NC1192 Station Annual Report (2023)

NC1192, "An integrated approach to the control of bovine respiratory disease"

Chair: Sarah Depenbrock, DVM, MS, DACVIM (LAIM), School of Veterinary Medicine, UC Davis.
Secretary: Manuel Chamorro Ortega, DVM, MS, PhD, DACVIM (LAIM), College of Veterinary Medicine, Auburn University

Experiment Stations submitting reports:

Auburn University
University of California Davis
South Dakota State University
Texas A&M University - VERO
Washington State University
University of Georgia
Mississippi State University

2023 meeting minutes:

Date: Jan 24th
Location: Chicago. Marriott in Chicago (CRWAD 2023 venue). Avenue Ballroom
Time: 1:30-5:00 pm Eastern Standard

In attendance: *(existing members, interested, and graduate students of members)*
Brad Vanderlay, Scott McVey, Kathe Bjork, John Richeson, Chris Chase, M Thoresen, Stephan Tam, Alexis Thompson, Mathew Scott, Roberto Palomares, Paul Morley, Amelia Woolums, Natalia Cernicchiaro, Mike Sanderson, Noelle Noyes, Chris Penritos, Max Chung, Robert Leres, Maggie Murphy, Paul Morley, Narissa Bectel, Santiago Cornejo, Will Crosby, Florencia Meyer, Robert Valeris-Chacin

Time	Topic
1:30-1:45	Introductions and welcoming new members

- All members and many graduate students of members in attendance introduced themselves.

Time	Topic
1:45-2:00	NIFA updates provided by Dr. Kathe Bjork

- Tips for success:
    - Follow the RFA for all the nuanced data; reviewers will look for any reason to disqualify an application
    - Join a grant review panel if you can; being on a panel gives you valuable insight
    - Talk to the NPL prior to submission (Kathe, Tim, etc)
    - Pay attention to the details- deadlines etc. Communicate early to NPL
    - Resubmissions are more successful when working with NIFA to improve a proposal

  - Use the page to respond provided in the re-submission; don’t fight the reviewers (vs resubmitting a fresh proposal)

2:00-4:00 Discussion of experiment station reports

- Note for discussion: some members were able to receive funding from their experiment station to pay for travel to this meeting.
- Order of station report presentations based on cattle per capita by state.
- South Dakota state: updated provided by Chris Chase, and was based on his presentation here at CRWAD
- Kansas State: updated provided by Natalia Cernicchiaro. Discussed predictive models, working with Woolums et al. at Miss; metaphylaxis - perceptions and information from feedlot managers to assess why they make antibiotic use decisions for various categories of BRD. Looking at economic risk of BRD outcomes
- Texas: Mathew Scott provided many research updates via Powerpoint on the topics of: Impact of management decisions during the cow-calf, backgrounding, and feedlot phases of beef production on BRD morbidity and mortality risks; Impact of the neonatal microbiome on morbidity and performance of beef cattle; Influence of tulathromycin metaphylaxis on the whole blood transcriptome of high-risk stocker cattle; Effects and interactions of vaccination and marketing strategies on host gene expression and bovine respiratory disease outcome.
- Texas: update provided by Dr. Valeris -Chacin: Sequencing, development of targeted enrichment for M. bovis to assess how many strains the methodology can detect; WGS of M. bovis isolates. Wants to use Nanopore which requires more DNA, but M. bovis doesn’t like to grow as well, using an amplification technique to then use for sequencing.
- Texas: update provided by Paul Morley: using a bait and sequence to avoid culture step (target enhanced sequencing for M. haemolytica); cooperative with another for group surveillance for M. haemolytica, using DNA extraction from rope samples or water bowl swabs, PCR and 16s; part of Stephen Tamm’s PhD; Will Crosby led a paper that was published in Animal Microbiome, from feedyard and tildipirosin metaphylaxis, and compared small nasal swab vs long double guarded swabs vs proctology swabs; notes different microbiomes with the different locations, but the trends for BRD are the same across sample types and changes in microbiome that are predictive of BRD (and it's not the Pasteurellaceae). Notes that they see is a large increase in Tenericutes (mycoplasma types) from 16s (So don’t know what species), also see a concomitant lowering of Moraxellaceae - this is a neat marker - very predictive of BRD.
- Mississippi: update provided by Amelia Woolums. Ppt presentation featuring collaboration with AL, CA, KS, SD, TX and topics of:
  - With KS and TX: (lead institution: TAMU) Quantify the impact of vaccination (MLV 5-way) twice preweaning BRD morbidity, mortality and performance in the feedlot.
  - Determine the impact of exposure to auction market and order buyer facility on health and performance in the feedlot

    - Evaluate inflammatory responses (TNF-a, IL-1b, HPTG) on d. 90, d. 97, d. 217, d. 220
    - Evaluate parasitism at feedlot arrival (d 220) on health and performance in feedlot
    - Also: using data from multiple feedlots, determine associations between pen and yard level management factors and health outcomes during the feedlot phase of production.
    - In progress: with TX and ARS (GA)
    - In high-risk stocker cattle given tulathromycin META or not, sampled over a 70-day backgrounding period:
    - Compare the prevalence of multidrug resistant (MDR) M. haemolytica on nasopharyngeal swabs at d. 0, 21, and 70;
    - Characterize the nasopharyngeal microbiome, using metagenomic 16S rRNA gene sequencing;
    - Characterize the nasopharyngeal resistome, including AMR genes and mobile genetic elements
    - Describe and compare the relative and absolute abundance of genome sequences for nasopharyngeal M. haemolytica, using a novel target-enriched metagenomic sequencing approach
    - Characterize morbidity, mortality and weight gain
- Mississippi collaboration with Tx VERO: Update provided by John Richeson: Completed a pen replicated study - 3 treatments in high risk cattle (parental pentavalent + MH, trivalent IN + BVD bivalent + MH, No viral vaccination). This was started due to practitioners seeing increased Histophilus mortality. Work that Laurel Gershwin did indicates that BRSV is immune modulating to shift to TH2 side, then H. somni takes advantage of this scenario; in this study, there was no difference between treatment groups, but there was sig more Histophilus by qPCR in IN vaccinated group, not a lot of concurrent BRSV shedding; antibody titres for BRSV showed evidence of a natural BRSV outbreak; J Richeson suspects BRSV is ubiquitous in the feedlot. Also working on ear tags for diagnosing BRD and done some beta testing. Measures points of movement (feed, water)+ has a thermometer; consulting DVM has the ability to adjust the algorithm. He notes Merck has a similar tag, except it has IR light down the ear canal for temp and instead of location tracking it has a 3 axis accelerometer. Cost of devices has been prohibitive however they are getting cheaper, Richeson believes feedyards may start trying them. Could this replace the clinical score? Tags can go cellular or wifi.
- Texas:discussion provided by Paul Morley: Regarding the vaccine field trial that Richeson mentioned - came together with several others from NC1192 - grad students helped with this project. Sick cattle have elevated Mycoplasma abundance, lower Moraxella abundance. Mycoplasma and Moraxella are large proportion of the microbiome. Vaccine was associated with a change in this ratio; the IN vaccinated were opposite the others with no difference in disease rate, but there was a difference in microbiomes. IN vaccination was associated more Histophilus on q PCR and 16s. On the deads, only Pasteurellaceae are cultured from the lungs. None of the IN vaccinated

animals had Mannheimia, but were more likely to have Histophilus in nose and lungs - published in JAS (a portion, from the PCR portion).
- Georgia: update provided by Roberto Palomares. Presented ppt topics on: Screening of the Nasal Microbiome in Dairy Calves (Route of vaccination, Trace mineral administration, Bovine Virus Infections);

4:00-4:15 Break

4:45-5:00 Future multistate research & extension collaborations:
- Group discussed a need for an NC1192 award for grad students at CRWAD ($500-1000 or a fancy related book. Ex:Chase immunology book). Ideas to fund the award: cash collection from members, funds from participating stations
- Amelia Woolums notes a need to set up collaborations with cow -calf herds at experiment stations (many of us have university cow-calf herds) on vaccines at pre weaning.

