Veterinary Services

Update on *Theileria equi* genotyping at NVSL

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EP genotyping at NVSL

• NVSL’s approach
• Progress
• Next steps
• Potential pitfalls
Whole genome sequencing

- NVSL has developed expertise in next-gen sequencing and bioinformatics
  - TB and *Brucella* programs
  - Organism typing moving towards WGS
- Can we successfully sequence the larger genome of *T. equi* using same approach?
Progress

• Proof of concept
  – *In vitro*-derived *T. equi*
  – Ct value 29.1
  – Captured 97% of the *T. equi* genome at a coverage of 200x
  – Sequencing results were 30% *T. equi* and 70% equine

• Sample inventory
  – Approx. 600 whole blood samples archived
Next steps

• Build database of sequences
  – Compare sequence data to known epi info
  – Compare WGS to other published genotyping studies

• Evaluate methods of concentrating *T. equi* DNA
  – Minimize horse DNA
  – Decreased cost
  – Increased sensitivity
Next steps (cont.)

- Archived vs. fresh samples
  - Archived stored in EDTA, significant lysis of cells
  - Two different approaches for DNA concentration
    - Affinity purification for archived samples
    - WBC depletion for fresh samples
      - Enrich by *in vitro* culture?
Potential pitfalls

• Sensitivity
  – Can’t be cultured/isolated like bacteria
  – Low parasitemia in chronic carriers
  – Extraction of sufficient amount of *T. equi* for sequencing

• Exchange of genetic information
Questions?