Plant Pathology Journal 7 (1): 109-113, 2008
ISSN 1812-5387

Diversity of the Rice Blast Pathogen Populations in Ghana and Strategies for Resistance Management

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Abstract: The present study describes the outputs of a collaborative research programme funded by the UK's Department for International Development-Crop Protection Program to investigate the genetic (lineages) and pathogenic (pathotypes) diversity of the blast fungus populations and characterize the key sites suitable for resistance screening. Seventy-one *Magnaporthe grisae* isolates were collected from seven regions where rice is grown, representing blast populations in Ghana. Following molecular characterization, these isolates were grouped into four distinct lineages designated as GH-1, GH-2, GH-3 and GH-4 and 25 pathotypes. GH-1 was the major lineage comprising 52% of all the isolates and was present across the country on up to 24 rice cultivars. GH-2 comprising of 30% of the isolates sampled was restricted in distribution mainly from Hohoe area on up to seven cultivars. GH-3 consisted of six isolates from Western, Eastern and Central Regions while GH-4 consisted of two isolates from Nyankpala in Northern Region. Occurrence of blast pathogen on wild rice and weed hosts has been observed and their potential impact needs to be considered in blast/weed management. Baseline data new to Ghana on the diversity and distribution pattern of the blast pathogen populations have been established and key sites identified. Adaptive research is continuing to develop technologies suitable for long-term pathogen monitoring, identify sources of resistance and develop appropriate blast management strategies.

Key words: Blast, lineages, *Magnaporthe grisea*, *Oryza sativa*, pathotypes, Ghana

INTRODUCTION

The demand for rice in Ghana is growing faster than any other staple food. Rice constitutes a major source of calories for the rural and urban people and is cultivated in all the ten regions. During 2003 cropping season, 238,810 metric tons (m t) of paddy rice was produced in Ghana from a land area of 117,720 ha (Anonymous, 2004). The current annual rice import into Ghana is 241,610 m t, which is equivalent to US $95.0 million. The average yield of 2.0 m t/ha (Anonymous, 2001) is among the lowest as compared to the rest of the world. A wide range of biophysical constraints reduces the yield potential of the cultivars in all the rice production systems.

Blast disease caused by *Pyricularia grisea* (syn. *P. oryzae*) (Rossman *et al*., 1990) (teleomorph = *Magnaporthe grisea* (Webster, 1980) remains a threat to rice production worldwide despite extensive research efforts at its control (Teng, 1994). *Magnaporthe grisea* is able to infect rice at different stages of growth and adapt to both upland and lowland rice ecosystems (Bonman *et al*., 1992; Teng, 1994). In the West African sub-region, blast is recognised as a primary constraint to rice production causing 3.2-77% yield losses (Notteghem and Baudin, 1981; Fomba and Taylor, 1994; Singh *et al*., 2000; Chipili *et al*., 2003). Deployment of resistant cultivars integrating good cultural practices is the most effective and economical way to combat the blast disease. However, breakdown of resistance is common due to the dynamic nature of the pathogen in responding to the host genotype and environment. Understanding the diversity and dynamics of the pathogen populations and identification of resistance sources based on this knowledge is critical to the development of blast resistance that is stable over space and durable over time.

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In this context, the West Africa Rice Development Association (WARDA), Benin, Savanna Agricultural Research Institute (SARI) and Crops Research Institute (CRI), Ghana and Warwick HRI (previously Horticulture Research International), UK have been involved in a collaborative strategic research program funded by the UK Department for International Development (DFID)-Crop Protection Programme (CPP). The objectives were to characterize the resistance screening sites, assess the genetic and pathogenic diversity of pathogen populations and identify potential resistance sources. This study describes the blast population and screening site characterization aspects based on the work done at Warwick HRI in co-ordination with WARDA, SARI and CRI.

MATERIALS AND METHODS

Blast samples were collected from rice screening sites and surrounding locations in Ghana from 2000-2002 and sent to Warwick HRI, UK for MGR586 fingerprint pattern or lineage determination and pathotype analysis. In all, seventy-one *M. grisea* isolates were obtained from the blast samples collected and characterized (Chipili, 2000; Chipili *et al*., 2002). DNA was extracted from mycelial powder by the CTAB method (Valent *et al*., 1991; Hamer and Givan, 1990; Sreenivasaprasad, 2000). DNA digestion and Southern hybridisation with the MGR586 probe were carried out following standard protocols (Levy *et al*., 1991). Virulence spectrum of the *M. grisea* isolates was determined on the international differential set of rice cultivars following the scale of Valent *et al*. (1991) and pathotype designations were assigned based on Ling and Ou (1969).

