



## Microbial Interactions with Humans and Animals

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### Abstract

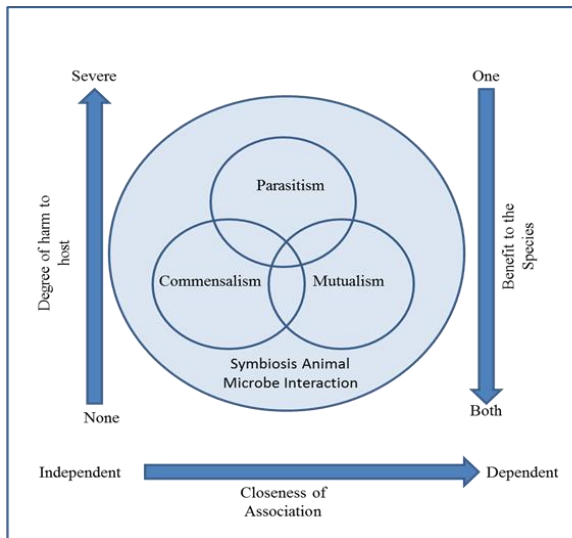
Each animal or human body is a complex macrocosm comprised of multiple interconnected ecological systems of different body sites, including numerous body surfaces which are highly populated by microorganisms. Each region differs from the others and thus, creating a selective environment where certain microorganisms are favored more than others. These residents participate in commensal, parasitic and mutualistic relationships with their hosts. The microorganisms that establish more or less permanent residence but do not produce disease under normal conditions are members of the normal microbiota. Others are called the transient microbiota which may be present for several days, weeks or months and then disappear. Within the gastrointestinal system, animals have established relationships with microbes that appear to benefit both in many cases. Normal microbiota are not only found in gastrointestinal system, but also localized in skin, eyes, upper respiratory system and urogenital system of mammals. Digestive symbioses are most common among insects feeding on wood or other lignified plant materials. The symbiotic relationship in gut of termite is completely mutual and is beneficial for the host termite, its gut protists and their associated prokaryotes. Nematophagus fungi are an important group of soil microorganisms that can suppress the populations of plant-parasitic and animal-parasitic nematodes. The pathogenic mechanisms of nematophagous fungi are diverse. The present review enlightens the microbial interactions in four sections. First two sections discuss microbial interactions with gastrointestinal system and other body sites of mammals. Other two sections include microbial interactions with nematodes and termites.

**Key words:** Microbial Interactions, Humans, Animals

### Introduction

Symbiosis is defined as an important biological strategy in which living organisms share beneficial functions with their partners to establish their ecological niche. Mutualism, commensalism and parasitism are the three types of symbiosis. In mutualism, both the

microorganism and the host are benefited. In commensalism, one of the organisms is benefited and the other is unaffected, whereas when one organism is benefited and the other is harmed, then the symbiosis is called as parasitism. The most microbial-animal interactions are considered commensal [1,2]. Figure 1 shows Venn diagram of different symbiotic relationships between microbes and host.



**Figure 1: Venn diagram showing symbiotic relationships between microbes and animals.**

The digestive system and the skin of mammals contain the most diverse and complex bacterial flora [3].

### Microbe-Animal Interaction in the Gastrointestinal System

The gastrointestinal (GI) tract begins at the mouth and ends at the anus. Food is consumed through the mouth and digested by host enzymes in the stomach and small intestine, and nutrients are extracted and absorbed in the small and large intestines. In this nutrient-rich environment, microorganisms can colonize and grow. The gastrointestinal ecosystem of mammals contains hundreds of species of microorganisms [4]. This diverse and dynamic population of bacteria in the system is referred to as the microflora or microbiota. The specific species or strains of microorganisms can vary with animal host,

diet, and environment, but in general the predominant species are associated with a limited number of bacterial genera [5,6]. The digestive tract can be divided into distinct units, each providing conditions for the growth of a specific microflora.

The oral cavity is one of the most complex and heterogeneous microbiological habitats of the body. The bacterial flora present in oral cavity includes both strict anaerobes and facultative anaerobic bacteria. Many antimicrobial substances including the most important enzymes such as lysozyme and lactoperoxidase are found in saliva. Despite the activity of these substances, the presence of food particles and epithelial debris makes the oral cavity a favorable habitat for microbial growth. The mouth presents a series of different ecological conditions with age. At birth the oral cavity is sterile, but is rapidly colonized from the environment mainly from the mother in the first feeding. *Streptococcus salivarius* is dominant oral flora until the appearance of the teeth in humans [7]. When teeth begin to erupt during the first year, leads to colonization by *Streptococcus mutans* and *S. sanguis*, *Bacteroids spp.*, *Fusobacterium spp.*, *Rothia* and *Capnocytophaga* (as shown in table 1). These bacteria need a non-epithelial surface for colonization. They will persist as long as teeth remain [8]. Other strains of *Streptococci* adhere strongly to the gums and cheeks but not to the teeth. The complexity of the oral flora continues to increase with time, and has diverse population of bacterial species such as *Streptococci spp.*, *Corynebacterium spp.*, *Haemophilus spp.*, *Bacteroides spp.*, *Fusobacterium spp.*, *Actinomyces spp.*, *Actinobacillus spp.*, *Treponema spp.*, *Micrococcus spp.*, *Moraxella spp.* and *Neisseria spp.* around puberty. Fungus *Candida albicans* is also present in the oral cavity [9,10,11]. *Bifidobacteria* are very early colonizers of GI tract and are regularly present in the oral cavity of children. Later, they can become the normal inhabitants of the adult dental plaque. The oral flora contributes to host nutrition through the synthesis of vitamins and also contribute to immunity by inducing low levels

