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Resistance of selected *Oryza glaberrima* landraces and their intra-specific breeding lines to Beninese *Rice yellow mottle virus* isolates

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ABSTRACT

Rice yellow mottle virus (RYMV) is a widespread and damaging pathogen, endemic to Africa and affecting rice in lowland, irrigated and upland ecologies. Yield losses of 10–100% have been recorded, depending on rice genotypes, time of infection, cropping system, vector abundance and isolate pathogenicity. Control measures for this disease are based mainly on cultural practices and the use of varietal resistance. Specifically, *Oryza glaberrima,* the cultivated African rice species, has provided several of the known resistance alleles/genes. In this study, 160 *O. glaberrima* landraces, 55 of their intra-specific progenies and two controls - Tog5681 (resistant) and IR64 (susceptible) - were screened against five RYMV isolates collected from Northern Benin. Disease severity was measured on plants at 21 and 42 days after inoculation. Two cultivars - IRGC104019 and IRGC96787 (Tog5644) - from Tanzania and Nigeria respectively - and 16 intra-specific lines were identified as highly resistant to all five isolates. The genotyping of IRGC104019 and IRGC96787 revealed that they share allele *rymv1-3,* identified in Tog5681 (the resistant control) and that confers resistance, bringing the number of *O. glaberrima* accessions known to date to harbor this allele to 11. The importance of this finding and the level of resistance displayed by these two accessions strengthen the hypothesis that the African rice collection is a potential RYMV resistance donor. It is, therefore, necessary to further screen it for valorizing its usefulness in breeding programs.

1. Introduction

Despite efforts at increasing production, rice yields in Africa range from 1 to 3 t ha^{-1} and remain far below the potentials (Traoré et al., 2006). Current production cannot meet the demand of the growing population. Several factors militate against optimum rice production in most African rice-growing countries, including the susceptibility of cultivars to diseases. *Rice yellow mottle virus* (RYMV) is a major constraint in several countries (Séré et al., 2013). The disease is endemic to and widespread the African continent, causes severe damage to rice plants (Abo et al., 1998), reduces grain yield by 10–100%, and severe attacks can lead to plant death (Calvert et al., 2003; Kouassi et al., 2005). The disease has been widely observed in lowland, irrigated and upland ecologies in most rice-producing countries.

RYMV belongs to the Sobemovirus genus, that includes the type species of the *Southern bean mosaic virus* which infects both dicotyledonous and monocotyledonous plants (ICTV, 2018). Symptoms of RYMV include yellowing, mottling, necrosis, stunting of rice plants, incomplete emergence of panicles, and plant death. In general, RYMV is highly infectious and stable in different environments. It also infects all wild rice species (*Oryza* spp.) particularly the perennial wild species *O. longistaminata* as well as several weeds that serve as inoculum reservoir in the Soudano-Sahelian zone of West Africa where it is endemic.

For a long time, breeders had access to only one resistance gene (*RYMV1*) that has four known resistance alleles which confer a high resistance level - *rymv1-2* available in Asian cultivated rice species, *O. sativa*, while *rymv1-3*, *rymv1-4* and *rymv1-5* are available in African cultivated rice species, *O. glaberrima* (Ndjiondjop et al., 1999; Albar et al., 2006; Thiemele et al., 2010). A few years ago, *RYMV2* was discovered in Tog7291, an *O. glaberrima* accession (Thiémélé et al., 2010) and a third resistance gene, *RYMV3 w*as recently found in Tog5307 (Pidon et al., 2017).

Previous molecular analyses showed that the two resistance alleles of the *RYMV1* gene (i.e *rymv1-3* carried by Tog5681 and *rymv1-4* carried by Tog5672) are characterized by a short deletion (RRD322-324) and substitution (E321K) of amino acids in the same central region of the MIF4G

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domain of the protein (Albar et al., 2006). The modeling of this domain shows that these mutations are very close and located on the surface of the protein. The second resistance gene (*RYMV2*) is governed by a recessive allele and codes for CPR5-1, a probable component of the nuclear pore complex involved in the regulation of defense mechanisms (Orjuela et al., 2013). The third gene (*RYMV3*), with a NLR as a very convincing candidate gene, is probably involved in the virus recognition mechanism (Pidon et al., 2017).

