

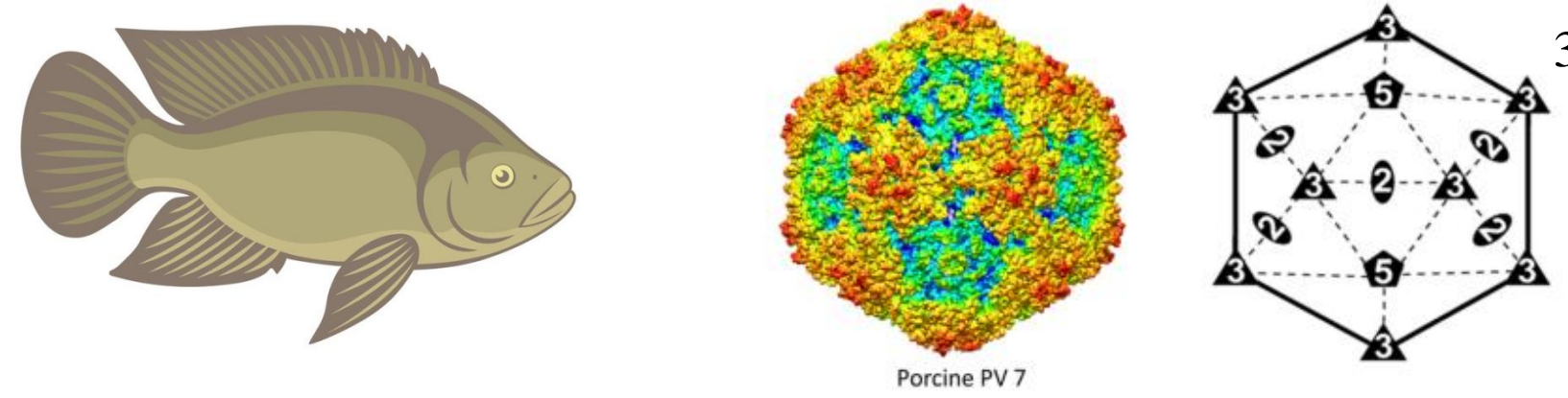
# Determination of a novel parvovirus pathogen associated with massive mortality in adult tilapia

Wenzhi Liu<sup>1a</sup>, Yecheng Zhang<sup>2a</sup>, Jie Ma<sup>3a</sup>, Nan Jiang<sup>1</sup>, Yuding Fan<sup>1</sup>, Yong Zhou<sup>1</sup>, Kenneth Cain<sup>3</sup>, Meisheng Yi<sup>4</sup>, Kuntong Jia<sup>4</sup>, Hua Wen<sup>1</sup>, Wei Liu<sup>1</sup>, Wuxiang Guan<sup>2\*</sup>, Lingbing Zeng<sup>1\*</sup>

<sup>1</sup>Yangtze River Fisheries Research Institute, Chinese Academy of Fishery Sciences. <sup>2</sup>Wuhan Institute of Virology, Chinese Academy of Sciences. <sup>3</sup>Department of Fish and Wildlife Sciences and the Aquaculture Research Institute, University of Idaho. <sup>4</sup>School of Marine Sciences, Sun Yat-sen University.

## Introduction

- Tilapia (*Oreochromis niloticus*), belonging to the family *Cichlidae* of the order *Perciformes*, are the third-ranking aquaculture species<sup>1</sup>.
- In 2015, a massive mortality event was reported in cage-farmed tilapia in China and this newly emerging disease developed rapidly<sup>2</sup>.
- The parvovirus pathogen (named TiPV) was isolated and determined to be the causative agent of an epidemic in tilapia in China<sup>2</sup>.

