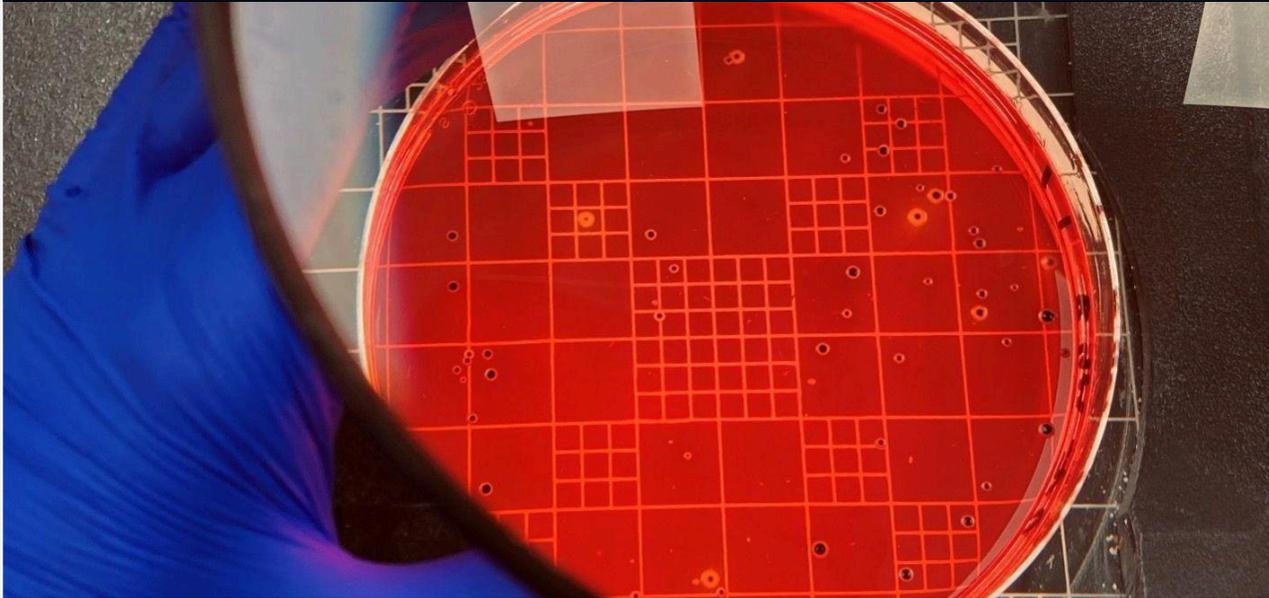


PATHKINEX UPDATE



Is *Salmonella* involved in coinfections?
A recent PathKinex™ meta-analysis reveals
that *Salmonella* is not present alone.

According to the World Health Organization (WHO), *Salmonella* is one of the four key causes of diarrheal disease in humans across the world and there are an estimated 550 million infections every year. *Salmonella* is a zoonotic pathogen, meaning it can spread from livestock to people. This makes *Salmonella* of major concern because it infects all major livestock species globally.¹ All *Salmonella*

serotypes can cause disease in humans, and certain serotypes can also cause disease in livestock, such as *S. Dublin* in cattle and *S. Choleraesuis* in swine.²



Multiple pathogens display greater abundance when *Salmonella* is present

Recent PathKinex meta-analyses revealed that there is an increased risk of disease when *Salmonella* is stacked in coinfection with other microorganisms (see the January Domino Effect PathKinex Update!). Using a large, curated subset of our PathKinex database comprised of 887 nursery pig, 1939 dairy, and 702 broiler samples, we investigated the relationship between *Salmonella* presence and quantities of other opportunistic pathogens in greater detail.

Across swine, dairy cattle, and poultry, we found that gene quantities of *E. coli* were significantly higher when *Salmonella* marker gene *invA* was also detected (**Figure 1**).

