M. ovi strain virulence subcommittee
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• NV: Mike Cox, Peri Wolff
• UT: Annette Roug
• ID: Frances Cassirer
• CA: Brandon Munk
• AZ: Anne Justice-Allen
• MT: Emily Almberg

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- Pauline Kamath (conservation & disease geneticist)
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Kezia’s task for WSWG: Touch base with reps from other states/provinces about participation

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Kamath et al. (2019) Scientific Reports

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Do we get cross-strain protection among closely-related strains?

Kamath et al. (2019) Scientific Reports

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Are strains from some parts of the tree consistently “worse” for bighorn than strains from other parts?

Do we get cross-strain protection among closely-related strains?

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M. ovi phylogeny

Do we get cross-strain protection among closely-related strains?

Are strains from some parts of tree consistently “worse” for bighorn than strains from other parts?

How much of the variation in disease outcomes is due to differences between strains?

Kamath et al. (2019) Scientific Reports
Approach

“Virulence” measurements
Approach

“Virulence” measurements
Approach

“Virulence” measurements ~ Strain’s location in *M. ovi* tree
Approach

“Virulence” measurements ~ Strain’s location in *M. ovi* tree

<table>
<thead>
<tr>
<th>State/Province</th>
<th>Begin Month</th>
<th>Begin Year</th>
<th>Herd_No</th>
<th>Location/Herd Name</th>
<th>Subspecies</th>
<th>Native or Reintroduced</th>
<th>Pop Trend Before Event</th>
<th>Pop Est Before 1</th>
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<td>Alberta</td>
<td>September</td>
<td>1978</td>
<td></td>
<td>Sheep River</td>
<td>Rocky Mtn</td>
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<td>2000</td>
<td>94</td>
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<td>November</td>
<td>1982/83</td>
<td>134</td>
<td>Yarrow/Westcastle</td>
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<td>1985/86</td>
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<td>Sheep River</td>
<td>Rocky Mtn</td>
<td>Native</td>
<td></td>
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</tr>
</tbody>
</table>

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Approach

“Virulence” measurements $\sim$ Strain’s location in *M. ovi* tree $+$ Everything else we can fit in

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Approach

“Virulence” measurements ~ Strain’s location in *M. ovi* tree

+ Everything else we can fit in

- Subspecies
- Heterozygosity/other
- Translocation history Other pathogens
- Sinus tumors — little data
- Drought/other environment

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Resources

WSF funding to support data aggregation and initial modeling

Help folks who need it to compile west-wide disease data

Pull together strain type, ELISA, and load data for individual animals from focal herds

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If you need help populating/updating the dies-off datasheet, this person could help

If you've got a good person who could do this, please contact me

Happy to set up data sharing agreements with any jurisdictions that need them
Resources

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Two big tasks:

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Immediate goals

• Map *M. ovi* strains by herd

• Compare demographic responses for well-studied herds to describe the relationship between strain type and:
  • Die-off size
  • Post-die-off population growth

• Build document that describes current knowledge / knowledge gaps around *M. ovi* virulence
Questions for the group

• Ideas on how to measure strain severity/virulence?
  • % decline in die-off
  • Years of poor recruitment
  • ???

• Thoughts re: additional key determinants of disease “severity” that should be included?

• What else have we forgotten?
Goal:
Set up methods/data to address the following

• Determine whether / how often novel *M. ovi* strain introductions pose big threats to already infected herds

• Describe current distribution of *M. ovipneumoniae* strain types and demographic responses for bighorn herds west-wide.
  • Estimated die-off size,
  • Lamb:ewe ratio in the five years following a die-off
  • Duration of persistence

• How much of the demographic response can be explained by variation in *M. ovi* strain virulence?