRRI, 2015)

Rice can grow from altitudes ranging from below sea level to over 2000m above sea level. The crop requires temperature ranging between 10-35^{o}C and optimum relative humidity between 70-80% for normal flowering (Chandrasekaran *et al.*, 2013). Rice requires soil pH of 6.5-8.5 and salinity of less than 3 dS/m (IRRI, 2015). Due to its versatility in growth requirements, the crop is grown almost worldwide, with the exception of Antarctica (Poehlman, 2013).

1.1.3 Global rice production

Asia is the largest producer and consumer of rice (Awika, 2011). Asia alone accounts for 90% paddy rice production around the world and consumes 90% of milled rice produced in the world (USDA, 2013). China (203 million Tons) and India (164 million Tons) are the largest rice producers in the world accounting for 27.4% and 21.5% of total world rice production respectively (USDA, 2018). India has the largest area under rice production (43.5 million hectares) (USDA, 2018). Rice is responsible for feeding over half of the world population especially in Asia, Africa and Latin America (IRRI, 2018).

In Africa, rice is the third most consumed cereal after maize and sorghum with the fastest growing consumption rate of 5.5% per year (ADB, 2015). In 2006 rice was identified as a region-wide strategic commodity with great potential to solve food insecurity and poverty in Africa. It is estimated that indigenous production in Africa supplies only 60% of the total quantity demanded and the remaining 40% is supplied by imports (ADB, 2015). Many African countries in the 21st Century, started investing heavily in rice sectors to enable self-sufficiency of rice production. (ADB 2015)

1.1.4 Rice production in Uganda

In Uganda, rice is not a traditional staple food but has experienced a fast growing consumption rate especially in urban areas (Haggblade & Dewina, 2010). However, it is the second most important grain crop after maize (MoFPED, 2015); about 246,551 tons of rice are produced in Uganda (FAOSTAT, 2018).

Rice production in Uganda was started in 1942 in Uganda mainly to feed World War 2 soldiers. Production, thus, remained marginal up to 1974 when the government took the first major step to invest in the rice sector by constructing Doho rice irrigation scheme following pleas from local farmers (UNRDS, 2008). The rice sector grew significantly between 2005 and 2010, with increased local production and a subsequent fall in rice imports between 2005 and 2008 (FAO, 2013) when the Government of Uganda introduced upland rice varieties NERICA 1, 4 and 10 (UNRDS, 2008and FAO, 2013).

Other varieties grown in Uganda include K85 and WITA9, which are more preferred by low-land rice farmers over the “Supa” rice variety because of their high yielding characteristics and resistance to lodging (Nanfumba *et al.,* 2013). Ugandan consumers, however, still prefer the local “supa” rice variety due to its aromatic characteristic (Masette *et al.,* 2013).

1.1.5 Hindrances to rice production

Rice production is faced by socio-economic, biotic, abiotic and management-related constraints (John & Fielding, 2014). Socio-economic constraints include inadequate farmer knowledge and difficulty in accessing irrigation water. Abiotic constraints include soil infertility and droughts. Management-related constraints include poor water management and poor use of fertilizers; while biotic constraints include pests, diseases and weeds (John & Fielding, 2014).

Mondal *et al.*, (2017) reported that rice diseases contribute to 15.6% yield loss in intensified rice production systems. These diseases are caused by viral, bacterial and fungal pathogens. Major diseases in Africa include bacterial blight, first observed by Buddenhagen, *et al.*, (1979) in Mali; rice blast and *Rice yellow mottle virus* disease (Séré *et al*., 2013). Amongst the over 30 viruses that infect rice worldwide, only five are known to naturally infect rice in Africa: *Rice stripe necrosis furovirus*, *Rice stripe necrosis virus*, *Maize streak geminivirus strain A*, *African cereal streak virus* and *Rice yellow mottle sobemovirus* (Abo & Sy, 1997).

1.1.6 *Rice yellow mottle virus* disease in Uganda

Rice yellow mottle virus is the most economically significant viral disease of rice endemic in Africa and nearby islands, affecting most of the rice growing areas on the continent (Séré *et al.*, 2013). The disease causes yield losses ranging from 0.64% for resistant varieties to 51.28% for susceptible varieties (Sereme *et al.*, 2016) and up to 100% for highly susceptible varieties (Salaudeen *et al.*, 2010). Although RYMV affects rice in both high and lowland agro-ecologies, the latter which account for 59% of total rice produced in Uganda (MoFPED, 2015), are the most severely affected (Zouzou *et al.*, 2008; Séré *et al.*, 2013). Ochola & Tusiime, (2011b) reported very high incidence and severity of the disease in Eastern Uganda, which is the leading rice producer in Uganda (UNRDS, 2008). RYMV is, therefore, a major threat to rice production in the country.

Management techniques for the disease include phyto-sanitation, control of insect vectors, use of resistant varieties and integrated pest and production management (Salaudeen *et al.*, 2008). Use of resistant varieties is, however, one of the most promising control methods (Munganyinka, 2013).

1.2 Problem statement

In Uganda, farmer preferred rice varieties such as WITA 9 and K85 are susceptible to RYMV (Ochola & Tusiime, 2011a). The consumer preferred variety "supa", has also been reported to be susceptible (Banwo *et al.*, 2002).

Promising varieties with resistance to the virus were identified (Rakotomalala *et al.*, 2008; Mogga *et al.*, 2012; Kam *et al.*, 2013) although they were later found to be only tolerant when tested in multi-locational trials (Dr. Jimmy Lamo, Head of Rice Breeding Program at NaCRRI, Personal communication). *Rice yellow mottle virus* is a highly evolving virus, with pathotypes that are reported to breakdown resistance (Poulicard *et al*., 2014; Lyimo & Luzi-Kihupi, 2017; Longue *et al.*, 2018).

There is, therefore, still need to identify rice varieties with durable resistance that can be transferred to farmer- and consumer-preferred varieties through breeding. This will also expand researchers' knowledge about the gene pool of resistance genes against RYMV for further research.

1.3 Justification to the study

Breeding remains the most effective control strategy for RYMV. With the virus' high tendency of breaking down resistance, continuous efforts must be made to breed varieties with improved resistance. Genes controlling RYMV resistance have been found to be highly heritable, (Munganyinka, 2013) enhancing the viability of gene transfer to preferred varieties. Sow (2012) showed that RYMV susceptible varieties when improved through breeding, yield better than the susceptible varieties even in the presence of the virus. This study was, therefore, vital for identification of RYMV resistant varieties for further breeding.

1.4 Objectives of the study

1.4.1 General objective

This study was done to identify rice varieties with resistance to RYMV in Uganda

1.4.2 Specific objectives

To establish the level of resistance to RYMV among diverse genotypes

1.5 Hypothesis

Rice genotypes with resistance to RYMV in Uganda will exhibit lower disease severity and produce higher yields under virus infection.

CHAPTER TWO

LITERATURE REVIEW

2.1 History, distribution and diversity of RYMV in Africa

Rice yellow mottle virus is endemic to Africa and has not been reported in other continents (Wilson, 2014). Fargette *et al.,* (2008a) reported that intra-specific diversification of RYMV occurred 200 years ago whereas inter-specific divergence occurred between 500 to 9,000 years ago in Africa. RYMV was first recorded in Kenya at a place called Otonglo near Kisumu around Lake Victoria in 1966 (Bakker 1970) and from then it has been reported in various rice growing parts of Africa (Sere *et al.,* 2008; Ndikumana *et al.,* 2011, 2012 & 2015). In Uganda, RYMV was first reported in 2006 by Pinel-Galzi, Fargette & Hull.

There are generally six strains reportedly distributed across Africa (Fargette *et al.,* 2004; Traore *et al.,* 2009). The strains are classified based on their coat protein (Sereme *et al.,* 2016). West Africa consists of RYMV strains S1, S2 and S3 while S4, S5 and S6 strains are found in East Africa (Fargette *et al.,* 2002). Genetic diversity of the RYMV in relation to land area is more in the East Africa and decreases towards West Africa (Abubakar *et al.,* 2003), therefore, East Africa might have been the primary center of diversification of the virus (Singh, 2017). Fargette *et al.,* (2004) reported that genetic distance between the strains is directly proportional to the distance between the localities from which the strains are found. However, Ochola *et al.,* (2015) reported S4ug strain in Eastern Uganda which is more closely related to S4mg, a strain in Madagascar which is 2000km away, compared to S4lv, a strain that has existed around Lake Victoria for the past five decades.

2.2 Genomic and morphological features of RYMV

The virus is a single stranded linear positive sense RNA virus measuring about 28 + 3 nm in diameter (Fauquet & Thouvenel, 1977), whose genome consists of about 4450 nucleotides that are organized into five Open Reading Frames (ORFs); ORF1, ORF2a ORF2b, ORF3 and ORFx (Ling *et al.,* 2013). ORF1 encodes proteins which suppress plant's defense mechanism of gene silencing and is also responsible for virus movement from cell to cells, and is hence very important in host infection (UniProt, 2018). ORF2a encodes poly-proteins for replication, serine proteases and Viral Protein genome-linked (VPg), a primer during RNA synthesis while ORF2b codes for RNA-directed RNA polymerase (UniProt, 2018). ORF3, translated from a sub-genomic RNA, codes for the coat protein while ORFx function is yet to be understood (Ling *et al.,* 2013). *Rice yellow mottle virus* has a high concentration of Guanine and Cytosine (29% and

26.3% respectively) compared to Adenine and Uracil (25% apiece) (CABI, 2018) The virus when seen under electron microscope is an icosahedral particle consisting of 180 subunits of capsids arranged in triplicate to form 60 triangulations (Konaté and Fargette, 2004).

2.3 Host range and spread of RYMV

Rice yellow mottle virus has a very narrow host range infecting mainly rice and a few other grasses such as *Cynodon dactylon*, *Cyperus esculentus*, *Cyperus rotundus*, *Eleocharis complanata*, *Eleusine indica*, *Fuirena umbellata*, *Imperata cylindrica*, *Kyllinga pumila* and *Paspalum vaginatum* which are potential virus natural reservoirs in the Poacae family closely related to rice (Fargette *et al.*, 2008a; Salaudeen, *et al.*, 2008 & 2010). *Rice yellow mottle virus* infects both rice species of *Oryza sativa* and *Oryza glaberrima* which are exotic and indigenous to Africa respectively and mostly infecting rice in lowland agro ecologies (Zouzou *et al.*, 2008; Salaudeen, 2014).

