

Supplementary materials for Journal of Wildlife Diseases DOI: 10.7589/2017-07-158: Kang-Seuk Choi, Ji-Ye Kim, Hyun-Jeong Lee, Min-Jun Jang, Hyuk-Moo Kwon, Haan-Woo Sung.

Suppl. Table 1. List of APMV-6 strains used in the study.

APMV-6 isolate(abbreviation)	Country	Year	Bird species ^b	Accession number
Eurasian wigeon/KR/KNU13/10(KNU13) ^a	Korea	2010	Eurasian wigeon	MF072423
Eurasian wigeon/KR/KNU14/10 (KNU14) ^a	Korea	2010	Eurasian wigeon	MF072424
Mallard/KR/KNU22/11(KNU22) ^a	Korea	2011	Mallard	MF072421
Mallard/KR/KNU26/11(KNU26) ^a	Korea	2011	Mallard	MF072422
Wild bird/KR/KNU57/13(KNU57) ^a	Korea	2013	Unknown	MF072425
Wild bird/KR/KNU58/13(KNU58) ^a	Korea	2013	Unknown	MF072426
Wild bird/KR/KNU59/13(KNU59) ^a	Korea	2013	Unknown	MF072427
Eurasian wigeon/KR/KNU60/13 (KNU60) ^a	Korea	2013	Eurasian wigeon	MF072428
Wild bird/KR/KNU61/13(KNU61) ^a	Korea	2013	Unknown	MF072429
Eurasian wigeon/KR/KNU62/13(KNU62) ^a	Korea	2013	Eurasian wigeon	MF072430
Eurasian wigeon/KR/KNU63/14(KNU63) ^a	Korea	2014	Eurasian wigeon	MF072431
Mallard/Jilin/190/11	China	2011	Mallard	JX522537.1
Mallard/Jilin/127/11	China	2011	Mallard	KF267717.1
red-crested pochard/Balkhash/5842/13	Kazakhstan	2013	Red-crested pochard	KP762799.1

Teal/Novosibirsk/455/09	Russia	2009	Eurasian teal	KT962980.1
Duck/Taiwan/Y1/98	Taiwan	1998	Domestic duck	AY029299.1
Goose/FE/4440/03	Russia(far East)	2003	Domestic goose	EF569970.1
Teal/IT/6895-1/07	Italy	2007	Teal	GQ406234.1
Duck/IT/4526/07	Italy	2007	Unknown	GQ406233.1
Mallard/BE/12245/07	Belgium	2007	Mallard	JN571486.1
Duck/HK/18/77	Hong Kong	1977	Unknown	EU622637.2
Red-necked stint/JP/8KS0813/08	Japan	2008	Red-necked stint	AB759118.1
Duck/IT/4524-2/07	Italy	2007	Unknown	GQ406232.1
Avian avulavirus 1(APMV-1)/La Sota	USA	1946	Chicken	DQ195265.1

^aAPMV-6 isolated during winter season (November to February) in the study.

^b Unknown= waterfowl of undetermined species.

Suppl. Table 2. Primers for amplification of the F gene of APMV-6

Primer ^A	Primer sequence	Position	Product size	PCR condition
Set 1	APMV-6 F1	5'-AATCACYRAATCAATACRCAG-3'	4369 to 4389	45°C 30 min-94°C 2 min-(94°C 30 s- 50°C 30 s-72°C 30s) x40- 72°C 7 min.
	APMV-6 R1	5'-TCCAAATCGAGATTCAAGCA-3'	5731 to 5712	
Set2	APMV-6 F1045	5'-ATGACCAAGCAAGCCAAATC-3'	5406 to 5425	
	APMV-6 R2110	5'-GTTGCAGTCAACCTCCTTCC-3'	6471 to 6452	
Set 3	APMV6 F4302	5'-GGGATTCAACCCGTTTCATAA-3'	4302 to 4321	1,197 bp
	APMV6 R5479	5'-TGAGGCCAGACACAGATGAG-3'	5498 to 5479	
Set4	APMV6 F5286	5'-CTGCGCTGTCAACCTTATCA-3'	5286 to 5305	1,357 bp
	APMV6 R6623	5'-CGCCGGAGGATCTGTATTAG-3'	6642 to 6623	