Planning BRD symposium: (*SD provided updates on Sharif Aly's behalf)*
- BRD symposium planning committee members: SA and Grant Dewell as co-chairs; other members: Depenbrock, Amelia Woolums, Paul Morley, Natalia Cernicchiaro, John Richeson, Chris Chase
- The committee meets regularly, 2nd Wednesday of every month
- We have met twice so far and members are preparing for the 2024 meeting tackling different subtasks
- BRD symposium dates are set for Aug 6-7 2024 (AVC will be August 8-10) (NOTE This should be 7,8th (Night of 6th is welcome reception); program all day on 7th and 8th - finish 5pm on 8th because the AVC dinner starts that night
- Sponsorship levels and networking with industry is ongoing
- That's all for now and more to come!

Planning projects, publications, courses, workshops
- Discussion regarding the groups' need to find a way to fulfill objective 6- economic impact of BRD. The work must be collaborative to count towards 1192.

Update on webinars- (*Depenbrock provided an update on Grant Dewall's behalf*)
- Webinars are going well; there was one in October and January.
- Getting good viewership; 50 or so
- Videos will be available at KSU Beef Cattle Institute website.
- Appreciate those that have contributed a presentation.
- Reminder next webinar will be in April; if anyone has something they would like to present or has a recommendation for what they would like to be presented, please contact Grant Dewell.

5:00- 5:15 Future meeting plans
- Meeting concurrent with CRWAD. General sentiment that this is working in terms of turnout. One downside is that we don't provide outreach to stakeholders, which would be good for generating research plans. CRWAD likes having multi-state projects here. Could be moved to Saturday before CRWAD.

- Alternatives: AABP. And could sponsor a student award.
- Another suggestion provided was to still have standard meeting at CRWAD and hold extra meetings or extra events at AABP
- An added goal should be to use our meetings to increase outreach to stakeholders
- Other discussion: should the group organize a listening session or student award or other activity at AABP?

5:15-5:30 Consensus statement and wrap up.

Accomplishments, impact and deliverables focused on the NC1192 project's objectives

Six stations sent reports for the semiannual 2023 activities (list of participating stations are on NIMSS website).

I. Accomplishments –

Objective 1: *To elucidate pathways by which host characteristics, pathogen virulence mechanisms, and environmental impacts interact to produce BRD, and to develop strategies to mitigate detrimental factors and enhance protective mechanisms.*

1. (TX) Pathogenomics of the respiratory *Mycoplasma bovis* strains circulating in cattle. In this project, *M. bovis* cultures isolated from ante and post-mortem specimens are subcultured in the VERO lab. Subsequently, the DNA is extracted and due to the low biomass of *M. bovis* growth, a whole genome amplification is performed as a previous step before library preparation. Oxford nanopore native barcoding and flow cells compatible with the new Q20+ chemistry are used for library preparation and sequencing. The long reads are filtered and assembled using Filtlong and Canu, respectively. The complete genomes are annotated in Prokka with a reference *M. bovis* annotated genome downloaded from NCBI. Roary is employed to elucidate the pangenome and Snippy is utilized for the detection of single nucleotide polymorphisms (SNPs). Phylogenetic trees are constructed in Mega and antibiotic resistance genes are characterized with ResFinder. The study collaborators at Texas A&M University (Matthew **Scott**, Sarah **Capik,** Paul **Morely**) and Mississippi State University (Amelia **Woolums**) characterized pathogenomics of different strains of *Mycoplasma* bovis circulating in cattle with the goal of developing a targeted enrichment methodology to evaluate the *M. bovis* strain diversity.

2. (TX) Impact of the neonatal microbiome on morbidity and performance of beef cattle is a collaboration between Texas A&M University (Matthew **Scott**, Sarah **Capik,** R. **Valeris-Chacin**), New Mexico State University (G.C **Duff**) and University of Nebraska-Lincoln (JD **Loy**). This project evaluated the temporality of BRD commensals on first colonization of the respiratory tract of neonatal calves and the composition of the neonatal respiratory microbiome of beef and dairy calves. Preliminary results indicate self-clustering of nasal samples (i.e., calf ID) at birth, with increasing similarity to dam nasal swab samples over 6, 12, and 24 (most similar) hours. Initial interpretation and hypothesis is that sequencing analysis has captured bacterial colonization events within the first 24 hours of live, and the dam's bacterial nasal flora is associated with the calf's nasal bacterial flora by 24 hours post-parturition.

3. (TX) Effects and interactions of vaccination and marketing strategies on host gene expression and bovine respiratory disease outcome. Collaborators at Mississippi State University (Amelia **Woolums,** BB **Karisch**) and Texas A&M University (Matthew **Scott,** SF **Capik**) evaluated cattle management decisions, related to reducing risk of disease, influence host immunity and cellular activity, and prompt changes in the composition of the microbial communities. Results from this study indicate that cattle, regardless of vaccine administration, demonstrate a continuous increase in gene expression related to specialized pro-resolving mediator (SPM) biosynthesis, which

regulates both acute and chronic airway inflammation, CD28-dependent T-cell survival and co-stimulation, and carbohydrate/fatty acid metabolism. In this case these mechanisms and pathway were driven by differentially expressed genes (DEGs) previously identified to be increased in expression at facility arrival in cattle that remain clinical healthy within high-risk populations, compared to cattle that eventually develop BRD. Additionally, MLV-vaccinated cattle possessed DEGs which enriched for the downregulation of complement/coagulation cascades and the upregulation of Th17-cell-mediated immunity. Importantly, MLV-vaccinated calves did not demonstrate a change in type I interferon-associated gene expression prior to weaning. The study also addresses NC 1192 objective 3.

4. (TX) Characterizing the impact of metaphylaxis on the microbiome and resistome of beef feedlot cattle. Researchers from Texas A&M University (Matthew **Scott,** R **Valeris-Chacin,** Paul **Morley**) compared effects of 6 different antimicrobial drugs when used for BRD metaphylaxis on the respiratory and fecal microbiome and resistome in feedlot 120 cattle. Results from this study are pending. The study also addresses NC 1192 objective 3.

5. (WA) Identification of pathogen profiles and loci associated with enhanced resistance to BRD in 1000 pre-weaned calves in Ohio. Researchers from Washington State University (Holly **Neibergs**) and Texas A&M University (C**. Seabury**) are using bacteriology and virology analytics and Illumina BovineHD BeadChips for genotyping of mid-nasal and deep pharyngeal swab samples collected from young calves in Ohio to identify pathogen profiles. Genome-wide association results will be compared with previous results in pre-weaned dairy calves in California and New Mexico. In the current time period 62 new calves have been added to this study and results are pending.

Objective 2: *To develop and validate methodologies for accurate BRD diagnosis, objective risk assessment, and surveillance to detect new trends in BRD occurrence.*

1. (SD) Researchers at South Dakota State University (C. **Chase**) are using RNA hybridization methods and deep sequencing to identify astroviruses associated with BRD. A new virus that could be part of the BRD complex has been identified. A manuscript has been submitted.