Konate *et al.,* (2001) reported that RYMV is not transmitted by rice seeds even though it may be detected in all parts of the seed during the growing stage. Konate *et al*., (2001) then suggested that this may be due to inactivation of the virus as a result of desiccation and seed maturation. Allarangaye, *et al*., (2006) also reported that RYMV cannot be transmitted by dried seeds of wild hosts. The RYMV is transmitted naturally when sap from an infected plant is injected into a healthy plant bringing the virus in close proximity to host cells. This can be due to insect bite, specifically insects in orders of Orthoptera such as *Conocephalous merumontanus* and *Oxya hyla*, Coleoptera such as *Sesselia pusilla* and *Dicladispa gestroi*, Homoptera such as *Confana spectra* and *Confana unimaculata* and one insect in Diptera order Diopsis *thoracica* (Salaudeen *et al.*, 2010; Uke *et al.*, 2014; Koudamiloro *et al.*, 2015). Other vectors such as rats and grazing animals have been found to spread the disease (Sastry & Zitter, 2013; Wilson, 2014; CABI 2018b). It can also be spread by intertwine of roots of infected with non-infected plants (CABI, 2018b), overlapping and contact of healthy with infected leaves (Traore *et al.*, 2008; Séré *et al*., 2013) in closely spaced plant density. Traore *et al.*, (2008) also reported that soil contaminated with RYMV-infected leaves can also spread RYMV to healthy rice plants. Contaminated hands when working with plants are reported to spread the virus either intentional or unintentional (Séré *et al.*, 2013; CABI, 2018b). Uke *et al.*, (2014) reported that soil contaminated with sap from RYMV-infected roots had high infectivity and also recorded a low infectivity from soil and water gotten from RYMV-infected ecosystems. Uke *et al*, (2014) also reported that straw kept at 27^0C for over 42 days is non-infective hence cannot spread the virus.

2.4 Symptoms of RYMV and impact on yield

Rice yellow mottle virus causes rice yellow mottle disease which is systemic hence affects the whole plant characterized by young leaves developing elongated chlorotic dots in the early stages of symptom emergence which appear to join and form yellow or orange streaks parallel to the leaf veins. It also causes reduction in tillering and grain weight, production of sterile spikelets, stuntedness and plant death before maturity (CABI 2018; IRRI, 2018). Kouassi *et al.*, (2005) reported grain yield losses to RYMV ranging from 10% to 100% depending on stage of infection, variety and other stress factors. Issaka *et al.*, (2012) reported a yield loss ranging between 35 to 71%. These different reporting indicate that yield loss also varies according to geographical region and variety. Generally, *Oryza glaberrima* species of rice have been reported to succumb to less grain yield loss compared to *Oryza sativa* species due to their relatively higher resistance to RYMV (Thottapilly & Rossel, 1993; Rakotomalala *et al.*, 2008).

2.5 Management of RYMV disease

Effective management strategies of the virus include phyto-sanitation, control of insect vectors, use of resistant varieties and integrated pest and production management (Salaudeen *et al.*, 2010). Phyto-sanitation practices include rogueing of volunteer plants and alternative hosts at the end of harvest period to prevent continuous RYMV survival. Phyto-sanitation however is only effective when the disease is not yet in the field and it is very laborious. Control of insect vectors can be biologically by use of parasitoids and predators (Woin, *et al.*, 2007). It can also be done by use of chemicals such as pesticides and pheromones. Control of insect vectors however is not the most effective way of managing RYMV because the RYMV virus can be transmitted by means other than insect vectors (Séré *et al*., 2013; Sastry & Zitter, 2013; Wilson, 2014). International Rice Research Institute (2018) suggests weeding during and even after harvest to reduce primary inoculum, large-scale planting combined with fallowing to prevent virus and vector population build up and establishing the rice crop before population buildup of the vectors among others.

Integrated pest management reduces the status of insect vectors hence reducing the rate of transmission of the virus (Nwilene, 1999). This approach, however, requires a lot of knowledge which may not be at the disposal of farmers. Therefore, use of resistance as RYMV management strategy which requires less inputs and knowledge is the best and most sustainable management strategy for the poor farmers in sub-Saharan Africa.

2.6 Host resistance as a management strategy to RYMV disease

Use of naturally resistant rice varieties is said to be the best and most promising method of RYMV management among the available management methods (IRRI, 2018). Resistance to RYMV has been demonstrated to be very low in exotic rice varieties and moderate to high in indigenous African varieties (Rakotomalala *et al.,* 2008). Varieties reported to have resistance in Uganda include: NERICA6, ITA257, ITA325, WAC116 and WAC117 (Ochola & Tusiime, 2011a) although they are not the most farmer preferred rice varieties (Nanfumba *et al.*, 2013).

Two types of natural resistance mechanisms have been identified, one type is polygenic controlled partial resistance identified mostly in *Oryza sativa* accessions (Albar *et al.,* 1998) while the other is a recessive monogenic controlled resistance found mostly in *Oryza glaberrima* accessions (Orjuela *et al.,* 2013). Three major genes have been identified to control resistance to RYMV in both *Oryza sativa* and *Oryza glaberrima*. The most widely studied resistance gene is the *rymv1* with four independent alleles *rymv1-2*, *rymv1-3*, *rymv1-4* and *rymv1-5* of which the first two are found mostly in accessions of *Oryza sativa* while the latter two found mostly in *Oryza glaberrima*. The other two major genes controlling resistance to RYMV are *rymv2* (Thiémélé *et al.,* 2010) and *rymv3* (Pidon *et al.,* 2017) which are found mostly in *Oryza glaberrima* accessions. Other derived resistances of rice other than natural resistance have been developed by irradiation with gamma rays to form resistant mutant rice varieties (Luzi-Kihupi *et al.,* 2008) and genetic engineering (Fulekar, 2010) to form transgenic rice varieties.

Rice yellow mottle virus has been reported to be as rapidly evolving as animal viruses (Fargette *et al.,* 2008b) and highly susceptible to mutational changes; it can hence easily overcome resistance in improved rice accessions (Poulicard *et al.,* 2014; Pinel-Galzi *et al.,* 2016; Longue *et al.,* 2018). Resistance from major genes creates a high selection pressure against pathogens enhancing susceptibility to breakdown (Brown, 2015). This is because such resistances are controlled by one or a few genes which become easily overcome by even single base substitution in the viral genome (Gomez *et al.,* 2009). However, Poulicard, *et al.,* (2010) explained that RYMV has a low efficiency to overcome resistance controlled by *rymv2* genes due to genetic and demographic contributions.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Description of study site

The study was done in a screen house at the National Crops Resources Research Institute (NaCRRI), Namulonge from August to December 2017. Namulonge is located in Wakiso district, 10 km along Gayaza-Zirobwe highway about 30 km Northeast of Kampala in the central region of Uganda. The area has a tropical climate with a bimodal annual rainfall. The first rainfall season is from March to May and the second from August to December. The average annual rainfall and temperature are 1242 mm and 21.7 ^{o}C respectively. The average amount of rainfall received and average temperature per month ranges between 55-170mm and 20.7-22.4 ^{o}C respectively. The least amount of rainfall is received in January while the highest amount of rainfall is received in April. July is the coldest month while March is the hottest.

The elevation of Namulonge is 1,160 meters above sea level with undulating topography. The coordinates of the area are 00^{o} 31'30"N 32^{o} 36'54"E (Latitude: 0.5250 and Longitude: 32.6150). The soils in Namulonge are mainly Oxisols in the plains and hills and Vertisols in the swamps and valleys. Vegetation is savannah with tall trees and grasses such as *Pennisetum purpureum.*

3.2 Experimental design and genotypes used

The experiment was done using a Type 1 alpha lattice design with four blocks and two replicates per RYMV isolate. Each genotype represented a treatment and each block contained 28 treatments per RYMV isolate.

One hundred and twelve rice genotypes, including 8 *Oryza sativa* and 104 *Oryza glaberrima* rice genotypes (Appendix 1), that had been introduced into the Rice Breeding Program to improve NaCRRI rice varieties for resistance against blast and RYMV were selected for evaluation. They included MET71, MET72 and Gigante, which are known resistant genotypes, and IR64, K34, K38 and K85, which are known susceptible genotypes, as check varieties. *Rice yellow mottle virus* infected rice plants were collected from farmers' rice fields in Iganga (Eastern Uganda), Lira (Northern Uganda) and Namulonge (Central Uganda) so as to generate virus isolates for inoculation. These isolates were mechanically inoculated to, and maintained on the highly susceptible IR64 rice variety at NaCRRI.

3.4 Trial establishment and management

Soil from around the NaCRRI screen house was collected, crushed and sieved to get fine particles. The sieved soil was then spread on raised beds and watered thoroughly. Six rice seeds of each genotype were planted in a line. Each block contained 28 lines of seedlings. Four blocks were made per RYMV isolate and replicated twice. Each set of four blocks under a single RYMV isolate was then boundary-enclosed with polythene sheets (Figure 1) to prevent any aerial thigmo-interaction between plants infected by different isolates or replicates of a given isolate.

Figure 1. Blocks within the screen house experimental setup at NaCRRI

Twenty-one days post-sowing (dps); the infected rice plants from each respective area were crushed using sterile mortar and pestle then mixed with distilled water in a ratio of 1:10 (50g of crushed infected leaves with 500ml of double distilled water). The mixture was decanted to obtain an infective RYMV solution. The first 3 plants within each line were inoculated with the infective solution by mechanical finger-rubbing of the whole plant from the lowest part. Inoculation was repeated 28 dps to prevent natural infection escape.

3.5 Data collection

3.5.1 Disease severity

Data collection on disease severity was done by scoring symptom severity on leaves using the IRRI standard evaluation scale (IRRI, 2013). The IRRI standard evaluation scale used had a range from 1 to 9 where; 1= no symptom observed, 3= plants whose leaves were green but with sparse dots or streaks and less than 5% of height reduction, 5= plants whose leaves were green or pale green with mottling and 6% to 25% of height reduction, flowering slightly delayed, 7= plants whose leaves were pale yellow or yellow and 26-75% of height reduced, flowering delayed, 9= plants whose leaves turned yellow or orange, more than 75% of height reduction, no flowering or some plants dead. Data on disease severity began 28 dps and was done six times following an interval of seven days as follows: First Scoring (S1)-28 dps, second scoring (S2)-35 dps, third scoring (S3)-42 dps, fourth scoring (S4)-49 dps, fifth scoring (S5)-56 dps and sixth scoring (S6)-63 dps.

