

GUT BACTERIAL DIVERSITY IN TRIBES OF INDIA: A REVIEW

CHAKRABORTY, S.¹ – MOLLIICK, S. A.¹ – ROY, B.^{1*}

¹ *Department of Physical Anthropology, Anthropological Survey of India, West Bengal, India.*

**Corresponding author
e-mail: bidyutroy8933[at]gmail.com*

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Abstract. Throughout the course of human history, populations have traversed diverse stages of subsistence such as hunting, foraging, horticulture and agriculture. Even in the contemporary world, numerous tribal communities inhabit geographically isolated regions and rely on their traditional subsistence practices for sustenance. Their enduring cultural and dietary practices of these populations have not only shaped their gut microbial composition, but have also played a significant role in influencing their metabolic processes and overall well-being. The exploration of the human gut microbiome is garnering increased attention over the past couple of decades. Comprehensive population-level investigations of gut microbiota in Indian tribes, incorporating representative samples across varied geographical and subsistence contexts, are notably scarce. Importance of intricate and diverse nature of gut microbiome in these healthy tribal populations is crucial, since it provides insights into the interplay between their dietary choices, gut microbiota, and health outcomes. This paper undertakes a thorough review of research into the gut microbiota of 21 Indian tribal populations hailing from diverse geographical regions of India. We also look into the variations in their gut microbiota and discuss possible reasons for similarities and dissimilarities in the gut microbial profiles in the various tribes.

Keywords: *human gut microbiota, bacterial diversity, tribes, India*

Introduction

Human gut microbiome consists of millions of distinct microbial species (Sankar et al., 2015) which have given rise to one of the most complex ecosystems. Previous estimates suggested bacterial cells outnumber human cells by the ratio 150:1 within an individual, but later estimates have put the ratio at a more moderate level of 1:1 (Sender et al., 2016). Human microbes are predominantly present in the oral cavity and gut, where the majority of digestion and absorption of nutrients takes place. They consist of bacteria, along with some other organisms such as archaea, eukaryotes, viruses etc. (Matijašić et al., 2020) which have co-evolved with their hosts to form intricate and mutually beneficial partnerships (Thursby and Juge, 2017). Over lifetime, the diversity and abundance of gut microbiome vary depending on health, environment, diet, diseases, age and other lifestyle factors of individuals (David et al. 2014; Karlsson et al., 2013; Yatsunencko et al., 2012). In India, human gut microbiota is fairly a recent domain of research which has focused on its diversity and abundance in different populations, variation with age (Marathe et al., 2012), diet (Kabeerdoss et al., 2011), obesity (Patil et al., 2012) and other diseases such as irritable bowel syndrome (IBS) (Verma et al., 2010).

Although few studies have been conducted in the Indian tribes, it has been realised that India warrants vigorous and comprehensive research into the gut microbiome from diverse ethnic populations in relation to geographies, culture and customs and dietary habits (Shetty et al., 2013). Numerous pre-industrial and pre-agricultural, mostly isolated, tribal societies exist in India which have been earmarked by the Government of India. Among total 705 Scheduled Tribes (ST) of the nation, 75 have been identified as

Particularly Vulnerable Tribal groups (PVTGs). These PVTGs, to an extent, have maintained much of their traditional lifestyle, such as diet and social cultural practices. Thus, investigations on the gut microbiota in these PVTGs are very crucial to understand a variety of consequences of metabolic processes, dietary affects and contributions towards health and well-being. Here, we have reviewed gut bacterial diversity among Indian tribes studied so far.

Materials and Methods

Previously published studies related to gut microbiota of healthy Indian tribal communities were searched. The entire process of exclusion and inclusion process of the research papers reviewed in this study (*Figure 1*) has been undertaken using PRISMA 2020 template. Different headings and keywords were used to search the articles; such as ‘tribe’, ‘India’, ‘human gut microbiota’, ‘human gut microbiome’, ‘metagenomics’, and ‘human gut microbial diversity’. A total number of 36 published articles were identified from electronic databases such as Research Gate (n=1), and metadata services such as PubMed (n=25) and Google Scholar (n=10). From these 36 articles, 14 records were removed as they did not match the keywords perfectly, so a total of 22 papers were selected for scrutiny. Again, one article was excluded due to the lack of proper description of quantitative data and access to its supplementary files, so, 21 papers (8 from PubMed, 1 from Research Gate and 12 from Google Scholar) were considered for further scrutiny. Again, a total of 16 papers were excluded for the reasons such as 4 articles overlapped with separate online sources, 8 articles proved to be insufficient in respect to the objectives of the present review, and 4 articles did not declare the appropriate names of the tribal populations. Finally, 5 articles fulfilled our inclusion criteria and, hence, were considered for the present review. These publications reported 22 tribal populations and 1 non-tribal rural population across 7 states of India (*Table 1* and *Figure 2*). The data from this non-tribal population was not included, so, finally 21 tribal populations were reviewed in the present manuscript

Table 1. Specifics of the studies conducted on the gut microbiota of Indian tribes.

