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First detection of porcine reproductive and respiratory syndrome virus in a wild rodent population in upstate new york

E-poster presentations - session 35: Virus discovery and virome studies

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Background and Aims

The meadow vole, *Microtus pennsylvanicus*, is a common rodent species widely distributed in North America, living in both natural and human-modified habitats and known to host zoonotic pathogens, some of which pose a threat, with significant economic impact, to the livestock industry. Using a whole virome detection method we explored the diversity of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in a wild reservoir, providing insight into its diversity.

Methods

The lung virome of six populations of meadow voles in Upstate New York, USA, was investigated with an adapted protocol from Plyusnin et al. 2020. Using partial PRRSV genomes recovered in four *M. pennsylvanicus* samples, we performed phylogenetic and network analysis to investigate the diversity and the relations of this rodent strain with other well-known Suidae lineage recovered from livestock infections.

Results

This study marks the first-ever evidence of PRRSV occurrence in meadow voles, with six partial genomes recovered from different populations. This provides insight into the genetic diversity of this virus and may have implications for PRRSV management.

Conclusions

This study revealed a new PRRSV lineage circulating in voles, no other evidence of this virus circulating in wild taxa other than Suidae had been shown before. Our results reinforce the importance of surveying wildlife viromes to identify and monitor possible sources of zoonoses, which is vital for making evidence-based decisions, with a One-Health perspective, regarding potential threats to the health of humans, animals, and the ecosystem as a whole.