Primer sets 1 and 2 were synthesized based on the sequence of the genome of APMV-6/mallard/BE/12245/07 (JN571486.1) while primer sets 3 and 4 were synthesized based on the sequence of the genome of APMV-6/duck/IT/4524-2/07 (GQ406232.1)

Suppl. Table 3. Comparison of the nucleotide and amino acid sequences from F protein gene of APMV-6 Korean isolates and reference APMV-6 strains. Nucleotide **sequence identity** above the diagonal; amino acid **sequence identity** below the diagonal.

		Nucleotide sequence identity (%)																						
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Amino acid sequence identity (%)	1		97.5	97.1	95.6	95.6	95.5	95.3	97.3	97.4	95.2	100	71.2	71.0	71.1	70.9	71.1	70.8	70.8	70.7	70.6	70.9	71.0	70.8
	2	99.2		98.7	96.9	96.9	96.8	96.6	97.3	97.4	96.5	97.5	71.3	71.0	71.0	70.9	71.1	70.9	70.7	70.6	70.6	71.1	71.1	70.8
	3	99.2	99.6		97.1	97.1	97.0	96.7	97.0	97.0	96.8	97.1	71.3	71.1	71.1	71.0	71.2	71.0	70.6	70.8	70.8	71.2	71.1	71.0
	4	98.5	98.8	99.2		100	99.8	99.3	95.1	95.3	99.4	95.6	71.2	71.2	71.3	71.2	71.4	70.7	70.7	70.5	70.7	71.3	71.1	70.7
	5	98.5	98.8	99.2	100		99.8	99.3	95.1	95.3	99.4	95.6	71.2	71.2	71.3	71.2	71.4	70.7	70.7	70.5	70.7	71.3	71.1	70.7
	6	98.5	98.8	99.2	100	100		99.2	95.0	95.2	99.3	95.5	71.2	71.3	71.4	71.2	71.4	70.8	70.8	70.6	70.8	71.4	71.1	70.8
	7	98.5	98.8	99.2	100	100	100		94.8	95.0	99.2	95.3	71.1	71.1	71.2	71.1	71.2	70.5	70.6	70.5	70.6	71.2	70.9	70.5
	8	99.0	98.7	98.7	97.9	97.9	97.9	97.9		99.8	95.0	97.3	71.5	71.2	71.2	71.1	71.2	71.1	70.9	70.8	70.8	71.2	71.2	71.0
	9	99.2	98.8	98.8	98.1	98.1	98.1	98.1	99.8		95.2	97.4	71.7	71.3	71.3	71.2	71.4	71.2	71.0	70.9	70.9	71.4	71.4	71.1
	10	98.3	98.7	99.0	99.8	99.8	99.8	99.8	98.1	98.3		95.2	71.0	71.1	71.1	71.0	71.2	70.5	70.5	70.3	70.5	71.1	70.9	70.5
	11	100	99.2	99.2	98.5	98.5	98.5	98.5	99.0	99.2	98.3		71.2	71.0	71.1	70.9	71.1	70.8	70.8	70.7	70.6	70.9	71.0	70.8
	12	84.3	84.1	83.9	83.9	83.9	83.9	83.9	84.1	84.3	83.7	84.3		97.7	97.6	97.7	97.5	98.2	94.9	96.7	97.1	97.6	98.5	96.8
	13	84.5	84.3	84.1	84.1	84.1	84.1	84.1	84.3	84.5	83.9	84.5	99.2		99.8	99.7	99.5	96.6	93.6	95.0	95.6	99.2	97.8	95.2
	14	84.6	84.5	84.3	84.3	84.3	84.3	84.3	84.5	84.6	84.1	84.6	99.2	99.6		99.7	99.5	96.5	93.5	95.0	95.5	99.2	97.7	95.1
	15	84.5	84.3	84.1	84.1	84.1	84.1	84.1	84.3	84.5	83.9	84.5	99.4	99.4	99.4		99.6	96.7	93.7	95.1	95.6	99.3	97.9	95.2
	16	84.8	84.6	84.5	84.5	84.5	84.5	84.5	84.6	84.8	84.3	84.8	99.4	99.4	99.4	99.6		96.4	93.4	94.9	95.4	99.1	97.6	95.0
	17	84.1	84.1	83.9	83.9	83.9	83.9	83.9	83.9	84.1	83.7	84.1	99.6	98.9	98.9	99.0	99.0		94.4	97.5	97.8	96.5	97.1	97.5
	18	84.1	83.9	83.7	83.7	83.7	83.7	83.7	83.9	84.1	83.6	84.1	99.0	98.3	98.3	98.5	98.5	99.0		93.2	93.2	93.5	94.1	93.2
	19	83.9	83.9	83.7	83.7	83.7	83.7	83.7	83.7	83.9	83.6	83.9	98.9	98.1	98.1	98.3	98.3	99.2	98.3		99.2	94.9	95.6	99.1