Specific molecular markers for the different alleles of *RYMV1* gene were developed for accelerating the cultivars' resistance improvement using Marker-Assisted Selection (MAS). These markers were used to introgress *rymv1-2* into popular RYMV-susceptible elite varieties, such as Bouake 189, a very popular cultivar in Côte d'Ivoire which subsequently became resistant to the virus (Bouet et al., 2013). However, the virus is able to evolve and some isolates are known to have overcome resistance (Fargette et al., 2002; Hebrard et al., 2006, 2018; Pinel-Galzi et al., 2016), thus making the identification of new resistance sources and genes critical in programs for sustainable resistance breeding. As *O. glaberrima* species appeared to be an interesting source of resistance to RYMV (Thiémélé et al., 2010), screening its landraces for resistance is continuously being conducted at AfricaRice and this study reports on the screening of 160 individuals and 55 intra-specific lines. In addition, resistance durability may be increased by combining different resistance genes/alleles in a single genetic background. Intra-specific lines were thus developed as suggested by Ghesquière et al. (1997) through crosses between the resistant accessions Tog5681, Tog5672 and Tog7291 in order to develop varieties with improved high yields and RYMV resistance as these varieties would combine several of these genes/alleles. Fifty-five of these derived progenies were selected based on their agro-morphological characters (Agnoun et al., 2012) and evaluated for their resistance to the virus.

2. Materials and methods

2.1. Plant materials and virus strains

The study evaluated 160 rice accessions from an *O. glaberrima* core sample of AfricaRice's GeneBank. These materials cover the wide phenotypic and eco-geographic diversity of an *O. glaberrima* collection originating from 20 African countries. Also screened were 55 intra-specific *O. glaberrima* lines (F7 generation), developed from two different crosses, 11 from the cross Tog5681/Tog5672 and 44 from Tog5681/Tog7291. All three parental lines of these crosses are resistant to the disease. Indeed, Tog5681 carries *rymv1-3,* the most widespread allele (Albar et al., 2006) while Tog7291 carries *RYMV2* gene (Thiémélé et al., 2010). Tog5672 harbors *rymv1-4* and is suspected to also carry *RYMV3* (Thiémélé et al., 2010; Pidon et al., 2017). This means that three resistance genes or alleles will potentially segregate in those derived progenies. IR64 (susceptible *O. sativa*) and Tog5681 (resistant *O. glaberrima*) served as controls. Plant materials were screened using five RYMV isolates - RBe24 and RBe25 from Malanville (N11°52.279′ E003°23.112), RBe73, RBe76, and RBe77 from Tanguieta (N10°39.315′ E001°15.033). Both localities are in the north of Benin and are very close to the border with Niger. All these isolates were diagnosed as belonging to the S1 serotype based on Triple Antibody Sandwich (TAS) ELISA with monoclonal antibodies (Oludare et al., 2016). To this end, micro-titre plates were coated with polyclonal antibody anti-RYMV. Thereafter, saps from leaves grinded in PBST x 1 buffer pH 7.2 (1/10 w:v ratio) were used as antigen. Six monoclonal antibodies (Mabs) A, B, D, E, G and M were used as secondary antibodies and bound Mabs were detected with goat anti-mouse globulin/alkaline phosphate conjugate. After incubating the samples with p-nitrophenyl phosphate for 1 and then 3 h at room temperature or after overnight incubation at 4 °C, absorbance at 405 nm was recorded using a spectrophotometer.

2.2. Establishment of the experimental trials

The experiment was established in 2012 in the experimental screenhouse of the AfricaRice research station at Abomey-Calavi, Benin. Rice plants (one plant/pot) were grown in 1 L pots filled with soil collected on the station. The pots were arranged in a randomized complete augmented block design and each block, replicated three times for each of the five RYMV isolates, comprised 20 *O. glaberrima* genotypes and the two controls (Tog5681 and IR64). Fertilizers were applied at the rate of 1 g of NPK/pot at sowing and 0.2 g of urea/pot one month later. Soil moisture was frequently checked and hand weeding was carried out throughout the experiment.

In a second experiment, only the selected resistant genotypes identified in the first experiment were again tested to confirm their resistance status. Ten pots each containing 5 plants (total of 50 plants for each resistant accession) were sown and tested as described below. For each accession, a water control set consisting of the same number of plants was also tested.