**Table 1: List of Some Microflora in Various Body Regions of Humans and Animals**

<b>Body Regions</b>	<b>Human/Animals</b>	<b>Microflora</b>
Oral cavity	Human	Various species of <i>Streptococcus</i> , <i>Corynebacterium</i> , <i>hemophilus</i> , <i>Bacteroides</i> , <i>Fusobacterium</i> , <i>Actinomyces</i> , <i>Treponema</i> , <i>Micrococcus</i> , <i>Moraxella</i> , <i>Neisseria spp.</i> and <i>Candida</i> (fungus)
Small intestine	Human	Various species of <i>Lactobacillus</i> , <i>Enterococci</i> , <i>Bacteroides</i> and family <i>Enterobacteriaceae</i>
Large intestine	Human	Various species of <i>Bacteroides</i> , <i>Fusobacterium</i> , <i>Peptostreptococcus</i> , <i>Escherichia coli</i> , <i>Klebsiella</i> , <i>Enterobacter</i> , <i>Shigella</i> , <i>Bifidobacterium</i> , <i>Proteus</i> , <i>Citrobacter</i> , <i>Enterococcus</i> and <i>Candida</i> (fungus)
	Ruminants	<i>Bacteroides succinogens</i> , <i>Ruminococcus flavefaciens</i> , <i>Ruminococcus albus</i> , fungi ( <i>Neocallimastix frontalis</i> , <i>Piromonas communis</i> , <i>Sphaeromonas communis</i> ), ciliated protozoa ( <i>Epidinium ecaudatum</i> , <i>Eudiplodinium maggii</i> , <i>Isotricha intestinalis</i> )
Skin	Human	<i>Staphylococcus epidermidis</i> , <i>S. aureus</i> , <i>Corynebacterium xerosis</i> , <i>Propionibacterium acnes</i> , <i>Streptococcus spp.</i> , <i>Candida spp.</i> (fungus), <i>Pityrosporum spp.</i> (fungus)
Eyes (conjunctiva)	Human	<i>Staphylococcus epidermidis</i> , <i>S. aureus</i> , <i>Propionibacterium acnes</i> and diphtheroids
	horse and deer	<i>Bacillus spp.</i> , <i>Diplococcus spp.</i> , <i>Corynebacterium spp.</i> , <i>Streptococcus spp.</i> , <i>Staphylococcus spp.</i> <i>Pseudomonas spp.</i> , <i>Micrococcus spp.</i> , <i>Sarcina spp</i> and <i>Aerobacter aerogenes</i>
Upper respiratory tract	Human	<i>Staphylococcus epidermidis</i> , <i>S. aureus</i> , <i>Corynebacterium spp.</i> , <i>Neisseria spp.</i> , <i>Moraxella catarrhalis</i> , <i>Streptococcus spp.</i> , and diphtheroids
	Donkey	<i>Streptococcus spp.</i> , <i>Corynebacterium spp.</i> , <i>Staphylococcus aureus</i> , <i>CNS spp.</i> , <i>E.coli</i> , <i>Rhodococcus</i> , <i>Proteus vulgaris</i> , <i>Pseudomonas spp.</i> , <i>Pasteurella spp.</i> , <i>Bacillus spp.</i> and <i>Klebsiella</i>
Urinary tract	Human	<i>Staphylococcus epidermidis</i> , <i>micrococci</i> , <i>Enterococcus</i> , diphtheroids, <i>Pseudomonas</i> , <i>Lactobacillus</i> , <i>Klebsella</i> and <i>Proteus</i>
	Human	<i>Lactobacillus spp.</i> , <i>Bacteroides</i> , <i>Staphylococcus</i> , <i>Streptococcus</i> ,

Genital tract (vagina)		diphtheroids, <i>Clostridium</i> , <i>Bifidobacteria</i> spp., <i>Trichomonas vaginalis</i> (protozoan) and <i>Candida albicans</i> (fungus)
	Cow	<i>Streptococcus</i> , <i>Micrococcus</i> , <i>Staphylococcus</i> , <i>Escherichia</i> , <i>Bacillus</i> , and <i>Corynebacterium</i> , species of <i>Candida</i> , <i>Penicillium</i> , <i>Aspergillus</i> , <i>Alternaria</i> and <i>Cladosporium</i> .
	Goat and Sheep	<i>Staphylococcus epidermidis</i> , <i>Pasteurella</i> spp., <i>Proteus</i> spp., <i>Streptococcus</i> spp., <i>Corynebacterium</i> spp., <i>Listeria</i> spp., <i>Lactobacillus</i> spp., <i>Micrococcus</i> spp.
	Nematodes	fungi ( <i>Arthrobotrys oligospora</i> , <i>Monoacrosporium haptotylum</i> , <i>Drechmeria coniospora</i> , <i>Dactylellina candidum</i> , <i>Coprinus comatus</i> and <i>Stropharia rugosoannulata</i> )
Gut	Termite	protozoa <i>Trichonympha</i> , <i>Methanobrevibacter</i> , spirochete-like bacteria

of circulating and secretory antibodies that may cross react with pathogens [12]. The oral bacteria also exert microbial antagonism against non-indigenous species by production of inhibitory substances such as fatty acids, peroxides and bacteriocins. The oral cavity of animals also contains variety of normal flora such as oral cavity of mouse is colonized with lactobacilli and low level of *Streptococcus gordonii* [13].

