Rapid identification and differentiation of Xanthomonas oryzae pv oryzae strain with primer 16S-23S rDNA from rice fields in Peninsular Malaysia.

ABSTRACT

Primer pairs XOR-F/XOR-R2 was used for rapid identification and differentiation of thirty strains of Xanthomonas oryzae pv. oryzae (Xoo) were collected from rice fields in Penang, Kedah, Selangor and Melaka during the period from 2008 to 2010. Purified DNA was extracted using a modified CTAB method and was used in the PCR. Four hundred and seventy bp product was amplified from DNA of 30 strain using XOR-F/XOR-R2 primer pairs. Sequence similarities of the intergenic region in the 16S-23S rDNA in the Malaysian strains were as high as 99-100%. Cluster analysis based on the sequencing shows that the strains are grouped one main cluster and four groups. The minimum role of varietal influence on strain variability is partly due to the almost homogenous planting of two popular rice varieties in Peninsular Malaysia during the period of the study. On the other hand, phylogenetic analysis by using intergenic region 16S-23S divided the strains into one main cluster and four groups. The first group is represented by isolates collected from Penang and the second groups from Selangor. The third and fourth groups represented strains collected from Melaka and Kedah, respectively. The present study confirmed that direct DNA extraction from infected rice tissue by using CTAB method, followed by PCR effective methods for the identification of Xoo. Further more the results indicated that strains differentiation may be affected by the geographical areas.

Keyword: 16S-23S rDNA; Differentiation; PCR; Rapid identification; Xanthomonas; Xanthomonas oryzae.