REPORT ON

GUT MICROBIAL GENOMIC STUDY AMONG THE PVTGs OF INDIA

2023-2024

PART-B

(TAXONOMY AND FUNCTIONAL ANALYSIS)

Anthropological Survey of India

Ministry of Culture
Government of India

भारतीय मानवविज्ञान सर्वेक्षण
संस्कृति मंत्रालय
भारत सरकार
इ एन 7-9, सेक्टर – V, साल्ट लेक सिटी
कोलकाता – 700 091
ANTHROPOLOGICAL SURVEY OF INDIA
MINISTRY OF CULTURE
GOVERNMENT OF INDIA
E N – 7-9, SECTOR – V, SALT LAKE CITY
KOLKATA – 700 091

TEL : 91-33-2357 0090/ 0092
E mail : director@ansi.gov.in
Pmi.anthropology@gmail.com
Website: www.ansi.com

FOREWORD

Anthropological Survey of India (AnSI) is committed to advancing the scientific understanding of India's diverse communities, particularly those classified as Particularly Vulnerable Tribal Groups (PVTGs). This commitment has led to groundbreaking research initiatives across multiple anthropological and biomedical domains. The present study on "Gut Microbial Genomic Study Among the PVTGs of India" reflects AnSI's dedicated pursuit of knowledge that transcends traditional anthropology, integrating molecular biology and genomics to gain deeper insights into the unique health, nutrition, and lifestyle aspects of India's indigenous communities.

The human gut microbiome, a complex community of trillions of microorganisms, plays a critical role in health and disease. It is influenced by various factors, including diet, lifestyle, and environmental exposure. By studying the gut microbial composition of PVTGs, we aim to understand how traditional diets, subsistence practices, and unique environmental exposures impact these communities' gut microbiota, thereby contributing to their health and resilience. Additionally, this research provides valuable insights into how modernization and gradual shifts in lifestyle are influencing the microbiomes of these communities, potentially affecting their health in the long term.

The findings of this study have far-reaching implications. By mapping the gut microbial diversity among PVTGs, we open doors to understanding the evolutionary adaptations that have allowed these communities to thrive in diverse ecosystems over centuries. This research can also inform public health interventions, helping to develop microbiome-centred strategies that are tailored to the specific needs of these groups. This report is part of a multi-phase research project. Part B, which you hold in your hands, focuses on the taxonomy and functional analysis of the gut microbiota of selected PVTGs, shedding light on the structure and functional potential of these microbial communities. We extend our gratitude to all those who have contributed to this significant body of work, especially the Officers of AnSI who participated in this study, sharing their lives and experiences with us.

We hope this report will stimulate further research, foster interdisciplinary collaboration, and inspire continued dialogue on the importance of microbiome research in understanding human health and cultural heritage.

Director
Anthropological Survey of India

Acknowledgement

We begin by expressing our heartfelt gratitude to the Ministry of Culture, Government of India, for their unwavering support and generous funding, which have been essential to the success of this project on the "Gut Microbial Genomic Study Among the PVTGs of India." This study would not have been possible without their commitment to advancing research that bridges culture, health, and science.

Our sincere appreciation goes to the State Governments of Telangana, Andhra Pradesh, Jharkhand, West Bengal, Odisha, and Maharashtra for their invaluable assistance in facilitating access to the PVTG communities. Their collaboration in coordinating local resources and supporting data collection efforts has been crucial in enabling us to gather meaningful and comprehensive insights.

We extend a special note of thanks to the School of Life Sciences, University of Hyderabad for their continuous guidance and encouragement throughout this phase of project. Their leadership and vision have been instrumental in shaping the direction of this study, and their support has been a source of motivation for our team at every stage.

We would like to extend our heartfelt gratitude to the Department of Systems and Computational Biology, DBT- Centre for Microbial Informatics, University of Hyderabad for their invaluable collaboration and for providing essential training that greatly contributed to the success of this work. The guidance and support have been instrumental in advancing our research, and we deeply appreciative of their dedication and expertise.

Finally, we wish to acknowledge the PVTG communities who graciously welcomed our research teams, sharing their knowledge, traditions, and experiences. Their participation and openness have enriched our study, providing a deeper understanding of the relationship between traditional lifestyles and gut health.

To all those who contributed to this endeavour, we extend our deepest thanks.

Anthropological Survey of India

ACRONYMS

BIR	Birhor
CHE	Chenchu
KAT	Katkari
KND	Konda Savara
KOL	Kolam
LOD	Lodha
PVTG	Particularly Vulnerable Tribal Groups
NGS	Next Generation Sequencing
HMP	Human Microbiome Project
MetaHIT	Metagenomics of the Human Intestinal Tract
BCAA	Branched Chain Amino Acid
SCFA	Short Chain Fatty Acid
PWY	Pathway

List of scientific staff in this project

Principal Advisors

Prof. H. A. Nagarajaram (HoD, Department of Systems and Computational Biology, Principal Investigator, DBT- Centre of Microbial Informatics, University of Hyderabad)

Prof. P. Appa Rao (Senior Professor, Department of Plant Sciences, Co-Principal Investigator, DBT- Centre for Microbial Informatics, University of Hyderabad)

Prof. Ch. Venkataramana (Senior Professor, Department of Plant Sciences, Co-Principal Investigator, DBT- Centre for Microbial Informatics, University of Hyderabad)

Dr. Bidyut Roy, Former Professor, Indian Statistical Institute and Presently, Rabindranath Tagore Felow, Anthropological Survey of India

Principal Investigators

Dr. Harsawaradhana, Deputy Director (P), Dr. B P Urade, Deputy Director (P), Dr. Mithun Sikdar, Superintendent Anthropologist (P)

Principal Coordinators

Dr. VenuGopal P N (Assistant Anthropologist), Dr. Abhishikta Ghosh Roy (Superintendent Anthropologist), Dr. Shiv Patel (Assistant Anthropologist)

Research team of Anthropological Survey of India

1	Shri S S Barik, Superintendent Anthropologist
2	Dr. Koel Mukherjee, Anthropologist
3	Dr. Murali Kotal, Anthropologist
4	Dr. Somorjit, Anthropologist
5	Dr. Moajungla Longkumer, Anthropologist
6	Dr. P Baruah, Anthropologist
7	Dr. Junumai Deori, Assistant Anthropologist
8	Dr. Priyanka Airi Goyal, Assistant Anthropologist
9	Shri. Reddy Narsimham Naidu, Assistant Anthropologist
10	Dr. Chitta Ranjan Mondal, Assistant Anthropologist
11	Dr. D. Sun, Assistant Anthropologist
12	Smt. P. Mangalalakshmi, Assistant Anthropologist
13	Smt. Subhra Bhattacharyya, Assistant Anthropologist
14	Dr. Yikham Gogoi, Assistant Anthropologist
15	Dilip Kumar Barik, RA (Physical)
16	Sh. Shubham Roy, RA (Physical)
17	Dr. Gin Khan Khual, RA (Physical)
18	Dr. Mopada Nani Babu, RA (Physical)
19	Dr. Nandini Bhattacharya, RA (Physical)
20	Shri. Kiran Uttaravalli, RA (Physical)
21	Dr. Chandrashekhar Roy, RA (Physical)
22	Dr. Dipak Kumar Adak, Assistant Anthropologist (Physical)
23	Dr. Manjulika Gautam, RA (Physical)
24	Ms. Alekhya, R.A. (Physical)
25	Dr. Imkongtenla Pongen, RA (Physical)
26	Shri. Balagani Venkatesh, RA (Physical)
27	Ms. Mamta, RA (Physical)
28	Shri. Narasimhulu T, RA (Physical)

29	Ms. Saloni Uniyal, RA (Physical)
30	Anup Raj. K, RA (Physical)
31	Mr. Kevi Dziivichii, RA (Physical)
32	Shri. Soumen Majumdar, RA (Physical)
33	Shri. Sanjay Gajbhiye, RA (Bio-Chem)
34	Sh. Joy Das, RA (Biochem.)
35	Dr. Tapas Kumar Biswas, RA (Biochem.)
36	Dr. Sujit Lal Bhakta, RA (Biochem.)

Other members participated in this project

1	Dr. Barnali Waugh, Visiting Fellow
2	Shahid Afrid Mollick, Senior Research Fellow
3	Ms. Ankitha Ghosh, Junior Research Fellow
4	Sh. Bimal Khanra, Junior Research Fellow
5	Sh. Sayak Chakraborty, Senior Research Fellow
6	Ms. Priya Dey, Junior Research Fellow
7	Ms. Pooja Pratiksha Swain, Junior Research Fellow
8	Ms. Soma Bhowmik, Junior Research Fellow
9	Ms. Arna Chatterjee, Junior Research Fellow
10	Ms. Maitrayee Mitra, Senior Research Fellow

Contents

Abstract

The transition of human subsistence across the world from hunting-gathering to settled agriculture and then followed by industrialization and globalization has impacted the environment and brought in significant changes in the lifestyles of communities across the world. The changes in the food habits in turn have a bearing on the evolution of human gut microbiome that coexist with humans since time immemorial. The gut microbiome is responsible for several outcomes such as digestion of complex molecules, synthesis of vitamin and minerals, providing immune function and supporting overall health in human. Certain tribal communities in India that are recognized with a constitutional status of Scheduled Tribes and are also designated as 'Particularly Vulnerable Tribal Groups (PVTGs)', still continue many of their traditional subsistence practices and have not significantly adopted the modern lifestyles. A study on the gut microbiome of the PVTGs is assumed to provide a profile on the composition, diversity and function of the beneficiary microorganisms across the gastrointestinal tract and their association with human health and disease. Thus, a study on the gut microbiota of six of the 75 such PVTGs of India, (namely Birhor, Chenchu, Konda Savara, Kolam, Katkari and Lodha was conducted based on Next Generation Sequencing (NGS) shotgun metagenomic sequencing technology. This study characterised and compared the taxonomic and functional profiles of the microbiome highlighting intra and inter community variations, key differences in microbial diversity, composition and potential metabolic functions among different populations. The study identified signature microbiome and discriminate metabolic functions which could be associated to the community-specific availability and accessibility of food and to the changing lifestyle practices and also to certain special ethnic characteristics and ecological features of the six communities. Though the samples were collected from different locations inhabited by the same group who were more acculturated and less acculturated, no significant differences in taxonomic and functional profiles were identified. This may be the reflection of some shared environmental and seasonal diversities. This study identified that *Firmicutes* is the most abundant phylum followed by *Bacteroidetes, Proteobacteria* and *Actinobacteria.* At Species level *Segatella copri (Prevotella copri), Eubacterium rectale, Faecalibacterium prausnitzii, Blautia wexleria* etc. are found as core microbiota in all six communities. Though the relative abundance of *Treponema* (an active microbiota for complex polysaccharide diet degradation) is low, it is found among all the studied communities. Earlier studies reported that this genus is depleted in urban-industrial communities due to modernised lifestyle. The core pathways are enriched in short chain fatty acid degradation, amino acid biosynthesis, starch degradation, pyruvate fermentation, super pathway of aromatic amino acid synthesis etc. Overall, this study revealed considerable diversity of the gut microbiome and enriched biochemical pathways among the studied communities.

Introduction

Introduction

Human gut harbours trillions of microorganisms which include bacteria, virus, fungi and other microbes that play major role in the digestion of complex proteins, synthesis of vitamins, providing immune function and supporting overall health. A balanced gut microbiome is provided by healthy diet, and lifestyle. To understand the modern-day health scenario vis-à-vis the adopted lifestyle, there is a need to study the gut microbiome in the communities which have retained their traditional dietary practices. Tribal populations, especially the Particularly Vulnerable Tribal Groups (PVTGs) in India offer a unique opportunity for such a study as they are distinct in their diet, lifestyle, and adaptation to their ecosystem. Those microorganisms harboured in their guts represent the oldest inhabitants and also help inferring that their high adaptability has continued to challenge our understanding of their coexistence with human and upon their health and well-being.

The Particularly Vulnerable Tribal Groups in India

The various definitions given to tribe by multitude of scholars is a testament to the complexity of understanding, especially in the context of India, what is a tribe. However, one of the early definitions by Sahlin (1961) for tribe will better serve as the more generally accepted meaning attached to this term. Accordingly, "tribe" is a system of the social association consisting of a common culture, name, language, simple economy, political system, religion, beliefs and ancient law. They have well defined life with definite rules, morals, customs, traditions, and way of worship (Levi, 1962). India, is the second largest country in the world in terms of tribal population after Africa (Ganesh et al., 2021). The tribal population in India comprises 8.6% of the total country's population with 705 scheduled tribes and sub tribes living among them and 75 ethnic groups who are classified as PVTGs (Ministry of Tribal Affairs; Government of India, 2019). The state wise list of 75 PVTGs as per the Government of India's notification is given in Table 1

Table – 1 List of PVTGs in India

State-wise list of Particularly Vulnerable Tribal Groups (PVTGs)					
Name of States/Union Territory	**S.No**	**Name of the Particularly Vulnerable Tribal Group**	**Name of States/Union Territory**	**S.No**	**Name of the Particularly Vulnerable Tribal Group**
Andhra Pradesh (Including Telangana)	1	Chenchu	Maharashtra	41	Katkaria /kathodi
	2	Bodo Gadaba			
	3	Gutob Gadaba		42	Kolam
	4	Dongaria Khond		43	Maria Gond
	5	Kutia Kondha	Manipur	44	Maram Naga
	6	Kolam	Orissa	45	Chukutia Bhunjia
	7	Konda Reddi			
	8	Kondasavara		46	Birhore
	9	Bondo Porja		47	Bondo
	10	Khond Porja		48	Didayi
	11	Parengi Porja		49	Dongaria Khond
	12	Tothi			
Bihar (Including Jharkhand)	13	Asur		50	Juang
	14	Birhor		51	Kharia
	15	Birjia		52	Kutia Kondha
	16	Hill Kharia		53	Lanjia Saura
	17	Korwa		54	Lodha
	18	Mal Paharia		55	Mankirdia
	19	Parhaiya		56	Paudi Bhuiya
	20	Sauria Paharia		57	Saura
	21	Savara	Rajasthan	58	Saharia
Gujarat	22	Kolgha	Tamil Nadu	59	Irular
	23	Kathodi		60	Kattunayakan
	24	Kotwalia		61	Kota
	25	Padhar		62	Korumba
	26	Siddi		63	Paniyan
Karnataka	27	Jenu Kuruba		64	Toda
	28	Koraga	Tripura	65	Raing
Kerala	29	Cholanaikayan	Uttar Pradesh (Including Uttrakhand)	66	Buksa
	30	Kadar		67	Raji
	31	Kattunayakan	West Bengal	68	Birhor
	32	Koraga		69	Lodha
	33	Kurumbas		70	Totos
Madhya Pradesh (Including Chhattisgarh)	34	Abujh Maria	Andaman & Nicobar island	71	Great Andamanese
	35	Baiga			
	36	Bharia		72	Jarawa
	37	Birhor		73	Onge
	38	Hill Korba		74	Sentinelese
	39	Kamar		75	ShomPen
	40	Sahariya			

**** Source – Ministry Tribal Affairs;2019

An overview of the study communities

The details provided in this section are intentionally concise, as more comprehensive information on each of the communities studied including the demographic profile of the six communities, their food practices, health and hygiene practices, and other relevant cultural aspect are thoroughly documented in Part 1 of this report on the current study of the *Gut Microbial Genomic Study among the PVTGs of India.* Part 1 serves as an in-depth introduction to the unique lifestyles and environmental factors that shape the gut microbial composition of these communities.

The Chenchu

The Chenchu community inhabits Nallamala Hills, which span across the district of Mahbubnagar, Nalgonda and Nagar kurnool of Telangana as well as parts of Andhra Pradesh. These hills are known for their dense forest and biodiversity. This tribal group is known for its traditional lifestyle that is closely connected to the forests. Chenchu live in small clusters and each of such settlements is locally called *Penta* or *Gudem* (Rao et al., 2013). They are traditionally hunter-gatherers (Reddy, G. N. 1989; Sharma BV & Srinivas. N, 2019). They consume leaves of all kinds which are not bitter. They also eat a variety of roots and tubers secured from the forest such as *Chenchu gadda, Venabala gadda, Urragadda, Nulugagadda, Thamoragadda* and *Kaluvagadda.* The tuber that specifically gives them a food identity is '*Chenchu gadda'* which is perhaps consumed frequently only by them. Occasionally they collect bamboo rice and shoots. The leafy vegetables they obtain from the forest are *Devadaru* leaves, *Biddaku, Chenchalaku, Pendlipeddikura, Nallakura, Alikamamidikura* and *Pullakura.* They also consume insects called *Usullu* (Termites) as well as meat of Monitor lizard (*Udumu*). They also consume the wild hunt available in the forest.

Rice is their staple food, which they consume twice a day. They also take gruel that is made out of finger millet *(ragi)* or rice. Chenchus consume a flat bread *(roti)* prepared from sorghum *(jowar)* flour. They, however, abstain from eating beef and pork. They take meat, chicken eggs and fish. They make *curries* with seasonally available vegetables like pumpkin, water gourd, beans, peas, brinjal, drumsticks, bamboo shoots etc., Chenchu also prepare *chutneys* and consume tamarind in the form of soup (*rasam).* Consumption of oil is very less in this community and often they use palm oil or groundnut oil supplied in the GCC Ration depots at subsidized rate. Both male and female smoke cigars (loose tobacco) and chew betel leaves and nuts along with loose tobacco. Consumption of intoxicating drinks like *toddy, sara (Vippa)*, rice beer and foreign liquor by both men and women is quite common.

The Katkari

The Katkari's are socio-economically, one of the most backward forest tribes who mostly live in Mulshi, Raigad, Pune, Nashik, Ratnagiri and Thane districts of Maharashtra. They now live in the boarders of multi-tribal villages by forming small hamlets known as *"Wadi" or "Pada"* largely (A Study on Katkari: A Primitive Tribal Group in Maharashtra No.214, 1995). They still collect fish, crabs, medicinal plants and vegetables from forest for their livelihood.
Traditionally Katkaris are hunter-gatherers and so still retained their nomadic tendency with no opportunity for accumulating non-movable assets. They engage in small scale trade of various

items Which also compel to be nomadic. They work as agricultural labourers in pre and post agricultural activities, brick making.

Katkaris eat wheat, *waroi* (millets) and rice as staple food. They have omnivorous diet, with pulses and vegetables in low quantity. They take pulses like urad, tur and moong. They eat fish, egg, meat, chicken and pork. Dry fish is adequately consumed by them. They consume wild roots and tubers collected from the forest. Fruit consumption is very meagre. as they consume fruits yielded in their gardens and forests seasonally. Use of edible oil in cooking is also very much restricted. They do not consume milk but drink tea. Katkaris brew liquor for their consumption from the *mahua* (Bassia latifolia). They smoke bidi and chew tobacco.

The Konda Savara

The Konda Savara are mainly found in the agency areas of Parvathipuram Seethampeta in Andhra Pradesh. Their traditional occupation is shifting cultivation (Podu) though many have recently shifted to horticulture, cultivating cashew, pine apple, banana etc. They collect non-timber forest produce and rear cattle, fowls and pigs. Thus, their food system is today characterized by agro-forest base associated with forest ecology, and supplemented by horticulture. Their staple food is rice which is largely obtained from the supplies of government public distribution system. They also consume all kinds of millets and cereals that are cultivated by themselves. They make gruels out of the millets. One unique feature of Savara dietary practice is that they ferment rice overnight and then consume on the next day. Besides Sorrel (*Gongora)* and Amaranthus *(thota kura)*, they collect leaves of Pumpkin, Drumstick, Bitter, Gongura, Amaranthus etc, available in their surroundings as well as in the forest and cook them in combination with dal or other vegetables. They also collect locally available roots and tubers like D*oldumpa, Puli dumpa, Uladumpa, Chilagada dumpa* and make curries. Savara community prepare special food items like *Jeedi ambali* made of mango kernel and tamarind seed powder. They consume beef, pork, chicken, fish etc., Both male and female consume intoxicating drinks. Female take *Jeelugu kallu* (sago palm extract), whereas males take all kinds of drinks though *Naatu sara (arrack)* is most frequent. Mostly the male smoke and chew tobacco and Ganja.

The Lodha

The Lodha community of West Bengal, are majorly concentrated in Paschim Medinipur district. They were originally semi-nomadic hunter gatherer people. Their traditional occupation is collection and sale of forest produce. They gather grass and leaves and make plates, collect cocoons and also sell wood, honey and wax. They mainly consume roots and tubers, mushrooms and leafy vegetables collected from the forest while wild reptiles, fish, tortoise, molluscs and such others are also hunted to consume. Consumption of liquor is more or less a part of their food habits. Both men and women drink country liquor and have the habit of chewing betel leaves with tobacco. Men also smoke bidi and cigarette.

Their principal food is rice in all forms including puffed rice and rice flakes. They take meals twice or thrice a day. Mustard oil is commonly used in making dishes. They eat all kinds of roots and tubers, fruits and nuts, vegetables, pulses, legumes and leaves available in their surroundings. They consume wild hunt when available and chicken, mutton, fish, snails, tortoise and dried fish is part of their everyday meal They make *Handia*, a fermented rice item by adding *Bakhor bori*

(locally available plant produce). This delicacy is consumed on every occasion and also offered to god during festivals. It is rich in carbohydrates and glucose which supports their energy consumption and is believed to help to stay 'cool' while working under scorching sun. Almost every household prepares *Mahua* by fermenting *Mahul* flowers.

The Birhor

The Birhor community is mainly present in the Hazaribagh, Ramgarh, Gridih, Dhanbad, Bokaro, Gumla, Ranchi and Singhbhum districts in Jharkhand. Birhor were largely a nomadic tribe with no fixed habitation; they used to shift their camps within the forest areas. After some families took to settled life, the community was divided into two groups – *Uthlus* (the wanderers) and *Janghi* (the settlers). But presently, most of the families of Birhor are settled in government colonies or *Tanda* (Village). These villages are setup on some hill top or on the outskirts of some forest. They move in small bands snaring Monkeys, tracking hare, deer and other game or collecting fibres for making ropes for sale. They also collect honey and bees wax and sell in the local markets. Though they have a settled life still they depend on hunting and food gathering. They collect leaves and wood from forest and also collect *Mahua* fruits in the season and dry them for several purposes. They use *mahua* as vegetable, medicine and also for making intoxicating drinks. They collect *Bhatua* sag and dry it, for use in their meal with rice. They eat variety of wild fruits, roots, tubers, honey and meat. As their entry into the forest is now restricted and the resources declined, they started consuming the food provided through the public distribution system.

