Risk-based surveillance and addressing PPR risk pathways through the episystem approach

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Aim

Introduce the episystem approach and how it can inform risk-based surveillance.

Sets the stage for next presentation, which will explore episystems in more depth.

Risk-based surveillance

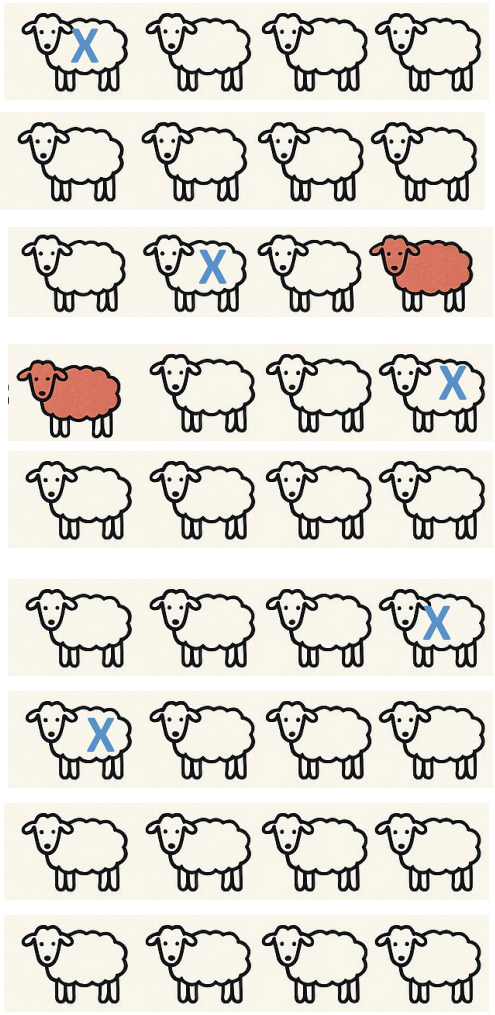
Surveillance for early detection:

Prioritize high-risk flocks!!!

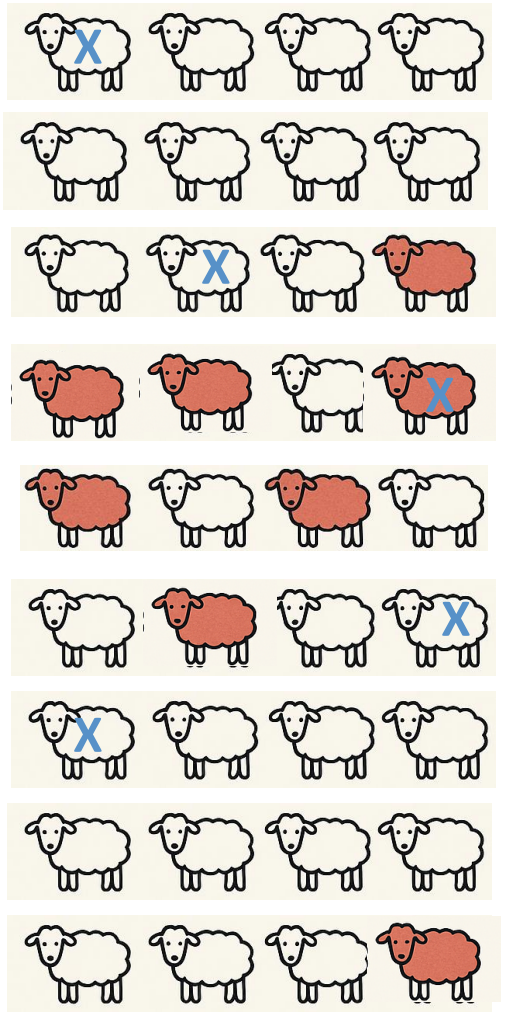
Surveillance that employs risk-based sampling is an example of risk-based surveillance.

