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“Development on the margin”

## Fatty Acid and Multilocus Sequence Analyses Based Genotypic Characterisation of the Rice Pathogen *Xanthomonas Oryzae* Pv. *Oryzae* from West Africa

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### Abstract

Bacterial leaf blight (BLB) of rice caused by *Xanthomonas oryzae* pv. *oryzae* is one of the most important diseases of rice limiting rice production and productivity. The pathogen causes a substantial yield loss of up to 50 % in severe epidemics. Host plant resistance is the most effective and environmentally friendly approach to control the pathogen, and to date more than 30 genes exhibiting resistance towards various strains of *X. oryzae* pv. *oryzae* have been identified and incorporated into high yielding rice cultivars. The high degree of pathogenic variability in the population structure of *X. oryzae* pv. *oryzae* demands genetic strategies to improve host plant resistance towards BLB. Prerequisite for improving host plant resistance is an understanding of the genetic diversity of the pathogen. In light of this, fatty acid and multilocus sequence analyses of the housekeeping genes *atpD*, *dnaK*, *efp* and *gyrB* was carried out to characterise *X. oryzae* pv. *oryzae* strains from West Africa. The fatty acid analysis for 23 strains of the pathogen identified them as *X. oryzae* pv. *oryzae*. However, African strains demonstrated a lower index of similarity ranging from 0.16 to 0.48 as compared to Asian ones with higher index of similarity (0.51–0.86). Moreover, the fatty acids 12:0 iso 3OH, 13:0 2OH and 18:0 iso are only found in African strains, in contrast to 16:0 3OH, only found in Asian strains. In the multilocus sequences analysis, the level of nucleotide polymorphism per gene varied from 4 (*efp*) to 24 (*gyrB*). Concatenation of the four housekeeping loci gave a 2785-bp nucleotide sequence of which 4.9% showed polymorphism among strains of the pathogen. Neighbour joining based phylogenetic analysis revealed that African strains of *X. oryzae* pv. *oryzae* are distinctly aggregated from Asian ones and from *X. oryzae* pv. *oryzicola*, which causes bacterial leaf streak of rice. The fatty acid and multilocus sequence analyses of four housekeeping genes demonstrated that African strains of *X. oryzae* pv. *oryzae* are genetically distant from Asian ones.

**Keywords:** Fatty acid analysis, MLSA , *x. oryzae* pv. *oryzae*