The Kolam

Kolam tribe is primarily found in the Vidarbh region of Maharashtra and Adilabad district of Telangana. They practice shifting cultivation and rely on forest for their subsistence. Occasionally they hunt and collect produce from the nearby forests. Their staple food consists of *Jowar, Bajra* along with rice and wheat. They cook *jowar* with tur dal or vegetables. They also consume *pej* (gruel) made of rice flour with vegetables or *chutney*. Kolam members gather variety of edible leaves as well as roots and tubers from the forest. Roots and tubers like *surankhand, karukand, thorkakadi, ghorkakadi* and *gadda* (bamboo shoot) are common. Earlier hunting of *wild boar, hare, ghorpad, deer, rola, bataru* etc. used to be consumed but due to limited access into the forest now they take meet of such animals occasionally. They consume seasonal fruits. The members of Kolam community practice three meals a day. The menu is more or less the same. During festivals they prepare special cuisine, *puran poli* with tur or gram pulses mixed with jaggery or sugar. The country liquor called Pakkel is very common. Smoking and chewing of tobacco are common among the male.

PVTGs and Traditional food system

Tribal communities have distinct food practices which often gives an insight into the way of living of these communities. Their food practices depict their close association with nature and dependency on the forest resources. They follow "traditional food system" where all kinds of foods are available from local natural resources (Kuhnlein & Receveur, 1996). The traditional food system of these communities is defined as being composed of items that are local, natural and culturally accepted (Bisai & Dutta, 2021).

As the available food resources as well as the traditional dietary practices of the tribal communities make them unique in the diversity, composition, and function of the gut microbiota of these communities could be used as a standard against which the modern-day health could be defined (De Filippo et al., 2010). Indeed, transition from the traditional subsistence to current lifestyle brought vast differences in environment and diet, which are the major determinants of gut microbial composition (Gupta et al., 2017). This led to continuous decrease in the diversity of gut microbiome as human communities passed through the many stages as they moved from hunting-gathering to modern agriculture. As a consequence, there is a growing awareness of the profound change in the diet that began with the introduction of agriculture and animal husbandry. The changes with industrialization, urbanization, and globalization are believed to have led to what are now called diseases of civilization.

Dietary habits adopted by the modern society make an important etiologic contribution to diseases like hypertension, diabetes and some types of cancer. These conditions emerged as dominant health problems in the past century and are believed to be unknown among the hunter-gatherers whose way of life and eating habits are completely different. (Eaton, 1985). During the Neolithic and industrial periods, the food staples and food processing procedures are introduced that had altered seven crucial nutritional characteristics of ancestral hominin diets like – glycemic load, fatty acid composition, macronutrient composition, micronutrient density, acid-base balance, sodium-potassium ratio and fibre content (Cordain et al., 2005). The diet of the remote population i.e., the PVTGs may stand as a reference for modern nutrition and a model for defence against those civilized diseases.

In order to understand the impact of lifestyle changes, dietary patterns, and the prevalence of modern diseases, it is crucial to study the gut microbial profile among the PVTGs of India, who still rely on traditional systems and food habits. This study enhances our understanding of how diet influences overall health and disease by scrutinizing the associated gut microbiome. It provides valuable insights into what constitutes a healthy gut and how traditional diets contribute to maintain gut health.

A study among the subsistence strategies demonstrated that there are distinct taxonomic and functional profiles of gut microbiome between hunter-gather, agricultural and urban-industrial populations (Conteville et al., 2019). The differences between the gut microbiome of these groups signifies that hunter-gatherers are more diversified in their gut microbiome, with high levels of fibre-degrading bacteria and these taxa are depleted in the urban-industrial population (De Filippo et al., 2010). As PVTGs in India are still indigenous, less exposed to urban lifestyle and consume food available from their own ecosystem, a study on the gut microbiota among these groups would illustrate the human development, nutritional needs, physiological variations and impact of westernization.

In the first phase of this study six PVTGs namely, Birhor of Jharkhand, Chenchu of Telangana, Savara of Andhra Pradesh, Kolam and Katkari of Maharashtra, Lodha of West Bengal were considered. This study on these communities provides an opportunity to explore and unravel the human gut microbiome before modernisation.

The origin of Gut Microbiome studies

The term "microbiome" is coined by Joshua Lederberg to describe an ecological system of commensal, symbiotic and perhaps pathogenic microorganisms that reside in the human body (X. Liu, 2016). It is the collection of genomes of the microorganisms living in a specific niche. Research to uncover the heterogeneity and complexity of the microbiomes and how the microorganisms of microbiomes impact our health in various ways is ongoing. Early attempt to determine the microbial community and their phylogenetic relationships comprised analysing the relatively well conserved 16s rRNA genes in mixtures of organisms (Woese & Fox, 1977). Mostly the understanding of human microbiome came from culture-based approaches using 16s rRNA technology. Yet 20 % to 60 % of the human-associated microbiome is uncultivable which led to underestimation of its diversity (Bik et al., 2006). Some recent studies on the gut microbiome at 16s rRNA gene level have revealed a significant diversity in the flora of individuals (Eckburg et al., 2005). 16s rRNA gene is also used as a metagenomic marker of the microbiome in the oral cavity (Faveri et al., 2008), vagina (Hyman et al., 2005), and skin (Gao et al. 2007). However, the 16s rRNA gene approach defines the evolutionary relationships among lower microbes including bacteria.

The most recent studies to examine the complexity of environmental samples by sequencing genome libraires made from the DNA extracted directly from mixed samples. This approach is termed as "metagenomics" and was applied in several studies of environmental microbial communities (Handelsman, 2004). The high throughput sequencing (Next Generation Sequencing, NGS) approach enable genomic analyses ideally of all microbes in a sample, not just those that are amenable to cultivation. One such method is shotgun metagenomics. It is untargeted sequencing of all microbial genome present in a sample (Quince et al., 2017). This laid the foundation for the study of human health and disease that offered insights into unknown and unpredicted role of gut microbiome in human life. Hence, by employing NGS-shot gut metagenomic sequencing, this study can uncover valuable insights into the intricate tapestry of the gut microbiome within these six tribal groups. These insights will contribute significantly to our understanding of human-microbe interactions and the diverse microbial communities that inhabit our bodies.

The Human Microbiome Project (HMP), 2008 is initiated by National Institute of Health to gain more complete and thorough understanding of human microbiomes at different locations of body and their associations with diseases (Peterson et al., 2009). This project developed and indexed fundamental reference set of microbial genome sequences from a population of 242 healthy adults generating 5177 microbial taxonomic profiles from 16s ribosomal RNA genes and over 3.5 terabases of metagenomic sequence so far. The HMP encountered 81-99 % of the genera, enzyme families and community configurations occupied by the healthy western microbiome. (Huttenhower et al., 2012; Methé et al., 2012). The European Metagenomics of the Human Intestinal Tract (MetaHIT) consortium produced Illumina sequences of fecal samples of 124 European individuals, including healthy, overweight and obese adults as well as patients with inflammatory bowel disease (IBD) (Qin et al., 2010). This project is extended to Japanese and American populations and established that worldwide population could be classified into three distinct enterotypes (Arumugam et al., 2011). These projects made substantial progress towards gut microbial studies and amount of metagenomic information is exponentially increased.

Interplay of food, culture, and Gut Microbiome

Food as a biological aspect for the human existence plays major role in good health. Food, dietary habits, lifestyle and existing ecosystem are associated with health outcomes. Food is both a biological and a social need and is vital to be satisfied on everyday basis. It is a prerequisite that shapes society through the activities related to social, cultural and economic practices as well as cultural values, customs and beliefs (Mohan, 2023). As a result, Anthropologists have now emphasized on empirical research for linking biological, social and cultural aspects for the development of knowledge on health. This led Anthropological Survey of India to prioritize studies on gut microbiome from biology to anthropology which reveals how cultural practices, traditional diet and environmental factors shape the gut microbiota of human populations.

There is a long history for Anthropology of food that began in 19th century with Garrick Mallery and William Robertson Smith. Earlier Anthropological structuralists defined the concept of food and its identity as negotiable and subject to social structures providing a nuanced understanding of how cultural, biological, and individual factors intersect in defining what we eat. This perspective aligns with other anthropological studies that emphasize the role of culture and society in shaping dietary practices and food perceptions (Borghini & Piras, 2021). But the contemporary anthropological study of food serves as a vehicle for the development of new methods for understanding the microbial world in the gut providing an opportunity to reevaluate the way to view human biological and cultural diversity (Sarkar et al., 2018).

Taxonomic Profile and Gut Microbiome

The studies conducted on the pre-industrialized societies including hunter-gatherers those still depend on wild plants and animals, consumption of medicinal plants and populations residing in geographically diverse locations have revealed specific gut microbiota adaptations based on food habits and lifestyle (Clemente et al., 2015; Obregon-Tito et al., 2015; Rampelli et al., 2015). A study among three tribal populations of Arunachal Pradesh residing in remote areas and following traditional lifestyle had higher gut microbiome diversity with a high prevalence of *Prevotella* and *Collinsella* in the Adi and Nyshi tribes and *Bifidobacterium* and *Catenibacterium* in Apatani tribe (Hazarika et al., 2022). The faecal bacterial diversity studied among fifteen tribal populations representing four geographical regions based on diet and location reveals that the gut bacterial profile of the Indian tribes is dominated by *Prevotella* and on comparison with worldwide data it is found that Indian population is similar to that of the Mongolian population (Dehingia et al., 2015). Human population passed through three stages of subsistence like foraging, rural farming and industrialised urban western life. In general, the gut microbiome of the hunter-gatherer populations is highly abundant with *Prevotella, Proteobacteria, Spirochaetes, Clostridiales, Ruminobacter* etc., while those of the urban communities are often enriched in *Bacteroides, Bifidobacterium* and *Firmicutes* (Gupta et al., 2017).

A study on the Nicobarese, a tribal group of Nicobar Islands, among the remote, rural and urban cohorts, reveals that life style and dietary habits are crucial for the alteration of gut microbiome. The life style transition among these three groups results in alteration of dominant bacterial groups. The remote cohort remains diverse and stable than the other two cohorts and had higher numbers of *Bacteriodetes* and the dominant genus in this phylum is *Prevotella*. This indicate that the remote Nicobarese take rich carbohydrate diet, whereas, the rural cohort is dominated by Clostridium the urban cohort is dominated by *Bifidobacterium* (Anwesh et al., 2016).

While characterizing the evolutionary transition of Indian gut microbiota from tribal to urban, different signatures with respect to diversity as well as taxonomic and functional composition were observed. The gut microbiota of tribal communities is found to harbour significantly higher species diversity and richness as compared to that in urban populations. Further there is no significant difference between tribal groups in the gut microbial diversity and the taxonomic profiles of different tribal communities cluster together irrespective of their geographical location (Singh et al., 2019).

A study on relationship between lifeways and gut microbiota through taxonomic and functional potential characterization of faecal samples from hunter-gatherer traditional agriculturalist communities in Peru and an urbanised industrialized community from the US. It is found that *Treponema* are diverse, and fall outside of pathogenic clades and are similar to *Treponema succinifaciens*, a known carbohydrate metabolizer in swine. The gut *Treponema* are found in non-human primates and all traditional peoples are symbionts and were lost in urban-industrialized societies (Obregon-Tito et al., 2015).

Human gut and their indigenous microbial communities need to optimize two basic biological functions, nutrient absorption and microbial fermentation of slowly digestible plant foods (De Filippo & Tuohy, 2015). The role of gut microbiome is to contribute metabolic and digestive functions that are not able to undergo in human gut. Human genome lacks most of the enzymes required for the degradation of plant polysaccharides and they are supplied by human gut microbiome, which can metabolise cellulose, starch and unusual sugars such as arabinose, mannose, xylose etc. (Gill et al., 2006).

The composition of gut microbiota varies according to the type of food consumed. Early studies also found that there is an increased diversity of microbial communities among those individual consuming plant-based diet than animal based (De Filippo & Tuohy, 2015). A study conducted on Indian gut microbiome among 110 healthy individuals from North-central India and South India, found that the North central India consuming a plant-based diet, was found associated with *Prevotella* and also showed an enrichment of branched chain amino acid (BCAA) and lipopolysaccharide biosynthesis pathways. Whereas the Southern India, which consume an omnivorous diet, showed associations with *Bacteroides, Ruminococcus* and Faecalibacterium and had an enrichment of short chain fatty acid biosynthesis pathway and BCAA transporters (Dhakan et al., 2019).

Diet affects the structure and function of the gut microbiome, whereas the microbiome in turn impacts the nutritional value of food and food ingredients (Walker et al., 2011). A recent study revealed that Indian gut microbial communities and comparing them with the microbiota from other populations shows the dominance of *Prevotella, Lactobacillus, Bifidobacterium*, and *Megasphaera* in Indian population (Bhute et al., 2016).

Functional annotations and Gut microbiome

The gut microbiota is central to human metabolism, affecting a wide range of pathways that contribute to health and disease. By fermenting undigested food, synthesizing essential vitamins, modulating immune responses, and processing xenobiotics, gut microbes play a critical role in

maintaining homeostasis. Humans have co-evolved with their microbiota through an interaction between the gastrointestinal tract and microbial community. Any change in the lifestyle, diet, and environmental conditions directly modulate the microbiota. The composition of microbiota is also decided by the geographical factors.

Early studies revealed that the rural populations showed an increase in Bacteroidetes responsible for degradation of polysaccharides, and decrease in the Firmicutes number due to attribution by the diet enriched with plant polysaccharides (De Filippo et al., 2010). The rural population showed presence of bacteria from the genus *Xylanibacter* and *Prevotella*, which are responsible for xylan and cellulose hydrolysis. These bacteria were completely absent in urban residents (De Filippo et al., 2010). Some studies say that many of the biochemical pathways that humans do not have, are provided by the gut microbiota genome (Qin et al., 2010).

The Gut microbiota is mainly associated with degradation of the dietary fibres, proteins and peptides by fermentation and anaerobic degradation to provide energy through metabolism (Acheson & Luccioli, 2004). The gut microbiota has been separately named as 'metabolic organ' because of its metabolic potential equivalent to the liver (O'Hara & Shanahan, 2006). The main functions include energy-derivation from non-digestible carbohydrates, glycoconjugates derived from the host (glycosphingolipids), deconjugation and dihydroxylation of bile acids, biosynthesis of vitamins (K and B) and isoprenoids, cholesterol reduction and metabolism of amino acids and xenobiotics

Objective of the study

1. To characterize the population specific microbiome/microbiota profile of the Particularly Vulnerable Tribal Groups.
2. To understand the diversity of microbiome composition with respect to diet and geographical locations.

Materials and Methods

Materials and Methods

A total of 228 stool samples were collected from all six communities of different geographical locations through conventional sampling process following exclusion and inclusion criteria. The exclusion criteria were based on the respondent with chronic illnesses, lactating and pregnant mothers, female with menstrual cycle, those with lifestyle disorders and gastrointestinal diseases. The inclusion criteria were healthy male and female belonging to age group of 18- 45 years and those were not under medication (antibiotics) for past 6 months. Indeed, each community is stratified as traditional and customised based on the availability and accessibility of food resources. The traditional groups are those who completely reside in the remote villages and have no accesses to the modernised food. Whereas the customised groups consume foods available from their own environment as well as those foods that are accessible to them. Nearly twenty samples from each cohort were collected.

Study design

A schedule was prepared based on which the anthropological as well as diet data of the respondents were taken. The data included socio-demographic profile, their life-style, aliments profile, sanitation and hygiene practices, personal habits, health and anthropometric measures and dietary information. Details of all the above data were collected from 228 respondents.

Sample collection, DNA isolation and Sequencing

Each participant was given instructions and training regarding the stool collection process. The faecal samples were collected into OMNIgene Gut Stool collection Kits and were stored in the ice box until the sample reached the laboratory. Then the sample tubes were stored at -80^0 C. DNA was extracted from the samples using QIAGEN DNA extraction following the protocol. The extracted DNA is kept in -4^0 C for further analysis. The sequencing of the isolated DNA was obtained by outsourcing using Illumina platform of NovaSeq 6000.

Bioinformatics and statistical analysis

The raw reads obtained from the sequencer were scrutinised using FastQC (Andrews, S. 2010) and MultiQC (Ewels et al., n.d.) tools to assess the quality of the high-throughput sequencing data. The total number of sequences generated were 12.4 – 24.3 million base pairs for each sample. The read lengths were of 150 bp pair-end reads. Short nucleotide sequences called adapters are added to the DNA fragment during the library preparation to facilitate sequencing. These adapters may interfere with the downstream analysis if they are not removed properly. Hence, using BBDuk (Brian Bushnell, 2014) tool these adapters were removed. FastP (Chen et al., 2018) tool was used to remove duplicates and the reads with high accuracy (Phred Score (Q30 = 99.9%) were taken. The classification of reads was done by Kraken2 (Wood & Salzberg, 2014) tool which utilizes pre-built reference database containing genomes from a wide range of organisms including bacteria, viruses, archaea and eukaryotes. It assigns taxonomic labels to the reads on Kmers matches against the databases. Kraken tool identifies the host DNA contamination in the sequence reads. This contamination was removed using Hostile tool (Constantinides et al., 2023). The MetaPhlAn 4.1 tool (Segata et al., 2012) was used to profile the composition of microbial communities in the given samples. MetaPhlAn 4.1 relies on ~5.1M unique clade-specific marker genes identified from ~1M microbial genomes (~236,600 references and 771,500 metagenomic assembled genomes) spanning 26,970 species-level

genome bins. The MetaPhlAn tool generated output of all the six communities were merged into a single OTU table and it is statistically analysed using R packages such as Phyloseq (McMurdie & Holmes, 2013), Microeco (C. Liu et al., 2021), Vegan (Jari Oksanen, vegan: Community Ecology Package, 2024), ggplot2 (H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016), and ggpubr (Kassambara A. (2020). ggpubr: 'ggplot2' Based Publication Ready Plots. R package version 0.4.0).

The functional profiling of the sequence reads of these six communities was done using HUMAnN 3.9 tool (Abubucker et al., 2012; Beghini et al., 2021). HUMAnN tool uses the UniRef (50 and 90) and Metacyc databases to explore the metabolic interactions of Microbial Communities. HUMAnN tool uses taxonomic profile files generated by MetaPhlAn tool to generate pathway abundance tables. These tables of 6 communities are merged into a single file for statistical analysis using the above R packages. The alpha, beta diversities and discriminant features identification were carried out for taxonomic and functional profiles.

Results

Results

Gut Microbial Composition and diversity

Alpha Diversity

It measures the variety of species within a particular sample reflecting the number of different species present. The diversity performed using both Observed and Shannon indices, revealed significant differences between the communities. Both Observed and Shannon indices are used together to provide a complete picture of microbial diversity. The Observed index reveals that how many species are present, while Shannon index reveals how evenly the species are distributed in the sample. Kruskal-Wallis test was employed to assess the differences, yielding p-values < 0.05 for both the observed as well as for the Shannon indices, indicating statistically significant differences among various communities (Figure-1). The pairwise comparison of observed index revealed notable differences between BIR (Birhor) vs KND (Savara) ($p \leq 0.01$) and KOL (Kolam) vs LOD (Lodha) ($p \leq 0.001$). For Shannon index the pairwise comparison suggested that the KND (Savara) vs LOD (Lodha) ($p \leq 0.01$) and KOL (Kolam) vs LOD (Lodha) ($p \leq 0.01$) show notable differences in species richness. This underscores that the communities like the Kolam community of Maharashtra and the Savara community of Andhra Pradesh exhibit higher species richness compared to others like Lodha of West Bengal and Birhor of Jharkhand.

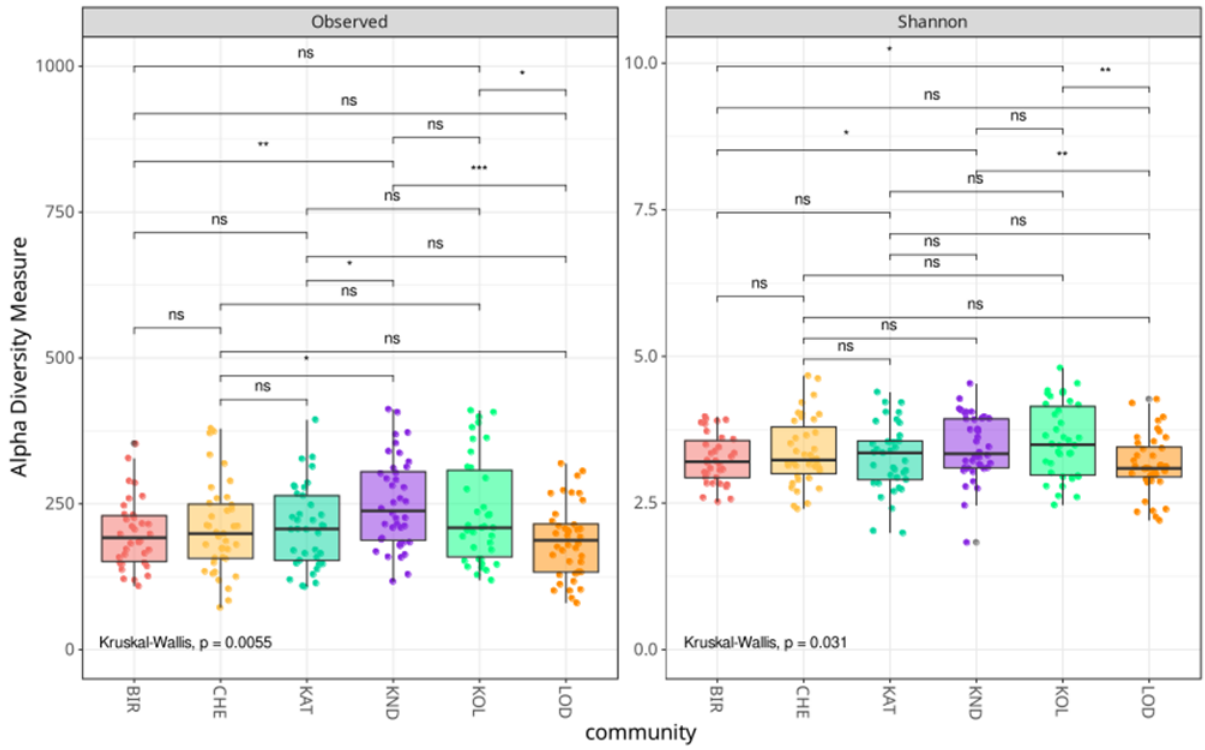

Figure 1 Alpha Diversity Plot, observed diversity index (Left panel) and Shannon index (Right panel) showing Kolam and Savara community with highest richness of microbiome and Lodha community with lowest species richness

Beta Diversity

Beta diversity refers to the differences in microbial communities between different samples. It essentially measures how the composition of the gut microbiome varies across individuals or groups. Beta diversity is usually quantified using distance or dissimilarity metrics, which measure how far apart microbial communities are from one another. The weighted UniFrac distances (Lozupone & Knight, 2005) consider phylogenetic relationships between microbes and species abundances into account. The distance matrix of Weighted UniFrac output showed the microbial compositions are not correlated among the communities (R^2 = 0.0856, $p \leq 0.001$, PERMANOVA). The pairwise comparison also revealed similar insignificant correlations between the communities (BIR vs KND -R^2 = 0.09903, $p \leq 0.1$; BIR vs KOL - R^2 = 0.11042, $p \leq 0.1$; KAT vs KND -R^2 = 0.08670, $p \leq 0.1$; KAT vs KOL - R^2 = 0.12993, $p \leq 0.1$ and KAT vs LOD -R^2 = 0.04834, $p \leq 0.1$) (Figure- 2).

