Microbial Diversity in Different Organs of Human System

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ABSTRACT

The parts of human body exposed to environment colonised by diversified group of microorganisms. Thus colonized microorganisms establish commensal or sometimes antagonistic interaction with the host and referred to as normal human microflora. The distribution of microorganisms in human body are site specific with distinct host benefits. These microorganisms offer front line defense against invading pathogens and environmental factors. Further, they produce an array of metabolites viz., antimicrobial compounds, enzymes, vitamins and many more with therapeutic properties that have beneficial effect on the host. Furthermore, these microorganisms also modulate host immune system and confers protection against wide range of pathogens. The present article discusses the distribution of normal microflora of different parts of human system and their role in health and disease.

INTRODUCTION

Humans live with an abundant, complex and dynamic microbial population that colonise many body sites. In a healthy human, the internal tissues such as blood, brain, muscles etc., are sterile, however, the parts which expose to environmental factors are readily colonised by microorganisms in the surroundings. In a healthy human, a combination of organisms regularly found at any anatomical site is referred to as normal flora or indigenous microbiota. The normal microflora of human consists of few fungi and majorly bacteria. These normal floras are found in skin, respiratory tract, intestine, genital tracts, ears, eyes etc. These microorganisms are the essential constituents of a man’s life. They are inhabitants of the body and establish an interaction, which may be mutualistic, commensals, parasitic or amensal. Based on the type of interaction they may become beneficial or harmful to man. Kong and Segre (2012) stated that the microbiota is generally considered as two groups namely resident microbes and transient microbes. Resident microflora belongs to a relatively fixed group of microorganisms and they reestablish themselves after a disturbance. Whereas transient flora are usually from environment and do not establish permanently on the surface and remains for hours to days.

SKIN

The skin, as the largest organ of human body, protects the underlying tissues and plays an important role as a front-line defense system against external environmental changes and invading pathogens. Skin surface does not provide favourable environment for the growth of microorganisms since it has several defensive mechanisms such as acidic pH, secretion of sebum, sweat with high concentration of sodium chloride and production of antimicrobial peptides. But still it is colonised by complex microbial ecosystem majorly including bacteria and fungi. Transient flora either dies or is removable after washing whereas resident microbial population can reestablish followed by a vigorous scrubbing. It is estimated that ~1 billion bacteria inhabit a typical square centimeter of skin – covering the surface and extending down into the appendages and glands. Skin flora is usually non-pathogenic, and either commensals (are not harmful to their host) or mutualistic (offer a benefit). The benefits usually skin flora can offer majorly include preventing transient pathogenic organisms from colonizing the skin surface, either by competing for nutrients, secreting chemicals against them, or stimulating the skin’s immune system (Cogen et al., 2008). However, resident microbes can cause skin diseases and enter the blood system creating life-threatening diseases particularly in immunosuppressed people. Hygiene to control such flora is important in preventing the transmission of infections. pH of the natural skin varies between pH 4 to 5. However, the kind of water and soaps used for cleaning, cosmetics applied and physiology of individual contributes to the variation in skin pH. An acid skin keeps the residential microflora attached to the skin whereas an alkaline pH (8–9) promotes the dispersal of microbial cells from the skin (Lambers et al., 2006). Actinobacteria, Bacilli, Clostridia, Betaproteobacteria, Alphaproteobacteria and Gammaproteobacteria are the six major Bacterial classes of normal microflora of skin