A	B	C	D	E	F	G	H	I
1	Dehingia et al. (2015)	Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake Meitei, Kuki, Tangkhul Nepali, Bhutia, Lepcha Gond, Kolam, Nayak, Koya	78 30 27 58	Assam Manipur Sikkim Telangana,	Rice is the staple food for all the tribal groups, with variations in consumption of vegetables, fish, meat, legumes, whole grains, fruits, and tubers. The tribes from Manipur and Sikkim consume a relatively higher quantity of fermented foods, and dairy, along with dried and smoked fish and meat	Bacillota, Bacteroidota, Actinomycetota, Pseudomonadota	Geography and diet	Geography and diet had significant effect on the gut bacterial profile of these Indian tribes which were dominated by <i>Prevotella</i>
2	Ramadas et al. (2017)	One Rural Population (Unknown Ethnic Group) One Rural Tribal Population (Malaiyali)	10 10	Tamil Nadu	Consume millets-based diet. Eat pork every day. Do not consume any dairy products.	Bacillota, Pseudomonadota, Bacteroidota, Actinomycetota	Dietary habits	<i>Actinobacteria</i> was significantly low in this group.

3	Ganguli et al. (2019)	Savar	3 (father, mother and child)	West Bengal	Foragers, (essentially 'carnivores') and dependent on forest produce.	Verrucomicrobiota, Bacillota, Actinomycetota, Bacteroidota	Geographic location and dietary habits	The propensity of transition of the gut microbial profiles from parents to son. Thus, revealing the parental contribution to the formation of the child's gut microbiome.
4	Basu et al. (2022)	Drukpa Bhutia	3 (father, mother and child)	West Bengal	Intake of locally produced vegetables and fruits, along with liquor and fermented dairy products.	Bacteroidota, Actinomycetota, Pseudomonadota	Traditional dietary practice	Parental contribution in the formation of the child's gut microbiome.
5	Hazarika et al. (2022)	Adi Apatani Nyshi Total	10 10 10 30	Arunachal Pradesh	The Nyshi consume cereals, millet, leaves, fish, and meat. The Apatani tribe consume boiled vegetables, boiled fish, meat, and dairy products. All three tribes also consume fermented bamboo shoots, smoked pork, and smoked fish. Rice is their main staple cereal	Verrucomicrobiota, Bacillota, Actinomycetota, Pseudomonadota, Fusobacteriota, Elusimicrobiota, Bacteroidota	Dietary factors, and the overall state of health	Higher gut microbiome diversity with a high prevalence of <i>Prevotella</i> and <i>Collinsella</i> in the Adi and the Nyshi. <i>Bifidobacterium</i> and <i>Catenibacterium</i> in the Apatani.

Note: A=SI No.; B=Publication used in this review; C=Studied tribal communities; D=Sample size; E=Region of the study; F=Diet/lifestyle/mode of subsistence; G=Composition of bacteria (Phylum-level); H=Proposed influential factors; I=Remarks/outcomes of the studies.

