

Swine Enteric Coronavirus evolution: Learning from the past to understand the future

Douglas Marthaler, Ph.D.

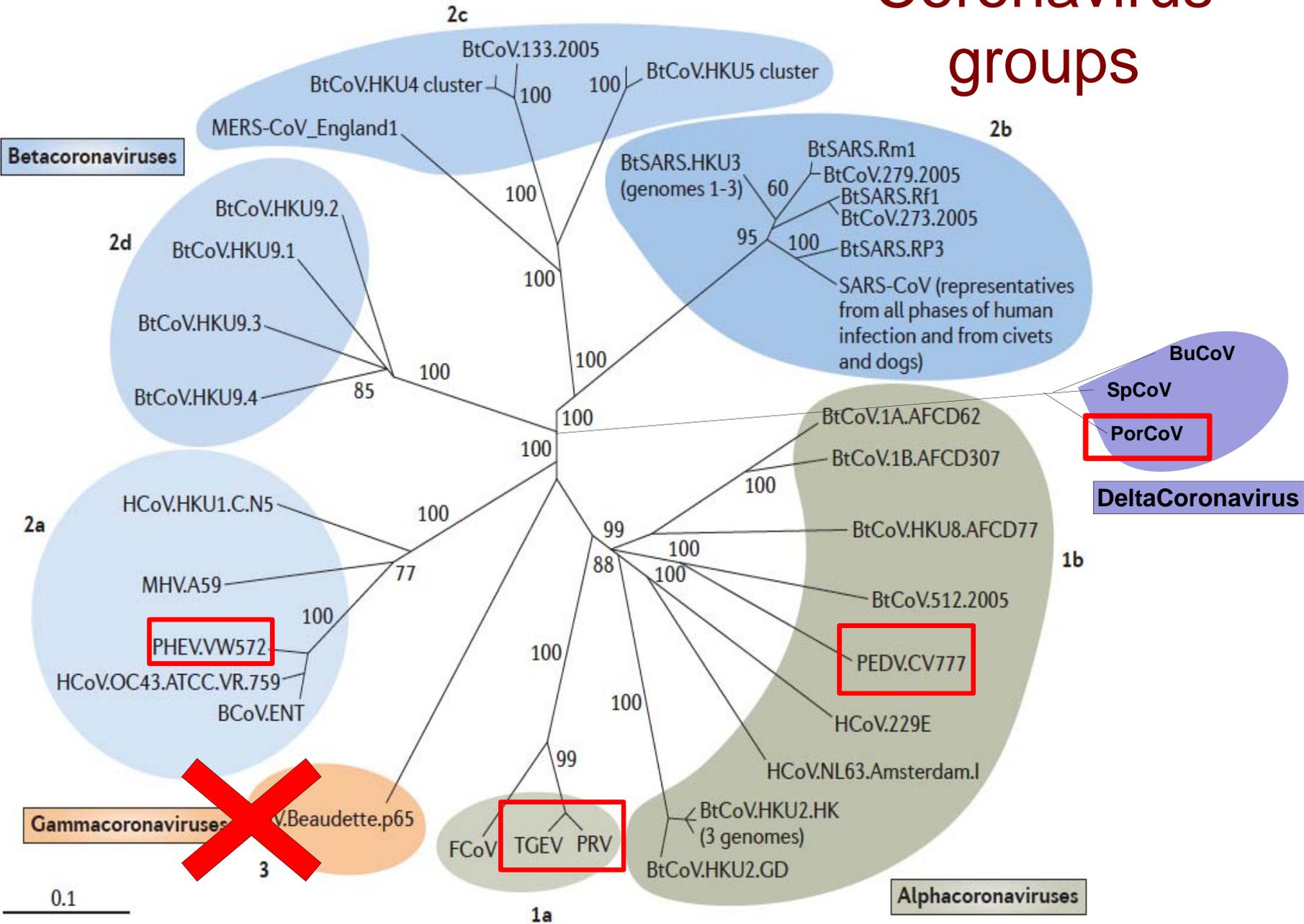
PEDV Diagnostics and Immunity
SECD International Meeting
September 25th, 2014



