Supporting Information

Woo et al. 10.1073/pnas.1119972109

Table S1. Pairwise amino acid identities of predicted gene products of FmoPV compared with other paramyxoviruses

	Percentage of amino acid sequence identity																	
	N			P			M			F			A			L		
Paramyxovirus	761U	776U	M252A	761U	776U	M252A	761U	776U	M252A	761U	776U	M252A	761U	776U	M252A	761U	776U	M252A
Morbillivirus																		
FmoPV 761U	—	99.2	96.0	—	97.4	89.2	—	98.8	95.8	—	98.9	96.3	—	99.0	96.3	—	99.4	97.0
FmoPV 776U	99.2	—	96.1	97.4	—	88.6	98.8	—	96.4	98.9	—	95.9	99.0	—	95.3	99.4	—	97.3
FmoPV M252A	96.0	96.1	—	89.2	88.6	—	95.8	96.4	—	96.3	95.9	—	96.3	95.3	—	97.0	97.3	—
CdiPV	56.8	56.5	56.2	29.7	29.3	27.5	58.8	58.5	58.8	36.0	35.8	36.1	20.4	20.6	20.6	55.5	55.4	55.4
DmoPV	54.5	54.3	55.0	26.4	25.8	25.6	59.3	59.6	59.5	43.0	42.2	42.4	24.1	24.1	23.9	56.4	56.4	56.5
MeaPV	55.4	55.2	54.6	29.0	28.8	27.8	60.0	59.7	59.0	44.0	44.0	43.9	20.7	20.9	20.7	56.0	55.9	55.8
PprPV	55.6	55.8	55.8	31.6	31.7	31.6	58.2	58.5	58.8	42.8	42.8	43.2	21.6	21.8	21.6	57.3	57.3	57.2
RinPV	55.5	55.5	55.6	28.4	28.4	26.8	59.5	59.2	58.2	44.6	44.3	45.1	21	21.1	22.4	55.4	55.3	55.2
PdiPV	56.6	56.2	56.2	30.6	30.4	28.8	57.9	57.9	57.6	42.7	42.9	42.9	20.6	20.8	20.9	55.4	55.4	55.7
Avulavirus																		
AviPV-6	29.1	29.3	28.1	18.3	17.9	18.6	23.5	23.5	22.9	26.8	27.0	26.6	17.7	17.6	17.3	28.5	28.6	29.1
NdiPV	27.1	27.1	28.0	19.8	18.8	18.1	19.5	20.0	20.9	25.8	25.8	25.4	17.5	17.2	16.2	27.7	27.5	27.6
Henipavirus																		
HenPV	33.6	33.2	32.8	21.1	22.2	23.3	43.9	44.2	44.2	32.4	32.6	33.0	17.8	17.8	18.9	43.4	43.4	43.4
NipPV	33.8	33.4	33.0	22.4	21.8	22.8	43.1	43.3	43.4	33.0	33.2	33.3	18.2	18.2	18.9	44.9	44.8	45.2
Respirovirus																		
BpiPV-3	25.7	25.9	25.4	18.0	18.7	19.2	33.9	33.6	34.2	28.5	28.2	28.5	18.9	18.9	18.2	38.4	38.6	38.9
SenPV	24.2	25.2	25.0	19.0	18.5	20.5	34.7	34.7	34.4	27.1	26.5	26.5	20.5	20.3	21.1	39.1	39.3	39.4
Rubulavirus																		
HpiPV-2	27.5	27.7	27.9	19.4	19.6	16.8	22.8	23.1	21.8	25.0	24.4	25.0	18.0	18.0	18.3	30.4	30.2	30.2
MumPV	27.6	27.8	27.7	19.6	19.9	17.2	20.4	20.0	20.7	26.4	26.2	25.7	18.1	17.8	18.7	30.0	30.1	29.9
Unclassified *Paramyxovirinae*																		
AsaPV	29.8	29.8	28.4	16.4	17.2	17.1	34.7	34.7	34.7	30.9	30.6	30.8	20.1	20.1	19.0	40.0	40.1	40.4
TlmPV	35.7	36.4	36.0	22.7	22.7	23.0	48.0	48.3	48.8	32.7	32.9	33.0	16.1	15.8	16.6	46.4	46.4	46.4
BeiPV	36.6	36.2	36.3	23.5	23.3	23.9	47.4	47.7	48.5	32.9	32.7	32.7	16.1	15.8	15.8	46.3	46.3	46.6
FdlPV	28.4	28.4	28.5	19.9	21.1	20.8	34.9	34.5	33.9	29.0	29.2	29.7	19.9	19.9	19.2	40.0	40.0	39.7
JPV	34.0	34.0	34.0	23.1	23.3	22.3	47.8	48.1	48.4	31.8	31.8	32.9	14.8	15.0	14.4	46.9	46.9	47.2
MosPV	38.6	38.6	37.6	22.9	22.9	22.0	47.5	48.2	46.9	36.3	36.3	35.8	19.0	19.2	19.9	48.6	48.8	48.8
TupPV	33.4	32.7	32.1	23.2	23.2	23.9	43.9	43.2	42.5	35.0	35.4	35.0	14.7	14.4	15.6	47.3	47.2	47.1
NarPV	37.2	36.9	38.1	22.7	23.8	22.6	51.5	51.5	50.6	33.0	32.5	32.6	18.6	18.4	18.7	47.7	48.0	47.9

