



New Insights on Cow Health, Transition Stress, and HPAI Coinfections from PathKinex™

Written by Amy Lange, Microbiologist III at Microbial Discovery Group

Since 2018, United Animal Health (UAH) and Microbial Discovery Group (MDG) have been uncovering new connections between gut microorganisms, environmental stressors, and emerging pathogens with the PathKinex™ program. At this year’s American Dairy Science Association (ADSA) meeting, we are sharing an updated analysis of key microorganisms based on cow health and production stage from our largest dataset yet, plus a new analysis of key pathogens in dairies infected with highly pathogenic avian influenza (HPAI). All these comparisons are drawn from our dairy PathKinex™ dataset, which now encompasses more than 2,000 cows tested between 2018 and 2024 and uses qPCR assays to detect relevant dairy pathogens in DNA from rectal swab samples.



Dairies Sampled After HPAI Outbreaks Harbor Higher Levels of *E. coli*, *Salmonella*, and *Clostridium perfringens* than Unaffected Herds

U.S. dairies experienced a major epidemic of viral disease starting in March 2024, when the first cases of avian influenza virus type A (H5N1; also known as HPAI) were detected in dairy herds in the southwest U.S. Confirmed and reported cases rose to over 1,000 in 17 states by June 2025. The genotypes of HPAI detected in U.S. dairy cows in 2024 are thought to have crossed over from wild birds and include the same types affecting U.S. poultry flocks. HPAI has also infected over 15 million chickens and turkeys in the current outbreak and has varying levels of severity and infectivity in other animals. Spread from dairy herds into poultry flocks in close proximity continues to be a risk.

While mortality and culling rate in dairy cows is generally under 2%—a stark contrast to the severe respiratory symptoms and sudden death seen in wild birds and poultry flocks—HPAI has a dramatic impact on feed intake and milk production in lactating dairy cows. This may have a cascading effect on gastrointestinal health through development of subacute ruminal acidosis, inflammation of the rumen and intestinal epithelium, and stimulation of pathogen growth.

We examined HPAI-infected farms to determine which pathogens were most impacted by HPAI infection. 113 cows from four farms in the midwestern and southwestern U.S. affected by HPAI within the previous month were compared to 571 cows from 19 farms from the same regions sampled during the same seasonal timeframe between 2023 and 2024. Cows from farms with recent HPAI outbreaks had significantly higher levels of multiple key pathogens, including *E. coli*, and several virulence factors from Shiga toxigenic and enteropathogenic strain types, *Salmonella enterica*, and *C. perfringens*, all species which may elevate the risk of gastrointestinal disease in the months following infection.