2. (TX) Evaluation of methods for group-based surveillance and characterization of *Mannheimia haemolytica* in beef feedlot cattle. Collaborators from Mississippi State University (Amelia **Woolums**) and Texas A&M University (SF **Capik,** R **Valeris-Chacin,** and P. **Morley**) evaluated sampling and testing methods that would facilitate investigation of *Mannheimia haemolytica* in groups of cattle to study relationships between the occurrence of BRD and members of the respiratory microbial community such as *Mannheimia haemolytica*. This study included 10 pens of cattle from a variety of sources (all >600 miles from the feedlot) that had an average of 18.8 days-on-feed at sampling. For each pen, ropes were placed the afternoon prior to sampling, and then

collected the following day. Swabs of the bottom and sides of the waterbowl were also collected at this time. Additionally, 10 cattle were randomly selected from each pen and sterile 16” rayon-tipped proctology swabs were used to sample the nasal passage and nasopharynx (NP swabs). Samples were cultured to detect Mh, and DNA was extracted for testing using qPCR for Mh, 16S sequencing to characterize the microbiome, and target-enriched sequencing to characterize Mh and AMR gene sequences. Results demonstrate significantly greater sensitivity of qPCR over culture for detection of *Mannheimia haemolytica* in swabs of the nasal passage and nasopharynx. Culture was unreliable for detection of *Mannheimia haemolytica* in other samples such as rope samples and waterbowl swabs. These investigations are being conducted to evaluate detection and characterization of Mh in 6 different demographic groups of beef cattle: a) Young (~5 cwt) beef-breed feedlot calves, b) Yearling (~9 cwt) beef-breed feedlot cattle, c) Young (~5 cwt) dairy-beef cross-breed feedlot calves, d) Young (~3-4 cwt) beef-breed backgrounding calves, e) Young (~200 cwt) dairy-beef cross-breed bull calves in pens. The study also addresses NC 1192 objective 4.

3. (TX) Comparison of sampling and diagnostic techniques for recovery of *Mannheimia haemolytica* and respiratory microbiome characterization from feedlot cattle. Collaborators from Mississippi State University (Amelia **Woolums**) and Texas A&M University (SF **Capik,** and P. **Morley**) compared the ability to recover *Mannheimia haemolytica* using 29.5 inch (74.9 cm) deep-guarded nasopharyngeal swabs, 16 inch (40.6 cm) unguarded proctology swabs, or 6 inch (15.2 cm) unguarded nasal swabs when characterized using culture, real time-qPCR, and 16S rRNA gene sequencing. Samples for aerobic culture to identify *M. haemolytica* and DNA extraction for qPCR and metagenomic sequencing were collected from the upper respiratory tract of high-risk cattle 2 weeks after feedlot arrival. Results indicated that there was high concordance of culture and qPCR results for all swab types (results for 77% and 81% of samples agreed completely across all 3 swab types for culture and qPCR respectively) and microbial communities differed only slightly between swabs, and were comparable across swab types with respect to treatment for BRD. qPCR showed high concordance as well (81% agreed completely), but deep-guarded (DG) swabbing had higher C_t and lower frequency of positive compared to nasal and proctology swabs (PS) [McNemar’s Chi-square test, *P* <0.05]. Each swab type demonstrated a similar shift between BRD negative and BRD positive animals: an increased abundance of the order Mycoplasmatales coupled with decreases in abundance of Pseudomonadales, Clostridiales, and Bacteroidales. Of the six phyla representing greater than 1% of the overall microbial community, four differed significantly in abundance between BRD-negative and -positive animals when sampled using DG swabs. Only two phyla differed if samples were collected using NS, while four differed significantly when sampled with PS. All three collection methods demonstrated a significant difference in Tenericutes, which was the most abundant phylum across all samples and was almost exclusively composed of the order Mycoplasmatales. However, sample collection using NS was less effective in characterizing changes within less abundant phyla than samples collected using DG swabs or PS. Slight differences exist

between swabs of individual cattle; however, NS and NS offer comparable results to DG nasopharyngeal swabs when identifying and characterizing *M. haemolytica* by culture, 16S rRNA microbiome, and qPCR. The study also addresses NC 1192 objective 4.

4. (GA) Clinical status and endoscopy of the upper respiratory tract of dairy calves infected with Bovine viral diarrhea virus 2 and Bovine herpes virus 1 after vaccination and trace minerals injection. Researchers from GA (Roberto A. **Palomares** and Alejandro **Hoyos**) in collaboration with AU (M**. Chamorro** and J. Rush) developed a respiratory endoscopic score (ES) for evaluation of the upper respiratory tract in dairy calves vaccinated and infected with BVDV and BHV1. Endoscopic evaluation of the calves' URT demonstrated: 1. differences in the appearance of the respiratory mucosa before and after BVDV2 + BHV1 challenge; 2. contrast between vaccinated and unvaccinated calves, and 3. demonstrated positive effects of trace minerals supplementation concurrent with IN vaccination on the URT mucosa health. This was the first study using endoscopy as an ancillary tool to evaluate the effects of BVDV2 + BHV1 co-infection on the characteristics of the respiratory tract mucosa and to assess clinical protection elicited by vaccination concurrent with trace mineral injection. Results from this study have been published in Res Vet Sci. 2022.

5. (AL) Serum Haptoglobin levels before and after transport to backgrounder farm in beef steers weaned by 3 different methods. Researchers from Auburn University (Maggie Justice, Kim Mullenix, Soren Rodning, and Manuel F. **Chamorro**) in collaboration with The University of Tennessee (Liesel **Schneider**) and West Texas A&M University (J. **Richeson**) assessed the effects of 3 different weaning methods (Abrupt, Fence-line, and Nose-flap) on the levels of serum Haptoglobin of beef steers from 3 different sources immediately before and 24h and 14 days after transport (6 hours) to a backgrounder farm. The mean serum Haptoglobin levels immediately before transport and 14 days after transport were similar and comparable among steers from different treatment groups; however, the mean serum Haptoglobin levels 24h after transport were significantly increased in Abruptly-weaned steers compared with Fence-line and Nose-flap groups (0.09 mg/mL vs. 0.02 and 0.02, respectively). The mean ADG during the first 15 days of arrival to the backgrounder farm was significantly lower in Abruptly-weaned steers compared with Fence-line and Nose-flap groups (0.4 kg/d vs. 1.1 and 0.8, respectively. Based on preliminary results of this study, abrupt weaning appeared to promote a pro-inflammatory phenotype and reduced performance in beef steers following transport. Reducing pro-inflammatory responses during weaning and transport improves performance of beef calves during the early backgrounding period.

6. (CA) Prevalence of in-vitro phenotypic and genotypic antibiotic resistance in respiratory bacterial isolates from weaned dairy heifers in California with and without respiratory disease and the association with farm level management variables and enteric bacterial minimum inhibitory concentrations. Researchers from University of California (S. **Depenbrock**, S. **Aly**) in collaboration with Washington State University (**Wenz**) are

evaluating performing genomic analysis of bacterial isolates from dairy heifers from California dairy operations and contrasting the results of health records for the presence or not of BRD with antibiotic resistance and enteric bacterial minimum inhibitory concentrations of antimicrobials. Since the last report, this group completed the analysis of the whole genome sequencing (WGS) of these respiratory isolates. There were 26 antimicrobial resistance (AMR) genes identified in the 326 respiratory isolates analyzed (*P. multocida, M. haemolytica, H. somni*). The most frequently identified AMR genes were those that confer resistance to tetracyclines, aminoglycosides, sulfonamides, penicillins, cephalosporins, phenicol and macrolides. Preliminary analysis demonstrates that the breakpoint analysis from culture and sensitivity is discordant with the AMR genes found with WGS. The largest discrepancies were observed with cephalosporin and fluoroquinolone class drugs. Isolates were never identified as resistant by breakpoint analysis to cephalosporin however > 70% of those isolates contained genes that encode resistance to cephalosporin class drugs; this suggests a potential problem with breakpoint analysis. Conversely, isolates were identified as resistant to fluoroquinolone class drugs however no genes encoding for fluoroquinolone resistance were identified in WGS of those isolates; this suggests a potential deficiency in the AMR gene database for these species of isolates for genes that encode AMR to fluoroquinolones.