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Coronavirus groups

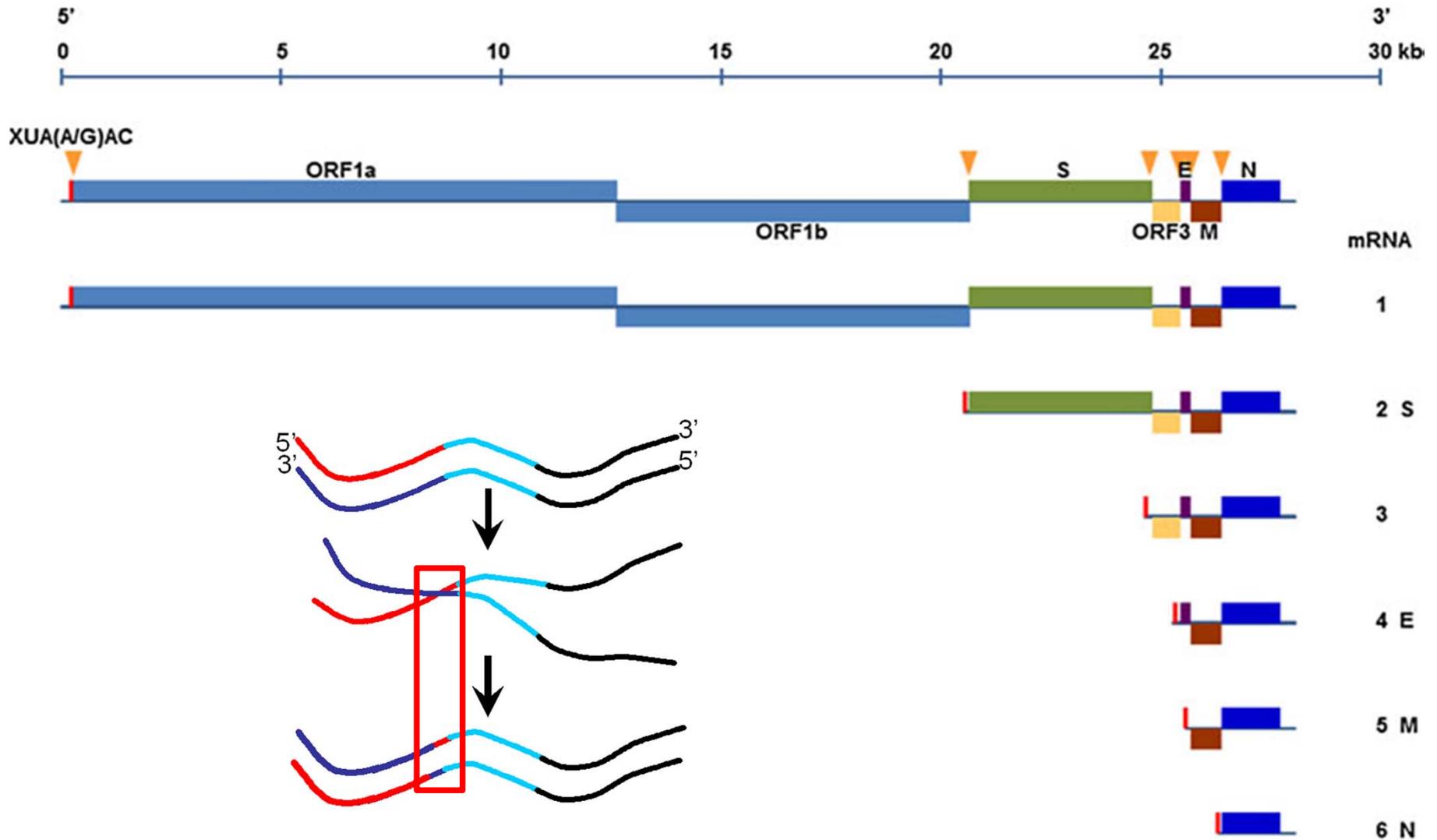


Graham RL, et al. Nat Rev Microbiol. 2013 Dec;11(12):836-48.
doi: 10.1038/nrmicro3143. Epub 2013 Nov 11. Review. PubMed PMID: 24217413.