RESULTS AND DISCUSSION

Seventy-one *M. grisea* isolates collected from seven rice producing regions, Ashanti, Central, Eastern, Northern, Upper East, Volta and Western, were grouped into four distinct lineages (genetic groups) designated as GH-1, GH-2, GH-3 and GH-4 (Table 1). GH-1 was the major lineage comprising 52% of all the isolates and was present in all but one of the region (Eastern) where isolates were collected. Lineage GH-1 occurred on at least 24 rice cultivars some of which could have related genetic background, for example Tox-related cultivars. Lineage GH-2 comprised 30% of the isolates sampled and except for three isolates from Asikam (Eastern), Kpachie and Galenkpegu (both from Northern) all were from the Hohoe area in the Volta Region recovered from seven different rice cultivars (two of which were Tox-related) and one weed host at Santrokofi # 7. Lineage GH-3 consisted of six isolates (8%) from Agya-Amoa (Sayerano, Nsuansua and Sefwi-Wiawso in Western), red rice in Otumi (Eastern) and Diaso (Central). Isolates B18 and B137 from unknown rice cultivars in Tono # 1 (Upper East) and Nyankpala # 1 (Northern), respectively formed lineage GH-4 (3%). Further, five *M. grisea* isolates from Tanoso (Western), Otumi # 2 (Eastern), Kwadaso # 4 (Ashanti) and Tono # 3 (Upper East) from elephant grass, wild rice and known/unknown rice cultivars produced 'atypical' fingerprints (non-rice pathogen-like MGR586 fingerprints) (Borromeo *et al*., 1993).

The virulence characteristics of the representative isolates were determined on the international rice differentials. Twenty-five pathotypes were recorded from more than 20 rice cultivars and also from a weed and wild rice across the seven rice producing regions (Table 1). Volta with 12 pathotypes and Upper East with eight were most diverse. A number of isolates showed distinct virulence spectrum defined by a particular pathotype, but there were also examples where different isolates belonged to the same pathotype. For example, IB-1 was recorded in all the regions except Eastern. Isolates 5038 and 60040 from weed hosts were pathogenic on the international rice differentials (Chipili *et al*., 2003). The most frequently observed pathotype groups were IB and IC (Table 1 and 2).

Analysis of the lineage-pathoytype data has provided some understanding of the lineage-pathotype relationships. Pathotypes represented in lineage GH-1 were mostly IB group. Some of the other isolates in this lineage originating from Tox-related cultivars at Hohoe also expressed related pathotypes. Similarly, pathotypes represented in lineage GH-2 were mostly IB group. Lineage GH-3 represented diverse pathotypes from groups IA, IB, IC, ID, IF and IH (Table 2).

Based on the diversity and distribution of the blast genetic groups (lineages) and pathotypes (Table 1 and 2), various key sites have been identified to be suitable for blast resistance screening. Hohoe in Volta Region with major lineages GH-1 and GH-2 and 12 pathotypes belonging to five pathotype groups (IA, IB, IC, ID and IG) is a high diversity site. In the North, Nyankpala and Bolgatanga with lineages GH-1, GH-2 and GH-4 and 12 pathotypes (IA, IB and IC groups) were characterized. Although six pathotypes belonging to groups IA, IB, IC and ID were recorded in Western Region (Sayerano and Sefwi-Wiawso) one of the major lineages GH-2 was not observed, which needs to be further monitored. At

Table 1: Details of site, host cultivar, lineage grouping and pathotype designation of *Magnaporthe grisea* isolates from Ghana

