Complete genome and molecular characterization of Cyprinid herpesvirus 2 (CyHV-2) SH-01 isolated from cultured crucian carp

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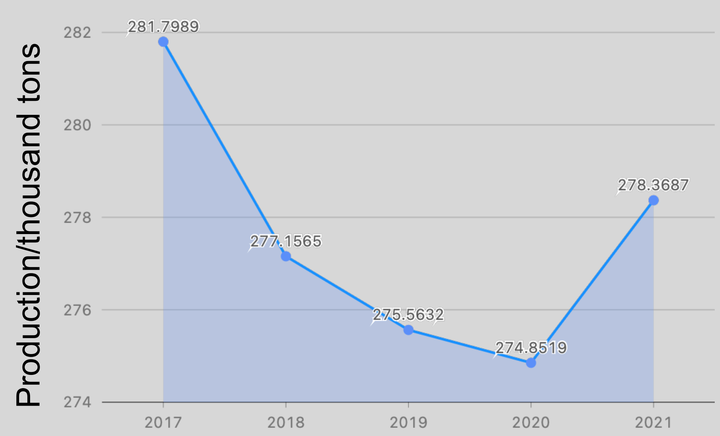
Summary

- We analyzed the genomic characteristics of a new CyHV-2 SH-01 strain isolated from disease crucian carp at a local fish farm near Shanghai in China.
- We further predicted the function features of proteins encoded by SH-01, then compared genome structures as well as evolutionary patterns among homologous or heterologous regions of SH-01 and another closely viruses in *Cyprinivirus*.

Background

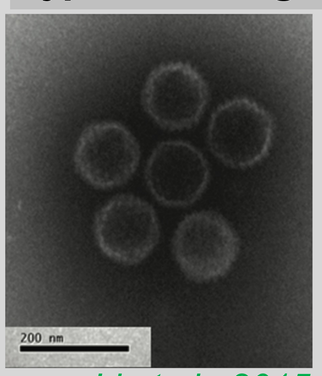


- Crussian carp (*Carassius carassius*) is one of the most important freshwater fish species in China, alongside goldfish (*Carassius auratus*) and gibel carp (*Carassius gibelio*) with production of 278.37 thousand tons in 2021.
- Cyprinid herpesvirus 2 (CyHV-2) causes herpesviral hematopoietic necrosis (HVHN) in crucian carp, goldfish and other inbred hybrids of *Carassius* with high susceptibility and mortality leading to considerable economic losses.

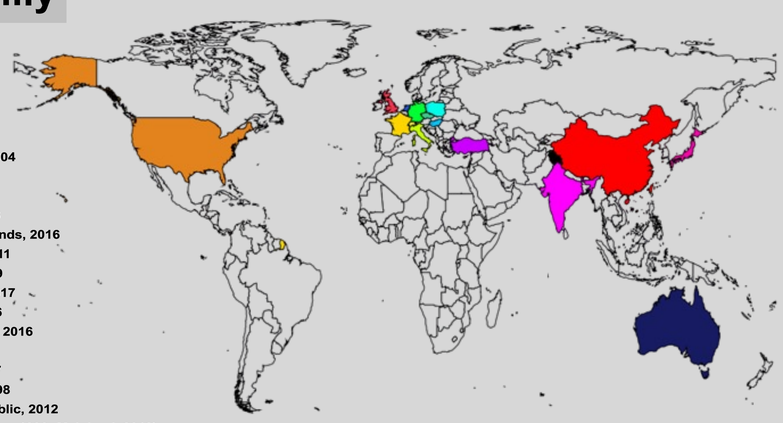
Xu et al., 2013; Zhao et al., 2019

***Alloherpesviridae* family**

***Cyprinivirus* genus**

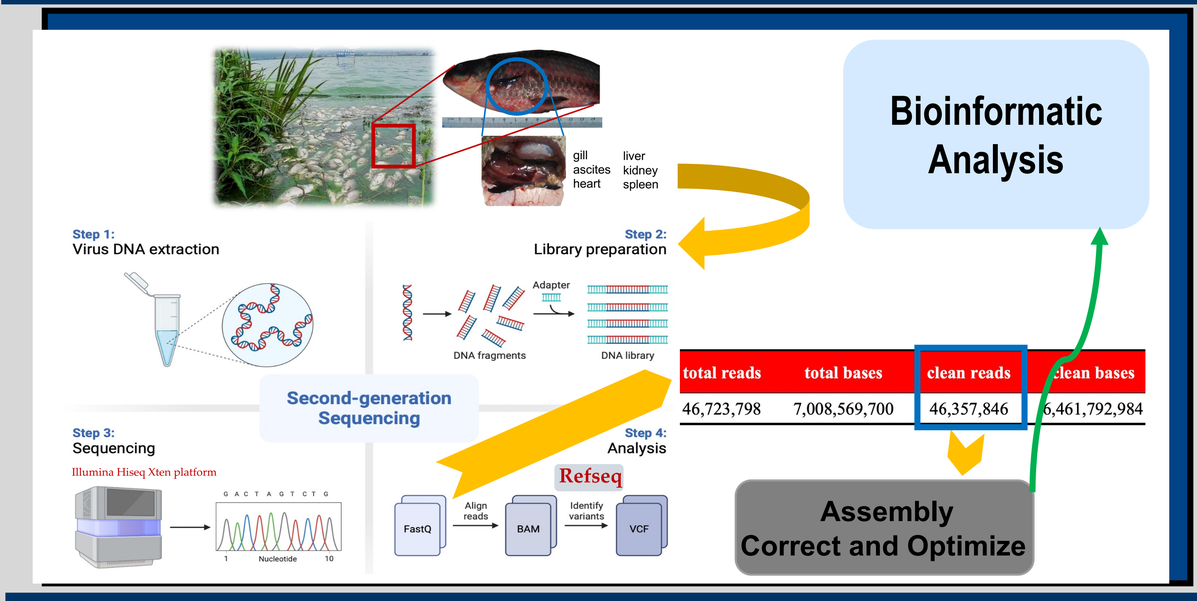


Li et al., 2015



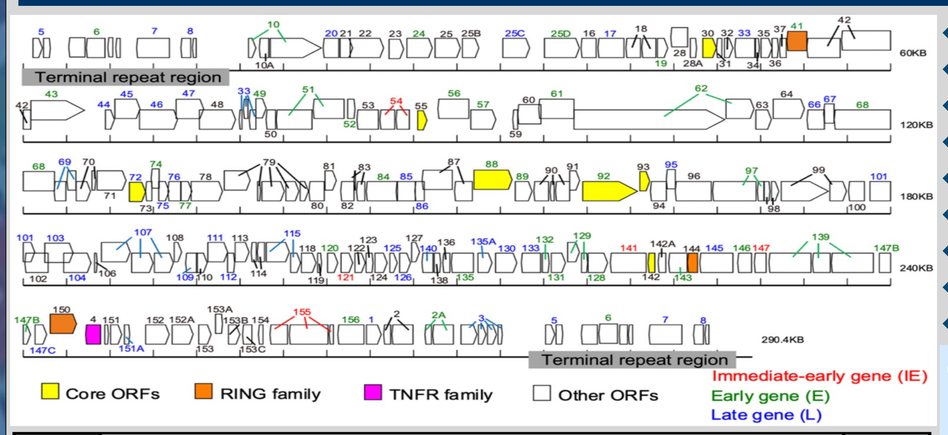
- CyHV-2 infection was originally reported in Japan, then has rapidly spread into many countries and regions worldwide.
- CyHV-2 is a double-stranded DNA virus with 290 kb of genome size in length.
- Research in the past decade has mainly involved detection and genome sequencing of CyHV-2. To date, seven CyHV-2 isolates have been cultivated and genome-sequenced.

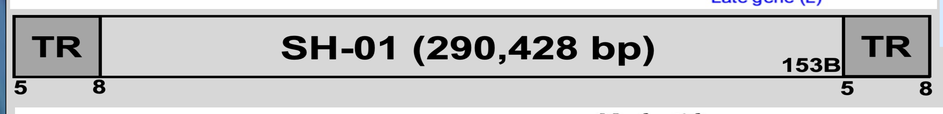
Materials and Methods



total reads	total bases	clean reads	clean bases
46,723,798	7,008,569,700	46,357,846	6,461,792,984