Table S2. Molecular features and predicted gene products of FmoPV and other morbilliviruses

	mRNA features, nt						Deduced protein			
Virus/gene	Total length	5′ UTR	ORF	3′ UTR	Hexamer phase	Intergenic regions, nt	Size, aa	MW, kDa	pI	Coding frame
FmoPV 761U										
Leader	55	—	—	—	—	(TTT)	—	—	—	—
N	1,659	52	1,560	47	2	CTT	519	57.01	5.27	3
P/V/C(P)	1,637	63	1,476	98	2	CTT	491	53.12	5.20	2
P/V/C(V)	1,638	63	831	744	2	CTT	276	29.97	4.85	2
P/V/C(C)	1,637	94	513	1,030	2	CTT	170	19.90	9.69	3
M	1,378	31	1,014	333	4	CTA	337	38.05	9.29	2
F	2,191	215	1,632	344	5	CTT	543	60.26	8.80	1
H	1,934	30	1,788	116	3	CTT	595	68.11	6.25	3
L	6,781	22	6,609	150	2	(CTT)	2,202	252.87	8.32	3
Trailer	400	—	—	—	—	—	—	—	—	—
FmoPV 776U										
Leader	55	—	—	—	—	(TTT)	—	—	—	—
N	1,659	52	1,560	47	2	CTT	519	57.06	5.15	3
P/V/C(P)	1,637	63	1,476	98	2	CTT	491	53.19	5.33	2
P/V/C(V)	1,638	63	831	744	2	CTT	276	29.99	4.91	2
P/V/C(C)	1,637	94	513	1030	2	CTT	170	19.87	9.69	3
M	1,378	31	1,014	333	4	CTA	337	38.02	9.29	2
F	2,191	215	1,632	344	5	CTT	543	60.21	8.79	1
H	1,934	30	1,788	116	3	CTT	595	68.24	6.03	3
L	6,781	22	6,609	150	2	(CTT)	2,202	253.01	8.23	3
Trailer	400	—	—	—	—	—	—	—	—	—
FmoPV M252A										
Leader	55	—	—	—	—	(TTT)	—	—	—	—
N	1,659	52	1,560	47	2	CTT	519	57.08	5.34	3
P/V/C(P)	1,637	63	1,476	98	2	CTT	491	53.41	5.44	2
P/V/C(V)	1,638	63	831	744	2	CTT	276	29.94	5.13	2
P/V/C(C)	1,637	94	513	1030	2	CTT	170	19.86	9.69	3
M	1,378	31	1,014	333	4	CTA	337	38.06	9.29	2
F	2,191	215	1,632	344	5	CTT	543	60.19	8.80	1
H	1934	30	1,788	116	3	CTT	595	68.18	6.25	3
L	6,781	22	6,609	150	2	(CTT)	2,202	252.91	8.28	3
Trailer	400	—	—	—	—	—	—	—	—	—
MeaPV										
Leader	55	—	—	—	—	(CTT)	—	—	—	—
N	1,689	52	1,578	59	2	CTT	525	58.02	5.11	3
P/V/C(P)	1,655	59	1,524	72	2	CTT	507	53.90	4.99	1
P/V/C(V)	1,656	59	900	697	2	CTT	299	31.85	4.66	1
P/V/C(C)	1,655	81	561	1013	2	CTT	186	21.11	10.36	2
M	1,466	32	1,008	426	4	CTT	335	37.71	9.07	3
F	2,373	583	1,653	137	3	CTT	550	59.53	8.78	1
H	1,958	20	1,854	84	3	CGT	617	69.17	7.88	2
L	6,643	22	6,552	69	2	(CTT)	2,183	247.74	8.43	3
Trailer	40	—	—	—	—	—	—	—	—	—
CdiPV										
Leader	55	—	—	—	—	(CTT)	—	—	—	—
N	1,683	52	1,572	59	2	CTT	523	58.14	5.20	3
P/V/C(P)	1,655	59	1,524	72	2	CTT	507	54.75	5.03	1
P/V/C(V)	1,656	59	900	697	2	CTT	299	33.11	4.66	1
P/V/C(C)	1,655	81	525	1049	2	CTT	174	20.26	10.30	2
M	1,447	32	1,008	407	4	CTT	335	37.77	8.87	3
F	2,206	85	1,989	132	2	CTT	662	72.95	9.18	3
H	1,946	20	1,815	111	3	CTA	604	67.99	6.74	2
L	6,642	22	6,555	65	2	(CAA)	2,184	248.19	8.39	3
Trailer	41	—	—	—	—	—	—	—	—	—
DmoPV										
Leader	55	—	—	—	—	(CTT)	—	—	—	—
N	1,683	52	1,572	59	2	CTT	523	57.49	5.14	3
P/V/C(P)	1,655	59	1,521	75	2	CTT	506	55.26	5.09	1
P/V/C(V)	1,656	59	912	685	2	CTT	303	33.69	4.75	1