Code	Location[1]	Host cultivar[2]	Lineage[3]	Pathotype[4]
Ashanti region				
B115	Kwadaso # 1	WAB 638-9-A36	GH-1	IB-1
B119	Kwadaso # 2	WAB 651-B-A-158	GH-1	ID-13
B124	Kwadaso # 3	WAB 651-B-9-B36	GH-1	IB-45
B336	Kwadaso # 4	WAB 638-9-H36	Atypical[5]	-[6]
60059	Aframso	More	GH-1	IB-1
60060	Dromankoma	More	GH-1	ID-1
60061	Offinso-Kayera	Asante-mo	GH-1	IB-13
60062	Anyinasuso	Asante-mo	GH-1	IB-1
Central region				
6007a	Diaso # 1	Local	GH-1	IC-1
6007b	Diaso # 2	Local	GH-3	IH-1
6007c	Diaso # 3	Local	GH-3	IB-9
60012a	Abora # 1	Red rice	GH-1	IB-1
60012b	Abora # 2	Red rice	GH-1	IB-1
60012c	Abora # 3	Red rice	GH-1	IC-9
Eastern region				
60021b	Otumi # 1	Red rice	GH-3	ID-9
60021c	Otumi # 2	Red rice	Atypical	IC-13
60035	Asikam	Red rice	GH-2	IC-25
Western region				
5010	Sayerano # 1	Agya-Amoa	GH-3	IC-9
5082	Sefwi-Wiawso	Agya-Amoa	GH-3	IA-9
5083	Sayerano # 2	Agya-Amoa	GH-1	IB-45
60013a	Nsuansua	Agya-Amoa	GH-3	IF-1
60025	Tanoso	Elephant grass	Atypical	II-1
60063	Adjakaa-Manso	Wassa-mo	GH-1	ID-13
Volta region				
B147	Hohoe # 1	Tox 3100-37-3-3-2-9	GH-2	IB-61
B149	Hohoe # 2	TGR 75	GH-2	IB-21
B150	Hohoe # 3	ITA 321	GH-2	IB-61
B151	Hohoe # 4	Tox 3416-170-2-1-1	GH-1	-
B152	Hohoe # 5	TCA 80-4	GH-2	IB-13
B153	Hohoe # 6	Tox 3880-38-1-1-2	GH-1	IA-2
B154	Hohoe # 7	WAB 450-24-3-2-P18-HB	GH-1	IB-1
B157	Hohoe # 8	WAB-IR-12979	GH-1	IB-1
B158	Hohoe # 9	CK 73	GH-2	IB-9
B159	Hohoe # 10	Tox 3792-10-1-2-1-1-3-2	GH-1	IB-1
B161	Hohoe # 11	Tox 3100-37-3-3-2-4	GH-2	IB-13
B163	Hohoe # 12	WAB 340-B-B-9-L3-L1-LB	GH-1	IB-5
B164	Hohoe # 13	Tox 728-1	GH-1	IB-1
B165	Hohoe # 14	Tox 3440-171-1-1-1	GH-1	IB-7
B167	Hohoe # 15	Tox 4004-43-1-2-1	GH-1	IA-1
5008	Gbi-Godenu # 1	Viwono	GH-2	IB-61
5009	Gbi-Godenu # 2	Viwono	GH-2	IB-61
5079	Santrokofi # 1	Viwono	GH-1	IB-1
5081	Gbi-Godenu # 3	Viwono	GH-1	IB-1
6005a	Fodome # 1	Viwono	GH-2	ID-13
6005b	Fodome # 2	Viwono	GH-2	IB-61
6005c	Fodome # 3	Viwono	GH-2	-
6005d	Fodome # 4	Viwono	GH-2	IC-1
6009a	Santrokofi # 2	Viwono	GH-2	IB-1
6009b	Santrokofi # 3	Viwono	GH-2	-
6009c	Santrokofi # 4	Viwono	GH-2	IB-1
60011a	Santrokofi # 5	Viwono	GH-2	IB-61
60011b	Santrokofi # 6	Viwono	GH-2	IG-1
60019b	Kpoeta # 1	Perfume rice	GH-1	IB-5
60019c	Kpoeta # 2	Perfume rice	GH-1	IB-1
60040	Santrokofi # 7	Weed	GH-2	IG-1
Northern region				
B137	Nyankpala # 1	Unknown	GH-4	-
60046	Nyankpala # 2	Mendi	GH-1	IB-1
60051	Golinga	Agongima	GH-1	IB-9
60053	Galenkpegu	More	GH-2	IB-13
60054	Kpachie	Local rice	GH-2	IC-29
60055	Salaga	Tox 3050	GH-1	IB-9

