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## Data Article

# Gut microbial dataset of a foraging tribe from rural West Bengal - insights into unadulterated and transitional microbial abundance



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## ABSTRACT

The human gut microbiome contributes to a broad range of biochemical and metabolic functions that directly or indirectly affect human system. Numerous factors such as age, geographical location, genetic makeup, and individual health status significantly influence the diversity, stability, and relative abundance of the gut microbiome. Of the mentioned factors, geographical location and dietary practices appears to explain a significant portion of microbiome variation. On the other hand tribal people living in geographically isolated areas and dependent on their traditional food sources are considered as having relatively unadulterated gut as their guts are least colonized by Western diet. The Western diet — low in fiber and high in refined sugars — is basically wiping out species of bacteria from our intestines. That's the conclusion Smits (2017) and his team reached after analyzing the Hadza microbiome at one stage of their year long study. The trend was clear: The further away people's diets are from a Western diet, the greater the variety of microbes they tend to have in their guts. And that includes bacteria that are missing from American guts."So whether it's people in Africa, Papua New Guinea or South America, communities that live a traditional lifestyle have common gut microbes — ones that we all lack in the industrialized world. In this work we present a pilot study data of the gut microbiome of an ethnic tribe

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of West Bengal, India, originating from Dravidian descent - the Savars. These are nomadic tribes and are still dependent on hunting and gathering for their livelihood. We identified a healthy family and have analysed their stool samples for gut microbial profiles.

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#### Specifications table

|                            |  |
|----------------------------|--|
| Subject area               | <i>Biology</i>   |
| More specific subject area | <i>Gut Microbial Profiling</i>   |
| Type of data               | <i>NGS Based Data represented in form of Pie chart and Heat Map</i>  |
| How data was acquired      | <i>Illumina HiSeq Next Gen Sequencing Platform; FASTQC, QIIME</i>  |
| Data format                | <i>Raw FASTQ files</i>   |
| Experimental factors       | Subjects were allowed to have their regular diet   |
| Experimental features      | <i>DNA isolation and sequencing from first faecal matter of the subjects</i>   |
| Data source location       | Bangabasi College, Kolkata   |
| Data accessibility         | <a href="https://www.ncbi.nlm.nih.gov/sra/SRX5459403[accn]">https://www.ncbi.nlm.nih.gov/sra/SRX5459403[accn]</a> - SRA<br><a href="https://www.ncbi.nlm.nih.gov/bioproject/525343">https://www.ncbi.nlm.nih.gov/bioproject/525343</a> - Bioproject  |
| Related research article   | Smits, S. A., Leach, J., Sonnenburg, E. D., Gonzalez, C. G., Lichtman, J. S., Reid, G., Knight, R., Manjuran, A., Chandalucha, J., Elias, J. E., Dominguez-Bello, M. G., ... Sonnenburg, J. L. (2017). Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania. <i>Science (New York, N.Y.)</i> , 357(6353), 802–806 [1]. |

#### Value of the data

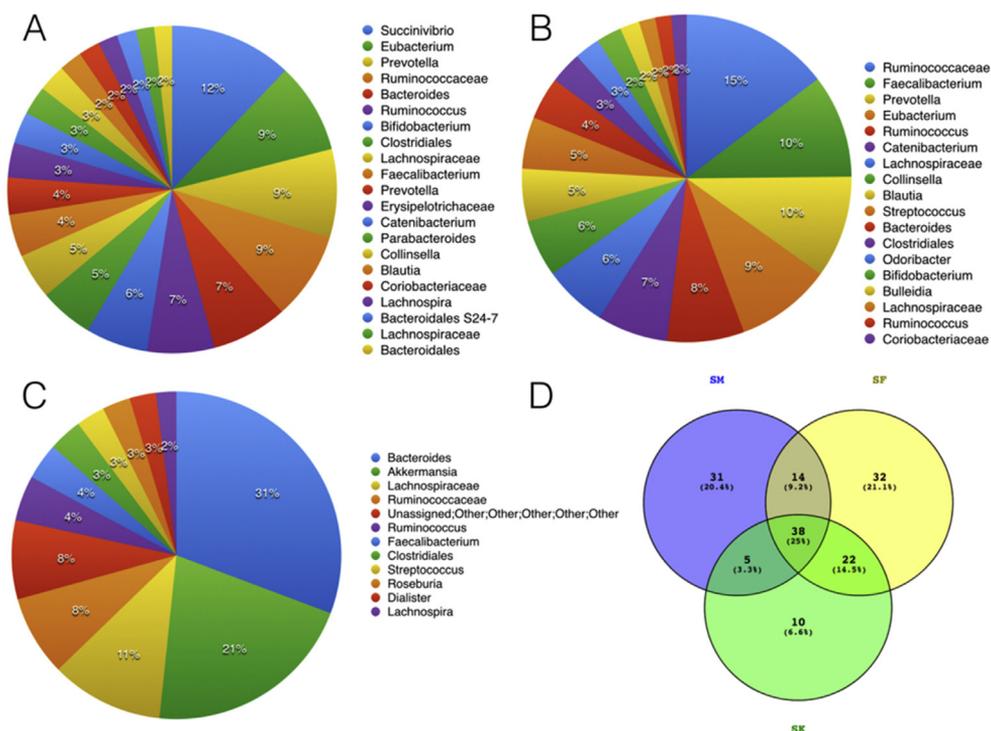
- The significance of this data stems from the fact that this is the first report of the gut microbial abundance from SAVARS of West Bengal, a nomadic tribe who are still basically foragers i.e. essentially carnivores and dependent on forest produce, having minimum or no direct agricultural practice. Thus future studies which plan to incorporate comparisons of urban and rural gut microbiomes can use this a reference point to compare and reveal the commonalities and variations that have been induced in the gut as a result of the socioeconomic lifestyle patterns.
- The gut microbial profiles identified represent unadulterated gut which has not been influenced by fast food and ready to cook frozen and stored commercial products. Further, these guts still are shielded from the overuse of medicines and antibiotics, thus antibiotic resistant microbes should be a rarity in the profiles.
- The data also reveals the propensity of transition of the gut microbial profiles from father to son and mother to son thus revealing the parental contribution to the formation of the child's gut microbiome.