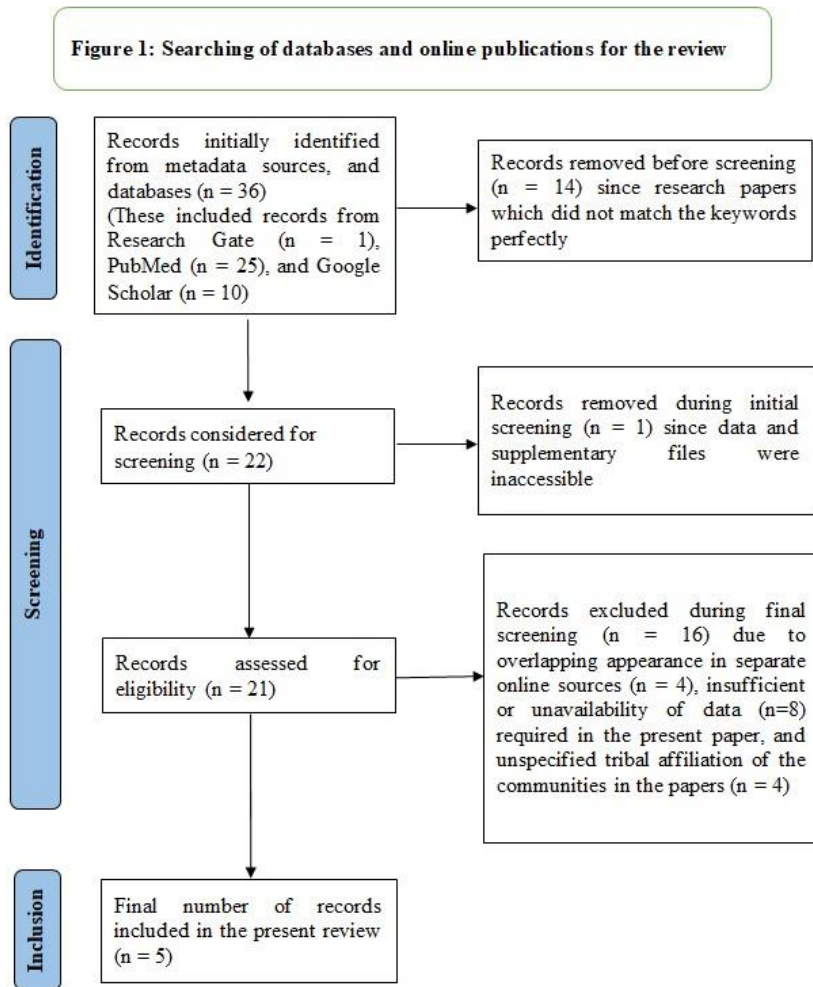


Figure 1. Publications from Research Gate, PubMed and Google Scholar were searched for this review.

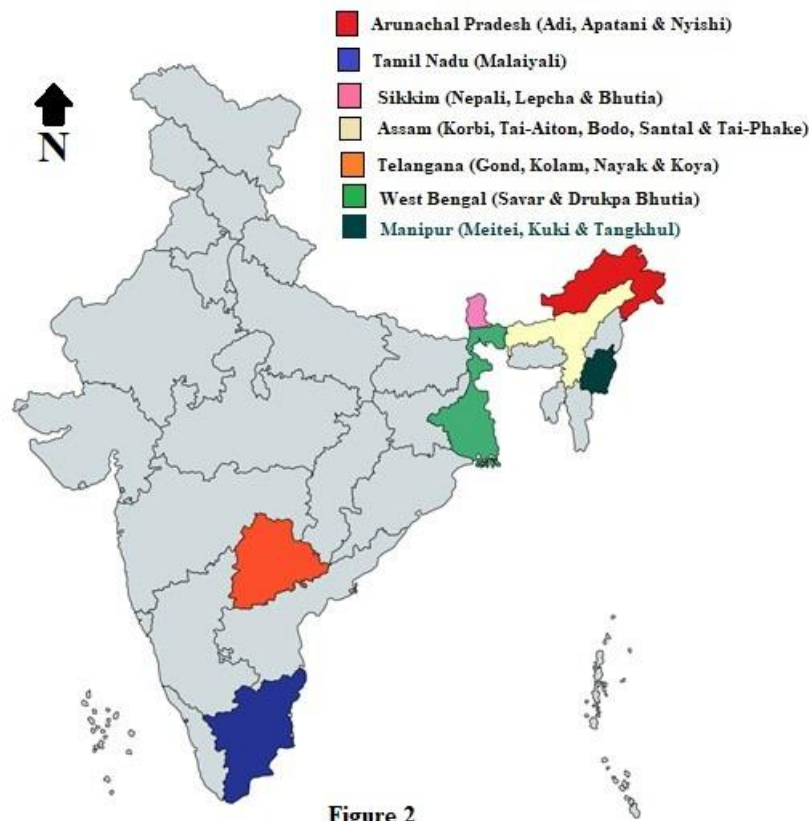


Figure 2. Locations of tribal populations studied from the different states of India as mentioned in the reported articles.

The articles, which had been reviewed for this paper, had used a mixture of both new and old nomenclature for the bacterial phyla. Thus, to avoid any confusion and to maintain uniformity, nomenclature provided by Oren and Garrity (2021) has been used in this paper. Therefore, older names of bacterial phyla have been replaced by updated ones (ending with-ota), such as, *Actinobacteria* renamed as *Actinomycetota* and similarly *Bacteroidetes*, *Elusimicrobia*, *Firmicutes*, *Fusobacteria*, *Proteobacteria* and *Verrucomicrobia* were renamed as *Bacteroidota*, *Elusimicrobiota*, *Bacillota*, *Fusobacteriota*, *Pseudomonadota* and *Verrucomicrobiota*, respectively. In the reported studies, the faecal samples were collected from all individuals, and then kept at $-20\text{ }^{\circ}\text{C}$, and used for bacterial DNA isolation using different methods (Table 2). Segments of bacterial ribosomal DNA, i.e. 16S DNA, were PCR amplified, sequenced in different NGS platforms and analysed to find diversity of gut bacteria in individuals of these populations. Analysed data were shown as heat maps of the bacterial phyla and genera (Figure 3 and Figure 4) using PAST 4.04.