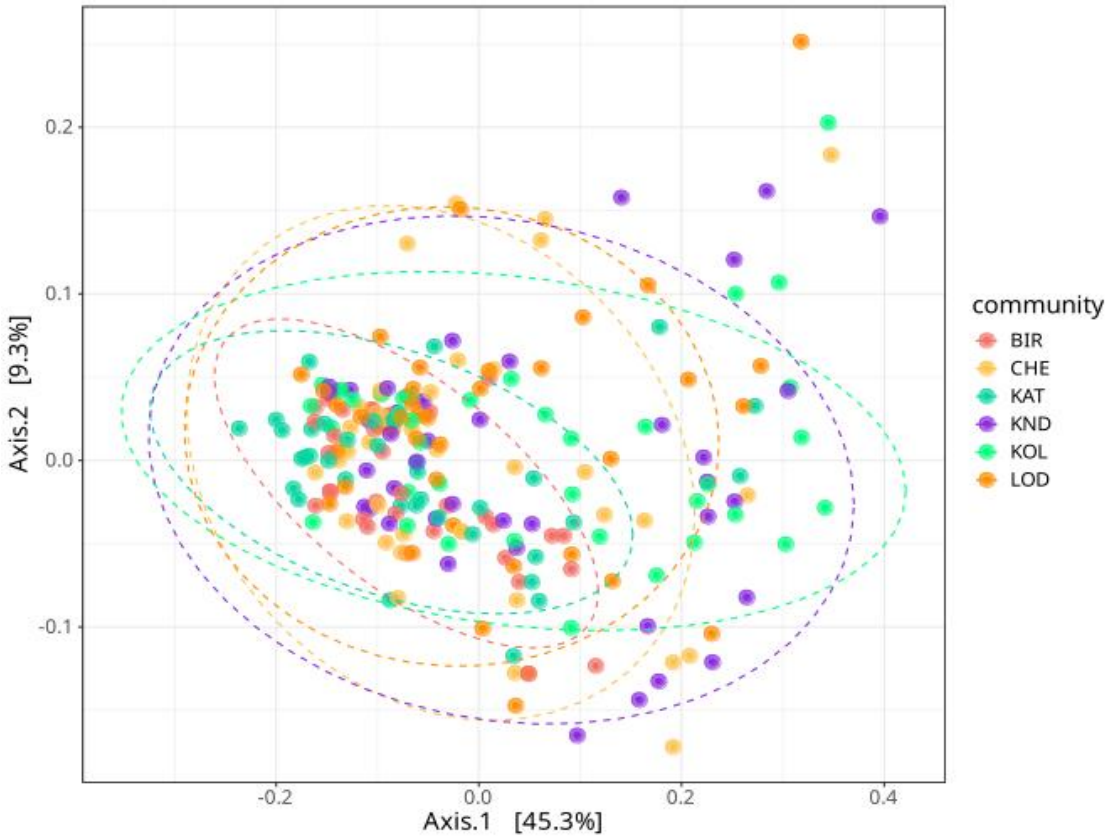

Figure 2 Beta Diversity – PCoA based on weighted UniFrac distance showing variation with Axis- 1 at 45.3% and Axis-2 at 9.3%

Dominant phyla among the PVTGs

Table 2, reveals that gut microbial diversity at the phylum level, is relatively conserved across the Indian sub-continent and neighbouring Bangladesh with Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria identified as the predominant phyla. In a comparative analysis with populations of other continents including USA, EU, Africa, and South America a similar pattern of dominant phyla is observed. Specifically, in hunter-gatherer populations, the major phyla include Bacteroidota (Prevotella), Proteobacteria (Ruminobacter), Spirochaetes, Firmicutes (Clostridiales), while in urban populations Bacteroides, Actinobacteria (Bifidobacterium), and Firmicutes predominate. These findings highlight the conservation of gut microbial profiles across different geographical setups as well as lifestyle groups.

Table – 2 Comparison of dominant phyla of six PVTGs (individual/ combined) with other communities

Community	Dominant phyla	References
Six PVTGs (combined)	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Chenchu	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Konda-Savara	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Lodha	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Katkari	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Birhor	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Kolam	Actinobacteria, Bacteroidota, Firmicutes, Proteobacteria	
Individuals residing in rural and urban (n = 49)	Actinobacteria, Bacteroidota, Firmicutes,	Analysis of the Gut Microbiome of Rural and Urban Healthy Indians Living in Sea Level and High-Altitude Areas. Scientific

Ballabhgarh (Faridabad) and in rural HIGH-ALTITUDE areas of Leh, Ladakh (n = 35)	Proteobacteria	Reports. 2018.(8), 10104
Healthy subjects from six joint families, Pune (Dongargaon and Shikrapur)	Bacteroidetes, Firmicutes, Proteobacteria, Actinobacteria	Gut, oral and skin microbiome of Indian patrilineal families reveal perceptible association with age. Scientific Reports. 2020. 10:5685.
The Himalayan populations include the Chepang (a foraging population), the Raute and Raji (two foraging communities that are currently transitioning to subsistence farming), and the Tharu (former foragers that have completely transitioned to farming within the last two centuries) + 10 Americans of European descent	The Himalayan populations were characterized by higher abundance of Proteobacteria, while abundances of Actinobacteria, Firmicutes, and Verricomicrobia were highest in the Americans, intermediate in the farmers (Tharu, Raji, and Raute), and lowest in the Chepang foragers. Higher levels of Proteobacteria and lower levels of Actinobacteria and Verricomicrobia are common features of many traditional human gut microbiomes around the world	Gut microbiome transition across a lifestyle gradient in Himalaya. PLOSBiology https://doi.org/10.1371/journal.pbio.2005396 November 15, 2018
Urban subjects, Ahmedabad	Bacteroidetes, Firmicutes, Proteobacteria, Actinobacteria	A snapshot of gutmicrobiota of an adult urban population from Western region of India. PLOSONE. https://doi.org/10.1371/journal.pone.0195643 April 6, 2018
Ladakh, Rajasthan, Madhya Pradesh (Indian ethnic	Ladakh had a higher proportion of Bacteroidetes, and	Metagenomics analysis reveals features unique to Indian distal gut microbiota. PLOSONE.

tribes; healthy subjects)	Jaisalmer and Khargone subjects had higher proportions of Actinobacteria and Firmicutes.	https://doi.org/10.1371/journal.pone.0231197 April 8, 202
Thirty individuals from the Adi, Apatani and Nyshi tribes of Arunachal Pradesh (ten in each cohort) tribal groups	Firmicutes, Actinobacteria, Proteobacteria, Bacteroidates	Elucidating the gut microbiome alterations of tribal community of Arunachal Pradesh: perspectives on their lifestyle or food habits. Scientific Reports. 2022. 12:18296
Bengali people as well as several indigenous ethnicities (Chakma, Marma, Khyang, and Tripura) residing in the Chittagong Hill Tracts areas of Bangladesh.	Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria	Gut microbiome composition reveals the distinctiveness between the Bengali people and the Indigenous ethnicities in Bangladesh. Communications Biology. 2024. 7:500
Gut microbiota of urban and tribal populations from multiple regions of India. A total of 80 healthy Indian "urban" individuals from Ahmedabad city. A total of 75 healthy Indian "tribals" from four different geographical regions in India namely, Andhra, Assam, Sikkim, and Manipur.	Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria	Lifestyle-Induced Microbial Gradients: An Indian Perspective. Frontiers in Microbiology. 2019. Volume 10. Article 2874
Fifteen tribal populations representing four geographic regions (Assam, Telangana,	Firmicutes, Bacteroidetes, Actinobacteria	Gut bacterial diversity of the tribes of India and comparison with the worldwide data. Sci Rep. 2015; 5: 18563

Manipur and Sikkim)		
Worldwide (USA, EU, Africa, South America)	Gut microbiome of the hunter-gatherer populations is highly abundant with Prevotella, Proteobacteria, Spirochaetes, Clostridiales, Ruminobacter etc. while those of the urban communities are often enriched in Bacteroides, Bifidobacterium, and Firmicutes	Review article. Geography, Ethnicity or Subsistence-Specific Variations in Human Microbiome Composition and Diversity. Frontiers in Microbiology. June 2017 Volume 8 Article 1162

Microbial composition at different taxa levels

The major dominant Phyla are *Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria*. Significant differences were observed between the *Actinobacteria*, *Firmicutes, Candidatus Melainobacteria, Candidatus Thermoplasmota, Elusimicrobia, Euryarchaeota, Fusobacteria, Lentispherae and Tenericutes* phyla (Figure -3). *Firmicutes* are significantly high in Kolam, Lodha, and Savara. They include *Eubacterium rectale, Holdemanella biformis, Faecalibacterium prausnitzii, Phascolarctobacterium succinatutens, Blautia massiliensis, Blautia wexlerae, Roseburia inulinivorans, Dorea longicatena, Anaerobutyricum soehngenii, Catenibacterium tridentinum, Clostridium_fessum* etc. as dominant species (Figure -4). The Phylum *Bacteroidota* includes *Segatella (Prevotella) sinensis, Segatella homins, Segatella sinica, Prevolella stercorea, Bacteroides uniformis, Alistipes onderdonkii* as dominant species. The phylum *Actinobacteria* is found significant (in abundance) in Kolam community of Maharashtra. At Species level *Collinsella_aerofaciens, Slackia isoflavoniconvertens, Senegalimassilia_faecalis, Bifidobacterium_longum* are abundant. Phylum Proteobacteria includes *Sutterella wadsworthensis*, *Sutterella_faecalis*, *Escherichia coli, Klebsiella variicola* as major species. *Candidatus Thermoplasmota* and *Euryarchaeota* belong to kingdom Archaea also show significant difference in abundance among few communities. It is found that Phylum *Candidatus Thermoplasmota* is fade in the Kolam community. Phylum *Euryarchaeota* includes *Methanosphaera stadtmanae, Methanobrevibacter smithii, Methanosphaera cuniculi* at the species level. The Phylum Fusobacteria includes *Fusobacterium mortiferum, Sneathia vaginalis, Fusobacterium ulcerans* etc at species level.

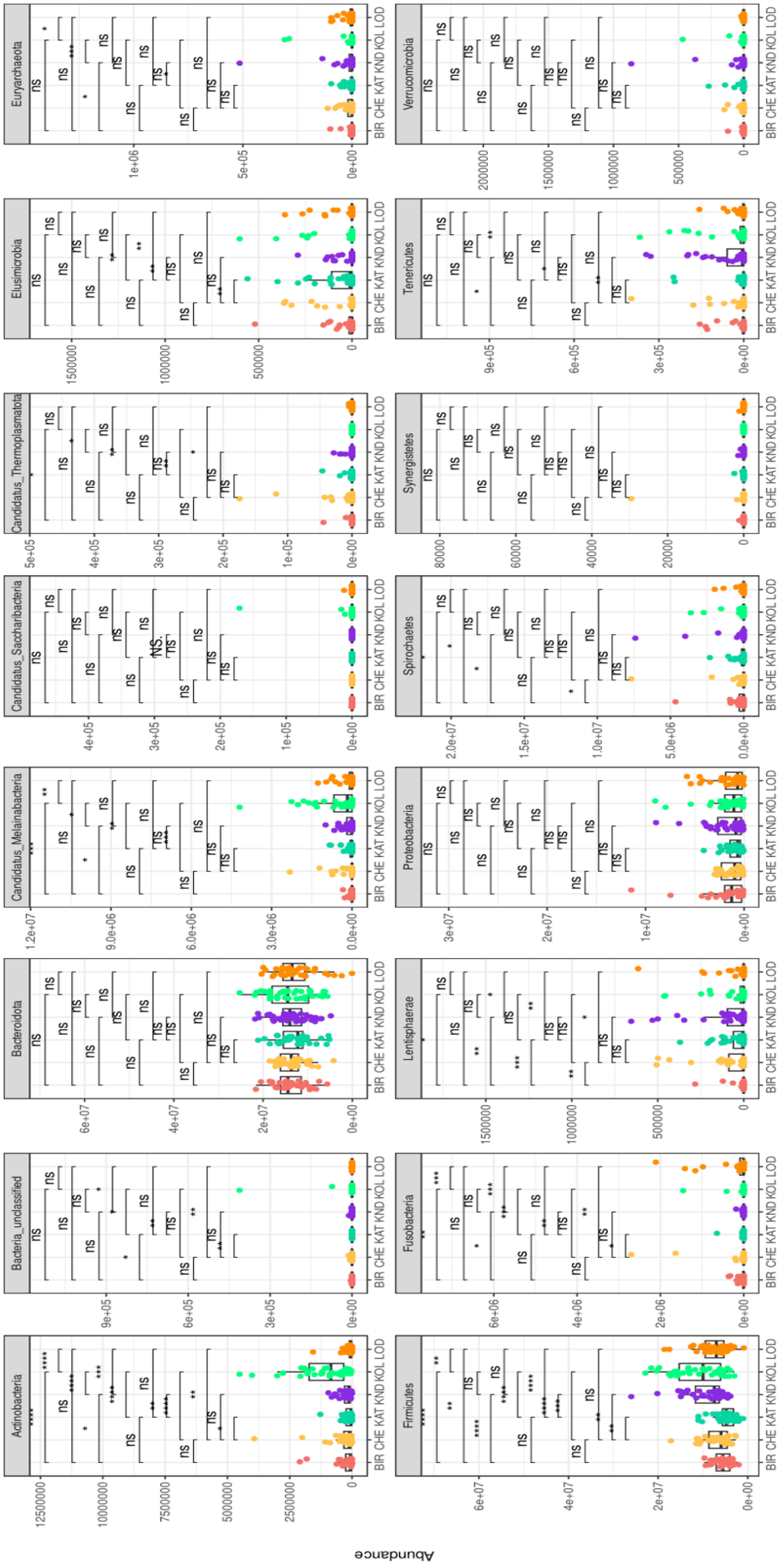

figure 3 Box plot at Phylum level relative abundance displaying the distribution of abundances and highlighting significant differences of various phyla across the six communities denoted by significance markers (‘*’ p ≤ 0.05, ‘**’ p ≤ 0.01, ‘***’ p ≤ 0.001)

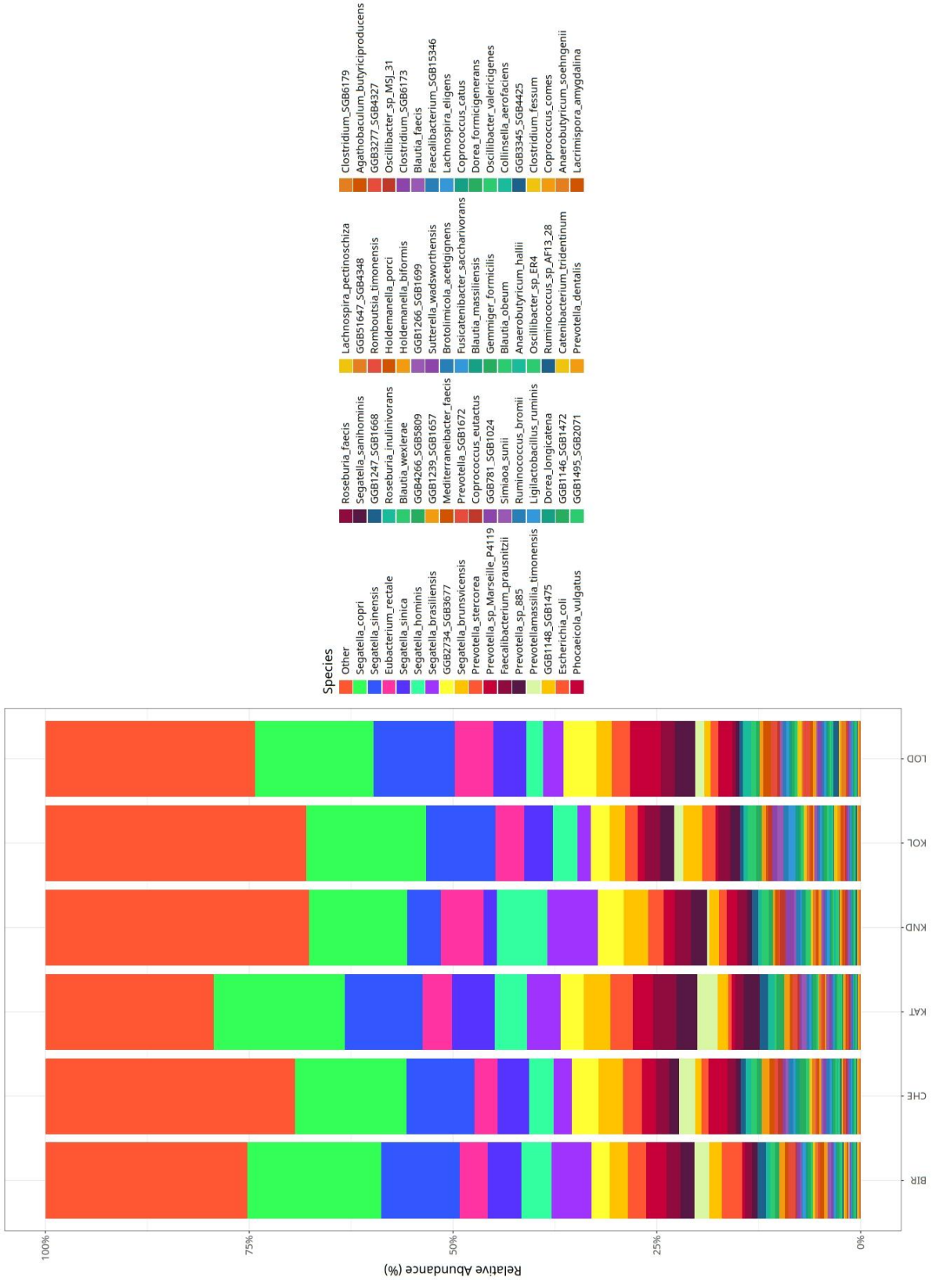

Figure 4 Species aggregate bar plot showing the relative abundance of microbial species across different communities

Firmicutes and Bacteroidetes ratio (F/B ratio)

F/B ratio is a common metrics to evaluate the balance between these two major phyla Firmicutes and Bacteroidetes, as they play an essential role in gut health, metabolism and immune function. The F/B ratio in healthy individuals can range from 1:1 to 2:1. The mean ratios among these six communities, Birhor (0.44), Chenchu (0.61), Katkari (0.50), Savara (0.82), Kolam (0.84), Lodha (0.60) is low and it is considered healthy. Although the mean ratios were within the healthy range, it is perhaps noteworthy to note that the PVTGs showed significant differences in their values t ($p < 0.0001$). The pairwise comparisons indicated significant differences between most of the communities (Figure - 5). Out of these 6 communities Kolam community exhibited the highest F/B ratio whereas, Birhor and Chenchu communities showed the lowest ratio. The elevated F/B ratio among the Savara and Kolam communities might signify a transition towards the modern food habits and lifestyle practices

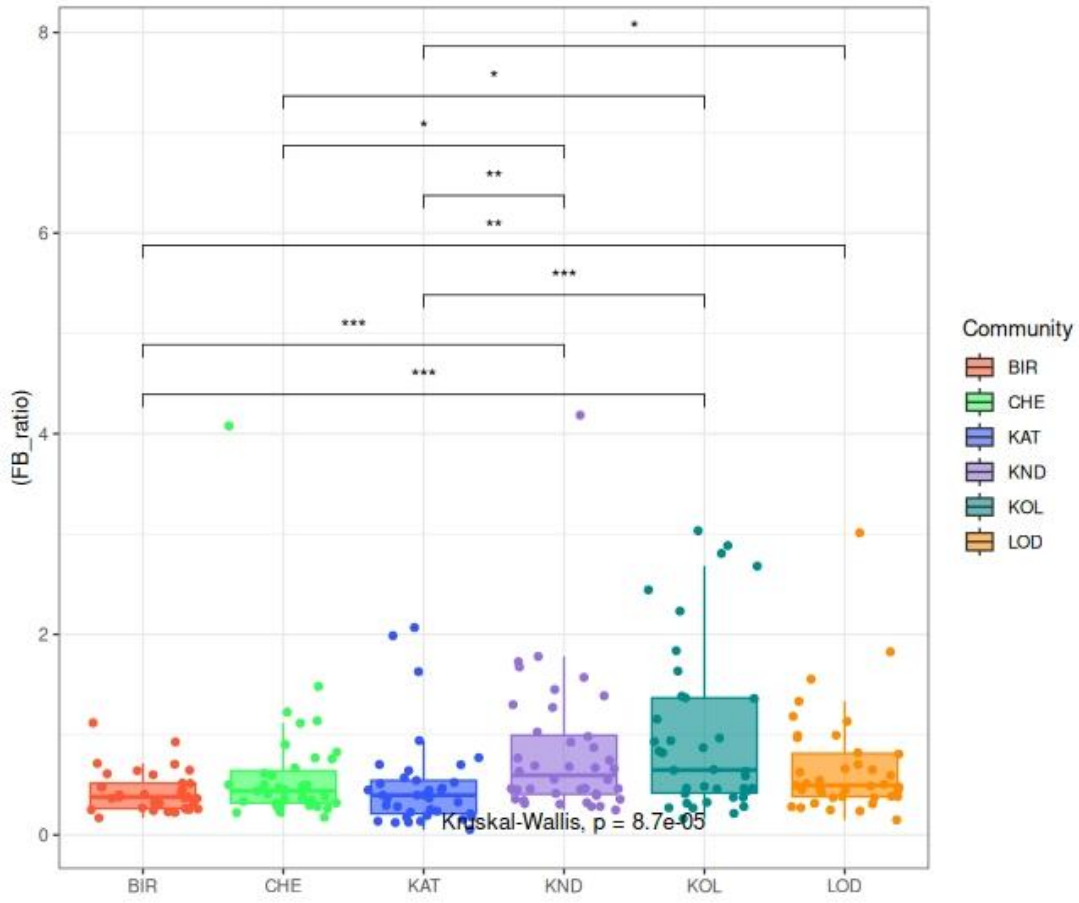

Figure 5 Firmicutes and Bacteroidetes ratio plot representing the distribution with Kruskal-Wallis p value ($p \leq 8.7e\text{-}05$) and pairwise comparison between the communities are denoted by significance markers ('*' $p \leq 0.05$, '**' $p \leq 0.01$, '***' $p \leq 0.001$).

Table – 3. The distinct features between six PVTGs were calculated using LDA technique.

