Revista Argentina de Microbiología 57 (2025) 307–308

asociación argentina de microbiología
aam

REVISTA ARGENTINA DE
MICROBIOLOGÍA

www.elsevier.es/ram

EDITORIAL

The transmission of viral diseases in wild boar using Rutherford’s atomic model

Transmisión de enfermedades virales en jabalíes utilizando el modelo atómico de Rutherford

Throughout history, different atomic models have been theoretical representations that describe the structure and behavior of atoms.

At the beginning of the last century, Rutherford proposed an atom with a centralized nucleus and electrons orbiting around it. Here, we use Rutherford’s atomic model as a metaphor to illustrate the dynamic role of wild boars in the spread of viral diseases under a One Health perspective. Although viral transmission is far from a static process, the concept of a ‘‘core’’ and its ‘‘orbits’’ provides a useful framework to reflect the interaction of wild boars with domestic swine in viral transmission.

In Argentina, wild boars were introduced early in the last century for hunting purposes. Today, they are widely distributed throughout various parts of the country, coinciding with, or in some cases orbiting around the regions with the highest agricultural and livestock activity. Wild boars cause significant economic losses due to direct and indirect impacts, including changes to flora and fauna, damage to the agricultural and livestock industry and the spread of diseases with public health relevance.

Due to their omnivorous diet, which consists mainly of grains, they tend to gather near livestock facilities where grains and water are stored.[1] In this context, their constant movement and contact with livestock farms can be viewed as the ‘‘orbital’’ component of this analogy, illustrating their role in the potential transmission of viral pathogens.

This proximity has led to crossbreeding between wild boars and domestic swine. The resulting hybrid specimens exhibit increased body mass and higher reproductive capacity. Additionally, the absence of natural predators in the environment has created optimal conditions for the species to thrive, enhancing their survival rate and the consequent viral spread.[1]

Domestic swine are susceptible to a wide range of viral diseases, including swine flu, classical swine fever, African swine fever, Aujeszky’s disease, porcine reproductive and respiratory syndrome, swine vesicular disease, and various circoviruses, parvoviruses, coronaviruses and hepatitis E.[2] Like protons confined in the nucleus, domestic swine are usually part of large production systems, which, under ideal conditions, tend to have biosecurity standards and sanitary measures that prevent the transmission of viral diseases among their animals. These measures also ensure the safety of animals being transported from one place to another. In contrast, wild boars, analogous to electrons in their constant pursuit of food, have the potential to interact with domestic swine and/or their fomites, thereby transmitting and becoming carriers of several diseases. Through these interactions, they can acquire and disseminate viral pathogens, thus expanding their geographic distribution.

These dynamics allow viruses to fluctuate between two replication substrates that are similar yet distinct. It is plausible that in the context of ‘‘production nuclei,’’ viruses employ ‘‘domestic’’ cellular substrates that are subject to regulation by vaccination. In contrast, ‘‘wild’’ cellular substrates, lacking the immune regulation of vaccination, facilitate viral replication and transmission. Regardless of the substrate utilized by viruses for replication, in addition to the high mutation rate of RNA viruses, the ability to fluctuate between both substrates offers viruses the potential to generate slight variations in their progeny. This macroscopic dynamics of viruses between wild boars and domestic swine will allow new microscopic replication dynamics, observable when disease events differ from the usual ones.

Assuming that swine act as a mixing vessel for the emergence of new strains of the influenza virus, we can extrapolate and infer that the same may be true for wild boars. Although further research is needed in this area, there is solid scientific evidence that shows the crucial role of wild boar in the propagation of African swine fever virus and hepatitis E [3] and several other diseases.

https://doi.org/10.1016/j.ram.2025.11.001

While large urban areas are not currently being explored by wild boars, urbanization is encroaching on the niches occupied by wild boars. This phenomenon has already been observed in the case of capybaras and pumas in several areas of our country. Consequently, wild boars tend to orbit around production areas, either because they approach them in search of food or because the production areas orbit and come increasingly closer to their habitats.

In Samborombón Bay, one of the areas with the highest concentration of wild boars in the country, and in the southern region of the province of Buenos Aires and northern Patagonia, molecular and serological surveys have been carried out for various viruses, detecting the presence of parvovirus, porcine circovirus, rotavirus, cytomegalovirus, and porcine herpesvirus.[4,5] Many of these viruses have the potential to spread among wild boars, domestic swine, and other animals. For example, cases of porcine herpesvirus-induced encephalitis in hunting dogs have been reported, and there is even serological evidence of this virus in humans.

While it is improbable that humans will acquire the infection through contact with wild boars, their meat, derivatives, and fomites could serve as a source of zoonotic diseases. Therefore, it is essential to implement control measures that put an end to this ''atomic'' model of transmission. At the same time, regular health checks on wild boars are necessary to detect diseases that are potentially zoonotic or problematic for other animals, consistent with the One Health approach that integrates animal, human, and environmental health.

References

1. Ballari SA, La Sala LF, Merino ML, Carpinetti B, Winter M, Gürtler RE, Barandarian S, Cuevas MF, Condori WE, Tammone A, Marcos A, Barrios-Garcia MN. El jabalí y el cerdo silvestre (*Sus scrofa*) en la Argentina. Ecología Austral. 2024;34:401–21, http://dx.doi.org/10.25260/EA.24.34.2.0.2389.
2. Di Cola G, Di Cola G, Fantilli A, Mamani V, Tamiozzo P, Martínez Wassaf M, Nates SV, Ré VE, Pisano MB. High circulation of hepatitis E virus (HEV) in pigs from the central region of Argentina without evidence of virus occurrence in pork meat and derived products. Res Vet Sci. 2023;164:105000, http://dx.doi.org/10.1016/j.rvsc.2023.105000.
3. Minassian ML. Acute viral hepatitis: What we do know and still do not know about hepatitis A and E in Argentina. Rev Argent Microbiol. 2024;56:1–3, http://dx.doi.org/10.1016/j.ram.2024.03.001.
4. De Maio FA, Winter M, Abate S, Birochio D, Iglesias NG, Barrio DA, Bellusci CP. Molecular detection of Porcine cytomegalovirus (PCMV) in wild boars from Northeastern Patagonia, Argentina Detección molecular de citomegalovirus porcino (PCMV) en jabalíes del noreste de la Patagonia argentina. Rev Argent Microbiol. 2021;53:325–32, http://dx.doi.org/10.1016/j.ram.2020.12.003.
5. Williman MM, Negrelli Pilar M, Carpinetti B, Colina SE, Ozaeta DS, Echeverría MG, Metz GE, Serena MS. Los cerdos silvestres *Sus scrofa* de la Bahía de Samborombón, Provincia de Buenos Aires, Argentina. Detección de patógenos virales de importancia en salud pública. Mastozoología Neotropical. 2024;31:e0994, http://dx.doi.org/10.31687/saremMN.24.31.01.19.e0994.

Germán Ernesto Metz*, María Gabriela Echeverría
Laboratorio de Virología-Centro de Microbiología Básica y aplicada (LAVIR-CEMIBA), Facultad de Ciencias Veterinarias, Universidad Nacional de La Plata. CONICET CCT-La Plata

* Corresponding author.
E-mail address: germanmetz@fcv.unlp.edu.ar (G.E. Metz).