

Not just a collection of bugs: the poultry microbiome organ

For decades, the complex microbial communities in the digestive tracts of animals have been viewed as a collection of bugs: some good, some bad. The resulting management strategies seem simple. Kill the bad bugs. Feed good bugs and hope they take hold in the gut to do something beneficial.

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But like most aspects of modern poultry production, life is not so simple, and hope is not a strategy. Fortunately, if we dig just a little deeper into the fundamentals of microbial communities, we unearth tremendous untapped potential to improve the health, performance, and sustainability of poultry production.

To access the novel modes of action that make this possible, we tap into recent advances in microbiome science. It all begins with a key realisation. The microbiome is not just bugs. It is an organ!

The trouble with taxonomy

Traditional efforts to understand the gut microbiota are based on taxonomy. That is, they characterise gut micro-organisms by kingdom, phylum, genus, etc, as a proxy for the role each organism plays. This approach evolved from the tools available to animal microbiologists: culturing organisms, PCR probes, and eventually sequencing technologies like 16s microbial profiling.

Without question, taxonomic methods have brought value to the industry. They have been used to identify pathogens and to associate certain bacterial and yeast strains with healthy birds. Taxonomic thinking led to many of the antimicrobials, vaccines, probiotics, and enzymes now associated with health and performance in modern commercial poultry operations.

So, with such decorated history, why change our thinking? To put it simply,

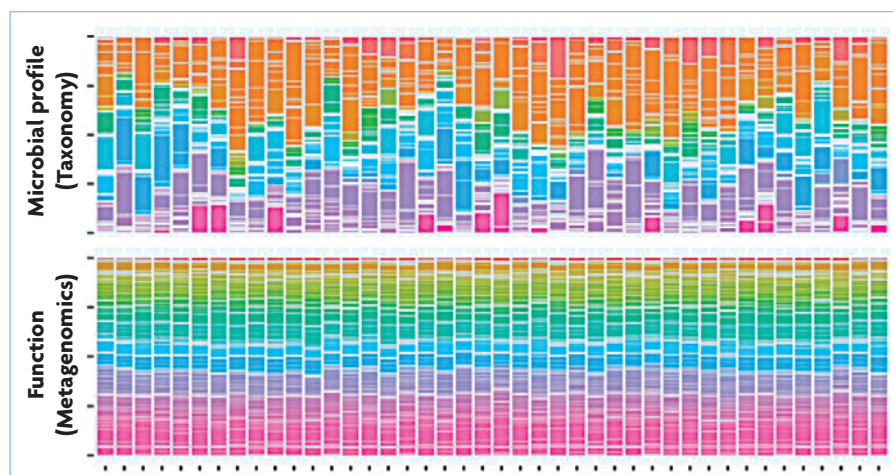


Fig. 1. Gut microbial composition (top) varies wildly between identical healthy birds, but their microbiome functions (bottom) remain highly consistent.

taxonomy has a major flaw. It misses the most important property of microbial communities: bugs are not individual actors. Far from it. They cooperate with one another and with their host. It is now recognised by microbiologists that what the microbiome does together is much greater than the sum of its parts.

A glimpse into how bugs cooperate is found in the ecology of non-starch polysaccharide (NSP) utilisation. Fibre is first broken down to short sugar chains by primary fibre degraders. The sugars are then upgraded to beneficial short chain fatty acids by secondary degraders.

Intuitively, we must already suspect that this example of NSP utilisation barely scratches the surface. The evidence lies in those dizzying reports generated by gut microbial profiling, now common in the literature and industry. Fig. 1 (top) shows such a profile obtained from our own work in broilers.

The taxonomic composition varies wildly. Yet these are otherwise genetically identical, healthy, high-performing birds fed the same diet, in the same house, at the same time. It simply must be that many different microbial profiles can perform the same essential tasks. Indeed, microbial profiling is a bit like measuring a team by its demographics.

If we want to leverage the full potential of

the microbiome, we simply must embrace its properties as a community and learn to manipulate microbial cooperativity.

Embracing the metagenome

As usual, it all comes down to finding the right tool for the job. Profiling only detects a small set of marker DNA to reveal the taxonomy.

Over the past decade, whole-genome sequencing (WGS) has become accessible to animal researchers. Unlike profiling, WGS reveals the entire metagenome: all the genes in the microbiome. The metagenome tells us the functions the microbiome can perform together. As a helpful analogy: if you think of the microbiome as an orchestra, the microbiota are the musicians, while the metagenome represents all the music the orchestra can play.