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Received: 21 May 2016 – Accepted: 24 June 2016 – Published: 28 July 2016
Bacteria are associated with eye since from birth. Bacteria from mother's vagina transmit to newborn. The protective mechanisms of eye are eyelashes, eyelids, lacrimal glands, and tear flora. The protec-
powerhouse, breaking food down into useful and nutritious components for us and for the microorganisms. Gut bacteria are known to produce vitamin K. Prolonged antibiotic therapy results in the declined gut flora and vitamin deficiency which leads to coagulopathy and bleeding (Bhat and Deshmukh, 2003). The diversity of regulatory signalling among the gut flora and host epithelium, lymphoid tissue, and neuromuscular apparatus is an untapped reservoir from which novel therapeutics may be mined. Moreover, the capacity to engineer food-grade or commensal bacteria to deliver therapeutic molecules to the intestinal mucosa promises to extend the scope of microbial manipulation for the benefit of mankind (Shanahan, 2005). Enteric bacteria form a natural defence barrier and exert many protective, structural and metabolic effects on the epithelium. Major functions of the gut flora include metabolic functions that result in salvage and absorbable nutrients, important tropic effects on intestinal epithelia and on immune structure and function, and protection of host against invading pathogens (G guarner and Malagelada, 2003). It’s only recently that new genomic techniques have opened the doors to detailed study of our gut microbiome, but understanding how it varies among different people is extremely important. Many researchers suspect that the make-up of the inhabitants of our guts might help explain why some people develop metabolic disorders and others do not. In the gut Bacteria and Archaea are dominant. Acid, bile and pancreatic secretions limit the colonization of most of the bacteria in stomach and proximal small intestine. However, in distal small intestine and in large intestine, the number increases to greater extent as the pH increases. Bacteria belonging to Bacteroidetes, non-Alphaproteobacteria, Cyanobacteria, Actinobacteria, Firmicutes, Fusobacteria and Alphaproteobacteria were frequently identified as gut flora of healthy adults (Eckburg et al., 2005). However, fetal gut is sterile but colonisation begins immediately after birth and is influenced by the mode of delivery, the infant diet, hygiene and medication. Enterobacteria and Bifidobacteria represent early colonisers, although differences in gut colonization begins immediately after birth and is influenced by the mode of delivery, the infant diet, hygiene and medication. Enterobacteria and Bifidobacteria represent early colonisers, although differences in gut microflora composition and the incidence of infection occur between breast- and formula-fed infants (Mountzouris et al., 2002). It seems that these pioneering bacteria may modulate gene expression in the host to create a suitable environment for themselves and can prevent growth of other bacteria introduced later to the ecosystem (Xu and Gordon, 2003). Enteric bacteria form a natural defence barrier and exert numerous protective, structural and metabolic effects on the epithelium. Commensal bacteria profoundly influence the development of humoral components of the gut mucosal immune system (Weinstein and Cebra, 1991) and also modulate the fine-tuning of T-cell repertoires and T-helper (Th)-cell type 1 or type 2 cytokine profiles (Cebra, 1999; Shanahan, 2002). Thus, it is possible that the composition of the colonising flora influences individual variations in immunity. Microbiota of esophagus includes *Streptococcus mitis, Streptococcus thermophilus, Streptococcus parasanguis, Veillonella atypica, Veillonella dispar, Rothia mucilaginosus, Megathurrha microcomiformis, Granulicatella adiacens, Prevotella pallens, Bacteroides, Clostridium AY 278618, Bulleidia moorei* and *Actinomyces odontofyticus* (Pei et al., 2004).

Studies and statistical analysis revealed that dietary pattern greatly influences the diversity of gut flora. Gut microflora mainly composed three enterotypes: *Prevotella, Bacteroides* and *Ruminococcus*. Always there is an association between these enterotypes and dietary components. *Prevotella* is related with carbohydrates and simple sugars, indicating an association with carbohydrate-based diet more typical of agrarian societies in South Asian countries like India, Pakistan, Nepal, Sri Lanka and others. While *Bacteroides* enterotype is associated with, species of *Bacteroides* which are associated with people practicing diet rich with animal proteins, aminoacids and saturated fats. Protein-rich milk and meat products are diet of Western countries (Wu et al., 2011). Study and characterisation of bacterial genes isolated from fecal bacteria of Amazonas of Venezuela, rural Malawi and US metropolitan areas showed that gut bacteria of US population has a high representation of glutamine degrading enzymes and enzymes required for vitamin and lipoic acid biosynthesis. Meanwhile, glutamate synthase and α amylase enzyme showed a high degree of representation in Malawi and Amerindian population (Yatsunenko et al., 2012). While in case of rural Africa, people mostly consume carbohydrate rich food with less fat and proteins. Accordingly, their gut flora is dominated by *Bacteroidetes* with a unique abundance of bacteria from genus *Prevotella* and *Xylanibacter*, known to produce a set of bacterial genes for cellulose and xylene hydrolysis which may aid in the digestion of indigestible plant sugars. However, these genes were completely lacking in the European children whose fecal flora mainly represented by *Firmicutes* and showed marked reduction in the bacterial diversity. The increased biodiversity and different composition of gut flora in the African population results in the reduction of non infectious colonic diseases (De Filippo et al., 2010).