Table 2. Methods employed in the reported studies.

SI No	Publications	Sample size (Age ranges)	Study objectives	Specimen type	Techniques
1.	Dehingia et al. (2015)	193 (20-35 years)	Gut bacterial diversity of the tribes	Faecal samples	DNA was extracted from the faecal samples using QIAGEN DNA Stool Mini-Kit (QIAGEN, Hilden, Germany). Sequencing of the V3- V4 regions of 16S rRNA was done on the Illumina MiSeq Platform.
2.	Ramadass et al. (2017)	20 (18-60 years)	Comparison of faecal microbiota of	Faecal samples	DNA was extracted from approximately faecal samples using QIAamp DNA stool mini kits. Sequencing the V3-V4 regions of 16s rRNA

			healthy adults in south India among the tribal and non-tribal population		was done using Roche 454 GLX Titanium sequencer (Roche Diagnostics GmbH)
3.	Ganguli et al. (2019)	3 (7, 26, and 30 years)	Gut microbiome of a foraging tribe.	Faecal samples	DNA isolation was done following the THSTI Method given by Bag et al. (2016). NGS Sequencing was done in the Illumina Hiseq sequencing platform.
4.	Basu et al. (2022)	3 (5, 27, and 29 years)	Gut microbiome of a tribal population	Faecal samples	DNA isolation was done following the THSTI Method given by Bag et al. (2016). NGS Sequencing was done in the Illumina Hiseq sequencing platform.
5.	Hazarika et al. (2022)	30 (20-60 years)	Gut microbiome of a tribal community	Faecal samples	DNA was extracted from stool samples using the QIAamp DNA Stool Mini Kit. Sequencing of the V3- V4 regions of 16S rRNA was done on the Illumina MiSeq sequencing platform.

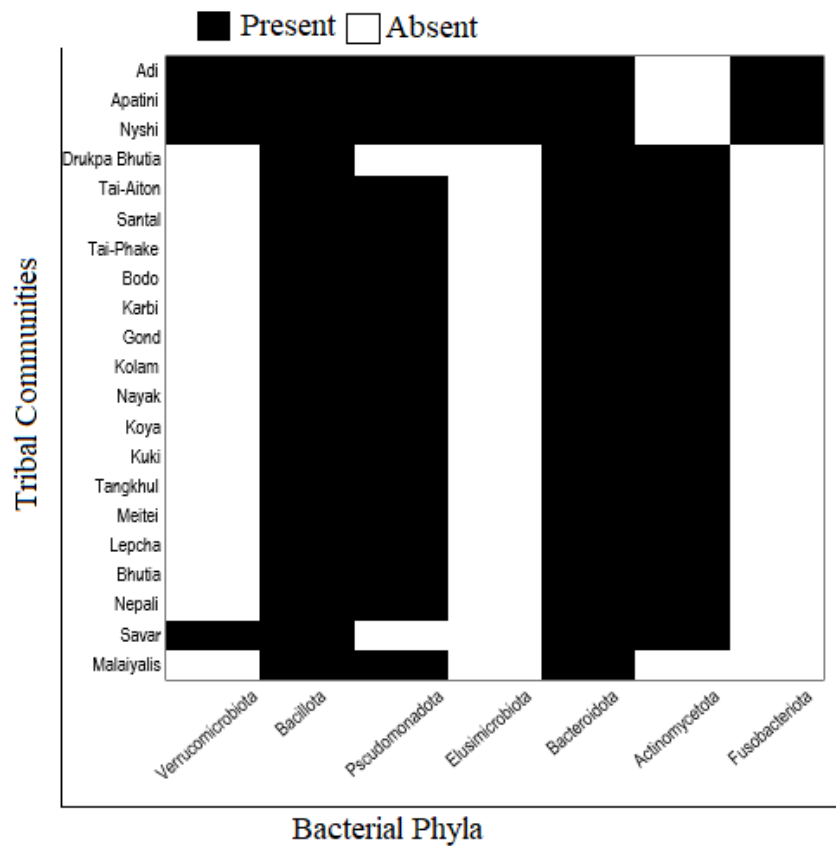


Figure 3. Presence/absence of bacterial phyla in different tribal population. Y-axis: populations, X-axis: phyla.