Objective 3: *To develop and validate management practices and responsibly applied therapeutic and preventative interventions, such as vaccines, antimicrobials, and immunomodulators, to minimize the impact of BRD on cattle, producers, and society.*

1. (SD) Dairy cow transition response to intranasal vaccines. Researchers from South Dakota State University (C. **Chase**) in collaboration with Mississippi State University (Amelia **Woolums)** evaluated dairy cow responses to intranasal vaccines during the transition period and demonstrated higher levels of IgA in vaccinates compared with controls.

2. (TX) Impact of management decisions during the cow-calf, backgrounding, and feedlot phases of beef production on BRD morbidity and mortality risks. Collaborators from Texas A&M University (S. **Capik,** M **Scott**) and Mississippi State University (A **Woolums,** BB **Karisch)** and Kansas State University examined 1) the effect of vaccination twice during preweaning on preweaning performance and BRD morbidity and mortality during backgrounding; 2) quantify the impact of marketing decisions on BRD morbidity, mortality, and performance by comparing weaned beef calves sent directly to a backgrounding operation or sent via an auction market and order buyer; 3) evaluate associations between pen and yard level management factors and health outcomes during the feedlot phase of production and 4) explored the impact of preweaning and marketing management decisions on inflammatory mediators and whether they are predictive of health outcomes or performance during backgrounding. The overarching goal of this project was to identify management interventions that reduce BRD incidence and thus decrease the need for therapeutic or preventative antimicrobials. Preliminary results include cattle weighing between 227–272 kg and

group sizes of 100–175 head having two water sources decreased respiratory disease risk compared to only one water source. Additionally, pen housing management factors were significantly associated with BRD incidence in the first 45 days of feed (DOF), but effects were modified by demographic factors, such as arrival weight. The study also addresses NC 1192 objective 4.

3. (AL) Effect of intranasal modified-live virus vaccination in weaning-age beef calves simultaneously challenged with BoHV-1 and BRSV shortly after weaning. About 60.6% of beef calves from cow-calf operations in the United States do not receive any vaccine before weaning. This is concerning for southeastern cow-calf operations where smaller producers market their naïve calves through local sale or auction barns and repeated exposure to respiratory pathogens may occur before arrival to feedlots or backgrounder operations. There is inconsistency on the benefits of vaccination at arrival or delayed vaccination. Researchers from Auburn University (Manuel F. **Chamorro**, David Martinez, Thomas Passler, Shollie Falkenberg, Laura Huber, and Paul H. Walz) in collaboration with Mississippi State University (Amelia **Woolums**) assessed the effect of vaccination of beef steers with a combination vaccine protocol at branding and weaning (MLV SC/MLV IN) or a single dose of an IN MLV vaccine at weaning on clinical protection against simultaneous experimental challenge with IBR and BRSV. Results from this study are preliminary. Clinical scores and performance outcomes (individual BW and ADG) following challenge were similar between treatment groups. Following challenge, a greater proportion of calves in all treatment groups shed BHV-1 compared with BRSV. Serum antibody titers (SNA) against BHV-1 and BRSV before challenge were greater in calves vaccinated with a parenteral MLV SC vaccine; however, following challenge SNA were similar among treatment groups. Results from nasal antibody responses are pending.

4. (GA) Collaborative research between UGA (R. **Palomares**), UC Davis (A. **Hoyos**) and UF (J. **Bittar**) investigators evaluated the effect of intranasal vaccination of dairy calves with high levels of maternally derived immunity on serum neutralizing (SNA) and nasal antibodies against BHV-1 and BRSV following intranasal MLV vaccination. Although SNA response was minimal a significant BHV1-IgA response in nasal secretion was detected. Supplementation with injectable trace minerals (ITM) was associated with a delayed decrease of BRSV-SNA titers on days 14 and 28 after primary vaccination. Administration of ITM was also associated with lower clinical scores and BRD morbidity and mortality. Treatment with ITM did not affect SNA titers to BHV1 and BPI3V or the BHV1-specific IgA level in nasal secretion. Results from this manuscript have been submitted for publication.

5. (GA) Assessing the nasopharyngeal microbiome following BVDV2+BHV1 challenge in dairy calves submitted to different vaccination protocols in combination or not with administration of trace minerals. Researchers from GA (R. **Palomares**) in collaboration with researchers at UC-Davis (A. **Hoyos**), MSU (Florencia **Meyer**) and Texas A & M (R.

Valeris) determined if administration of trace minerals and route of booster vaccination (IN vs. SC) affected the richness, diversity and relative abundance of the nasopharyngeal bacterial phyla and genera. Six major phyla were identified with a relative abundance >1% (*Protobacteria*, *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, *Tenericutes* and *Fusobacteria*). Relative abundance of bacteria Phyla changed following BVDV2 + BHV1 challenge episodes. Administration of trace minerals or the route of vaccination were not associated with changes in relative abundance of bacteria Phyla. Relative abundance of bacteria commonly involved in BRD (*Mannheimia*, *Pasteurella*, and *Mycoplasma*) was not influenced by mineral supplementation, booster vaccination 49 days before microbiome assessment or after BVDV2 + BHV1 challenge. Virus challenge was associated with changes ($P< 0.001$) in relative abundance of some bacteria genera (*Ruminococcus*, *Prevotella*, *Pseudomonas*, *Blautia*, *Acinetobacter*, *Psycrobacter*, *Corynebacterium*, *Bacteroides*). Additional results are still pending.

6. (GA) Effects of injectable trace minerals on cortisol concentrations during different stress events (vaccination, BVDV-2 challenge and liver biopsy) in newly received stressed beef calves. Researchers from FL (Joao **Bittar**) in collaboration with researchers at UC-Davis (Alejandro **Hoyos**), and UGA (Roberto A. **Palomares**) evaluated the effect of injectable trace minerals on plasma cortisol levels of recently received beef calves undergoing several stressful events such as vaccination, BVDV-2 experimental challenge and liver biopsy. This was a side project derived from a field trial performed at GA in which supplementation with Se, Cu, Zn and Mn helped reducing the levels of cortisol in stressed beef calves. Results from this study have been submitted for publication.

7. <u>(MS) Quantification of the impacts of pre-weaning vaccination and post-weaning commingling on BRD morbidity and mortality during postweaning backgrounding</u>: In work including MS (Brandi Karisch, Florencia Meyer, Amelia **Woolums**) and KS, and collaborators at Texas A&M (all participants: KS: Brad **White**, Bob Larson, David Amrine; MS: Brandi **Karisch**, Kelsey Harvey, Jane Parish, Amelia **Woolums**; Texas A&M: Sarah **Capik**, Matt **Scott**) we are determining the impacts of preweaning vaccination and postweaning commingling through an auction market on BRD morbidity and mortality in weaned beef calves during the postweaning backgrounding period. Calves born in one of the cow-calf herds in the Mississippi Ag and Forestry Experiment Station (MAFES) are randomly allocated to groups to be vaccinated against respiratory viruses or not preweaning; calves in each of vaccinated or not-vaccinated treatment groups will be randomly allocated to travel through an auction market and order buyer facility, or not, after weaning. Cattle will then all be transferred to TX for backgrounding. While vaccination and commingling are widely recognized risk factors for BRD, little properly-controlled research has been published to allow objective quantification of the degree of effects of these factors. Funding: This work is funded by a USDA NIFA proposal, lead institution TAMU, with KS and MS receiving subcontracts. As of January 2023 we have completed 2 of 3 scheduled trials.

Assessment of inflammatory mediator expression in cattle in year 1 is completed and analysis is pending.