Table 1: Continued

Code	Location[1]	Host cultivar[2]	Lineage[3]	Pathotype[4]
Upper east region				
B18	Tono # 1	Unknown	GH-4	IC-17
B175	Bolgatanga # 1	Red rice	GH-1	-
B179	Bolgatanga # 2	Red rice	GH-1	IC-13
B200	Bolgatanga # 3	Red rice	GH-1	IA-88
B201	Bolgatanga # 4	Red rice	GH-1	IC-25
B202	Bolgatanga # 5	Red rice	GH-1	IB-1
B236	Bolgatanga # 6	Red rice	GH-1	-
5033	Tono # 2	Unknown	Atypical	IC-29
5038	Tono # 3	Wild rice	Atypical	IB-29
60056	Nyorigu # 1	Local rice	GH-1	IC-9
60057	Nyorigu # 2	More	GH-1	IB-1

[1]: Location where the cultivar was collected, [2]: Rice cultivar or wild rice or weed host at the survey site from which the isolate was collected, [3]: Ghanaian *M grisea* isolates belonging to different lineages (genetic groups and diversity) based on the similarity of the fingerprint patterns, [4]: Pathotyping of *M grisea* based on virulence spectrum on eight international rice differentials, [5]: Atypical fingerprint patterns have few (up to 9) MGR586 hybridising bands which is different from typical rice-pathogen-like fingerprints (with 30-50 MGR586 hybridising bands) (Borromeo *et al*., 1993) and [6]: Not tested

Table 2: Pathotype designation and lineage grouping of *Magnaporthe grisea* isolates from Ghana

	Lineage				
Pathotype	GH-1	GH-2	GH-3	GH-4	Atypical[1]
IA-1	+				
IA-2	+				
IA-9			+		
IA-88	+				
IB-1	+	+			
IB-5	+				
IB-7	+				
IB-9	+	+	+		
IB-13	+	+			
IB-21		+			
IB-25					+
IB-45	+				
IB-61		+			
IC-1	+	+			
IC-9	+		+		
IC-13	+				
IC-17				+	
IC-25	+	+			
IC-29		+			
ID-1	+				
ID-9			+		
ID-13	+	+			
IF-1			+		
IG-1		+			
IH-1			+		
TOTAL	15	10	6	1	1

[1]: *Magnaporthe grisea* isolates from wild rice produced atypical fingerprint patterns with few (up to 9) MGR586 hybridising bands (Borromeo *et al*., 1993)

Bolgatanga, pathotypes IA-88, IC-13, IC-25 and IB-1 were recorded from red rice, indicating the susceptibility of this type of rice to a wider range of pathotypes. On the other hand, there were examples where the same pathotype occurred on different cultivars; IB-1 from two Tox-related varieties from Hohoe and a third red rice variety from Bolgatanga. This suggests that the host genetic background could be related and/or that common genetic factors could be governing these interactions. Screening of a range of rice cultivars under controlled conditions against 15 Ghanaian blast lineage representatives and at some of the characterized sites has led to the identification of potential blast resistances (Nutsugah *et al*., 2005) that need to be further tested and/or developed.

The distribution pattern of the *M. grisea* lineages varied (Table 1) across the rice producing regions in Ghana. For instance lineage GH-1 was found in all regions except Eastern, while GH-2 and GH-3 tended to be more site specific. This suggests that the agro-environmental conditions, particularly the host genotypes present influence the shape of the pathogen population.

The blast characterization work has identified the occurrence of blast pathogen on wild rice and weed hosts common in the rice farming systems. Several of these isolates are closely related to rice pathogenic isolates in their genetic profile and are pathogenic on rice under controlled conditions (Chipili *et al*., 2003). The epidemiological significance of these isolates and their impact on blast management merit further investigation.

Baseline data on the diversity and distribution pattern of the pathogen populations in Ghana has been established and key screening sites identified. SARI and CRI are continuing with adaptive research to understand the dynamics of the blast pathogen populations, develop technologies suitable for long-term local monitoring of blast, identify sources of resistance to characterised pathogen groups and develop appropriate blast management strategies.

ACKNOWLEDGMENTS

The research was supported by DFID-CPP managed by the Natural Resources International, UK through Project R7552 coordinated by Dr. S. Sreenivasaprasad. The MGR586 probe was kindly provided by Dr. J.E. Hamer, Purdue University/Paradigm Genetics, USA. The authors wish to express their gratitude to the field technical staff for their assistance.

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