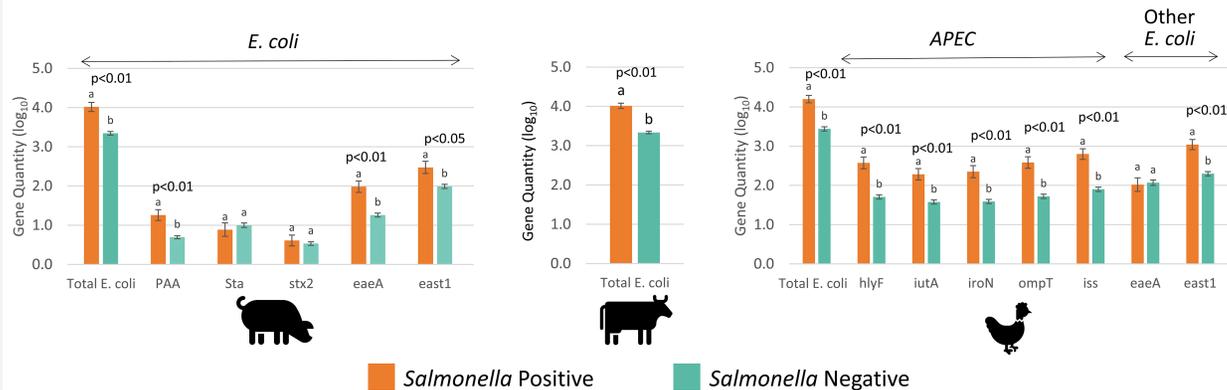


Figure 1. Pathogen gene quantities in the presence or absence of *Salmonella* (*invA*).

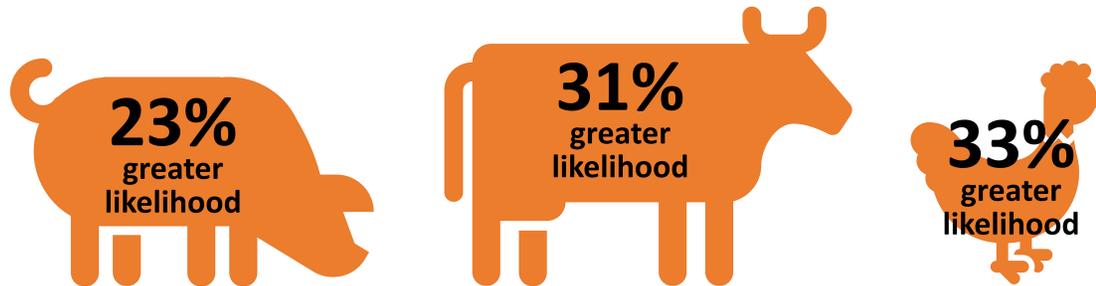
Other important pathogens were also detected at elevated quantities when *Salmonella* was present. In swine, a variety of different opportunistic pathogens were significantly elevated when *Salmonella* was positive, including *C. perfringens*, *Campylobacter*, and *Aspergillus* (all $p < 0.05$). Dairy cattle positive for the *Salmonella* marker also displayed increased levels of *C. perfringens* ($p = 0.09$). In poultry, gene quantities of all avian pathogenic *E. coli* (APEC) markers tested, as well as *Campylobacter*, and *Enterococcus cecorum* were greater when *Salmonella* was present (all $p < 0.05$). Elevation of these additional microorganisms may be occurring due to disruption of the normal microbiome by an initial pathogen, allowing others to follow suit and gain a foothold.



When *Salmonella* is present, there is a greater proportion of sick animals

While examining the incidence of sick vs. healthy animals, we discovered that for every host animal species there was a higher proportion of sick animals within the population positive for *Salmonella*. For swine, when *Salmonella* was present there was a 23% greater likelihood that the sample came from a sick pig (**Figure 2**). Similarly, when *Salmonella* was present, there was a 31% greater likelihood the sample came from a sick cow and 33% greater likelihood for poultry.

When *Salmonella* is present, there is a...



...the sample came from a sick animal

Figure 2. When *Salmonella* is present, there is a greater proportion of sick animals.



What can we do about *Salmonella* coinfections?

Because our PathKinex data shows *Salmonella* is not alone, controlling other opportunistic pathogens, such as *E. coli* and *Clostridium perfringens*, may in turn help reduce *Salmonella*. Therefore, a whole system approach may be the most effective control strategy. Program approaches that take into consideration best practices for feed quality, sanitation, veterinary interventions, as well as products like our *Bacillus*-based DFMs are likely to yield the best results.



**What tools are your customers using to manage *Salmonella* infections?
Would these tools be useful in combination with our *Bacillus*-based DFM
products?**

Interested to Learn More on the Topic of Coinfections?

Respond to MDG

Is there a topic you'd like to learn more about in a future newsletter? We enjoy hearing from you! We welcome your questions, comments, and suggestions on PathKinex updates. Please contact us at AnimalAg@mdgbio.com

References

1. World Health Organization. 2018. Salmonella (non-typhoidal). [https://www.who.int/news-room/fact-sheets/detail/salmonella-\(non-typhoidal\)](https://www.who.int/news-room/fact-sheets/detail/salmonella-(non-typhoidal)).
2. Merck Manual. Salmonellosis in animals. 2022. <https://www.merckvetmanual.com/digestive-system/salmonellosis/salmonellosis-in-animals>



[Click Here to Unsubscribe](#)