

Genetic diversity of bacterial communities associated with bacterial leaf blight of rice in Sri Lanka

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Bacterial leaf blight, caused by the bacterium *Xanthomonas oryzae* pv *oryzae* (*Xoo*), is one of the main devastating diseases in rice. Due to the shifting genetic structure, associated microbial consortia and environmental conditions of *Xoo*, it is difficult to identify them according to their pathotype, for better management. This study aims to determine the genetic diversity of bacterial communities associated with bacterial leaf blight in rice through molecular perspectives. A total of 41 isolates were collected from different rice-growing areas belonging to wet zone, dry zone and intermediate upcountry zones in Sri Lanka. All the samples were cultured in yeast dextrose carbonate agar medium. Based on the morphological and geographical perspectives, six groups were selected. Polymerase Chain Reaction was performed with universal primers 27F and 1492R for selected groups. PCR restriction fragment length polymorphism with Hae III restriction enzyme and virulence analyses were performed to evaluate the genetic diversity of associated microbial communities in rice bacterial blight. Pathogenicity test was conducted for IRRI 61, IRRI 57, IRRI 03 (International Rice Research Institute) and TN1 (Taichung Native 1) rice lines. These results revealed significant differences in disease severity among the selected rice lines and their locations. Furthermore, results revealed significant genetic diversity among isolates. RFLP analysis revealed four distinct genetic clusters, indicating genetic diversity among six isolates. Based on the sequencing results, it was highlighted that, *Xanthomonas oryzae*, *Stenotrophomonas* sp., *Sphingomonas* sp and *Pantoea ananatis* were associated with bacterial leaf blight in rice cultivation in Sri Lanka. This finding would greatly help to develop new bacterial leaf blight resistance in rice for better disease management.

Keywords: Bacterial leaf blight, Restriction fragment length polymorphism, Rice, *Xanthomonas oryzae*