Area Under Disease Progress Stairs (AUDPS) was calculated from the weekly severity scores as described by Campbell & Madden, (1990) and converted to Relative Area Under Disease Progress Stairs (rAUDPS) using a formula by Simko & Piepho (2012);

$$\text{rAUDPS} = \frac{\text{sAUDPS} - \text{ymin}}{\text{ymax} - \text{ymin}}$$

where; sAUDPS= Average interval severity scores across all the six scoring intervals, $ymin$ = least possible score and ymax = highest possible score.

Figure 2. Pictoral representation of RYMV severity using evaluation scale of IRRI. Left to Right: Severity scores 9, 7, 5, 3 and 1

3.5.2 Yield

Data on yield were collected at 135 dps and used to calculate percentage loss in weight of grains due to inoculation with RYMV. One hundred (100) grains from both inoculated and non-inoculated plants within a line were harvested separately, dried to 13% moisture content, weighed using an electronic weighing scale and the percentage loss in weight determined using a formula from Zouzou *et al.,* (2008)

$$\text{Percentage loss in grain weight due to disease} = \frac{\text{weight of grains from noninoculated} - \text{weight of grains from inoculated}}{\text{weight of grains from non} - \text{inoculated}} \text{x} 100\%$$

3.6 Data analysis

Data were subjected to a Restricted Maximum Likelihood (ReML) analysis using GENSTAT data analysis software (11^{th} edition) with optimization method set at Fisher scoring and maximum iteration of 20 to establish effectiveness of the lattice design. In cases where the lattice design wasn't effective, ANOVA was established directly from the data analysis software by handling the ineffective treatments as Randomized Complete Block Design (RCBD). In cases where the lattice design was effective, an ANOVA was calculated from ReML table. Subsequently, an ANOVA table was drawn to easily visualize the information.

Using the sixth scoring interval (S6) scores and percentage grain weight reduction effect of each isolate, virulence of the isolates was established and the most virulent isolate used for determining the resistance levels of the evaluated genotypes. Disease severity scores were used

to categorize resistance in a scale developed by Zouzou *et al.*, (2008) as follows: Scores: 1 – 1.5; Highly Resistant (HR), 1.6 – 3.5; Resistant (R), 3.6 – 5.5; Moderately resistant (MR), 5.6-7.5; Susceptible (S) and 7.6-9; Highly Susceptible (HS).

TABLE 1. Skeletal ANOVA for the Lattice design experiment

Source of variation	**D. F**	**S.S**	**MS**	**F-Test denominator**
Replicate	1	$S.S_{rep}$	MS_{rep}	$MS_{Block/replicate}$
Block/replicate		$S.S_{block/replicate}$	$MS_{block/replicate}$	$MS_{residual}$
Genotype (treatment)	111	$S.S_{genotype}$	$MS_{genotype}$	MS_{LEE}
LEE		$S.S_{LEE}$	MS_{LEE}	

CHAPTER FOUR

RESULTS

4.1 Isolate virulence

By comparing the mean effect of each isolate in the sixth scoring interval and on grain weight, the Iganga isolate was found to cause the greatest mean severity score and grain weight reduction percentage (Table 2). The Namulonge and Lira RYMV isolates were found to have no significant difference in virulence. The mean isolate effect of the three RYMV isolates on grain weight reduction percentage was significant ($p \leq 0.05$) whereas the mean isolate effects in the sixth scoring interval was insignificant ($p=0.278$) (Appendix 2)

The mean isolate effect on grain weight was 78.7% reduction for Iganga isolate, 72.8% reduction for Lira isolate and 70.8% reduction for the Namulonge isolate. The difference in mean grain weight reduction of Namulonge and Lira isolate was not significant.

Table 2. Average severity score and average grain yield reduction of three RYMV isolates from farmers' fields in Uganda

Isolate	S6	rAUDPS	%GW reduction
Iganga	5.85	0.451	78.7[a]
Namulonge	5.56	0.424[a]	72.8
Lira	5.72	0.471[b]	70.8[b]
LSD	0.43	0.03	7.3

[a,b] Values with different letters in the same column are significantly different

4.2 Foliar symptom severity

Differences in mean severity score of all the genotypes across all weeks were significant ($p \leq 0.001$) (Appendix 3) and ranged between scores 1 and 9. Typical RYMV disease symptoms were observed on some genotypes seven days after inoculation most severely on MET P48. Symptoms were sparse pale green dots and yellow mottling on leaves. Generally, *Oryza glaberrima* genotypes were showed less symptoms compared to *Oryza sativa* genotypes

The mean severity score in the first scoring ranged between 1 and 5 where 61 genotypes which represent 54.5% of the evaluated genotypes, did not show symptoms of the disease on the leaves at the first scoring whereas genotype MET P48 scored 5. Most genotypes exhibited the typical RYMV symptoms by the second scoring interval (Table 3).

Basing on the mean severity score at the sixth scoring interval, five classifications of the genotypes were generated (Table 4) using the Zouzou *et al*., (2008) scale which grouped the genotypes according to level of resistance to RYMV. The Highly Resistant (HR) genotypes were 5.4%, 4.5% were Resistant (R), 38.4% were Moderately Resistant (MR), 32% were Susceptible (**S**) and 19.6% of the genotypes were Highly Susceptible (HS) (Table 4). Genotypes MET P72 and MET P71 which had been introduced in the experiment as check resistant genotypes instead turned out to be Susceptible whereas Gigante which was also introduced as check resistant was found to be highly resistant based on mean severity score. The susceptible check genotypes IR 64, K34, K38 and K85 were classified as HS. Farmer preferred genotype WITA 9 was found to be Susceptible.

The genotypes classified as resistant showed RYMV symptoms in the fourth, fifth and sixth scoring intervals. Generally, *Oryza sativa* genotypes showed more severity symptoms than *Oryza glaberrima* genotypes. All *Oryza sativa* genotypes apart from Gigante were classified as HS (Table 3)

Table 3. Mean severity score and rAUDPS of selected genotypes

Category	Genotypes	Species	S1	S2	S3	S4	S5	S6	rAUDPS
HR	Gigante [RCK]	*O. sativa*	1	1	1	1	1	1	0.000
	ARS126-3-B-1-2 (11)	*O. Glaberrima*	1	1	1	1	1	1	0.000
	ARC36-2-P-2 (2)	*O. Glaberrima*	1	1	1	1	1	1	0.000
	ARC39-145-P-3 (4)	*O. Glaberrima*	1	1	1	1	1	1	0.000
	ARC39-145-P-2 (5)	*O. Glaberrima*	1	1	1	1	1	1	0.000
R	ARC36-4-EP-2 (3)	*O. Glaberrima*	1	1	1	1	1	2	0.021
	IRL 4 (69 GP 54)	*O. Glaberrima*	1	1	1	1	2	2	0.042
	ARC36-2-1-2 (1)	*O. Glaberrima*	1	1	1	2	2	2	0.063
	IRL 2 (GP 54)	*O. Glaberrima*	1	1	1	1	2	2	0.042
	IRL 5 (GP 54)	*O. Glaberrima*	1	1	1	1	2	3	0.063
MR	MET P44	*O. Glaberrima*	1	2	4	5	5	5	0.333
	MET P50	*O. Glaberrima*	2	4	5	5	5	5	0.417
	MET P64	*O. Glaberrima*	2	4	5	5	5	5	0.417
S	MET P72[RCK]	*O. Glaberrima*	2	5	5	6	6	6	0.500
	WITA 9	*O. Glaberrima*	2	5	6	6	7	6	0.542
	MET P71[RCK]	*O. Glaberrima*	1	5	5	5	5	7	0.458
HS	K34[SCK]	*O. sativa*	2	7	7	7	7	9	0.688
	K38[SCK]	*O. sativa*	3	8	8	9	9	9	0.833
	K85[SCK]	*O. sativa*	3	7	7	7	7	8	0.688
	KOMBOKA	*O. sativa*	4	7	7	8	8	8	0.750
	IURON (2014) 37	*O. sativa*	1	5	7	7	7	8	0.604
	IURON (2014) 41	*O. sativa*	2	5	7	7	8	9	0.667
	IURON 2014 (230)	*O. sativa*	4	7	8	9	9	9	0.833
	IR64[SCK]	*O. sativa*	3	9	9	9	9	9	0.875
Mean Isolate score			1.7	4.2	5.0	5.4	5.5	5.8	0.455
CV%			49.8	20.3	18.9	14.3	15.3	17.1	14.4
LSD (5%)			1.74	1.66	1.84	1.49	1.67	1.97	0.127

[RCK]: Resistant check, [SCK]: Susceptible check

The maximum disease severity score attained by genotypes that at least showed the disease symptoms in the six scoring intervals varied between 2-9 depending on genotype (Table 3). Maximum disease severity was attained by only genotype MET P48 in the first scoring interval,

13.4% of the genotypes in the second scoring, 21.4% in the third scoring, 23.2% in the fourth scoring, 9.8% in the fifth scoring and 25.9% in the six scoring whereas 6 genotypes which represent 5.4% of the genotypes did not show any foliar symptom of the disease throughout the six scoring intervals. The trend of mean severity score of individual genotypes varied across the six scoring intervals. Before stabilizing, some genotypes had an increasing and consequently a decreasing trend while others maintained an increasing trend. Some genotypes showed symptom early while others delayed symptom expression (Figure 3)

