

The Fecal Virome of Red-crowned Cranes

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Fig. S1. Phylogenetic analysis of the novel picornaviruses identified in red-crowned cranes. Phylogenetic analysis based on the complete amino acid sequence of P2 proteins of Gapovirus, Grusavirus, and 35 representative strains of all the 35 genera in *Picornaviridae*.

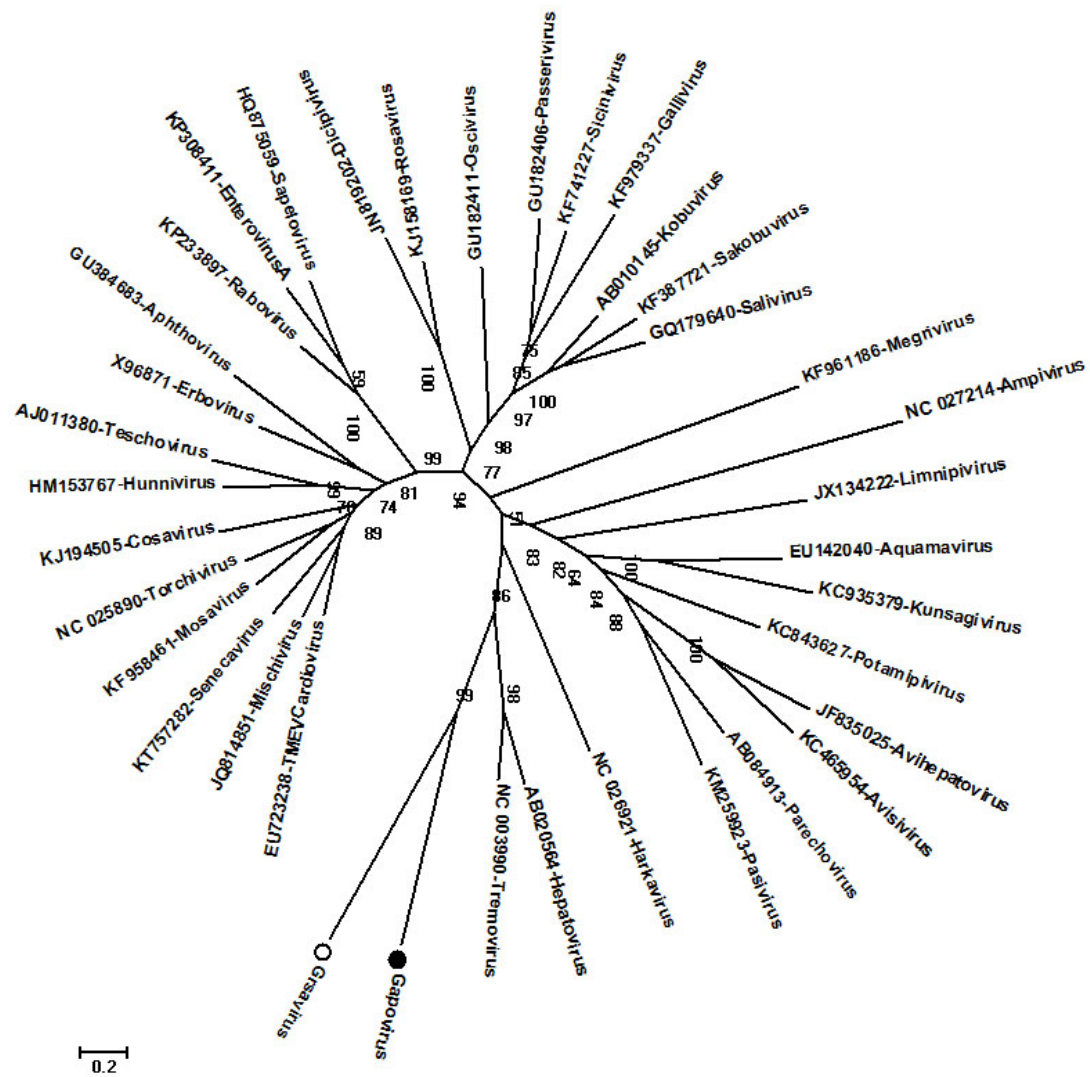


Fig. S2. Sequence comparison of four novel picornaviruses of genus *Avihepatovirus* identified in red-crowned cranes with the representative strain (NC_008250) based on the VP1-2A2 protein region.