PEDV Genome and Phylogenetics

PEDV Genome



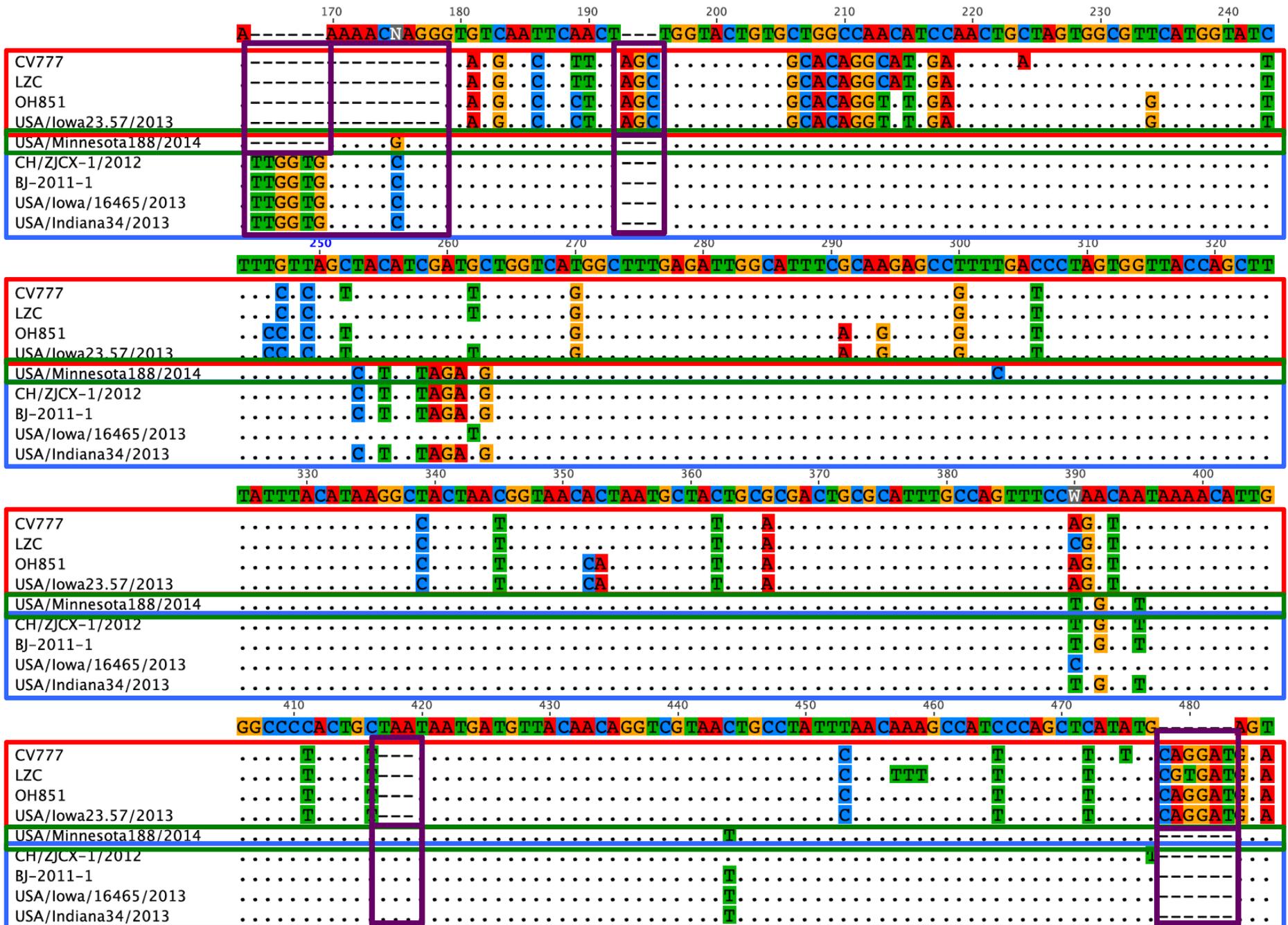
. Mechanism of recombination on nucleic acid strands