Table S2. Cont.

	mRNA features, nt						Deduced protein			
Virus/gene	Total length	5′ UTR	ORF	3′ UTR	Hexamer phase	Intergenic regions, nt	Size, aa	MW, kDa	pI	Coding frame
P/V/C(C)	1,655	81	534	1040	2	CTT	177	20.41	10.19	2
M	1,453	32	1,008	413	4	CTT	335	37.97	8.97	3
F	2,212	421	1,659	132	2	CTT	552	59.87	8.81	3
H	1,946	20	1,815	111	3	CTT	604	68.04	6.18	2
L	6,643	22	6,552	69	2	(CAA)	2,183	248.07	8.52	3
Trailer	40	—	—	—	—	—	—	—	—	—
PprPV										
Leader	55	—	—	—	—	(CTT)	—	—	—	—
N	1,689	52	1,578	59	2	CTT	525	57.78	5.21	3
P/V/C(P)	1,655	59	1,530	66	2	CTT	509	54.79	5.14	1
P/V/C(V)	1,656	59	897	700	2	CTT	298	31.34	4.58	1
P/V/C(C)	1,655	81	534	1040	2	CTT	177	19.93	9.92	2
M	1,483	32	1,008	443	4	CTT	335	37.95	8.97	3
F	2,411	634	1,641	136	2	CTT	546	59.12	8.71	3
H	1,957	20	1,830	107	4	CTT	609	68.76	6.64	3
L	6,643	22	6,552	69	2	(CTA)	2,183	247.27	7.73	3
Trailer	40	—	—	—	—	—	—	—	—	—
RinPV										
Leader	55	—	—	—	—	(CTT)	—	—	—	—
N	1,689	52	1,578	59	2	CTT	525	58.04	5.08	3
P/V/C(P)	1,655	59	1,524	72	2	CTT	507	54.36	4.82	1
P/V/C(V)	1,656	59	900	697	2	CTT	299	32.57	4.56	1
P/V/C(C)	1,655	81	534	1040	2	CTT	177	19.93	10.29	2
M	1,460	32	1,008	420	4	CTT	335	37.54	9.15	3
F	2,367	589	1,641	137	3	CTT	546	58.73	8.43	1
H	1,958	20	1,830	108	3	CGT	609	67.90	6.61	2
L	6,643	22	6,552	69	2	(CTT)	2,183	248.21	8.48	3
Trailer	40	—	—	—	—	—	—	—	—	—