Chenchu	Konda Savara	Lodha	Katkari	Birhor	Kolam
Fusobacterium mortiferum	GGB_781_SGB_1024	Segatella sinensis	GGB_1247_SGB_1668		Bifidobacterium adolescentis
	Bacteroides ovatus	Mediterraneibacter faeces			Roseburia faeces
		Romboutsia timonensis			Ligilactobacillus ruminis
		Ruminococcus_sp_AF13_20			Blautia wexlerae
		Roseburia sp AM23_20			Bifidobacterium angulatum
					Dialister succinatiphilus
					Mitsuokella jalaluddini
					Bifidobacterium catenulatum
					Lachnospiraceae bacterium
					Enterococcus hirae

The discriminative species for the six PVTGs identified by a linear discriminant analysis technique (LDA score > 3.0). Recently, it was found that Bacteroides ovatus, a distinct feature in Savara (Table - 5), takes part in cellulose degradation in human gut (Li et al. 2023). Roseburia species are the distinct features in Lodha and Kolam communities. A decrease in gut Roseburia species level have been linked with malnutrition and other human pathologies (Mondot et al. 2022).

Biochemical Pathways of the Gut microbiome

The biochemical pathways of gut microbiome are categorized based on their metabolic and functional characteristics. In MetaCyc, these pathways are hierarchically organized into various levels as Superclass 1, Superclass 2 and Pathway level. The superclass 1 is a broad metabolic category representing major functions like biosynthesis, degradation of complex molecules, generation of precursors, super pathways etc. The superclass 2 includes sub category of metabolic processes *viz.* carbohydrate metabolism, lipid metabolism, nucleotide metabolism etc. The third level shows specific pathways *viz.* methanogenesis, amino acid biosynthesis, TCA

cycle etc. At Superclass 1 level, the biosynthesis pathways were found to be more abundant in all the communities followed by degradation/utilization/assimilation, generation of precursor metabolites and energy etc. Significant differences were observed between the communities with Kolam community ($p \leq 0.0001$) is showing the highest abundance for biosynthesis pathways, when compared to Birhor and Katkari (Figure - 6). The difference may be due to variations in dietary intake, environmental exposure and lifestyle between the communities. Significant differences were identified amongst the six communities at the level of biosynthesis pathways, degradation/assimilation/utilization, generation of precursor metabolites and energy and macromolecule modification.

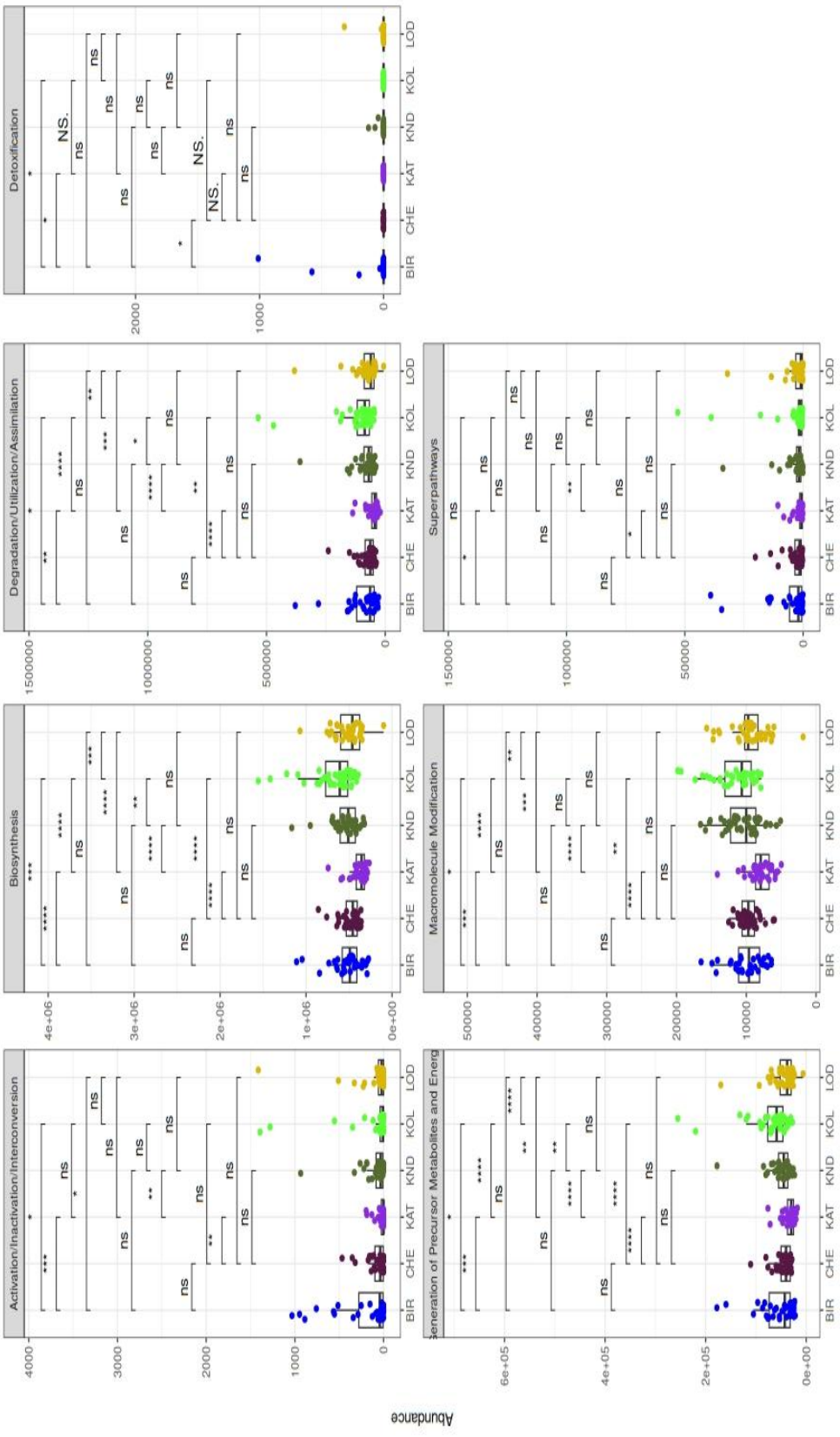

Figure 6 Boxplot of biochemical pathways at superclass 1 level illustrating the relative abundance of functional pathway categories across six communities with each panel representing a specific category of metabolic function with significance markers reported (‘*’ $p \leq 0.05$, ‘**’ $p \leq 0.01$, ‘***’ $p \leq 0.001$,)

Core biochemical pathways of six communities

The species level taxonomic profiling was performed using MetaPhlAn 4.1 with the rel_ab option activated (Blanco-Míguez *et al*. 2023). The MetaPhlAn 4 database includes 18.4k more species compared to MetaPhlan 3, offers superior resolution of many species described by kSGBs and includes ~5k yet to be characterised microbial species (uSGBs). These led to improved phylogenetic reconstructions for both known and uncharacterised taxa.

The package HUMAnN (3.9) was used to profile the abundances of gut microbial metabolic pathways and gene families from the metagenomic sequencing data (Franzosa *et al*. 2018). The gene length normalized (RPK) path abundance files for the six PVTGs were sequencing depth normalized (CPM) and used for further analysis.

In order to identify the core-metabolic pathways, a minimum relative abundance detection threshold (0.1%) was set. A cut-off was also set on the proportion of samples that share a pathway (50% prevalence threshold). All the six communities were found to share 287 pathways (conserved core pathways) [Table 6, Annexure I]. In addition, some of the communities possessed distinct pathways at the given detection and prevalence thresholds (distinct core pathways) [Annexure II].

Table -4 Conserved core pathways of six communities

Superclass I	%	Superclass II	%
Biosynthesis	174/287 = 60.6	Cofactor, Carrier, and Vitamin Biosynthesis	42/174=24.1
		Amino Acid Biosynthesis	40/174=23.6
		Nucleoside and Nucleotide Biosynthesis	28/174=16.1
		Fatty Acid and Lipid Biosynthesis	20/174=11.5
		Carbohydrate Biosynthesis	16/174=9.2
		Cell Structure Biosynthesis	11/174=6.3
		Secondary Metabolite Biosynthesis	4/174=2.3
		Amine and Polyamine Biosynthesis	3/174=1.7
		Aromatic Compound Biosynthesis	2/174=1.1
		Polyprenyl Biosynthesis	2/174=1.1
		Tetrapyrrole Biosynthesis	2/174=1.1
		Amide, Amidine, Amine, and	1/174=0.57

		Polyamine Biosynthesis	
		Aminoacyl-tRNA Charging	1/174=0.57
		Metabolic Regulator Biosynthesis	1/174=0.57
		Other Biosynthesis	1/174=0.57
Degradation/Utilization/Assimilation	74/287=25.7	Carbohydrate Degradation	19/74=25.7
		Nucleoside and Nucleotide Degradation	14/74=18.9
		Carboxylate Degradation	12/74=16.2
		C1 Compound Utilization and Assimilation	5/74=6.8
		Inorganic Nutrient Metabolism	5/74=6.8
		Amine and Polyamine Degradation	4/74=5.4
		Amino Acid Degradation	3/74=4.0
		Alcohol Degradation	3/74=4.0
		Secondary Metabolite Degradation	3/74=4.0
		Degradation/Utilization/Assimilation - Other	2/74=2.7
		Fatty Acid and Lipid Degradation	2/74=2.7
		Aromatic Compound Degradation	1/74=1.4
		Cyclitol Degradation	1/74=1.4
Generation of Precursor Metabolites and Energy	32/287=11	Fermentation	12/32=37.5
		TCA cycle	5/32=15.6
		Glycolysis	4/32=12.5
		Pentose Phosphate Pathways	3/32=9.4
		Photosynthesis	3/32=9.4
		Generation of Precursor Metabolites and Energy	2/32=6.3
		Superpathways	2/32=6.3
		Respiration	1/32=3.1
Superpathways	5/287=1.74	Superpathways	5/5=100
Macromolecule Modification	2/287=0.7	Nucleic Acid Processing	2/2=100

Table-6 shows the percentage constituents of the Superclass I and Superclass II metabolic pathway levels. At the Superclass I level, the conserved pathways consisted of Biosynthesis (60.6%), Degradation/Utilization/Assimilation (25.7%), Generation of Precursor Metabolites and Energy (11%), Super pathways (1.74%) and Macromolecule Modification (0.7%) (Table 2). At the Superclass II level, the majority of the Biosynthesis superclass consisted of 'Cofactor, Carrier, and Vitamin Biosynthesis' (24.1%), Amino Acid Biosynthesis (23.6%), Nucleoside and Nucleotide Biosynthesis (16.1%), Fatty Acid and Lipid Biosynthesis (11.5%), Carbohydrate Biosynthesis (9.2%), Cell Structure Biosynthesis (6.3%) and Secondary Metabolite Biosynthesis (2.3%). The major subclasses of the superclass 'Degradation/ Utilization/ Assimilation' were Carbohydrate Degradation (25.7%), Nucleoside and Nucleotide Degradation (18.9%), Carboxylate Degradation (16.2%), C1 Compound Utilization and Assimilation (6.8%), Inorganic Nutrient Metabolism (6.8%), Amine and Polyamine Degradation (5.4%), Amino Acid Degradation (4.0%), Alcohol Degradation (4.0%) and Secondary Metabolite Degradation (4.0%).

The Superclass 'Generation of Precursor Metabolites and Energy' consisted of Fermentation (37.5%), TCA cycle (15.6%), Glycolysis (12.5%), Pentose Phosphate Pathways (9.4%), Photosynthesis (9.4%), Generation of Precursor Metabolites and Energy (6.3%), Super pathways (6.3%) and Respiration (3.1%). Finally, the Superclass I member 'Super pathways' itself had 5 members (1.74%) and Macromolecule Modification (0.7%) had 2 Nucleic Acid Processing pathways.

Distinct core pathways for the six PVTGs

The Chenchu and the Katkari communities do not possess any pathway that is unique to the community. The Savara's have six distinct pathways. One pathway is a member of the 'Biosynthesis → Amino Acid Biosynthesis' super pathways. Four pathways are from the Degradation/Utilization/Assimilation super pathways and the last one is a member of the Generation of Precursor Metabolites and Energy. The Lodhas have a single distinct pathway belonging to the 'Biosynthesis → Secondary Metabolite Biosynthesis' Super pathway. The Birhor have two distinct pathways belonging to the Generation of Precursor Metabolites and Energy super pathway and a single pathway from the 'Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation' super pathway. Finally, the Kolam are enriched in three pathways belonging to the 'Biosynthesis → Fatty Acid and Lipid Biosynthesis', 'Biosynthesis → Aromatic Compound Biosynthesis' and 'Biosynthesis → Nucleoside and Nucleotide Biosynthesis' super pathway.

Pathways associated with food habits

The two microbial pathways- 'L-carnitine degradation I' (CARNMET-PWY) and 'super pathway of cytosolic glycolysis (plants), pyruvate dehydrogenase and TCA cycle' (PWY-5464) are enriched in the Birhor tribes. Mammals can synthesize carnitine. The main sources of carnitine are animal products such as meat, milk, egg and green leaves. Although bacteria cannot synthesize carnitine, yet it is a source of carbon and nitrogen and serve as electron acceptors (Ghonimy et al., 2018). Carnitine mediates the metabolism of SCFAs by regulating their concentrations in the cytosol and also protects microbial cells from different stressors. Carnitine is required to maintain high fibre fermentation ability of the gut microbes. Dietary fibre may trap

element iron. Iron conjugated to fibre is absorbed more in the large intestine as bacterial fermentation can release bound iron.

Humans rely on gut microbes to extract nutrients from resistant starch and a wide variety of fibres (Oliphant & Allen-Vercoe, 2019). Gut microbes have developed several fermentation strategies to generate energy from pyruvate. Pyruvate is either catabolized into succinate, lactate or acetyl-CoA or further metabolized to produce SCFAs, acetate, propionate and butyrate. Thus, enrichment of CARNMET-PWY and PWY-5464 in Birhor reflect their resistance-starch and fibre rich diet. A gut microbiome study conducted on breastfed pre-term versus full-term infants reported an enrichment of a number of microbial metabolic pathways (Aguilar-Lopez et al., 2022). The Lodha and Birhor tribes are enriched in phospholipases (LIPASYN-PWY) pathway. Chenchu, Savara, Katkari, Birhor and Kolam are enriched in 1,4-dihydroxy-6-naphthoate biosynthesis II (PWY-7371). In addition, enrichment of several conserved core pathways such as peptidoglycan biosynthesis V (β-lactam resistance) (PWY-6470), L-glutamine biosynthesis III (PWY-6549) and starch degradation III (PWY-6731) indicate that diverse pathways and probably different microbial species take part in the assimilation of milk derived nutrients in different tribal communities.

Enrichment of gut microbial pathways associated with various diseases

The gut microbial metagenomes of the three PVTGs- Chenchu, Savara and Birhor are enriched in the super pathway of menaquinol-6 biosynthesis (PWY-5850), super pathway of demethylmenaquinol-6 biosynthesis I (PWY-5860), super pathway of menaquinol-9 biosynthesis (PWY-5845), super pathway of histidine, purine, and pyrimidine biosynthesis (PRPP-PWY) and super pathway of demethylmenaquinol-9 biosynthesis (PWY-5862). In addition, Chenchu and Savara share the super pathway of menaquinol-10 biosynthesis (PWY-5896), and Chenchu and Birhor share the super pathway of (Kdo)2-lipid A biosynthesis (KDO-NAGLIPASYN-PWY). The 'TCA cycle IV (2-oxoglutarate decarboxylase)' (P105-PWY) is a conserved core pathway among the six communities. All these pathways had previously been reported to be enriched in the gut microbiomes of children suffering from atopic dermatitis (Patumcharoenpol et al., 2023). Although the said study was conducted on children, yet high occurrence of skin diseases among PVTGs indicate that enrichment of these pathways might be associated with the observed disease conditions in these tribal communities.

The field data collected by Anthropological Survey of India on a previous occasion showed that gastrointestinal disorders are common across the six PVTGs. The microbial metabolic pathways of the Chenchu, Kond-Savara and Birhor are enriched in 'enterobacterial common antigen biosynthesis pathway' (ECASYN-PWY) while Chenchu, Kond-Savara and Kolam are enriched in starch biosynthesis (PWY-622). The 'super pathway of heme b biosynthesis from glutamate' (PWY-5918), methanogenesis from acetate (METH-ACETATE-PWY), Bifidobacterium shunt (P124-PWY) and the 'super pathway of glycerol degradation to 1,3-propanediol' (GOLPDLCAT-PWY) form a part of the conserved core pathways of the six tribes. Enrichment of these pathways are known to be associated with irritable bowel syndrome (Phan et al., 2021). Enrichment of the 'enterobacterial common antigen biosynthesis pathway' may indicate an increase in the abundance of the gram negative Enterobacterales in the gut microbiome. Enterobacterial common antigen is speculated to promote virulence and protect the enteric pathogens from bile salts and antibiotics.

The Chenchu and Kond-Savara are enriched in super pathway of menaquinol-10 biosynthesis (PWY-5896). Chenchu, Birhor and Kond-Savara are enriched in super pathway of demethylmenaquinol-6 biosynthesis I (PWY-5860), and super pathway of menaquinol-6 biosynthesis (PWY-5850) while Kond-Savara and Birhor are enriched in 'super pathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass' (GLYCOLYSIS-TCA-GLYOX-BYPASS). The super pathway of glyoxylate bypass and TCA (TCA-GLYOX-BYPASS) are enriched in all tribes except Katkari. The aspartate super pathway (PWY0-781), nitrate reduction V (assimilatory) (PWY-5675), super pathway of fatty acids biosynthesis (E. coli) (PWY-6285), super pathway of menaquinol-7 biosynthesis (PWY-5840) and palmitate biosynthesis (type II fatty acid synthase) (PWY-5971) are a part of the conserved core pathways. These pathways have been reported to be distinct for patients suffering from enteric infection (Hansen et al., 2024). Enrichment of these pathways in six tribal communities thus reflect their vulnerability towards gastro-intestinal disorders.

The super pathway of (Kdo)2-lipid A biosynthesis (KDO-NAGLIPASYN-PWY) is enriched in Chenchu and Birhor; ‘super pathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass’ (GLYCOLYSIS-TCA-GLYOX-BYPASS) is present in Kond-Savara and Birhor and ‘enterobacterial common antigen biosynthesis’ (ECASYN-PWY) in Chenchu, Kond-Savara and Birhor. In addition to these pathways, enrichment of other pathways, that are conserved in six communities, such as L-lysine biosynthesis II (PWY-2941), TCA cycle IV (2-oxoglutarate decarboxylase) (P105-PWY), super pathway of menaquinol-11 biosynthesis (PWY-5897), super pathway of menaquinol-12 biosynthesis (PWY-5898), super pathway of menaquinol-13 biosynthesis (PWY-5899), palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate) (PWY-6282), palmitate biosynthesis (type II fatty acid synthase) (PWY-5971), stearate biosynthesis II (bacteria and plants) (PWY-5989) and oleate biosynthesis IV (anaerobic) (PWY-7664) have been implicated in the progression of non-alcoholic fatty liver disease and significant liver fibrosis (Rodriguez-Diaz et al., 2022; Si et al., 2021). Enrichment of these pathways in tribal communities could be due to their adoption to a sedentary lifestyle effected by various ‘food support schemes’ which abstains them from rigorous physical activities such as foraging and hunting gathering.

The Chenchu, Savara and Birhor share the super pathway of purine nucleotides de novo biosynthesis II (DENOVOPURINE2-PWY) and the pyrimidine deoxy ribonucleotides de novo biosynthesis II pathway (PWY-7187). The gut microbiome has been associated with several neurological and behavioural disorders such as attention deficit disorder, anxiety, and depression (Laue et al., 2022). A study was conducted on children to relate their gut microbial pathways to the level of anxiety, depression, hyperactivity and social behaviour (Laue et al., 2022). In this study, the super pathway of purine de novo biosynthesis II was found to be associated with better 'Attention Problems', 'Developmental Social Disorders', and 'Social Skills' scores, and de novo pyrimidine biosynthesis was associated with better 'Developmental Social Disorders' scores. In contrast, a second study found that the 'Super pathway of purine nucleotides de novo biosynthesis II' was differently enriched in patients with high-grade dysplastic polyps that have the malignant potential to initiate colorectal cancer (Clavenna et al., 2023).

Functional potential of differentially enriched pathways through Lefse (Linear discriminant analysis effect size)

The Linear Discriminant Analysis (LDA) Effect Size (LEfSE) provides insight into the differential abundance of metabolic pathways across microbial communities. The LDA score is a statistical method reflecting the magnitude of the differences in specific microbial pathways between these six communities with higher scores indicating a stronger association with the respective community. The relative abundance of these pathways further quantifies the representation of these metabolic functions across the communities. The gut microbiota of the Chenchu community is enriched with genes involved in preQ0 and L-arginine biosynthesis (Figure -7). Queuosine, Phosphopentothenate biosynthesis, L-histidine degradation pathways are enriched in Katkari community. Lodha community have abundance of pathways encoding for stachyose and purine ribonucleosides degradation. The Konda savara community have the pathways abundant for pyruvate fermentation to acetate and lactate, starch degradation, super pathway of thiamine diphosphate biosynthesis pathways. Acetylene degradation, flavin biosynthesis ethanolamine utilization pathways are enriched in Birhor community and in Kolam community their gut microbiome has genes encoding for starch biosynthesis, super pathway for glucose and xylose degradation, thiazole biosynthesis pathways etc.