PEDV, prototype strain CV777

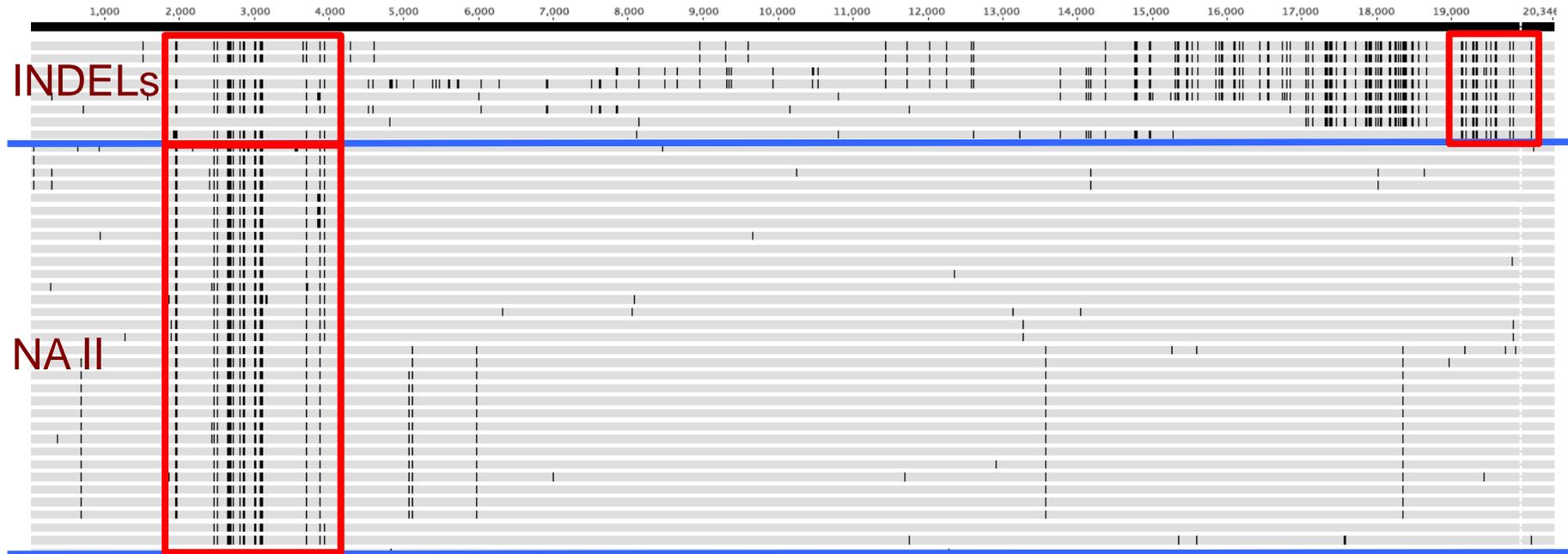
- First PEDV strain adapted to cell culture
- Caused pathogenesis in both piglets and growing pig
- Cell adapted sequence is available in GenBank
 - Cell adapted strain was disrupted throughout Europe
 - The progeny strains from CV777 have different sequences
- When CV777 is compared to the “virulent” PEDV strains, CV777 has a deletion in the spike gene. Or, the “virulent” strain gained an insertion in the spike gene.