Results





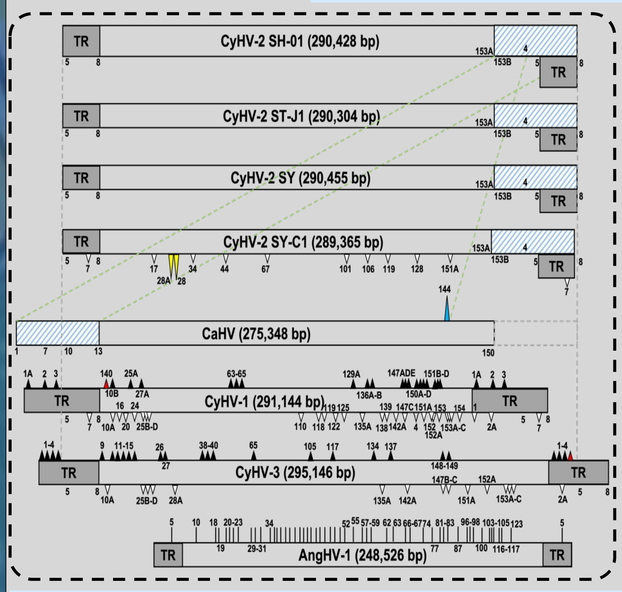
- U (Unique) region
- TR (Terminal repeat) regions
- G+G content: 51.79%
- 154 ORFs (4 ORFs in TR)
- Positive strand: 86 ORFs
- Negative strand: 28 ORFs
- 5 immediate-early (IE) genes
- 34 early (E) genes
- 39 late (L) genes

Genome structure and composition of SH-01

Figure 1

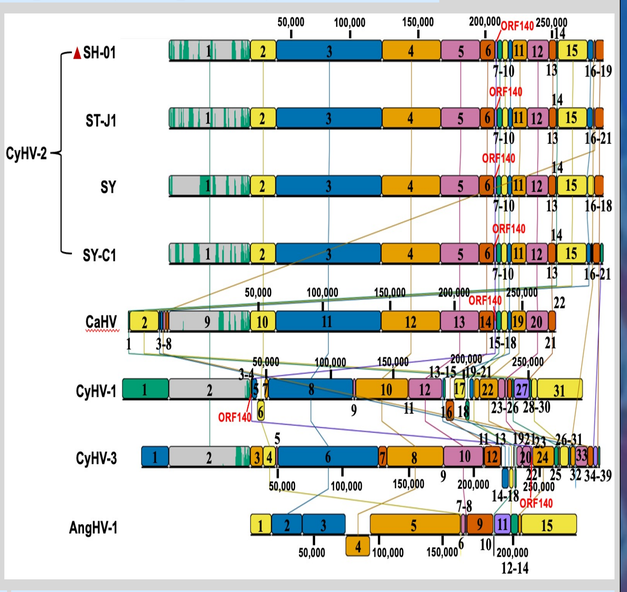
Virus		Size (bp)			Nucleotide composition (%)	No. of ORFs				Identity (%)[f]
		Genome	U[e]	TR[f]	G+C	Genome[g]	Unique[h]	U[e]	TR[f]	
CyHV-2	SH-01	290,428	260,586	14,921	51.79	154	150	146	4	***
	ST-J1[a]	290,304	260,238	15,033	51.70	154	150	146	4	99.98
	SY-C1[b]	289,365	259,555	14,905	51.60	143	140	137	3	99.79
	SY[c]	290,455	259,749	15,353	51.60	154	150	146	4	99.84
CyHV-1[a]		291,144	224,784	33,180	51.30	143	137	131	6	55.48
CyHV-3[a]		295,146	250,208	22,469	59.20	163	155	147	8	62.70
AngHV-1[a]		248,526	227,258	10,634	53.00	134	129	124	5	44.36
CaHV[d]		275,348	—	—	51.73	150	150	—	—	99.82

Table 1 **Genome features of CyHVs, AngHV-1, and CaHV**



Comparison of genome structure and ORFs arrangement

Figure 2



Evolutionary patterns among SH-01 and other seven strains

Figure 3

Conclusions

- ✓ Several variations were found in SH-01, including nucleotide mutations, deletions and insertions, as well as gene duplications, rearrangements and horizontal transfers.
- ✓ Notably, the genome of SH-01 isolated from crucian carp shares 99.98% identity with that of ST-J1 isolated from goldfish, implying that SH-01 may have originated from goldfish and been introduced to crucian carp.
- ✓ The results provide new clues to better understand the CyHV-2 genome and potential molecular pathogenic mechanisms through sequencing and sequence mining.

Acknowledgements

The present study received grant support from the National Natural Science Foundation 465 of China (Grant No.32102842), the Key Research and Development Plan of Jiangsu Province (No. 466 BE2021369).

By Jia Yang