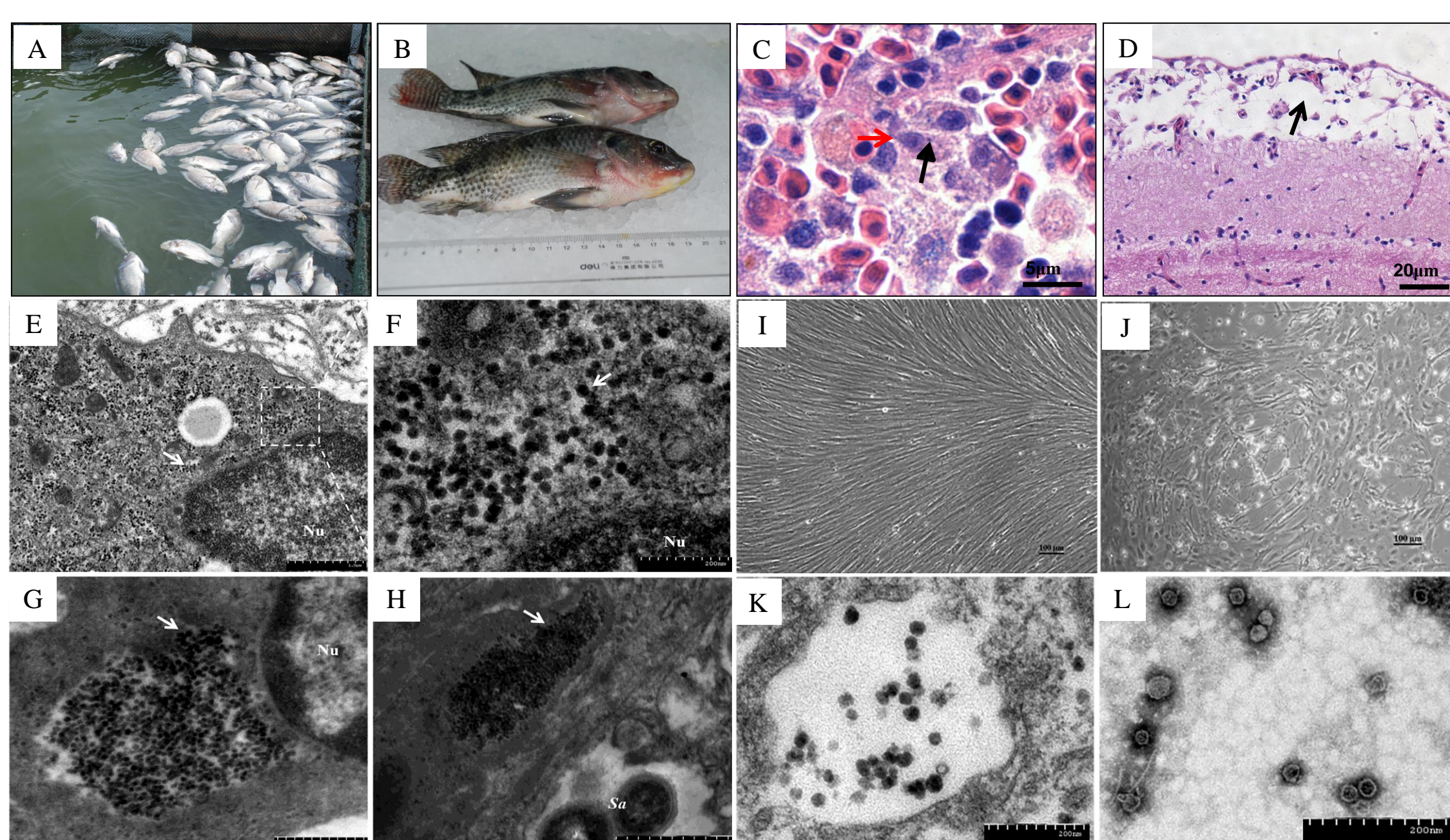


## Materials & Methods



- Diseased tilapia were collected for diagnosis and pathogen determination.
- Identification of the causative pathogen and virus isolation.
- Genome sequencing analysis of TiPV.
- Detection, transmission and distribution of TiPV.