Fully developed leaves of IR64 infected with each of the five isolates and conserved at −20 °C were used to infect new sets of IR64 plants to get fresh inoculum. Plant leaves that developed visible and severe symptoms were collected and ground in phosphate buffer (0.01 M pH 7.0) at a ratio of 1:10 (w/v). The virus content of the inocula was checked with the ACP ELISA test as described by Afolabi et al. (2009). Thereafter, 0.5 g carborundum (600-mesh) was added to the solution and the resulting mixture was used to mechanically inoculate rice plants by gently rubbing it on leaves (2–3 leaves/plant) of 21-day old plants.

2.3. Data collection

The Standard Evaluation System (IRRI, 2002) was used to score disease symptoms at 21 and 42 DAI. Disease scoring was done by using a scale (Table 1) in which the rating "0″ was assigned to plants with no visible symptoms and "9″ to those that showed full infection. Ratings 1, 3, 5, and 7 correspond to the other plant infection levels. The average disease severity per plant was then calculated as follows:

Disease Severity (DS) = {((n1*1)+(n3*3)+(n5*5)+(n7*7)+(n9*9)) ×100/((n1+n2+n3+n5+n7+n9)* 9}where, n1, n3, n5, n7 and n9 represent the number of leaves/plant scored 1, 3, 5, 7 and 9 respectively. A mean disease severity for each accession was then calculated by averaging the means of all plants assessed.

2.4. Statistical analysis

Data were analyzed with Excel and JMP Pro12.01 software. The averages of the three replicated plants/isolate were subjected to ANOVA test for means comparison using Newman-Keuls test at 5% level of probability for all isolates.

Table 1
Disease rating scale used for assessing *O. glaberrima* accessions for resistance to RYMV.

Scale	Symptoms	Code	Nature of resistance
0	Leaves green with no symptom observed	HR	Immune
1	Leaves pale or green with no symptom observed	HR	Highly resistant
3	Leaves greens, with sparse dots or streaks	R	Resistant
5	Leaves pale or green with mottling	MR	Moderate resistant
7	Leaves pale yellow or yellow with mottling	S	Susceptible
9	Leaves turned yellow or orange with often plant dead	HS	Highly susceptible

2.5. Genotyping

Genotyping of highly resistant accessions for *RYMV1* and *RYMV2* resistance genes was conducted as follows: PCR amplification was performed on 1 mm-diameter discs of dried leaves (with two discs/10 µl reaction) using the Terra PCR Direct Polymerase Mix (Clontech) as described in Orjuela et al. (2013). A CAPS marker was used to detect the mutation of the *RYMV2* allele in Tog7291 as described in Orjuela et al. (2013). The central domain of *RYMV1* gene, containing the mutations known to be involved in resistance, was amplified using the primers 5′-CCTTGGTCAGCTAGAAGAGGCA-3′ and 5′-CCTCGGTACAACCAAGA GAC-3′ and the amplification product was sent to Beckman Coulter Genomics for sequencing with the primer 5′-CTCTTCACGTCGAGGCA CCCA-3’.

3. Results

3.1. Severity of RYMV disease on O. glaberrima accessions and intraspecific lines infected with RYMV

As disease severity (DS) at both 21 and 42 DAI were highly correlated ($r = 0.8561$), only data for 42 DAI are presented because symptom development was maximum at this period and differences between isolates were best expressed.

The results confirmed the susceptible and resistant status of the controls, thus indicating that rice accessions could be properly screened for resistance to RYMV. DS on the susceptible control, IR64, ranged from 41.93 (isolate RBe76) to 100% (isolate RBe24) with the latter isolate being the most aggressive (Figs. 1 and 2). Conversely, DS on the resistant Tog5681 ranged from 11.1 to 16%.

The DS value for all accessions tested varied according to both the pathogenicity of the isolates and genetic background of the accessions (Fig. 1). ANOVA results (Table 2) show a significant “isolate” effect with considerable differences, thus revealing a strong variability of the isolates’ pathogenicity. The most pathogenic isolates were RBe24 and RBe25 that attacked many *O. glaberrima* landraces which exhibited DS of 60–80 (RBe24) and 80 to 100 (RBe25). Isolate RBe77 displayed medium pathogenicity while RBe73 and RBe76 caused very weak symptoms ($0 < DS < 20$) on most of the lines tested. There was a significant genotype effect ($P < 0.0001$) and significant interactions between the fixed effects, such as isolates, genotypes and blocks, were also observed.

About 98% of the screened *O. glaberrima* accessions expressed moderate or severe susceptibility to all five RYMV isolates while only three (1.9%) (including IRGC104019 and IRGC96787 [or Tog5644]) were as resistant as the resistant control Tog5681. These two newly identified resistant accessions also displayed good vegetative growth (data not shown) and the virus was not detected in their plants. The third accession, IRGC96851, differed from the previous two by its susceptibility to the RBe24 isolate.

