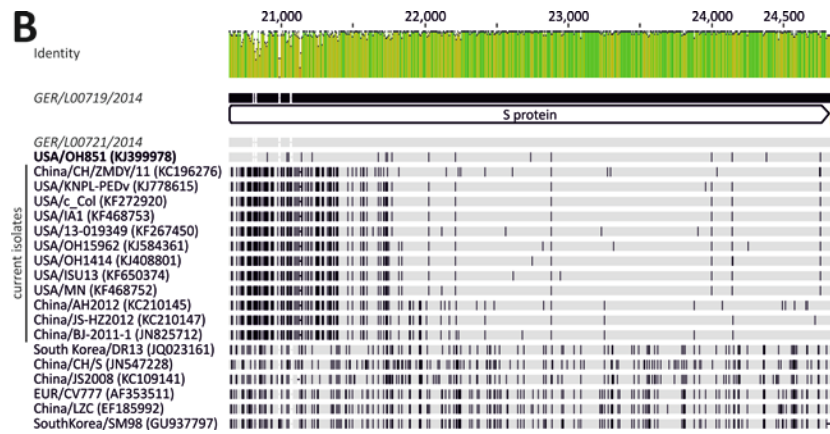# Comparison of Porcine Epidemic Diarrhea Viruses from Germany and United States, 2014

