

# PATHKINEX UPDATE

## Pathkinex™ at ADSA – Assessing the relationship between health and production stressors and enteric gene quantities in dairy cows

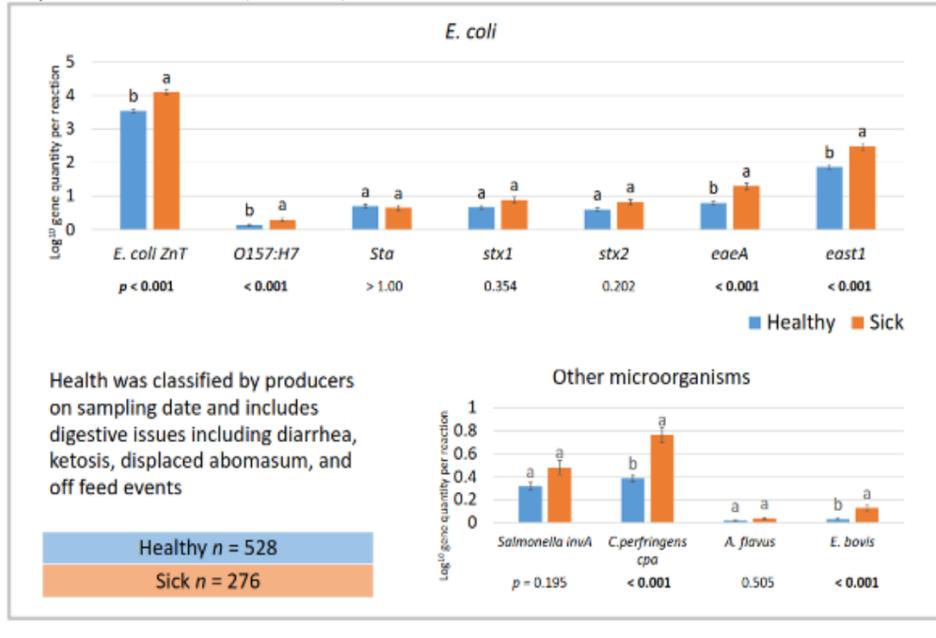
Our PathKinex™ platform and growing database of rectal and intestinal swab samples provide a unique resource for identifying and exploring connections between microorganisms and host or environmental factors. For this year's American Dairy Science Association meeting we shared an overview of the impact of stressors associated with season, bovine coccidial infection, gastrointestinal (GI) symptoms, and lactation stage on quantities of enteric virulence and marker genes.

## *E. coli*, *C. perfringens*, and *Eimeria bovis* are linked with GI symptoms in commercial dairy herds

### PathKinex™ Data Analysis Overview

Our PathKinex™ dataset consists of qPCR data from rectal swab DNA collected from healthy and sick primiparous and multiparous cows at US dairies participating in surveillance studies. For this analysis of stressors and microbial genes, data from 856 multi- and primiparous cows collected between 2018 and 2021 from US commercial dairies was used. Gene data was log-transformed and analyzed via Welch's T test or one-way ANOVA with Bonferroni correction to assess difference in virulence gene abundance.

When tracking microbial virulence gene targets, it is important to establish which species-specific marker genes or virulence genes are associated with symptoms of GI disorders in animals in commercial dairies. For this dairy survey, healthy cows were compared to cows classified as sick based on GI symptoms observed on the day of sampling or in recent records. These symptoms included diarrhea, displaced abomasum, ketosis, and off feed events.



