

Lower Digestive Tract Microbiology

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INTRODUCTION

The lower digestive tract of animals is often referred to as the hindgut and normally denotes the large intestine, which includes the cecum, colon, and rectum. The cecum is a branch from the junction of the small intestine and colon. There is a great diversity among animals in hindgut morphology, mainly in relation to diet of the animal. Carnivores have a small hindgut and a cecum may be absent. However, herbivores, such as the horse, have a large hindgut capacity. The hindgut of nonruminant animals is the primary site for retention of food residues and endogenous substrates for microbial fermentation. Conditions in the hindgut include a constant temperature, pH between 6.5 and 7.5, and low concentrations of oxygen, thus providing an environment for 10^9 to 10^{11} microorganisms of up to 400 different species per gram of lumen contents.^[2] The fermentation end products of the microorganisms—short-chain volatile fatty acids, primarily acetate, propionate, and butyrate—are absorbed throughout the hindgut and used as energy by the animal. Humans have continuously tried to influence the microbial species present in the intestinal tract with the objective to increase meat-animal production efficiency. This has occurred primarily with the use of antibiotics, prebiotics, probiotics, or other dietary additives.

COLONIZATION OF HINDGUT

The digestive tract (Table 1) is an open ecosystem; therefore any microorganism taken in with food or water has the potential to colonize the hindgut and influence the fermentation. Microorganisms remain permanent residents if they can attach to the lining of the intestine or grow at a faster rate than the rate at which the digesta flow. The microbial species found in the digestive tract are affected by the host's diet, environment, drug administration, and stress to the animal. All animals are microbially sterile at birth, but microorganisms from the animal's environment rapidly colonize the gastrointestinal tract. Lactose content of mammalian milk encourages growth of lactic acid bacteria in the intestine.^[3] The lactic acid bacteria are gradually overgrown by strictly anaerobic microorganisms

as the gut lumen enlarges and the feed becomes more solid. However, the lactic acid bacteria (*Lactobacillus*) coexist with the *Bacteroides* and other strict anaerobes. Some of the common bacterial species found in the pig hindgut are listed in Table 2. Lactic acid-producing bacteria are thought to suppress other microorganisms and are now generally recognized as desirable, thus they are given as supplements (probiotics) to promote health.

Microorganisms associated with the hindgut can be divided into two groups: 1) autochthonous microorganisms are indigenous organisms that colonize a particular region of the gut early in life, multiply to high population levels soon after colonization, and remain in the gut throughout the lives of a healthy host; 2) nonautochthonous microorganisms are indigenous organisms that colonize the hindgut of animals living in a given area, but may not be present in all individuals of a given animal species.^[4] Stewart^[5] and Hillman^[3] have recently reviewed the microorganisms found in the hindgut of the pig through the use of conventional identification techniques. More recent studies using identification of bacterial 16S rDNA genes by polymerase chain reaction, cloning, and DNA sequencing suggest that 50% or more of the microflora of the pig hindgut is unidentified.^[6] This is likely true for most other animals because they have been studied much less than the pig. This suggests that the current classification systems for the major genera of microorganisms in the hindgut are inadequate. Recent studies have also demonstrated that the genetic diversity within existing taxonomic groups has been greatly underestimated. Future challenges will involve evaluating this large biodiversity and determining the link between diversity and metabolic function. Sensitive methods are needed that follow in detail, at short time intervals, the individual population changes occurring in the hindgut.

Composition of the hindgut microbiota is thought to be relatively stable. Several hundred species coexist without one or a few becoming dominant. The stability appears to be a function of inhibition of bacterial multiplication by such compounds as volatile fatty acids, hydrogen sulfide, bile salts, and bacteriocins. These bacterial inhibitors may prolong the lag phase of invading bacteria sufficiently that they are washed out of the hindgut. Competition for limiting nutrients is another method by which a balance of

Table 1 Classification of some animals based on gastro-intestinal anatomy

Class	Species	Dietary habit
Pregastric fermenters		
Ruminants	Cattle, sheep, deer	Grazing herbivores
	Antelope, camel	Selective herbivores
Nonruminants	Colobine monkey	Selective herbivore
	Hamster, vole	Selective herbivores
	Kangaroo, hippopotamus	Grazing and selective herbivores
Hindgut fermenters		
Cecal (rodents)	Capybara	Grazer
	Rabbit	Selective herbivore
	Rat	Omnivore
Colonic digesters		
Sacculated	Horse	Grazer
	New World monkey	Selective herbivore
	Pig, man	Omnivores
Unsacculated	Dog	Carnivore
	Cat	Carnivore

(From Ref. 1.)

microbial species is selected. The greater the number of limiting nutrients in the hindgut, the greater the diversity of the bacterial population, since each limiting nutrient will support the one bacterial species that is most efficient at using it.^[2] Protozoa and fungi are also found in the

hindgut of some animal species, but their occurrence is not universal and their roles are poorly understood.