Table S3. FmoPV viral load and antibody level of RT-PCR positive stray cats in this study

Cat no.	Date of sample collection	Type of positive sample(s)	FmoPV	
			Viral load, copies/mL	Western blot
543	14 May 2009	Urine	1.4×10^4	+
545	14 May 2009	Fecal swab	3.8×10^5	–
557	12 June 2009	Urine	9.5×10^2	+
572	24 June 2009	Urine	1.2×10	+
587	2 July 2009	Urine	4.88	++
591	8 July 2009	Urine	2.7×10^4	+++
592	8 July 2009	Urine	3.0×10^3	+++
670	27 Aug 2009	Urine	2.7×10^3	+
680	31 Aug 2009	Urine	8.8×10^3	+++
688	3 Sep 2009	Urine	7.1×10^3	+++
725	3 Nov 2009	Fecal swab	2.7×10^3	++
761	24 Nov 2009	Urine	5.9×10^5	+++
773	1 Dec 2009	Urine	6.4×10^4	+
776	4 Dec 2009	Urine	2.3×10^3	+++
802	24 Dec 2009	Urine	2.76	–
810	29 Dec 2009	Urine	1.6×10^2	–
818	12 Jan 2010	Urine	1.06	–
835	22 Jan 2010	Urine	2.4×10^4	+
850	29 Jan 2010	Urine	2.1×10^4	++
851	29 Jan 2010	Urine	2.6	++
		Fecal swab	5.0×10^2	
858	26 Feb 2010	Urine	6.9×10^4	+
898	23 Mar 2010	Urine	2.4×10^4	+
900	23 Mar 2010	Urine	1.6×10^4	+
906	23 Mar 2010	Urine	9.8×10^3	++
		Fecal swab	2.0×10^4	
908	25 Mar 2010	Urine	8.8×10^2	+
909	25 Mar 2010	Urine	2.6×10^3	–
938	29 Apr 2010	Urine	2.1×10^2	++
962	6 May 2010	Urine	8.0×10^3	+++
968	10 May 2010	Urine	4.7×10^2	+++
970	10 May 2010	Blood	3.1×10^4	+++
979	17 May 2010	Urine	5.3×10^3	+++
990	24 May 2010	Urine	1.4×10^3	++
997	31 May 2010	Urine	5.0×10^3	++
1012	10 June 2010	Urine	9.5×10^3	+
1036	28 June 2010	Urine	1.6×10^4	++
1055	2 Aug 2010	Urine	1.0×10^3	+
1057	2 Aug 2010	Urine	9.7×10^3	++
1078	9 Sep 2010	Urine	2.0×10^5	+
1091	24 Sep 2010	Urine	7.0×10^3	+
1096	27 Sep 2010	Urine	2.0×10^1	+++
1107	7 Oct 2010	Urine	4.6×10^3	++
1148	25 Oct 2010	Urine	1.4×10^5	++
1155	28 Oct 2010	Urine	3.2×10^{-1}	+
1189	25 Nov 2010	Urine	6.9×10^3	+
1226	6 Jan 2011	Urine	3.7×10^{-2}	+++
1297	28 Feb 2011	Urine	2.7×10^2	+
1312	9 Mar 2011	Urine	3.8	++
1314	9 Mar 2011	Urine	1.6×10^3	–
1325	14 Mar 2011	Urine	2.3×10^3	++
1327	24 Mar 2011	Urine	3.7×10^4	+
1336	31 Mar 2011	Urine	5.4×10^5	++
1357	28 Apr 2011	Urine	1.0×10^2	++
1359	28 Apr 2011	Urine	2.0×10^5	+
1392	30 May 2011	Urine	5.2×10^4	–
1407	13 June 2011	Urine	3.5×10	++
1409	16 June 2011	Urine	1.4×10^6	+