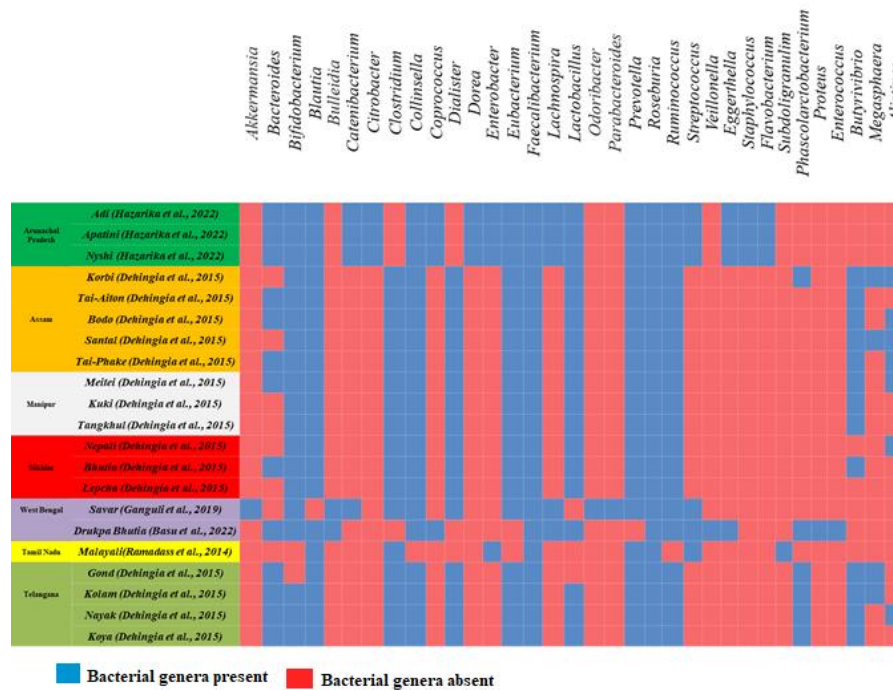


Figure 4. Bacterial genera present/absent in different population. X-axis: genera, Y-axis: populations.

Results and Discussion

All reviewed articles mainly attempted to address the gut bacterial diversity in these tribal populations based on three major factors such as dietary habits, ethnicity, and geographic location (as shown in *Table 1*). Sample sizes in the studies were different ranging from 193 (Dehingia et al., 2015) to merely 3 (Basu et al. 2022; Ganguli et al., 2019). Presence of different bacterial phyla and their corresponding bacterial genera in the tribal communities (*Table 3*) revealed that dietary practices, geography and ethnicity play important roles in composition of gut microbiota (as shown in *Table 1*). Thirty four bacterial genera, belonging to 7 phyla, have been reported in these studies (as shown in *Figure 3* and *Figure 4*). *Bacteroidota* and *Bacillota* phyla were present in all 21 tribes. Six other phyla (*Actinomycetota*, *Pseudomonadota*, *Elusimicrobiota*, *Pseudomonadota*, *Verrucomicrobiota*, and *Fusobacteriota*) have been reported in these tribal populations with varying distributions. *Fusobacteriota* and *Elusimicrobiota* were unique among the Adi, Apatani and Nyshi tribes from Arunachal Pradesh. But information on bacterial genera present in the tribes from Arunachal Pradesh was not provided. The phylum *Verrucomicrobiota* was unique to the Savar tribe of West Bengal. The phylum *Pseudomonadota* was reported from all the tribes studied, except for the Savar and Drukpa Bhutia of West Bengal. Fifteen tribes, from Manipur, Assam, Sikkim, and Telangana (as shown in *Figure 3*), have the common phyla *Bacillota*, *Pseudomonadota*, *Bacteroidota* and *Actinomycetota*. These North-East Indian tribes such as Adi, Apatani, Nyshi, Nepali, Bhutia, and Lepcha were found to have similar food habits, though they belongs to different geo-political boundaries and shared ethnic affiliation.

Table 3. Phyla and genera of the various gut microbes present in the studied Indian tribes.