Among the intraspecific lines (Fig. 2), DS varied from 0 to 100%. Sixteen of the 55 intra-specific breeding lines were resistant to all five isolates and did not significantly differ from the resistant control Tog5681. Seven of them (S5-8, S7-1, S19–4, S21–6, S24-9, Pl 49–7 and S2-6) were among the11 genotypes from the cross Tog5681/Tog5672 (cross 1) while nine (PL55-7, PL82-7, PL85-1, PL85-3, PL85-4, PL85-5, PL87-1, PL87-3 and PL87-8) were among the 44 derived from the cross Tog5681/Tog7291. The rest either had weak symptoms or were as susceptible as the susceptible control IR64.

3.2. RYMV1 resistance gene sequencing in the newly documented resistance sources

The highly resistant accessions IRGC104019 and IRGC96787 (Tog5644) were checked for the presence of the *RYMV1* resistance alleles previously shown to be present in Gigante, Tog5681, Tog5672 and Tog5674 and the *RYMV2* allele identified in Tog7291 (Albar et al., 2006; Thiémélé et al., 2010). None of the accessions had *RYMV2*. The central domain of the *RYMV1* gene was sequenced in the new immune genotypes IRGC96787 and IRGC104019 and the sequences obtained were compared to the known alleles at this locus (Fig. 3). The accessions IRGC96787 and IRGC104019 showed the deletion that characterizes the *rymv1-3* resistance allele in Tog5681, suggesting that the high resistance of these two accessions is conferred by this allele.

4. Discussion

Despite the eco-geographic diversity and the presence of two serogroups (S1 and S2) of RYMV in Benin, variability of RYMV population is quite low (Oludare et al., 2016). While both serotypes were found in all rice-growing areas, S1 serotype, to which the five isolates tested in this study belong, is the most frequent in Northern Benin where these isolates originate from. Isolates RBe24 and RBe25, collected from an irrigated scheme in Malanville, were more pathogenic than the other three (RBe73, RBe76 and RBe77) that originated from lowland ecologies

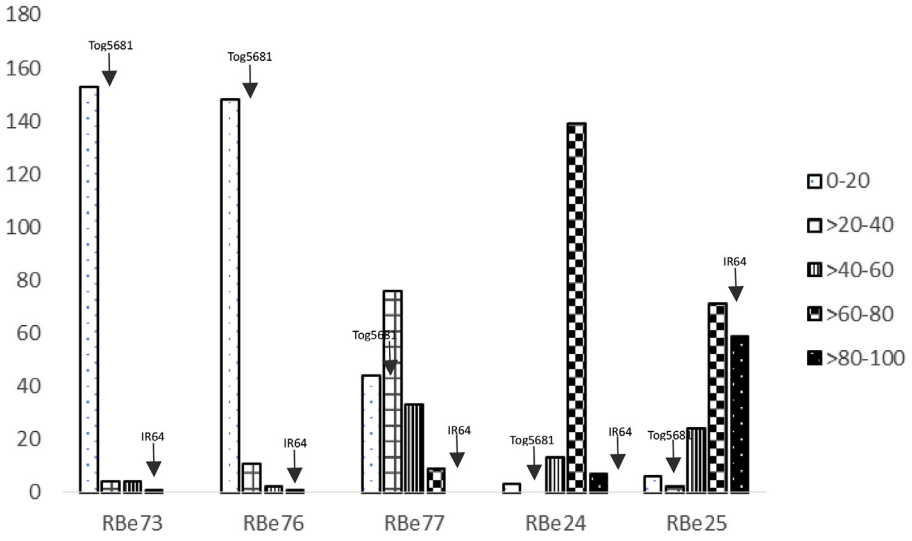

Fig. 1. Distribution of the number of *O. glaberrima* landraces arranged by disease severity (DS) values measured for all five RYMV isolates at 42 DAI. Legend: Five classes of DS were defined and range from 0 to 100. The position of the two controls (Tog5681 and IR64) were reported for each RYMV isolate (RBe73, RBe76, RBe77, RBe24 and RBe25) according to their DS values.

