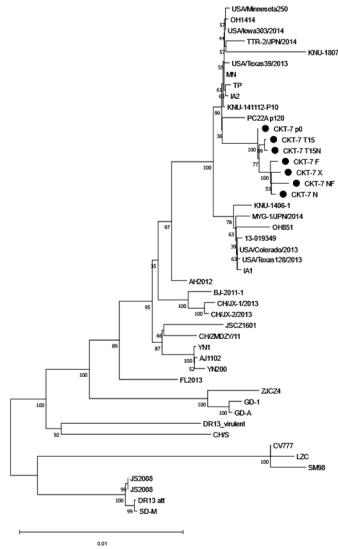
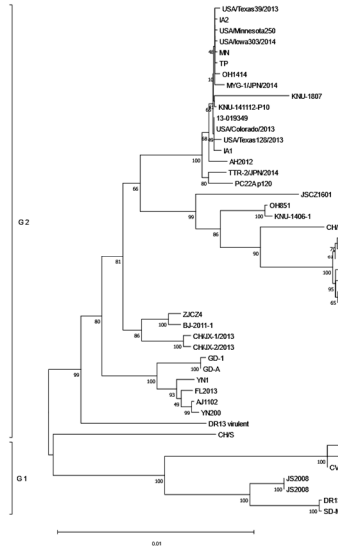


Supplementary Materials

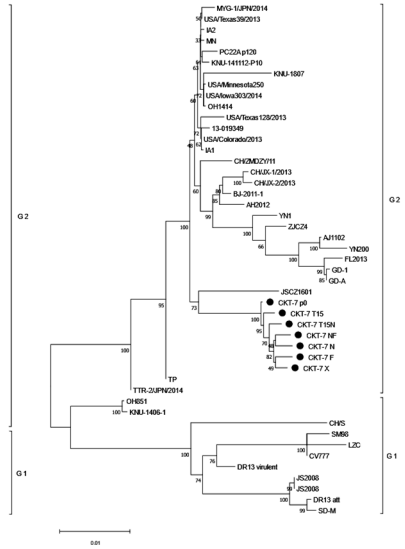
(A) ORF 1a



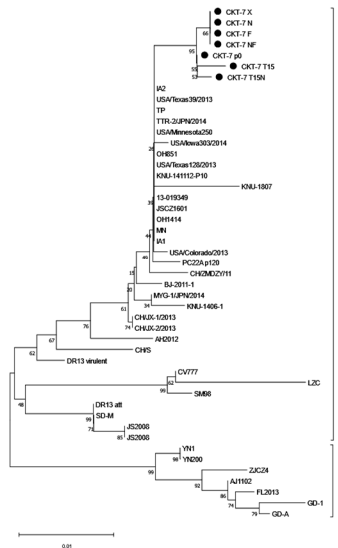
(B) ORF 1b



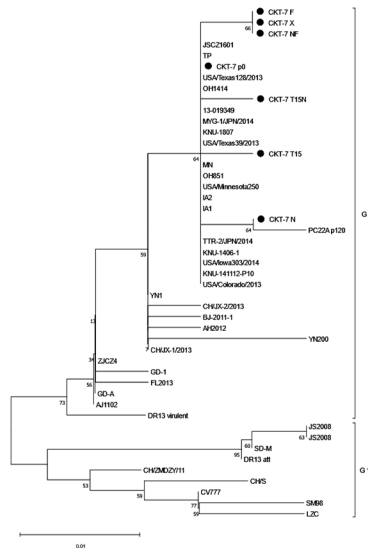
(C) Spike



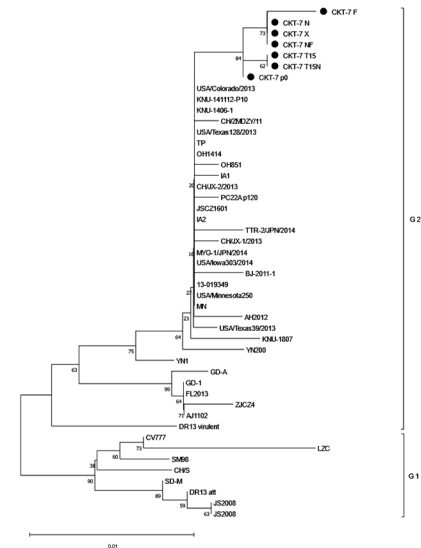
(D) ORF 3



(E) Envelope



(F) Membrane



Phylogenetic tree of the Cxorf11 gene region. The tree shows relationships between various sequences, with bootstrap values indicated at the nodes. A scale bar of 0.04 is provided at the bottom left. A bracket on the right side groups several sequences together, labeled 'G1'.