Spike gene diversity



PEDV ORF1



RESEARCH

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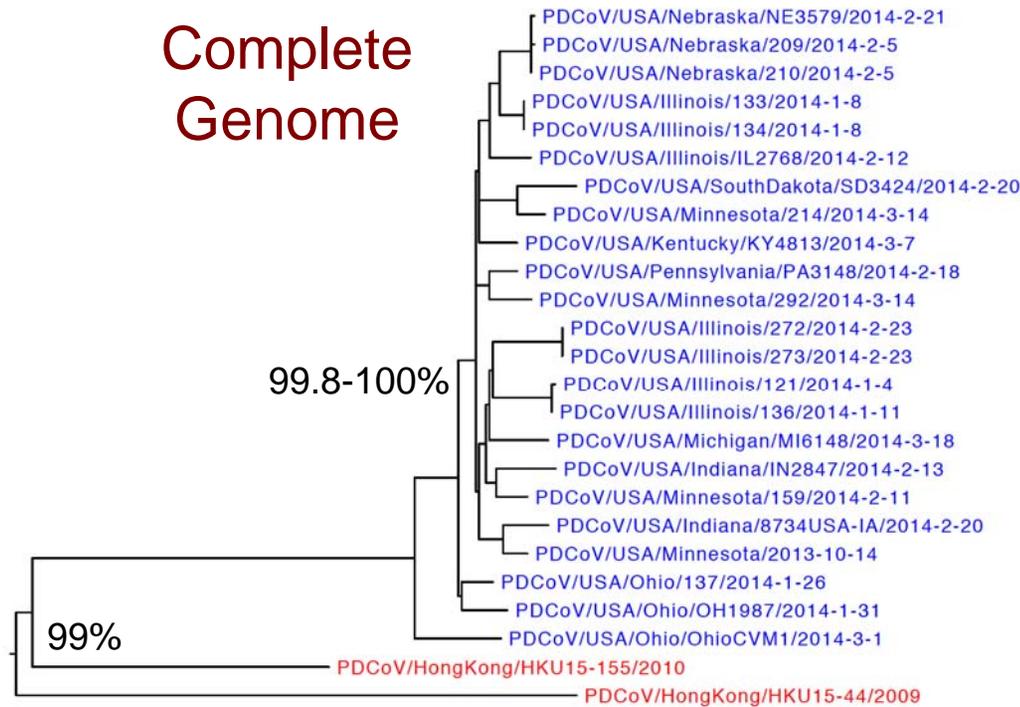
RESEARCH

Distinct Characteristics and Complex Evolution of PEDV Strains, North America, May 2013–February 2014

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Kurt D. Rossow, Albert Rovira, James Collins, and Linda J. Saif

Porcine Deltacoronavirus

Complete Genome

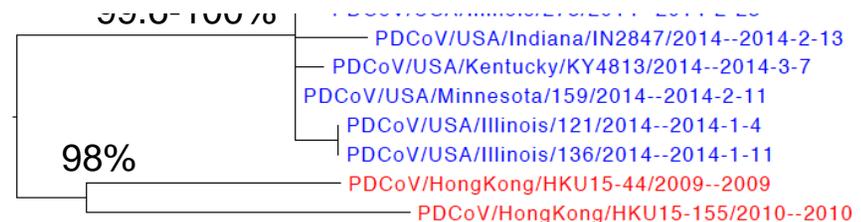


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 infection, The University of Hong Kong, Hong Kong, and Guangdong Center for Disease Control and Prevention, Guangzhou, China^e

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. Lau,^a Alan K. L. Tsang,^a John H. N. Lau,^a Ru Bai,^a
 -Hung Chan,^a and Kwok-Yung Yuen^{a,b,c,d}

Centre of Infection and Immunology,^c and the Carol Yu Centre for



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Conclusion

- PEDV strain diversity is expected and changes will occur over time. The question is, “Are these changes important?”
- 3 Wild type strains have been identified; Original, INDEL/variant, and S2aa-del.
 - The US PEDV strain with the spike gene deletion is not novel. It’s a characteristic of prototype strain CV777. The ORF1b is novel in the INDEL strains.
- The limited global PEDV sequences impedes our analysis.
- PEDV phylogenetic analysis and interpretation must include complete genomic data. Otherwise, incorrect assumptions will be made.
 - The most recent common ancestor for the US strains is AH2012.
 - However, recombination events occurred with other global PEDV strains before PEDV was introduced into the US.
- PDCoV genetic diversity in the US is very limited.



Acknowledgements

- Kurt Rossow
 - Yin Jiang
 - Marie Culhane
 - Martha Nelson
 - Jim Collins
 - Albert Rovira
 - Lindsey Raymond
 - Linda Saif
 - Quihong Wang
 - Anastasia Vlasova
 - Laura Bruner
- **Funding Sources**
 - Minnesota Agricultural Experimental Station, RARF
 - University of Minnesota Veterinary Diagnostic Laboratory



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