SI No.	Phylum	Genera	Tribal populations
1	Actinomycetota	<i>Bifidobacterium</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Malaiyali
		<i>Collinsella</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond
		<i>Egerthella</i>	Drukpa Bhutia, Adi, Apatani, Nyshi
2	Bacillota	<i>Faecalibacterium</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Roseburia</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Ruminococcus</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond
		<i>Blautia</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Eubacterium</i>	Adi, Apatani, Nyshi, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond
		<i>Enterococcus</i>	Drukpa Bhutia
		<i>Clostridium</i>	Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Dialister</i>	Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond
		<i>Veillonella</i>	Drukpa Bhutia
		<i>Lactobacillus</i>	Adi, Apatani, Nyshi, Drukpa Bhutia, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya
		<i>Catenibacterium</i>	Adi, Apatani, Nyshi, Savar
		<i>Streptococcus</i>	Adi, Apatani, Nyshi, Savar, Drukpa Bhutia, Malaiyali
		<i>Bulleidia</i>	Savar, Drukpa Bhutia
		<i>Coprococcus</i>	Adi, Apatani, Nyshi, Drukpa Bhutia
		<i>Dorea</i>	Adi, Apatani, Nyshi
		<i>Lachnospira</i>	Adi, Apatani, Nyshi, Savar, Drukpa Bhutia
		<i>Staphylococcus</i>	Adi, Apatani, Nyshi
		<i>Subdoligranulum</i>	Malaiyali
		<i>Phascolarctobacterium</i>	Drukpa Bhutia, Korbi, Kolam, Gond, Nayak, Koya
		<i>Butyrivibrio</i>	Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Bhutia, Kolam, Gond, Nayak, Koya
		<i>Megasphaera</i>	Korbi, Santal, Gond, Kolam
3	Bacteroidota	<i>Prevotella</i>	Adi, Apatani, Nyshi, Savar, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Odoribacter</i>	Savar
		<i>Parabacteroides</i>	Savar
		<i>Bacteroides</i>	Adi, Apatani, Nyshi, Tai-Aiton, Bodo, Tai-Phake, Meitei, Bhutia, Drukpa Bhutia, Kolam, Gond, Nayak, Koya
		<i>Flavobacterium</i>	Adi, Apatani, Nyshi
		<i>Alistipes</i>	Korbi, Bodo, Santal, Tai-Phake, Meitei, Nepali, Nayak
4	Elusimicrobiota	-	Adi, Apatani, Nyshi
5	Fusobacteriota	-	Adi, Apatani, Nyshi
6	Pseudomonadota	<i>Enterobacter</i>	Adi, Apatani, Nyshi, Korbi, Tai-Aiton, Bodo, Santal, Tai-Phake, Meitei, Kuki, Tangkhul, Nepali, Bhutia, Lepcha, Kolam, Nayak, Koya, Gond, Malaiyali
		<i>Proteus</i>	Drukpa Bhutia
		<i>Citrobacter</i>	Adi, Apatani, Nyshi
7	Verrucomicrobiota	<i>Akkermansia</i>	Savar

At the genus-level, the most abundant bacteria were *Faecalibacterium* and *Roseburia* which have been reported in all the tribal populations. The bacterial genera *Ruminococcus* and *Blautia*, and *Prevotella* were present in nearly all the studied populations, followed by *Bifidobacterium* and *Eubacterium*. The bacterial genera with minimal presence were *Akkermansia* (Phyla, Verrucomicrobiota), *Odoribacter* and

Parabacteroides (Phyla, Bacteroidota) and were reported only in the Savar tribe. Similar minimal presence was detected in cases of *Veillonella*, *Enetrococcus*, and *Proteus* in the Drukpa Bhutia tribe, and *Subdoligranulum* in the Malaiyali tribe (as shown in *Figure 4*). The core gut bacteria in the tribes of Telangana and Assam consisted of *Prevotella*, *Faecalibacterium*, *Eubacterium*, *Clostridium*, *Blautia*, *Collinsella*, *Ruminococcus* and *Roseburia*. Core bacteria in the tribes from Manipur were *Bacteroides*, *Dialister* and *Veillonella*. The genera *Bacteroides*, *Dialister*, *Bifidobacterium* and *Lactobacillus* were found in the tribes of Sikkim. The Adi and Nyshi tribes from Arunachal Pradesh have high prevalence of *Prevotella* and *Collinsella*, but the Apatani tribes have high prevalence of *Bifidobacterium* and *Catenibacterium*, even though these tribes live in the same geographical region and have similar dietary practices. *Egerthella* (Phyla, Actinomycetota), *Catenibacterium*, *Coprococcus*, *Dorea*, *Staphylococcus* (Phyla, Bacillota), and *Flavobacterium* (Phyla, Bacteroidota) were prevalent only among the tribes from Arunachal Pradesh, with only *Egerthella* and *Coprococcus* being shared with the Drukpa Bhutia Tribe. Considering the Savar and Drukpa Bhutia tribes from West Bengal, the common bacterial genera in them were *Bacteroides*, *Bifidobacterium*, *Streptococcus*, *Faecalibacterium*, *Ruminococcus*, *Prevotella*, *Roseburia*, *Collinsella* despite they live in separate geographic regions of the state but separated by nearly 600 km, and had different dietary practices (as shown in *Table 1*, *Figure 2* and *Figure 4*). *Megasphaera* (Phyla, Bacillota) was unique to the tribes of Telangana, i.e. among the Gond, Kolam, Nayak, and Koya. These tribes contained the same 4 bacterial phyla (*Pseudomonadota*, *Bacteroidota*, *Actinomycetota*, and *Bacillota*) in their guts and share 18 similar bacterial genera in themselves. The Gond, Kolam, and Koya tribes from Telangana are Dravidian tribes enlisted as STs. However, the identity of the fourth tribe, the Nayak is unclear because it is a surname adopted by various communities in Telangana (Singh, 1993) and may not be a single tribal identity. Gut microbial composition of 3 Tibeto-Burmese tribes (Nepali, Bhutia, and Lepcha) of Sikkim showed presence of 4 common bacterial phyla (*Pseudomonadota*, *Bacteroidota*, *Actinomycetota*, and *Bacillota*) (as shown in *Figure 3*) and 20 common bacterial genera (as shown in *Figure 4*). It should be noted that bacterial phyla present in the tribes of Telangana and Sikkim are similar, despite being separated by a distance of 2000 km from each other, and having geographic, cultural, dietary, and ethnic differences.