Table S4. Association between TIN and evidence of FmoPV infection

		Evidence of FmoPV infection							
			Antibody response						
				IF (IgG) with serum dilution					
Sample no.	TIN	Urine RT-PCR	Western blot	1:10	1:40	1:160	1:640	1:2,560	1:10,240
1357	+	+	++	+	+	+	+	–	–
1359	+	+	+	+	+	+	–	–	–
1363	–	–	+	–	–	–	–	–	–
1364	–	–	–	–	–	–	–	–	–
1365	–	–	+	–	–	–	–	–	–
1366	+	–	–	–	–	–	–	–	–
1367	–	–	–	–	–	–	–	–	–
1368	–	–	–	–	–	–	–	–	–
1391	–	–	–	–	–	–	–	–	–
1392	+	+	–	+	+	–	–	–	–
1393	+	–	+	+	+	–	–	–	–
1394	–	–	–	–	–	–	–	–	–
1395	–	–	–	–	–	–	–	–	–
1396	–	–	–	–	–	–	–	–	–
1397	–	–	++	+	+	–	–	–	–
1402	–	–	+	–	–	–	–	–	–
1403	–	–	+	–	–	–	–	–	–
1404	–	–	–	–	–	–	–	–	–
1405	–	–	–	–	–	–	–	–	–
1406	–	–	–	–	–	–	–	–	–
1407	+	+	++	+	+	+	–	–	–
1408	+	–	–	–	–	–	–	–	–
1409	+	+	+	+	+	+	–	–	–
1417	+	–	+	–	–	–	–	–	–
1418	–	–	–	–	–	–	–	–	–
1419	–	–	–	–	–	–	–	–	–
1420	–	–	–	–	–	–	–	–	–

Table S5. Viruses and GenBank accession numbers

Abbreviation	Virus name	GenBank accession no.
AsaPV	Atlantic Salmon paramyxovirus	EU156171
AviPV-5	Avian paramyxovirus 5	GU206351
AviPV-6	Avian paramyxovirus 6	NC_003043
AviPV-7	Avian paramyxovirus 7	FJ231524
BeiPV	Beilong virus	NC_007803
BpiPV-3	Bovine parainfluenza virus 3	NC_002161
CdiPV	Canine distemper virus	NC_001921
DmoPV	Dolphin morbillivirus	NC_005283
FdlPV	Fer-de-lance virus	NC_005084
FmoPV 761U	Feline morbillivirus strain 761U	JQ411014
FmoPV 776U	Feline morbillivirus strain 776U	JQ411015
FmoPV M252A	Feline morbillivirus strain M252A	JQ411016
GooPV	Goose paramyxovirus SF02	NC_005036
HenPV	Hendra virus	NC_001906
HpiPV-1	Human parainfluenza virus 1	NC_003461
HpiPV-2	Human parainfluenza virus 2	NC_003443
HpiPV-3	Human parainfluenza virus 3	NC_001796
HpiPV-4a	Human parainfluenza virus 4a	BAJ11741
HuRSV	Human respiratory syncytial virus	NC_001781
JPV	J-virus	NC_007454
MeaPV	Measles virus	NC_001498
MosPV	Mossman virus	NC_005339
MumPV	Mumps virus	NC_002200
NarPV	Nariva virus	FJ362497
NdiPV	Newcastle disease virus	NC_002617
NipPV	Nipah virus	NC_002728
PdiPV	Phocine distemper virus	P35944, P35939, BAA01205, BAA01206, CAA12080, CAA70843
PprPV	Peste-des-petits-ruminants virus	NC_006383
RinPV	Rinderpest virus	NC_006396
SenPV	Sendai virus	NC_001552
SpiPV-3	Swine parainfluenza virus 3	EU439429
ThkPV-1	Tuhoko virus 1	GU128080
ThkPV-2	Tuhoko virus 2	GU128081
ThkPV-3	Tuhoko virus 3	GU128082
TlmPV	Tailam virus	JN689227
TupPV	Tupaia paramyxovirus	NC_002199

Fig. S1 shows phylogenetic analysis of amino acid sequences of 72-bp fragment of L gene of paramyxoviruses identified from cats in the present study.