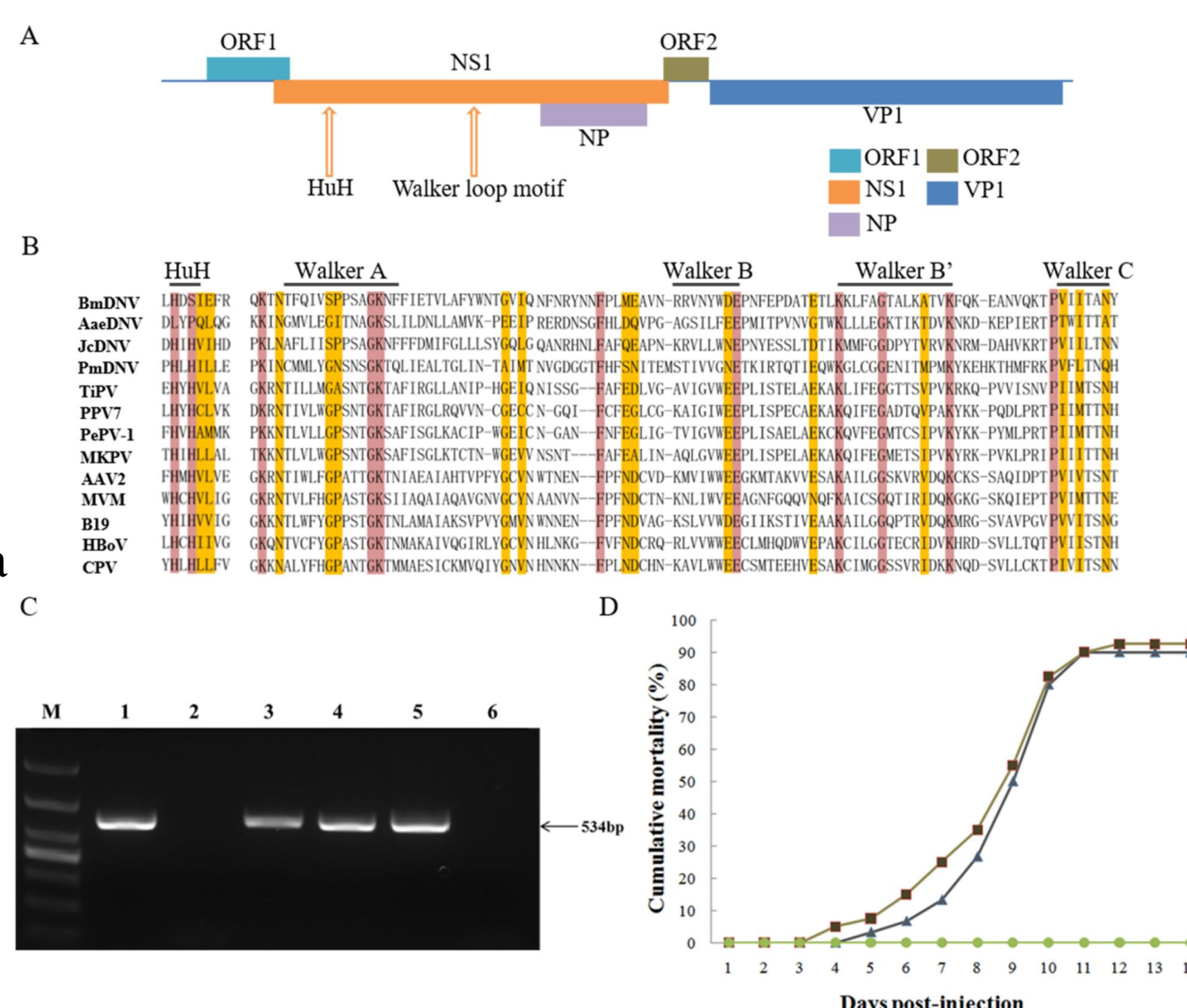
## Clinical signs, pathological features and viral observation



- Clinical signs of the disease in tilapia.
- Various degrees of pathological features were observed in visceral tissues.
- Electron microscopy revealed large aggregates of parvovirus particles located in visceral tissues and in TiK cells.

