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Complexity and Pathogen Variability of Rice Sheath Rot Disease Causal Organisms and Their Virulence Spectrum: Review

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Abstract

Knowledge about the causal agents and their genetic variability as well as pathogenicity mechanisms is essential to develop strategies and practices for control and prevention of rice sheath rot disease. Successful management of plant diseases is mainly dependent on the accurate and efficient detection of plant pathogens, amount of genetic and pathogenic variability present in pathogen population. Cognizant of this, the current paper was prepared with the aim of reviewing of genetic variability within and among causal pathogens of rice sheath rot disease. Number of researchers reported and agreed that rice sheath rot is a devastating disease associated a complex of bacterial pathogen *P. fuscovaginae*, the fungal pathogen *S. oryzae* and the fungal complex pathogen of *Fusarium* spp. Moreover, each of these pathogens have also their close related strains. Therefore, further study is needed to describe the detail of the all the responsible pathogens associated with rice sheath rot disease.

Keywords: rice, sheath rot, complex disease, *Pseudomonas fuscovaginae*, *Sarocladium oryzae*, *Fusarium fujikuroi*

Introduction

Sheath rot is a widespread rice disease reported in several rice growing parts of the world. It is one of the major diseases of lowland rice growing countries like Ethiopia (Desalegn2022). The pathogen mainly infects the upper most flag leaf sheaths that enclose the emerging young panicle

during the boot stage. It is one of the most serious and devastating rice diseases in wetland rice growing regions (Lanoiselet *et al.*, 2012). It causes yield losses resulted mainly from poor panicle formation and exertion, spikelet sterility (80-100%), reduced grain filling, and losses in milling (Simon, 2016).

Successful management of plant diseases is mainly dependent on the accurate and efficient detection of plant pathogens, amount of genetic and pathogenic variability present in pathogen population, development of disease resistant cultivars and development of effective resistant gene in different epidemiological regions (Sunil and Shalini, 2019). Assessment of variability provides a basis of breeding cultivar with durable resistance and designing strategies for long term management of major diseases. Moreover, Sharma (2003) also stated that, all the disease management strategies based on host resistant require the knowledge of variability in pathogens.

Knowledge about the causal agents and their genetic variability as well as pathogenicity mechanisms is essential to develop strategies and practices for control and prevention, and also paves the way for breeding for resistance against sheath rot-causal pathogens (Bigirimana, 2016). Therefore, the objective of this paper was to review different literatures about the genetic variability within and among disease causal pathogens of rice sheath rot and draw a conclusion.

Rice Sheath Rot Causal Pathogens

Rice sheath rot is a disease complex that can be caused by various fungal and bacterial pathogens. Major pathogens associated with rice sheath rot are fungi such as *Sarocladium oryzae* and *Fusarium* sp. belonging to the *Fusarium fujikuroi* complex and the bacterial pathogen *Pseudomonas fuscovaginae* (Bigirimana *et al.*, 2015).

The studies conducted by Samson (2020) demonstrated that the *P. fuscovaginae* pathogen is abundantly present in symptomatic samples in the highland in both dry and wet seasons, whereas the fungal rice pathogen *S. oryzae* is significantly present only in diseased samples from the lowland especially during the wet season.

Each of the abovementioned pathogens have different races with in a particular species. The pathogenicity/degree of virulence each race also

differs one from others depending the molecular and morphological characteristics the race possessed. Consequently, the diseases caused by different races are also different, in which the management method also would accordingly the nature of the race. Therefore, it is important to know detail characteristic of each causal pathogen as well as it associated races.