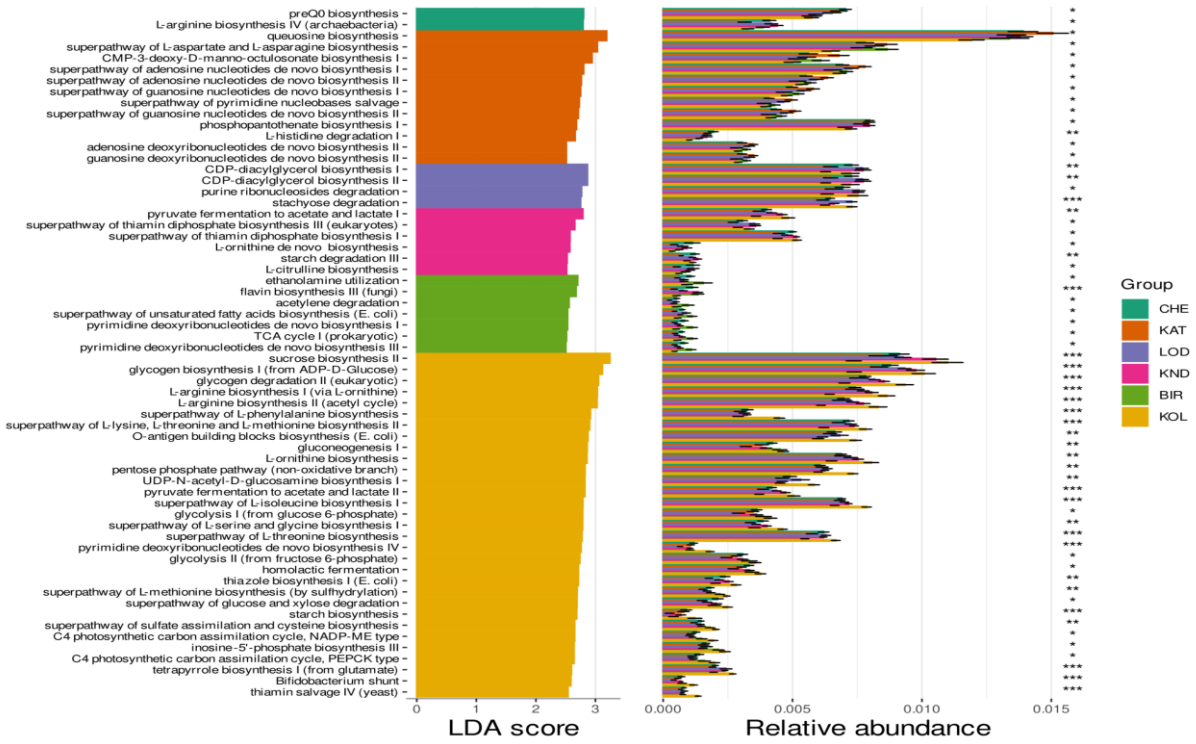

Figure 7 LDA vs Relative abundance plot at pathway level across six communities with significance markers reported ('*' $p \leq 0.05$, '**' $p \leq 0.01$, '***' $p \leq 0.001$)

Discussion & Conclusion

Discussion

Human gut microbiome is unique and stable in each individual living in different geographical locations. There are several ethnic groups, so-called particularly vulnerable tribal groups recognised by the Government of India, who still remain isolated and rely on the food resources available from their surrounding environment. Nevertheless, our knowledge on the gut microbiome profile of the healthy tribal groups is limited. This study on six PVTGs of India namely Birhor of Jharkhand, Chenchu of Telangana, Katkari and Kolam of Maharashtra, Konda Savara of Andhra Pradesh and Lodha of West Bengal belonging to different geographical setup will provide us the insights into the composition and diversity of healthy gut microbiome as well as their function profile. These tribal populations mostly consume food rich in dietary fibre which include wild leaves and vegetables, millets, roots and tubers etc. The common food among these communities is rice with differences in consumption of cereals, millets, meat and fish. For instance, the consumption of millets is more in Savara and Chenchu population when compared to the other communities, whereas the Birhor and Lodha communities consume more wheat, puffed rice and rice flakes.

The gut microbiome analysis in our study revealed that *Actinobacteria, Proteobacteria, Firmicutes* and *Bacteroidota* are the dominant phyla and core microbiota at species level is more or less same in all the six communities with slight variations in their abundance. Phylum *Firmicutes* is the most abundant among all these communities. At Genus level *Actinobacteria*, *Bifidobacterium, Roseburia* and *Lachinospira* show high abundance in Kolam community of Maharashtra. Whereas *Faecalibacterium* is highly abundant in Savara community followed by Kolam. A comparative study among the Indian population of different geographical locations with that of worldwide data revealed that the gut microbial profile of the Indian population was similar to the Mongolian population and the bacterial genera *Faecalibacterium, Eubacterium*, *Clostridium, Blautia, Ruminococcus* and *Roseburia* were found to be core genera in the representative population of the world (Dehingia et al., 2015). The same is found in the present study of Six PVTGs of India belonging to different geographical locations. Prevalence of *Faecalibacterium, Lachinospira*, and *Bifidobacterium* contribute anti-inflammatory and antimicrobial activities that act as barrier effect (Lievin et al., 2000). The *Lactobacillus sp* are in low abundance among all the communities and they are found absent in Lodha community. This could be because the Lodha community do not consume milk and milk products. The Lodha and Katkari/Kathodi community show high abundance of *Segatella (Prevotella)* species when compared to the other communities. High abundance of *Segatella (Prevotella)* in gut is associated with food highly rich in carbohydrates derived from plant and fibre in the Indian diet (Arumugam et al., 2011; De Filippo et al., 2010). This study observed high abundance of Bacteroidetes and proportionally low abundance of *Proteobacteria* among all the six communities. Increase of *Bacteroidetes* and reduced *Proteobacteria* may be linked with energy consumption and high animal fat diet consumption (Hazarika et al., 2022).

F/B Ratio as a Biomarker of Gut Microbiome Diversity and Health

The ratio of Firmicutes to Bacteroidetes (F/B) is often explored as a key indicator of gut microbiota balance, and it plays a notable role in metabolic processes. Studies have found that a higher F/B ratio is frequently linked to conditions like obesity and metabolic syndrome, as well as more efficient energy absorption from food. On the other hand, a lower F/B ratio tends to be

associated with issues like malnutrition or inflammatory bowel diseases. In this study the F/B ratio of Kolam (0.84) community followed by Savara (0.82) community suggests a distinct gut microbial composition that could linked to their dietary patterns or lifestyle. The communities with lower F/B ratios like Birhor (0.44) and Katkari (0.50) have different dietary habits, lower caloric intake or more fibre-rich diets. These findings are consistent with studies reporting indigenous populations, such as the Hadza hunter-gatherers of Tanzania, tend to have a more diverse gut microbiome with different F/B ratios. Such populations are often characterised by a high intake of fibre and unprocessed foods that supports a more balanced microbiota. The variation in F/B ratio between the communities could point the differences in dietary intake, particularly the intake of fibre, animal protein and processed foods. There is no universally optimal F/B ratio because it varies depending on several factors like diet, lifestyle and geography. But early studies suggests that a balanced F/B ratio is beneficial for overall health, typically ranging between 1:1 and 2:1 (Rinninella et al., 2019). There may be significant differences among the communities in the F/B ratio but the overall ratio is below suggesting that these communities have a healthy gut.

Core gut microbiota and biochemical pathways

Core microbiota at species level in all the six communities are predominant by *Prevotella copri (Segatella copri), Segatella sinensis, Eubacterium rectale, Faecalibacterium prausnitzii, Blautia wexlerae, Roseburia faecis, Dorea longicatena, Lachnispira pectinoschiza, Gemmiger formicilis, Blautia massilensis, Escherichia coli, Ruminococcus bromii, Coprococcus eutactus, Holdemanella bioformis* etc. The abundance of Eubacterium rectale is more in Savara when compared to other communities which plays major role in the biochemical pathways such as Amino acid biosynthesis, Super pathway of branched amino acid biosynthesis, CoA biosynthesis, Super pathway of aromatic amino acid biosynthesis etc. *Faecalibacterium prausnitzii* is found abundant in all the six communities and this species is functionally active members of the microbiome (Li et al., 2008). *F. prausnitzii* is one of the most abundant butyrate-producing bacteria in gut (Flint et al., 2012). Butyrate plays a major role in gut physiology and it has multiple effects in intestinal cell life cycle and numerous beneficial effects for health through protection against pathogen invasion and modulation of immune system (G. T. Macfarlane & Macfarlane, 2011). Though the genus *Treponema (Spirochetes)* is less abundant in these primitive groups when compared to other microbial communities, their proportion is more in Katkari/Kathodi and Savara communities. Earlier studies revealed that abundance of Treponema in gut is due to consumption of plant tubers (Schnorr et al., 2014), and are depleted in urban-industrial communities (De Filippo et al., 2010). The Species of *Treponema* like *Treponema berlinense, Treponema succinifaciens* play major role in several pathways such as L- ornithine biosynthesis (GLUTORN-PWY), Coenzyme A biosynthesis (COA-PWY), chorismate biosynthesis (ARO-PWY), pyruvate fermentation to acetate and lactate (P41-PWY), queuosine biosynthesis etc. These pathways work together to support crucial functions in the gut such as immune response, production of important fatty acids that nourish the gut lining, production of key aromatic compound that play a role in immune regulation and gut brain interactions and production of SCFAs. Together, these pathways underscore the importance of a balanced and functional gut microbiota that is vital for maintaining healthy gut environment and promoting overall health.

Carbohydrate metabolism and Gut microbiome

Humans lack the capacity to degrade complex polysaccharides and non-digestible carbohydrates such as resistant starch, oligosaccharides and plant fibres, glycans etc. (Cummings, 1987). The majority of carbohydrates in the diet of these primitive groups are resistant starch, non-digestible polysaccharides, oligosaccharides and unabsorbed sugars such as raffinose, lactose and stachyose etc. (Scott et al., 2008). The gut microbiota plays an important role in the fermentation of these complex molecules through a series of processes. They are characterised on the basis of functional groups based on metabolite formed and substrate utilized. The initial degradation of insoluble carbohydrates was performed by colonic microbes *Firmicutes sp*, *Bacteroides sp, and Ruminococcus sp*. (Flint et al., 2012). In the present study the carbohydrate degradation pathways (PWY-6527, PWY-6731, PWY-6902, PWY-7294) are associated with bacterial species like *Bifidobacterium angulatum, Bifidobacterium bifidum, Blautia obeum, Blautia wexlerae, Ruminococcus torques, Clostridium baratii, Faecalibacterium prausnitzii, Bacteroides cellulosilyticus* etc. that produce Methane, Carbon dioxide, Hydrogen and short chain fatty acids (SCFA) such as acetate, propionate, butanoate etc. as the byproducts. Figure -7 shows the discriminant pathways among all the communities. In Lodha community Stachyose degradation pathway (PWY-6527) found highly significant ($p \leq 0.001$), in Birhor community Lactose and galactose degradation (LACTOSECAT-PWY) pathway is significant ($p \leq 0.05$), Katkari/Kathodi, CMP-3-deoxy-D-manno-octulosonate biosynthesis I (PWY-1269) pathway is significant ($p \leq 0.05$), Savara community starch degradation III (PWY-6731), 1,5-anhydrofructose degradation (PWY-6992) pathways are significant ($p \leq 0.01$) and in Kolam community glycogen degradation (PWY-5941) pathway found highly significant ($p \leq 0.001$)

Amino acid metabolism and Gut microbiome

The gut microbiota uses amino acids produced from food or the host as elements for protein synthesis and synthesize nutritionally essential amino acids de novo, which are potential regulatory factors in host amino acid homeostasis (Lin et al., 2017). *Bacteroides, Clostridum, Propionibacterium, Fusobacterium, Lactobacillus and Streptococcus* were identified microbial species for their role in proteolysis (S. Macfarlane & Macfarlane, 2006). Among the core biochemical pathways BRANCHED-CHAIN-AA-SYN-PWY is one of the most abundant among these six primitive groups. BCAAs including leucine (Leu), isoleucine (Ile), and valine (Val), play critical roles in the regulation of energy homeostasis, nutrition metabolism, gut health, immunity, and diseases. BCAAs are not only substrates for synthesis of nitrogenous compounds but they also serve as signalling molecules regulating metabolism of glucose, lipid and protein synthesis (Nie et al., 2018). Degradation of aspartate, alanine, threonine and methionine lead to the formation of propionate, while degradation of glutamate, lysine, histidine, cysteine, serine and methionine generates butyrate (Yadav et al., 2018). The gut microbial species responsible for the biosynthesis and degradation pathways of amino acids are *Escherichia coli, Klebsiella oxytoca, Bacteroides cellulosilyticus, Alistipes shahii, Acidaminococcus fermentans, Blautia hansenii, Catenibacterium mitsuokai* etc. The most abundant amino acid pathways are biosynthesis pathways and found discriminant in Kolam community of Maharashtra (Figure -7). The pathways include L-arginine biosynthesis ($p \leq 0.001$), superpathway of L-lysine, L-threonine and L-methionine biosynthesis II ($p \leq 0.001$), superpathway of L-threonine biosynthesis ($p \leq 0.001$), superpathway of L-methionine biosynthesis (by sulfhydrylation) ($p \leq 0.01$).

Vitamin biosynthesis and Gut microbiome

The other essential biochemical pathways include bile acid metabolism, vitamin synthesis, aromatic compound metabolism, immunomodulatory pathways etc. The gut bacteria in human synthesizes a wide variety of vitamins that are important for their own metabolism as well as for the host to maintain host physiology. The role of microbiome is essential in the synthesis of vitamin B, vitamin K, pantothenic acid, riboflavin, thiamine, pyridoxine, nicotinic acid, folate etc. The pathways like flavin biosynthesis (RIBOSYN2-PWY) and biotin biosynthesis (BIOTIN-BIOSYNTHESIS-PWY) are associated with gut microbiota such as Bacteroides vulgatus, Citrobacter koseri, Cronobacter sakazakii, Escherichia coli, Klebsiella aerogenes, Ruminococcus torques, Veillonella atypica, etc. The gut microbiota like *Alistipes fingoldii, Alistipes onderdonkii, Bacteroides dorei, Blautia obeum, Barnesiella intestinihominis, Citrobacter portucalensis, Haemophilus haemolyticus, Klebsiella michiganensis, Neisseria perflava, Saccharomyces cerevisiae* etc are associated with the biosynthesis of folate pathway (1CMET2-PWY, FOLSYN-PWY, PWY-2201, PWY-3841).

Table -5 Communities, core microbiota (with prevalence 50 % and detection 0.001), signature microbiota (threshold 2.5) and pathways (threshold 2.5)

Sno.	Population studied	Subsistence pattern	Diet	core species	Gut Composition (Discriminant)	enrichment of pathways (Discriminant)
1	Birhor	Monkey catchers, gather food from forest and rope makers	wild fruits and leaves, tubers and roots, fermented drinks (Rice and Mahua), occasional wild hunt, molluscs	*Segatella sp., Eubacterium rectale, Faecalibacterium praustnitzii, Prevotella sp.,* as core	High abundance of *Anaerovibrio_lipolyticus* and unclassified proteobacterial species *Phascolarctobacterium_succinatutens*	Flavin biosynthesis III (fungi), Petroselinate biosynthesis
2	Chenchu	Hunter-gatherers of Telangana	wild roots and tubers, fermented millet flour and rice, wild hunt, fermented drinks, insects	*Segatella sp., Eubacterium rectale, Faecalibacterium praustnitzii, Prevotella sp.*, as core	High abundance of Fusobacterium mortiferum, Bifidobacterium longum, Roseburia sp.	PreQ0 Biosynthesis, L-arginine biosynthesis
3	Katkari	Hunter-gatherers of Maharasthra	pulses, fish, meat, fermented drinks	*Segatella sp., Eubacterium rectale, Faecalibacterium praustnitzii, Prevotella sp.,* as core	Enriched with abundance of unclassified sp of *Bacteroidetes*	L-histidine degradation I
4	Konda savara	Shifting cultivators and gather	diet rice in millets, local pulses,	*Segatella sp., Eubacterium rectale, Faecalibacte*	High abundance of *Bacteoides ovatus, unclassified Blautia sp. Rumminococcus lactaris, Faecalibacillus intestinalis*	Pyruvate fermentation to acetate and lactate I, Starch

		forest produce	wild tubers and roots, wild leaves and meat, wild hunt	*rium praustnitzii, Prevotella sp.,* as core		degradation III, purine nucleobases degradation I (anaerobic), 1,5-anhydrofructose degradation
5	Kolam	Shifiting cultivators and gather forest produce	vegetables, roots and tubers, bamboo shoots, meat and fish	*Segatella sp., Eubacterium rectale, Faecalibacterium praustnitzii, Prevotella sp*., as core	Enriched with *Bifidobacterium adolescentis, Blautia wexlerae, Mitsuokella jalaludinii, Enterococcus hirae, Dorea longlcatena*	Sucrose biosynthesis II, Glycogen biosynthesis I (from ADP-D-Glucose), L-arginine biosynthesis II (acetyl cycle), L-arginine biosynthesis I (via L-ornithine), Superpathway of L-threonine biosynthesis
6	Lodha	Semi nomadic Hunter gatherers	vegetables, legumes, wild leaves and tubers, snails, dry fish	*Segatella sp., Eubacterium rectale, Faecalibacterium praustnitzii, Prevotella sp.,* as core	*Mediterraneibacter faecis, romboutsia timonensis, streptococus gallolyticus, clostridium saudiense, cetobacterium somerae* etc.	CDP-diacylglycerol biosynthesis I, CDP-diacylglycerol biosynthesis II, Stachyose degradation

Table – 6 Summary of early studies on gut microbiota of primitive groups. Source: Geography, Ethnicity or Subsistence-Specific Variations in Human Microbiome Composition and Diversity. Frontiers in Microbiology. June 2017 Volume 8 Article 1162

Sno.	Population studied	Diet/Subsistence pattern	Gut Composition	enrichment of pathways	Reference
1	Native Africans and African Americans	Higher intake of animal protein, fat and low fibre by African Americans than native Africans	Dominance of *Prevotella* and butyrate-producing groups and Higher	Genes of hydrogen sulfide production, saccharolytic fermentation, butyrogenesis and methanogenesis, genes of secondary	O'Keefe et al., 2007; Ou et al., 2013

			abundance of *bacteroides*	bile acid production	
2	The Hadza- a hunter-gatherer community of Tanania, Africa	Ancient foraging subsistence Diet: Game meat, honey, baobab, berries and tubers	Enriched in *Succinovibrio sp. Ruminobacter, Spirochaetes (Treponema), Prevotella, unclassified Bacteroidetes, Firmicutes, Proteobacteria*, and *Clostridiales*	Propionate producers	Schnorr et al., 2014
3	Amerindian population of Venezuela	Ancient subsistence Diet: corn, cassava	High abundance of *Prevotella* and *Enterococcaceae*	460 Ecs including those involved in glutamate synthase, alpha-amylase etc are enriched in nin-US populations and 433 Ecs including those involved in vitamin biosynthesis, xenobiotics metabolism, sugar catabolism, bile salt metabolism etc, are enriched in US populations.	Yatsunenko et al., 2012
4	The Matses from the Peruvian Amazon	Isolated hunter-gatherer community Diet: tubers invasive plantains, fish, game meat	High abundance of *succinovibrio, Treponema, Cynobacteria, Tenericutes, prevotella, Firmicutes (Clostridium, Catenibacterium, Eubacterium, Lachnospira* etc.), *Proteobacteria, Spirochaetes* and *Euryarchaeota*	78 KEGG ortholog groups (Kos), mostly associated with metabolism and gentic information processing and 79 Ecs (some involved in Tricarboxylic acid cycle) are enriched in Traditional groups. 20 Kos, mostly associated with membrane transport	Obregon-Tito et al., 2015

5	Pygmy hunter-gatherers	Ancient foraging subsistence Diet: cassava, nuts occasional game meat	higher frequencies of *Proteobacteria,* especially of *Succinivibrio* and *Samonella*, depeted in *Lachnospiraceae* family	only one pathway associated with bacterial invasion of epithelial cells, has been reported to differ significantly across all subsistence types, with highest across all subsistence types, with the highest relative abundance in the hunter-gatherers and lowest in the farmers	Morton et al., 2015
6	Bantu farming populations	Rural agricultural subsistence Diet: locally grown cereals, vegetables, meat	Higher abundance of *Firmicutes*, especially of *Ruminococcus*, *Treponema*		Morton et al., 2015
7	Bantu fishing populations all three populations were from southwest Cameroon, Africa	Fishing population diet: cassava, fish meat yogurt	Enriched in *Bifidobacteria, Bacteroidales,* depleted in *Ruminococcus*		Morton et al., 2015
8	BaAka pygmies from the Central African Republic	Ancient hunter-gatherer subsutence, no exposure to antibiotics or modern therapeutics or modern therapeutics Diet: wild game, fish fibrous leaves nuts and fruits	High abundance of *Prevotella* and *Clostridiaceae* and *Treponema*, depleted in *Bacteroidales*	14 pathways includinf those involved in pathogenecity, peptidoglycan biosynthesis, purine/pyramidine metabolism etc, Increased abundance of virulence, amino acid, lipid and vitamin metabolism pathways	Gomez et al., 2016

9	Bantu population from the Central African Republic	Traditional agriculturist group, partial exposure to western lifestyle and modern therapeutics Diet" flour like products, goat meat.	Intermediate abundance of *Prevotella, Clostridiaeae* and *Treponema*, relatively enriched in *Rickenellaceae* and *Bacteroides*. Bantu gut microbiome is dominated by *Firmicutes*	22 pathways including transporters, secretion system, signal transduction mechanism etc. increased abundance of carbohydrate and xenobiotics metabolism pathways	Gomez et al., 2016

Conclusion

The world underwent a metamorphosis from simple to complex life strategies but there are still some communities so-called particularly vulnerable tribal groups (PVTGs) depending on natural resources for their subsistence. However, these groups are still traditional, practicing hunting gathering, shifting cultivation etc. though some of the inhabitants (customised) have a modern lifestyle access. A study on the gut microbiota of these primitive tribal groups provided us insights into the composition, diversity of the microbiome and the functional annotations of these microbes. The study is conducted using shotgun metagenome sequencing technology. The metagenomic sequences are analysed using various tools. Metadata is obtained from the schedules designed to collect various aspects related to their health and food consumption. Table -3 shows an outline of the current study on the six primitive tribal groups in India belonging to different geographical locations. The communities are compared within (intra) and among (inter) based on their availability and accessibility of food as well as the geographical location. Within the community the people are grouped into traditional and customised. The traditional groups are those who still depend on the food available from their natural resources and unexposed to modern lifestyle. The customised groups are those who have availability and accessibility to the modern lifestyle and food habits. However, there is no significant difference in the gut microbiota within the two cohorts. On comparison among these six communities significant differences were found in the microbiota as well as their biochemical pathways. These differences may be the result of dietary practices and variation in the food types. All the six communities showed signature microbiota and biochemical pathways.

The core gut microbiota is almost the same. This is may be because they still depend on the traditional food system. The core microbiota at species level includes *Segatella (Prevotella) Copri, Eubacterium rectale, Faecalibacterium prausnitzii, Mediterraneibacter faecis, Dorea longicatena* etc. There are keynote species that are discriminant in each community. For instance, in Lodha community *Romboutsia timonensis, Cetabacterium somerae, Turicibacter sanguinis, Turicibacter bills* etc are discriminant. *Turicibacter sanguinis* plays a major role in several core pathways like chorismate biosynthesis (ARO-PWY). Chorismate is an intermediate in the biosynthesis of aromatic amino acids (Phenylalanine, Tyrosine and Tryptophan) and other compounds. It helps as a branching point to produce various essential molecules. Indeed, Lodha community is enriched with the pathways responsible for CDP-diacylglycerol biosynthesis I, CDP-diacylglycerol biosynthesis II, Stachyose degradation (PWY-6527). The Stachyose is an oligosaccharide present in certain foods, especially legumes, like beans, lentils etc. The gut microbial species like *Bifidobacterium angulatum, Blautia obenum, Citrobacter braaki, Clostridium ventriculi, Enterobacter mori, Hungatella effluvia, Klebsiella oxytoca* etc. are responsible for the degradation of chorismate.