MICROBIAL EFFECTS ON HOST ANIMALS

A stable intestinal microflora is inherently more resistant to pathogenic infection than an unstable one. The health of the gastrointestinal tract has a direct bearing on the growth and productivity of livestock animals, since the gut comprises the body's largest organ and represents a considerable part of the animal's protein and energy requirements.^[3] Some of the benefits and negative effects of intestinal microorganisms in the intestinal tract are given in Table 3. The large mass of adherent autochthonous bacterial population is in itself an important physiological contribution to the health of the animal. It provides a

Table 2 Common bacteria in the hindgut of pigs

<i>Bacteroides fragilis</i>
<i>Bacteroides thetaiotaomicron</i>
<i>Bacteroides uniformis</i>
<i>Bacteroides suis</i>
<i>Butyrivibrio fibrisolvens</i>
<i>Clostridium perfringens</i>
<i>Escherichia coli</i>
<i>Eubacterium aerofaciens</i>
<i>Fibrobacter succinogenes</i>
<i>Lactobacillus acidophilus</i>
<i>Lactobacillus brevis</i>
<i>Lactobacillus cellobiosus</i>
<i>Lactobacillus fermentum</i>
<i>Lactobacillus salivarius</i>
<i>Methanobrevibacter</i> spp
<i>Peptostreptococcus productus</i>
<i>Prevotella bryantii</i>
<i>Prevotella ruminicola</i>
<i>Proteus</i> spp
<i>Ruminococcus flavefaciens</i>
<i>Selenomonas ruminantium</i>
<i>Streptococcus bovis</i>
<i>Streptococcus equinus</i>
<i>Streptococcus faecalis</i>
<i>Streptococcus intestinalis</i>
<i>Streptococcus salivarius</i>
<i>Veillonella</i> spp

Table 3 The effects of gut microorganisms

Benefits	Negative effects
Synthesis of vitamins B and K	Production of toxic metabolites
Detoxification of food components or endogenous products	Modification of nutrients
Recovery of endogenous nitrogen	Release of toxins from nontoxic precursors
Production of digestive enzymes, e.g., bacterial amylase for starch digestion	Uptake of nutrients, e.g., amino-acids.
	Decreased digestibility of fat due to altering lipids and bile salts

(From Ref. 7.)



formidable barrier through which a pathogen must penetrate to establish itself. However, perturbations such as antibiotic treatment, stress, and abrupt diet modification can disrupt the adherent flora and allow a pathogen to temporarily flourish in the gastrointestinal tract.

The microbial end products of the hindgut fermentation include the short-chain fatty acids acetate, propionate, and butyrate, along with the gases methane, hydrogen, and carbon dioxide. In the young pig, the short-chain fatty acids can contribute up to 30% of the maintenance energy of the animal, while in the adult pig this may be even greater. Among other animals, large variations exist in the amount of energy derived from hindgut volatile fatty acids, with the dog and human being at the low end (<5%) and the horse at the high end (>30%). Although volatile fatty acids and vitamins synthesized in the hindgut benefit the animal, the microbes also impose a considerable burden to the animals in terms of replacement of epithelial cells, detoxification of microbial metabolites, and production of inflammatory and immunological cells. The benefits and negative effects of microbes in the hindgut are further discussed elsewhere in this encyclopedia.

MANIPULATION OF THE HINDGUT FERMENTATION

In order to maintain a healthy intestinal microflora for efficient animal growth, growth promotants, primarily in the form of antibiotics, have been therapeutically fed to livestock for several decades. This practice is suspected to be linked to development of antibiotic-resistant microorganisms. Thus, alternatives to antibiotics are being sought.^[3] These include supplementary enzymes to diets, organic acids, prebiotics, and probiotics. However, many of these alternatives are viewed with skepticism because the results obtained are variable and few have been studied sufficiently to adequately explain a mode of action.

Other efforts to increase animal growth efficiency are the use of genetically modified grains and forages that contain appropriate hydrolytic enzymes in vacuoles or in the cytosol to be released after crop harvest and animal consumption. These enzymes will assist microbial enzymes in extracting nutrients for animal growth. Recent studies have also demonstrated that it is possible for transgenic mice to produce key microbial enzymes that degrade fiber or plant phosphorous more efficiently.^[8] Generation of transgenic animals that secrete xylanase from the pancreas suggests that this may prove to have a dual benefit. Intestinal secretion of xylanase by swine would enhance nutrient absorption and the xylooligosaccharide products from xylanase action would enrich *Bifidobacterium* spp. in the intestine, thus providing a more favorable intestinal environment.

CONCLUSIONS

The gastrointestinal tract is the largest organ in an animal. The population of microorganisms in the tract will outnumber the tissue cells making up the entire body of the animal. The microflora in the hindgut are critical to the well-being of an animal and provide nutrients (volatile fatty acids, vitamins) and protection from invading pathogens that constantly enter the open ecosystem with food and water. Currently, a large proportion of hindgut microorganisms is unknown (50%). New methods and techniques are needed to identify this large mass of diverse microorganisms. Once this capability is obtained, efforts are needed to follow the changing population of microorganisms on a short-term basis. This will allow us to more fully understand the significance of the microflora in animal growth efficiency and health.

ARTICLE OF FURTHER INTEREST

GI Tract: Animal/Microbial Symbiosis, p. 449

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