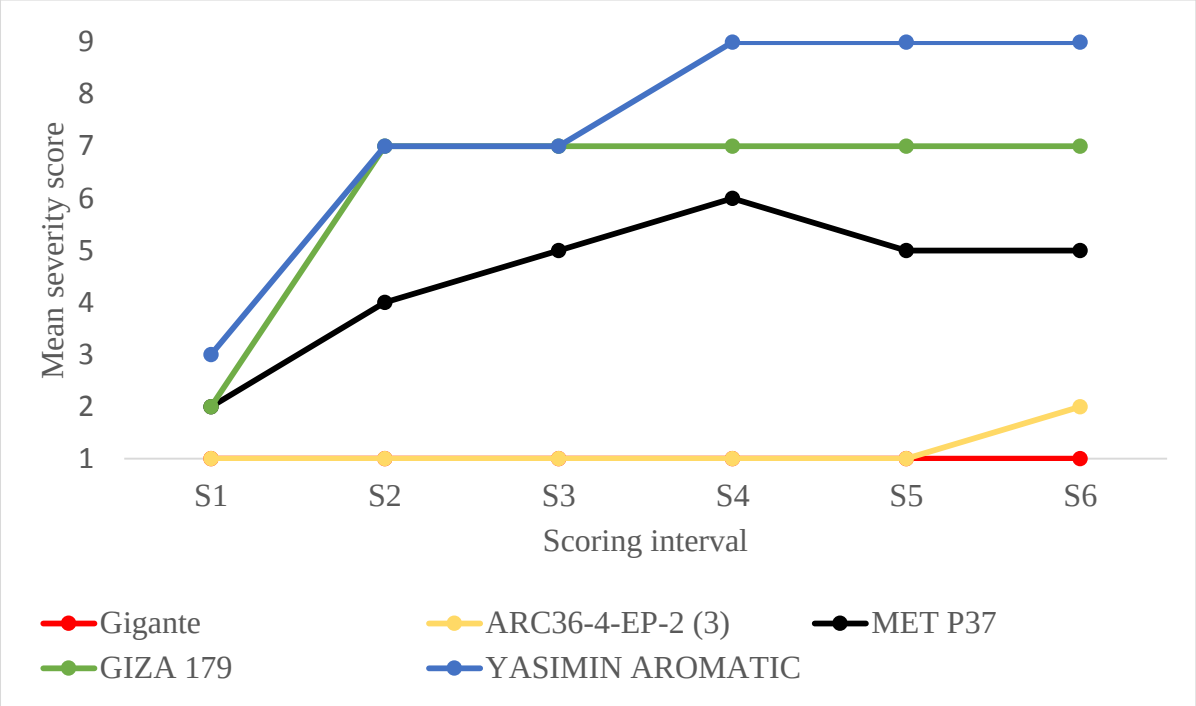

Figure 3 Mean severity score of five selected genotypes each from a resistance category

Generally, the resistance categories followed different trends of reaction to Iganga RYMV isolate across the six scoring intervals. (Figure 4). The HR genotypes did not show signs of RYMV across all the six scoring intervals. The genotypes categorized as R delayed expression of RYMV symptoms until at least the fourth scoring interval. Moderately Resistant, Susceptible and Highly susceptible genotypes showed symptoms in the first scoring interval and rapidly increased intensity of symptoms by the second scoring interval then a gradual increase in intensity of the symptoms to the sixth scoring interval.

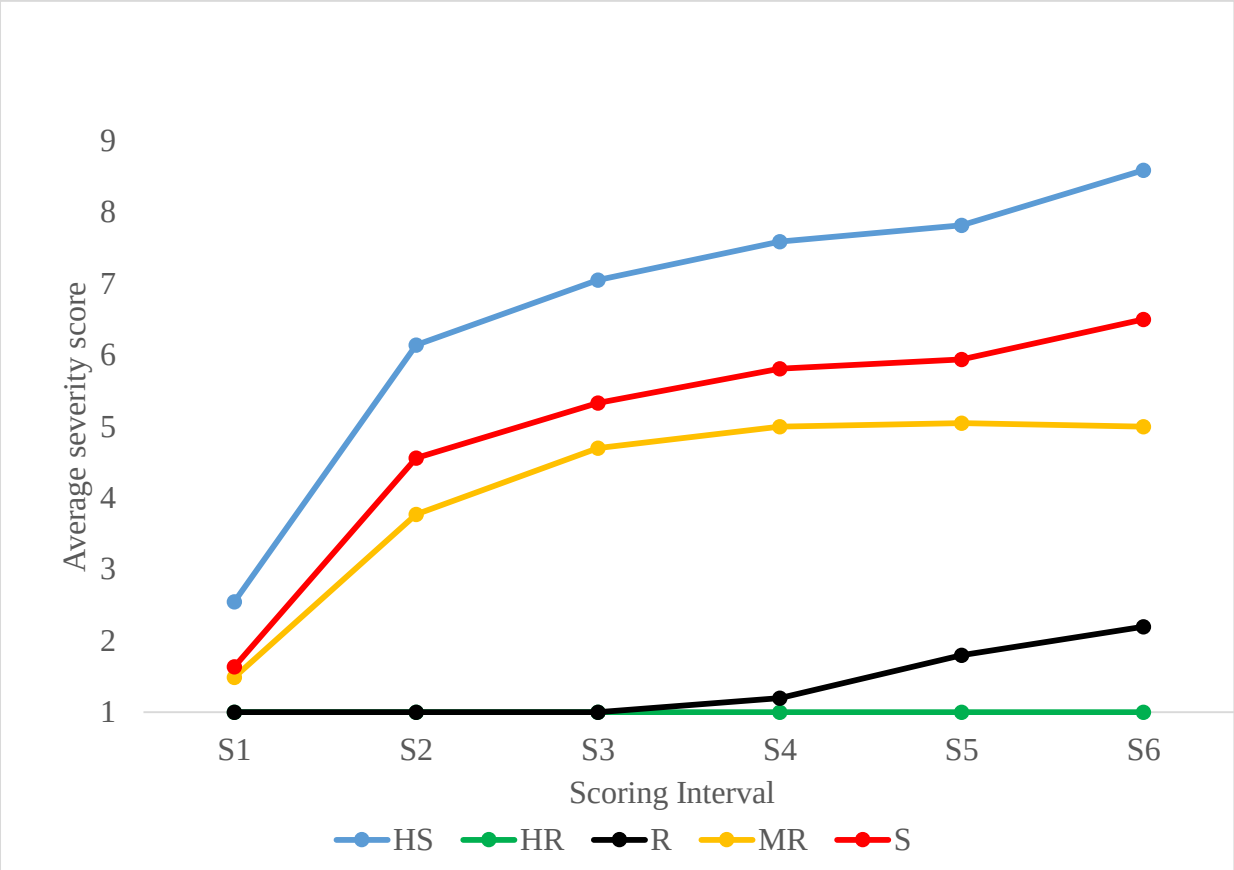

Figure 4 Average severity score across the six scoring intervals

The Relative Area Under Disease Progress Stairs of the genotypes was highly significant ($p \leq 0.001$). The rAUDPS ranged between 0 and 0.875. Genotypes Gigante, IRL 53(GP 54), ARC36-2-P-2 (2), ARC39-145-P-2 (5), ARC39-145-P-3 (4) and ARS126-3-B-1-2 (11) had the lowest rAUDPS whereas IR 64 had the highest rAUDPS. Check susceptible genotypes K34 and K85 had rAUDPS of 0.688 apiece while K38 had 0.833. Farmer preferred genotype WITA 9 had rAUDPS of 0.542 (Table 3). Check resistant genotypes MET P71 and MET P72 had rAUDPS of 0.458 and 0.5 respectively. All genotypes classified as HR had rAUDPS of 0 whereas genotypes classified as R had rAUDPS ranging from 0.021 and 0.063. (Appendix 4)

Table 4. Classification of the genotypes inoculated with Iganga RYMV isolate based on foliar response

Classification	No.	Genotypes
HR	06	ARC36-2-P-2 (2), ARC39-145-P-3 (4), ARC39-145-P-2 (5), ARS126-3-B-1-2 (11), Gigante[os], IRL 53 (GP 54).
R	05	ARC36-2-1-2 (1), ARC36-4-EP-2 (3), IRL 2 (GP 54), IRL 4 (69 GP 54), IRL 5 (GP 54)
MR	43	AGRA 41, AGRA 55, AGRA 60, AGRA 65, AGRA 78, E 20, MET P10, MET P13, MET P14, MET P16, MET P23, MET P24, MET P27, MET P28, MET P29, , MET P32, MET P34, MET P35, MET P37, MET P38, MET P39, MET P4, MET P40, MET P41, MET P42, MET P44, MET P47, MET P48, MET P49, MET P5, MET P50, MET P57, MET P58, MET P59, MET P61, MET P62, MET P64, MET P65, MET P66, MET P67, MET P7, MET P8, MET P9,
S	36	E 22, GIZA 179, GIZA 182, MET P1, MET P2, MET P11, MET P12, MET P17, MET P18, MET P19, MET P21, MET P22, MET P25, MET P26, MET P3, MET P30, MET P31, MET P33, MET P36, MET P43, MET P45, MET P46, MET P51, MET P52, MET P53, MET P55, MET P56, MET P6, MET P60, MET P63, MET P68, MET P69, MET P70, MET P71, MET P72, WITA 9
HS	22	E-YASIMIN, GIZA 177, GIZA 178 (7), GIZA 178 HIGH YIELDER, IR64[os], IRL 29 (GP 54), IRL 47 (GP 54), IRL 69 (GP 54), IURON (2014) 37 [os], IURON (2014) 41 [os], IURON Module-2 (230) [os], K34 [os], K38 [os], K85[os], KOMBOKA [os], MET P15, MET P20, MET P54, MGC 5-(51), Namche 2, SANDY, YASIMIN AROMATIC

[os] *Oryza sativa* genotype

4.3 Effect of Iganga RYMV isolate on grain yield

The percentage grain weight reduction of the genotypes was significant ($p \leq 0.001$) (Appendix 5). Generally, *Oryza sativa* genotypes exhibited more grain weight loss than *Oryza glaberrima*. All the *Oryza sativa* genotypes apart from Gigante lost 100% grain weight whereas *Oryza glaberrima* genotypes exhibited grain weight reduction between 0-100% (Table 5).

