ORAL 24: Regional evolutionary dynamics of peste des petits ruminants virus in West Africa: influence of livestock trade

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Keywords: PPRV, morbilivirus, phylogenetics, animal movement, transboundary

Peste des petits ruminants (PPR) is a highly contagious and devastating viral disease of small ruminants. It represents a serious risk for the economy and food security in regions of Africa, Middle East and Asia where the disease is endemic. Integrated knowledge of evolutionary and epidemiological factors underlying PPR virus (PPRV) emergence, persistence and spread are necessary for better guidance of PPR control strategies and their practical implementation. Efforts are especially needed to better understand the regional dynamics of PPRV evolution and endemic transmission.

Here we studied the regional evolutionary dynamics of endemic PPRV in West Africa, focussing on Senegal and neighbouring countries, and assessed the role of livestock trade in explaining the observed viral diversity and phylogenetic patterns. Sheep and goats were sampled in livestock markets and villages across Senegal between 2010 and 2014 and tested for PPRV infection. Other samples were obtained from Mauritania, Mali, and Guinea during the same period. Historical samples (1972-1994) were also collected from the region. In addition, livestock movement data, particularly livestock trade were collected during specific surveys implemented in Mauritania and Senegal.

A total of 55 samples collected from 2010 to 2014 were positive for PPRV. Partial sequencing of the N gene showed that 54 belonged to the PPR virus lineage II (PPRV-II) and one to lineage I. We obtained the sequence of the full N and H genes for all PPRV-II samples, and sequenced the full genome for a subset of recent and historical samples. Phylogenetic analyses showed the presence of at least 4 different, geographically delimited, clades within PPRV-II in West Africa. Samples from Mali were distributed across 3 of these clades, suggesting a central position of the country in regional movement of PPR.

All PPRV-II samples from Senegal were situated within a single clade, but could be separated in distinct clusters. These clusters pointed to virus movement across long distances within Senegal and between Senegal and its neighbours. Transboundary movements involved mainly major sites for commercial animal movement, but also transhumant movement between Senegal and Mauritania. A statistical model of virus genetic distance was fitted with environment and animal movement data to assess if the genetic patterns observed can be predicted by commercial connectivity. We discuss how such landscape resistance analyses based on animal movement can be used to predict PPR transmission pathways and control effort within endemic regions.

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EPIZONE
10th Annual Meeting

GOING VIRAL

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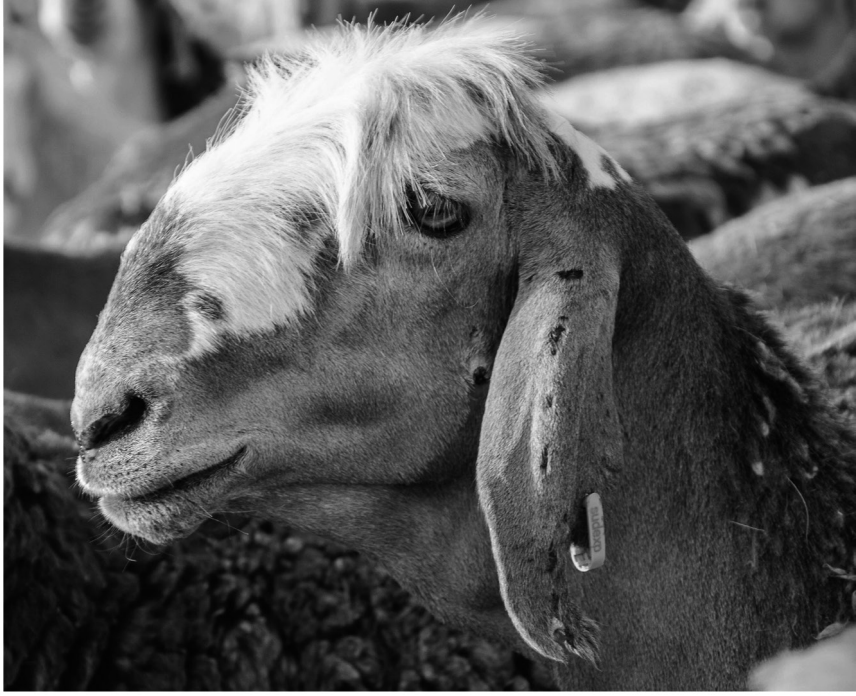

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Welcome
10th Annual Meeting EPIZONE "Going Viral"

It is a great honour and a privilege for me to give you all our warmest welcome to the Xth Annual Meeting of EPIZONE, the first to be celebrated in Spain. INIA-CISA, as the host institution, has been fully committed on this challenge from the beginning, and we do hope that the final result will be satisfactory for participants, sponsors and organizers. We wish to thank specially to them, as this event could not be possible without any of these essential parts. The financial support from sponsors, the availability and contributions from keynote speakers, the high scientific level of oral and poster presentations from participants and, at the end, curious, active and interested assistants, will contribute to the success of the meeting. From the organizing committee I want also to thank the EPIZONE secretariat and coordinator for their continuous help and implication in the effort. Finally, my gratitude to the people at the local and international scientific and organizing committees that have been working together very hard to yield a balanced, wide-scoped and intense (maybe too intense?) programme. Special thanks to Jovita Fernandez Piñero, who has been in charge of many tasks, and has fulfilled a brilliant labour. And will not forget about the enthusiastic Young Epizone people; thank you for your work and for organizing such a well-designed session.

Under the general title of "Going Viral", and from a *One Health* perspective, we have outlined three concentric circles defining the main topics:

Topic I: Animal Health in a changing World, dealing with global threats for animal health.

Topic II: Threats at the European border, paying attention to diseases in the neighbouring areas.

Topic III: Current challenges inside Europe, where the main diseases affecting the European countries will be discussed.

As in previous EPIZONE meetings, diagnostics, intervention strategies, epidemiology and surveillance, risk analysis and some other aspects will be approached by recognized experts in specific sessions. Many diseases which are familiar to us will receive attention, from Foot and Mouth Disease to West Nile Virus Disease or the more recent episodes by Lumpy Skin Disease, Pest des Petits Ruminants and some others. African Swine Fever and Bluetongue have been the most "popular" diseases among contributors, this revealing their current relevance.

I hope that the efforts of contributors, sponsors, participants and organizers will provide an opportunity for the "epizootic community" to work together, to plan new initiatives, to interact and to share a good time in Madrid.

Victor Briones

Acknowledgements

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National Institute for the Agricultural and food Research and Technology (INIA)

Spanish Technology Platform for Animal Health (Vet+i)

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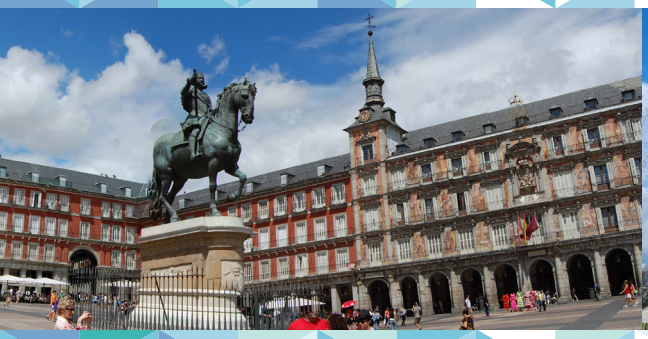

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