Legend:

- Cxorf11 T15
- Cxorf11 X
- Cxorf11 NF
- Cxorf11 N
- Cxorf11 F
- Cxorf11 T15N
- Cxorf11 p6

Sequences and Bootstrap Values:

- JA1
- NI1
- TP
- USA/Texas/29/2013
- JA2
- GD-A
- USA/Israel/12/2013
- KNU3.141112.F10
- PC204-120
- USA/Columbia/2013
- USA/Mexico/250
- KNU3.1887
- CH1414
- MYG-1/UPN/2014
- 13-01909
- CH161
- 61 KNU3.1406-1
- TIR-2/UPN/2014
- 61 USA/New/20/2014
- BA-2011-1
- AV012
- NI1
- YIN20
- CH12/MZ/111
- JSC29801
- CH16A-1/2013
- 100 CH16A-3/2013
- DR13 isolate
- GD-A
- A1102
- FL2613
- GD-1
- ZC24
- SM6
- 100 CVT7
- L2C
- CH15
- DR13.at
- SD-M
- 12 ZC2000
- 12 ZC2000

Scale bar: 0.04

Group G1: CH16A-1/2013, CH16A-3/2013, CH15, DR13.at, SD-M, ZC2000, ZC2000

Figure S1. Analysis of phylogenetic relationship based on the nucleotide sequence of the ORF1a, ORF1b, spike (S), ORF3, envelope (E), membrane (M), and N genes. Phylogenetic tree of (A) the ORF1a gene; (B) the ORF1b gene; (C) the S gene; (D) the ORF3 gene; (E) the E gene; (F) the M gene; (G) the N gene. The trees were determined using the neighbor-joining method of MEGA X software. The bootstrap analysis was generated using 1000 replicates.

Table S1. Analysis of genomic alteration depend on strains

Gene	Nucleotide	Amino-acid position	PEDV strains						
			Parental	T15	T15N	N	NF	F	X
ORF 1a/b	4-6	2	GCT (A)	GCT (A)	GCT (A)	GCT (A)	--- (-)	GCT (A)	GCT (A)
	7-9	3	AGC (S)	AGC (S)	AGC (S)	AGC (S)	--- (-)	AGC (S)	AGC (S)
	10-12	4	AAC (N)	AAC (N)	AAC (N)	AAC (N)	--- (-)	AAC (N)	AAC (N)
	13-15	5	CAT (H)	CAT (H)	CAT (H)	CAT (H)	--- (-)	CAT (H)	CAT (H)
	16-18	6	GTT (V)	GTT (V)	GTT (V)	GTT (V)	TTA (L)	GTT (V)	GTT (V)
	19-21	7	ACA (T)	ACA (T)	ACA (T)	ACA (T)	CAT (H)	ACA (T)	ACA (T)
	23	8	TTG (L)	TTG (L)	TTG (L)	TTG (L)	TGG (W)	TTG (L)	TTG (L)
	25-26	9	GCT (A)	GCT (A)	GCT (A)	GCT (A)	CTT (L)	GCT (A)	GCT (A)
	31-33	11	GCC (A)	GCC (A)	GCC (A)	GCC (A)	AAA (K)	GCC (A)	GCC (A)
	34-36	12	AAT (N)	AAT (N)	AAT (N)	AAT (N)	CGA (R)	AAT (N)	AAT (N)
	37-39	13	GAT (D)	GAT (D)	GAT (D)	GAT (D)	CCG (P)	GAT (D)	GAT (D)
	40	14	GCA (A)	GCA (A)	GCA (A)	GCA (A)	TCA (S)	GCA (A)	GCA (A)
	43	15	GAA (E)	GAA (E)	GAA (E)	GAA (E)	CAA (Q)	GAA (E)	GAA (E)
	518	173	ACA (T)	ACA (T)	ACA (T)	ACA (T)	ACA (T)	ATA (I)	ATA (I)
	536	179	ACT (T)	ATT (I)	ACT (T)	ACT (T)	ACT (T)	ACT (T)	ACT (T)
	833	278	TGC (C)	TGC (C)	TGC (C)	TTC (F)	TTC (F)	TGC (C)	TTC (F)
	1601	534	CGC (R)	CGC (R)	CTC (L)	CGC (R)	CGC (R)	CGC (R)	CGC (R)
	2254	752	GTT (V)	GTT (V)	TTT (F)	GTT (V)	GTT (V)	GTT (V)	GTT (V)
	2815	939	AAG (K)	AAG (K)	AAG (K)	AAG (K)	GAG (E)	AAG (K)	AAG (K)
	2858	953	GTT (V)	GTT (V)	GTT (V)	GCT (A)	GTT (V)	GTT (V)	GTT (V)
	2941	981	CCC (P)	TCC (S)	TCC (S)	TCC (S)	TCC (S)	TCC (S)	TCC (S)
	3329	1110	GCA (A)	GCA (A)	GCA (A)	GCA (A)	GCA (A)	GCA (A)	GTA (V)
	4106	1369	GGT (G)	GGT (G)	GGT (G)	GAT (D)	GAT (D)	GAT (D)	GAT (D)
	4156	1386	GAG (E)	GAG (E)	GAG (E)	GAG (E)	GAG (E)	CAG (Q)	GAG (E)
	4369-4371	1457	TTT (F)	TTT (F)	TTT (F)	--- (-)	TTT (F)	TTT (F)	TTT (F)
	4592	1531	ACT (T)	AAT (N)	AAT (N)	ACT (T)	ACT (T)	ACT (T)	ACT (T)
	4691	1564	TCT (S)	TCT (S)	TCT (S)	TTT (F)	TTT (F)	TTT (F)	TTT (F)

