

OHIO STATE UNIVERSITY EXTENSION



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Research

Rossi, G., Grohn, Y. T., Schukken, Y. H., & Smith, R. L. (2017). **The effect of *Mycobacterium avium* subspecies *paratuberculosis* infection on clinical mastitis occurrence in dairy cows.** *Journal of Dairy Science*. Advance online publication. doi: 10.3168/jds.2017-12721

BACKGROUND: Existing models meant to identify optimal disease control strategies rarely tackle more than one issue at a time and thus miss the potential interdependent effect of Johne's disease and other clinical conditions. Higher mastitis incidences as well as a higher culling rate due to clinical mastitis have been found in Johne's-positive farms, but the effect of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) on individual animals' clinical mastitis rates has not been determined.

PURPOSE: The objective was to understand whether MAP infection represents a significant risk factor for clinical mastitis occurrence, particularly in animals with different MAP infection status. The results of this work can be further used in epidemiological modeling to obtain more accurate evaluation of the benefits of on-farm MAP control strategies.

RESULTS: Results, obtained by survival analysis, suggest that MAP-infected cows had an increased probability of experiencing clinical mastitis during lactation.

CONCLUSIONS: The authors concluded that the added value of this analysis, as well as one of the motivating factors, was to provide a sound estimate of the clinical mastitis risk parameters for different stages of MAP-infected animals. By using 3 different observable criteria for MAP infection categorization, the results can be applied to economic analyses using different assumptions about MAP biology. By including the combined effect of Johne's disease and clinical mastitis in economic and epidemiological dynamic models, they could provide a more accurate estimate of the real burdens caused by some of the most common health issues in dairy farms.

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Location

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[Department of Veterinary Preventive Medicine](#)

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Pempek, J., Trearchis, D., Masterson, M., Habing, G., & Proudfoot, K. (2017). **Veal calf health on the day of arrival to growers in Ohio.** *Journal of Animal Science*. Advance online publication. doi: 10.2527/jas2017.1642

BACKGROUND: There is some evidence that calves arrive to growers in poor condition, and poor condition has been linked to long-term health of the calves. Research is still needed to determine the impact of other health conditions at arrival on morbidity and mortality later in life, as well as pre-arrival risk factors for poor condition at arrival.

PURPOSE: The objectives were to 1) estimate the prevalence of health outcomes in calves on arrival to growers, 2) determine risk factors for poor health outcomes on the day of arrival, and 3) determine if poor health outcomes on the day of arrival predict early calf mortality.

RESULTS: Upon arrival, 6% (95% CI: 4.4 to 7.6) of calves had failure of passive transfer, 14% (9.1 to 18.8) had diarrhea, 0.5% (0 to 1.3%) had respiratory disease, 14% (8.5 to 19.3) were depressed, and 27% (22.7 to 30.7) had inflamed navels. In addition, 35.1% (23.5 to 46.6) of calves were dehydrated using a skin tent test, but only 1.3% (0.0 to 2.9) were dehydrated based on the packed cell volume threshold. Auction site was associated with depression on arrival ($P = 0.008$), and tended to be associated with skin tent on arrival ($P = 0.08$). None of the health variables were predictors of early mortality; however, mortality was generally low for all cohorts (4.3%; range 1.7 to 6.8). These results estimate the prevalence of dehydration, diarrhea, navel inflammation, and depression in veal calves on arrival to growers, and demonstrate that some health outcomes are dependent on auction site.

CONCLUSIONS: The authors concluded that there are many opportunities to intervene before the calves arrive to the grower to improve their health and welfare. Efforts should be made to reduce transport time and provide hydration and energy (glucose and electrolytes) at the auction, during transport, and upon immediate arrival to the grower.

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Martin, B. E., Sun, H., Carrel, M., Cunningham, F. L., Baroch, J. A., Hanson-Dorr, K. C.,... Wan, X. F. (2017). **US feral swine were exposed to both avian and swine influenza A viruses.** *Applied and Environmental Microbiology*, 83(15). doi: 10.1128/AEM.01346-17

BACKGROUND: Feral swine in the US are domestic swine that escaped from commercial operations or were intentionally released, descendants of Eurasian wild boar introduced for hunting purposes, or hybrids of the two. In 2013, an estimated 5 million feral swine were found in at least 35 US states, with both numbers and geographic range increasing. Feral swine are free ranging and have the unique opportunity for contact with wildlife, livestock, and their habitats; thus, they could potentially serve as hosts for the generation of novel influenza A viruses (IAVs) at the interface of feral swine, wild birds, domestic swine, and humans.

PURPOSE: The objective was to conduct a serological survey of feral swine for IAV exposure. Utilizing 8,239 serum samples collected from feral swine in 35 US states between 2010-2013, this study explored patterns of IAV seropositivity and further characterize seropositive samples' cross-reaction to 45 antigenically diverse prototype IAVs from avian, domestic swine and human hosts.