Suppl. Table 4. Estimates of the evolutionary distances among APMV-6s, inferred from the nearly complete nucleotide sequence of the F gene.

The number of base substitutions (per site) between sequences is shown below the diagonal. Standard error estimate(s) are shown above the diagonal.

		Standard error estimate(s)																						
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
No. of base substitutions per site in sequence	1		0.007	0.007	0.011	0.011	0.011	0.012	0.007	0.007	0.012	0.000	0.385	0.395	0.396	0.397	0.393	0.396	0.395	0.402	0.398	0.398	0.391	0.393
	2	0.025		0.004	0.008	0.008	0.008	0.008	0.007	0.007	0.008	0.007	0.385	0.395	0.395	0.397	0.392	0.396	0.398	0.405	0.400	0.393	0.391	0.395
	3	0.029	0.012		0.007	0.007	0.007	0.008	0.008	0.008	0.008	0.007	0.386	0.395	0.395	0.396	0.392	0.393	0.403	0.400	0.395	0.393	0.392	0.390
	4	0.046	0.032	0.029		0.000	0.001	0.002	0.012	0.012	0.002	0.011	0.385	0.390	0.390	0.392	0.387	0.397	0.395	0.403	0.394	0.390	0.389	0.393
	5	0.046	0.032	0.029	0.000		0.001	0.002	0.012	0.012	0.002	0.011	0.385	0.390	0.390	0.392	0.387	0.397	0.395	0.403	0.394	0.390	0.389	0.393
	6	0.047	0.033	0.030	0.001	0.001		0.002	0.012	0.012	0.002	0.011	0.384	0.389	0.389	0.391	0.387	0.396	0.395	0.402	0.394	0.389	0.389	0.392
	7	0.049	0.035	0.034	0.006	0.006	0.007		0.013	0.012	0.003	0.012	0.388	0.393	0.394	0.395	0.391	0.401	0.399	0.405	0.398	0.393	0.393	0.397
	8	0.027	0.027	0.031	0.051	0.051	0.053	0.055		0.001	0.012	0.007	0.372	0.384	0.384	0.386	0.381	0.383	0.388	0.391	0.386	0.382	0.380	0.382
	9	0.027	0.026	0.030	0.049	0.049	0.051	0.053	0.002		0.012	0.007	0.370	0.381	0.381	0.383	0.379	0.381	0.386	0.389	0.384	0.379	0.377	0.380
	10	0.050	0.036	0.033	0.006	0.006	0.007	0.008	0.053	0.051		0.012	0.389	0.394	0.394	0.396	0.392	0.402	0.400	0.407	0.398	0.394	0.393	0.398
	11	0.000	0.025	0.029	0.046	0.046	0.047	0.049	0.027	0.027	0.050		0.385	0.395	0.396	0.397	0.393	0.396	0.395	0.402	0.398	0.398	0.391	0.393
	12	0.472	0.470	0.470	0.473	0.473	0.471	0.475	0.462	0.459	0.476	0.472		0.006	0.006	0.006	0.007	0.005	0.013	0.008	0.007	0.007	0.004	0.008
	13	0.479	0.478	0.475	0.473	0.473	0.471	0.476	0.472	0.469	0.476	0.479	0.024		0.001	0.001	0.002	0.009	0.016	0.012	0.011	0.003	0.006	0.012
	14	0.477	0.478	0.475	0.471	0.471	0.469	0.474	0.471	0.468	0.474	0.477	0.025	0.001		0.001	0.002	0.009	0.016	0.012	0.011	0.003	0.006	0.012
	15	0.479	0.480	0.478	0.473	0.473	0.472	0.476	0.474	0.471	0.477	0.479	0.023	0.002	0.002		0.002	0.008	0.016	0.012	0.011	0.002	0.006	0.012
	16	0.475	0.475	0.473	0.469	0.469	0.467	0.471	0.469	0.466	0.472	0.475	0.026	0.005	0.005	0.004		0.009	0.017	0.013	0.011	0.003	0.006	0.012
	17	0.481	0.479	0.476	0.484	0.484	0.482	0.488	0.471	0.469	0.489	0.481	0.018	0.035	0.036	0.034	0.037		0.014	0.006	0.006	0.009	0.007	0.006
	18	0.483	0.484	0.487	0.485	0.485	0.483	0.487	0.478	0.475	0.488	0.483	0.053	0.069	0.069	0.068	0.071	0.060		0.017	0.017	0.017	0.015	0.017

19	0.485	0.487	0.482	0.489	0.489	0.487	0.490	0.479	0.477	0.494	0.485	0.034	0.052	0.052	0.051	0.054	0.025	0.074	0.002	0.012	0.011	0.003
20	0.485	0.486	0.480	0.483	0.483	0.482	0.486	0.478	0.475	0.487	0.485	0.029	0.046	0.046	0.045	0.048	0.022	0.073	0.008	0.011	0.010	0.003
21	0.481	0.476	0.473	0.471	0.471	0.469	0.473	0.470	0.467	0.474	0.481	0.025	0.008	0.008	0.007	0.009	0.036	0.070	0.053	0.047	0.006	0.012
22	0.478	0.476	0.476	0.476	0.476	0.475	0.479	0.470	0.467	0.480	0.478	0.015	0.023	0.023	0.022	0.025	0.030	0.063	0.046	0.040	0.024	0.011
23	0.481	0.482	0.476	0.483	0.483	0.482	0.488	0.474	0.471	0.488	0.481	0.032	0.050	0.051	0.050	0.052	0.025	0.073	0.009	0.008	0.052	0.044

1, Eurasian wigeon/KR/KNU13/2010; 2, Duck/Italy/4524-2/2007; 3, Red-necked stint/Japan/8KS0813/2008; 4, Wild bird/KR/KNU57/2013; 5, Wild bird/KR/KNU58/2013; 6, Wild bird/KR/KNU59/2013; 7, Eurasian wigeon/KR/KNU60/2013; 8, Wild duck/KR/KNU61/2013; 9, Eurasian wigeon/KR/KNU62/2013; 10, Eurasian wigeon/KR/KNU63/2014; 11, Eurasian wigeon/KR/KNU14/2010; 12, Duck/Taiwan/Y1/1998; 13, Mallard/Jilin/190/2011; 14, Mallard/Jilin/127/2011; 15, Mallard/KR/KNU22/2011; 16, Mallard/KR/KNU26/2011; 17, Goose/FE/4440/2003; 18, Duck/HK/18/1977; 19, Duck/IT/4526/2007; 20, Teal/IT/6895-1/2007; 21, Red-crested pochard/Balkhash/5842/2013; 22, Teal/Novosibirsk/455/2009; 23, Mallard/BE/12245/2007.