Fifty-four genotypes which is 48.2% of all the evaluated genotypes lost 100% grain weight when inoculated with the Iganga RYMV isolate (Appendix 6). Ninety-one genotypes which represent 81.25% of the evaluated genotypes lost more than 60% grain weight when inoculated with the Iganga RYMV isolate. However, only 7 genotypes which represent 6.3% of the evaluated genotypes lost 20% or less grain weight (Figure 5)

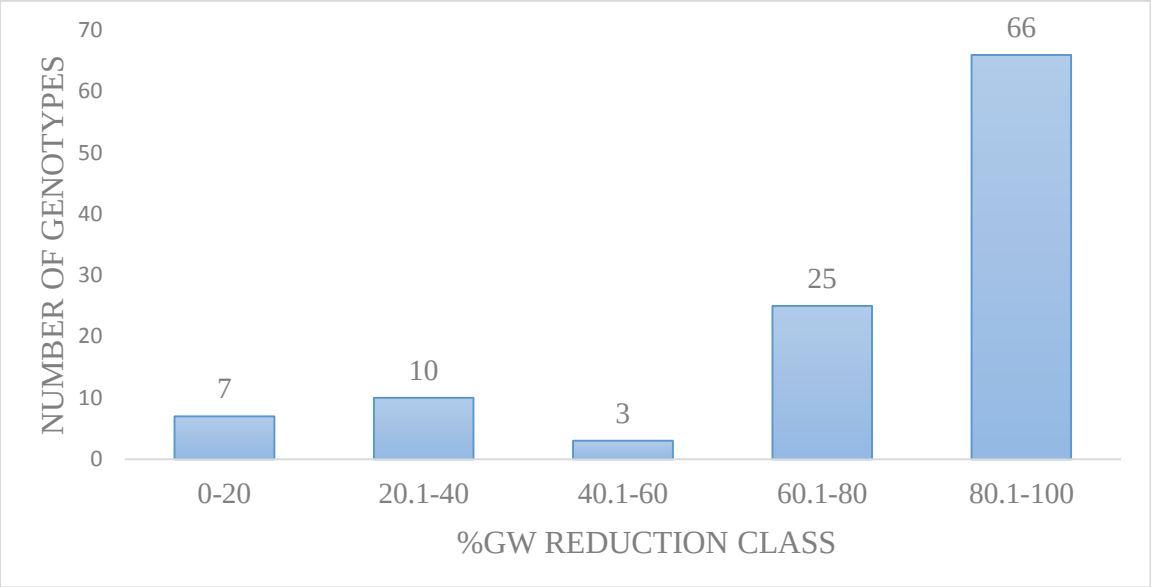

Figure 5 Grain weight reduction of the 112 genotypes[1]

[1] Gigante genotype which had net grain-weight increase was considered to have 0 loss of grain weight; Genotype IRL 53 (GP 54) had no yield data

No effect on grain yield was observed in genotypes ARC36-4-EP-2 (3), ARC36-2-P-2 (2) and IRL 4 (69 GP 54) whereas yield was increased by 33.3% in Gigante when inoculated with the Iganga RYMV isolate (table 5). No other genotype increased grain yield when inoculated with the Iganga RYMV isolate. Other check resistant genotypes MET 71 and MET 72 lost 66.7% and 80% grain weight respectively. All the check Susceptible genotypes lost 100% grain weight. Farmer preferred genotypes WITA 9 lost 71.4% grain weight (table 5)

Genotypes categorised as HR based on severity score lost up to 40% grain weight due to Iganga RYMV isolate. Among the HR genotypes, ARC39-145-P-2 (5) lost the most percentage grain weight whereas Gigante had a net grain-weight increase of 33.3% due to inoculation with Iganga RYMV Isolate (table 5)

Genotypes categorized as R lost between 0 and 66.7% of grain weight due to Iganga RYMV isolate. Among the R Genotypes, grain weight of ARC36-4-EP-2 (3) was not affected by RYMV whereas IRL 5 (GP 54) lost the most grain weight in this category (Table 5).

Genotypes categorised as MR lost between 20% and 100% grain weight due to Iganga RYMV isolate. Genotype MET P44 lost the least grain weight in this category whereas 18 genotypes which is 42% of genotypes categorized as MR lost 100% grain weight (Appendix 6).

Genotypes categorised as S lost between 33.3% and 100% grain weight. Genotype MET P3 lost the least percentage grain weight whereas 21 genotypes which is 58% of genotypes in the S

category lost 100% grain weight in the Susceptible classification. Genotypes categorised as HS lost between 85.7% and 100% grain weight due to Iganga RYMV isolate. The differences in loss of grain weight of all the genotypes in the HS category were not significant. Genotype MET P54 lost the least grain weight in this category while 15 genotypes which is 68% of genotypes in the HS classification lost 100% grain weight (Appendix 6).

TABLE 5 . Percentage grain weight reduction for selected genotypes inoculated with Iganga RYMV isolate

CATEGORY	**GENOTYPES**		**%GW reduction**
	Gigante [RCK]	*O. sativa*	-33.3
	ARS126-3-B-1-2 (11)	*O. glaberrima*	0
HR	ARC36-2-P-2 (2)	*O. glaberrima*	20
	ARC39-145-P-3 (4)	*O. glaberrima*	22.2
	ARC39-145-P-2 (5)	*O. glaberrima*	40
	ARC36-4-EP-2 (3)	*O. glaberrima*	0
	IRL 4 (69 GP 54)	*O. glaberrima*	0
R	ARC36-2-1-2 (1)	*O. glaberrima*	25
	IRL 2 (GP 54)	*O. glaberrima*	20
	IRL 5 (GP 54)	*O. glaberrima*	66.7
	MET P44	*O. glaberrima*	20
	MET P66	*O. glaberrima*	28.6
	MET P8	*O. glaberrima*	28.6
MR	MET P50	*O. glaberrima*	40
	MET P64	*O. glaberrima*	40
	MET P72[RCK]	*O. glaberrima*	80
	MET P3	*O. glaberrima*	33.3
S	WITA 9	*O. glaberrima*	71.4
	MET P71[RCK]	*O. glaberrima*	66.7
	K34[SCK]	*O. sativa*	100
	MET P54	*O. glaberrima*	85.7
	K38[SCK]	*O. sativa*	100
HS	K85[SCK]	*O. sativa*	100
	KOMBOKA	*O. sativa*	100
	IR64[SCK]	*O. sativa*	100
Mean Isolate score			79.4
CV%			38.6
LSD (5%)			20.2

[RCK]: Resistant check, [SCK]: Susceptible check

CHAPTER FIVE

DISCUSSION, CONCLUSONS AND RECOMMENDATIONS

5.1 Discussion

5.1.1 Isolate virulence

This study comprised of 112 rice genotypes tested against three RYMV isolates from Iganga, Lira and Namulonge. Evaluation of virulence of the 3 RYMV isolates by comparing the mean isolate percentage grain weight reduction and the mean isolate score of the sixth scoring interval revealed that the Iganga isolate was the most virulent. Similar results were reported with RYMV virus isolates from Iganga (Mogga *et al.,* 2012; Munganyinka, 2013) and simply confirm the existence of RYMV isolates with different virulence levels in Uganda. Variability in virulence levels of RYMV isolates is not new and has been documented elsewhere (Amancho *et al*., 2009; Kam *et al.,* 2012; Hubert *et al*., 2017).

5.1.2 Foliar symptom severity

The study recorded high variability in the foliar response of the genotypes shown by high significance in severity score of the sixth scoring interval and rAUDPS. The resistance levels ranged from highly resistant to highly susceptible. Variability in resistance and foliar response to RYMV in rice genotypes has also been reported by Kam *et al.,* (2012) and Mogga *et al.,* (2012). The high variability could be due to difference in mechanisms of resistance against RYMV and hence existence of different genes controlling such resistance mechanisms, which elicits genotypic responses in a range of categories. Very few genotypes were found to be highly resistant or at least resistant. Most were Moderately resistant or susceptible. Similar results were also reported by Kam *et al.,* (2012). This is indicative that there are few naturally resistant rice genotypes against RYMV and hence a low frequency of RYMV resistance genes in the rice gene pool. The frequency is even lower in *Oryza sativa* species compared to *Oryza glaberrima* species of rice.

The incubation period of the Iganga RYMV isolate varied among genotypes shown by difference in time of first showing of RYMV symptoms. The shortest incubation period was observed in genotype MET P48 where severity score was 5 in the first scoring interval whereas the longest incubation period was observed in genotypes categorized as Resistant. Incubation period of RYMV in rice genotypes could be controlled by genetic factors that vary in genotypes hence variation in incubation period of RYMV in the different rice genotypes.

The maximum severity score was attained by most genotypes between the third and fourth scoring interval, which was consistent with Mogga *et al.*, (2012), who used an isolate from a similar location (Iganga). This could be a sign of co-evolution of RYMV isolates to specific niches hence often exhibiting similar characteristics.

Gigante genotype did not show any RYMV symptom across the six scoring intervals and fell within the highly resistant category. Similar reaction has been reported with this genotype by Rakotomalala, *et al.*, (2008), Kam *et al*., (2013) and Salaudeen, (2014). Contrarily, Mogga *et al.*, (2012) observed some foliar symptoms on Gigante genotype. Similar to this study, Mogga *et al.*, (2012) studied the response of rice genotypes to RYMV in a screen house but other environmental factors which may have been different from those in this study could have suppressed host expression of resistance hence favoring RYMV to stimulate symptom development in his study.

Resistance break-down was observed in check resistant genotypes MET P71 and MET P72 which exhibited resistance to RYMV in West Africa. Nevertheless, resistance suppression by RYMV is not new and has been reported by Lyimo & Luzi-Kihupi, (2017) and Longue *et al.*, (2018) due to high rate of evolution of the RYMV.

5.1.3 Effect of Iganga RYMV isolate on grain yield

Complete loss of grain weight occurred in 48.2% of the evaluated genotypes; in addition, most of the genotypes lost more than 80% grain weight. This kind of reaction supports the virulent nature of the Iganga isolate.

Genotype MET P44 was classified as MR based on severity score but lost only 20% of grain weight which was significantly different from grain weight lost by most genotypes classified as MR but not significant to the mean of the genotypes classified as R and HR. MET P44 could, thus, exhibit a mechanism of resistance characterized by virus suppression until later stages of growth, preventing the virus from significantly reducing yield. Similar reactions have been reported by Zouzou *et al.*, (2008). In contrast, genotype IRL 5 (GP 54), which was classified as R, lost 66.7 yield which was significant to all the other genotypes in the same classification. This could be because RYMV took a longer incubation period in this genotype hence by the sixth scoring interval, less severe symptoms were recorded. The reactions of MET P44 and IRL 5 (GP 54) support the idea that foliar symptom expression alone in evaluation of genotypes for resistance against RYMV is not effective (Zouzou *et al.,* 2008). However, the evaluation criteria remain very vital in evaluation of genotypes for resistance to RYMV.