The stomach contains relatively few microorganisms due to its acidic environment. Some acid-tolerant species are capable of colonizing this part of digestive tract; such bacteria include species of lactobacilli and streptococci. The gastric pathogen *Helicobacter pylori* is able to colonize the stomach of humans. *H. pylori* has also been isolated from the stomach of pigs and cats, and several other species of *Helicobacter* occur in the stomach of various animals [14].

The anterior part of the small intestine is also acidic and it is similar to stomach in terms of its microbial content (a microflora mainly consisting of Gram-positive species). The distal region of the small intestine has a less acidic pH value. This creates favorable environment for bacterial flora resulting in a

richer and more complex microbiota. The present microflora includes *Pseudomonas aeruginosa*, *Lactobacilli* spp., *Enterococci* spp., *Bacteroides* spp. and the family *Enterobacteriaceae* includes genera *Escherichia*, *Enterobacter*, *Proteus*, etc. [15]. The large intestine contains an enormous microbial population. More than four hundred microbial species have been discovered in large intestine. The bacterial population of the large intestine comprises mainly strict anaerobic bacteria such as *Bacteroides* spp., *Fusobacterium* spp., *Clostridium* spp., and *Peptostreptococcus* spp. Considerable numbers of facultative anaerobes such as *Escherichia coli*, *Klebsiella* spp., *Enterobacter* spp., *Proteus*, *Shigella*, *Hemophilus* spp. and *Enterococcus* spp. are also present [16]. Todar suggests that the concentration of the various bacteria in the intestines varies with species. *E. coli* and enterococci are the two most widespread bacteria among pets and farm [5].

The gastrointestinal tract microflora has profound effects on the anatomical, physiological and immunological development of the host. Mutualistic bacteria can contribute some energy, amino acids, and vitamins, but the commensal bacteria appear

to stimulate development of the gastrointestinal capillary system and intestinal villi. The presence of commensal bacteria helps fortify the GI barrier, regulate postnatal maturation, affect nutrient uptake and metabolism, and help in the processing of xenobiotics [17]. Moreover, commensal bacteria appear to interact with specialized cells, known as Paneth cells in the intestine of the host to produce antimicrobial factors called angiogenins, which can help to shape the microflora composition [18,19]. Not all examples of commensal bacterial interactions are advantageous to the host. Some *Clostridium* species can transform secreted bile acids to form secondary products that may impact nutrient digestion and absorption. The normal flora plays an essential role in stimulating the host immune system to respond more quickly against pathogenic challenges and thereby preventing infection or invasion [20]. Moreover, the normal flora stimulates the development of certain tissues, like lymphatic tissue in the GI tract. A healthy commensal population such as enterobacterial flora also protects the animal body against colonization of invading pathogens by competing for nutrients and for attachment sites. This phenomenon is known as bacterial antagonism [21]. In addition, lactobacilli produce antagonistic substances including organic acids such as lactic acid and antimicrobial substances such as reuterin and bacteriocins (toxic proteins). All these substances are able to suppress growth and interfere with the adhesion of pathogenic strains of bacteria [22]. Similarly, in mouth, streptococci produce compounds that prevent growth of most Gram-positive and Gram-negative cocci. In large intestine, *E. coli* produce bacteriocins that inhibit the growth of pathogenic bacteria, *Salmonella* and *Shigella* (as shown in table 1). However, indigenous GI bacteria are also opportunistic pathogens and can translocate across the mucosal barrier to cause systemic infection in hosts [23]. For example, *E. coli* is harmless as long as it resides in the large intestine, but if it reaches other body sites like lungs, spinal cord, urinary bladder or wounds then it causes

pulmonary infection, meningitis, urinary tract infection or abscesses, respectively [6].

The intestinal flora of mammals is responsible for a wide variety of metabolic reactions and helps in the enzymatic breakdown of food. The production of useful vitamins like niacin, vitamins B1, B2, B6, and B12, folic acid, biotin, and vitamin K involves the activity of microorganisms [24]. The intestinal microflora is strongly influenced by diet. For instance, the addition of organic acids to the feed of fattening pigs contributes to reduction in the total number of bacteria, and to changes in the composition of the gut bacterial flora [25]. Numerous studies with animals such as swine and rats reared in microbiota-free environments suggest that microorganisms are not essential for the animal's survival, but they are beneficial [26].