8. (MS) Metaphylaxis for respiratory disease in high-risk stocker cattle: impacts on Mannheimia haemolytica, the microbiome and the resistome: Bovine respiratory disease (BRD) is the leading cause of morbidity and mortality in beef cattle, and mass antimicrobial administration (metaphylaxis) is the most effective prevention. Metaphylaxis can also be life-saving in other livestock and humans, but the practice may be compromised by spread of multidrug resistant (MDR) pathogens. MDR isolates of the BRD pathogen *Mannheimia haemo*lytica can be found in 90% of some cattle 14 days after metaphylaxis. The mechanisms leading to MDR after metaphylaxis are unknown, but rapid transfer of mobile genetic elements (MGE) encoding antimicrobial resistance (AMR) is likely. In conjunction with TX, we (MS: Brandi **Karisch**, Amelia **Woolums**, Bill Epperson; TX: Paul **Morley**, Sarah **Capik**)are using a randomized field trial assessing treated and untreated conventionally managed cattle, we are 1) comparing prevalence of nasopharyngeal (NP) MDR M. haemolytica isolates, AMR genes, and MGE, using culture, susceptibility testing, and whole genome sequencing; 2) comparing NP metagenomes, using 16S amplicon sequencing; 3) comparing the NP resistome, using target-enriched sequencing of AMR and MGE gene sequences; and 4) using target-enriched sequencing to compare absolute abundance of M. haemolytica and sequences specific to other BRD pathogens. This approach will provide never before reported description of the ecology of respiratory AMR in cattle receiving metaphylaxis, revealing targets for mitigating AMR. As of January 2023 we have completed the field data collection for all 4 trials for this research and we have completed the analysis of the phenotypic antimicrobial susceptibility testing of the *M. haemolytica* isolates collected. Importantly, multidrug resistance (MDR), defined by resistance to 3 or more classes of antimicrobials (AM) was significantly higher in META cattle than NO META cattle at 21 and 70 days post metaphylaxis with the long acting macrolide tulathromycin. However, the proportion of cattle treated for BRD after metaphylaxis was significantly lower for META cattle. Whole genome sequencing (WGS) of 244 *M. haemolytica* isolates (138 from META cattle and 106 from NO META cattle) collected at on day 0, 21, or 70 from cattle across all 4 trials is completed, and assessment of AMR and MGE genes in these isolates is underway. Results of preliminary assessment were presented at the January 2023 NC-1193 meeting, these indicate that more of the *M haemolytica* isolates from META cattle contained AMR genes. A total of 434 AMR genes were identified in the 138 *M haemolytica* isolates from META cattle while 189 AMR genes were identified in 106 *M haemolytica* isolates from NO META cattle. Sequencing to allow us to characterize the 16S metagenome and the resistome in DNA isolated from nasopharyngeal swabs collected from all cattle in all 4 trials has been completed and analysis is underway. Funding: This work is funded by a USDA NIFA proposal, lead institution MSU, with TAMU receiving a subcontract.

Objective 4: *To determine how attributes of cattle production systems including epidemiologic, societal, and economic forces contribute to BRD, and to develop ways to promote changes in those systems to reduce the occurrence of BRD and improve cattle health, welfare, productivity and antimicrobial stewardship.*

1. (TX) Evaluation of methods for group-based surveillance and characterization of *Mannheimia haemolytica* in beef feedlot cattle. Collaborators from Mississippi State University (Amelia **Woolums**) and Texas A&M University (SF **Capik,** R. **Valeris-Chacin,** and P. **Morley**) evaluated sampling and testing methods that would facilitate investigation of *Mannheimia haemolytica* in groups of cattle to study relationships between the occurrence of BRD and members of the respiratory microbial community such as *Mannheimia haemolytica*. This study included 10 pens of cattle from a variety of sources (all >600 miles from the feedlot) that had an average of 18.8 days-on-feed at sampling. For each pen, ropes were placed the afternoon prior to sampling, and then collected the following day. Swabs of the bottom and sides of the water bowl were also collected at this time. Additionally, 10 cattle were randomly selected from each pen and sterile 16" rayon-tipped proctology swabs were used to sample the nasal passage and nasopharynx (NP swabs). Samples were cultured to detect Mh, and DNA was extracted for testing using qPCR for Mh, 16S sequencing to characterize the microbiome, and target-enriched sequencing to characterize Mh and AMR gene sequences. Results demonstrate significantly greater sensitivity of qPCR over culture for detection of *Mannheimia haemolytica* in swabs of the nasal passage and nasopharynx. Culture was unreliable for detection of *Mannheimia haemolytica* in other samples such as rope samples and water bowl swabs. These investigations are being conducted to evaluate detection and characterization of Mh in 6 different demographic groups of beef cattle: a) Young (~5 cwt) beef-breed feedlot calves, b) Yearling (~9 cwt) beef-breed feedlot cattle, c) Young (~5 cwt) dairy-beef cross-breed feedlot calves, d) Young (~3-4 cwt) beef-breed backgrounding calves, e) Young (~200 cwt) dairy-beef cross-breed bull calves in pens. The study also addresses NC 1192 objective 2.

2. (TX) Impact of management decisions during the cow-calf, backgrounding, and feedlot phases of beef production on BRD morbidity and mortality risks. Collaborators from Texas A&M University (S. **Capik,** M **Scott**) and Mississippi State University (A **Woolums,** BB **Karisch)** and Kansas State University examined 1) the effect of vaccination twice during preweaning on preweaning performance and BRD morbidity and mortality during backgrounding; 2) quantify the impact of marketing decisions on BRD morbidity, mortality, and performance by comparing weaned beef calves sent directly to a backgrounding operation or sent via an auction market and order buyer; 3) evaluate associations between pen and yard level management factors and health outcomes during the feedlot phase of production and 4) explored the impact of preweaning and marketing management decisions on inflammatory mediators and whether they are predictive of health outcomes or performance during backgrounding. The overarching goal of this project was to identify management interventions that reduce BRD incidence and thus decrease the need for therapeutic or preventative antimicrobials. Preliminary results include cattle weighing

between 227–272 kg and group sizes of 100–175 head having two water sources decreased respiratory disease risk compared to only one water source. Additionally, pen housing management factors were significantly associated with BRD incidence in the first 45 days of feed (DOF), but effects were modified by demographic factors, such as arrival weight. The study also addresses NC 1192 objective 3.

Objective 5: *To promote dialogue and exchange among scientists, veterinarians, allied industry professionals and cattle producers to advance BRD research initiatives, to implement outreach, to disseminate research results, and to facilitate the translation of research findings to practical field applications*.

- **SD** station members contributed to an International collaboration with University of Sao Paulo on BRD symposium with WI and MS in November 2022.
- **SD** station members developed a 2-day preconference seminar on bovine vaccinations with OH, MO and MS in September 2022.
- **SD** station members presented a BRD Webinar for NC1192 in January 2023.
- **GA** station members (R. **Palomares**) presented a seminar on future research perspectives on the use of trace minerals for the prevention and control of BRD at Mississippi State University.
- **GA** station members (R. **Palomares**) was invited to the American Association of Bovine Practitioners PodCasts, Have You Herd? Dr. Fred Gingrich interviewed him about the impact of trace minerals on health and immunity of cattle in November 2022.
- **AL** station members (M. **Chamorro)** presented two BRD lectures at the University of Tennessee Livestock Health and Nutrition Conference in January 2023.
- **WA** station members delivered 3 lectures on genomic and BRD to undergraduate students.