I. *Sarocladium oryzae*

Sarocladium oryzae was established in 1975 which was earlier described as *Acrocyndrium oryzae*, the first organism to be associated with rice sheath rot symptoms isolated in Taiwan in 1922 (Mew and Gonzales, 2002). The genus *Sarocladium* currently encompasses 16 species including plant pathogens, saprobes, mycoparasites, endophytes, and potential human pathogens (Giraldo *et al.*, 2015). According to Giraldo and his coworkers' study, the genus belongs to the order of the Hypocreales in the Phylum Ascomycota. Furthermore, Bigirimana *et al.* (2015) reviewed that *Sarocladium attenuatum* was originally described as a distinct species causing rice sheath rot, and nowadays it is considered as a synonym of *Sarocladium oryzae*. Similarly, Bills *et al.* (2004) also reported that the cerulenin producing fungus *Cephalosporium caerulans* conspecific with *Sarocladium oryzae*. Therefore, despite the earlier reports explained the four species viz., *Acrocyndrium oryzae*, *Sarocladium attenuatum*, *Cephalosporium caerulans* and *Sarocladium oryzae* as distinct species each cause rice sheath rot disease, nowadays researchers agreed that all the four species are similar and referred as *Sarocladium oryzae*.

As shown in the figure 1 below, *Sarocladium oryzae* grows slowly (about 2.5 mm/day on potato dextrose agar at 28 C) and produces a sparsely branched white mycelium. The colony reverse of isolates obtained from rice is generally orange. Moreover, conidiophores can be simple or branched. Conidia are cylindrical, aseptate, and hyaline, 4–7×1–2µm in size, and arranged in slimy heads (fig. 2) (Bigirimana *et al.*, 2015).

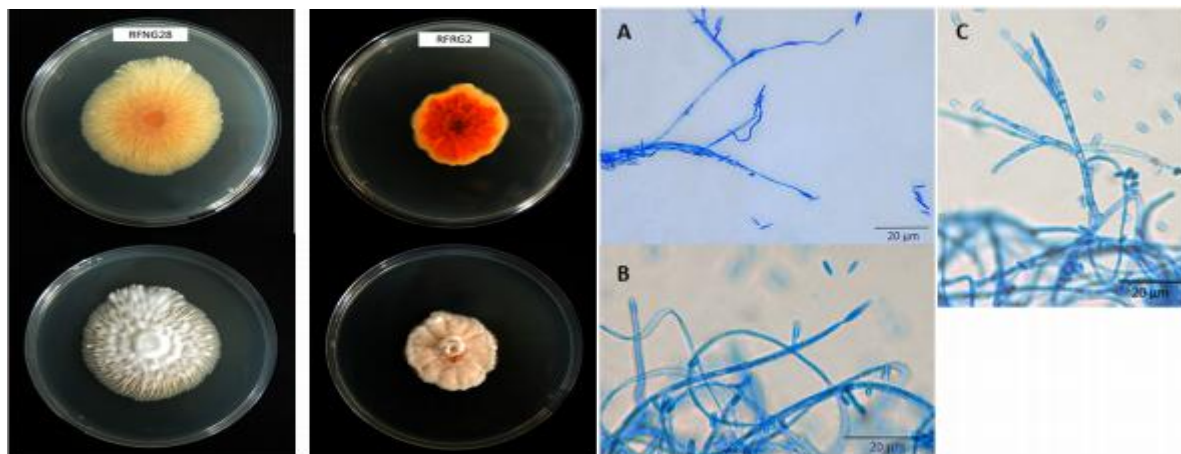


Figure1. Morphology of two different *Sarocladium oryzae* isolates from Rwanda on PDA medium after 14 days of growth at 28 C. Top is reverse view, and bottom is front view.

Figure 2. Microscopy of *S. Oryzae* grown on PDA medium. All structures were stained with lactophenol blue. (A) Conidia; (B) Conidiogenous cell; (C) Aerial conidiophores.

Source: Bigirimana *et al.* (2015)

According to Samson (2020), the pathogenicity determinants of this pathogen are the secondary metabolites helvolic acid and cerulenin. In addition, *S. oryzae* also produces a cellulolase, a protease, a pectinase, and oxidative enzymes that are thought to play a role in pathogenicity. Regarding variability within *S.oryzae* isolates, Bigirimana, (2016) evaluated and characterized 16 *S. oryzae* isolates and obtained different results, indicating that there was variability within *S. oryzae* isolates. Similar Giraldo *et al.*, (2015) also reported about the presence of variability with in *S.oryzae* isolates. Therefore, there is variability not only among causal organisms of shea rot but also within isolates of a particular causal pathogen.