Random vs. risk-based sampling

Random sampling



Risk-based sampling



Random vs. risk-based sampling

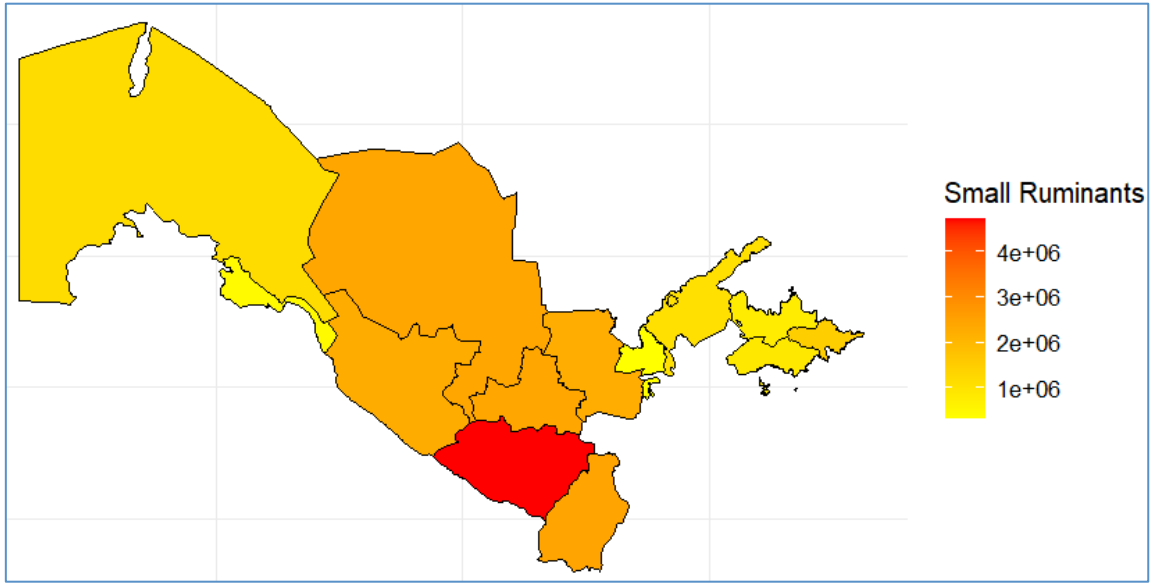
		Conventional sampling	Risk-based sampling
Prevalence in the sampled population: P	This is the "assumed" prevalence in the population from which flocks will be selected. In our example the unit of interest is the flock and we are assessing the capacity of our surveillance strategy (either conventional or risk-based) to detect the disease if it is present in the sampled population at the specified level. For conventional sampling the sample population is the entire population (e.g. all the flocks in the region). For risk-based sampling, the sampled population is the high-risk subpopulation. The prevalence will therefore be higher in the population sampled by risk-based sampling than in the population sampled when we use conventional sampling.	0.01	0.05
Number of flocks sampled: n	The number of flocks that we test in order to assess if the disease is present in the population. Here we assume that we sample the same number of herds in conventional sampling than in risk-based sampling.	100	100
Sensitivity at flock level: Se	The probability that an infected flock included in our sample is identified as infected. It depends on the performance of the diagnostic test in individual animals, the number of animals tested within the flock, and the number of infected animals in infected flocks. We assume that the flock level sensitivity is the same for conventional and risk-based sampling.	0.90	0.90
P one flock sampled is infected: P(I)	This is simply the prevalence in the sampled population (P). P(I) = P.	0.0100	0.0500
P one flock sampled is infected and tests positive: P(I,+)	The value of P(I,+) can be obtained as a product of P(I) * Se	0.0090	0.0450
P one flock sampled tests negative: P(-)	We are assuming that the specificity at flock level is 100%, therefore, there are no false positive flocks. Only infected flocks can be positive. The probability that a sampled flock is negative, P(-) is 1 - P(I,+).	0.9910	0.9550
P all flocks sampled test negative: P(All -)	The probability that all sampled flocks test negative is P(-) to the nth power.	0.4049	0.0100
P at least one herd sampled tests positive: P(at least one +)	The probability that at least one flock is positive is 1 - P(All -)	0.5951	0.9900

Prioritize based on a-priori risk

- Geographical location (flock typologies, population/density, proximity to border…)
- Connectivity
- Gaps in vaccination / immunity
- …

Other criteria could be used, but in the context of PPR surveillance, the above are probably the main ones.

Risk-based sampling - example



Small ruminant population by region in Uzbekistan (based on 2022 data from the Uzbekistan statistics agency, www.stat.uz)

Random sampling to ensure representativeness (useful for prevalence estimation)

Risk-based sampling concentrating in areas considered of higher risk (useful for disease detection)

Risk-based sampling - example

Organisation des Nations Unies
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Large-Scale Active Seromonitoring for PPR Virus in Small Ruminants begins in Uzbekistan

05/11/2024

In cooperation with the Food and Agriculture Organization of the United Nations (FAO) and the Veterinary and Livestock Development Committee of Uzbekistan, an extensive active seromonitoring project has been launched to detect the presence of Peste des Petits Ruminants (PPR) virus in small ruminants in the all Uzbekistan's border regions. This initiative is a critical step toward preventing the spread of the disease and enhancing food security across the country.

What are episystems and why are they important?

Episystems: interconnected populations maintaining virus transmission indefinitely.

