

## **Genome analysis of Betanodavirus from cultured marine fish species in Malaysia**

### **Abstract**

Betanodavirus is the causative agent of the viral nervous necrosis (VNN) or viral encephalopathy and retinopathy disease in marine fish. This disease is responsible for most of the mass mortalities that occurred in marine fish hatcheries in Malaysia. The genome of this virus consists of two positive-sense RNA molecules which are the RNA1 and RNA2. The RNA1 molecule contains the RdRp gene which encodes for the RNA-dependent RNA polymerase and the RNA2 molecule contains the Cp gene which encodes for the viral coat protein. In this study, total RNAs were extracted from 32 fish specimens representing the four most cultured marine fish species in Malaysia. The fish specimens were collected from different hatcheries and aquaculture farms in Malaysia. The RNA1 was successfully amplified using three pairs of overlapping PCR primers whereas the RNA2 was amplified using a pair of primers. The nucleotide analysis of RdRp gene revealed that the Betanodavirus in Malaysia were 94.5-99.7% similar to the RGNNV genotype, 79.8-82.1% similar to SJNNV genotype, 81.5-82.4% similar to BFNNV genotype and 79.8-80.7% similar to TPNNV genotype. However, they showed lower similarities to FHV (9.4-14.2%) and BBV (7.2-15.7%), respectively. Similarly, the Cp gene revealed that the viruses showed high nucleotide similarity to RGNNV (95.9-99.8%), SJNNV (72.2-77.4%), BFNNV (80.9-83.5%), TPNNV (77.2-78.1%) and TNV (75.1-76.5%). However, as in the RdRp gene, the coat protein gene was highly dissimilar to FHV (3.0%) and BBV (2.6-4.1%), respectively. Based on the genome analysis, the Betanodavirus infecting cultured marine fish species in Malaysia belong to the RGNNV genotype. However, the phylogenetic analysis of the genes revealed that the viruses can be further divided into nine sub-groups. This has been expected since various marine fish species of different origins are cultured in Malaysia.