		Percent Identity						
		1	2	3	4	5		
Divergence	1	■	24.5	17.4	17.1	15.8	1	NC_008250
	2	200.0	■	30.7	64.8	26.5	2	VP1-2A2-GrHAV1
	3	268.0	122.5	■	21.6	29.0	3	VP1-2A2-GrHAV2
	4	223.0	40.4	163.7	■	21.0	4	VP1-2A2-GrHAV3
	5	248.0	142.6	131.0	177.0	■	5	VP1-2A2-GrHAV4
		1	2	3	4	5		

Table S1. The summary of library information of red-crowned crane

Library ID	Sample type	No. of Sample	Healthy status	habitation	Total no. of raw reads	No. of unique reads	No. of viral reads with E value <10 ⁻⁵
1	Feces	14	Normal	Wild	642,992	558,303	37,298
2	Feces	15	Normal	wild	589,512	448,999	28,898
3	Feces	12	Normal	wild	208,348	155,485	11,258
4	Feces	20	Normal	Breed	519,160	299,263	8,709
5	Feces	16	Normal	Ornamental	269,889	145,887	36,574
6	Feces	16	Normal	Ornamental	957,290	331,497	104,925

Table S2. Eukaryotic viral sequences of wild, breed and ornamental libraries, the families marked with highlight yellow were mainly studied in this study.

Virus Families	Virus Type	No. of viral reads with E value <10 ⁻⁵					
		Library1 (wild)	Library2 (wild)	Library3 (wild)	Library4 (breed)	Library5 (ornamental)	Library6 (ornamental)
Adenoviridae	Mammalian virus	3	1	4	10	42	14
Alphaflexiviridae	Plant virus	2	1	0	0	0	0
Alphatetraviridae	Insect virus	229	0	0	0	0	0
Alvernaviridae	Plant virus	1	0	0	0	0	0
Astroviridae	Mammalian virus	2	0	1	3	2	24
Baculoviridae	Insect virus	17	8	1	7	2	8
Barnaviridae	Plant virus	8	0	0	0	0	0
Betaflexiviridae	Plant virus	0	1	0	1	1	0
Bidnaviridae	Insect virus	7	9	2	0	2	0
Bromoviridae	Plant virus	22	6	0	1	0	0
Caliciviridae	Mammalian virus	65	4	2,274	30	20	8
Caulimoviridae	Plant virus	3	0	1	0	2	1
Circoviridae	Mammalian virus	1,669	2,218	1,034	69	156	69
Closteroviridae	Plant virus	15	4	2	0	0	3
Dicistroviridae	Insect virus	716	222	67	101	384	472
Endomaviridae	Plant virus	4	0	0	0	0	0
Geminiviridae	Plant virus	184	281	123	330	67	32
Hepeviridae	Mammalian virus	27	0	0	1	7	2
Iflaviridae	Insect virus	39	16	2	22	65	37
Iridoviridae	Insect virus	37	70	8	16	0	7
Luteoviridae	Plant virus	51	6	3	2	4	6

Malacoherpesviridae	Molluscs virus	4	2	0	0	0	0
Mamaviridae	Plant virus	29	29	9	3	2	0
Mesoniviridae	Insect virus	1	0	0	0	0	0
Nanoviridae	Plant virus	391	195	78	8	4	4
Nimaviridae	crustaceans virus	2	2	1	0	0	0
Nodaviridae	Aquatic virus	26	34	4	11	2	1
None	unclassified	16,254	14,596	5,708	1,637	929	893
Nudiviridae	Insect virus	0	2	0	0	0	1
Ophioviridae	Plant virus	0	1	0	0	0	0
Partitiviridae	Plant virus	3	1	1	4	32	21
Parvoviridae	Mammalian virus	8,935	3,765	1,167	6,052	21,626	17,912
Permutotetraviridae	Insect virus	9	24	14	0	0	1
Phycodnaviridae	Plant virus	639	602	246	38	24	49
Picornaviridae	Mammalian virus	7,158	6,295	397	276	13,159	85,270
Polydnaviridae	Insect virus	1	2	1	0	0	7
Potyviridae	Plant virus	10	5	3	0	0	0
Reoviridae	eukaryote	19	3	1	0	3	1
Roniviridae	crustaceans virus	0	1	0	1	0	0
Secoviridae	Plant virus	50	21	15	12	7	9
Tombusviridae	Plant virus	608	327	58	40	18	43
Totiviridae	protozoa virus	2	0	0	0	4	0
Tymoviridae	Plant virus	0	1	0	0	0	0
Virgaviridae	Plant virus	7	2	5	6	5	2

Table S3. Comparison of the cleavage sites of GrHAV1-4 and the representative strain

Virus strains	Cleavage sites of different proteins of <i>Avihepatovirus</i>									
	VP0/VP3	VP3/VP1	VP1/2A1	2A1/2A2	2A2/2B	2B/2C	2C/3A	3A/3B	3B/3C	3C/3D
NC_008250	Q/G	Q/G	E/S	G/P	Q/S	Q/S	Q/S	Q/S	Q/S	Q/G
GrHAV1	Q/G	Q/G	N	N	Q/G	M/E	Q/G	Q/S	Q/G	Q/G
GrHAV2	Q/G	L/G	N	N	Q/A	D/L	Q/G	H/N	Q/P	Q/G
GrHAV3	Q/G	Q/G	N	N	Q/G	Q/S	Q/G	Q/S	Q/G	Q/G
GrHAV4	Q/G	V/G	N	N	Q/G	E/S	Q/S	N/G	Q/G	Q/G