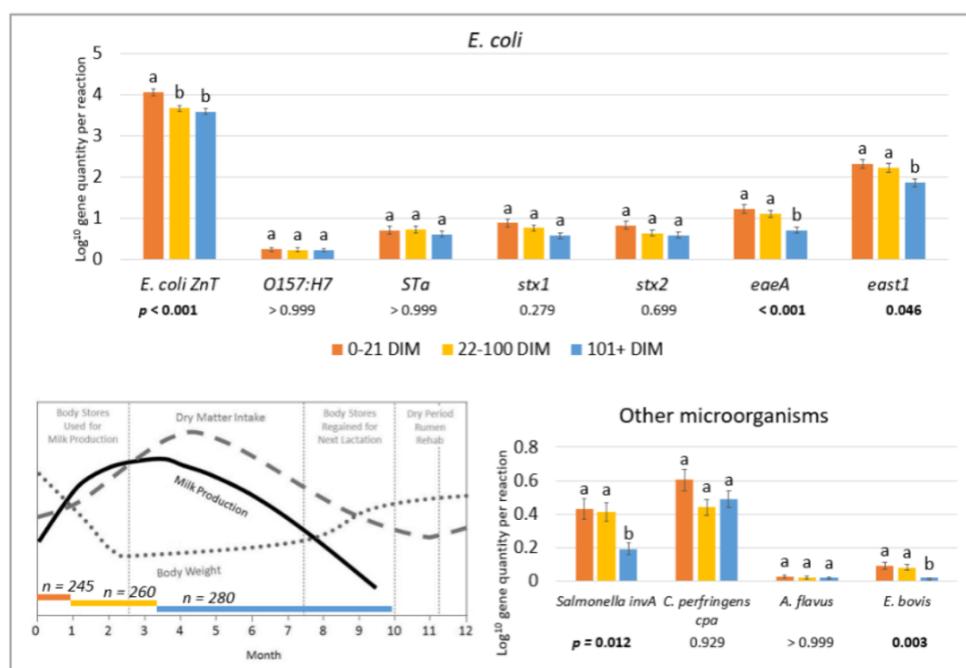
When we compared sick and healthy cows and heifers, we found that total *E. coli*, an *O157* marker gene, *eaeA* (intimin) and the *EAST1* toxin gene were significantly higher in sick animals than in healthy animals. *eaeA* and *EAST1*-positive *E. coli* are frequently associated with disease in swine,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

*Clostridium perfringens* alpha toxin gene (*cpa*) and the bovine coccidia *Eimeria bovis* 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. *Eimeria bovis* is frequently disregarded as a disease of calves, but coccidial shedding in mature cows is associated with elevated levels of other opportunistic pathogens.

Link: [Bacterial pathogen burden in dairy cows harboring bovine coccidia](#)

## *Salmonella*, virulent *E. coli*, and *Eimeria bovis* are associated with fresh and early periods of lactation

The lactation cycle of the dairy cow covers large contrasts in immune status and energy balance, starting with a period of immunosuppression, systemic stress, and high risk of metabolic and reproductive disorders in the first three weeks after calving, or the fresh period. Early lactation (3 weeks to 3 months post-calving) is also energetically expensive and associated with systemic stress, with milk production increasing faster than feed intake to create a negative energy balance.



In this comparison, *Salmonella* joined *eaeA* and *EAST1 E. coli*, *C. perfringens*, and *Eimeria bovis* as microbes significantly associated with fresh and early lactation. *Salmonella* carriage is sporadic overall in cows with GI symptoms but was closely linked to lactation stage and persisted at elevated levels into early lactation. Our previous work has indicated that *Salmonella* has been on the rise at US dairies since 2018, further underscoring the need for additional tools for management of infection and fecal shedding.

Link: [Salmonella on the rise in US dairies](#)

### Findings

- Virulent *E. coli*, *C. perfringens*, and *Eimeria bovis* are significantly elevated in cows with gastrointestinal symptoms.
- The same core group of GI symptom-associated microbes plus *Salmonella* are elevated in fresh and/or early lactation cows.
- Microbes with virulence factors involved in intestinal colonization and aggregation were predominant in both the sick group and the fresh/early lactation groups.

### Action

These PathKinex™ findings emphasize the role of a core group of pathogen species in gastrointestinal disease in dairy cows, especially bacteria like *E. coli*, *Clostridium perfringens*, and *Salmonella* for which direct-fed microbials like Strateris® have demonstrated antimicrobial activity. The key species and virulence types peak in the fresh period, persist at high levels throughout early lactation, and never fully disappear, overlapping with species important in gastrointestinal disease. These microbial patterns point to opportunities for DFM success throughout the lactation cycle.

### Interested In More?

Check out the ADSA Poster entitled "Microbial virulence genes in rectal swab samples are correlated with environmental, metabolic, and gut health stressors in US dairy cows" on Pitcher under Dairy > Topics > ADSA.

### Discussion Question

Are your pathogen challenges linked to reproductive cycles? Which parts of your production cycles are critical points for microbial challenge and microbial control?

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We enjoy hearing from you! We welcome your questions, comments and suggestions on PathKinex updates. Please contact us at [AnimalAg@mdgbio.com](mailto:AnimalAg@mdgbio.com)



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