

A Longitudinal study to gain insights into the Gut Bacterial Abundances and Associated Diet Practices of important ethnic tribes of West Bengal

ABSTRACT

**THESIS SUBMITTED FOR THE DEGREE OF
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Abstract:

Tribals of West Bengal are divided into geographically separate regions with distinctive ecological characteristics, and many of them still maintain a traditional lifestyle that excludes the consumption of western foods. Therefore, it can be anticipated that they should possess a pristine gut. Globalization has resulted in considerable growth in the metropolitan sprawl of various cities as the world becomes increasingly urban. Dietary patterns and lifestyle choices have changed dramatically as a result of this spread across individuals. Till date, no study has reported on the gut microbiome of the West Bengal tribal population despite the fact that there are 40 identified tribes in the state comprising 5.8 percent of the total population of the state as per 2011 Census.

Nomadic tribe Sabar currently stationed near Jharkhand, Purulia side; Foothill Mech tribe of Alipurduar; Hilly Bhutia tribe of Lepchakha. Along with these three tribal families we have also recruited an urban family as a control for this longitudinal study over a period of three years. Each family consisted of a male, female and kid member (essentially a male and would not attain puberty during the period of our study). Anthropometric measures such as BMI was evaluated to understand the nutritional status of the subjects. In order to evaluate the gut bacterial diversity, 16S rRNA from first fecal matter was subjected to Illumina Miseq™ sequencing. Quality control (FASTQC), taxonomic (QIIME2) and functional profiling was performed for metagenomic analysis.

Our study involving the Bhutia, Mech and Sabar tribes indicate that association of *Prevotella*, *Bifidobacterium*, *Akkermansia*, *Holdemanella* form a core consortium, which allows consistency in their subsistence to find the alterations in gut bacterial assemblages and finally would be able to map the gut microbial consortia among the tribals and the urbanized population based on their subsistence pattern. From the urban subjects selected

as control, we were able to identify significant increase of genera *Metanobrevibacter*, *Faecalibacterium*, *Alcaligenes*, *Romboutsia* etc. can be correlated with their lifestyle and dietary patterns.

Non-Timber Forest Produces (NTFPs) were also used as a part of their regular diet, and get an insight into their probable utility as drug-like molecules which can be used to address a number of diseases that have become a subject of major concern in recent times. The compounds identified showed satisfactory bioavailability and drug-likeness score we were able to identify functional implications on key disease associated targets using suitable probability indices in the human body involved in various important metabolic pathways and disease regulation.

Our aim was also to be able to explain the disease risk estimation obtained from genome variant analyses performed on the subject candidates and draw a relationship between the lack of phenotypic expression of the diseases even though genetic variants were observed. These observations may be further explored in targeted nutrigenomics studies to evaluate the impact of the dietary components as a preventive arsenal for many diseases. Finally, this study will enable us to create a roadmap for evaluating the interplay between dietary practice and indigenous lifestyle, gut bacteriome structure and function among the Sabar, Bhutia, Mech tribes along with the urban population of West Bengal.

Keywords: *Ethnic Tribes, Pristine Gut, Gut Bacteriome, Anthropometry, Diet, Metagenomics. Microbiological Profiling, GC-MS.*

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