

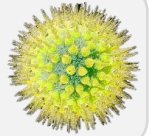
TORQUE TENO SUS VIRUS: AN INNOCENT BYSTANDER OR A TRUE EMERGING VIRUS PATHOGEN IN SWINE FARMS?

M. Polinas*, S. Hawko*, S. Dei Giudici†, P.P. Angioi†, A. Alberti*, E. Antuofermo*, A. Oggiano† and G.P. Burrai*

*Department of Veterinary Medicine, University of Sassari and †Department of Animal Health, Istituto Zooprofilattico Sperimentale della Sardegna, Sassari, IT

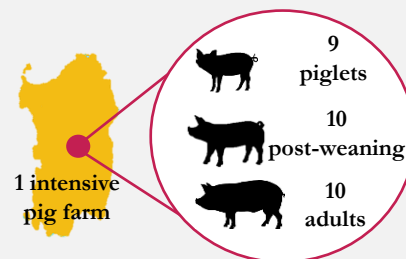
Introduction

Torque teno sus virus (TTSuV, Anelloviridae) is a non-enveloped circular ssDNA virus detected in pigs worldwide. Suspected to be involved in several swine diseases as a primary agent or as an opportunistic pathogen.



Work aims Detecting TTSuV in different swine age categories from an intensive pig farm in Sardinia (Italy) with respiratory signs (dyspnea).

Materials and Methods



Gross evaluation and histopathology

Lung, heart, liver, spleen, kidney, intestine, mediastinal, and mesenteric lymph nodes were macroscopically and histologically evaluated.

Molecular biology

Real-time PCR (RT-PCR) for TTSuV detection
Sanger sequencing to characterize viral strains in a subset of samples.

Results

Histopathology

Moderate, diffuse chronic macrophagic and lymphoplasmacytic interstitial pneumonia in:

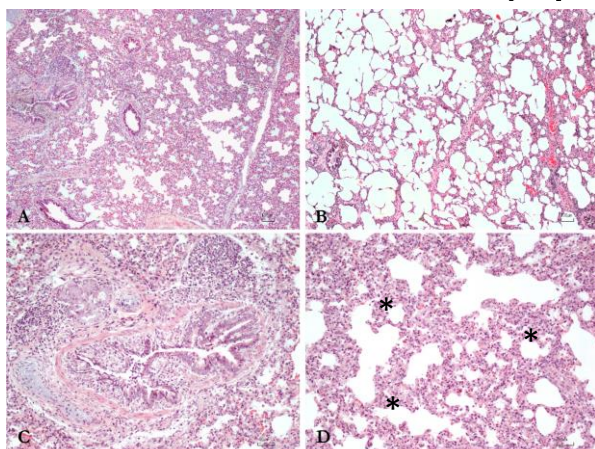
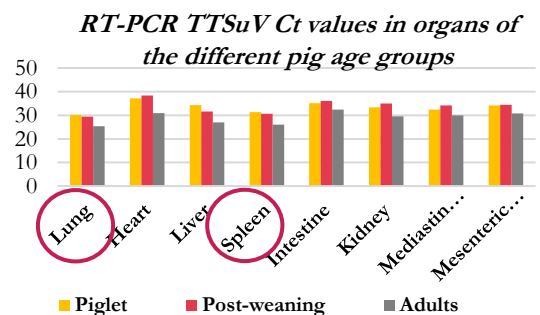


Figure 1. A-D. Morphological features of swine lungs positive to TTSuV. A-B. Moderate interstitial bronchopneumonia. C. Moderate diffuse lymphoplasmacytic and macrophagic chronic bronchitis. D. High number of lymphocytes and macrophages expanding the interstitium (asterisks). A, B = HE, bar 100µm; C, D = HE, bar 50µm.

Molecular biology

RT-PCR

- in 100% of pigs (higher viral loads in adults)
- lowest CT's values in lung and spleen ($P < 0.05$)



Sanger sequencing

TTSuV1 and TTSuV2k strains were identified:

- *TTSuV1*: highest homology with Brazilian and South Korean strains.
 - *TTSuV2k*: 98% similarity to Chinese strains.
- Other tested viruses, including PCV2 and PRRS, were detected with low viral loads.

Conclusions

Based on data, TTSuV may play a role in swine lung disease, but further studies are needed to clarify if it represents an innocent bystander or play a synergistic role with other swine pathogens.

This work was supported by Italian Ministry of Health, Grant N° IZS SA 06/21 RC and by DM 737/2021 risorse 2021–2022, Finanziato dall'Unione Europea - NextGenerationEU