* Description of considerations for enrolling a herd
  + Dairy farms who responded to the survey (cite previous paper), indicated they met enrollment criteria AND were interested in further participation
    - Responded to survey in Winter 2018-2019
    - Responded at least "sorta" or "very" interested (no "not really"/"nope")
    - Testing with DHIA at least monthly
    - Herd size 35-120 lactating cows
  + Contacted if they were interested, met criteria, and in 1 of 4 categories of bedding/housing combination we were interested in
    - What we WANTED
      * 10 FREESTALL with SAND
      * 10 FREESTALL with WOOD
      * 10 BEDDED PACKS
      * 10 TIESTALL with WOOD
    - What we GOT
      * 1 FREESTALL with SAND
      * 5 FREESTALL with WOOD
      * 5 BEDDED PACKS
      * 10 TIESTALL with WOOD
* Description of administration of survey, sample collection
  + Collection of BTM and bedding
    - Agitate, dipper, etc.
    - Description of collecting used, unused bedding- grabs from different spots? Mixed them? Subsampled?
  + Survey- used KoboCollect, tablet
* Description of culture procedures at Minnesota for BTM and bedding, St. Albans for culture data from them?

***Bedding and BTM M and M from patel’s paper:***

Frozen bedding and BTM samples were shipped on ice to the Laboratory for Udder Health (University of Minnesota Veterinary Diagnostic Laboratory, St. Paul) for analysis. After thawing at room temperature, 50 cm3 of packed bedding material was weighed and measured into a new Whirl-Pak bag Nasco, Fort Atkinson, WI), 250 mL of sterile water was added, and the contents were mixed and left to stand for 10 min. Serial 10-fold dilutions of the samples were made using sterile water (Becton Dickinson and Company, Franklin Lakes, NJ). Sample dilutions were plated onto MacConkey agar (gram-negative bacteria selection) and colistin naladixic acid agar (gram-positive bacteria selection, Becton Dickinson and Company) plates and incubated overnight at 37°C. For the MacConkey plates, lactose fermenting (pink) colonies were counted as coliform bacteria and all other colonies were counted as non-coliform gram-negative bacteria. Colonies with a confluent appearance on MacConkey agar were identified to the genus level using a MALDI Biotyper (Bruker Daltonics, Billerica, MA), and colonies identified as Klebsiella spp. were counted and reported as a percentage of total coliform count. For colistin naladixic acid plates, colony morphology in conjunction with catalase reaction and Gram stain were used to differentiate colonies of Staphylococcus spp., SSLO, and Bacillus spp. Total bacteria count (TBC) and counts of Bacillus spp., coliforms, Klebsiella spp., non-coliform gram-negatives, Staphylococcus spp., and SSLO were recorded as colony-forming units per cubic centimeter of wet bedding. The minimum limit of detection was 25 cfu/cm3 (max count of 6,250,000 cfu/mL).

After thawing to room temperature, bulk tank milk and a 10-fold dilution of the bulk tank milk sample were plated onto MacConkey, Factor (gram-positive selective agar; University of Minnesota, 2016), and Focus (University of Minnesota, St. Paul, selective for SSLO bacteria) media plates and incubated for 2 d at 37°C. Lactose fermenting (pink) colonies on MacConkey medium were counted and reported as coliform bacteria. All β-hemolytic colonies on Focus medium were counted and identified to the species level using a MALDI Biotyper, as these colonies were suspect for *Streptococcus agalactiae*. All colonies on Focus medium that were not identified as *Strep. agalactiae* were counted and recorded as SSLO. β-Hemolytic colonies on Factor medium were counted and identified to the species level using a MALDI Biotyper, and those with a confidence score ≥2.0 for *Staph. aureus* were counted and reported as such. Non-hemolytic colonies of Staphylococcus spp. (based on colony morphology, catalase reaction, or Gram stain) were counted and reported as NAS. For Mycoplasma spp., 0.1 mL of BTM was swabbed across the entire surface of a Mycoplasma agar plate and incubated for 7 d in a 7% CO2 incubator at 37°C. Plates were examined for Mycoplasma spp., and colonies were counted by a trained microbiology technician. For each BTM sample, total counts of coliforms, NAS, SSLO, *Staph. aureus*, *Strep. agalactiae*, and Mycoplasma spp. were recorded as colony-forming units per milliliter of milk. The minimum limit of detection for the BTM culture protocol was 5 cfu/mL (max count of 62,500 cfu/mL).

For the beddings, we use MacConkey and CNA agar.

Bulk Tanks use Factor (gram positive selective), Focus (Strep selective; FKA MKTK) and MacConkey

* Considerations for dealing with 40 herd bedding data
  + Cut points from culture data (e.g., less than 10 CFU; max count of 6,250,000)
    - Make them categorical?
  + Zeroes in bedding culture data
    - Make difficult to just log transform bedding bacteria counts

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***Data analysis notes***

For Patel’s Objective 1, linear regression model:

