Indian J Microbiol (Jan–Mar 2018) 58(1):123–125
https://doi.org/10.1007/s12088-018-0706-4

NEWS & VIEWS

Infection and Microbiome: Impact of Tuberculosis on Human Gut Microbiome of Indian Cohort

Utkarsh Sood[1] · Abhay Bajaj[1] · Roshan Kumar[1] · Sachin Khurana[1] · Vipin Chandra Kalia[2]

Human Microbiome plays a key role in maintaining a healthy state by imparting normal metabolism and immunity to the host. In fact maintenance of good health has been contributed to the presence of healthy microbiome in human beings [1]. Any imbalance can lead to many diseases and make humans susceptible to attack by a variety of pathogens. While smooth functioning of the metabolic pathways ensures fitness and a state of well-being [2], a strong correlation has been established between human health and microbial diversity, which harbors on and within the body [3, 4]. Recent estimates have revealed that our body is inhabited by as many bacteria as our body cells [5]. Skin harbours a wide range of microbes, the dominant ones being those belonging to Bacteroidetes, Corynebacteria, Propionibacteria, Proteobacteria, and *Staphylococcus* [6]. These microbes help in protecting skin from getting infected by pathogens. Within the human gut, bacteria belonging to around 160 species have been identified [7] and 44–48% of the total population is represented by Firmicutes and Bacteroidetes [8, 9]. There are various factors, which modulate the human gut flora including diet [10], diseases like rheumatoid arthritis [11], type I diabetes [12], obesity [13] and inflammation of gut due to IBD and Crohn disease [14]. These studies have shown a significant shift in the community of gut microbes between healthy and diseased individuals mainly in lifestyle diseases [15]. But the role of gut microflora in infectious diseases like tuberculosis (TB) and the impact of antibiotic treatment has not been studied to great extent worldwide with only a few reports [16, 17] concerning the dysbiosis in the diversity of gut microflora during TB infection. Additionally, there is no study from the Indian subcontinent that took into account the shift in the bacterial community of gut and the functional implications of microbes on the gut-lung axis, especially during tuberculosis.

Tuberculosis (TB) has high burden both socially and economically in a developing country like India. The patients are prescribed with directly observed treatment, short course (DOTS) regimen and the treatment can extend up to 6–9 months. The treatment using the DOTS regimen has led to instances of Multi-Drug Resistant (MDR) in strains of *Mycobacterium tuberculosis.* MDR strains are very difficult to treat as *M. tuberculosis* has evolved in a way that it can develop resistance by way of developing mutation against multiple antibiotics if exposed for prolong duration below minimum inhibitory concentration (MIC) [18]. Therefore, studying the modulation of gut microbiome can provide insights into the pathophysiology of the infectious disease and thus can open new avenues for the research and development of new drugs and therapies for curing the disease. Restoration of gut microbiota has been shown as an effective treatment for patients suffering from *Clostridium difficile* infection (CDI) [19] and this can act as a primer for initiating therapies based on probiotics and faecal microbiome transplant.

A few attempts have been made to catalog the diversity of gut microbes in Indian ethnic cohort. But the majority of these studies reported only the taxonomic diversity of normal individuals like children [20], tribal people [21], or individuals suffering from type-I diabetes [22], IBD and colon cancer [23]. The major lacunae of these study were

---

✉ Vipin Chandra Kalia
vckalia@igib.res.in; vc_kalia@yahoo.co.in

[1] Department of Zoology, University of Delhi, Delhi 110007, India

[2] Microbial Biotechnology and Genomics, CSIR - Institute of Genomics and Integrative Biology (IGIB), Delhi University Campus, Mall Road, Delhi 110007, India