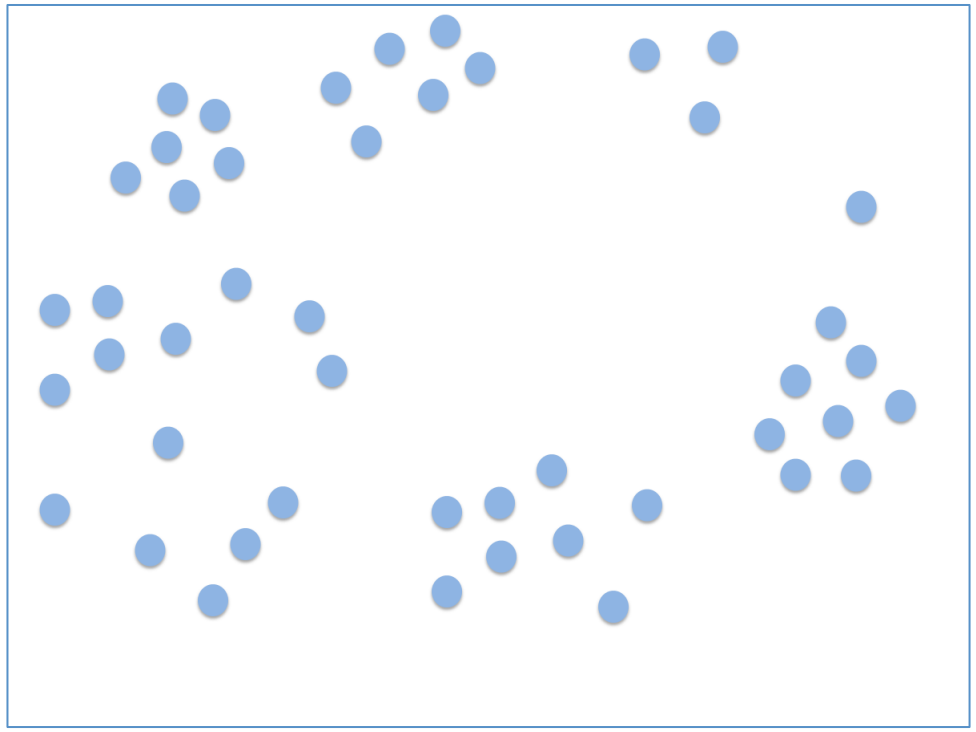
Understanding them allows:

- Identification of populations critical for PPR persistence.
- Targeting surveillance and vaccination to interconnected populations rather than just geographical areas.
- Identify how to break chains of transmission, essential for elimination.

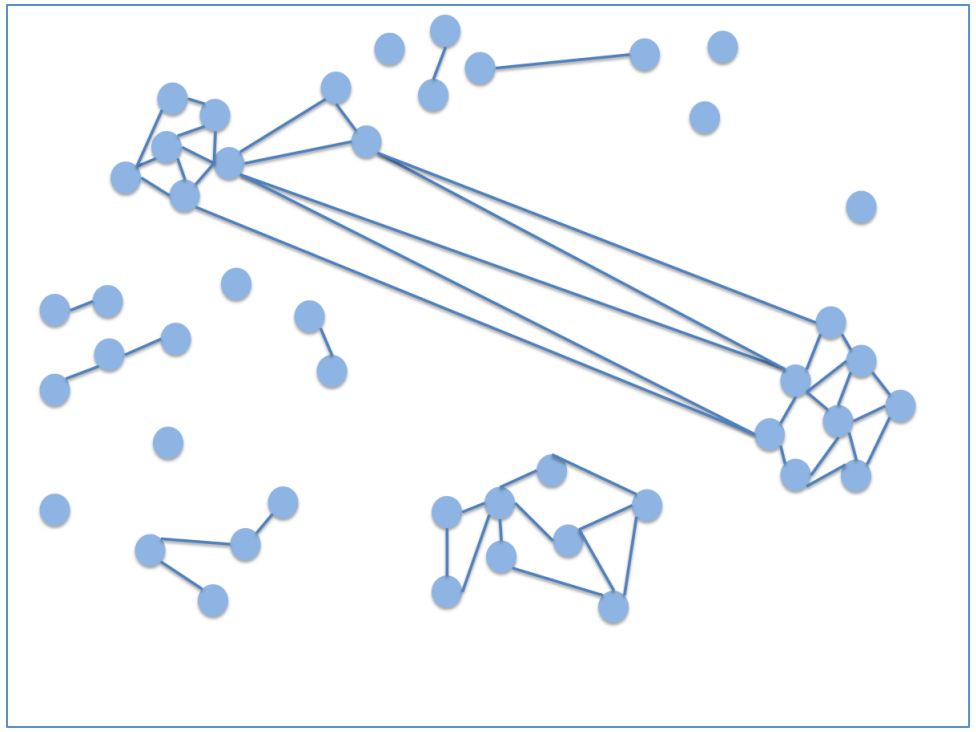
Episystem approach →shift in surveillance & control:

Geographically-based → Epidemiologically-based

From geographically-based to epidemiologically-based surveillance & control

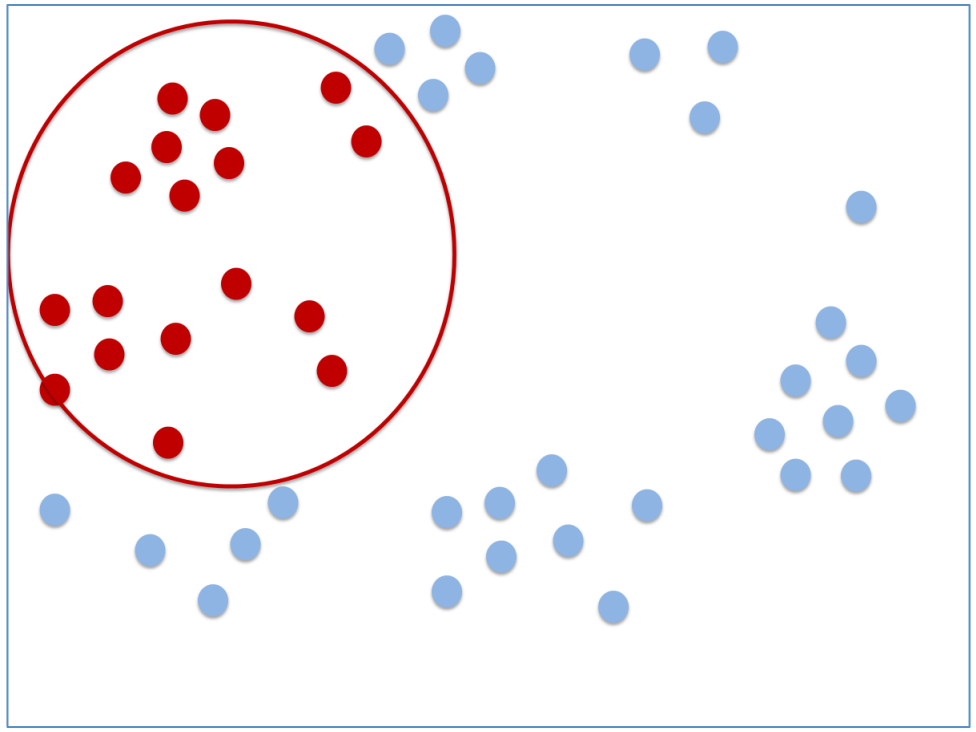


Purely geographical approach – connectivity ignored.

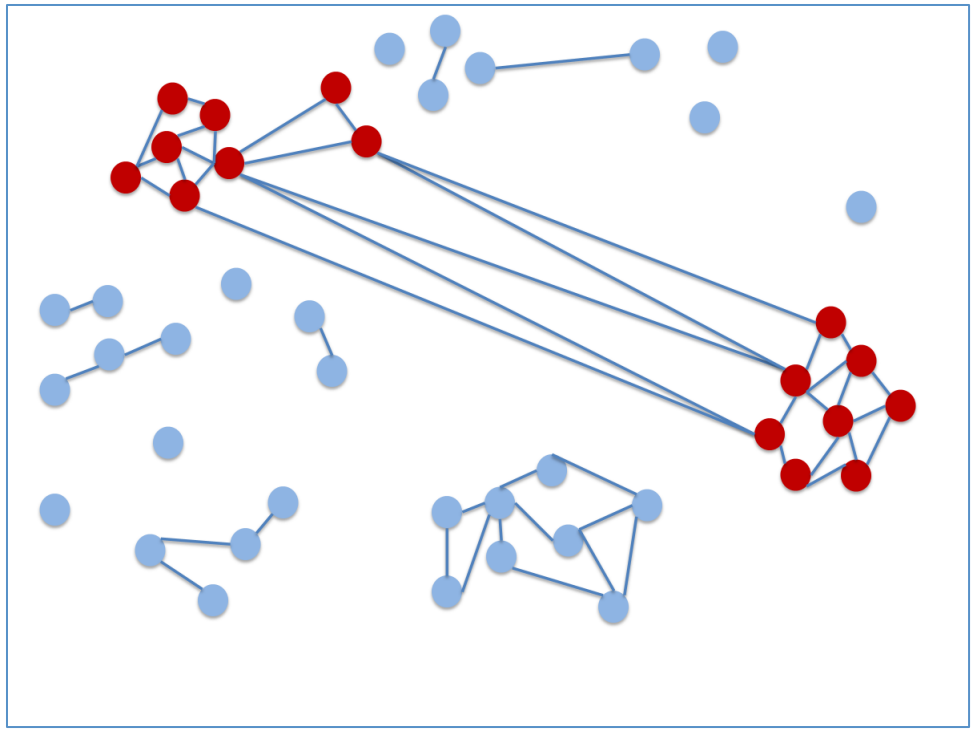


Episystem approach – connectivity considered.

From geographically-based to epidemiologically-based surveillance & control



Purely geographical approach – connectivity ignored.



Episystem approach – connectivity considered.

Risk pathways and connectivity

Risk of PPR spread follows animal movements, trade networks, social connections.

Risk pathways are shaped by:

- Animal mobility (transhumance, nomadism)
- Market networks
- Gaps in vaccination/immunity

Identifying and characterizing risk pathways

What data sources can we use:

1. Population and movement data
2. Outbreak and vaccination data
3. Molecular/Phylogenetic data

Population and movement data

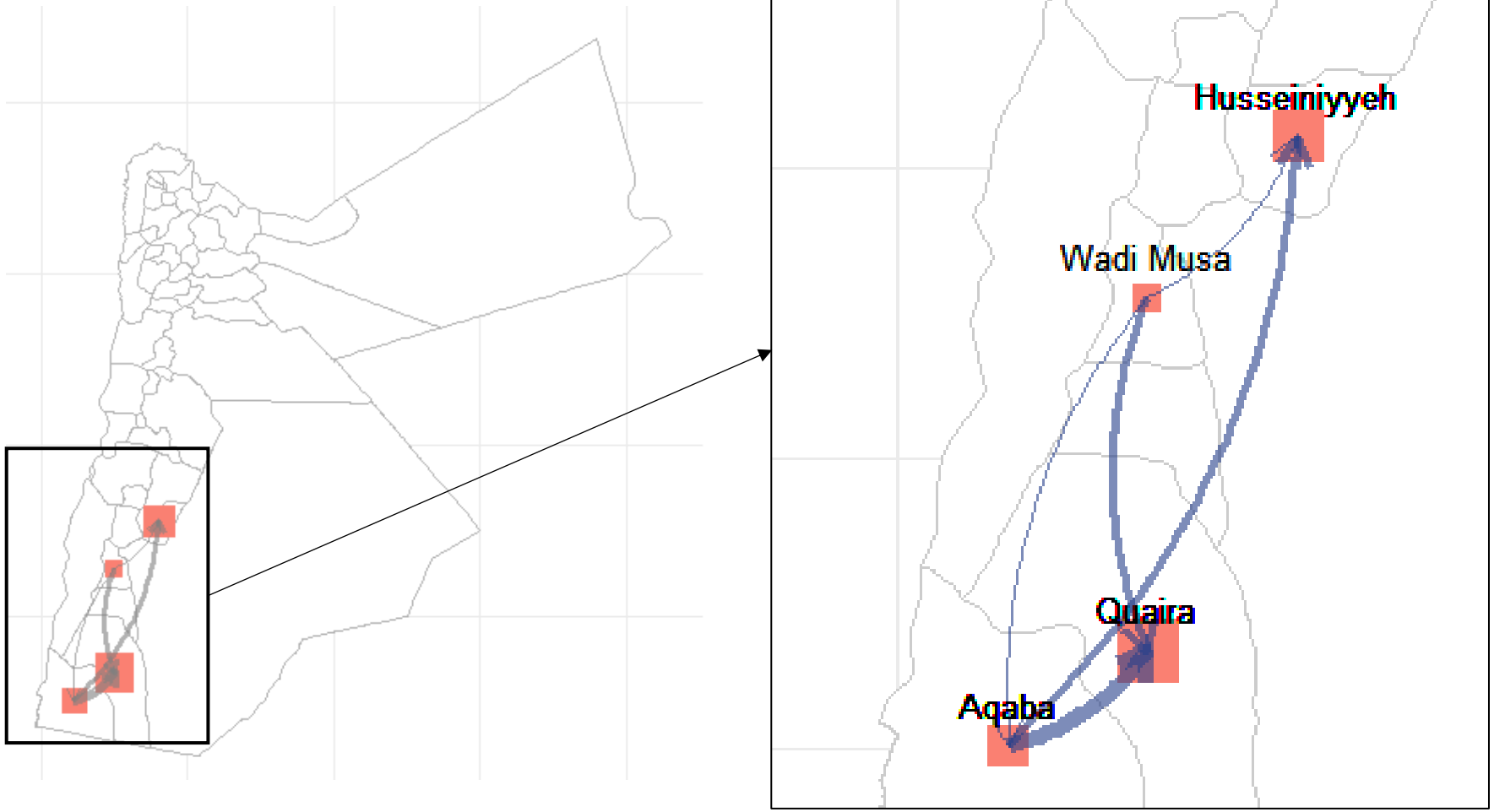
To map connectivity

- Small ruminant density and distribution (e.g. census data)
- Movement patterns (e.g. seasonal migration / transhumance)
- Livestock trade networks (trading hubs, flows of live animals)

Geospatial data integration (e.g. integrate census with participatory mapping).

Population and movement data

Mapping flows of small ruminants to local markets in Southern Jordan based on field surveys.