[illegible]

	3667	1223	ATT (I)	ATT (I)	GTT (V)	GTT (V)	GTT (V)	GTT (V)	GTT (V)
	3679	1227	GTG (V)	GTG (V)	GTG (V)	TTG (L)	GTG (V)	GTG (V)	GTG (V)
	3683	1228	GTC (V)	GTC (V)	GTC (V)	GTC (V)	GTC (V)	GCC (A)	GTC (V)
	3757	1253	GAT (D)	TAT (Y)	GAT (D)	GAT (D)	GAT (D)	GAT (D)	GAT (D)
	3818	1273	AAT (N)	AAT (N)	ACT (T)	ACT (T)	ACT (T)	ACT (T)	ACT (T)
	4061	1354	TGT (C)	TTT (F)	TGT (C)	TGT (C)	TGT (C)	TGT (C)	TGT (C)
	4070	1357	TGC (C)	TGC (C)	TGC (C)	TGC (C)	TGC (C)	TTC (F)	TGC (C)
	4139-4140	1380	TTT (F)	TGA (*)	TGA (*)	TGA (*)	TGA (*)	TGA (*)	TGA (*)
	4141-4143	1381	GAA (E)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4144-4146	1382	AAG (K)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4147-4149	1383	GTC (V)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4150-4152	1384	CAC (H)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4153-4155	1385	GTG (V)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4156-4158	1386	CAG (Q)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
	4159-4161	1387	TGA (*)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)	--- (-)
ORF3	506	169	TTG (L)	TCG (S)	TTG (L)	TTG (L)	TTG (L)	TTG (L)	TTG (L)
	571	191	GAT (D)	GAT (D)	GAT (D)	TAT (Y)	TAT (Y)	TAT (Y)	TAT (Y)
	602	201	CAT (H)	CGT (R)	CAT (H)	CAT (H)	CAT (H)	CAT (H)	CAT (H)
	607	203	ATT (I)	ATT (I)	GTT (V)	ATT (I)	ATT (I)	ATT (I)	ATT (I)
Envelope	119	40	ACT (T)	ACT (T)	ATT (I)	ACT (T)	ACT (T)	ACT (T)	ACT (T)
	168	56	TTG (L)	TTG (L)	TTG (L)	TTG (L)	TTC (F)	TTC (F)	TTC (F)
	191	64	ATG (M)	ACG (T)	ATG (M)	ATG (M)	ATG (M)	ATG (M)	ATG (M)
	209	70	CCT (P)	CCT (P)	CCT (P)	CTT (L)	CCT (P)	CCT (P)	CCT (P)
Membrane	70	24	ATC (I)	ATC (I)	ATC (I)	TTC (F)	TTC (F)	TTC (F)	TTC (F)
	352	118	GCG (A)	TCG (S)	TCG (S)	GCG (A)	GCG (A)	GCG (A)	GCG (A)
	656	219	AGT (S)	AGT (S)	AGT (S)	AGT (S)	AGT (S)	AAT (N)	AGT (S)
Nucleocapsid	497	166	AGA (R)	AGA (R)	AGA (R)	ATA (I)	AGA (R)	AGA (R)	AGA (R)
	551	184	CGT (R)	CGT (R)	CGT (R)	CCT (P)	CTT (L)	CGT (R)	CGT (R)
	1130	377	GGG (G)	GGG (G)	GGG (G)	GAG (E)	GGG (G)	GGG (G)	GGG (G)
	1139	380	AAA (K)	ATA (I)	AAA (K)	AAA (K)	AAA (K)	AAA (K)	AAA (K)