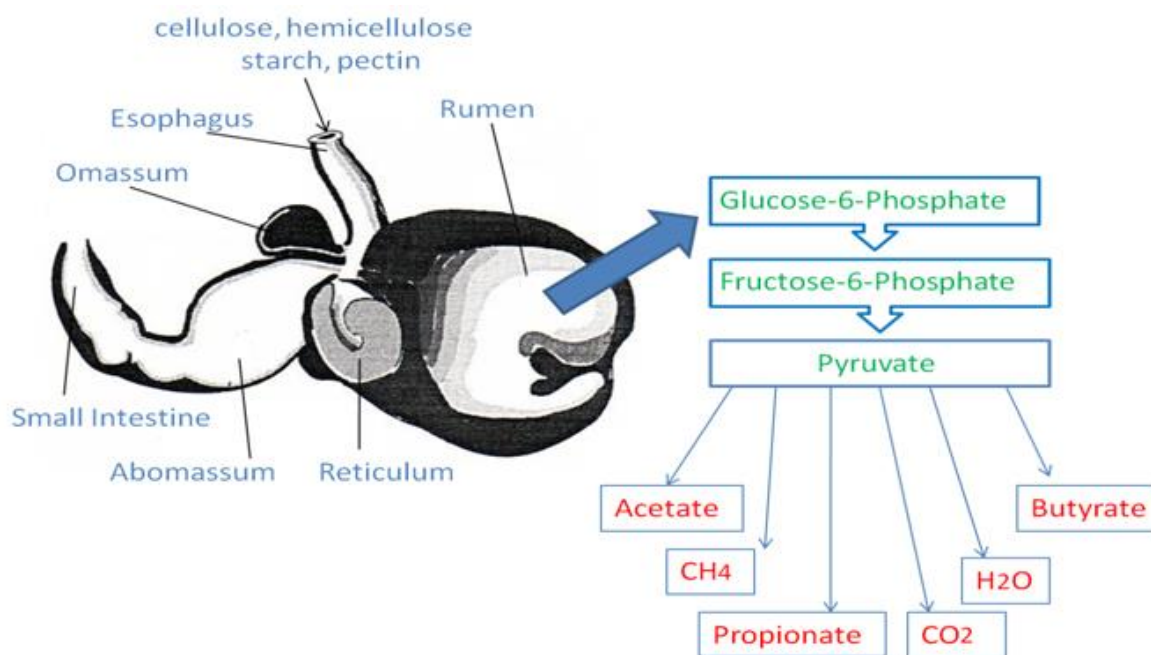
### Rumen

The microflora of ruminants plays a crucial role in the development of the rumen in the young ruminants. In herbivores, the stomach is divided into four compartments- rumen, reticulum, omasum and abomasums (Figure 2). The microbial fermentation occurs in a series of sacs called the rumen, reticulum and omasum. Rumen is the largest of the three sacs and may comprise 80% of the total volume. The microbial population of the rumen is complex and containing many different types of interacting prokaryotic and eukaryotic microorganisms including bacteria, ciliate protozoa, flagellate protozoa, phycomycete fungi, amoebae, and bacteriophages [27,28]. The rumen may be considered as a continuous culture microbial system, with regular inputs of nutrients, removal of waste products and an overflow system which passes the digesta to the abomasums and small intestine. Carbohydrates are fermented, lipids and proteins are also hydrolyzed in rumen. Volatile fatty acids (VFA) are produced during fermentation. The VFA are chiefly acetate, propionate and butyrate which are absorbed by the host animal through rumen epithelium and used as major energy sources. Rumen increases transit time of the dietary

material through the alimentary canal and allowing slow microbial fermentation of the plant polymers to proceed [29]. The principal components of the plant cell wall are insoluble carbohydrate such as cellulose and hemicelluloses. Herbivorous animals have no ability to digest these polysaccharides, but the microflora of rumen synthesizes enzymes which are capable of degrading cellulose and hemicelluloses into smaller oligosaccharides and eventually into disaccharides and monosaccharides. Thus, herbivorous animals can digest cellulose and hemicelluloses by means of a symbiotic association with cellulolytic bacteria (*Bacteroides succinogens*, *Ruminococcus flavefaciens*, *Ruminococcus albus*, *Selenomonas ruminantium*, etc.), rumen phycomycete fungi (*Neocallimastix frontalis*, *Piromonas communis*, *Sphaeromonas communis*), ciliated protozoa (*Epidinium ecaudatum*,

*Eudiplodinium maggii*, *Isotricha intestinalis*) [30,31]. Most fibrolytic ruminal bacteria are generally acetate and butyrate producers are sensitive to low ruminal pH [29]. In contrast, the amylolytic bacteria are acid-tolerant and are responsible for most of the production of propionate in rumen. Other products of fermentation, CO<sub>2</sub> and methane are lost from the animal by eructation [32].

Some microbial fermentation of cellulose also occurs in the large intestine of all animals. The degree of fermentation and energy contribution to the host is dependent on the transit time of digesta through the intestine. Some herbivores, such as monkey, pigs and chickens derive additional energy from fermentation occurs postgastric compartment (cecum). The amount of energy harnessed through fermentation in this compartment is much less than in rumen [33,34].



**Figure 2: Schematic diagram showing fermentation in rumen.**

Postgastric fermenters do not gain much from microbial biosynthesis because fermentation occurs beyond the sites of digestion and absorption. However, animals which practice coprophagy, such as rabbits get out of limitations associated with postgastric fermentation [35].