Gigante genotype exhibited a yield increase when inoculated with RYMV, just like another resistant genotype, Moroberekan, in West Africa (Zouzou *et al.,* 2008). This reaction is similar to overcompensation often observed in plant reaction to mild herbivory (Belsky *et al.,* 1993)

5.1.4 Resistance of the genotypes to RYMV

From this study, it was observed that some genotypes showed resistance to the less virulent isolates but were susceptible to the most virulent isolate. However, no genotype that showed resistance to the most virulent isolate was susceptible to the less virulent isolates. This therefore shows that all the genotypes that showed resistance to the Iganga RYMV isolate had non-isolate specific resistance. However, that does not necessarily mean that the genotypes resistant to only the less virulent isolates are not useful in breeding programs because such genotypes may be important in gene pyramiding breeding programs so that a wider range of resistance mechanisms are integrated for sustainable resistance.

Oryza sativa genotypes exhibited more susceptibility to RYMV than *Oryza glaberrima* genotypes. All *Oryza sativa* genotypes except Gigante were categorized as HS and lost 100% grain weight due to RYMV. This indicates the high virulence of RYMV against *Oryza sativa* rice genotypes which are exotic to Africa compared to the indigenously African *Oryza glaberrima* (Sweeney and McCouch, 2007). These findings are similar to results by Thottapilly & Rossel, (1993); Zouzou *et al.,* (2008); Kam *et al.,* (2012) and could be due to existence of unique resistance genes in *Oryza glaberrima* genotypes that are not present in *Oryza sativa* genotypes. These unique genes could be due to co-evolution of RYMV, endemic to the African continent, and *Oryza glaberrima* for the past decades

5.2 Conclusions

This study classified genotypes into resistant and highly resistant groups based on foliar symptom expression, however the grain yield between the two classifications was overlapping for most genotypes and the relative area under disease progress curves of these genotypes were not insignificantly different. Genotypes in both classifications are, therefore, potential sources of resistance to RYMV apart from IRL 5 (GP 54) which had a long incubation period for the virus but was not necessarily resistant. The tolerant variety MET P44 is also a potential source of genes for resistance. Farmer preferred genotypes WITA 9 and K85 were still susceptible and if not improved will negatively impact on breeding gains so far made

5.3 Recommendations

1. By coupling percentage grain weight reduction and foliar symptom severity score ten genotypes namely, Gigante, ARC36-4-EP-2 (3), ARS126-3-B-1-2 (11), IRL 4 (69 GP 54), ARC36-2-P-2 (2), ARC36-2-1-2 (1), MET P44, ARC39-145-P-3 (4), ARC39-145-P-2 (5) and IRL 2 (GP 54) were promising candidates for breeding with farmer preferred genotypes to confer resistance against RYMV disease. Due to the high rate of evolution of RYMV, genes from genotypes with varying RYMV resistance mechanisms could later be pyramided to confer durable RYMV resistance to the farmer preferred genotypes.
2. Further yield evaluations should be done on genotype IRL 53 (GP 54) so as its yield data is captured because basing on foliar symptom, it could be another promising genotype.

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APPENDICES

Appendix 1 Additional information about the 112 rice genotypes used in the evaluation at NaCCRI in 2017B[1]

List name	Pedigree	Other information	Source	Maturity period (days)	Yield (kg/Ha)	Status
MET P1	ART35-52-2-7N-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	119	2958	
MET P2	ART34-82-1-7N-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	119	2875	
MET P3	ART35-114-1-6N-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	119	3140	
MET P4	ART34-146-1-8N-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	112	3827	
MET P5	ART34-79-1-2N-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	121	3440	
MET P6	ART35-49-1-4N-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	120	3575	
MET P7	ART34-76-2-8D-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	113	4787	
MET P8	ART35-100-1-7D-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	123	2954	
MET P9	ART35-4-1-5D-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	132	3631	
MET P10	ART35-200-2-2-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	111	3275	
MET P11	ART34-86-2-1-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	108	3266	
MET P12	ART34-88-1-2-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	109	3531	
MET P13	ART34-113-3-2-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	107	3476	
MET P14	ART34-256-3-1-B-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	110	3146	
MET P15	ART35-159-1-2-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	121	4016	
MET P16	ART35-272-1-2-B-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	116	3196	
MET P17	ART27-58-7-1-2-2-2-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	125	3778	
MET P18	ART27-58-3-2-1-4	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	125	4631	
MET P19	ART27-190-6-4-2-1-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	135	3423	
MET P20	ART27-58-7-2-2-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	134	3169	
MET P21	ART27-58-7-1-2-4-2-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	129	3271	
MET P22	ART27-58-3-2-1-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	138	4744	
MET P23	ART27-58-8-1-1-4	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	157	6466	
MET P24	ART3-7L9P8-3-B-B-2-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	132	4700	

MET P25	ART27-58-6-2-1-1-3-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	132	5090
MET P26	ART27-190-6-1-4-2-2-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	149	5329
MET P27	ART27-190-1-3-3-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	135	3993
MET P28	ART27-58-6-2-2-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	148	5081
MET P29	ART27-58-8-1-2-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	139	4684
MET P30	ART27-58-6-2-1-1-3-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	142	3956
MET P31	ART15-7-16-38-1-B-B-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	135	5200
MET P32	ART27-190-7-3-2-4-3-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	143	4218
MET P33	ART27-58-6-2-1-1-3-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	136	4756
MET P34	ART27-58-6-2-1-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	139	3716
MET P35	ART27-58-3-2-2-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	124	3808
MET P36	ART27-122-19-3-1-2-1-1	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	143	4091
MET P37	ART27-122-19-3-1-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	154	4125
MET P38	ART16-5-9-22-3-B-B-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	105	6400
MET P39	ART27-190-7-6-4-2	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	131	3049
MET P40	ART27-190-1-4-2-1-1-3	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	150	5863
MET P41	PCT-11\0\0\2,Bo\2\1>181-9-1-3-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	116	4160
MET P42	PCT-11\0\0\2,Bo\2\1>32-M-1-1-4-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	118	4430
MET P43	PCT-11\0\0\2,Bo\2\1>32-M-1-1-5-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	116	4500
MET P44	PCT-11\0\0\2,Bo\2\1>404-1-1-1-1-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	112	4000
MET P45	PCT-11\0\0\2,Bo\2\1>46-M-3-4-3-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	117	4030
MET P46	PCT-11\0\0\2,Bo\2\1>46-M-4-1-2-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	115	4000
MET P47	PCT-11\0\0\2,Bo\2\1>487-1-6-2-1-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	111	4130
MET P48	PCT-11\0\0\2,Bo\2\1>487-1-6-2-3-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	125	3800
MET P49	PCT-11\0\0\2,Bo\2\1>82-3-1-1-3-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	107	3860
MET P50	PCT-11\0\0\2,Bo\2\1>82-3-1-1-3-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	108	4160
MET P51	PCT-11\0\0\2,Bo\2\1>82-3-1-1-3-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	101	4000
MET P52	PCT-11\0\0\2,Bo\2\1>82-3-3-1-3-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	95	3760
MET P53	PCT-11\0\0\2,Bo\2\1>94-1-1-2-1-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	115	4100
MET P54	PCT-11\0\0\2,Bo\2\1>94-1-1-2-1-5-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	108	3630

MET P55	PCT-11\0\0\2,Bo\3\1>1-M-3-1-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	105	4500	
MET P56	PCT-11\0\0\2,Bo\3\1>44-M-1-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	109	3900	
MET P57	PCT-11\0\0\2,Bo\3\1>44-M-4-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	110	2950	
MET P58	PCT-11\0\0\2>Bo\2\1>87-1-1-2-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	91	2930	
MET P59	PCT-4\0\0\1>295-2-3-1-2-4-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	113	4480	
MET P60	PCT-4\0\0\1>295-2-3-1-3-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	116	4300	
MET P61	PCT-4\0\0\1>295-2-6-1-3-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	115	2700	
MET P62	PCT-4\0\0\1>295-2-6-3-3-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	104	2950	
MET P63	PCT-4\0\0\1>4-2-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	112	4350	
MET P64	PCT-4\SA\1\1,Bo\3\1>161-3-2-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	109	4060	
MET P65	PCT-4\SA\1\1,Bo\3\1>204-1-3-3-M-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	106	3780	
MET P66	PCT-4\SA\1\1,SA\2\1>746-1-1-4-1-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	90	3450	
MET P67	PCT-4\SA\1\1,SA\2\1>746-1-2-2-1-3-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	100	3500	
MET P68	PCT-4\SA\1\1,SA\2\1>746-1-5-2-2-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	103	3180	
MET P69	PCT-4\SA\5\1>1754-5-1-3-2-2-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	116	4060	
MET P70	PCT-4\SA\5\1>1754-5-1-5-3-1-M	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria	100	4550	
MET P71	NERICA 4 (Check)	O.glaberrima	AfricaRice-Ibadan, Nigeria			resistant check
MET P72	NERICA 8 (Check)	WAB 450 IBP91HB.	AfricaRice-Ibadan, Nigeria			resistant check
IURON 2014 (230)	CR 2340-4	CR 2340-5	IRRI			
AGRA 65	AGRA-CRI-UPL-4-18	AGRA-CRI-UPL-4-18	CRI, Ghana			
AGRA 60	AGRA-CRI-UPL-4-13	AGRA-CRI-UPL-4-13	CRI, Ghana			
AGRA 55	AGRA-CRI-UPL-4-4	AGRA-CRI-UPL-4-4	CRI, Ghana			
AGRA 78	AGRA-CRI-UPL-2-1	AGRA-CRI-UPL-2-1	CRI, Ghana			
E 22	WAB 450-1-BL1-136-HB /WAB 450-B-136-HB	NM7-22-11- B-P-1-1	NARO, Uganda			
SANDY	O.barthi interspecific lines	O.barthi interspecific lines	AfricaRice-Ibadan, Nigeria			
E 20	IRAT 325/WAB 365-B-1H1-HB	NM7-20-4- B-P-1-1	NARO, Uganda			
IURON (2014) 41	IR 88628-B-B-16	IR 88628-B-B-16	IRRI			