Surveillance and outbreak data

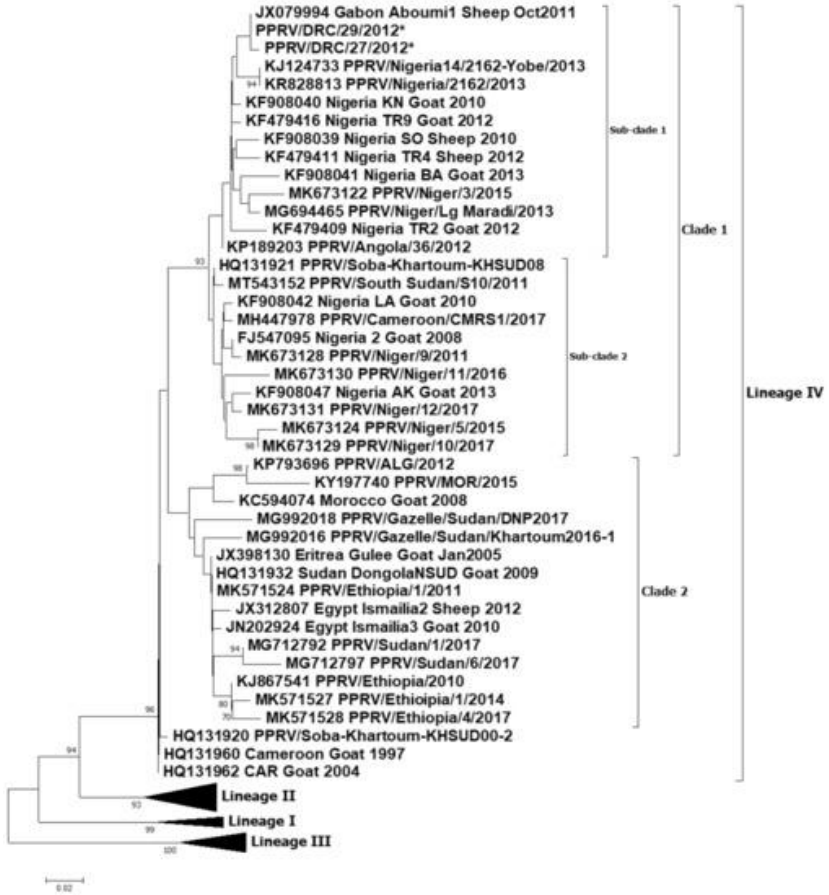
To track transmission events and risk factors

- Surveillance data and outbreak investigations
- Vaccination coverage (identify immunity gaps)

Molecular data

To identify circulating strains and their transmission pathways:

- Identification of circulating lineages/strains
- Molecular clustering and mapping distribution.



Neighbor-joining tree constructed using partial N gene sequences of peste des petits ruminants virus (PPRV), showing relationships among the PPRV lineage IV isolates circulating in Africa. Source: Mulumba-Mfumu, et al (2021). https://doi.org/10.3390/v13122373

From risk pathways to surveillance design

- Outline / identify risk pathways.
  - Qualitatively assess the risk for different subpopulations.
    - Target high risk subpopulations.

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A Qualitative Assessment of the Risk of Introducing Peste des Petits Ruminants into Northern Zambia from Tanzania

R. Chazya, J. B. Muma, K. K. Mwacalimba, E. Karimuribo, E. Mkandawire, M. Simuunza

First published: 12 January 2014 | https://doi.org/10.1155/2014/202618 | Citations: 1

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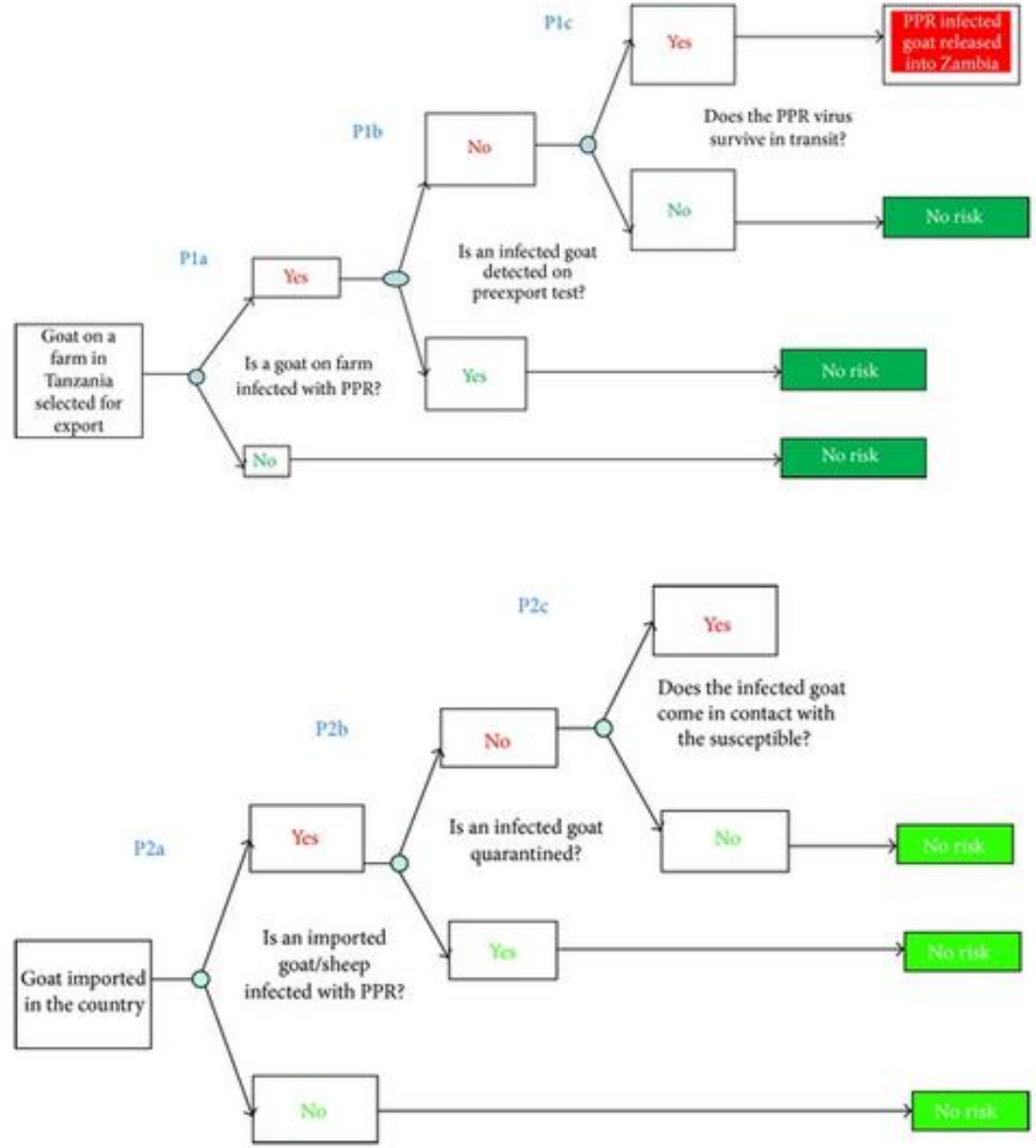