Ruminants do not require vitamin supplementation to their diet because vitamins B and K are synthesized by the rumen microflora. Postgastric fermentation also generates vitamins, but their absorption is limited. In addition, microbes serve as protein source for the ruminant animals and can

contribute about 50% of the animal's proteins needs [36].

There are three interconnecting environments in the rumen- the liquid phase (rumen fluid), the solid phase (digested materials or digesta) and the rumen epithelium. Microbial movement occurs between all the three environments. Overlying the rumen contents is a gaseous phase consisting of carbon dioxide, hydrogen and methane and low levels of oxygen and hydrogen sulphide. Many rumen bacteria are associated with the digesta [37]. The bacteria associated with the solid phase may be more than twice as numerous as in the rumen fluid. The rumen epithelium supports a population of adherent bacteria. Microorganisms within the GI system play major role in rumen ecology by scavenging oxygen from the GI system and helps in the growth of the obligate anaerobes. Many of the bacteria are ureolytic, facultative anaerobes which may be important in controlling the transport of urea into the rumen. The number of all rumen microorganisms varies from animal to animal and fluctuates with the time after feeding the diet and the health of the animal [29].

### Microbial interaction with other body sites Skin

The majority of skin microorganisms are found in the most superficial layers of the epidermis and the upper parts of the hair follicles in mammals. The microflora is especially rich and abundant in warm and humid parts of the skin. The microflora mainly consists of *Micrococci*, coagulase-negative staphylococci (CNS), *Staphylococcus spp.*, *Propionibacterium spp.* and *Corynebacterium xerosis*, *Pseudomonas aeruginosa* (as shown in table 1). These are generally non-pathogenic and are considered to be commensal. For example, *Staphylococci* and *Propionibacteria* produce fatty acids that inhibit the growth of fungi and yeast on the skin [38]. However, if *Propionibacterium acnes* is trapped in hair follicle, it may grow rapidly and cause inflammation and acne. Similarly, CNS are often related to infections in hospitalized humans and are reported to be

responsible for bovine mastitis. In some individuals of a population, potentially pathogenic bacteria such as *Staphylococcus aureus* are part of the skin flora. *Staphylococcus epidermidis* and *Malassezia furfur* reside in the outer dead regions of the skin as commensal [39,40]. Species within the CNS-group are often associated with multiple drug resistance. In addition to being normal flora bacteria, multiresistant coagulase-negative *Staphylococcus spp.* could possibly serve as gene donors to the more virulent *S. aureus* and *Staphylococcus epidermidis* in dogs, cats and horses [41,42].

In human, eccrine sweat glands have separate openings to the skin surface. In cattle, the eccrine ducts open into the common sebaceous duct and hair follicle. Thus water and lipid soluble nutrients are available to microbes at the human skin surface separately but in cattle the secretion may appear as emulsion which percolates throughout the stratum corneum [43]. Some microbes, such as aerobic microorganisms appear to reproduce at skin surface while the anaerobes are present in sebaceous ducts. For example, in human, yeast such as *Pityrosporum spp.* are found in the mouths of sebaceous ducts, *Micrococcaceae* are found in the upper part of the duct and anaerobe *Propionibacterium spp.* are found in deep of the duct. In cattle, bacteria are mostly associated with areas of disorganized stratum corneum or with hair follicle infundibula. Skin flora of man and animals are found not only at the surface but also in the deeper layers of the skin, in loose squamous layers or in sebaceous follicles [38,43].

### Eyes (conjunctiva)

Although the number of bacteria found in normal human conjunctiva is usually small but a variety of bacteria may be cultivated. *Staphylococcus epidermidis*, *Bradyrhizobium* and certain coryneforms (*Propionibacterium acnes*) are dominant species. *Staphylococcus aureus*, some *Streptococci*, Cyanobacteria and Bacteroidetes are occasionally found [44]. The conjunctiva is kept moist and healthy by the continuous secretions from the lachrymal

glands (tears). Blinking wipes the conjunctiva every few seconds and washing away foreign objects including bacteria. Tears also contain bactericidal substances including lysozyme. There is little or no opportunity for microorganisms to colonize the conjunctiva. Only by special mechanisms to attach to the epithelial surfaces and some ability to withstand attack by lysozyme, microorganism may be colonized in conjunctiva [44,45]. In animals such as in cattles, horses and deer, wide varieties of conjunctival flora is identified including *Bacillus spp.*, *Diplococcus spp.*, *Corynebacterium spp.*, *Streptococcus spp.*, *Staphylococcus spp.*, *Pseudomonas spp.*, *Micrococcus spp.*, *Sarcina spp* and *Aerobacter aerogenes* (as shown in table 1). Most microorganisms revealed in the domestic and wildlife animals are similar to human flora because of the human contact and urban inhabit [45,46,47].

