The Microbes We Can't Ignore

By Vanessa L. Hale, MAT, DVM, PhD

You have heard it all before. The mice were moved to a new institution, or the feed or bedding brand was switched, or the same mouse line was purchased from a different vendor, and suddenly, the mouse phenotype changes. The disease is less severe, or the cancer spreads more rapidly, or susceptibility to the infection changes. Six months or 6 years or 16 years of predictable disease outcomes become unreproducible. We scratch our heads and consult with managers, technicians, and veterinarians at the old institution, investigate feed labels, do health checks, and in the end, we are sometimes still left with a mystery. Enter the microbiome.

Over the past decade, our knowledge and understanding of the microbial communities that live within and on our bodies have grown exponentially. We have learned that the microbiome is critical to health, immune development and response, pathogen defense, and even behavior. We have also learned that changes in diet, bedding, caging, and moving laboratory animals across the country, or even just across campus can have varying and profound effects on the gut microbiome.[1,2] In many cases, we have yet to determine why and how some microbial community alterations affect host or disease phenotypes. Certainly, microbes can alter the metabolic landscape of the gut—interacting with host genes, host diet, and xenobiotics— affecting things like tumor progression, susceptibility to pathogen invasion, and rendering some medications more or less effective or more or less toxic. Through the gut-brain axis, microbial metabolites can also interact with the host nervous system and influence anxiety or depressive-like behaviors in both mice and humans. Unintended or unrecognized changes in the gut microbial community as a result of dietary changes, moves, or the acquisition of a new batch of mice with different microbiota can lead to unpredictable or unexpected changes in experimental outcomes.

Laboratory animals—including gnotobiotic animals—are some of our best models for understanding and manipulating complex microbial communities. But how can we potentially account for or prevent changes in these complex communities when microbes are not the focus of a study? This session will explore what we know about the microbiome, its role in health and disease, the factors within our control and management that can change the microbiome, as well as measures, such as banking stool samples for sequencing or fecal microbiota transplants, to assess, prevent, or respond to unintended microbial community changes. The use and management of gnotobiotic (or germ-free) animals will also be described as well as current efforts to standardize microbiome research in laboratory animals. As we gain insights on how microbial communities impact animal health, the selective and targeted manipulation of these communities via feed or pre-, pro-, and synbiotics (a combination of pre- and probiotics) may become an additional resource in our animal care and management toolkits.

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REFERENCES
1. **Ericsson AC, Gagliardi J, Bouhan D, Spollen WG, Givan SA, Franklin CL.** 2018. The influence of caging, bedding, and diet on the composition of the microbiota in different regions of the mouse gut. Sci Rep **8(1):** 4065.
2. **Ma BW, Bokulich NA, Castillo PA, Kananurak A, Underwood MA, Mills DA, Bevins CL.** 2012. Routine habitat change: a source of unrecognized transient alteration of intestinal microbiota in laboratory mice. PLOS ONE **7(10):** e47416.

What Could Possibly Go Wrong? Everything You Never Wanted to Know about the Microbiome

Date: Wednesday, October 31, 11:00 AM-12:00 PM
Room: Ballroom II
Speaker: Vanessa L. Hale
Moderator: Thomas R. Meier
Facilitator: TBN