Objective 6: *To assess the economic impact of BRD across different sectors of cattle industry.*

II. Impact

Objective 1:

- (TX) several research projects conducted by Texas A&M University and Mississippi State University members increased the understanding of the molecular mechanisms used by *M. bovis* to help induce the pathogenesis of BRD, including virulence, persistence, and antibiotic resistance factors. Additionally these projects resulted in the development and validation of a molecular technique to study *M. bovis* molecular epidemiology at the strain level.
- (TX) a research project conducted and currently in development by Texas A&M University, New Mexico State University and University of Nebraska Lincoln members identified that bacterial colonization in the nasal mucosa of newborn calves within the first 24 hours of life correlates with the dam’s nasal flora.
- (TX) a research project conducted and currently in development by Texas A&M

University and Mississippi State University members defined host gene expression patterns and genomic mechanisms involved in BRD risk and development based on common management practices such as vaccination and marketing strategies. Utilizing cutting-edge next generation sequencing techniques, these findings distinguish potential predictive biomarkers of BRD development and severity, and capture genomic mechanisms indicative of cattle which remain healthy in high-risk settings. Specifically the mechanisms and pathways that drive differentially expressed genes (DEGs) previously identified to be increased in expression at facility arrival in cattle that remain clinical healthy within high-risk populations, compared to cattle that eventually develop BRD in addition to differences induced by modified-live virus (MLV) vaccination.

- (WA) Further the understanding of the etiology of BRD and the role that specific pathogens play in BRD in beef feedlot animals and in dairy calves. Provide additional genomic tools for selection of animals resistant/resilient to BRD

Objective 2:

- (TX) research projects conducted and currently in development by Texas A&M University and Mississippi State University members identified optimal sampling methods (including nasopharyngeal swabs, rope samples and water bowl swabs and proctology swabs) for group-based surveillance and characterization of *Mannheimia haemolytica* by qPCR and culture methodologies in different demographic groups of beef cattle.
- (SD) research from SD State University identified a new virus that could be part of the BRD complex.
- (GA) research from UGA in collaboration with Auburn University (AL) developed an upper respiratory tract endoscopy technique that permitted prompt detection of mucosal inflammation and damage caused by BVDV2 and BHV1, before bronchial and lung lesions appear. This tool allowed to demonstrate the positive effects of vaccination (and injectable trace minerals) protecting calves from URT damage caused by BVDV2 + BHV1 infection.
- (AL) preliminary results of research from Auburn University (AL) identified a greater pro-inflammatory profile (higher serum Haptoglobin levels) 24 hours after transport in beef calves abruptly weaned compared with beef calves weaned by different methods (i.e., fence-line).
- (CA) preliminary results of research from University of California Davis suggests that incongruences between whole genome sequencing (WGS) and CLSI breakpoint analysis reveal questions about breakpoint analysis for Cephalosporins for BRD pathogens, and potential deficiencies in AMR gene databases for WGS of respiratory isolates. Further research is needed to determine ideal methods for AMR definitions and surveillance in BRD pathogens. Additionally, Farm level management factors appear to be associated with AMR outcomes as defined by selective isolation and sensitivity testing of respiratory isolates from weaned dairy heifers. Individual animal antimicrobial drug treatment history appears to be less frequently and less significantly associated with AMR outcomes than

management factors, suggesting that to mitigate AMR, farm level management factors will need to be addressed.

Objective 3:

- (TX) current research from Texas A&M University, Mississippi State University and Kansas State University identified that management interventions that cattle weighing between 227–272 kg and group sizes between 100–175 head, having two water sources had a lower BRD risk compared to only one water source. Additionally, they identified pen housing management factors that were significantly associated with BRD incidence in the first 45 DOF; however, effects were modified by demographic factors, such as arrival weight.
- (TX) current research from Texas A&M University and Mississippi State University identified that metaphylaxis with Tulathromycin (META) and no metaphylaxis (NOMETA) cattle groups had similar inflammatory and immunological gene expression patterns at day 0 (arrival), but differentially expressed genes (DEGs) were identified within the META group over time, associated with inflammatory modulation, cellular clearance, and inflammatory regulation mechanisms. Differential expression analysis of cattle free of BRD indicated specific inflammatory and immunological modulation pathways associated with tulathromycin administration.
- (TX) Texas A&M University and Mississippi State University research defined host gene expression patterns and genomic mechanisms involved in BRD risk and development based on common management practices such as vaccination and marketing strategies. Specifically the mechanisms and pathways that drive differentially expressed genes (DEGs) previously identified to be increased in expression at facility arrival in cattle that remain clinical healthy within high-risk populations, compared to cattle that eventually develop BRD in addition to differences induced by modified-live virus (MLV) vaccination.
- (TX) research from Texas A&M University identified that the route of MLV vaccine administration to feedlot cattle (intranasal vs. parenteral) resulted in changes in the upper respiratory tract microbiome during the first 28 days in feed of cattle that remained healthy and those that died from BRD.
- (SD) research from SD State University demonstrated several important vaccine findings 1) the development of a protective IgA immune mucosal response with a mucosal vaccines and 2) established a controlled study that demonstrated IFN levels are increased in transition cows at freshening with intranasal (IN) vaccines
- (GA) research from UGA demonstrated improving the immune response to primary vaccination in young dairy calves using IN booster vaccination and administration of injectable trace minerals (ITM) might have a significant impact on prevention of BRD and future health status of dairy heifers.
- (GA) research from UGA elucidated the influence of trace mineral supplementation concurrent with vaccination on the microbiome ecosystem in weaned dairy calves that were challenged with BVDV2 and BHV1 might help to understand the mechanisms of action of Se, Cu, Zn and Mn to improve the efficacy of vaccination against BRD pathogens in dairy calves.

- (GA) research from UGA advanced in the understanding of the mechanisms by which ITMs enhance the immune response after vaccination (increase antibody production and cell mediated immunity) in stressed beef calves and the possible association with the reduction in cortisol levels may have a significant impact on the design of management and vaccination protocols for weaned and shipped beef calves.
- (AL) research from Auburn University developed a combination MLV vaccine protocol to protect recently weaned beef calves against simultaneous experimental challenge with BRSV and BHV-1.
- (MS) Research from Mississippi State University and collaborators will provide objective data regarding the relative impacts of preweaning vaccination and postweaning auction market exposure on BRD incidence. Such data are surprisingly rare. This information will support the development of models that identify the most cost effective management strategies to prevent BRD.
- (MS) Research from Mississippi State University and collaborators has provided new information regarding the impact of metaphylaxis on AMR. Importantly, the administration of long acting macrolide metaphylaxis at arrival was associated with decreased BRD morbidity. However, it is also associated with significant increase in the proportion of *M. haemolytica* isolated from cattle receiving metaphylaxis that are MDR, compared to control cattle not receiving metaphylaxis.
- (MS) Findings from Mississippi State University and collaborators could indicate that cattle that receive metaphylaxis and then require subsequent treatment will not respond to antimicrobials, due to MDR. However, future research will be needed to test this hypothesis, as the number of cattle that required treatment for BRD following metaphylaxis was too low to identify such an effect in this study.

Objective 4:

- (TX) current research from Texas A&M University, Mississippi State University and Kansas State University identified that management interventions that cattle weighing between 227–272 kg and group sizes between 100–175 head, having two water sources had a lower BRD risk compared to only one water source. Additionally, they identified pen housing management factors that were significantly associated with BRD incidence in the first 45 DOF; however, effects were modified by demographic factors, such as arrival weight.
- (TX) research projects conducted and currently in development by Texas A&M University and Mississippi State University members identified optimal sampling methods (including nasopharyngeal swabs, rope samples and water bowl swabs and proctology swabs) for group-based surveillance and characterization of Mannheimia haemolytica by qPCR and culture methodologies in different demographic groups of beef cattle.

Objective 5:

- (SD) researchers from SD State University (C. **Chase**) participated in BRD symposium with University of Sao Paulo- SD, WI and MS. Presented a 2-day preconference seminar on bovine vaccinations with OH, MO and MS. Presented a webinar for NC1192 to increase visibility of the group.

