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Disease Notes

First Report of *Xanthomonas oryzae* pv. *oryzicola* Causing Bacterial Leaf Streak of Rice in Uganda

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Published Online: 14 Oct 2014 | https://doi.org/10.1094/PDIS-07-14-0745-PDN

Abstract

In June 2013, symptoms reminiscent of bacterial leaf streak (BLS) caused by *Xanthomonas oryzae* pv. *oryzicola* were observed on rice plants at the booting stage in the Doho rice irrigation scheme, Butaleja district, and at the tillering stage in Nambale, Iganga district and Magada, Namutumba district of Uganda. In areas surveyed, disease incidence was about 80, 40, and 30% in Doho, Nambale, and Magada, respectively. Outside the irrigation schemes, it was lower but widespread. Affected leaves showed typical BLS symptoms, such as water-soaked lesions, translucent stripes, and yellow-brown to black streaks, sometimes with visible exudates at the leaf surfaces. To check for the presence of the bacteria, symptomatic leaves were ground in sterile water and the suspension obtained was subjected to a multiplex PCR assay for *X. oryzae* pathovars, leading to the three diagnostic DNA

fragments for *X. oryzae* pv. *oryzicola* (3). In parallel, bacterial strains were isolated from surface-sterilized symptomatic leaves. To this end, rice leaves were ground in sterile distilled water and serial dilutions of the cell suspensions were plated on semi-selective PSA medium (4). Each of the three samples yielded yellow, mucoid *Xanthomonas*-like colonies that resembled the positive control strain MAI10 (1). These isolates were named Ug_1, Ug_10, and Ug_14, which originated from Doho, Magada, and Nambale, respectively. Multiplex PCR on the pure cultures strongly supported that these isolates corresponded to *X. oryzae* pv. *oryzicola*. Two isolates, Ug_1 and Ug_14, were further subjected to partial DNA sequence analysis of the *gyrB* gene upon PCR amplification using the primers XgyrB1F and XgyrB1R (5). The 467-bp DNA sequence was identical to the *gyrB* sequences from the *X. oryzae* pv. *oryzicola* strains BLS256 (Philippines), ICMP 12013 (China), and MAI3 (Mali) (2). The partial nucleotide sequence of the *gyrB* gene of strain Ug_1 was submitted to GenBank (KJ921786). Pathogenicity tests were performed on greenhouse-grown 4-week-old rice plants of the cultivars Nipponbare, Azucena, IRBB 1, IRBB 2, IRBB 3, FKR 14, PNA64F4-56, TCS 10, Gigante, and Adny 11. For this purpose, bacterial cultures were grown overnight in PSA medium and re-suspended in sterile water at a concentration of 1×10^8 CFU/ml. Bacterial suspensions were sprayed on leaves of rice seedlings. Four seedlings per accession and isolate were inoculated. Fifteen days after incubation in a BSL-3 containment facility (27 ± 1°C with a 12-h photoperiod), inoculated leaves exhibited typical water-soaked lesions with yellow exudates that were similar to the symptoms seen in the fields. Re-isolation of the bacteria from the diseased leaves yielded colonies with the typical morphology of *Xanthomonas*. Multiplex PCR and sequence analysis of portions of the *gyrB* gene confirmed that these isolates are *X. oryzae* pv. *oryzicola*, thus fulfilling Koch's postulates. One of the three isolates, Ug_1, has been deposited in the Collection Française de Bactéries Phytopathogènes (CFBP) as strain CFBP 8171 (http://www.angers-nantes.inra.fr/cfbp/). Further surveys and strain collections in East and Central Africa will help assess the geographic distribution and importance of BLS.

References: (1) C. Gonzalez et al. Mol. Plant Microbe Interact. 20:534, 2007. (2) A. Hajri et al. Mol. Plant Pathol. 13:288, 2012. (3) J. M. Lang et al. Plant Dis. 94:311, 2010. (4) L. Poulin et al. Plant Dis. 98:1423, 2014. (5) J. M. Young et al. Syst. Appl. Microbiol. 31:366, 2008.