Technical Appendix

A

	GER/L00719/2014	GER/L00721/2014	KJ399978	KC196276	KJ778615	KF272920	KF468753	KF267450	KJ584361	KJ408801	KF650374	KF468752	KC210145	KC210147	JN825712	JQ023161	JN547228	KC109141	AF353511	EF185992	GU937797
GER/L00719/2014		100,0%	99,5%	98,9%	98,7%	98,7%	98,7%	98,7%	98,7%	98,6%	98,6%	98,6%	98,5%	98,6%	98,5%	97,9%	97,6%	97,3%	97,1%	96,8%	96,6%
GER/L00721/2014	100,0%		99,5%	98,9%	98,7%	98,7%	98,7%	98,7%	98,7%	98,6%	98,6%	98,6%	98,5%	98,6%	98,5%	97,9%	97,6%	97,3%	97,1%	96,8%	96,6%
USA/OH851 (KJ399978)	99,5%	99,5%		98,8%	99,1%	99,1%	99,1%	99,1%	98,9%	99,0%	99,0%	99,0%	98,7%	98,7%	98,7%	97,9%	97,6%	97,4%	97,1%	96,8%	96,6%
China/CH/ZMDY/11 (KC196276)	98,9%	98,9%	98,8%		99,0%	99,0%	99,0%	99,0%	99,1%	99,1%	99,1%	99,1%	99,1%	99,1%	99,1%	97,6%	97,2%	97,0%	96,8%	96,5%	96,3%
USA/KNPL-PEDv (KJ778615)	98,7%	98,7%	99,1%	99,0%		100,0%	100,0%	99,9%	99,8%	99,8%	99,9%	99,9%	99,5%	99,4%	99,3%	97,6%	97,3%	97,0%	96,8%	96,5%	96,3%
USA/c_Col (KF272920)	98,7%	98,7%	99,1%	99,0%	100,0%		100,0%	99,9%	99,7%	99,8%	99,9%	99,9%	99,5%	99,4%	99,3%	97,6%	97,3%	97,0%	96,8%	96,5%	96,3%
USA/IA1 (KF468753)	98,7%	98,7%	99,1%	99,0%	100,0%	100,0%		99,9%	99,7%	99,8%	99,8%	99,8%	99,5%	99,4%	99,3%	97,6%	97,3%	97,0%	96,7%	96,5%	96,3%
USA/13-019349 (KF267450)	98,7%	98,7%	99,1%	99,0%	99,9%	99,9%	99,9%		99,7%	99,8%	99,8%	99,8%	99,5%	99,3%	99,3%	97,6%	97,3%	97,0%	96,7%	96,5%	96,3%
USA/OH15962 (KJ584361)	98,7%	98,7%	98,9%	99,1%	99,8%	99,7%	99,7%	99,7%		99,8%	99,9%	99,9%	99,5%	99,3%	99,2%	97,7%	97,3%	97,0%	96,8%	96,5%	96,3%
USA/OH1414 (KJ408801)	98,6%	98,6%	99,0%	99,1%	99,8%	99,8%	99,8%	99,8%	99,8%		99,9%	99,9%	99,6%	99,3%	99,3%	97,7%	97,3%	97,1%	96,8%	96,5%	96,3%
USA/ISU13 (KF650374)	98,6%	98,6%	99,0%	99,1%	99,9%	99,9%	99,8%	99,8%	99,9%	99,9%		100,0%	99,6%	99,4%	99,3%	97,7%	97,3%	97,0%	96,8%	96,5%	96,3%
USA/MN (KF468752)	98,6%	98,6%	99,0%	99,1%	99,9%	99,9%	99,8%	99,8%	99,9%	99,9%	100,0%		99,6%	99,4%	99,3%	97,7%	97,3%	97,1%	96,8%	96,5%	96,3%
China/AH2012 (KC210145)	98,5%	98,5%	98,7%	99,1%	99,5%	99,5%	99,5%	99,5%	99,5%	99,6%	99,6%	99,6%		99,5%	99,4%	97,7%	97,3%	97,1%	96,8%	96,6%	96,3%
China/JS-HZ2012 (KC210147)	98,6%	98,6%	98,7%	99,1%	99,4%	99,4%	99,4%	99,3%	99,3%	99,3%	99,4%	99,4%	99,5%		99,7%	97,8%	97,4%	97,2%	96,9%	96,6%	96,4%
China/BJ-2011-1 (JN825712)	98,5%	98,5%	98,7%	99,1%	99,3%	99,3%	99,3%	99,3%	99,3%	99,3%	99,3%	99,3%	99,4%	99,7%		97,8%	97,3%	97,1%	96,9%	96,7%	96,5%
SouthKorea/DR13 (JQ023161)	97,9%	97,9%	97,9%	97,6%	97,7%	97,6%	97,6%	97,6%	97,7%	97,7%	97,7%	97,7%	97,7%	97,8%	97,8%		98,1%	97,8%	97,7%	97,4%	97,2%
China/CH/S (JN547228)	97,6%	97,6%	97,6%	97,2%	97,3%	97,3%	97,3%	97,3%	97,3%	97,3%	97,3%	97,3%	97,3%	97,4%	97,3%	98,1%		97,5%	97,4%	97,1%	96,9%
China/JS2008 (KC109141)	97,3%	97,3%	97,4%	97,0%	97,0%	97,0%	97,0%	97,0%	97,0%	97,1%	97,0%	97,1%	97,1%	97,2%	97,1%	97,8%	97,5%		97,7%	97,4%	97,2%
EUR/CV777 (AF353511)	97,1%	97,1%	97,1%	96,8%	96,8%	96,8%	96,7%	96,7%	96,8%	96,8%	96,8%	96,8%	96,9%	96,9%	96,9%	97,7%	97,4%	97,7%		99,7%	99,5%
China/LZC (EF185992)	96,8%	96,8%	96,8%	96,5%	96,5%	96,5%	96,5%	96,5%	96,5%	96,5%	96,5%	96,5%	96,6%	96,6%	96,7%	97,4%	97,1%	97,4%	99,7%		99,2%
SouthKorea/SM98 (GU937797)	96,6%	96,6%	96,6%	96,3%	96,3%	96,3%	96,3%	96,3%	96,3%	96,3%	96,3%	96,3%	96,3%	96,4%	96,5%	97,2%	96,9%	97,2%	99,5%	99,2%	

current isolates

B

Identity — S protein (alignment view, positions ~21,000–24,500)

Appendix Figure. Nucleotide sequence alignment (MAFFT) (*1*) of whole-genome sequences of 21 isolates of porcine epidemic diarrhea virus (PEDV). The new strains PEDV/GER/L00719/2014 and PEDV/GER/L00721/2014 (italics) from Germany and the new 2014 PEDV US variant OH851 (boldface) were included and compared with current circulating strains from the United States and China (current isolates). A) Pairwise similarity matrix based on full-length genomes. Similarity is given in percent identity.

B) Schematic representation of the nucleotide sequence alignment of the complete spike protein coding sequences to depict the variable region in the 5′ part. Sequence identity is given in the upper color-coded graph (dark green, high similarity; light green, lower similarity; red, low similarity). Nucleotide positions that differ relative to the recent German strains are marked in black.

Reference

1. Katoh K, Misawa K, Kuma K, Miyata T. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 2002;30:3059–66. PubMed http://dx.doi.org/10.1093/nar/gkf436