India is a melting pot where traditional lifestyles and indigenous dietary practices of the tribal communities are being infiltrated by mainstream societal influences (Dehingia et al., 2015), thus resulting in the alteration of the gut microbiome profile (Hazarika et al., 2022; Ganguli et al., 2019). Even today, some communities remain isolated, which gives us the opportunity to study the gut bacterial diversity in these populations and use them as a reference point for future research on changes in their gut bacterial diversity due to external influences. Striking disparities between the gut microbial composition of urban populations and rural tribal populations have already been reported (Singh et al., 2019) which indicate such shifts may have been caused by different dietary and lifestyle practices. Dehingia et al. (2015) claimed that geographical locations, culture and diet had significant influence on gut bacterial profile of the Indian tribes and are dominated by the genus *Prevotella*. The Drukpa Bhutia in northern part of West Bengal follow their traditional agriculture based diet along with some foraging and livestock rearing products (Basu et al., 2022). But the Savar tribe in southern part of West Bengal led a relatively more foraging lifestyle (Ganguli et al., 2019), but both of them may have

retained their ancestral gut microbiome profile since they were not impacted much by external influences such as present-day life style factors and food. These two studies also claimed parental contribution to the composition of the gut microbiota of the child from same family, although this claim has not been substantiated by large-scale studies. The Adi, Apatani, and Nyshi communities seemed to have same bacterial phyla (as shown in *Table 3* and *Figure 3*) and genera (as shown in *Table 3* and *Figure 4*) in their gut. This might be due to similar dietary patterns supported by agricultural subsistence economy (as shown in *Table 2*) and shared highland ecology of Arunachal Pradesh. In addition, all of them share a common ancestral cultural identity given that they are all speakers of the Tani sub-group of languages in the Sino-Tibetan language family (Sun, 1993). These three indigenous groups from Arunachal Pradesh are also unique in the context that they had the highest diversity of phyla among all the reported tribes (as shown in *Figure 3*). An interesting observation was that apart from the three aforementioned tribes of Arunachal Pradesh; the Drukpa Bhutia and the Savar from West Bengal; the Malaiyalis from Tamil Nadu and other indigenous communities, spread across the states of Manipur, Assam, Telangana, and Tamil Nadu contained the same 4 bacterial phyla (Pseudomonadota, Bacteroidota, Actinomycetota, and Bacillota) (as shown in *Figure 3*) in their gut samples. So, similarities of phyla were observed in tribal populations living over such a large ecological range and unrelated linguistic communities (such as Tibeto-Burmese, Dravidian, and Austro-Asiatic groups) but there were differences at the level of the bacterial genera in these populations (as shown in *Figure 4*).