IURON (2014) 37	IR 88628-B-B-46	IR 88628-B-B-46	IRRI
ARC36-2-1-2 (1)	ARC36-2-1-2	ARC36-2-1-2	AfricaRice-Benin,
ARC36-2-P-2-54 (2)	ARC36-2-P-2-54 (2)	ARC36-2-P-2-54 (2)	AfricaRice-Benin,
ARC36-4-ET-2 (3)	ARC36-4-ET-2 (3)	ARC36-4-ET-2 (3)	AfricaRice-Benin,
ARC39-145-P-3 (4)	ARC39-145-P-3 (4)	ARC39-145-P-3 (4)	AfricaRice-Benin,
ARC39-145-P-2 (5)	ARC39-145-P-2 (5)	ARC39-145-P-2 (5)	AfricaRice-Benin,
ARS126-3-B-1-2 (11)	ARS126-3-B-1-2 (11)	ARS126-3-B-1-2 (11)	AfricaRice-Benin,
MGC5 (51)	Unknown	Unknown	AfricaRice-Benin,
IRL 4	ARC 39-145-P-3	ARC 39-145-P-3	AfricaRice-Benin,
1RL 5	ARC 39-145-P-2	ARC 39-145-P-2	AfricaRice-Benin,
IRL 2	ARC 36-2-P-2	ARC 36-2-P-2	AfricaRice-Benin,
IRL 29	HHZ 8-SAL6-SAL3-SAL1	HHZ 8-SAL6-SAL3-SAL1	AfricaRice-Senegal,
IR 47	ARS 759-1-1-1-B	ARS 759-1-1-1-B	AfricaRice-Benin,
IRL 53	Unknown	Unknown	AfricaRice-Benin,
IRL 69	Unknown	Unknown	AfricaRice-Benin,
YASIMIN	Unknown	Unknown	Egypt
AROMATIC			
GIZA 178 HIGH YIELDER	Unknown	Unknown	Egypt
GIZA 179	Unknown	Unknown	Egypt
GIZA 177	Unknown	Unknown	Egypt
GIZA 182	Unknown	Unknown	Egypt
E-YASMIN	Unknown	Unknown	Egypt
GIZA 178	Unknown	Unknown	Egypt
AGRA 41	AGRA-CRI-UPL-3-4	AGRA-CRI-UPL-3-4	AfricaRice-Benin,

Gigante	Unknown	Unknown	AfricaRice	resistant check
K85	Unknown	Unknown	China	Susceptible
K38	Unknown	Unknown	China	Susceptible
WITA 9	TOX 3058-28-1-1-1	TOX 3058-28-1-1-1	IR 2042-178-1/CT19	
K34	Unknown	Unknown	China	Susceptible
Namche 2	NM7-8-2-B-P-11-6	NM7-8-2-B-P-11-6	Caiapo/CT 16324-CA-9-M – 1	
KOMBOKA	IR 79253-55-1-4-6	IR 79253-55-1-4-6	IRRI	
IR 64	Unknown	Unknown	IRRI	Susceptible

[1] Missing data is unknown

Appendix 2 ANOVA for percentage grain weight and severity score of the sixth scoring interval across the three isolates

Source of variation	D.F	%GW reduction		S6	
		M.S	p-value	M.S	p-value
Isolate	2	4602.6	0.046	3.091	0.278
rep(isolate)	3	451.667	0.543	1.532	0.257
Genotype	110^{gw} and 111^{S6}	3887.2	3.002×10^{-35}	19.773	4.662×10^{-82}
Isolate.Genotype	220	899.6		1.0474	
pooled error	283.85^{gw} and 286.02^{S6}	630.628		1.131	

^{gw} value for %GW reduction; ^{S6} Value for S6

Appendix 3 ANOVA for mean disease severity score of genotypes under Iganga RYMV isolate treatment

SOURCE OF VARIATION	D.F	MEAN SUMS OF SQUARES						
		S1	S2	S3	S4	S5	S6	rAUDPS
Rep	1	5.84*	1.13^{ns}	0.6567^{ns}	3.01*	1.7977^{ns}	0.88^{ns}	0.010^{ns}
Block/Rep or Block	5.81-5.95 or 3^{rc}	0.77^{ns}	1.59^{ns}	1.60^{ns}	10.30***	0.80^{ns}	1.06^{ns}	0.007^{ns}
Cultivar	111	1.67***	6.78***	6.45***	6.64***	6.68***	7.68***	0.078***
Residual	104.05-104.19 or 107^{rc}	0.77	0.70	0.86	0.57	0.71	0.99	0.0041
Total	107				3.75			
LEE	58.2-104.19	0.72	0.73	0.89		0.72	1	0.004

^{ns} not significant at $p \leq 0.05$; * significant at $p \leq 0.05$; ***significant at $p \leq 0.001$; ^{rc} value from RCBD analysis for parameters analyzed as RCBD; ^{prc} Parameter analyzed as RCBD

Appendix 4 Means of severity score, relative area under disease progress stairs and %GW reduction under Iganga RYMV isolate

DESIGNATION	S1	S2	S3	S4	S5	S6	rAUDPS
AGRA 78	1.0	5.0	5.0	5.0	5.0	5.0	0.417
E 20	1.0	5.0	6.0	5.0	5.0	5.0	0.438
E 22	3.0	6.0	6.0	6.0	6.0	6.0	0.563
E-YASIMIN	3.0	7.0	8.0	9.0	9.0	9.0	0.813
GIZA 177	3.0	6.0	7.0	7.0	7.0	8.0	0.667
GIZA 178 (7)	3.0	7.0	8.0	8.0	8.0	9.0	0.771
GIZA 179	2.0	7.0	7.0	7.0	7.0	7.0	0.646
GIZA 182	3.0	7.0	7.0	7.0	7.0	7.0	0.667
IR64	3.0	9.0	9.0	9.0	9.0	9.0	0.875
IRL 69 (GP 54)	3.0	7.0	8.0	9.0	9.0	9.0	0.813
IURON (2014) 37	1.0	5.0	7.0	7.0	7.0	8.0	0.604
IURON (2014) 41	2.0	5.0	7.0	7.0	8.0	9.0	0.667
IURON 2014 (230)	4.0	7.0	8.0	9.0	9.0	9.0	0.833
K34	2.0	7.0	7.0	7.0	7.0	9.0	0.688
K38	3.0	8.0	8.0	9.0	9.0	9.0	0.833

K85	3.0	7.0	7.0	7.0	7.0	8.0	0.688
KOMBOKA	4.0	7.0	7.0	8.0	8.0	8.0	0.750
MET P10	1.0	5.0	5.0	5.0	5.0	5.0	0.417
MET P12	1.0	3.0	4.0	6.0	6.0	7.0	0.438
MET P14	2.0	4.0	5.0	5.0	5.0	5.0	0.417
MET P15	1.0	4.0	6.0	7.0	7.0	9.0	0.583
MET P16	1.0	3.0	4.0	5.0	5.0	5.0	0.354
MET P19	1.0	3.0	5.0	5.0	6.0	6.0	0.417
MET P2	1.0	4.0	5.0	6.0	6.0	6.0	0.458
MET P24	1.0	4.0	5.0	5.0	5.0	5.0	0.396
MET P25	1.0	4.0	5.0	6.0	6.0	7.0	0.479
MET P26	2.0	5.0	6.0	6.0	6.0	7.0	0.542
MET P29	3.0	5.0	5.0	5.0	5.0	5.0	0.458
MET P30	1.0	3.0	5.0	5.0	5.0	7.0	0.417
MET P32	2.0	5.0	5.0	5.0	5.0	5.0	0.438
MET P33	2.0	5.0	6.0	7.0	7.0	7.0	0.583
MET P38	2.0	5.0	5.0	5.0	5.0	5.0	0.438
MET P4	1.0	4.0	5.0	5.0	5.0	5.0	0.396
MET P40	1.0	2.0	3.0	4.0	5.0	5.0	0.292
MET P41	1.0	3.0	5.0	5.0	5.0	5.0	0.375
MET P43	1.0	5.0	6.0	6.0	6.0	6.0	0.500
MET P45	3.0	5.0	5.0	5.0	5.0	6.0	0.479
MET P46	1.0	5.0	5.0	5.0	5.0	6.0	0.438
MET P48	5.0	5.0	5.0	5.0	5.0	5.0	0.500
MET P49	1.0	3.0	5.0	5.0	5.0	5.0	0.375
MET P5	1.0	3.0	5.0	5.0	5.0	5.0	0.375
MET P51	2.0	5.0	5.0	7.0	7.0	7.0	0.563
MET P55	1.0	5.0	6.0	6.0	6.0	7.0	0.521
MET P56	2.0	5.0	7.0	7.0	7.0	7.0	0.604
MET P59	1.0	5.0	5.0	5.0	5.0	5.0	0.417
MET P6	1.0	4.0	5.0	6.0	6.0	7.0	0.479
MET P60	2.0	5.0	5.0	6.0	6.0	7.0	0.521
MET P63	2.0	3.0	5.0	6.0	6.0	6.0	0.458
MET P67	1.0	5.0	5.0	5.0	5.0	5.0	0.417
MET P68	3.0	5.0	5.0	6.0	6.0	6.0	0.521
MET P69	1.0	3.0	5.0	6.0	6.0	7.0	0.458
MET P9	1.0	3.0	4.0	5.0	6.0	5.0	0.375
MGC 5-(51)	4.0	7.0	8.0	9.0	9.0	9.0	0.833
YASIMIN AROMATIC	3.0	7.0	7.0	9.0	9.0	9.0	0.792
GIZA 178 HIGH YIELDER	4.0	7.0	8.0	8.0	8.0	9.0	0.792
SANDY	2.0	5.0	7.0	7.0	8.0	8.0	0.646
AGRA 55	1.0	3.0	4.0	4.0	5.0	5.0	0.333
MET P17	2.0	5.0	6.0	6.0	6.0	6.0	0.521
MET P27	3.0	5.0	5.0	5.0	5.0	5.0	0.458
MET P54	1.0	4.0	5.0	6.0	8.0	9.0	0.563
MET P57	1.0	4.0	5.0	5.0	5.0	5.0	0.396
IRL 47 (GP 54)	3.0	7.0	8.0	8.0	8.0	8.0	0.750
MET P11	1.0	4.0	6.0	5.0	5.0	6.0	0.438
MET P22	2.0	5.0	5.0	5.0	5.0	6.0	0.458
MET P23	1.0	1.0	4.0	5.0	5.0	5.0	0.313
MET P42	1.0	3.0	5.0	5.0	5.0	5.0	0.375
MET P61	3.0	5.0	6.0	6.0	6.0	5.0	0.521
MET P65	1.0	2.0	4.0	5.0	5.0	5.0	0.333
MET P70	1.0	4.0	5.0	5.0	6.0	6.0	0.438
IRL 29 (GP 54)	2.0	7.0	7.0	8.0	8.0	8.0	0.708