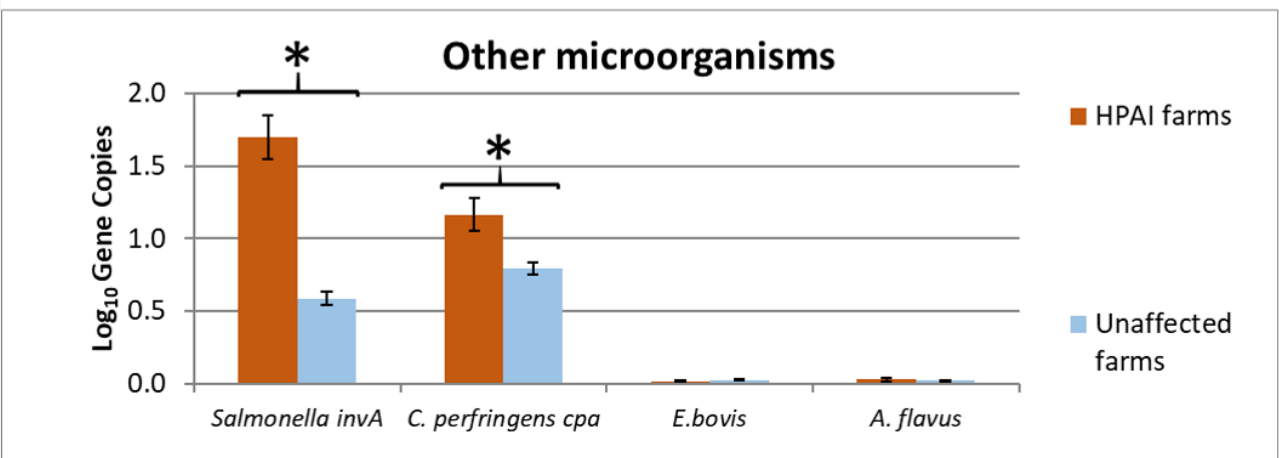
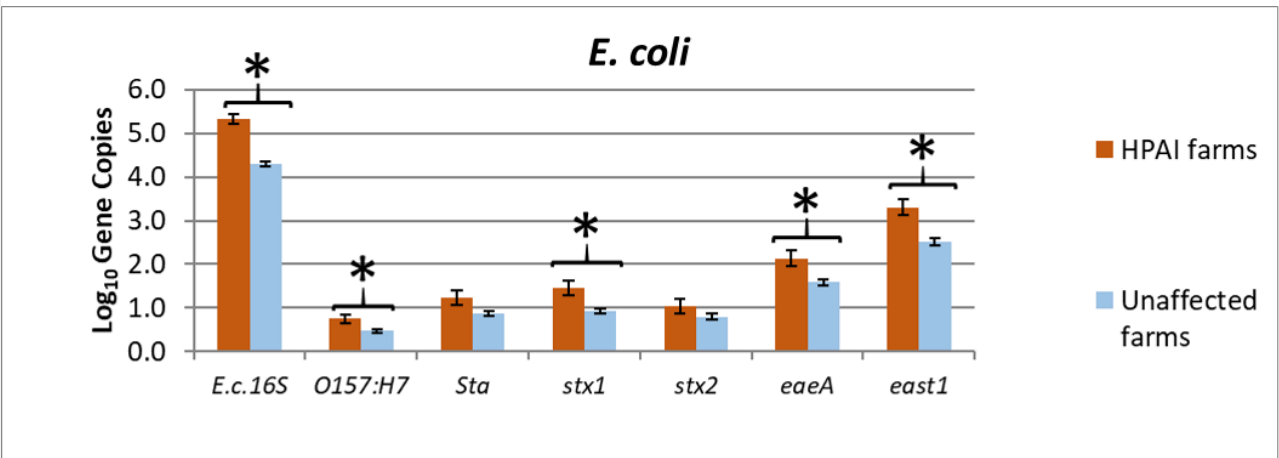


Figure 1: Virulence gene quantities in cows from HPAI-infected and uninfected herds matched by region and timeframe. An asterisk (*) indicates a significant difference (p<0.05).



E. coli, *C. perfringens*, and *Salmonella* Are Linked with GI Symptoms in Commercial Dairy Herds

In our updated analysis of cow health and key gastrointestinal pathogens, healthy cows were compared to cows classified as sick based on gastrointestinal and metabolic symptoms observed on the day of sampling or in recent records. These symptoms included diarrhea, displaced abomasum, ketosis, and off-feed events.

We found that total *E. coli*, an *O157* marker gene, *eaeA* (intimin), and the *EAST1* toxin gene were significantly higher in sick animals than in healthy animals. *eaeA* and *EAST1*-positive *E. coli* are frequently associated with disease in swine, poultry, and dairy, and these virulence factors are directly involved in intestinal colonization.