The Kolam community is showing highest abundance of gut microbiota as well as the biochemical pathways. *Roseburia faecis, Mitsuokella jalaludinii, Dialister succinatiphilus, Anaerostipes hadrus, Gemmiger formicillis, Coprocossus catus, Blautia luti* etc. are found discriminant in this community. The microbiome plays a major role in the most of the core pathways like L- arginine biosynthesis (ARGSYNBSUB-PWY), super pathway of branched chain amino acid biosynthesis (BRANCHED-CHAIN-AA-SYN-PWY), chorismate biosynthesis (ARO-PWY) etc. These biochemical pathways are involved in amino acid

biosynthesis and degradation. The signature pathways include Sucrose biosynthesis II, Glycogen biosynthesis I (from ADP-D-Glucose), L-arginine biosynthesis II (acetyl cycle), L-arginine biosynthesis I (via L-ornithine), Super pathway of L-threonine biosynthesis. Intake of rich protein diet is responsible for the enrichment of these pathways. The Kolam community of Maharashtra intake protein from both plant and animal sources. Consumption of fish, meat, legumes, pulses etc is found more in this community.

Among the Savara community of Andhra Pradesh *Bacteroides ovatus, Blautia SGB4833*, *Ruminococcus intestinismiae* are the signature gut microbiota. These species are also responsible for amino acid biosynthesis pathways. Pyruvate fermentation to acetate and lactate I, Starch degradation III, purine nucleobases degradation I (anaerobic), 1,5-anhydrofructose degradation are the enriched pathways in this community. It is found that the intake of roots and tubers in Savara community is more. These foods are rich in dietary fibres and produce the short chain fatty acids (SCFA) which are in turn contribute for good for healthy gut.

The Katkari community have unclassified bacterial species as discriminant gut microbiota. It has high significance of L-histidine degradation pathway. The L-histidine degradation (HISDEG-PWY) is an essential pathway leads to histamine production which is involved in allergic reactions and immune responses. Earlier studies suggested that the gut derived histamine can have anti-inflammatory effects. Katkari community is also enriched with nucleotide *de novo* pathways. Intake of foods such as meat, legumes, fish and sea foods, mushrooms, dairy products are responsible for the enrichment of these pathways.

The Chenchu community has *Fusobacterium mortiferum, Bifidobacterium longum* and *Roseburia sp AF02_12* as the signature gut microbiome and they have a major role in several essential pathways. The pathways like coenzyme A biosynthesis (COA- PWY), super pathway of coenzyme A biosynthesis, super pathway of aromatic amino acid (COMPLETE-ARO-PWY), glycogen degradation (GLYCOCAT-PWY) etc are associated with *Bifidobacterium longum*. It corresponds to the degradation of dietary fibres. The other signature species are involved in the amino acid biosynthesis pathways.

Anaerovibrio lipolyticus, Clostridium perfringens, Phascolarctobacterium succinatutens etc are the discriminant gut microbiota in the Birhor community of Jharkhand. This community is enriched with genes associated with pathways like Flavin biosynthesis III (fungi), Petroselinate biosynthesis. Flavin is an essential coenzyme that play an important role in vitamin B2 synthesis. Intake of high dietary fibre and plant-based foods like fruits, vegetables and herbs are associated with this pathway.

The Gut microbiota of these six communities is diverse and they possess healthy gut as depicted by their microbiome composition. Though some inhabitants (customised) have access to modern lifestyle and exposed to few urbanised foods, most of them have diverse beneficial gut microbiota. Their gut is enriched with several species of *Segatella (Prevotella), Eubacterium rectale, Faecalibacterium prausnitzii* etc. because of their rich intake of dietary fibre. The study of six particularly vulnerable tribal groups in India, each from different geographical regions, revealed that they have healthy guts characterized by rich microbial diversity and composition.

References

References

100_A_Study_on_Katkari_A_Primitive_Tribal_Group_in_Maharashtra_No.214Final. (n.d.).

Abubucker, S., Segata, N., Goll, J., Schubert, A. M., Izard, J., Cantarel, B. L., Rodriguez-Mueller, B., Zucker, J., Thiagarajan, M., Henrissat, B., White, O., Kelley, S. T., Methé, B., Schloss, P. D., Gevers, D., Mitreva, M., & Huttenhower, C. (2012). Metabolic reconstruction for metagenomic data and its application to the human microbiome. *PLoS Computational Biology*, *8*(6). https://doi.org/10.1371/journal.pcbi.1002358

Acheson, D. W. K., & Luccioli, S. (2004). Mucosal immune responses. *Best Practice & Research Clinical Gastroenterology*, *18*(2), 387–404. https://doi.org/10.1053/ybega.2004.449

Aguilar-Lopez, M., Wetzel, C., MacDonald, A., Ho, T. T. B., & Donovan, S. M. (2022). Metagenomic profile of the fecal microbiome of preterm infants consuming mother's own milk with bovine milk–based fortifier or infant formula: a cross-sectional study. *American Journal of Clinical Nutrition*, *116*(2), 435–445. https://doi.org/10.1093/ajcn/nqac081

Aitor Blanco-Míguez, Francesco Beghini, Fabio Cumbo, Lauren J. McIver, Kelsey N. Thompson, Moreno Zolfo, Paolo Manghi, Leonard Dubois, Kun D. Huang, Andrew Maltez Thomas, William A. Nickols, Gianmarco Piccinno, Elisa Piperni, Michal Punčochář, Mireia Valles-Colomer, Adrian Tett, Francesca Giordano, Richard Davies, Jonathan Wolf, Sarah E. Berry, Tim D. Spector, Eric A. Franzosa, Edoardo Pasolli, Francesco Asnicar, Curtis Huttenhower & Nicola Segata. Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4. Nature Biotechnology. 2023. Volume 41, 1633–1644.

Anwesh, M., Kumar, K. V., Nagarajan, M., Chander, M. P., Kartick, C., & Paluru, V. (2016). Elucidating the richness of bacterial groups in the gut of Nicobarese tribal community - Perspective on their lifestyle transition. *Anaerobe*, *39*, 68–76. https://doi.org/10.1016/j.anaerobe.2016.03.002

Arumugam, M., Raes, J., Pelletier, E., Paslier, D. Le, Yamada, T., Mende, D. R., Fernandes, G. R., Tap, J., Bruls, T., Batto, J. M., Bertalan, M., Borruel, N., Casellas, F., Fernandez, L., Gautier, L., Hansen, T., Hattori, M., Hayashi, T., Kleerebezem, M., … Zeller, G. (2011). Enterotypes of the human gut microbiome. *Nature*, *473*(7346), 174–180. https://doi.org/10.1038/nature09944

Beghini, F., McIver, L. J., Blanco-Míguez, A., Dubois, L., Asnicar, F., Maharjan, S., Mailyan, A., Manghi, P., Scholz, M., Thomas, A. M., Valles-Colomer, M., Weingart, G., Zhang, Y., Zolfo, M., Huttenhower, C., Franzosa, E. A., & Segata, N. (2021). Integrating taxonomic, functional, and strain-level profiling of diverse microbial communities with bobakery 3. *ELife*, *10*. https://doi.org/10.7554/eLife.65088

Bhute, S., Pande, P., Shetty, S. A., Shelar, R., Mane, S., Kumbhare, S. V., Gawali, A., Makhani, H., Navandar, M., Dhotre, D., Lubree, H., Agarwal, D., Patil, R., Ozarkar, S., Ghaskadbi, S., Yajnik, C., Juvekar, S., Makharia, G. K., & Shouche, Y. S. (2016). Molecular characterization and meta-analysis of gut microbial communities illustrate enrichment of prevotella and megasphaera in Indian subjects. *Frontiers in Microbiology*, *7*(MAY). https://doi.org/10.3389/fmicb.2016.00660

Bik, E. M., Eckburg, P. B., Gill, S. R., Nelson, K. E., Purdom, E. A., Francois, F., Perez-Perez, G., Blaser, M. J., & Relman, D. A. (2006). *Molecular analysis of the bacterial microbiota in the human stomach*. www.pnas.orgcgidoi10.1073pnas.0506655103

Bisai, S., & Dutta, S. (2021). *TRADITIONAL FOOD PRACTICES OF LODHA: A GATHERING-HUNTING INDIGENOUS COMMUNITY OF WEST BENGAL, INDIA*. https://www.researchgate.net/publication/355436368

Borghini, A., & Piras, N. (2021). On Interpreting Something as Food. *Food Ethics*, *6*(1). https://doi.org/10.1007/s41055-020-00082-5

Bray, J. R., Curtis, J. T., & Roger, J. (1957). This content downloaded from 147.8.31.43 on Mon. In *Source: Ecological Monographs* (Vol. 27, Issue 4).

Chen, S., Zhou, Y., Chen, Y., & Gu, J. (2018). Fastp: An ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics*, *34*(17), i884–i890. https://doi.org/10.1093/bioinformatics/bty560

Clavenna, M. G., La Vecchia, M., Sculco, M., Joseph, S., Barberis, E., Amede, E., Mellai, M., Brossa, S., Borgonovi, G., Occhipinti, P., Boldorini, R., Robotti, E., Azzimonti, B., Bona, E., Pasolli, E., Ferrante, D., Manfredi, M., Aspesi, A., & Dianzani, I. (2023). Distinct Signatures of Tumor-Associated Microbiota and Metabolome in Low-Grade vs. High-Grade Dysplastic Colon Polyps: Inference of Their Role in Tumor Initiation and Progression. *Cancers*, *15*(12). https://doi.org/10.3390/cancers15123065

Clemente, J. C., Pehrsson, E. C., Blaser, M. J., Sandhu, K., Gao, Z., Wang, B., Magris, M., Hidalgo, G., Contreras, M., Noya-Alarcón, Ó., Lander, O., McDonald, J., Cox, M., Walter, J., Oh, P. L., Ruiz, J. F., Rodriguez, S., Shen, N., Song, S. J., … Dominguez-Bello, M. G. (2015). The microbiome of uncontacted Amerindians. *Science Advances*, *1*(3). https://doi.org/10.1126/sciadv.1500183

Constantinides, B., Hunt, M., & Crook, D. W. (2023). Hostile: accurate decontamination of microbial host sequences. *Bioinformatics*, *39*(12). https://doi.org/10.1093/bioinformatics/btad728

Conteville, L. C., Oliveira-Ferreira, J., & Vicente, A. C. P. (2019). Gut microbiome biomarkers and functional diversity within an Amazonian semi-nomadic hunter-gatherer group. *Frontiers in Microbiology*, *10*(JULY). https://doi.org/10.3389/fmicb.2019.01743

Cordain, L., Eaton, B., Sebastian, A., Mann, N., Lindeberg, S., Watkins, B. A., O'keefe, J. H., & Brand-Miller, J. (2005). *Origins and evolution of the Western diet: health implications for the 21st century 1,2*.

cummings1987. (n.d.).

De Filippo, C., Cavalieri, D., Di Paola, M., Ramazzotti, M., Poullet, J. B., Massart, S., Collini, S., Pieraccini, G., & Lionetti, P. (2010). Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa. *Proceedings of the National Academy of Sciences of the United States of America*, *107*(33), 14691–14696. https://doi.org/10.1073/pnas.1005963107

De Filippo, C., & Tuohy, K. M. (2015). A Nutritional Anthropology of the Human Gut Microbiota. In *Diet-Microbe Interactions in the Gut: Effects on Human Health and Disease* (pp. 17–26). Elsevier Inc. https://doi.org/10.1016/B978-0-12-407825-3.00002-2

Dehingia, M., Devi, K. T., Talukdar, N. C., Talukdar, R., Reddy, N., Mande, S. S., Deka, M., & Khan, M. R. (2015). Gut bacterial diversity of the tribes of India and comparison with the worldwide data. *Scientific Reports*, *5*. https://doi.org/10.1038/srep18563

Dhakan, D. B., Maji, A., Sharma, A. K., Saxena, R., Pulikkan, J., Grace, T., Gomez, A., Scaria, J., Amato, K. R., & Sharma, V. K. (2019). The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. *GigaScience*, *8*(3). https://doi.org/10.1093/gigascience/giz004

eaton1985. (n.d.).

Eckburg, P. B., Bik, E. M., Bernstein, C. N., Purdom, E., Dethlefsen, L., Sargent, M., Gill, S. R., Nelson, K. E., & Relman, D. A. (n.d.). *Diversity of the Human Intestinal Microbial Flora*. www.sciencemag.org/cgi/content/full/1110591/DC1

Eric A. Franzosa, Lauren J. McIver, Gholamali Rahnavard, Luke R. Thompson, Melanie Schirmer, George Weingart, Karen Schwarzberg Lipson, Rob Knight, J. Gregory Caporaso, Nicola Segata & Curtis Huttenhower. Species-level functional profiling of metagenomes and metatranscriptomes. Nat Methods. 2018. 15(11): 962–968.

Ewels, P., Magnusson, M., Lundin, S., & Käller, M. (n.d.). *Data and text mining MultiQC: Summarize analysis results for multiple tools and samples in a single report*. http://www.bioinformatics.babraham.ac.uk/projects/fastqc

Faveri, M., Mayer, M. P. A., Feres, M., De Figueiredo, L. C., Dewhirst, F. E., & Paster, B. J. (2008). Microbiological diversity of generalized aggressive periodontitis by 16S rRNA clonal analysis. *Oral Microbiology and Immunology*, *23*(2), 112–118. https://doi.org/10.1111/j.1399-302X.2007.00397.x

Flint, H. J., Scott, K. P., Duncan, S. H., Louis, P., & Forano, E. (2012). Microbial degradation of complex carbohydrates in the gut. In *Gut Microbes* (Vol. 3, Issue 4). https://doi.org/10.4161/gmic.19897

Fukuyama, J., Mcmurdie, P. J., Dethlefsen, L., Relman, D. A., & Holmes, S. (n.d.). *COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES*. http://stat.stanford.edu/~susan/projects/psb2012.pdf

Ganesh, B., Rajakumar, T., Acharya, S. K., Vasumathy, S., Sowmya, S., & Kaur, H. (2021). Particularly vulnerable tribal groups of Tamil Nadu, India: A sociocultural anthropological review. In *Indian journal of public health* (Vol. 65, Issue 4, pp. 403–409). NLM (Medline). https://doi.org/10.4103/ijph.IJPH_2_21

Ghonimy, A., Zhang, D. M., Farouk, M. H., & Wang, Q. (2018). The impact of carnitine on dietary fiber and gut bacteria metabolism and their mutual interaction in monogastrics. In *International Journal of Molecular Sciences* (Vol. 19, Issue 4). MDPI AG. https://doi.org/10.3390/ijms19041008

Gill, S. R., Pop, M., DeBoy, R. T., Eckburg, P. B., Turnbaugh, P. J., Samuel, B. S., Gordon, J. I., Relman, D. A., Fraser-Liggett, C. M., & Nelson, K. E. (2006). Metagenomic analysis of the human distal gut microbiome. *Science*, *312*(5778), 1355–1359. https://doi.org/10.1126/science.1124234

Gupta, V. K., Paul, S., & Dutta, C. (2017). Geography, ethnicity or subsistence-specific variations in human microbiome composition and diversity. In *Frontiers in Microbiology* (Vol. 8, Issue JUN). Frontiers Media S.A. https://doi.org/10.3389/fmicb.2017.01162

Handelsman, J. (2004). Metagenomics: Application of Genomics to Uncultured Microorganisms. *MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS*, *68*(4), 669–685. https://doi.org/10.1128/MBR.68.4.669-685.2004

Hansen, Z. A., Schilmiller, A. L., Guzior, D. V., Rudrik, J. T., Quinn, R. A., Vasco, K. A., & Manning, S. D. (2024). Shifts in the functional capacity and metabolite composition of the gut microbiome during recovery from enteric infection. *Frontiers in Cellular and Infection Microbiology*, *14*. https://doi.org/10.3389/fcimb.2024.1359576

Hassan Zafara and Milton H. Saier, Jr. Gut Bacteroides species in health and disease. Gut Microbes. 2021; 13(1): 1848158.

Hazarika, P., Chattopadhyay, I., Umpo, M., Choudhury, Y., & Sharma, I. (2022). Elucidating the gut microbiome alterations of tribal community of Arunachal Pradesh: perspectives on their lifestyle or food habits. *Scientific Reports*, *12*(1). https://doi.org/10.1038/s41598-022-23124-w

Huttenhower, C., Gevers, D., Knight, R., Abubucker, S., Badger, J. H., Chinwalla, A. T., Creasy, H. H., Earl, A. M., Fitzgerald, M. G., Fulton, R. S., Giglio, M. G., Hallsworth-Pepin, K., Lobos, E. A., Madupu, R., Magrini, V., Martin, J. C., Mitreva, M., Muzny, D. M., Sodergren, E. J., … White, O. (2012). Structure, function and diversity of the healthy human microbiome. *Nature*, *486*(7402), 207–214. https://doi.org/10.1038/nature11234

Hyman, R. W., Fukushima, M., Diamond, L., Kumm, J., Giudice, L. C., & Davis, R. W. (2005). *Microbes on the human vaginal epithelium*. www.psb.ugent.be

Laue, H. E., Karagas, M. R., Coker, M. O., Bellinger, D. C., Baker, E. R., Korrick, S. A., & Madan, J. C. (2022). Sex-specific relationships of the infant microbiome and early-childhood behavioral outcomes. *Pediatric Research*, *92*(2), 580–591. https://doi.org/10.1038/s41390-021-01785-z

Lévi, C., & Chapter One, S. (1962). *THE SAVAGE MIND*.

Li, M., Wang, B., Zhang, M., Rantalainen, M., Wang, S., Zhou, H., Zhang, Y., Shen, J., Pang, X., Zhang, M., Wei, H., Chen, Y., Lu, H., Zuo, J., Su, M., Qiu, Y., Jia, W., Chaoni, X. ¶, Smith, L. M., … Zhao, L. (2008). *Symbiotic gut microbes modulate human metabolic phenotypes*. www.pnas.org/cgi/content/full/

Liévin, V., Peiver, I., Hudault, S., Rochat, F., Brassart, D., Neeser, J.-R., & Servin, A. L. (n.d.). *Bifidobacterium strains from resident infant human gastrointestinal microflora exert antimicrobial activity*. www.gutjnl.com

Lin, R., Liu, W., Piao, M., & Zhu, H. (2017). A review of the relationship between the gut microbiota and amino acid metabolism. In *Amino Acids* (Vol. 49, Issue 12, pp. 2083–2090). Springer-Verlag Wien. https://doi.org/10.1007/s00726-017-2493-3

Liu, C., Cui, Y., Li, X., & Yao, M. (2021). Microeco: An R package for data mining in microbial community ecology. *FEMS Microbiology Ecology*, *97*(2). https://doi.org/10.1093/femsec/fiaa255

Liu, X. (2016). *Microbiome*.

Lozupone, C., & Knight, R. (2005). UniFrac: A new phylogenetic method for comparing microbial communities. *Applied and Environmental Microbiology*, *71*(12), 8228–8235. https://doi.org/10.1128/AEM.71.12.8228-8235.2005

Macfarlane, G. T., & Macfarlane, S. (2011). *Fermentation in the Human Large Intestine Its Physiologic Consequences and the Potential Contribution of Prebiotics*. www.jcge.com

Macfarlane, S., & Macfarlane, G. T. (2006). Composition and metabolic activities of bacterial biofilms colonizing food residues in the human gut. *Applied and Environmental Microbiology*, *72*(9), 6204–6211. https://doi.org/10.1128/AEM.00754-06

McMurdie, P. J., & Holmes, S. (2013). Phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. *PLoS ONE*, *8*(4). https://doi.org/10.1371/journal.pone.0061217

Meixia Li, Yeqing Wang, Ciliang Guo, Sheng Wang, Liangzhen Zheng, Yifan Bu, Kan Ding. The claim of primacy of human gut Bacteroides ovatus in dietary cellobiose degradation. Gut Microbes. 2023 Jan-Dec;15(1):2227

Methé, B. A., Nelson, K. E., Pop, M., Creasy, H. H., Giglio, M. G., Huttenhower, C., Gevers, D., Petrosino, J. F., Abubucker, S., Badger, J. H., Chinwalla, A. T., Earl, A. M., Fitzgerald, M. G., Fulton, R. S., Hallsworth-Pepin, K., Lobos, E. A., Madupu, R., Magrini, V., Martin, J. C., … White, O. (2012). A framework for human microbiome research. *Nature*, *486*(7402), 215–221. https://doi.org/10.1038/nature11209

Mohan, R. (2023). Food and Culture: An Anthropological Analysis. *International Journal of Research and Review*, *10*(8), 479–484. https://doi.org/10.52403/ijrr.20230860

Nicola Segata, Jacques Izard, Levi Waldron, Dirk Gevers, Larisa Miropolsky, Wendy S Garrett & Curtis Huttenhower. Metagenomic biomarker discovery and explanation. Genome Biology. 2011, 12:R60

Nie, C., He, T., Zhang, W., Zhang, G., & Ma, X. (2018). Branched chain amino acids: Beyond nutrition metabolism. In *International Journal of Molecular Sciences* (Vol. 19, Issue 4). MDPI AG. https://doi.org/10.3390/ijms19040954

Obregon-Tito, A. J., Tito, R. Y., Metcalf, J., Sankaranarayanan, K., Clemente, J. C., Ursell, L. K., Zech Xu, Z., Van Treuren, W., Knight, R., Gaffney, P. M., Spicer, P., Lawson, P., Marin-Reyes, L., Trujillo-Villarroel, O., Foster, M., Guija-Poma, E., Troncoso-Corzo, L., Warinner, C., Ozga, A. T., & Lewis, C. M. (2015). Subsistence strategies in traditional societies distinguish gut microbiomes. *Nature Communications*, *6*. https://doi.org/10.1038/ncomms7505

O'Hara, A. M., & Shanahan, F. (2006). The gut flora as a forgotten organ. In *EMBO Reports* (Vol. 7, Issue 7, pp. 688–693). https://doi.org/10.1038/sj.embor.7400731

Oliphant, K., & Allen-Vercoe, E. (2019). Macronutrient metabolism by the human gut microbiome: Major fermentation by-products and their impact on host health. *Microbiome*, *7*(1). https://doi.org/10.1186/s40168-019-0704-8

Patumcharoenpol, P., Kingkaw, A., Nakphaichit, M., Chatchatee, P., Suratannon, N., Panagiotou, G., & Vongsangnak, W. (2023). Exploring Longitudinal Gut Microbiome towards Metabolic Functional Changes Associated in Atopic Dermatitis in Early Childhood. *Biology*, *12*(9). https://doi.org/10.3390/biology12091262

Paul J. McMurdie, Susan Holmes. Phyloseq: An R package for reproducible interactive analysis and graphics of microbiome census data. 2013. PLoS ONE. 8(4):e61217

Peterson, J., Garges, S., Giovanni, M., McInnes, P., Wang, L., Schloss, J. A., Bonazzi, V., McEwen, J. E., Wetterstrand, K. A., Deal, C., Baker, C. C., Di Francesco, V., Howcroft, T. K., Karp, R. W., Lunsford, R. D., Wellington, C. R., Belachew, T., Wright, M., Giblin, C., … Guyer, M. (2009). The NIH Human Microbiome Project. *Genome Research*, *19*(12), 2317–2323. https://doi.org/10.1101/gr.096651.109

Phan, J., Nair, D., Jain, S., Montagne, T., Flores, D. V., Nguyen, A., Dietsche, S., Gombar, S., & Cotter, P. (2021). *Alterations in Gut Microbiome Composition and Function in Irritable Bowel Syndrome and Increased Probiotic Abundance with Daily Supplementation*. https://doi.org/10.1128/mSystems

Pnas, M. J. (2007). designed research. In *Z.G. performed research* (Vol. 104, Issue 8).