II. *Fusarium fujikuroi*

Sheath rot in rice has also been associated with *Fusarium* sp. belonging to the *F. fujikuroi* complex. The *F. fujikuroi* complex largely corresponds to the Section Liseola, established by Wollenweber and Reinking (1935), in which Nelson *et al.*(1983) recognized four species (including *F.moniliforme* and *F. proliferatum*), but also accommodates certain species

originally classified in other *Fusarium* sections. Furthermore, Kvas *et al.* (2009) reviewed that there are around 50 species in the *F. Fujikuroi* complex and the number keeps increasing as far as progress in molecular taxonomy increases. However, Bigirimana *et al.*(2015) reviewed and summarized as the complex is currently grouped in three large clades, the African clade, the Asian clade and the American clade. Moreover, within these clades, the main organisms associated with rice are *F. Verticillioides* from the African clade and the closely related species *F. proliferatum* and *F. fujikuroi* from the Asian clade.

Samson (2020) reported that the two metabolites involved in plant pathogenicity of *Fusarium* sp. were gibberellins and mycotoxins. On the other hand, only strains of *Fusarium fujikuroi* were able to produce gibberellin A causing abnormal elongation of rice plants, the so-called bakanae disease. The *Fusarium proliferatum* species is known as specie producing mycotoxins, like fumonisin B and has been associated to rice sheath rot (Wulff *et al.*, 2010). Generally, there are a lot of species/strains under this complex which require further detail study.

III. *Pseudomonas fuscovaginae*

Since its isolation in association with rice sheath rot in Japan by Tani *et al.* (1976), *Pseudomonas fuscovaginae* is considered as the main bacterium causing rice sheath brown rot. Zeigler and Alvarez (1987) stated that rice sheath brown rot, caused by *P. fuscovaginae* in Latin America, is characterized by the following features: longitudinal brown to reddish brown necrosis 2-5

mm wide extending the entire length of the leaf sheath and blade; affected sheaths enclosing the panicle may show extensive water soaking and necrosis with poorly defined margins; glumes discolor before emerging from such panicles; grains on affected tillers may be completely discolored and sterile to nearly symptomless with only small brown spots as shown in the figure below.



Figure 3. Symptoms of rice sheath rot caused by *P. fuscovaginae* (Source: Samson, 2020).

The generation of sheath rot symptoms is caused by three different types of phytotoxic metabolites produced by *P. fuscovaginae*, syringotoxin, fuscopeptin A (FP-A) and fuscopeptin B (FP-B). Similarly, several genetic loci have been implicated in the pathogenicity of this bacterium even though very few molecular and genetic studies related to the virulence of *P. fuscovaginae* have been performed (Samson, 2020).

Since its first identification in Japan, sheath rot caused by *P. fuscovaginae* is reported in many countries including: Mexico, Guatemala, Panama, Suriname, Colombia, Peru and Brazil, South

America, Burundi, Madagascar, South Korea. Furthermore, Duveiller *et al.* (1990) explained that based on biochemical and serological tests, *P. fuscovaginae* strains isolated from Madagascar, Burundi and Japan displayed a higher similarity and aggressiveness in pathogenicity tests. Moreover, Quibod *et al.*, (2015) reported that from few *P. fuscovaginae* strains genomes that have been sequenced, at least two sub groups have been identified and strains from Madagascar, Japan, China, and Australia clustered separately from *P. fuscovaginae*- like strains from the Philippines.

The genus *Pseudomonas* belongs to the subclass Gamma-proteobacteria of the Gram-negative bacteria and currently comprises 144 species. Furthermore, Samson (2020) reviewed that Based on multi locus sequence analysis, *P. fuscovaginae* belongs together with *Pseudomonas asplenii* to the *Pseudomonas asplenii* subgroup in which these two species are closely related and some authors consider them as synonymous.

Conclusion

Rice sheath rot is a devastating disease associated a complex of bacterial pathogen *P. fuscovaginae*, the fungal pathogen *S. oryzae* and the fungal complex pathogen of *Fusarium* spp.

Recommendation

Further investigations are necessary for deciphering their possible interkingdom interactions, potential effect on the microbiome and whether sheath rot is a complex disease involving the interaction/cooperation of different pathogens.

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