- (GA) researchers from UGA (R. **Palomares**) discussed. future research projects on the use of trace minerals to contribute to prevention and control of pathogens involved in BRD in a seminar at MSU.
- (WA) Educate students on the importance of BRD in animal breeding and dairy production classes; Educate students on the role of genetics on predisposition to disease; Educate students on the use of genomic selection to reduce infectious disease

III. Publications/deliverables-

Peer-reviewed scientific publications:

Scott MA, **Woolums AR**, Swiderski CE, Finley A, Perkins AD, Nanduri B, **Karisch BB**. Hematological and gene co-expression network analyses of high-risk beef cattle defines immunological mechanisms and biological complexes involved in bovine respiratory disease and weight gain. PLOS One. 2022 Nov 3; 17(11): e0277033. doi: 10.1371/journal.pone.0277033

Scott MA, **Woolums AR**, **Karisch BB**, Harvey KM, **Capik SF**. Impact of preweaning vaccination on host gene expression and antibody titers in healthy beef calves. Frontiers in Veterinary Science (Vetinformatics: An Insight for Decoding Livestock Systems Through In Silico Biology) 2022 Sep 26; 9:1010039. doi: 10.3389/fvets.2022.1010039

Crosby WB, Pinnell LJ, **Richeson JT**, Wolfe C, Loy JD, Gow SP, Seo KS, **Capik SF**, **Woolums AR***, **Morley PS***. Does swab type matter? Comparing methods for *Mannheimia* haemolytica recovery and upper respiratory microbiome characterization in feedlot cattle. Anim Microbiome 2022; 4:49 doi: 10.1186/s42523-022-00197-6

Crosby WB, Pinnell LJ, **Richeson JT**, Wolfe C, Loy JD, Gow SP, Seo KS, **Capik S**, **Woolums AR***, **Morley PS***. Comparison of sampling and diagnostic techniques for recovery of *Mannheimia haemolytica* and respiratory microbiome characterization from feedlot cattle. Research Square Preprint 2022 doi: 10.21203/rs.3.rs-1054768/v1

Hoyos-Jaramillo A, **Palomares RA***, Bittar JH, Divers SJ, **Chamorro MF**, Berghaus R, Kirks SJ, Rush J, Edmondson M, Rodriguez A, Gonzalez-Altamiranda EA. Clinical status and endoscopy of the upper respiratory tract of dairy calves infected with Bovine viral diarrhea virus 2 and Bovine herpes virus 1 after vaccination and trace minerals injection. Res Vet Sci. 2022; 152:582-595.

Martinez DA, **Chamorro MF***, Passler T, Huber L, Walz PH, Silvis S, Raithel G, Thoresen M, Stockler R, **Woolums AR**. The titers, duration, and residual clinical protection of passively-transferred nasal and serum antibodies are similar among beef calves that nursed colostrum from vaccinated or unvaccinated dams and were experimentally challenged with bovine respiratory syncytial virus (BRSV) at 3 months of age. Am J Vet Res 2022; 83 (11): 1-9 doi: 10.2460/ajvr.22.07.0118

Martinez DA, **Chamorro MF*,** Passler T, Huber L, Walz PH, Silvis S, Raithel G, Thoresen M, Stockler R, **Woolums AR**. Local and Systemic Antibody Responses in Beef Calves Vaccinated with a Modified-Live Virus Bovine Respiratory Syncytial Virus (BRSV) Vaccine at Birth following BRSV Infection. Vet. Sci. 2023**;** 10(1): 20 doi: 10.3390/vetsci10010020

Martínez DA, **Chamorro MF**, Passler T, Huber L, Walz PH, Thoresen M, Raithel G, Silvis S, Stockler R, **Woolums AR**. Local and systemic antibody responses in beef calves vaccinated with a modified-live virus bovine respiratory syncytial virus (BRSV) vaccine at birth following BRSV infection. Vet Sci. 2022. 10:20. doi: 10.3390/vetsci10010020.

Scott MA, **Woolums AR**, Swiderski CE, Finley A, Perkins AD, Nanduri B, **Karisch BB**. Hematological and gene co-expression network analyses of high-risk beef cattle defines immunological mechanisms and biological complexes involved in bovine respiratory disease and weight gain. 2022. PLoS One. 17:e0277033. doi: 10.1371/journal.pone.0277033.

Scott MA, **Woolums AR**, **Karisch BB**, Harvey KM, **Capik SF**. Impact of preweaning vaccination on host gene expression and antibody titers in healthy beef calves. 2022. Front Vet Sci. 9:1010039. doi: 10.3389/fvets.2022.1010039.

Martínez DA, **Chamorro M**F, Passler T, Huber L, Walz H, Thoresen M, Raithel G, Silvis S, Stockler R, **Woolums AR.** The titers, duration, and residual clinical protection of passively-transferred nasal and serum antibodies are similar among beef calves that nursed colostrum from vaccinated or unvaccinated dams and were experimentally challenged with bovine respiratory syncytial virus (BRSV) at 3 months of age. Am J Vet Res. 2022. 83:1-9. doi: 10.2460/ajvr.22.07.0118.

Powledge SA, McAtee TB, **Woolums AR**, Falkner TR, Groves JT, Thoresen M, **Valeris-Chacin R**, **Richeson JT**. Clinical and microbiological effects in high-risk beef calves administered intranasal or parenteral modified-live virus vaccines. J Anim Sci. 2022. 100:skac249. doi: 10.1093/jas/skac249.

Crosby WB, **Pinnell LJ, Richeson JT**, Wolfe C, Castle J, Loy JD, Gow SP, Seo KS, **Capik SF**, **Woolums AR**, **Morley PS**. Does swab type matter? Comparing methods for *Mannheimia haemolytica* recovery and upper respiratory microbiome characterization in feedlot cattle. Animal Microbiome. 2022. 4:49. https://doi.org/10.1186/s42523-022-00197-6

Scientific abstract presentations in national/international conferences:

Ramirez BI, Crosby WB, **Woolums AR**, **Karisch BB**, Harvey KM, **Scott MA**. 2022. Tulathromycin-induced gene expression evaluated in high-risk beef cattle through whole blood transcriptomics. Conference of Research Workers in Animal Diseases (CRWAD). Chicago, IL, USA.

McAllister HR, **Capik SF**, **Woolums AR**, **Karisch BB**, Harvey KM, **Scott MA**. 2022. Effect of vaccination and marketing strategies on gene expression patterns in beef cattle via time course RNA-Seq. Conference of Research Workers in Animal Diseases (CRWAD). Chicago, IL, USA.

Chung MN, **Scott MA**, Pinnell LJ, **Morley PS**, **Valeris-Chacin R**. 2022. Short versus long reads for microbiome profiling of the respiratory tract and environment of feedlot cattle. Conference of Research Workers in Animal Diseases (CRWAD). Chicago, IL, USA.

Capik SF, **Larson RL**, **White BJ**, Amrine DE, **Karisch BB**, Harvey KM, **Parish JA**, **Woolums AR**, McAllister HR, **Scott MA**. 2022. Update on the impact of management decisions on BRD morbidity, mortality, and performance in beef calves. Conference of Research Workers in Animal Diseases (CRWAD). Chicago, IL, USA.

Green MM, **Woolums AR**, **Karisch BB**, Harvey KM, **Capik SF**, **Scott MA**. 2022. Transcriptome analysis of beef cattle reveals influence of marketing on bovine respiratory disease risk. Conference of Research Workers in Animal Diseases (CRWAD). Chicago, IL. USA.

Scott MA, **Woolums AR**, Swiderski CE, Perkins AD, Nanduri B, Smith DR, **Karisch BB**, Epperson WB. 2022. Identification of potential predictive biomarkers and molecular mechanisms contributing to BRD-associated mortality in post-weaned beef cattle. World Buiatrics Congress. Madrid, Spain.

