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Evolutionary Dynamics of Classical Swine Fever Virus in the First Half of the 20th Century

Inhalt

Classical swine fever virus (CSFV) has been a major pathogen of domestic pigs for over a century. However, its early evolutionary history remains poorly understood due to the lack of historical genomic data, with current phylogenetic frameworks relying on sequences obtained since the 2000s. Archival tissue collections represent a valuable yet underexplored resource for investigating the historical diversity of economically important livestock viruses.

This project presents a paleogenomic study of CSFV based on 132 archival samples collected from seven European institutions and dating to the first half of the 20th century. Using optimized high-throughput sequencing protocols, we successfully recovered historical viral RNA genomes. Phylogenetic analyses revealed distinct lineages that are absent from contemporary datasets, indicating a greater level of viral diversity in the past. These results suggest that vaccination and eradication programs may have substantially reduced CSFV diversity over time.

Our findings provide direct genomic insights into the early evolutionary history of CSFV, contributing to a better understanding of long-term viral diversity and population dynamics. More broadly, this study demonstrates the potential of paleogenomic approaches to reconstruct the evolutionary trajectories of RNA viruses from archival material.

Keywords

Classical swine fever virus, Paleogenomics, Viral diversity, Ancient genomes, Phylogenetic analysis, Livestock pathogens, Archival material

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Professional Status of the Speaker

Graduate Student

Junior Scientist Status

No, I am not a Junior Scientist.

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Kommentare:

Oral presentation is preferred.

Eingereicht von **Frau KADOW, Laura** <laura.kadow@helmholtz-hioh.de> am **Montag, 22. Juni 2026**