Fig. S1. Phylogenetic analysis of amino acid sequences of 72-bp fragment of L gene of paramyxoviruses identified from cats in the present study. The tree was constructed by neighbor-joining method. The scale bar indicates the branch length that corresponds to 2 amino acid differences per sequence. The three strains from stray cats numbered 761U, 776U, and M252A with genome sequences determined are shown in bold. RSV, respiratory syncitial virus (U39661); DmoPV, dolphin morbillivirus (NC_005283); PprPV, Peste-des-petits ruminants virus (NC_006383); MeaPV, measles virus (NC_001498); CdiPV, canine distemper virus (NC_001921); MosPV, Mossman virus (NC_005339); NarPV, Nariva virus (FJ362497); ThkPV3, Tuhoko virus 3 (GU128082); ThkPV2, Tuhoko virus 2 (GU128081); ThkPV, Tuhoko virus 1 (GU128080); JPV, J-virus (NC_007454); BeiPV, Beilong virus (NC_007803); NipPV, Nipah virus (NC_002728); HenPV, Hendra virus (NC_001906); FdlPV, Fer-de-lance virus (NC_005084); SenPV, Sendai virus (NC_001552); HpiPV-1, human parainfluenza virus 1 (NC_003461).

Fig. S1

Fig. S2. 5′ Trailer sequences and ends of L genes in the genomes of the three strains of FmoPV (400 nt in all three genomes), two strains of avian paramyxovirus 3 (681 and 707 nt), and one strain each of avian paramyxovirus 5 (552 nt) and Tupaia paramyxovirus (590 nt). The ruler above the sequences shows the nucleotide positions in the 5′ trailer sequences.

Fig. S2

Fig. S3. Polymorphic nucleotide sites in the genes among the three FmoPV genomes. All polymorphic nucleotide sites are highlighted in yellow and all polymorphic nucleotide sites and their codons resulting in amino acid changes are highlighted in rectangles.

Fig. S3

Fig. S4. Multiple alignments of N proteins of FmoPV and other morbilliviruses. The conserved MA(S,T)L motif in morbilliviruses and the three conserved motifs in paramyxoviruses are marked in open boxes and reported consensus sequences are indicated above the alignment (where x represents any amino acid residue and Ø represents an aromatic amino acid residue). Amino acid residue numbers for each protein are shown to the right of each sequence. Dots indicate identical residues and dashes indicate gaps. The nuclear export signals are highlighted in yellow and the NLS highlighted in green.

Fig. S4

Fig. S5. Western blot analysis with stray cat sera against the purified $(His)_6$-tagged recombinant FmoPV N protein antigen. Prominent immunoreactive protein bands of approximately 69 kDa, consistent with the expected size of 68.7 kDa of the recombinant protein, were detected in three of the six cat serum samples shown, indicating antigen–antibody interactions between the recombinant FmoPV N protein and serum antibodies. Results of RT-PCR of the corresponding urine samples for FmoPV are also shown.

Fig. S5

Fig. S6. Representative images of cauxin-immunohistochemical stained paraffin-embedded renal sections of cats with and without histological evidence of tubulointerstitial nephritis (TIN). (*A*) In cats without histological evidence of TIN, cauxin-positive proximal straight renal tubules are observed between the inner cortex and outer medulla; (*B*) in cats with histological evidence of TIN, the number of cauxin-positive tubules is significant reduced compared with cats without histological evidence of TIN.

Fig. S6

Fig. S7. Double staining of the lymph node of an FmoPV infected stray cat for (*A*) mouse anti-human myeloid/histocyte antigen and then labeled with Texas red-conjugated goat anti-mouse IgG and (*B*) guinea pig antiserum against the N protein of FmoPV, followed by FITC-conjugated rabbit anti-guinea pig IgG. (*C*) Merged photo shows yellow, indicating that both antigens colocalized in cytoplasm of the cells.

Fig. S7

Fig. S8. Recombination analysis of the three complete genomes of FmoPV (761U, 776U, and M252A) using Recombination Analysis Tool (RAT), indicating that no evidence of recombination was observed among the three strains of FmoPV. The *y* axis represents the similarity between the test sequence (*A*, 761U; *B*, 776U; *C*, M252A) and other sequences. The *x* axis represents the location on the sequence. Default parameters were used and Auto Search was performed to search for possible recombination events.

Fig. S8