The Genera, *Faecalibacterium* and *Roseburia* have been reported to be present in the gut of all the tribal groups. *Faecalibacterium* (its sole species, *F. prausnitzii*) is known to be a beneficial bacterium in the human gut as it produces butyrate (a small chain fatty acid metabolite) in the intestine for the metabolism of sugar. Further, it helps in protecting diseases of the bowel such as Crohn's Disease (Wright et al., 2015) and irritable bowel disease (Lopez-Siles et al., 2015). *Roseburia* has similar functions like *Faecalibacterium*, but *Faecalibacterium* requires the presence of some other bacteria such as *Bacteroides thetaiotaomicron* in the gut (Wrzosek et al., 2013) in order to produce more butyrate. Among the populations mentioned in the review, 14 out of 21 tribes had *Bacteroides* alongside *Faecalibacterium* in their gut. The Savars of West Bengal happened to have 3 bacterial genera unique to them: *Akkermansia*, *Odoribacter* and *Parabacteroides*. *Akkermansia* has been reported to have several benefits towards human health such as reduction of body weight, resistance towards bowel diseases, and even cancer (Jayachandran et al., 2020). A decreased level of *Odoribacter* in the human gut has been reported to be related to various microbiota-associated diseases such as non-alcoholic fatty liver, cystic fibrosis, and inflammatory bowel disease (Hiippala et al., 2020). Abundance of *Parabacteroides* in the gut is known to be useful in the fight against obesity and other gut-associated diseases (Wang et al., 2019, Wu et al. 2019, Zeng et al., 2019). On the other hand, the Drukpa Bhutia, from the northern part of West Bengal, had unique bacterial genera such as *Veillonella*, *Enterococcus* and *Proteus* in their gut. *Veillonella* helps in enhancement of performance of individuals via lactic acid metabolism and production of sugar (Scheiman et al., 2019). The Drukpa Bhutia inhabits remote regions of semi-forested land. The occurrence of a bacterium associated with work performance enhancement may be related to the dairy consumption which is a key source of sugar for energy. On the other hand, *Enterococcus* is infamous for its virulence and association with various diseases such as sepsis, urinary tract infections,

and meningitis (Murray, 1990). Its presence in the gut of Drukpa Bhutia was not reported to have been associated with any of the above-mentioned diseases, possibly because the sample size was small. Similarly, *Proteus* is another pathogenic bacterium which can cause urinary tract infections. Thus, further investigation is crucial with more samples and involvement of clinicians

While considering the details of the research papers reviewed here, it was noticed that these studies had several limitations. Ramadass et al. (2017) used two broad sample groups, one consisting of individuals from the Malaiyali community (termed as a ‘rural tribal population’) and a ‘rural population’. The latter “rural population” hints a generic term used to designate individuals of a non-homogeneous non-tribal group consisted of individuals from different religion, caste, etc. Using such a sample of rural inhabitants to compare with one single homogeneous tribal community, inhabiting the same region/district in Tamil Nadu, may yield the spurious results. So, data of this “rural population” was excluded from this review. After all; abundance, composition, richness and evenness of human gut microbiota depends on lifestyle and dietary pattern specific to communities. Dehingia et al. (2015) used a large sample size (n=193) from 15 tribal communities. But they mentioned that these tribal communities belonged to different states with low sample size in each case: Assam state (5 communities, n=78), Manipur state (3 communities, n=30), Sikkim state (3 communities, n=30), and Telangana state (4 communities, n=58). The lack of availability of sample size of each community and non-uniformity of sample size in each community limited the study for comparing tribal specific gut microbiota. Those studies seem to be preliminary reports since none of them mentioned the sample size required for this type of study with sufficient power. In case of the studies on the Savar (Ganguli et al., 2019) and Drukpa Bhutia (Basu et al., 2022), from West Bengal state, the sample sizes were very low (n=3) and constituted a single nuclear family unit (mother, father and child). These two papers aimed at visualizing the diversity of bacterial phyla and genera in the guts of these family members and the transmission of bacterial genera or taxa from parents to child in the same family. The researchers should have considered several nuclear family units consisted of mother, father, and child to get proper statistical power and similarity index (Czekanowski Coefficient and Squared Euclidean Distance) to know the transmission of bacterial taxa and genera from parents to child.

Conclusion

Healthy tribal groups of India are important populations to understand the gut bacterial diversity, as most of them are isolated populations with limited contact with urban populations. Relative similarity in gut microbiota of tribes was noted as they had close geographical proximity, similar dietary practices and common ethno-linguistic group. Although, Chaudhari et al. (2020) reported association of age of individuals with the frequencies of different gut bacteria, but we were unable to study such association from the reviewed research papers because the sample sizes were low and detailed demographic details were unavailable. Large-scale research into the gut microbiome of the Indian tribal communities is certainly an inviting area of research for the near-future. With a large number of isolated tribal populations across India, the gut microbial diversity of these tribes can provide new insights into diet and microbiome association. Then the data from Indian tribal communities can be compared to other tribal populations from across the world. The scope of such research can have far-reaching

and widespread effects since understanding of gut and overall health, transmission and propagation of such bacteria could enhance the knowledge of association between gut microbiome and human health. Knowledge of gut microbiota and metabolites can have widespread applications in public health, community medicine, and other medical interventions which may help these tribes and other communities.

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Conflict of interest

The authors confirm that there is no conflict of interest involve with any parties in this research study.

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