Qualitatively assess the risk for different subpopulations

Qualitative risk assessment:

Evaluation, in non numerical terms, of the overall probability of the pathway of events from hazard to outcome

- The result of a qualitative risk assessment is a probability, described by words
- Example of qualitative likelihoods:
  - Negligible
  - Very Low
  - Low
  - Medium
  - High
  - Very High

Must be clearly defined at the beginning of the risk assessment

Table 4 Example of qualitative risk (or likelihood) terminology for risk assessments

RISK ESTIMATE	DEFINITION
NEGLIGIBLE	So rare that it does not need to be considered
VERY LOW	Very rare but cannot be excluded
LOW	Rare but does occur
MEDIUM	Occurs regularly
HIGH	Occurs very often
VERY HIGH	Almost certainly occurs

From: OIE compartmentalization guidelines – African Swine Fever

Qualitatively assess the risk for different subpopulations

Qualitative risk assessment:

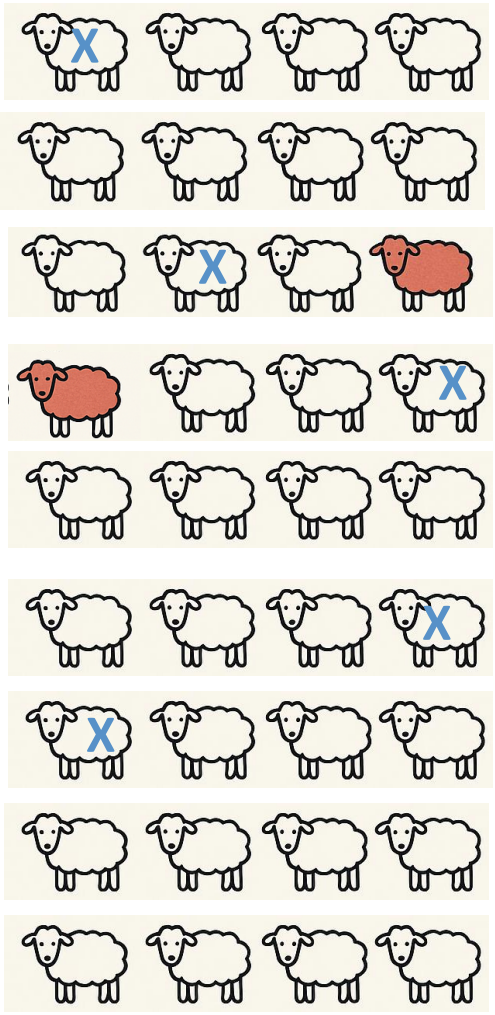
How to combine qualitative likelihoods along the pathway?

LIKELIHOOD 2	LIKELIHOOD 1					
	NEGLIGIBLE	VERY LOW	LOW	MEDIUM	HIGH	VERY HIGH
NEGLIGIBLE	Negligible	Negligible	Negligible	Negligible	Negligible	Negligible
VERY LOW	Negligible	Very low	Very low	Very low	Very low	Very low
LOW	Negligible	Very low	Low	Low	Low	Low
MEDIUM	Negligible	Very low	Low	Medium	Medium	Medium
HIGH	Negligible	Very low	Low	Medium	High	High
VERY HIGH	Negligible	Very low	Low	Medium	High	Very high

