# Understanding the Intestinal Microbiome in Health and Disease

Marcio Carvalho Costa, DVSc, PhD[a,*], Jeffrey Scott Weese, DVSc[b]

**KEYWORDS**

- Intestinal microbiota • Next-generation sequencing • 16S rRNA • Equine • Horse

**KEY POINTS**

- New technologies have allowed a better understanding of the equine intestinal microbiota and how it interacts with the host.
- The intestinal microbiome is now considered essential for the maintenance of health. Disturbances of this complex ecosystem are associated with several diseases.
- There is abundant interindividual variation in the microbiome and it can be influenced by a range of factors, such as diet, management, and antimicrobial exposure.
- Changes in the intestinal microbiome of horses have been associated with various clinical conditions, including colitis, laminitis, and colic.

## INTRODUCTION

The intestinal tract contains a complex polymicrobial community that consists of viruses, archaea, fungi, parasites, and bacteria. The bacterial community is the most extensively studied and is thought to be the most important in maintaining the homeostasis of this complex environment. Overall, the members of this microbial community (the microbiota) and the genetic composition of these microbes (the microbiome) dwarf that of the host. It has been estimated that only 10% to 50% of the human body consists of human cells; within that, human genes only make up 1% (or less) of the overall gene content.[1] Only recently, with high throughput and cost-effective DNA-sequencing technologies, has this area been explored in depth.[1,2] Recent study of these complex microbial communities and their interactions with the host have shown that gut bacteria cause or contribute to the occurrence of conditions such as allergies, inflammatory bowel diseases, rectal cancer, diabetes, and obesity; they are even able to induce alterations of behavioral and mood status.[3]

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[a] Department of Veterinary Biomedicine, University of Montreal, 3200 Rue Sicotte, Saint-Hyacinthe, Quebec J2S 2M2, Canada; [b] Department of Pathobiology, University of Guelph, 50 Stone Road East, Guelph, Ontario N1G 2W1, Canada
* Corresponding author.
*E-mail address:* marcio.costa@umontreal.ca

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The objectives of this article are to familiarize readers with the new concepts and terms used in this research, to provide the necessary knowledge for a good understanding and interpretation of those studies, and to provide an update on the current knowledge of the intestinal microbiome of horses. This article focuses on recent studies using culture-independent methods, mainly next-generation sequencing (NGS). Another article discussing the characterization the intestinal microbiome of horses can be found in the literature.[4]

### *Basic Concepts*

Understanding of some basic microbial ecology concepts is necessary for proper assessment of data and publications. **Table 1** summarizes the definitions of some of the most used concepts.[5,6]

Studies investigating purely the taxonomic classification of bacterial communities (which bacteria are present) should adopt the term microbiota and, if their overall genetic makeup or functional potential is being investigated (eg, shotgun metagenomics), the term microbiome is the most appropriate.

Changes in beta-diversity are noteworthy and differential changes in membership and structure can allow for some useful inferences. For example, if there is a change in membership but not structure, it implies that changes are most likely from rare members being added or dropped. Conversely, if structure changes and membership remains the same, it implies that there are changes in relative numbers (overgrowth or depletion) of existing members, with little deletion or addition of new taxa.

To illustrate these concepts, consider the number of horse breeds found in a 100 km (62 miles) radius of a specified area. If 5 different breeds, Thoroughbred, Standardbred, Belgian, Dutch Warmblood, and Canadian Horse, are identified during sampling, that constitutes a richness of 5. This is a representation of the community

**Table 1**
**Definition of the main concepts used in microbial ecology**

| | |
|---|---|
| Microbiota | All microorganisms of a particular environment |
| Microbiome | All microorganisms along with their genetic material and their interaction with an environment |
| Alpha diversity | Describes characteristics of individual samples (eg, richness, evenness, and diversity) |
| Richness | Total number of taxa (eg, species or genera, families, phyla) present in an environment, either through direct measure (observed richness) or through calculations to estimate the true richness that would have been detected if the entire population had been studied (estimated richness)<br>Alpha diversity indices can be described and compared between groups (eg, newborn foals have a richer microbiota than older animals)[7] |
| Evenness | Distribution of species (eg, prevalence or relative abundance of each population within a community) |
| Diversity | Mathematical equation that takes into account richness and evenness (ie, it quantifies how equal a microbial community is) |
| Beta-diversity | Comparisons between samples or groups assessed in a variety of ways with different indices<br>Compares the overall composition of the microbiota, typically based on membership or community structure |
| Membership | Members (eg, species) that are or are not present |
| Structure | Broader comparison that takes into account the members that are or are not present, and their relative abundance |