ARPHA Conference Abstracts 9: e203358
doi: 10.3897/aca.9.e203358

OPEN ACCESS

Conference Abstract

The interplay of drivers behind disease spillover risk from invasive alien mammals in Europe

Chiara Magliozzi‡, Joaquin Vicente Baños§, Ana Cristina Cardoso‡

‡ European Commission, Joint Research Centre, Ispra, Italy
§ University of Castilla-La Mancha, Ciudad Real, Spain

Corresponding author: Chiara Magliozzi (chiara.magliozzi@ec.europa.eu)

Received: 09 Jun 2026 | Published: 09 Jun 2026

Citation: Magliozzi C, Vicente Baños J, Cardoso AC (2026) The interplay of drivers behind disease spillover risk from invasive alien mammals in Europe. ARPHA Conference Abstracts 9: e203358. https://doi.org/10.3897/aca.9.e203358

Abstract

Invasive alien species (IAS) pose a considerable threat to European ecosystems, with the risk of disease spillover from IAS to native wildlife, livestock, and human populations being an increasingly significant concern. Despite heightened research efforts, the complex interactions of factors driving disease transmission from IAS remain poorly understood.

A systematic review and analysis of 545 pathogen-host-environment-driver records from 85 studies on invasive alien mammals in Europe was undertaken. The results revealed that ecological and biological factors, such as host density and reservoir host abundance, predominate the dataset (51.7% of records). Additionally, human-driven environmental change (14.1% of records) and pathogen-related factors (21.5% of records) play a substantial role in disease transmission. Notably, the study highlighted considerable variation in factor profiles across different invasive alien mammal species, including the American mink, raccoon dog, and raccoon.

The analysis showed that host density was the most frequently documented driver, appearing in 116 records (21.3% of the dataset), followed by reservoir host abundance (7.2%, n = 39) and presence/abundance of other invasive species (5.9%, n = 32). Urbanization and peri-urban expansion were also identified as significant drivers,

© Magliozzi C et al. This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

particularly for species such as the raccoon, which exhibited a strong association with human-driven environmental change (27.3%, n = 30).

The study further revealed that the most frequently documented pathogens were *Baylisascaris procyonis* (raccoon roundworm, n = 36 records), *Toxoplasma gondii* (n = 29), Aleutian mink disease virus (AMDV, n = 23), squirrelpox virus (SQPV, n = 20), and SARS-CoV-2 (n = 19). The pathogen assemblage included diverse taxonomic groups and transmission modes, reflecting the broad pathogen reservoir potential of invasive alien mammals in Europe.

The findings underscore the necessity for targeted management strategies to mitigate host density, reservoir host abundance, and human-driven environmental change, as well as species-specific and landscape-scale approaches to disease management and control. Furthermore, the study highlights the need for continued research into the dynamics of disease transmission from IAS, including the development of quantitative models to predict the risk of disease spillover and the implementation of effective disease surveillance and monitoring systems.

Keywords

wildlife, humans, pathogen, transmission, factors

Presenting author

Chiara Magliozzi

Presented at

Neobiota 2026, the 14th International Conference on Biological Invasions

Funding program

European Commission, Joint Research Centre (JRC)

Author contributions

CM: Conceptualization, Investigation, Analysis, Coordiantion and Supervision

JVB: Investigation, Expert Knoledge, Analysis, Writing

ACC: Coordination and Supervision, Review

Conflicts of interest

The authors have declared that no competing interests exist.