Qin, J., Li, R., Raes, J., Arumugam, M., Burgdorf, K. S., Manichanh, C., Nielsen, T., Pons, N., Levenez, F., Yamada, T., Mende, D. R., Li, J., Xu, J., Li, S., Li, D., Cao, J., Wang, B., Liang, H., Zheng, H., … Zoetendal, E. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, *464*(7285), 59–65. https://doi.org/10.1038/nature08821

Quince, C., Walker, A. W., Simpson, J. T., Loman, N. J., & Segata, N. (2017). Shotgun metagenomics, from sampling to analysis. In *Nature Biotechnology* (Vol. 35, Issue 9, pp. 833–844). Nature Publishing Group. https://doi.org/10.1038/nbt.3935

Rampelli, S., Schnorr, S. L., Consolandi, C., Turroni, S., Severgnini, M., Peano, C., Brigidi, P., Crittenden, A. N., Henry, A. G., & Candela, M. (2015). Metagenome Sequencing of the Hadza Hunter-Gatherer Gut Microbiota. *Current Biology*, *25*(13), 1682–1693. https://doi.org/10.1016/j.cub.2015.04.055

R Core Team. R: A language and environment for statistical computing. Foundation for Statistical Computing, Vienna, Austria. 2013.

Rao, K. M., Kumar, R. H., Krishna, K. S., Bhaskar, V., & Laxmaiah, A. (n.d.). *Diet & nutrition profile of Chenchu population-a vulnerable tribe in Telangana & Andhra Pradesh, India*.

Rodriguez-Diaz, C., Taminiau, B., García-García, A., Cueto, A., Robles-Díaz, M., Ortega-Alonso, A., Martín-Reyes, F., Daube, G., Sanabria-Cabrera, J., Jimenez-Perez, M., Isabel Lucena, M., Andrade, R. J., García-Fuentes, E., & García-Cortes, M. (2022). Microbiota diversity in nonalcoholic fatty liver disease and in drug-induced liver injury. *Pharmacological Research*, *182*. https://doi.org/10.1016/j.phrs.2022.106348

SAHLINS, M. D. (1961). The Segmentary Lineage: An Organization of Predatory Expansion 1 . *American Anthropologist*, *63*(2), 322–345. https://doi.org/10.1525/aa.1961.63.2.02a00050

Sarkar, P., Chatterjee, D., Bandyopadhyay, A. R., Dey, S., & Ratan Bandyopadhyay, A. (2018). To cite this article Saheli Dey, Pranabesh Sarkar, Diptendu Chatterjee, Arup Ratan Bandyopadhyay. Anthropology of Microbes: A Study on Kitchen Micro Flora from West Bengal. *India. International Journal of Microbiology and Application*, *5*(3), 46–49. http://www.openscienceonline.com/journal/ijma

Schnorr, S. L., Candela, M., Rampelli, S., Centanni, M., Consolandi, C., Basaglia, G., Turroni, S., Biagi, E., Peano, C., Severgnini, M., Fiori, J., Gotti, R., De Bellis, G., Luiselli, D., Brigidi, P., Mabulla, A., Marlowe, F., Henry, A. G., & Crittenden, A. N. (2014). Gut microbiome of the Hadza hunter-gatherers. *Nature Communications*, *5*. https://doi.org/10.1038/ncomms4654

Scott, K. P., Duncan, S. H., & Flint, H. J. (2008). Dietary fibre and the gut microbiota. In *Nutrition Bulletin* (Vol. 33, Issue 3, pp. 201–211). https://doi.org/10.1111/j.1467-3010.2008.00706.x

Segata, N., Waldron, L., Ballarini, A., Narasimhan, V., Jousson, O., & Huttenhower, C. (2012). Metagenomic microbial community profiling using unique clade-specific marker genes. *Nature Methods*, *9*(8), 811–814. https://doi.org/10.1038/nmeth.2066

Si, J., Lee, G., You, H. J., Joo, S. K., Lee, D. H., Ku, B. J., Park, S., Kim, W., & Ko, G. P. (2021). Gut microbiome signatures distinguish type 2 diabetes mellitus from non-alcoholic fatty liver disease. *Computational and Structural Biotechnology Journal*, *19*, 5920–5930. https://doi.org/10.1016/j.csbj.2021.10.032

Singh, R., Haque, M. M., & Mande, S. S. (2019). Lifestyle-Induced Microbial Gradients: An Indian Perspective. *Frontiers in Microbiology*, *10*. https://doi.org/10.3389/fmicb.2019.02874

Stanislas Mondot, Laurine Lachkar, Joël Doré, Hervé M Blottière, Mouna Hanachi. Roseburia, a decreased bacterial taxon in the gut microbiota of patients suffering from anorexia nervosa. European Journal of Clinical Nutrition volume 76, pages1486–1489 (2022)

Walker, A. W., Ince, J., Duncan, S. H., Webster, L. M., Holtrop, G., Ze, X., Brown, D., Stares, M. D., Scott, P., Bergerat, A., Louis, P., McIntosh, F., Johnstone, A. M., Lobley, G. E., Parkhill, J., & Flint, H. J. (2011). Dominant and diet-responsive groups of bacteria within the human colonic microbiota. *ISME Journal*, *5*(2), 220–230. https://doi.org/10.1038/ismej.2010.118

Woese, C. R., & Fox, G. E. (1977). *Phylogenetic structure of the prokaryotic domain: The primary kingdoms (archaebacteria/eubacteria/urkaryote/16S ribosomal RNA/molecular phylogeny)* (Vol. 74, Issue 11). https://www.pnas.org

Wood, D. E., & Salzberg, S. L. (2014). *Kraken: ultrafast metagenomic sequence classification using exact alignments*. http://ccb.jhu.edu/software/kraken/.

Yadav, M., Verma, M. K., & Chauhan, N. S. (2018). A review of metabolic potential of human gut microbiome in human nutrition. In *Archives of Microbiology* (Vol. 200, Issue 2, pp. 203–217). Springer Verlag. https://doi.org/10.1007/s00203-017-1459-x

Annexures

ANNEXURE- I

Conserved gut-microbial core pathways among six PVTGs (detection = 0.001, prevalence = 0.5)

Pathways	Superclass I	Superclass II
GOLPDLCAT-PWY: superpathway of glycerol degradation to 1,3-propanediol	Degradation/Utilization/Assimilation	Alcohol Degradation
PWY-7013: (S)-propane-1,2-diol degradation	Degradation/Utilization/Assimilation	Alcohol Degradation
PWY66-389: phytol degradation	Degradation/Utilization/Assimilation	Alcohol Degradation
PWY-6305: superpathway of putrescine biosynthesis	Biosynthesis	Amide, Amidine, Amine, and Polyamine Biosynthesis
ARG+POLYAMINE-SYN: superpathway of arginine and polyamine biosynthesis	Biosynthesis	Amine and Polyamine Biosynthesis
POLYAMINSYN3-PWY: superpathway of polyamine biosynthesis II	Biosynthesis	Amine and Polyamine Biosynthesis
POLYAMSYN-PWY: superpathway of polyamine biosynthesis I	Biosynthesis	Amine and Polyamine Biosynthesis
GLCMANNANAUT-PWY: superpathway of N-acetylglucosamine, N-acetylmannosamine and N-acetylneuraminate degradation	Degradation/Utilization/Assimilation	Amine and Polyamine Degradation
GLUDEG-I-PWY: GABA shunt	Degradation/Utilization/Assimilation	Amine and Polyamine Degradation
ORNDEG-PWY: superpathway of ornithine degradation	Degradation/Utilization/Assimilation	Amine and Polyamine Degradation
PWY0-1477: ethanolamine utilization	Degradation/Utilization/Assimilation	Amine and Polyamine Degradation
ARGSYN-PWY: L-arginine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis

(via L-ornithine)		
ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)	Biosynthesis	Amino Acid Biosynthesis
ASPASN-PWY: superpathway of L-aspartate and L-asparagine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched chain amino acid biosynthesis	Biosynthesis	Amino Acid Biosynthesis
CITRULBIO-PWY: L-citrulline biosynthesis	Biosynthesis	Amino Acid Biosynthesis
COMPLETE-ARO-PWY: superpathway of aromatic amino acid biosynthesis	Biosynthesis	Amino Acid Biosynthesis
DAPLYSINESYN-PWY: L-lysine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis
GLUTORN-PWY: L-ornithine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis
HISTSYN-PWY: L-histidine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
HOMOSER-METSYN-PWY: L-methionine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis
HSERMETANA-PWY: L-methionine biosynthesis III	Biosynthesis	Amino Acid Biosynthesis
ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)	Biosynthesis	Amino Acid Biosynthesis
METSYN-PWY: superpathway of L-homoserine and L-methionine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
P4-PWY: superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis

PWY-2941: L-lysine biosynthesis II	Biosynthesis	Amino Acid Biosynthesis
PWY-2942: L-lysine biosynthesis III	Biosynthesis	Amino Acid Biosynthesis
PWY-3001: superpathway of L-isoleucine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis
PWY-5097: L-lysine biosynthesis VI	Biosynthesis	Amino Acid Biosynthesis
PWY-5103: L-isoleucine biosynthesis III	Biosynthesis	Amino Acid Biosynthesis
PWY-5154: L-arginine biosynthesis III (via N-acetyl-L-citrulline)	Biosynthesis	Amino Acid Biosynthesis
PWY-5345: superpathway of L-methionine biosynthesis (by sulfhydrylation)	Biosynthesis	Amino Acid Biosynthesis
PWY-5347: superpathway of L-methionine biosynthesis (transsulfuration)	Biosynthesis	Amino Acid Biosynthesis
PWY-5505: L-glutamate and L-glutamine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
PWY-6292: superpathway of L-cysteine biosynthesis (mammalian)	Biosynthesis	Amino Acid Biosynthesis
PWY-6549: L-glutamine biosynthesis III	Biosynthesis	Amino Acid Biosynthesis
PWY-6628: superpathway of L-phenylalanine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
PWY-6629: superpathway of L-tryptophan biosynthesis	Biosynthesis	Amino Acid Biosynthesis
PWY-6630: superpathway of L-tyrosine biosynthesis	Biosynthesis	Amino Acid Biosynthesis

PWY-6936: seleno-amino acid biosynthesis (plants)	Biosynthesis	Amino Acid Biosynthesis
PWY-702: L-methionine biosynthesis II	Biosynthesis	Amino Acid Biosynthesis
PWY-724: superpathway of L-lysine, L-threonine and L-methionine biosynthesis II	Biosynthesis	Amino Acid Biosynthesis
PWY-7400: L-arginine biosynthesis IV (archaebacteria)	Biosynthesis	Amino Acid Biosynthesis
PWY-821: superpathway of sulfur amino acid biosynthesis (Saccharomyces cerevisiae)	Biosynthesis	Amino Acid Biosynthesis
PWY-I9: L-cysteine biosynthesis VI (from L-methionine)	Biosynthesis	Amino Acid Biosynthesis
PWY0-1061: superpathway of L-alanine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis I	Biosynthesis	Amino Acid Biosynthesis
THRESYN-PWY: superpathway of L-threonine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
TRPSYN-PWY: L-tryptophan biosynthesis	Biosynthesis	Amino Acid Biosynthesis
VALSYN-PWY: L-valine biosynthesis	Biosynthesis	Amino Acid Biosynthesis
ARGININE-SYN4-PWY: L-ornithine biosynthesis II	Biosynthesis	Amino Acid Biosynthesis
PWY-7977: L-methionine biosynthesis IV	Biosynthesis	Amino Acid Biosynthesis
HISDEG-PWY: L-histidine degradation I	Degradation/Utilization/Assimilation	Amino Acid Degradation
PWY-5030: L-histidine	Degradation/Utilization/Assimila	Amino Acid Degradation

degradation III	tion	
PWY-8187: L-arginine degradation XIII (reductive Stickland reaction)	Degradation/Utilization/Assimilation	Amino Acid Degradation
TRNA-CHARGING-PWY: tRNA charging	Biosynthesis	Aminoacyl-tRNA Charging
ARO-PWY: chorismate biosynthesis I	Biosynthesis	Aromatic Compound Biosynthesis
PWY-6163: chorismate biosynthesis from 3-dehydroquinate	Biosynthesis	Aromatic Compound Biosynthesis
PWY-6210: 2-aminophenol degradation	Degradation/Utilization/Assimilation	Aromatic Compound Degradation
P185-PWY: formaldehyde assimilation III (dihydroxyacetone cycle)	Degradation/Utilization/Assimilation	C1 Compound Utilization and Assimilation
P23-PWY: reductive TCA cycle I	Degradation/Utilization/Assimilation	C1 Compound Utilization and Assimilation
P42-PWY: incomplete reductive TCA cycle	Degradation/Utilization/Assimilation	C1 Compound Utilization and Assimilation
PWY-6969: TCA cycle V (2-oxoglutarate synthase)	Degradation/Utilization/Assimilation	C1 Compound Utilization and Assimilation
PWY-1861: formaldehyde assimilation II (assimilatory RuMP Cycle)	Degradation/Utilization/Assimilation	C1 Compound Utilization and Assimilation
CALVIN-PWY: Calvin-Benson-Bassham cycle	Biosynthesis	Carbohydrate Biosynthesis
COA-PWY: coenzyme A biosynthesis I (prokaryotic)	Biosynthesis	Carbohydrate Biosynthesis
COLANSYN-PWY: colanic acid building blocks biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
DTDPRHAMSYN-PWY: dTDP-β-L-rhamnose biosynthesis	Biosynthesis	Carbohydrate Biosynthesis

GLUCONEO-PWY: gluconeogenesis I	Biosynthesis	Carbohydrate Biosynthesis
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)	Biosynthesis	Carbohydrate Biosynthesis
OANTIGEN-PWY: O-antigen building blocks biosynthesis (E. coli)	Biosynthesis	Carbohydrate Biosynthesis
PWY-5659: GDP-mannose biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
PWY-7238: sucrose biosynthesis II	Biosynthesis	Carbohydrate Biosynthesis
PWY-7315: dTDP-N-acetylthomosamine biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
PWY-7323: superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
PWY-7328: superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
PWY0-1241: ADP-L-glycero-β-D-manno-heptose biosynthesis	Biosynthesis	Carbohydrate Biosynthesis
PWY66-399: gluconeogenesis III	Biosynthesis	Carbohydrate Biosynthesis
UDPNAGSYN-PWY: UDP-N-acetyl-D-glucosamine biosynthesis I	Biosynthesis	Carbohydrate Biosynthesis
PWY-1269: CMP-3-deoxy-D-manno-octulosonate biosynthesis	Biosynthesis	Carbohydrate Biosynthesis → Sugar Biosynthesis
FUCCAT-PWY: fucose degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
GLUCOSE1PMETAB-	Degradation/Utilization/Assimila	Carbohydrate Degradation

PWY: glucose and glucose-1-phosphate degradation	tion	
LACTOSECAT-PWY: lactose and galactose degradation I	Degradation/Utilization/Assimilation	Carbohydrate Degradation
P124-PWY: Bifidobacterium shunt	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-5384: sucrose degradation IV (sucrose phosphorylase)	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-5941: glycogen degradation II	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-6527: stachyose degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-6731: starch degradation III	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-6901: superpathway of glucose and xylose degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-6902: chitin degradation II (Vibrio)	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-6992: 1,5-anhydrofructose degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-7118: chitin deacetylation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-7345: superpathway of anaerobic sucrose degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-8004: Entner-Doudoroff pathway I	Degradation/Utilization/Assimilation	Carbohydrate Degradation
RHAMCAT-PWY: L-rhamnose degradation I	Degradation/Utilization/Assimilation	Carbohydrate Degradation
GLUCUROCAT-PWY: superpathway of β-D-glucuronosides degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
GLYCOCAT-PWY:	Degradation/Utilization/Assimila	Carbohydrate Degradation

glycogen degradation I	tion	
PWY-6317: D-galactose degradation I (Leloir pathway)	Degradation/Utilization/Assimilation	Carbohydrate Degradation
PWY-7456: β-(1,4)-mannan degradation	Degradation/Utilization/Assimilation	Carbohydrate Degradation
GALACTARDEG-PWY: D-galactarate degradation I	Degradation/Utilization/Assimilation	Carboxylate Degradation
GALACTUROCAT-PWY: D-galacturonate degradation I	Degradation/Utilization/Assimilation	Carboxylate Degradation
GLUCARDEG-PWY: D-glucarate degradation I	Degradation/Utilization/Assimilation	Carboxylate Degradation
KETOGLUCONMET-PWY: ketogluconate metabolism	Degradation/Utilization/Assimilation	Carboxylate Degradation
P441-PWY: superpathway of N-acetylneuraminate degradation	Degradation/Utilization/Assimilation	Carboxylate Degradation
P461-PWY: hexitol fermentation to lactate, formate, ethanol and acetate	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY-5100: pyruvate fermentation to acetate and lactate II	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY-5130: 2-oxobutanoate degradation I	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY-6961: L-ascorbate degradation II (bacterial, aerobic)	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY-7242: D-fructuronate degradation	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY0-301: L-ascorbate degradation I (bacterial, anaerobic)	Degradation/Utilization/Assimilation	Carboxylate Degradation
PWY0-42: 2-	Degradation/Utilization/Assimila	Carboxylate Degradation

methylcitrate cycle I	tion	
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Biosynthesis	Cell Structure Biosynthesis
PWY-5265: peptidoglycan biosynthesis II (staphylococci)	Biosynthesis	Cell Structure Biosynthesis
PWY-6385: peptidoglycan biosynthesis III (mycobacteria)	Biosynthesis	Cell Structure Biosynthesis
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Biosynthesis	Cell Structure Biosynthesis
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Biosynthesis	Cell Structure Biosynthesis
PWY-6470: peptidoglycan biosynthesis V (β-lactam resistance)	Biosynthesis	Cell Structure Biosynthesis
PWY-8073: lipid IVA biosynthesis (P. putida)	Biosynthesis	Cell Structure Biosynthesis
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)	Biosynthesis	Cell Structure Biosynthesis
NAGLIPASYN-PWY: lipid IVA biosynthesis (E. coli)	Biosynthesis	Cell Structure Biosynthesis
PWY-7953: UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)	Biosynthesis	Cell Structure Biosynthesis

1CMET2-PWY: folate transformations III (E. coli)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
COBALSYN-PWY: superpathway of adenosylcobalamin salvage from cobinamide I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
FOLSYN-PWY: superpathway of tetrahydrofolate biosynthesis and salvage	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
HEME-BIOSYNTHESIS-II: heme b biosynthesis I (aerobic)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PANTO-PWY: phosphopantothenate biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-3841: folate transformations II (plants)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-4041: gamma;-glutamyl cycle	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5005: biotin biosynthesis II	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5838: superpathway of menaquinol-8 biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5840: superpathway of menaquinol-7 biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5861: superpathway of demethylmenaquinol-8 biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5897: superpathway of menaquinol-11 biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis

PWY-5898: superpathway of menaquinol-12 biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5899: superpathway of menaquinol-13 biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-5918: superpathway of heme b biosynthesis from glutamate	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6147: 6-hydroxymethyl-dihydropterin diphosphate biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6151: S-adenosyl-L-methionine salvage I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6612: superpathway of tetrahydrofolate biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6823: molybdopterin biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6895: superpathway of thiamine diphosphate biosynthesis II	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6897: thiamine diphosphate salvage II	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-7282: 4-amino-2-methyl-5-diphosphomethylpyrimidine biosynthesis II	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-7356: thiamine diphosphate salvage IV (yeast)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-7761: NAD salvage pathway II (PNC IV cycle)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis

PWY-7851: coenzyme A biosynthesis II (eukaryotic)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY0-845: superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY3O-4107: NAD salvage pathway V (PNC V cycle)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PYRIDNUCSAL-PWY: NAD salvage pathway I (PNC VI cycle)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PYRIDNUCSYN-PWY: NAD de novo biosynthesis I (from aspartate)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PYRIDOXSYN-PWY: pyridoxal 5'-phosphate biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
RIBOSYN2-PWY: flavin biosynthesis I (bacteria and plants)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
BIOTIN-BIOSYNTHESIS-PWY: biotin biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
COA-PWY-1: superpathway of coenzyme A biosynthesis III (mammals)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
HEME-BIOSYNTHESIS-II-1: heme b biosynthesis V (aerobic)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
HEMESYN2-PWY: heme b biosynthesis II (oxygen-independent)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PANTOSYN-PWY: superpathway of coenzyme A biosynthesis I (bacteria)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis

PWY-5837: 2-carboxy-1,4-naphthoquinol biosynthesis	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-6892: thiazole component of thiamine diphosphate biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-7357: thiamine phosphate formation from pyrithiamine and oxythiamine (yeast)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY0-1415: superpathway of heme b biosynthesis from uroporphyrinogen-III	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
THISYN-PWY: superpathway of thiamine diphosphate biosynthesis I	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
THISYNARA-PWY: superpathway of thiamine diphosphate biosynthesis III (eukaryotes)	Biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis
PWY-7237: myo-, chiro- and scyllo-inositol degradation	Degradation/Utilization/Assimilation	Cyclitol Degradation
PWY-7883: anhydromuropeptides recycling II	Degradation/Utilization/Assimilation	Degradation/Utilization/Assimilation - Other
PWY0-1261: anhydromuropeptides recycling I	Degradation/Utilization/Assimilation	Degradation/Utilization/Assimilation - Other
FASYN-ELONG-PWY: fatty acid elongation -- saturated	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PHOSLIPSYN-PWY: superpathway of phospholipid biosynthesis I (bacteria)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-5367: petroselinate biosynthesis	Biosynthesis	Fatty Acid and Lipid Biosynthesis

