

**Genome characterization of a novel vibriophage VpKK5 (*Siphoviridae*)
specific to fish pathogenic strain of *Vibrio parahaemolyticus***

Abstract

Vibrio parahaemolyticus has long been known pathogenic to shrimp but only recently it is also reported pathogenic to tropical cultured marine finfish. Traditionally, bacterial diseases in aquaculture are often treated using synthetic antibiotics but concern due to side effects of these chemicals is elevating hence, new control strategies which are both environmental and consumer friendly, are urgently needed. One promising control strategy is the bacteriophage therapy. In this study, we report the isolation and characterization of a novel vibriophage (VpKK5), belonging to the family *Siphoviridae* that was specific and capable of complete lysing the fish pathogenic strain of *V. parahaemolyticus*. The VpKK5 exhibited short eclipse and latent periods of 24 and 36 min, respectively, but with a large burst size of 180 pfu/cell. The genome analysis revealed that the VpKK5 is a novel bacteriophage with the estimated genome size of 56,637 bp and has 53.1% G + C content. The vibriophage has about 80 predicted open reading frames consisted of 37 complete coding sequences which did not match to any protein databases. The analysis also found no lysogeny and virulence genes in the genome of VpKK5. With such genome features, we suspected the vibriophage is novel and could be explored for phage therapy against fish pathogenic strains of *V. parahaemolyticus* in the near future.