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Hidden diversity of rinderpest virus uncovered in historical pathology collections

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Rinderpest virus (RPV; Morbillivirus pecoris) and measles virus (MeV; Morbillivirus hominis) are RNA viruses that belong to the Paramyxoviridae family which have had a major impact on livestock and human health. RPV caused the death of billions of cattle, with fatality rates reaching up to 90%, until its eradication in 2011. MeV causes measles in humans; a disease that, despite the availability of a vaccine since the 1960's, still leads to approx. 110,000 deaths annually. RPV and MeV are each other's closest relatives. It is believed that MeV emerged in humans from a cattle-infecting ancestor of RPV. Using historical measles specimens to recover MeV genomes and applying tailored phylodynamic methods, we recently suggested that MeV may have emerged as early as 600 BCE, correlating with the rise of big cities.

Here, we intended to reassess this notion by investigating the evolution of RPV across a century of control measures by generating ancient RPV genomes from historical specimens. We applied pathogen genomic approaches to analyze 41 pathology specimens, sourced from three different pathology collections.

While we have not fully completed this study, our preliminary phylogenetic analyses already revealed that our RPV sequences fall outside of the known diversity of RPV, highlighting previously unrecognized viral diversity.

We expect that this project will ultimately unveil key elements of the evolution of morbilliviruses in their human and domestic hosts.

Keywords

RNA virus evolution, ancient genomics, Morbillivirus evolution, Measles Virus, Rinderpest Virus, pathological specimens

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Junior Scientist Status

Yes, I am a Junior Scientist.

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