The analysis of different levels of microbiota between Han and Tibetan people on the Tibet Plateau

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Abstract: *The study systematically evaluated the differential changes of microbiota between Han and Tibetan people on the Tibet Plateau. Subjects had accepted systematically medical test, IBS patients were diagnosed. Race, migration, genetic background, eating habits, living environment and altitude play important roles in shaping intestinal microbial population (16, 17). Hypobaric hypoxia environment is easy to induce intestinal inflammatory reaction and changes of flora (18). The human gut microbiota is closely related to the immunological, hormonal, and Metabolic homeostasis of human beings as well as various diseases and specific environmental adaptations. Moreover, the gut microbiota is an important indicator of human adaptation to the environment. We compared the changes of intestinal flora between IBS patients at high altitude and healthy people at high altitude.*

Keywords: *microbiota, IBS, the changes of intestinal flora, high altitude*

1. Introduction

16SrRNA analysis showed that the hypobaric and hypoxia environment in Tibet had a phased impact on the intestinal microbiota of Han migrants. In the study, the intestinal microbiota of Han people living in Tibet is significantly different from those of Tibetans, and also significantly different from those of Han people in plain areas. In another study showed that people in high-altitude and middle altitude Han HPs (hypertension patients) presented greater α-diversities and β-diversities, lower ratio of Firmicutes/ Bacteroidetes (F/B), and higher abundance of beneficial Verrucomicrobia and Akkermansia than the low-altitudes HPs (4,17) .The relative abundance of Prevotella (phylum: Bacteroidetes) in AMS patients was higher than that in healthy population, and the change of microbiota was significant. That higher Prevotella abundance was associated with worse AMS symptomology. A higher ratio of Prevotella to Bacteroides is generally considered a marker of a healthy high-fiber, plant-rich diet(4,5,6), and certain Prevotella species have been associated with improved glucose homeostasis (7). The differences among species are significant in the paper, Ruminococcus_torque, Candidatus_Gastranaerophilales, Thauera_terpenica (P=0.003573533, P=0.011058018, P=0.028997857 Respectively), and in one study that Sequences amplified with Nitrospira primers were most similar to sequences of several unclassified Ruminococcus clones. Nonetheless, clones having 94% identity with Ruminococcus torques were present in greater abundance in IBS patients and were correlated with greater pain severity (8). According to the results of Uparse platform, the abundance of Ruminococcaceae in HC012 sample accounts for 30.60%, and the abundance of Porphyromonadaceae in HC033 sample accounts for 2.25%. whereas the abundance of Ruminococcaceae in HC012 sample accounted for 14.33%, and that of Porphyromonadaceae in HC033 sample accounted for 17.98% (19). Ruminococcus_torque maybe become a focus in our study in the future.

2. Methodology And Result

2.1. At the genus level

At the genus level, 449 genera were detected. The four core taxa of the fecal bacteria in the native Tibetans were unclassified Prevotellaceae (13.69%), Bacteroides (8.30%), Faecalibacterium (6.62%), and Blautia (5.31%). The four core taxa of fecal bacteria in the Han immigrants were Bacteroides (21.79%), Faecalibacterium (9.96%), unclassified Prevotellaceae (8.85%), and Veillonella (6.91%). The relative abundance of unclassified Prevotellaceae was higher in the native Tibetans than in the Han immigrants, whereas the abundance of Bacteroides was higher in the Han immigrants than in the native

Tibetans, but the differences were not statistically significant (p > 0.05) (2). A meta-analysis included 13 studies on the relationship between intestinal flora and IBS, involving 360 patients with IBS and 268 healthy subjects. The results showed that the abundance of Lactobacillus, Bifidobacterium and F. Prausnitzii decreased in patient with IBS, especially in patients with IBS-D (9). Therefore, probiotics related to Lactobacillus and bifidobacterium have been gradually popularized in clinical practice and used in the adjuvant treatment of D-IBS (1).

Some scholars analyzed the intestinal flora of D-IBS patients based on 16SrRNA amplification sequencing and real-time quantitative polymerase chain reaction technology, and found that the abundance of Prevotella increased, while the abundance of Bifidobacteria, Lactobacillus and Bacteroides decreased, which was the main expression of intestinal flora disorder in D-IBS patients. These findings suggest that the increased abundance of "harmful" bacteria while the decreased abundance of "beneficial" bacteria may be an important link in the pathogenesis of D-IBS (10). Prevobacterium can also degrade the mucus layer covered by intestinal epithelial cells through its own enzymes, and then destroy the intestinal epithelial defense barrier, providing suitable conditions for the infection of opportunistic pathogens in the intestinal cavity, and 11.5% of IBS patients are related to enterogenic infection (11,12,13).At the genus level

2.2. At the genus level

As to phylum, In healthy individuals, the largest group of taxonomic phyla (contributing roughly 70% the intestinal tract) are Bacteroidetes and Firmicutes(8), Most studies have focused on investigating F/B (Firmicutes and Bacteroides) (1,2,3), One study showed that the sequencing depth employed here revealed a total of 228 bacterial genera and 9 different phyla among all the 84 subjects. Overall, the fecal microbiomes across the three cohorts were dominated by Firmicutes (62%) followed by Bacteroidetes (24%), Actinobacteria (5.2%) and Proteobacteria (4.2%)(2), At present, intestinal flora disorder in IBS patients has been confirmed by numerous studies at home and abroad (5,6), and the relatively consistent manifestations are decreased abundance and diversity of intestinal flora and increased firmicutes/bacteroidetes ratio (4,6,7), High F/B ratios and a high proportion of Firmicutes have been shown to be associated with the highly efficient extraction of energy from food(14) Similar resultswere reported by Li and Zhao (2015), who found that the F/B ratio was higher, Firmicutes was significantly more abundant, and Bacteroidetes was significantly less abundant in the intestinal microbiota of Tibetans and Han immigrants living at high altitudes than in Han subjects living at low altitudes(15).

2.3. α-Diversity Analysis

Four α-diversity measures were calculated: Simpson's index, Shannon's index, the abundance-based coverage estimator (Ace) index, and Chao 1. We found no significant differences in community richness (Ace and Chao 1) between the native Tibetans and the Han immigrants (p > 0.05), but the native Tibetan feces had significantly greater microbial diversity (more different species, Simpson's and Shannon's indices) than that of the Han immigrants (p < 0.05).

2.4. β-Diversity Analysis

The relationship between the community structures of the microbiota of the native Tibetans and Han immigrants was examined with NMDS ordination plots, which revealed clear differences in the community compositions and structures of the two groups.

3. Discussion

With the continuous progress of microbiota analysis technology, from the determination of changes in the level of a specific flora in feces to the systematic analysis of the whole flora, the research on the intestinal flora of IBS patients has also made great progress. Although most clinical studies have different results, there is a general agreement on the reduced gut microbiome diversity in patients with IBS.

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