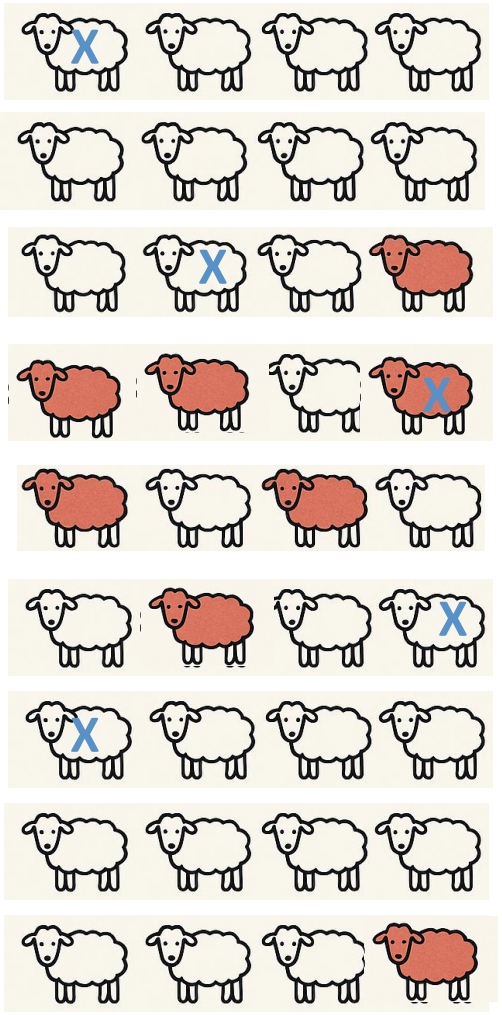
From: OIE compartmentalization guidelines – African Swine Fever

Target surveillance activities in high-risk subpopulations

General population



High-risk subpopulation



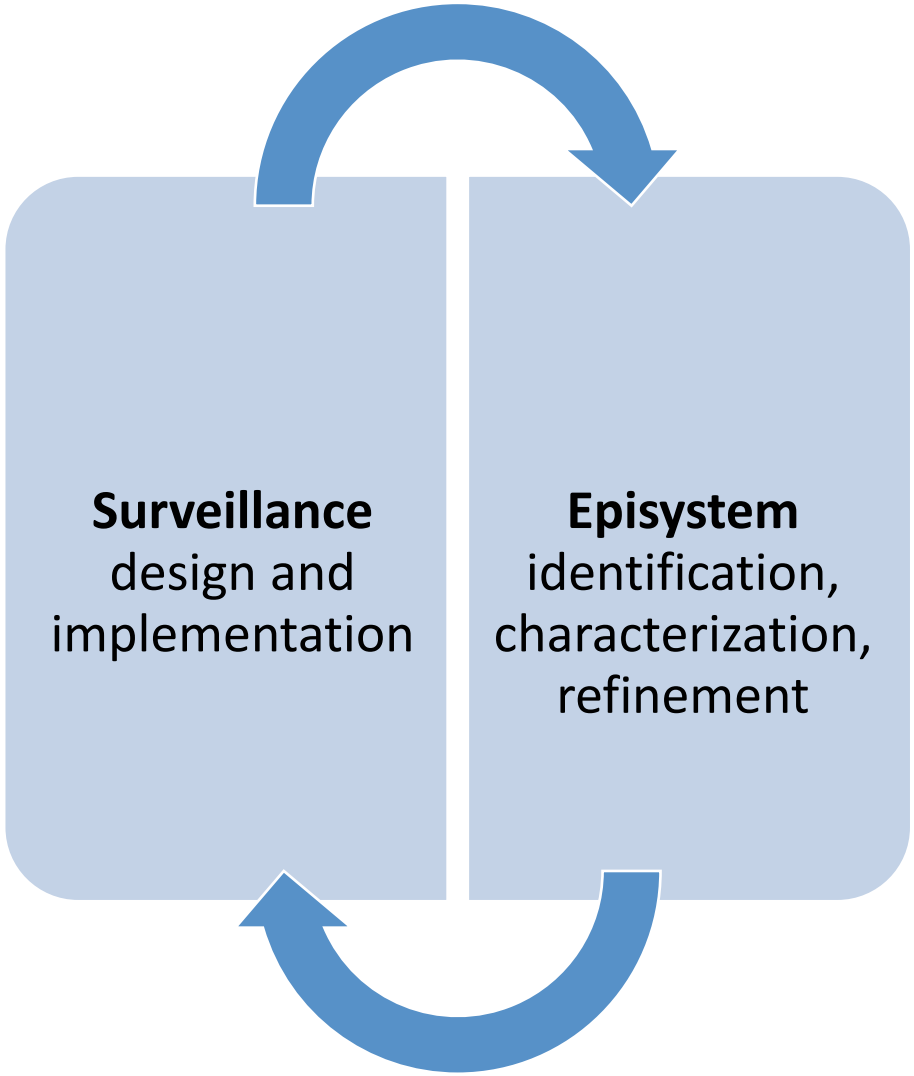
Data integration and feedback loop

From Episystems to Surveillance:

- Identifying/characterize episystems to target surveillance.
- Knowledge of connectivity to guide where & how to monitor.

From Surveillance to Episystems:

- Surveillance data:
  - continuously refines episystem characterization.
  - validates assumptions about connectivity & transmission.
  - Example: Identifying unexpected linkages between outbreaks using molecular data.



Recommendations

- Adopt risk-based sampling to increase chances of detection.
- Identify high-risk subpopulations to be targeted based on risk pathways
- Main criteria to consider:
  - Geographical location (flock typologies, population/density, proximity to border…)
  - Connectivity
  - Gaps in vaccination / immunity
- Start outlining risk pathways and characterizing episystems based on the “best available data”