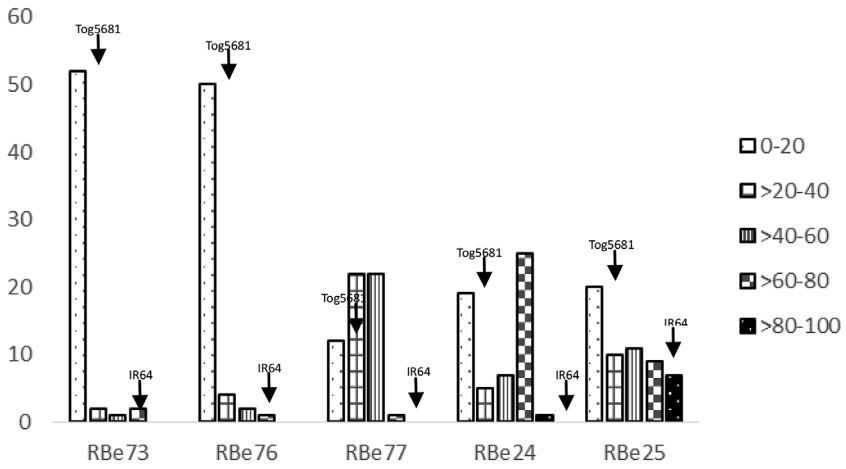

Fig. 2. Distribution of intra-specific *O. glaberrima* lines derived from crosses between resistant lines (Tog5681, Tog5672 and Tog7291) and arranged by disease severity (DS) values measured for all five RYMV isolates at 42 DAI. Legend: Five classes of DS were defined and range from 0 to 100. The position of the two controls (Tog5681 and IR64) were reported for each RYMV Isolate (RBe73, RBe76, RBe77, RBe24 and RBe25) according to their DS values.

Table 2
Analysis of variance performed on the disease severity data collected at 21 and 42 DAI.

Source	Ddl	P-value 21 DAI	P-value 42 DAI
Isolates	4	<0.001	<0.001
Genotypes	117	<0.001	<0.001
Blocks	10	<0.001	<0.001
Isolates * Genotypes	467	<0.001	<0.001
Genotypes * Block	50	<0.001	<0.001
Isolates * Block	40	<0.001	<0.001
Isolates *Gnotypes*Block	200	<0.001	<0.001

Legend: Highly significant ($P < 0.001$). ANOVA test performed on *O. glaberrima* accessions and intra-specific breeding lines.

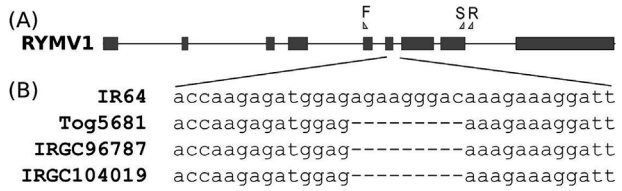

Fig. 3. (A) Structure of the RYMV1 gene with introns represented by lines and exons represented by black boxes. F and R represented the primers used for amplification of RYMV1 central domain and S the primer used for the sequencing of the amplified fragment. (B) Part of the sequences obtained on accessions IRGC96787 and IRGC104019 compared with the corresponding sequences in the susceptible accession IR64 and the resistant one Tog5681. Both accessions showed the same deletion in RYMV1 like in Tog5681.

in Tanguiéta. The higher pathogenicity of RBe24 and RBe25 (with RBe24 being more pathogenic than RBe25) might be due to intensive rice cultivation in Malanville. As this area is also very close to the Republic of Niger, which is a hotspot of the disease, migration into Benin of highly virulent isolates cannot be ruled out. The hypothesis that pathogenicity increases as one moves from Southern Benin to Niger was drawn and there is thus a need to verify this assumption by testing more isolates originating from this area. Indeed, previous studies (Reckhaus and Amadou, 1986; Séré et al., 2005) reported highly pathogenic isolates devastating rice production in Niger.

The current study tested an *O. glaberrima* collection representing the diversity of the species. The centers of origin of *O. glaberrima* are in West Africa. However, introductions and adoption of some accessions from within and outside the continent explain that some of the accessions used in this study do not originate from West Africa but, for instance, from Tanzania. The existing rice accessions in the genebank were collected at different times in several African countries. Collection was initiated in 1974 by the Office de la Recherche Scientifique et Technique Outre-Mer (ORSTOM) (now known as Institut de Recherche pour le Développement or IRD) with the aim of preserving the species' genetic diversity (Besançon and Second, 1984).