Woolums AR, **Scott MA**, Swiderski CE, Perkins AD, Nanduri B, **Karisch BB**. 2022. Transcriptomics to define mechanisms of bovine respiratory disease (BRD) resistance. World Buiatrics Congress. Madrid, Spain.

Green MM, **Woolums AR**, **Karisch BB**, Harvey KM, **Scott MA**, **Capik SF**. 2022 Impact of the host transcriptome on bovine respiratory disease treatment during backgrounding. Conference of the American Association of Bovine Practitioners. Long Beach, CA, USA.

Scott MA, **Woolums AR**, **Karisch BB**, Harvey KM, **Capik SF**. 2022. Impact of preweaning vaccination on host response in healthy calves during the cow-calf phase of production. Conference of the American Association of Bovine Practitioners. Long Beach, CA, USA.

Scott MA, **Woolums AR**, Thompson AC, **Karisch BB**. 2022. Time-course RNA-Seq analysis defines immunological and inflammatory mechanisms influenced by bovine respiratory disease. Conference of the American Association of Bovine Practitioners. Long Beach, CA, USA.

Crosby WB, Pinnell LJ, **Richeson JT**, Wolfe C, Castle J, Loy JD, Gow SP, Seo KS, **Capik SF**, **Woolums AR***, **Morley PS***. Comparison of sampling and diagnostic techniques for recovery of *Mannheimia haemolytica* from feedlot cattle. Proceedings of the 31st World Buiatrics Congress, September 2022, Madrid, Spain.

Crosby WB, Pinnell LJ, **Richeson JT**, Loy JD, Gow SP, Seo JS, **Capik SF**, **Woolums AR***, **Morley PS***. Comparison of sampling and diagnostic techniques for recovery of Mannheimia haemolytica from feedlot cattle. Proceedings of the 102nd Annual Conference of Research Workers in Animal Disease, 2021.

Crosby WB, **Valeris-Chacin R**, Wolfe C, Gow SP, **Woolums AR***, **Morley PS***. Environmental sampling for characterization of *Mannheimia haemolytica* shedding by feedlot cattle. 31st World Buiatrics Congress, September 2022, Madrid Spain.

Depenbrock, Schlesener, Weimer. 2023. Presence and expression of antimicrobial resistance genes in respiratory bacterial isolates from weaned dairy heifers. Poster. Annual Conference of Research Workers in Animal Disease (CRWAD). Chicago, IL, USA.

Hoyos-Jaramillo A; **Palomares RA**; Bittar JH; Divers SJ; Kirks SJ; Urdaneta J; Mohammad Ibrahim M; Miller K; Skrada K; Rodriguez A; Hurley DJ; **Chamorro MF**; Edmonson M; Rush J; Gonzalez E. Immune response and status of the upper respiratory tract of dairy calves challenged with BVDV2 and BHV1 after intranasal vaccination and trace minerals injection. 31st World Buiatrics Congress. September 2022, Madrid, Spain.

Martinez DA, **Chamorro MF***, Passler T, Huber L, Walz PH, Silvis S, Raithel G, Thoresen M, Stockler R, **Woolums AR**. The effect of local and systemic passive immunity acquired from maternal colostrum on clinical protection of beef calves against experimental challenge with BRSV. World Buiatrics Congress 2022, September 2022, Madrid, Spain.

Capik S, **Larson R, White B, Amrine D, Karisch** B, Harvey K, Parish J, **Woolums AR**, McAllister H, **Scott M**. Update on the impact of management decisions on BRD morbidity, mortality, and performance in beef calves. Conference for Research Workers in Animal Disease (CRWAD). Chicago IL. January 22-24, 2023. #P137.

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Tamm SC, Crosby WB, **Pinnell LJ, Richeson JT**, Wolfe C, Gow SP, **Capik S**, Newcomer B, Funk J, **Valeris-Chacin R**, **Woolums AR**, **Morley PS**. Surveillance of *Mannheimia haemolytica* through novel group-based sampling and molecular detection. Conference for Research Workers in Animal Disease (CRWAD). Chicago IL. January 22-24, 2023. #138.

Green MM, **Woolums AR, Karisch BB**, Harvey KM, **Scott MA, Capik SF**. Impact of the host transcriptome on bovine respiratory disease treatment during backgrounding. American Association of Bovine Practitioners (AABP) Conference Proceedings. Long Beach CA. September 22-24, 2022.

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Scott MA, Woolums AR, Karisch BB, Harvey KM, **Capik SF**. Impact of preweaning vaccination on host response in healthy cavles during the cow-calf phase of production. American Association of Bovine Practitioners (AABP) Conference Proceedings. Long Beach CA. September 22-24, 2022.

Scott MA, Woolums AR, Thompson AC, **Karisch BB**. Time-course RNA-seq analysis defines immunological and inflammatory mechanisms influenced by bovine respiratory disease. American Association of Bovine Practitioners (AABP) Conference Proceedings. Long Beach CA. September 22-24, 2022.

Crosby WB, Pittman A, **Karisch BB**, Hiott LM, Loy JD, Epperson WB, **Capik SF, Morley PS**, Frye JG, Jackson CR, **Woolums AR.** Tulathromycin metaphylaxis increases prevalence of multidrug resistant *Mannheimia haemolytica* while improving health in stocker calves. American Association of Bovine Practitioners (AABP) Conference Proceedings. Long Beach CA. September 22-24, 2022.

Chamorro M, Martínez D, Passler T, Stockler R, Raithel G, Silvis S, Thoresen M, Walz P, **Woolums A.** The effect of local and systemic passive immunity acquired from maternal colostrum on clinical protection of beef calves against experimental challenge with BRSV. 31st World Buiatrics Congress. Madrid, Spain. September 4-8, 2022. #IV-22.

Crosby WB, **Pinnell LJ, Richeson JT**, Wolfe C, Castle J, Loy JD, Gow SP, Seo KS, **Capik SF, Woolums AR**, **Morley PS**. Comparison of sampling and diagnostic techniques for recovery of *Mannheimia haemolytica* from feedlot cattle. 31st World Buiatrics Congress. Madrid, Spain. September 4-8, 2022. #ID-59.

Crosby WB, **Valeris-Chacin R**, Wolfe C, Gow SP, **Woolums AR**, **Morley PS**. Environmental sampling for characterization of *Mannheimia haemolytica* shedding by feedlot cattle. 31st World Buiatrics Congress. Madrid, Spain. September 4-8, 2022. #FE-10.

Scott M, Woolums A, Swiderski C, Perkins A, Nanduri B, Smith DR, **Karisch B,** Epperson W, Blanton Jr, JR. Identification of potential predictive biomarkers and molecular mechanisms contributing to BRD-associated mortality in post-weaned beef cattle. 31st World Buiatrics Congress. Madrid, Spain. September 4-8, 2022. #AH-16.

Martínez DA, **Chamorro MF**, Passler T, Huber L, Stockler R, Thoresen M, Raithel G, Silvis S, Walz PH, **Woolums AR**. Role of nasal BRSV-IgG1 titers on clinical protection of calves against experimental challenge with BRSV. American College of Veterinary Internal Medicine Annual Forum. Dallas, TX. June 22, 2022.

Crosby WB, Pittman A, **Karisch BB,** Loy DJ, Epperson WB, **Capik SF, Morley PS,** Frye JG, Jackson CR, **Woolums AR**. Effect of tulathromycin metaphylaxis on *Mannheimia haemolytica* isolation and health outcomes in stocker heifers. American College of Veterinary Internal Medicine Annual Forum. Dallas, TX. June 22, 2022.

Other activities:

WA station

1. **Three lectures on BRD host genomics to undergraduate students in:**

ANIM SCI 330	Animal Breeding and Genetics
ANIM SCI 472	Dairy Production