PWY-5667: CDP-diacylglycerol biosynthesis I	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-5973: cis-vaccenate biosynthesis	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-5981: CDP-diacylglycerol biosynthesis III	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-5989: stearate biosynthesis II (bacteria and plants)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-6282: palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-6284: superpathway of unsaturated fatty acids biosynthesis (E. coli)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-6285: superpathway of fatty acids biosynthesis (E. coli)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-6803: phosphatidylcholine acyl editing	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-7663: gondoate biosynthesis (anaerobic)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-7664: oleate biosynthesis IV (anaerobic)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-7858: (5Z)-dodecenoate biosynthesis II	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY0-1319: CDP-diacylglycerol biosynthesis II	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY0-862: (5Z)-dodecenoate biosynthesis I	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY4FS-7: phosphatidylglycerol	Biosynthesis	Fatty Acid and Lipid Biosynthesis

biosynthesis I (plastidic)		
PWY4FS-8: phosphatidylglycerol biosynthesis II (non-plastidic)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY-5971: palmitate biosynthesis (type II fatty acid synthase)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
PWY66-429: fatty acid biosynthesis initiation (mitochondria)	Biosynthesis	Fatty Acid and Lipid Biosynthesis
FAO-PWY: fatty acid β-oxidation I (generic)	Degradation/Utilization/Assimilation	Fatty Acid and Lipid Degradation
PWY-5136: fatty acid β-oxidation II (plant peroxisome)	Degradation/Utilization/Assimilation	Fatty Acid and Lipid Degradation
ANAEROFRUCAT-PWY: homolactic fermentation	Generation of Precursor Metabolites and Energy	Fermentation
CENTFERM-PWY: pyruvate fermentation to butanoate	Generation of Precursor Metabolites and Energy	Fermentation
FERMENTATION-PWY: mixed acid fermentation	Generation of Precursor Metabolites and Energy	Fermentation
P108-PWY: pyruvate fermentation to propanoate I	Generation of Precursor Metabolites and Energy	Fermentation
P122-PWY: heterolactic fermentation	Generation of Precursor Metabolites and Energy	Fermentation
PWY-5676: acetyl-CoA fermentation to butanoate II	Generation of Precursor Metabolites and Energy	Fermentation
PWY-6588: pyruvate fermentation to acetone	Generation of Precursor Metabolites and Energy	Fermentation
PWY-6590: superpathway of Clostridium acetobutylicum acidogenic fermentation	Generation of Precursor Metabolites and Energy	Fermentation

PWY-7111: pyruvate fermentation to isobutanol (engineered)	Generation of Precursor Metabolites and Energy	Fermentation
PWY-7383: anaerobic energy metabolism (invertebrates, cytosol)	Generation of Precursor Metabolites and Energy	Fermentation
PWY4LZ-257: superpathway of fermentation (Chlamydomonas reinhardtii)	Generation of Precursor Metabolites and Energy	Fermentation
P41-PWY: pyruvate fermentation to acetate and (S)-lactate I	Generation of Precursor Metabolites and Energy	Fermentation
GLYOXYLATE-BYPASS: glyoxylate cycle	Generation of Precursor Metabolites and Energy	Generation of Precursor Metabolites and Energy
PWY-5723: Rubisco shunt	Generation of Precursor Metabolites and Energy	Generation of Precursor Metabolites and Energy
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)	Generation of Precursor Metabolites and Energy	Glycolysis
GLYCOLYSIS: glycolysis I (from glucose 6-phosphate)	Generation of Precursor Metabolites and Energy	Glycolysis
PWY-1042: glycolysis IV	Generation of Precursor Metabolites and Energy	Glycolysis
PWY-5484: glycolysis II (from fructose 6-phosphate)	Generation of Precursor Metabolites and Energy	Glycolysis
PWY-4984: urea cycle	Degradation/Utilization/Assimilation	Inorganic Nutrient Metabolism
PWY-5675: nitrate reduction V (assimilatory)	Degradation/Utilization/Assimilation	Inorganic Nutrient Metabolism
PWY1ZNC-1: assimilatory sulfate reduction IV	Degradation/Utilization/Assimilation	Inorganic Nutrient Metabolism
SULFATE-CYS-PWY: superpathway of sulfate assimilation and cysteine biosynthesis	Degradation/Utilization/Assimilation	Inorganic Nutrient Metabolism

SO4ASSIM-PWY: assimilatory sulfate reduction I	Degradation/Utilization/Assimilation	Inorganic Nutrient Metabolism
PPGPPMET-PWY: ppGpp metabolism	Biosynthesis	Metabolic Regulator Biosynthesis
PWY0-1479: tRNA processing	Macromolecule Modification	Nucleic Acid Processing
PWY-6700: queuosine biosynthesis I (de novo)	Macromolecule Modification	Nucleic Acid Processing
PWY-5686: UMP biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6123: inosine-5'-phosphate biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6124: inosine-5'-phosphate biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6125: superpathway of guanosine nucleotides de novo biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6126: superpathway of adenosine nucleotides de novo biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6545: pyrimidine deoxyribonucleotides de novo biosynthesis III	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-6609: adenine and adenosine salvage III	Biosynthesis	Nucleoside and Nucleotide Biosynthesis

PWY-7184: pyrimidine deoxyribonucleotides de novo biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7197: pyrimidine deoxyribonucleotide phosphorylation	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7198: pyrimidine deoxyribonucleotides de novo biosynthesis IV	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7199: pyrimidine deoxyribonucleosides salvage	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7208: superpathway of pyrimidine nucleobases salvage	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7211: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7221: guanosine ribonucleotides de novo biosynthesis	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7229: superpathway of adenosine nucleotides de novo biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7234: inosine-5'-phosphate biosynthesis III	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7790: UMP biosynthesis II	Biosynthesis	Nucleoside and Nucleotide Biosynthesis

PWY-841: superpathway of purine nucleotides de novo biosynthesis I	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY0-162: superpathway of pyrimidine ribonucleotides de novo biosynthesis	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY0-166: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY66-409: superpathway of purine nucleotide salvage	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
PWY-7791: UMP biosynthesis III	Biosynthesis	Nucleoside and Nucleotide Biosynthesis
P161-PWY: acetylene degradation (anaerobic)	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-5497: purine nucleobases degradation II (anaerobic)	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6353: purine nucleotides degradation II (aerobic)	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6595: superpathway of guanosine nucleotides degradation (plants)	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6606: guanosine nucleotides degradation II	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6607: guanosine nucleotides degradation I	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6608: guanosine nucleotides degradation III	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-8131: 5'-deoxyadenosine degradation II	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation

PWY0-1296: purine ribonucleosides degradation	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY0-1297: superpathway of purine deoxyribonucleosides degradation	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY0-1298: superpathway of pyrimidine deoxyribonucleosides degradation	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
SALVADEHYPOX-PWY: adenosine nucleotides degradation II	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
P164-PWY: purine nucleobases degradation I (anaerobic)	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-5695: inosine 5'-phosphate degradation	Degradation/Utilization/Assimilation	Nucleoside and Nucleotide Degradation
PWY-6519: 8-amino-7-oxononanoate biosynthesis I	Biosynthesis	Other Biosynthesis
NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch) I	Generation of Precursor Metabolites and Energy	Pentose Phosphate Pathways
PENTOSE-P-PWY: pentose phosphate pathway	Generation of Precursor Metabolites and Energy	Pentose Phosphate Pathways
PWY-8178: pentose phosphate pathway (non-oxidative branch) II	Generation of Precursor Metabolites and Energy	Pentose Phosphate Pathways
PWY-241: C4 photosynthetic carbon assimilation cycle, NADP-ME type	Generation of Precursor Metabolites and Energy	Photosynthesis
PWY-7115: C4 photosynthetic carbon assimilation cycle, NAD-ME type	Generation of Precursor Metabolites and Energy	Photosynthesis

PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type	Generation of Precursor Metabolites and Energy	Photosynthesis
POLYISOPRENSYN-PWY: polyisoprenoid biosynthesis (E. coli)	Biosynthesis	Polyprenyl Biosynthesis
PWY-5121: superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	Biosynthesis	Polyprenyl Biosynthesis
METH-ACETATE-PWY: methanogenesis from acetate	Generation of Precursor Metabolites and Energy	Respiration
NONMEVIPP-PWY: methylerythritol phosphate pathway I	Biosynthesis	Secondary Metabolite Biosynthesis
PWY-6270: isoprene biosynthesis I	Biosynthesis	Secondary Metabolite Biosynthesis
PWY-6703: preQ0 biosynthesis	Biosynthesis	Secondary Metabolite Biosynthesis
PWY-7560: methylerythritol phosphate pathway II	Biosynthesis	Secondary Metabolite Biosynthesis
GALACTITOLCAT-PWY: galactitol degradation	Degradation/Utilization/Assimilation	Secondary Metabolite Degradation
PWY-6507: 4-deoxy-L-threo-hex-4-enopyranuronate degradation	Degradation/Utilization/Assimilation	Secondary Metabolite Degradation
PWY-6531: mannitol cycle	Degradation/Utilization/Assimilation	Secondary Metabolite Degradation
FUC-RHAMCAT-PWY: superpathway of fucose and rhamnose degradation	Superpathways	Superpathways
GALACT-GLUCUROCAT-PWY: superpathway of hexuronide and	Superpathways	Superpathways

hexuronate degradation		
GLUCARGALACTSUPER-PWY: superpathway of D-glucarate and D-galactarate degradation	Superpathways	Superpathways
MET-SAM-PWY: superpathway of S-adenosyl-L-methionine biosynthesis	Superpathways	Superpathways
PWY-561: superpathway of glyoxylate cycle and fatty acid degradation	Generation of Precursor Metabolites and Energy	Superpathways
PWY0-781: aspartate superpathway	Superpathways	Superpathways
GLYCOLYSIS-E-D: superpathway of glycolysis and the Entner-Doudoroff pathway	Generation of Precursor Metabolites and Energy	Superpathways
P105-PWY: TCA cycle IV (2-oxoglutarate decarboxylase)	Generation of Precursor Metabolites and Energy	TCA cycle
PWY-5690: TCA cycle II (plants and fungi)	Generation of Precursor Metabolites and Energy	TCA cycle
PWY-5913: partial TCA cycle (obligate autotrophs)	Generation of Precursor Metabolites and Energy	TCA cycle
REDCITCYC: TCA cycle VI (Helicobacter)	Generation of Precursor Metabolites and Energy	TCA cycle
TCA: TCA cycle I (prokaryotic)	Generation of Precursor Metabolites and Energy	TCA cycle
PWY-5188: tetrapyrrole biosynthesis I (from glutamate)	Biosynthesis	Tetrapyrrole Biosynthesis
PWY-5189: tetrapyrrole biosynthesis II (from glycine)	Biosynthesis	Tetrapyrrole Biosynthesis

ANNEXURE- II

Distinct gut-microbial core pathways among the six PVTGs (detection = 0.001, prevalence = 0.5)

KND	Superclasses	LOD	Superclasses
ALLANTOINDEG-PWY: superpathway of allantoin degradation in yeast	Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation → Allantoin Degradation Superpathways	PWY-922: mevalonate pathway I (eukaryotes and bacteria)	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid Biosynthesis → Hemiterpene Biosynthesis → Isopentenyl Diphosphate Biosynthesis → Mevalonate Pathways
ARGDEG-PWY: superpathway of L-arginine, putrescine, and 4-aminobutanoate degradation	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-arginine Degradation Superpathways		
ORNARGDEG-PWY: superpathway of L-arginine and L-ornithine degradation	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-arginine Degradation Superpathways		
PWY-5004: superpathway of L-citrulline metabolism	Biosynthesis → Amino Acid Biosynthesis → Other Amino Acid Biosynthesis → L-citrulline Biosynthesis Superpathways		
PWY-5392: reductive TCA cycle II	Degradation/Utilization/Assimilation → C1 Compound Utilization and Assimilation → CO2 Fixation →		

	Autotrophic CO2 Fixation → Reductive TCA Cycles		
PWY-8086: (S)-lactate fermentation to propanoate, acetate and hydrogen	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Propanoate		
BIR	**Superclasses**	**KOL**	**Superclasses**
CARNMET-PWY: L-carnitine degradation I	Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation → L-Carnitine Degradation; Generation of Precursor Metabolites and Energy → Respiration → Anaerobic Respiration	FASYN-INITIAL-PWY: superpathway of fatty acid biosynthesis initiation	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis → Fatty Acid Biosynthesis Initiation -Superpathways
PWY-5464: superpathway of cytosolic glycolysis (plants), pyruvate dehydrogenase and TCA cycle	Generation of Precursor Metabolites and Energy - Superpathways	PWY-6435: 4-hydroxybenzoate biosynthesis III (plants)	Biosynthesis → Aromatic Compound Biosynthesis → 4-Hydroxybenzoate Biosynthesis
PWY-6876: isopropanol biosynthesis (engineered)	Generation of Precursor Metabolites and Energy	PWY-7196: superpathway of pyrimidine ribonucleosides salvage	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide Salvage - Superpathways
CHE/KND	**Superclasses**	**CHE/BIR**	**Superclasses**
PWY-5896: superpathway of menaquinol-10 biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis →	KDO-NAGLIPASYN-PWY: superpathway of (Kdo)2-lipid A biosynthesis	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis; Biosynthesis → Fatty Acid and Lipid Biosynthesis; Glycan Pathways → Lipopolysaccharide Biosynthesis - Superpathways

	Menaquinol Biosynthesis - Superpathways		
		PWY-5705: allantoin degradation to glyoxylate III	Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation → Allantoin Degradation - Superpathways
KND/BIR	**Superclasses**	**LOD/BIR**	**Superclasses**
GLYCOLYSIS-TCA-GLYOX-BYPASS: superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass	Generation of Precursor Metabolites and Energy - Superpathways	LIPASYN-PWY: phospholipases	Degradation/Utilization/Assimilation → Fatty Acid and Lipid Degradation; Metabolic Clusters
PWY-7446: sulfoquinovose degradation I	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sulfoquinovose Degradation		
PWY-7616: methanol oxidation to carbon dioxide	Degradation/Utilization/Assimilation → Alcohol Degradation; Detoxification - Superpathways		
PWY0-1221: putrescine degradation II	Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation → Putrescine Degradation		
CHE/KND/BIR	**Superclasses**	**CHE/KND/KOL**	**Superclasses**
DENOVOPURINE2-PWY: superpathway of purine nucleotides de novo biosynthesis II	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Purine Nucleotide Biosynthesis → Purine Nucleotide De Novo Biosynthesis- Superpathways	PWY-5022: 4-aminobutanoate degradation V	Degradation/Utilization/Assimilation → Amide, Amidine, Amine, and Polyamine Degradation → 4-Aminobutanoate Degradation; Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Short-Chain Fatty Acids → Fermentation to Butanoate

ECASYN-PWY: enterobacterial common antigen biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Polysaccharide Biosynthesis; Glycan Pathways → Polysaccharide Biosynthesis	PWY-622: starch biosynthesis	Biosynthesis → Carbohydrate Biosynthesis → Polysaccharide Biosynthesis → Glycogen and Starch Biosynthesis; Glycan Pathways → Polysaccharide Biosynthesis → Glycogen and Starch Biosynthesis
PRPP-PWY	Superpathways	PWY-7992: superpathway of menaquinol-8 biosynthesis III	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis- Superpathways
PWY-5845: superpathway of menaquinol-9 biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis- Superpathways		
PWY-5850: superpathway of menaquinol-6 biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Menaquinol Biosynthesis - Superpathways		
PWY-5855: ubiquinol-7 biosynthesis (early decarboxylation)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Ubiquinol		

	Biosynthesis
PWY-5860: superpathway of demethylmenaquinol-6 biosynthesis I	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Demethylmenaquinol Biosynthesis → Demethylmenaquinol-6 Biosynthesis-Superpathways
PWY-5862: superpathway of demethylmenaquinol-9 biosynthesis	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → Demethylmenaquinol Biosynthesis-Superpathways
PWY-7187: pyrimidine deoxyribonucleotides de novo biosynthesis II	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → 2'-Deoxyribonucleotide Biosynthesis → Pyrimidine Deoxyribonucleotide De Novo Biosynthesis; Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide De Novo Biosynthesis → Pyrimidine Deoxyribonucleotide De Novo Biosynthesis
PWY-7204: pyridoxal 5'-phosphate	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis

salvage II (plants)	→ Enzyme Cofactor Biosynthesis → Vitamin B6 Biosynthesis; Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Vitamin Biosynthesis → Vitamin B6 Biosynthesis
PWY-7269: mitochondrial NADPH production (yeast)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → NAD Metabolism; Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → NAD Metabolism
PWY0-1277: 3-phenylpropanoate and 3-(3-hydroxyphenyl) propanoate degradation	Degradation/Utilization/Assimilation → Aromatic Compound Degradation-Superpathways
PWY0-1338: polymyxin resistance	Biosynthesis → Cell Structure Biosynthesis → Lipopolysaccharide Biosynthesis; Detoxification → Antibiotic Resistance; Glycan Pathways → Lipopolysaccharide Biosynthesis
THREOCAT-PWY: superpathway of L-threonine metabolism	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-threonine Degradation-Superpathways

KND/LOD/BIR	**Superclasses**	**CHE/KND/LOD/**	**Superclasses**

BIR

P125-PWY: superpathway of (R,R)-butanediol biosynthesis	Biosynthesis → Other Biosynthesis → Butanediol Biosynthesis- Superpathways	DARABCATK12-PWY: D-arabinose degradation II	Degradation/Utilization/Assimilation → Carbohydrate Degradation → Sugar Degradation → D-arabinose Degradation
		GLYCOL-GLYOXDEG-PWY: superpathway of glycol metabolism and degradation	Degradation/Utilization/Assimilation → Alcohol Degradation- Superpathways
		HCAMHPDEG-PWY: 3-phenylpropanoate and 3-(3-hydroxyphenyl)propanoate degradation to 2-hydroxypentadienoate	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Phenolic Compound Degradation
		P221-PWY: octane oxidation	Degradation/Utilization/Assimilation → Degradation/Utilization/Assimilation - Other
		PWY-6168: flavin biosynthesis III (fungi)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Flavin Biosynthesis; Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Flavin Biosynthesis
		PWY-6690: cinnamate and 3-hydroxycinnamate degradation to 2-hydroxypentadienoate	Degradation/Utilization/Assimilation → Aromatic Compound Degradation → Phenolic Compound Degradation
		PWY-6922: L-Nδ-acetylornithine biosynthesis	Biosynthesis → Amino Acid Biosynthesis → Other Amino Acid Biosynthesis → L-Ornithine Biosynthesis
		PWY-7385: 1,3-propanediol biosynthesis (engineered)	Generation of Precursor Metabolites and Energy → Fermentation → Fermentation to Alcohols

CHE/KND/KAT/KOL	Superclasses	CHE/KND/BIR/KOL	Superclasses
PWY-7209: superpathway of pyrimidine ribonucleosides degradation	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Pyrimidine Nucleotide Degradation → Pyrimidine Nucleobase Degradation; Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Pyrimidine Nucleotide Degradation → Pyrimidine Ribonucleoside Degradation - Superpathways	AST-PWY: L-arginine degradation II (AST pathway)	Degradation/Utilization/Assimilation → Amino Acid Degradation → Proteinogenic Amino Acid Degradation → L-arginine Degradation
		PWY-7094: fatty acid salvage	Biosynthesis → Fatty Acid and Lipid Biosynthesis → Fatty Acid Biosynthesis
		PWY0-1337: oleate β-oxidation	Degradation/Utilization/Assimilation → Fatty Acid and Lipid Degradation → Fatty Acid Degradation

CHE/KND/LOD/KAT/BIR	Superclasses	CHE/KND/LOD/BIR/KOL	Superclasses
METHGLYUT-PWY: superpathway of methylglyoxal degradation	methylglyoxal degradation I, methylglyoxal degradation III, methylglyoxal degradation IV, L-lactaldehyde degradation (aerobic)	HEXITOLDEGSUPER-PWY: superpathway of hexitol degradation (bacteria)	Degradation/Utilization/Assimilation → Alcohol Degradation → Alditol Degradation; Degradation/Utilization/Assimilation → Carbohydrate Degradation → Alditol Degradation- Superpathways
NAD-BIOSYNTHESIS-II: NAD salvage pathway III (to nicotinamide riboside)	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → NAD Metabolism → NAD Biosynthesis;	PWY-5138: fatty acid β-oxidation IV (unsaturated, even number)	Degradation/Utilization/Assimilation → Fatty Acid and Lipid Degradation → Fatty Acid Degradation

	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → NAD Biosynthesis; Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → NAD Metabolism → NAD Biosynthesis		
PWY-6859: all-trans-farnesol biosynthesis	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid Biosynthesis → Sesquiterpenoid Biosynthesis	PWY-5656: mannosylglycerate biosynthesis I	Biosynthesis → Metabolic Regulator Biosynthesis → Organic Solute Biosynthesis → Mannosylglycerate Biosynthesis
PWY-7392: taxadiene biosynthesis (engineered)	Biosynthesis → Secondary Metabolite Biosynthesis → Terpenoid Biosynthesis → Diterpenoid Biosynthesis- Superpathways	PWY-5747: 2-methylcitrate cycle II	Degradation/Utilization/Assimilation → Carboxylic Acid Degradation → Propanoate Degradation → 2-Methylcitrate Cycle
		PWY-5920: superpathway of heme b biosynthesis from glycine	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Enzyme Cofactor Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis; Biosynthesis → Tetrapyrrole Biosynthesis → Porphyrin Compound Biosynthesis → Heme Biosynthesis → Heme b Biosynthesis- Superpathways
		PWY-6293: superpathway of L-cysteine biosynthesis (fungi)	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-cysteine Biosynthesis- Superpathways
		PWY-7254: TCA cycle VII (acetate-producers)	Generation of Precursor Metabolites and Energy → TCA cycle
		PWY-7942: 5-oxo-L-proline	Macromolecule Modification → Protein Modification

		metabolism
		PWY-801: homocysteine and cysteine interconversion → Metabolite Activation/Inactivation/Interconversion
		TCA-GLYOX-BYPASS: superpathway of glyoxylate bypass and TCA → Superpathways

CHE/KND/KAT/BIR/KOL	Superclasses
PWY-5104: L-isoleucine biosynthesis IV	Biosynthesis → Amino Acid Biosynthesis → Proteinogenic Amino Acid Biosynthesis → L-isoleucine Biosynthesis
PWY-7185: UTP and CTP dephosphorylation I	Degradation/Utilization/Assimilation → Nucleoside and Nucleotide Degradation → Pyrimidine Nucleotide Degradation → Pyrimidine Ribonucleoside Degradation → UTP and CTP Dephosphorylation
PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP	Biosynthesis → Nucleoside and Nucleotide Biosynthesis → Pyrimidine Nucleotide Biosynthesis → Pyrimidine Nucleotide Salvage; Metabolic Clusters
PWY-7371: 1,4-dihydroxy-6-naphthoate biosynthesis II	Biosynthesis → Cofactor, Carrier, and Vitamin Biosynthesis → Carrier Biosynthesis → Electron Carrier Biosynthesis → Quinol and Quinone Biosynthesis → 1,4-dihydroxy-6-

	naphthoate biosynthesis
PWY490-3: nitrate reduction VI (assimilatory)	Degradation/Utilization/Assimilation → Inorganic Nutrient Metabolism → Nitrogen Compound Metabolism → Nitrate Reduction

सत्यमेव जयते

Ministry of Culture
Government of India

GUT MICROBIAL GENOMIC STUDY AMONG THE PVTGs OF INDIA

Published by
Anthropological Survey of India,
Head office, EN-79,
Salt Lake, Sector - III
Kolkata-700091.

TEL : 91-33-2357 0090/ 0092
E mail : director@ansi.gov.in
Pmi.anthropology@gmail.com
Website: www.ansi.com