The *O. glaberrima* landraces screened in this study exhibited great variability for resistance to the disease. Artificial inoculation resulted in greater infections than what is obtained naturally in the field. Most of the 160 *O. glaberrima* landraces tested were susceptible to all the five RYMV isolates and only three of them (1.9%) were resistant. The ACP ELISA Test (data not shown) revealed differences in the virus content of each isolate and zero or low virus content was detected beyond 42 DAI in the newly identified resistant accessions. This strengthens the hypothesis that *O. glaberrima* is a potential source for high resistance to the disease (Futakuchi and Sie, 2009; Thiémélé et al., 2010). Moreover, two levels of RYMV resistance were reported by Ndjondjop et al. (2001) - high resistance which results in an absence of symptoms, and partial resistance which delays their onset. The variability of the response observed among the moderately resistant accessions confirms that *O. glaberrima* may also be an interesting source of partial resistance as previously suggested by Thiemele et al. (2010).

Specifically, this study identified two novel high disease resistance sources, namely IRGC104019 from Tanzania and IRGC96787 (Tog5644) from Nigeria that resisted all five isolates. They did not exhibit any detectable symptoms and had features comparable to those of the resistant control Tog5681. The partial sequencing of the *RYMV1* gene in the two novel resistance sources showed that they harbor the *rymv1-3* allele (Fig. 3), the most widespread *O. glaberrima* resistance allele of this gene (Albar et al., 2006; Thiemele et al., 2010). *RYMV1* is a recessive gene located on chromosome 4 and codes protein eIF(iso)4G, a factor of the host interacting with the virus (Hébrard et al., 2010).

IRGC96851, another genotype from Nigeria, was resistant to all isolates except RBe24 and did not express any visible symptom. Further investigations are needed to identify the genes/alleles involved in its resistance.

A second group of *O. glaberrima* material was developed with the objective of pyramiding known resistance genes/alleles in progenies - *RYMV1* (alleles *rymv1-3* and *rymv1-4* carried, respectively, by Tog5681 and Tog5672); *RYMV2* carried by Tog7291; and *RYMV3* carried by Tog5672 (Albar et al., 2006; Thiémélé et al., 2010; Pidon et al., 2017). This material consisted of 55 lines that had already been selected by breeders for interesting agronomic characteristics. Among this material,

16 genotypes (29.1%) exhibited high resistance to all five isolates tested with no visible symptoms developed. Seven of them were derived from the cross Tog5681/Tog5672 while nine came from Tog5681/Tog7291.

The presence of two resistance *RYMV1* alleles (*rymv1-3* and *rymv1-4*) in the Tog5681/Tog5672 cross should confer resistance to all the derived lines but some infected lines were observed in the progenies. Moreover, an unbiased population derived from the Tog5681/Tog7291 cross involving *rymv1-3* and *RYMV2* should result in more than nine resistant lines. Selection for agronomic traits might have modified the segregation ratio or resistance-breaking may have occurred in some resistant lines. Resistance-breaking might specially concern lines with the *rymv1-4* allele or lines with *RYMV2* as these alleles and genes are known to be more frequently overcome than *rymv1-3* or *RYMV3* (Pinel-Galzi et al., 2016: Hébrard et al., 2018). Regarding the plant's response to all virus attacks and the serological results obtained, the significant interaction ($P \leq 0.001$) between the main factors - isolates and genotypes - (Table 2) suggests that the effects of isolates (expressed by disease severity) depended on the resistance/susceptibility status of the genotypes and showed that some accessions were more resistant or susceptible than others.

Further molecular analysis is, however, needed to identify the number and nature of the resistance alleles in the 16 resistant lines identified. Lines combining the *rymv1-3* allele, *RYMV2* and *RYMV3* would constitute an interesting material for evaluating the durability of resistance as this combination has so far not been identified in wild genotypes. This perspective supports the initiation of an intra-specific plant breeding approach using these genetic crosses for developing lines with added values. In addition, the development of interspecific *O. sativa/O. glaberrima* lines with RYMV resistance inherited from *O. glaberrima* is a good perspective for valorizing the African rice species (Ghesquière et al., 1997). The resulting progenies will also combine *O. glaberrima's* adaptability to and tolerance to many local stresses with the high yielding potential of the Asian species *O. sativa* - this was the key to the success of NERICA varieties. Therefore, the use of phenotypic characteristics and molecular tools, such as MAS, could be one option for unravelling the secrets of the offspring derived from such crosses.

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