## 1. Data

This data describes the gut microbiome profile of a nomadic tribe of west bengal - "Savar". This tribe has till date not adapted to the agricultural practices and is still dependent on hunting and forest produce for their livelihood, making their gut a quintessential reservoir for unadulterated microbes. Three datasets are presented - one belonging to a SAVAR male (Age: 30 years), the other of a female (Age: 26 years) and the third of their male child (Age: 7 years) who is yet to attain puberty. Ruminococcaceae (15%); Succinovibrio(12%) and Bacterioides(31%) were identified to be the most abundant of the microbial communities in female, male and child respectively (Fig. 1).

## 2. Experimental design, materials, and methods

The collection of data was performed in two important steps:



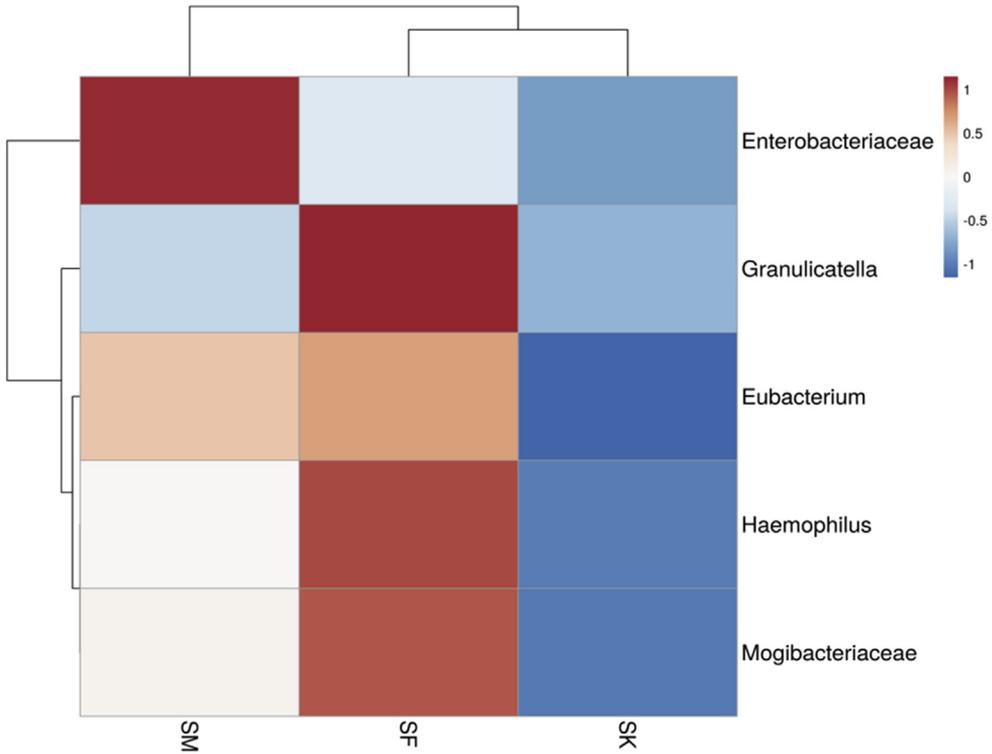
**Fig. 1.** Gut Microbial Profile of the Savar family under study. A: Male; B: Female and C: Child (male); D: Common taxa between the members; where SM = Male; SF=Female and SK=Child.

#### a) Counselling and Medical Evaluation of the Subjects:

The subjects were initially counselled on the requirement of the first faecal matter and were allowed to feed on their regular diet comprising of staple rice, poultry meat, fish and forest produce such as fruits for a week. Basic health check up of blood pressure and BMI (Body Mass Index) were performed to ensure that they were healthy, with no previous history of ailment or chronic infection in the last six months prior to sample collection with the help of a skilled medical professional.

#### b) Collection of First Faecal Matter and Sequencing:

The first faecal matter was collected at 5.30am in the morning in sterile containers previously autoclaved. The medical profiling of the candidates were again performed following the procedure and all of the subjects. The faecal matter was packed in containers and sealed with paraffin and transported to the sequencing facility within 10 hours of collection. Sequencing was performed using Illumina chemistry in the Hiseq platform using the protocol described in Bag et al. [2], with the Bioinformatics pipeline as previously described [3]. Following this, standard bioinformatics pipeline utilizing FASTQC, QIIME [4], and Krona, SILVA [5] and Greengenes [6] databases were used to first quality check the data and then identify the taxa. Following this the common taxa between the subjects [male vs female; male vs kid and female vs kid; Fig. 1D] were identified and the most abundant of the members were analysed using a heat-map [Fig. 2].



**Fig. 2.** Heatmap representing the top common taxa between the members under study, where SM = Male; SF=Female and SK=Child.

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## Transparency document

Transparency document associated with this article can be found in the online version at <https://doi.org/10.1016/j.dib.2019.103963>.

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