**PROBIOTICS**

Probiotics are the microorganisms which when administered in a required amount confer a health benefit on the host (FAO/WHO, 2002). The representatives of probiotics mainly include Lactic acid bacteria such as *Lactobacillus acidophilus, L. plantarum, L. johnsonii, L. gasseri, L. casei, L. rhamnosus* and *Bifidobacterium longum*, *B. breve*, *B. infantis, B. thermophilum, B. pseudolongum* and others (Gayathri et al., 2011). During last decade, several research works showed that probiotic therapy in combination with conventional therapies helps to fight existing diseases and protect future infections since probiotics have the potential to fight infection, and to modulate the immune system. The mechanism of probiotics includes competition with...
harmful gut flora for adhesion to the epithelium of the gastrointestinal tract, struggle for nutrients, enhancing the host immunity to pathogens by modulating immune system, producing antibacterial substances. Substances which are responsible for non-specific inhibition of pathogen development are primarily hydrogen peroxide, bacteriocins, lactic and acetic acids (Bielecka et al., 1998a; Asha and Gayathri, 2012b). These antagonistic properties are useful in probiotic products. Lactic acid bacteria as well as products in which they occur show anti-carcinogenic action and also take part in alleviating symptoms of lactose intolerance and other gastrointestinal disorders (Fooks et al., 1999; Asha et al., 2012; Asha and Gayathri 2012a; Rashmi and Gayathri 2014; Gayathri and Rashmi 2014b, Gayathri 2016). Probiotic bacteria can reduce the risk of occurrence of bacterial intestinal disorders and prevent diarrhea. Moreover, they are also characterised by anti-cholesterol activities (Fooks et al., 1999; McNaught and MacFie, 2001). The ability to activate and enhance the immunological system of the host which enhances the resistance to infections is one of the beneficial aspects of probiotics on human health (Gill, 1998).

Apart from this, successful probiotic bacteria should be able to survive gastric conditions and colonize the intestine, at least temporarily, by adhering to the intestinal epithelium (Lee and Salminen, 1995). In the gut number of beneficial bacteria can be maintained in good number by regular consumption of probiotic and prebiotic products. Prebiotic is a selectively fermented ingredient that allows specific changes, both in the composition and/or activity in the gastrointestinal microflora that confers benefits upon host well being and health. Trans-galactooligosaaccharides, inulin, fructooligosaccharide, lactulose serve as prebiotics (Gibson and Roberfroid, 1995; Roberfroid, 2007).

All the time, not all the gut flora are beneficial to human. Many of them may be potential pathogens and sometimes even commensals become opportunistic pathogens in immune compromised individuals. Among the numerous intestinal bacteria that affect beneficially to the host intestine could be selected as probiotics. The kind of food we ingest decides the kind of species that dominate in the gut. Both maintenance of good number of beneficial flora and ingestion of food that benefits essential gut flora are important and it can be achieved by the application of probiotics and prebiotics.

Study of such complex microbiota is difficult since non cultivable microorganisms predominate in the nature. To overcome, metagenomic analysis is widely used to study the extensively diverse human microbiome. In this context, Human Microbiome Project (HMP) is launched with the mission to comprehensively characterise human microbiota and analyse its role in human health and disease state by studying samples from multiple body sites (http://nihroadmap.nih.gov/hmp/) (Fig. 1).

CONCLUSION

Diverse microbiota have been found on various parts of human body; the body part which has an exposure to the external environment such as skin, eye, mouth, respiratory tract, urogenital tract and gastrointestinal tract, being colonised by microorganisms and these organisms establish a commensal/mutualistic/antagonistic interaction with the host. Some of these microbiota are transient while some are resident. The distribution and diversity of normal microbiota is often site specific. By their mechanism of action-like production of antimicrobial products, pharmacological compounds, immune modulation and competition, commensal flora benefits host in many ways. Diversity of human microbiota mainly depends on diet, culture and hygiene practice of individual that mainly varies with races and surrounding environment which are further strongly correlated with the geographical distribution. Study of such diverse microbiota is very interesting and opens ways to research that helps to understand the human microbial interaction for the betterment of human life.

REFERENCES


Statement of originality of work: The manuscript has been read and approved by all the authors, the requirements for authorship have been met, and that each author believes that the manuscript represents honest and original work.

Sources of funding: None.

Competing interest / Conflict of interest: The author(s) have no competing interests for financial support, publication of this research, patents, and royalties through this collaborative research. All authors were equally involved in discussed research work. There is no financial conflict with the subject matter discussed in the manuscript.

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