### Respiratory tract

The upper respiratory tract (anterior nares, nasopharynx and oropharynx part) harbors a flora that consists of various strains of aerobic (eg, *Staphylococcus*, *Corynebacterium*, *Stomatococcus*, *Neisseria*, *Micrococcus*, and *Mycoplasma*) and anaerobic (eg, *Veillonella*, *Peptostreptococcus*, *Fusobacterium*, *Porphyromonas*, *Bacteroides*, *Prevotella*, *Actinomyces*, *Lactobacillus*, *Bifidobacterium*, and *Propionibacterium* and *Haemophilus spp.*) microorganisms (as shown in table 1) [48,49]. Within these genera, there are several strains that have a pathogenic potential. *Staphylococcus aureus* is one of the most important, but *Streptococcus pneumoniae*,  $\alpha$ -hemolytic streptococci, and *Haemophilus influenzae* are also potentially pathogenic bacteria. The nares or nostrils are heavily colonized, predominantly with *Staphylococcus epidermidis* and *Corynebacteria* and with *Staphylococcus aureus* [50]. Healthy animals usually have no bacterial flora in the sinuses of upper respiratory tract. The pharynx (throat) is normally colonized by *Streptococci* and various Gram-negative cocci [51]. Sometimes pathogens such as *Streptococcus pneumoniae*,

*Streptococcus pyogenes*, *Haemophilus influenzae* and *Neisseria meningitidis* colonize the pharynx [52]. In healthy animals, the lower respiratory tract (trachea and lungs) is normally free of bacterial flora because of the efficient cleansing action of the ciliated epithelium which lines the tract. Any bacteria reaching the lower respiratory tract are removed upward by the action of the mucociliary layer that lines the bronchi. This is followed by coughing, sneezing, swallowing, etc. to expel out them. If the respiratory tract epithelium gets damaged, as in bronchitis or viral pneumonia, the individual may become susceptible to infection by pathogens such as *H. influenzae* or *S. pneumoniae* moving down from the nasopharynx [52,53].

Bacterial isolates are also present in upper respiratory tract of cattles and pets such as in donkey, bacterial species include *Streptococcus spp.*, *Corynebacterium spp.*, *Staphylococcus aureus*, *CNS spp.*, *E.coli*, *Rhodococcus*, *Proteus vulgaris*, *Pseudomonas spp.*, *Pasteurella spp.*, *Bacillus spp.* and *Klebsiella* [54].

### Urogenital tract

Both urinary tracts exhibit tremendous microbial diversity. Microorganisms have problems gaining access and becoming established in urinary tract because the urinary tract is flushed with urine every few hours and urine is normally sterile. The lower urethra in both human sexes is inhabited by a relatively consistent normal flora consisting of resident of many bacterial species including *Staphylococcus epidermidis*, *Enterococcus faecalis*, some  $\alpha$ -hemolytic streptococci, *Bacteroids*, *Lactobacillus*, aerobic diphtheroids, aerobic micrococci, *Pseudomonas*, *E. coli*, *Proteus* and *Klebsiella* [55].

The microflora of healthy vagina of women is made up of a large number of aerobic, facultative anaerobic and obligate anaerobic species. The most prevalent microorganisms isolated are members of the genus *Lactobacillus*. Aerobic Gram-positive cocci such as *Staphylococcus epidermidis* and other



*Staphylococcus spp.*, *Streptococcus spp.*, *Actinomyces spp.*, *Bifidobacteria spp.* (such as *Bifidobacterium breve*, *B. adolescentis*) and *Enterococcus spp.* are the second most frequently detected microbes [11]. Other predominant species are often seen in the vaginas of healthy women include *Gardnerella vaginalis*, *Corynebacterium spp.*, *Bacteriodes spp.*, *Fusobacterium spp.* and *Veillonella spp.* In addition, fungus *Candida albicans* and protozoan *Trichomonas vaginalis* reside in vagina (as shown in table 1). Species of symbiotic *Lactobacillus* and *Bifidobacteria* in the vagina helps in maintaining vaginal homeostasis by producing organic acids and bacteriocins that protects against infection by other microorganisms [56].

In vaginal microbiota of cow, the predominant bacterial species belong to genera *Streptococcus*, *Micrococcus*, *Staphylococcus*, *Escherichia*, *Bacillus*, and *Corynebacterium*. The genera *Proteus*, *Klebsiella*, *Pasteurella*, *Neisseria*, *Actinomyces*, *Moraxella*, *Acinetobacter*, *Haemophilus* and *Kurthia* constituted a minor proportion of the isolates. [57]. Mycotic flora was also detected in vagina of cow such as species of *Candida*, *Penicillium*, *Aspergillus*, *Alternaria* and *Cladosporium*. High numbers of CNS, streptococci, micrococci have been observed in the vaginal flora of dogs, rats and rabbit [58]. Sheep and goat genital tracts are also residence of many microflora such as *Staphylococcus epidermidis*, *Pasteurella spp.*, *Proteus spp.*, *Streptococcus spp.*, *Corynebacterium spp.*, *Listeria spp.*, *Lactobacillus spp.*, *Micrococcus spp.* [59].

