



# Molecular Characterization and Genogrouping of an Aquatic Birnavirus GC1 Isolated from Rockfish in Korea

Seong-Joon Joh, Chae-Ik Son, Sung-Won Kang, Byoung-Han Kim, Byung-Yul Jeong, Kyung-Gi Lee, Jun-Hun Kwon

Avian Diseases Division, National Veterinary Research & Quarantine Service, MAF, Anyang, Korea

## I. INTRODUCTION

Members of the family Birnaviridae have 2-segmented genomes - A and B. This family comprises 3 main genera, including the genus *Aquabirnavirus*, *Avibirnavirus*, and *Entomobirnavirus*. Aquatic birnaviruses are the largest and most diverse group of viruses within the family *Birnaviridae*. The genome segment B of birnaviruses encodes the VP1 protein, which is the presumptive virion-associated RNA-dependent RNA polymerase (RdRp). In the present study, we investigated the genetic characteristics of the VP1 protein and compared the genetic relationship between aquatic birnaviruses and other genres of birnaviruses within *Birnaviridae*.

## II. MATERIALS & METHODS

We performed nucleotide sequencing and genetic characterization of VP1 protein of GC1 isolate. The amino acid sequence of VP1 of GC1 was compared to those of other birnaviruses. By using phylogenetic cladogram, we investigated phylogenetic relationships of the VP1 protein of GC1 among *Birnaviridae*.

## III. RESULTS

The nucleotide sequence of VP1 gene of GC1 isolate was found to be 2,776 bp long. The predicted molecular weight of the VP1 was 94,263 Daltons, and the gene was known to contain a single large open reading frame (ORF) encoding the 846-amino acids. We also observed that the VP1 sequence contained 6 potential Asn-X-Ser/Thr motifs, 8 potential Ser phosphorylation sites and 1 Tyr phosphorylation site. The amino acid sequence of VP1 did not contain the GDD motif, which exists commonly in the RdRps of RNA viruses; however, we could identify the Leu-Lys-Asn (LKN) motif at position 521.

## IV. CONCLUSION

The study of genetic relationships using a phylogenetic cladogram revealed that Korean aquatic birnavirus GC1 is more closely related to genogroup 1 than genogroup 2. This result indicates that genetic relationships may be influenced by the geographical distributions of the isolates.

## V. REFERENCES

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Table 1. Pairwise similarity and distances between the RdRp amino acid sequences of 22 birnavirus strains.

Percent divergence amino acid sequence of VP1	Percent identity amino acid sequences of VP1																					
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	100	98	95	95	96	96	96	47	47	28	90	90	90	90	90	88	90	90	90	90	90	1
2	0	100	98	95	95	96	96	46	46	28	90	90	90	90	90	88	90	90	90	90	90	2
3	2	2	100	94	94	95	95	46	46	28	89	89	89	89	89	87	89	89	89	89	89	3
4	5	5	6	100	99	98	98	47	46	27	89	89	89	89	90	88	90	90	90	90	90	4
5	5	5	6	1	100	99	99	47	46	27	89	89	89	89	90	88	90	89	90	90	90	5
6	4	4	5	2	1	100	100	48	47	28	90	90	90	90	91	89	91	90	91	91	91	6
7	4	4	5	2	1	0	100	48	47	28	90	90	90	90	91	89	91	90	91	91	91	7
8	4	4	5	2	1	0	0	48	47	28	90	90	90	90	91	89	91	90	91	91	91	8
9	53	53	54	53	53	52	52	50	100	98	98	97	94	95	95	96	96	96	96	96	96	9
10	53	53	54	54	53	53	53	50	98	100	98	97	94	95	95	96	96	96	96	96	96	10
11	72	72	72	72	73	72	72	73	29	29	100	98	97	94	95	95	96	96	96	96	96	11
12	10	10	11	11	11	10	10	53	53	71	100	98	98	97	94	95	95	96	96	96	96	12
13	10	10	11	11	11	10	10	53	53	71	0	100	98	97	94	95	95	96	96	96	96	13
14	10	10	11	10	11	10	10	53	53	71	2	2	100	98	97	94	95	95	96	96	96	14
15	10	10	11	11	11	10	10	53	54	71	2	2	1	100	98	97	94	95	95	96	96	15
16	10	10	11	10	10	9	9	53	53	71	3	3	2	94	100	98	97	94	95	95	96	16
17	11	11	12	12	11	11	11	53	54	71	6	6	6	6	6	100	98	97	97	97	97	17
18	9	10	11	10	10	9	9	53	53	71	5	4	4	4	5	3	100	99	99	99	99	18
19	10	10	11	10	10	9	9	53	54	71	5	4	4	4	5	3	1	100	99	99	99	19
20	9	10	11	10	10	9	9	53	54	71	4	4	4	4	4	3	1	0	100	100	100	20
21	9	10	11	10	10	9	9	52	53	71	4	4	4	4	4	3	1	1	0	100	100	21
22	9	10	11	10	10	9	9	52	54	71	4	4	4	4	4	2	1	1	0	0	100	22

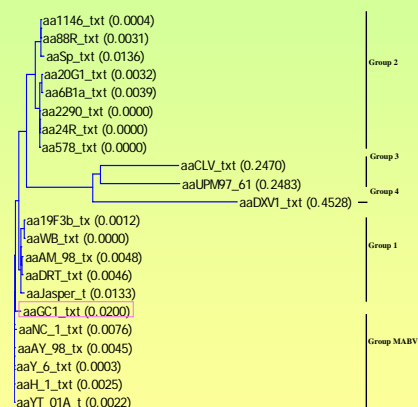


Fig. 1. Cladogram representing phylogenetic relationships between birnaviruses based on deduced amino acid sequences of VP1. The length of each pair of branches represents the distance between the sequence pairs, and the numbers in parentheses indicate the bootstrap values