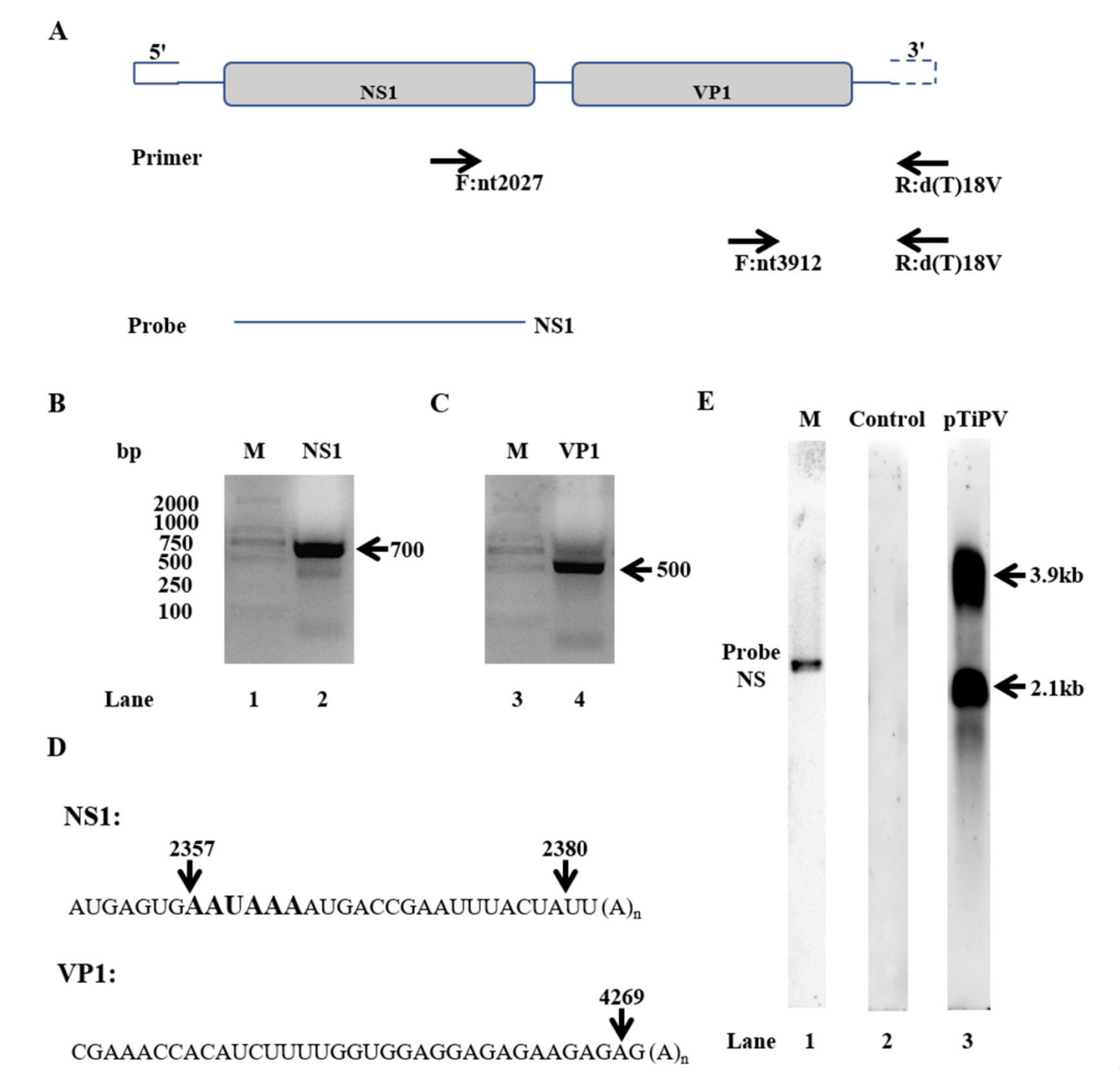
## Characterization of the TiPV genome and cumulative mortality of artificial infected tilapia

- A nearly complete genome (4269 bp) of TiPV was obtained, containing two major open reading frames (ORFs), with the left and right ORFs encoding NS1 and VP1, respectively.
- The HuH motif (where u indicates a hydrophobic residue) was found located at aa 78-80 in NS1.
- The mortality reached approximately 90% within 12 dpi.