### Nematode-Killing Fungi

Plant-parasitic nematodes cause severe damages to world agriculture every year. Similarly, animal-parasitic nematodes infect grazing animals such as sheep and can kill the host animal, leading to significant financial loss for the farmers [60,61]. Treatment is almost exclusively with chemicals, nematicides that kill the worms. However, nematodes are now becoming resistant to the chemicals and also causing significant

environmental pollutions. In recent years, nematophagus fungi, one of the natural enemies of nematodes, have been proposed as biological agents to control the harmful nematodes because of they have ability to infect and kill these nematodes [62]. Nematophagus fungi include a wide and diverse range of fungi that can antagonize nematodes [63]. More than 150 species of fungi are known to attack nematodes or their eggs. According to the different pathogenic mechanisms nematophagus fungi can be classified into three categories:

**parasitic fungi** which produce spores that infect nematodes.

**nematode-trapping fungi** which catch their prey with specialized hyphal devices.

**toxic fungi** which produce toxin.

### Parasitic Nematophagus Fungi

These fungi are obligate parasite and thus spend almost all their life cycle inside infected nematodes and only emerge to sexually reproduce and disperse their spores. Parasitic fungi infect nematodes mainly by ingestive spores (*Harposporium spp.*) or adhesive spores (*Drechmeria coniospora*) [64,65].

They use the nematode as their only food source. The spores release a chemical which attracts the nematodes towards it as potential food. This helps to ensure that attachment takes place. The fungal spores are either directly ingested by the nematode, where they attach to the gut cuticle or are sticky and adhere to the external cuticle of nematode. Once attached, the spore germinates, producing a germ tube which penetrates the nematode's cuticle. The fungus grows and creating a network of hyphae that produce enzymes which breakdown the nematode. The fungus generates aerial hyphae along the length of the dead nematode. These break through the cuticle and produce aerial spores which are dispersed by the wind and rain. If conditions are not favorable, the fungus can produce resistant spores within the dead free-living nematodes [66].

They produce traps at intervals along the length of their hyphae that capture, penetrate, kill and digest a nematode's contents. The

traps are usually formed in response to the presence of substances produced by the nematodes. Some endoparasites, for example, *Catenaria anguillulae* can produce zoospores that are attracted to nematodes before adhesion (as shown in table 1). The attachment is followed by encystment on the cuticle surface [67].

### Nematode-Trapping Fungi

Nematode-trapping fungi are facultative parasites. The primary function of predatory fungi is wood decay. Wood is mainly composed of carbohydrates-cellulose and lignocellulose. Wood has very high carbon:nitrogen (C:N) ratio. Most organisms require a C: N ratio of 30: 1 to produce nucleic acids, proteins and enzymes for their good growth. For predatory fungi nitrogen is the limiting factor for growth. Nematode-trapping or predatory nematophagus fungi get their extra nitrogen from digesting the nematode's biomass. Thus, predatory fungi have two phases—the predatory parasitic phase and the saprotrophic phase that run in parallel to supply them with the correct nutrients for growth [68].

Over 200 species of fungi use specialized structures, called traps to capture nematode. Nematode-trapping fungi include *Arthrobotrys oligospora*, *Monoacrosporium haptotylum* and many more. The type of trap produced will depend on the fungal species involved. The predatory fungus secretes chemicals that attract the nematode towards it by chemotaxis, leading quickly to its death. Two basic trapping mechanisms have been observed in carnivorous fungi that are predatory on nematodes—constricting rings (active traps) and adhesive structures (passive traps) [69,70].

### Constricting Rings

This is the most sophisticated of the trapping devices and is common in the species *Drechlerella*. The nematode wriggles into the ring hoping to find food, but as it touches the ring it triggers a response. Three curved cells at the end of a short stalk, which make

up the closed loop, swell rapidly inwards, and immediately crush the worm. Once ensnared, the fungus pierces the nematode's cuticle using a narrow penetration peg, which swells inside the host to form an infection bulb that the hyphae grow from. Fungal enzymes breakdown the contents of the nematode and the nutrients are translocated within the hyphal system for growth or spore production [71].

### Adhesive Traps

Nematode-trapping fungi form different nematode-trapping devices that include adhesive hyphae, adhesive networks, adhesive knobs or branches, and non-adhesive rings. Adhesive traps capture their prey by means of an adhesive layer covering all or part of the trap [70]. The adhesive on the fungal trap binds strongly to sugar compounds on the surface of the nematode. Different kinds of adhesive traps include: Networks resemble a mesh of interlocking loops which ramify through the soil. It is the most common type of adhesive trap (e.g., *Arthrobotrys oligospora*) [69]. Knobs are erect stalks with an adhesive bulb at the end that are spaced out along the length of the hyphae (*Deuteromycetes* and *Basidiomycetes*) [72,73].

**Non-constricting rings** – composed of three cells that do not change in size or shape. Fungi produce adhesive knobs often produce these rings as an alternative trapping device (*Dactylellina candidum*). The traps have extensive layers of extracellular polymers which have been considered important for the attachment of the traps to nematode surfaces. As with other pathogens, the nematode-trapping fungi enter into the host through both enzyme degradation and mechanical pressure. Several extracellular hydrolytic enzymes including serine proteases, collagenase, chitinase and other hydrolytic enzymes (such as having lipolytic activity) are key virulence factors involved in the penetration process. After penetration, the hosts will be eventually degraded by the invading fungi. These fungi

obtain nutrients from the nematodes for their growth and reproduction [74].