AGRA 65	2.0	5.0	5.0	5.0	5.0	5.0	0.438
MET P1	1.0	4.0	5.0	6.0	7.0	7.0	0.500
MET P13	1.0	4.0	5.0	5.0	5.0	5.0	0.396
MET P18	1.0	4.0	5.0	5.0	5.0	6.0	0.417
MET P20	1.0	4.0	6.0	6.0	6.0	8.0	0.521
MET P21	1.0	4.0	4.0	5.0	5.0	7.0	0.417
MET P28	2.0	5.0	5.0	6.0	6.0	5.0	0.479
MET P36	2.0	5.0	7.0	7.0	7.0	6.0	0.583
MET P37	2.0	4.0	5.0	6.0	5.0	5.0	0.438
MET P39	1.0	4.0	5.0	5.0	5.0	5.0	0.396
MET P53	2.0	5.0	5.0	6.0	6.0	6.0	0.500
MET P58	2.0	3.0	4.0	5.0	5.0	5.0	0.375
MET P72	2.0	5.0	5.0	6.0	6.0	6.0	0.500
Namche 2	1.0	1.0	2.0	3.0	4.0	8.0	0.271
WITA 9	2.0	5.0	6.0	6.0	7.0	6.0	0.542
MET P31	1.0	5.0	5.0	6.0	6.0	6.0	0.479
MET P62	1.0	3.0	5.0	5.0	5.0	5.0	0.375
AGRA 41	2.0	4.0	5.0	5.0	5.0	5.0	0.417
AGRA 60	1.0	5.0	5.0	5.0	5.0	5.0	0.417
MET P34	1.0	3.0	4.0	5.0	5.0	5.0	0.354
MET P52	2.0	5.0	5.0	5.0	5.0	7.0	0.479
MET P71	1.0	5.0	5.0	5.0	5.0	7.0	0.458
IRL 5 (GP 54)	1.0	1.0	1.0	1.0	2.0	3.0	0.063
MET P47	1.0	4.0	4.0	5.0	5.0	5.0	0.375
MET P35	1.0	3.0	5.0	5.0	5.0	5.0	0.375
MET P50	2.0	4.0	5.0	5.0	5.0	5.0	0.417
MET P64	2.0	4.0	5.0	5.0	5.0	5.0	0.417
MET P7	1.0	1.0	3.0	4.0	4.0	5.0	0.250
MET P3	2.0	2.0	3.0	4.0	5.0	7.0	0.354
MET P66	1.0	2.0	4.0	5.0	5.0	5.0	0.333
MET P8	2.0	5.0	4.0	5.0	5.0	5.0	0.417
ARC39-145-P-2 (5)	1.0	1.0	1.0	1.0	1.0	1.0	0.000
IRL 2 (GP 54)	1.0	1.0	1.0	1.0	2.0	2.0	0.042
ARC39-145-P-3 (4)	1.0	1.0	1.0	1.0	1.0	1.0	0.000
ARC36-2-1-2 (1)	1.0	1.0	1.0	2.0	2.0	2.0	0.063
MET P44	1.0	2.0	4.0	5.0	5.0	5.0	0.333
ARC36-2-P-2 (2)	1.0	1.0	1.0	1.0	1.0	1.0	0.000
IRL 4 (69 GP 54)	1.0	1.0	1.0	1.0	2.0	2.0	0.042
ARS126-3-B-1-2 (11)	1.0	1.0	1.0	1.0	1.0	1.0	0.000
ARC36-4-EP-2 (3)	1.0	1.0	1.0	1.0	1.0	2.0	0.021
IRL 53 (GP 54)	1.0	1.0	1.0	1.0	1.0	1.0	0.00
Gigante	1.0	1.0	1.0	1.0	1.0	1.0	0.000
Mean Isolate score	1.7	4.2	5.0	5.4	5.5	5.8	0.455
CV%	49.8	20.3	18.9	14.3	15.3	17.1	14.4
LSD (5%)	1.74	1.66	1.84	1.49	1.67	1.97	0.127

Appendix 5 Analysis of Variance table for percentage grain weight loss of genotypes evaluated with Iganga RYMV isolate[1]

Source of variation	D.F	MS	F-test	p-value
Rep	1	535.2	0.87	0.394
block/rep	5.89	615.1	5.908	7.5741×10^{-5}
genotype	110	1677.02	3.91	4.182×10^{-9}
Residual	104.11	104.11		
LEE	69.8	428.9		

[1] Genotype IRL 53 (GP 54) died before reaching reproductive maturity hence ANOVA excludes its data

Appendix 6 Percentage grain reduction of the 112 genotypes

category (Based on severity score)	Genotypes	Inoculated	non-inoculated	%GW reduction
HR	ARC36-2-P-2 (2)	2	2.5	20.0
	ARC39-145-P-2 (5)	1.5	2.5	40.0
	ARC39-145-P-3 (4)	3.5	4.5	22.2
	ARS126-3-B-1-2 (11)	3.5	3.5	0.0
	Gigante	4	3	-33.3
	IRL 53 (GP 54)	NA	NA	NA
R	ARC36-2-1-2 (1)	1.5	2	25.0
	ARC36-4-EP-2 (3)	2	2	0.0
	IRL 2 (GP 54)	2	2.5	20.0
	IRL 4 (69 GP 54)	2.5	2.5	0.0
	IRL 5 (GP 54)	1.5	4.5	66.7
MR	AGRA 41	1	4	75.0
	AGRA 55	0.5	3	83.3
	AGRA 60	1	3	66.7
	AGRA 65	1	3.5	71.4
	AGRA 78	0	2	100.0
	E 20	0	2	100.0
	MET P10	0	2	100.0
	MET P13	0.5	1.5	66.7
	MET P14	0	3.5	100.0
	MET P16	0	2.5	100.0
	MET P23	0.5	2	75.0
	MET P24	0	1	100.0
	MET P27	0.5	4	87.5
	MET P28	0.5	1.5	66.7
	MET P29	0	3.5	100.0
	MET P32	0	3	100.0
	MET P34	1	2	50.0
	MET P35	1.5	2.5	40.0
	MET P37	0.5	3	83.3

	MET P38	0	3	100.0
	MET P39	0.5	1.5	66.7
	MET P4	0	2	100.0
	MET P40	0	4	100.0
	MET P41	0	2	100.0
	MET P42	0.5	2	75.0
	MET P44	2	2.5	20.0
	MET P47	0.5	2.5	80.0
	MET P48	0	1	100.0
	MET P49	0	2.5	100.0
	MET P5	0	3.5	100.0
	MET P50	1.5	2.5	40.0
	MET P57	0.5	3.5	85.7
	MET P58	0.5	3	83.3
	MET P59	0	3.5	100.0
	MET P61	0.5	2.5	80.0
	MET P62	1.5	4.5	66.7
	MET P64	1.5	2.5	40.0
	MET P65	0.5	2.5	80.0
	MET P66	2.5	3.5	28.6
	MET P67	0	3	100.0
	MET P7	1.5	2.5	40.0
	MET P8	2.5	3.5	28.6
	MET P9	0	1.5	100.0
S	E 22	0	1.5	100.0
	MET P11	0.5	4	87.5
	MET P17	0.5	4.5	88.9
	MET P18	1	2.5	60.0
	MET P19	0	2	100.0
	MET P2	0	1.5	100.0
	MET P22	0.5	2	75.0
	MET P31	1.5	3	50.0
	MET P36	0.5	1.5	66.7
	MET P43	0	3	100.0
	MET P45	0	2	100.0
	MET P46	0	2	100.0
	MET P53	0.5	3	83.3
	MET P63	0	2	100.0
	MET P68	0	3	100.0
	MET P70	0.5	2.5	80.0
	MET P72	0.5	2.5	80.0
	WITA 9	1	3.5	71.4
	GIZA 179	0	3.5	100.0
	GIZA 182	0	4.5	100.0
	MET P1	0.5	1.5	66.7

	MET P12	0	1	100.0
	MET P21	0.5	2	75.0
	MET P25	0	3	100.0
	MET P26	0	3	100.0
	MET P3	2	3	33.3
	MET P30	0	4.5	100.0
	MET P33	0	2.5	100.0
	MET P51	0	1.5	100.0
	MET P52	1	3	66.7
	MET P55	0	3.5	100.0
	MET P56	0	4	100.0
	MET P6	0	2	100.0
	MET P60	0	2	100.0
	MET P69	0	4.5	100.0
	MET P71	1	3	66.7
HS	GIZA 177	0	4.5	100.0
	IRL 29 (GP 54)	1	3.5	71.4
	IRL 47 (GP 54)	0.5	4	87.5
	IURON (2014) 37	0	3	100.0
	K85	0	3.5	100.0
	KOMBOKA	0	3.5	100.0
	MET P20	0.5	2.5	80.0
	Namche 2	0.5	2.5	80.0
	SANDY	0.5	4.5	88.9
	E-YASIMIN	0	3	100.0
	GIZA 178 (7)	0	2	100.0
	GIZA 178 HIGH YIELDER	0.5	5	90.0
	IR64	0	4.5	100.0
	IRL 69 (GP 54)	0	2	100.0
	IURON (2014) 41	0	3.5	100.0
	IURON Module-2 (230)	0	6	100.0
	K34	0	2.5	100.0
	K38	0	4	100.0
	MET P15	0	2.5	100.0
	MET P54	0.5	3.5	85.7
	MGC 5-(51)	0	2.5	100.0
	YASIMIN AROMATIC	0	3.5	100.0
Mean				79.1
CV%				38.6
LSD (5%)				20.2

NA; Data not available due to death before reproductive maturity