RESULTS: There were 8,239 serum samples from feral swine across 35 US states tested against contemporary antigenic variants of avian, swine, and human IAVs; of these, 406 (4.9%) samples were IAV-antibody positive. Among 294 serum samples selected for antigenic characterization, 271 cross-reacted with ≥ 1 testing virus whereas the other 23 did not cross-react with any testing virus. Of the 271 IAV-positive samples, 236 cross-reacted with swine IAVs, 1 with avian IAVs, and 16 with avian and swine IAVs, indicating that feral swine were exposed to both swine and avian IAVs but predominantly

to swine IAVs. Feral swine were predominantly exposed to H1 and H3 swine IAV, but 5.4% of IAV seropositive samples cross-reacted with avian IAV.

CONCLUSIONS: The authors concluded that there is potential for feral swine to generate novel IAVs by hosting and re-assorting IAVs from wild birds with those from domestic swine facilitating adaptation of avian IAVs before their spillover to other hosts, including humans. Continued surveillance is warranted to monitor the distribution and genomic/antigenic diversity of IAVs in feral swine to assess their risk to human health and commercial livestock producers.

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Kim, M., Kuehn, L. A., Bono, J. L., Berry, E. D., Kalchayanand, N., Freetly, H. C.,... Wells, J. E. (2017). **The impact of the bovine fecal microbiome on *Escherichia coli* O157:H7 prevalence and enumeration in naturally infected cattle.** *Journal of Applied Microbiology*. Advance online publication. doi: 10.1111/jam.13545

BACKGROUND: Gut microbiome may play an important role in controlling pathogens via direct interaction with each other and stimulation of host immunity; therefore, bovine fecal microbiome also may affect *E. coli* O157:H7 passage through the gastrointestinal tract and colonization thus affecting the prevalence and concentration in feces. Understanding the variance explained by bovine fecal microbiome towards *E. coli* O157:H7 colonization and shedding may provide new insights into strategies to understand the complex ecosystem driving fecal *E. coli* O157:H7 shedding in cattle.

PURPOSE: The objective was to determine if the fecal microbiome has an association with *E. coli* O157:H7 prevalence and enumeration.

RESULTS: In the LC diet group, OTUs assigned to the orders Clostridiales and RF39 (placed within the class Mollicutes) were positively correlated with both *E. coli* O157:H7 prevalence and enumeration. In the MC diet group, OTUs assigned to *Prevotella copri* were positively correlated with both *E. coli* O157:H7 prevalence and enumeration, whereas OTUs assigned to *Prevotella stercorea* were negatively correlated with both *E. coli* O157:H7 prevalence and enumeration. In both the MC diet group and the HC diet group, OTUs assigned to taxa placed within Clostridiales were both positively and negatively correlated with both *E. coli* O157:H7 prevalence and enumeration. However, all correlations were weak. In both the MC diet group and the HC diet group, stepwise linear regression through backward elimination analyses indicated that these OTUs were significantly correlated ($P < 0.001$) with prevalence or enumeration, explaining as much as 50% of variability of *E. coli* O157:H7 prevalence or enumeration.

CONCLUSIONS: Individual colonic bacterial species have little impact on *E. coli* O157:H7 shedding but collectively groups of bacteria were strongly associated with pathogen shedding. The authors concluded that bacterial groups in the bovine colon may impact fecal shedding of the zoonotic pathogen *Escherichia coli* O157:H7, and manipulation of the intestinal microbiota to alter these bacteria may reduce shedding of this pathogen and foodborne illnesses.

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Calendar



A full calendar of all upcoming events and continuing education opportunities offered by the College of Veterinary Medicine is available on the website at <http://vet.osu.edu/>

Ohio Dairy Health and Management Certificate Program

Module 11 – " Dairy Cattle Facility Design with Emphasis on Animal Welfare"

- August 17-18, 2017
- Hilton Garden Inn; Columbus, Ohio

Spots are always available for specific module plan

Poultry Medicine Workshops

- October 3rd, 4th, & 5th, 2017

One-day workshops to be held in Cleveland, Columbus, and Cincinnati areas.

Details and registration information to be forthcoming.

Farm Science Review

Sept 19-21, 2017

Molly Caren Agricultural Center, London, Ohio

Please stop by and visit the College of Veterinary Medicine tent and the "Ask the Expert" program in the OSU Central Area.

Ohio Dairy Veterinarians Meeting

- January 3-5, 2018

Save the date – details coming this fall.

Information presented above and where trade names are used, they are supplied with the understanding that no discrimination is intended and no endorsement by Ohio State University Extension is implied.

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