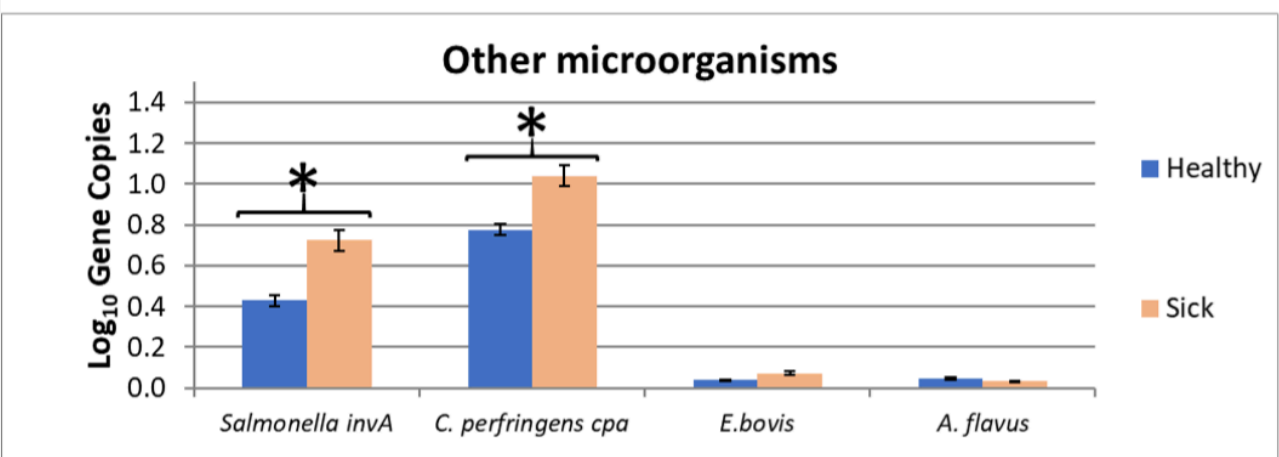
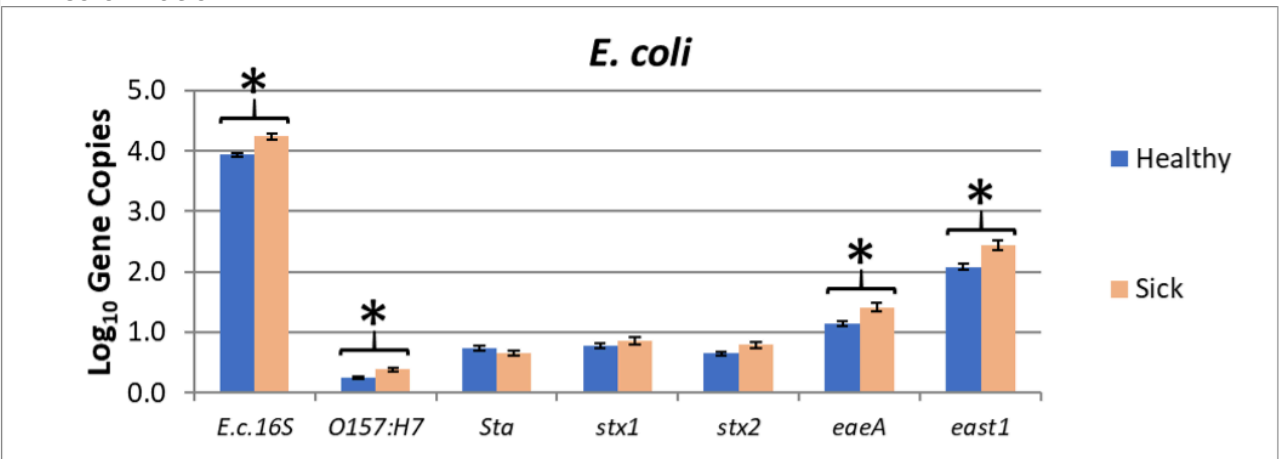


Figure 2: Virulence gene quantities in sick and healthy cows. An asterisk (*) indicates a significant difference (p<0.05).

Salmonella invasion protein gene (*invA*) and *C. perfringens* alpha toxin gene (*cpa*) were also significantly elevated in sick animals. *C. perfringens* Type A (alpha toxin only) is rarely included in bovine *C. perfringens* vaccines but is frequently involved in polymicrobial infections alongside virulent *E. coli*, *Salmonella*, and other pathogens.



Action

These PathKinex™ findings emphasize the effect of viral infection and cow health status on pathogen populations. In turn, the core group of pathogens that flourish during periods of disease challenge can have significant consequences on immune status and feed intake. Direct-fed microbials such as Strateris® ECL for cattle, ProVent® ECL for pigs, and Novela® ECL for poultry may allow producers to mitigate the aftereffects of these health stressors, decrease the risk of gastrointestinal disease, and improve animal health.



Discussion Question

Have your customers been challenged by viral diseases in their livestock and poultry, including avian flu, PRRS, or others? If so, how has it affected them?



About the Author:



Amy Lange is a Microbiologist III at Microbial Discovery Group. Her main research focus is in the use of direct-fed microbials to influence ruminant health and nutrition and the development of large-scale microbial surveillance platforms in animal agriculture.