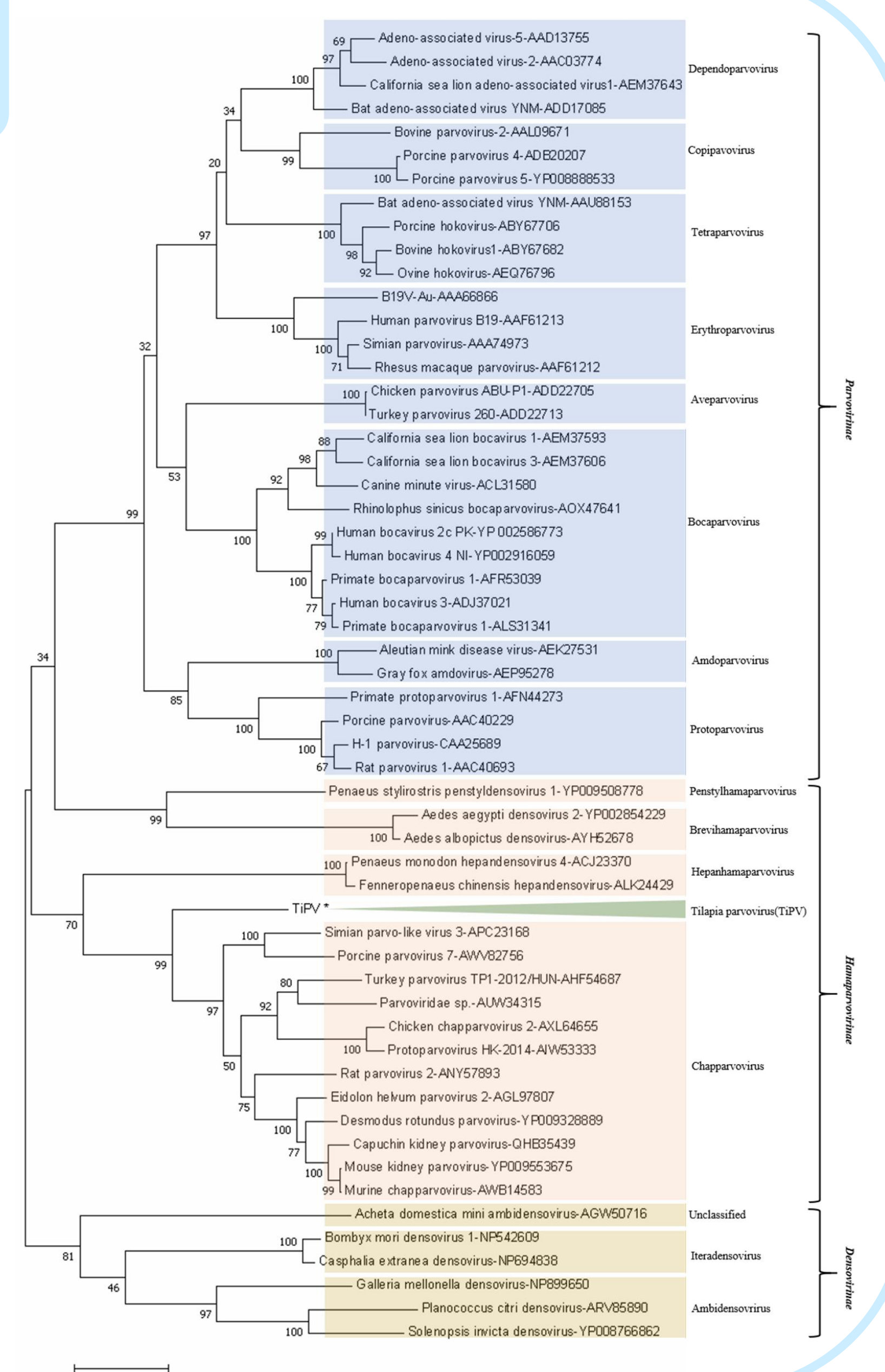
## Northern blot analysis

- Sequence analysis revealed that there were two bands terminated at nt 2380 and nt 4269, respectively, suggesting that NS1 and VP1 mRNAs of TiPV are polyadenylated at nt 2380 and nt 4269.
- A consensus poly (A) signal (AATAAA) was identified at nt 2357-2362 in the TiPV genome, which can be used for the (pA)p.



## Phylogenetic analysis and classification

- A phylogenetic tree was constructed based on the completed non-structural (NS1) protein amino acid sequences of 55 representative viruses in the family *Parvoviridae*.
- The deduced TiPV NS1 protein has the highest homology of 36.7% identical amino acid residues to the NS1 protein of Porcine parvovirus 7 (PPV7).
- Phylogenetic analysis showed that TiPV is a novel parvovirus, and forms a separate branch in the proposed genus *Chapparovirus* of *Parvoviridae*.



## Conclusion

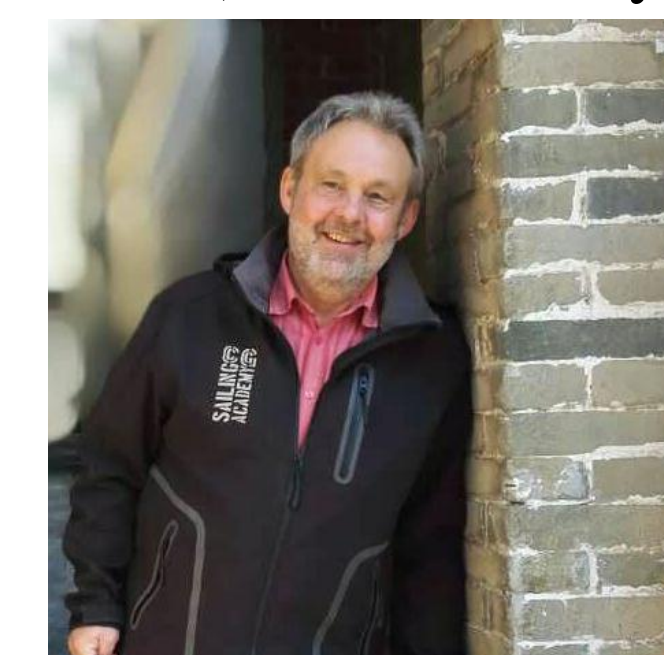
- The causative agent of a new emerging disease associated with massive mortality in farmed tilapia, in China was identified as a novel parvovirus.
- This novel virus is tentatively named tilapia parvovirus (TiPV).
- TiPV appears to be an emerging viral pathogen in tilapia with implications for culture of this species in China and elsewhere.

## Acknowledgements

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Sven Bergmann



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