

Comparative genomics of *Xanthomonas oryzae* pv. *oryzae* bacteriophages

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Xanthomonas oryzae pv. *oryzae* (*Xoo*) is the causative agent of bacterial leaf blight (BLB) of rice. BLB of rice is a devastating disease causing severe economic losses, especially on Asia and western Africa. Bacteriophages may provide an environmentally friendly, effective solution against *Xoo*. Isolated *Xoo* bacteriophages were grouped into two major groups: OP₁- and OP₂-like phages (Wakimoto et al 1960).

In our laboratory – Enviroinvest Corp. in Hungary – ten different OP₂-like phages were isolated from Vietnam and from Philippines previously, they were characterized and their complete genomes were determined (Kovács et al 2019). As a result of our cooperation with Ralf Koebnik's laboratory in the IRD Montpellier, two more bacteriophages were isolated against *Xoo*. These new phages were characterized and sequenced as well. Based on terminase large subunit encoding gene sequences, OP₁- and OP₂-like bacteriophages build a distinct phylogenetic group and OP₂-like phages could be further divided into 2 major groups. Comparative full genomic analysis of the 12 newly isolated OP₂-like bacteriophages revealed the phylogenetic relationship among the different isolates. A 322 bp conserved intergenic region in the OP₂-like phage genomes were discovered when genome sequences of the 12 novel OP₂-like phages were compared to OP₂'s genome. Analyzing mutation frequencies along the OP₂-like phage genomes enabled us to track steps of the molecular evolution of OP₂-like bacteriophages. Host-specificity of these newly isolated bacteriophages were tested on representative strains of *X. oryzae* (*Xoo* and *Xoc* from Asia and Africa, on strains of *X. oryzae* from the USA and on *X. oryzae* isolated from southern cutgrass). All of the examined phages (two from Vietnam, two from Philippines and two from Montpellier) could infect only *X. oryzae* pv. *oryzae* strains from Asia, contrarily, these phages were produced no effect against *Xoo* strains from Africa and against *X. oryzae* pv. *citri* strains.

Our study provides data on the genomic characteristics, phylogenetic relationships and a route of molecular evolution of mostly novel *Xoo* OP₂-like bacteriophages.

Wakimoto S. 1960. Classification of strains of *Xanthomonas oryzae* on the basis of their susceptibility against bacteriophages, J Phytopathol 25:193-198.

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