Zoonotic Case Study
Facilitator Guide

<u>Scenario</u>
- The nation-wide prevalence of Bruntellosis has been increasing in animals and people
- Most human cases can be epidemiologically linked to cattle (*B. bovis* is the suspected agent)
- Only large-scale agricultural operations (> 500 animals) are included in current surveillance
- Primary transmission routes between herds unknown
- Test and cull of positive animals is only current control strategy

Facilitators
Encourage participants to discuss answers using context from their home countries and personal experiences.

Questions for discussion - ~5 to 6 minutes per question

Q1: What are some questions for which genomic data could add actionable information about this disease system? For each question, describe a public health intervention that could be designed, refined, or improved using genomic surveillance data.
Prompts:
- If new strains are identified, what changes might need to be made in existing vaccines or treatments?
- Could understanding transmission patterns influence quarantine or movement restrictions of livestock?
- What impact might the identification of antibiotic resistance genes have on the local antimicrobial stewardship programs?
- Would specific interventions be more effective in certain regions based on geographic differences in strain diversity?

Potential responses:

Public Health Questions	Public Health Actions
Do different species/strains result in different disease outcomes?	Develop PCR assays to genotype identified species/strains and virulence factors
Can we improve treatment success by characterizing AMR markers?	Develop treatment guidelines based on markers/strains
How many strains are circulating and how are they distributed across the country?	Compare baseline data before, during, after interventions
Is the animal vaccine equally effective in preventing disease across all subtypes?	Inform investment case for vaccination intervention Target vaccination campaign where it will be most effective Determine if new/different vaccines are needed
What are the transmission networks leading to spread/increase of the pathogen among animals?	-Targeted public education/communications campaign -Focus non-pharmaceutical interventions to decrease transmission among animals (regulations for quarantine, disposal of carcasses, testing of animals before/after sale)
Are certain species/subtypes more or less likely to infect humans?	Target interventions based on characteristics of the pathogen rather than prevalence alone

Q2. Why might it be important to understand if/how cross-species transmission among different animal reservoirs is occurring?
Prompts:
- How might identifying cross-species transmission change the approach to control strategies?
- Could certain animal species act as key reservoirs in sustaining the pathogen in both wildlife and livestock populations? How would you mitigate this?
- What role does genomic surveillance play in tracking pathogen spillover between animals and humans?

Q3. What sampling strategies and metadata would you want to inform the following?

- **Differences in animal vaccine effectiveness across bacterial species/strains**
  - Prompts:
    - What data about animal populations would you need to collect?
    - What animal populations would you sample?
    - How would genomic data from vaccinated vs. unvaccinated populations provide insights into vaccine effectiveness?
    - What metadata would be crucial to track during your planned control efforts?
- **Potential impact of genotype on phenotype disease outcomes**
  - Prompts:
    - What are some components of a sampling strategy that would be needed to identify virulence factors?
    - What populations of animals and humans would you want to sample?
    - What non-genetic data would you need to support your findings?
- **Identification of AMR markers**
  - Prompts:
    - What are some components of a sampling strategy that you would need to characterize AMR markers?
    - What non-genomic data would you need to inform this?
    - What human and animal populations would you want to sample?
    - How could genomic data help tailor antibiotic regimens based on specific bacterial genotypes?
- **Identifying key transmission pathways among animals within the country**
  - Prompts:
    - How would spatial and temporal data from genomic sequencing help map transmission routes?
    - What role might environmental factors or animal movements play in pathogen spread?
    - What animal populations/species would you want to sample?
- **Determine if import of new cases from neighboring countries is a major factor in the epidemiology**
  - Prompts:
    - How might genomic comparisons between local and foreign strains provide evidence to support or refute cross-border transmission?
    - What populations of animals would you want to sample?
      What geographic considerations do you need to consider when analyzing data for this goal (include sequences from local, national, regional, global)
    - What metadata, such as trade routes or livestock import records, would support this analysis?

Q4. What stakeholders should be involved and what roles would they play in the surveillance efforts you are planning?
- Some things to think about…

- Surveillance strategy design
- Sample collection (humans and animals)
- Diagnostics
- Sequencing
- Data sharing
- Reporting
- Analysis/interpretation/downstream actions
- Are human and animal health systems linked in your country?

Prompts:
- How would human and animal health systems need to collaborate in your country for effective zoonotic disease surveillance?
- What roles would veterinarians, epidemiologists, genomic scientists, and industrial farms, small/local farmers play in the effort?
- Who would be responsible for ensuring the ethical collection of samples from both humans and animals?
- How could policymakers, agricultural departments, and public health agencies work together to implement control measures based on genomic data?
- How would you determine what interventions have the biggest return on your investment?

Q5. What components of this system are unique because the focal pathogen is zoonotic?
Prompts:
- How does the involvement of both human and animal health sectors enhance or complicate surveillance efforts?
- What additional challenges arise from the need to monitor multiple species for the same pathogen?
- In what ways does genomic surveillance have to adapt to account for cross-species transmission and reservoirs in the wild?
- What control measures can be implemented in animals that may not be possible in people?