General notes:

* Yellow highlights are just for my reading and paying attention – general denote what I think are key points.
* I can tell you totally know this, but just pay attention to micro nomenclature and when things (e.g. species level names) should be italicized. I fixed the once that I noticed ☺
* I think you can shorten/tighten a lot of the writing however for a thesis with no word limit I actually often enjoyed the extra words being very explicit in what was done etc. but would suggest editing for more scientific/pithy writing for manuscript submissions.

**Q’ I noted for defene**

**Q – Selection bias – high quality of milk observed. How to enroll farms less likely to volunteer survey data.**

**Q – SCC freeze thaw issue – is that how is it done clinically?** Are samples assessed fresh or frozen. If frozen, this is a good point to make if people/reviewers bring it up. Otherwise, your response regarding comparability within study ok but beware between studies is perfect.

**Q- Can you describe the difference in cow management (tie stall etc) and say what you think is happening to cause differences in infection rates?**

**Q - Wouldn’t the below bias those cows to certain SCC levels bc impact of time in milk on SCC levels?**

The goal was to enroll 35 cows of varying parity in early- to mid-lactation from each herd for the duration of the study. In 1 herd with approximately 35 lactating cows, all cows were sampled. In 8 herds with ≥ 35 cows and with available DHIA data, a stratified random approach was used with cows stratified by SCC, lactation number, and DIM and then randomly selected across these variables. In 1 herd with ≥ 35 cows and no DHIA data, the producer generated a list of 35 cows in early lactation so that they would continue to be milking for the duration of the study.

REPEATED MEASUREMENTS  
The mean number of observations per quarter included was 2.1 (2; 1-4). Twenty-seven percent of observations were the sole observation contributed to the data set by a given quarter, 41% came from quarters contributing 2 time points, and 31% and 1% came from quarters contributing 3 and 4 observations, respectively. The average time elapsed between sequential observations of a quarter was 37.1 days (median: 34.5; SD: 11.6), with an overall range of 27-96 days.

**Q- STAU order of prevenance change – why do you think Staph aureum may be more common w tiestalls? I recognize numbers are small, but this finding has meaningful clinical implications and is worth hyping up as a reason to pursue additional studies…**

Quarter-level prevalence of IMI by pathogen was similar between bedded pack and tiestall farms, with slight variability found for the most prevalent species. For the bedded pack farms, the most commonly identified pathogens were *Staph. chromogenes,* followed by *Strep. uberis*, *Staph. haemolyticus,* and then *Staph. aureus.* For the tiestall farms, the most commonly identified pathogens were *Staph. chromogenes,* followed *Staph. aureus*, *Strep. uberis*, and then *Corynebacterium* spp*.*

**Q – where are the staph spp. coming from?**

* We discussed this, but focusing and framing from public health perspective is important. Could consider as future direction – swabbing of udders to establish/explore colonization vs. environmental exposures etc. . Understanding pathogen transmission and colonization dynamics has a big impact on public health and clinical interventions.

**Q – you assessed clonality in persistent infecitons (by MLST) – but did you look at clonality within herds? (related to contagiousness)**

* We discussed, but perhaps good fodder for future directions.

**Q- while # of VF didn’t a/w SCC – what about a modeling approach to identify specific VF a/w SCC? – not enough variation between isolates….**

* *Neither overall number of virulence factors nor blaZ carriage was found to be a significant predictor of SCC category. blaZ carriage, number and type of virulence factor instead appeared to be a function of strain type (Table  
  -* Once again, may be good fodder for future directions.

I love the below figure. Noted in document, but also providing here:

* Potential clinical impact of this is meaningful I think - for those w lines farther apart (e.g. S Warner vs S. Devriesei) - a single SCC level may be clinically useful while for others, infection overlaps w healthy depending on day. Can extrapolate to how this could play out clinically – by knowing species level ID, can more appropriately interpret SCC and need to treat.

A group of graphs showing different types of growth

Description automatically generated