Studying the metagenome provides pivotal insights into how we might harness the gut microbiome. In the past decade, human microbiome scientists found that, like animals, microbiota composition varies remarkably between healthy people even when corrected for diet and ethnicity. But their metagenomes do not. The functions that the various microbiomes perform (for example, their collective metabolic

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pathways) are often stable from person to person.

The same property holds for animals. Fig. 1 (bottom) shows metagenome data for the very same broilers we profiled in Fig. 1 (top). To generate this plot, we analysed WGS data and grouped genes according to their associated metabolic pathways instead of their taxonomy. Many pathways are nearly constant from bird to bird, despite the variability of their profiles.

The microbiome organ

Unearthing such consistency in the microbiome teaches us that function is more fundamental than composition. As such, modern microbiome science has come to view the microbiome as an organ – a group of tissues or cells adapted for specific functions. The detailed cellular makeup can vary without sacrificing the overall purpose and, like other organs, the microbiome has its own associated physiology and pathology.

Taken together, the gut microbiome organ connects the diet, the host animal, and the environment (Fig. 2). This is because the microbiome converts unabsorbed components of the feed into thousands of primary and secondary metabolites.

Some of these metabolites are directly nutritional, while others are potent biomolecules that are absorbed into the blood stream and communicate with the bird's systemic functions. Other metabolites are excreted in the litter or released to the atmosphere.

Treating the microbiome as an organ reduces complexity. Instead of interpreting hundreds of species, we focus efforts on a small number of key functions (for example, metabolic pathways) that lead directly to

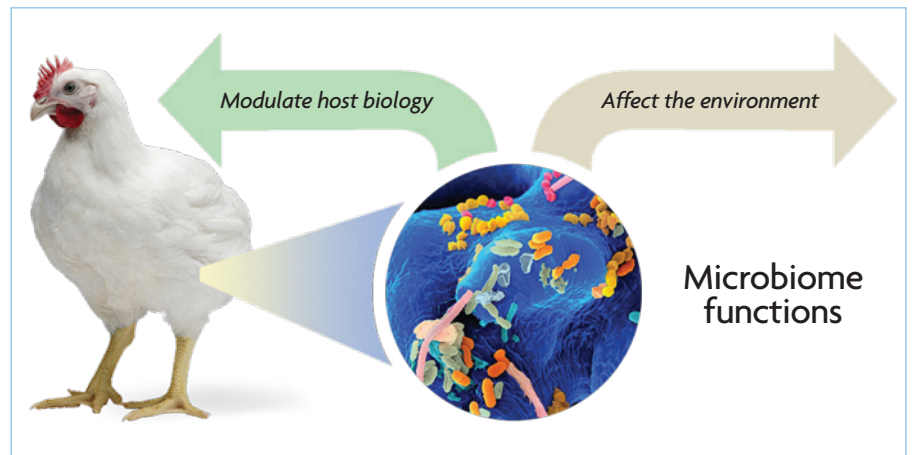


Fig. 2. The gut microbiome organ connects the diet, the host animal, and also the environment.

mechanisms known to create value for the industry.

This change in mindset opens enormous possibilities for novel modes of action that bring consistency to the microbiome. Immediate opportunities include optimising microbiome carbon and nitrogen utilisation, both of which affect the host's resilience to enteric dysbiosis, immunoinflammatory homeostasis, and nitrogenous emissions.

Further opportunities involve improving host animal behaviour, meat quality, vaccine effectiveness, and even novel therapeutics, to name but a few.

In search of a conductor

The movement away from medicated feed additives has already transformed how the industry views gut functionality. With antibiotics reduction, nutritionists and veterinarians have started to embrace aspects of the microbiome as a tool rather

than a limitation. Experience gained across Europe, the Americas, and a growing list of pioneering countries and growers around the world have shown us that high quality poultry production systems are still possible.

These approaches have successfully leveraged the scientific concepts of gut microbial taxonomy. But as we all know too well, microbial composition is highly variable and so are many current gut health products. Solutions based on taxonomy face inherent limitations to their consistency.

Harnessing the stable metagenomic functions of the microbiome is the next frontier in animal science. Rather than changing the musicians, our goal is to tune the music. Our search is not for new organisms, but a conductor – a maestro that directs microbiome function to benefit our customers. ■

References are available
from the authors on request