### Toxic and Other Nematophagus Fungi

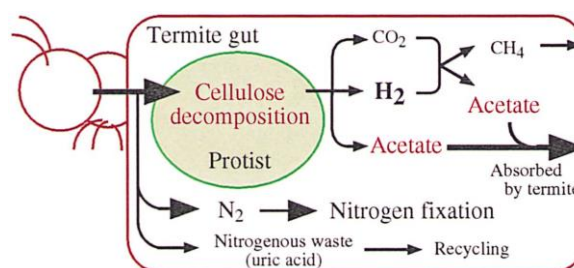
Toxin-producing fungi can attack plant-parasitic nematodes by the production of nematocidal toxins. The modes of action of these compounds against nematodes are diverse and complex. Luo et al. reported a novel nematocidal mode in basidiomycetous fungi *Coprinus comatus* and *Stropharia rugosoannulata* [73,75]. These two species produce sharp, sword-like device, canthocyte that could cause damage to the nematode cuticle, resulting in leakage of nematode inner materials. This shows that mechanical force is an important virulence factor in these fungi.

### Microbial-Termite Interaction

Digestive symbioses are most common among insects feeding on wood or other lignified plant materials [76,77]. The symbiotic community in the termite gut is a sophisticated system in which diverse population of both eukaryotic (many unique genera and species of protists, primarily mastigotes) and prokaryotic (unique bacterial species such as of phylum spirocheta) microorganisms have been identified. The symbiotic flagellated protists in the termite gut belong to the orders Hypermastigida, Trichomonadida, and Oxymonadida (as shown in table 1). These protist species are all anaerobic, and have lack many organelles [76]. All termites eat cellulose in its various forms as plant fibre. Cellulose is a rich source of energy, but it is difficult to digest. Termites rely mainly upon symbiotic protozoa *Trichonympha* (order Hypermastigida) and other microbes for cellulose digestion. Gut protozoa, such as *Trichonympha* in turn depends on symbiotic bacteria present on their surface to produce some necessary digestive enzymes. The cellulolytic flagellates degrade cellulose to produce acetate, which is absorbed by termites as energy and carbon source [78,79]. Figure 3 depicts cellulose degradation in termite gut. The digestive processes in the hindgut are largely controlled by the symbiotic gut microbiota while, the

digestive events in foregut and midgut are due mainly to host activities. In the evolutionarily lower termites (such as families Mastotermitidae, Kalotermitidae), the hindgut is predominantly occupied by unicellular eukaryotes (flagellate protozoa) that are unique to termites. These protozoa are essential for wood digestion and represent the major source of cellulolytic and xylanolytic (breakdown of xylan in hemicellulose) activities in the hindgut [80,81].

The gut flagellates are colonized by prokaryotic ectobionts attached to the surface and by endosymbionts located in the cytoplasm or in the nucleus. Microorganisms within smaller gut flagellates are methanoarchaea or methane-producing archaea (methanogens) inhabit the gut of termites and release methane from termites.



**Figure 3: Metabolism of cellulose by termite-gut protists.**

Methanogens occur on and within the cells of symbiotic protists. The endobiotic methanogens have been identified are of the genus *Methanobrevibacter*. Methanogens, which are different from endobionts, also occur onto the gut epithelium. In addition to the endobiotic methanogens, a variety of associations of prokaryotes with eukaryotic symbionts occur in the gut microbial community [82]. The ectobionts such as spirochete-like bacteria are attached with oxymonad protist's cell membrane via special structures. Some spirochete ectobionts in oxymonads are *Treponema*-related spirochetes. In a few cases, the spirochetal ectobionts contribute to the locomotion of the host protists by waving in synchronization. This relationship is known as motility symbiosis [83].

Methanogens utilize hydrogen (H<sub>2</sub>) and CO<sub>2</sub> produced by the protist hosts during the decomposition of cellulose. The relationship between hydrogen consumer and H<sub>2</sub> producer in anaerobic microbes is known as syntrophy. In this relationship inter-species hydrogen transfers stimulate decomposition of the producer. It is because of efficient removal of the reducing equivalents, released as H<sub>2</sub> by the consumer [84]. Spirochete shows acetogenic activity from H<sub>2</sub> and CO<sub>2</sub>. In the gut of termites, acetogenesis dominates methanogenesis from the same substrates. As termites absorb acetate but not methane as their energy source, therefore acetogenesis is more profitable than methanogenesis. It is assumed that many of the endobiotic and ectobiotic symbionts of the gut protists are acetogens which consume hydrogen produced by cellulose decomposition in protists. Nitrogen is released during cellulose decomposition and is fixed by nitrogen-fixing bacteria. This is the major source of nitrogen in termite. There may be other important sources of nitrogen such as termite carcasses, fungi and fecal waste [85].

### Conclusion

The presence of the various associations among members of the gut community indicates that the gut symbiotic system is highly structured and accumulates many kinds of symbiotic interactions among the members. The normal microbiota can benefit the host by preventing the colonization of potentially pathogenic microbes. In addition, normal microbiota helps to provide nutrients essential for animal or human survival. The symbiotic relationship in gut of termite is completely mutual and is beneficial for the host termite, its gut protists and their associated prokaryotes. On the other hand, nematophagus fungi kill nematodes which cause harm to cattles and plants and are good nonpolluting and environmentally safe biocontrol agents against parasitic nematodes.

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