



Case Studies for Exploring the Indian human metagenomes through multiomics and AI-

31st July 2025

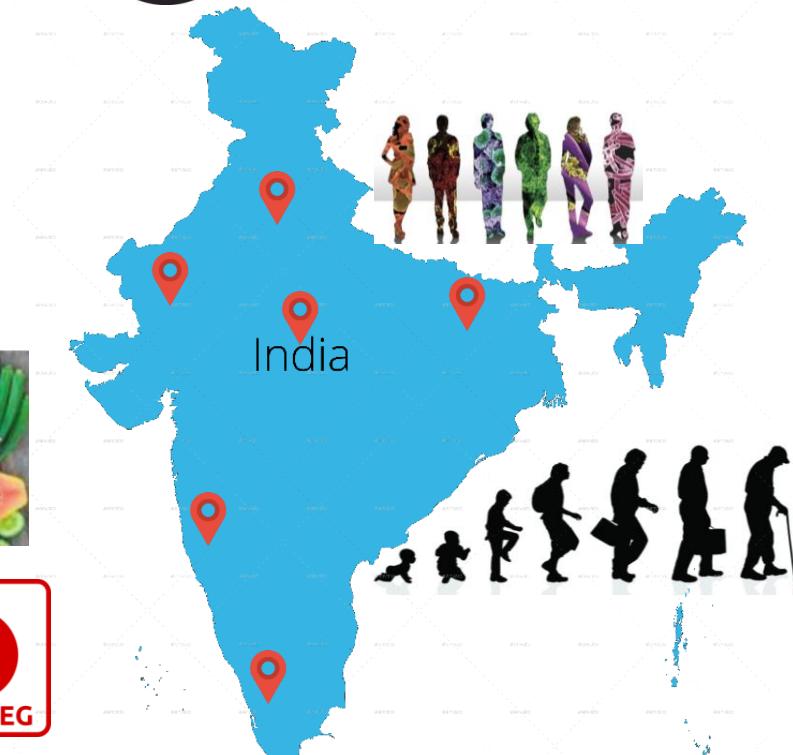
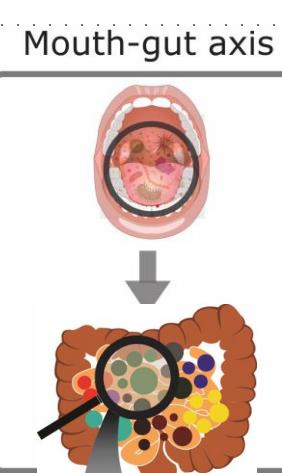
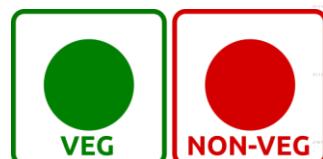


Vineet K. Sharma

Professor,

Department of Biological Sciences,
IISER Bhopal, India

Integrated Omics and Bioinformatics Lab



Microbes in various environmental systems

One teaspoon of garden soil



>1 million
microbes

On your hands



More than
World's
Human
Population

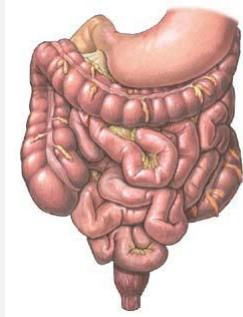
- Microbes outnumber all other species
- Make up most of the living matter on the planet

One Litre of Sea water



> 1 billion
microbes

In Our Gut— Gut feeling



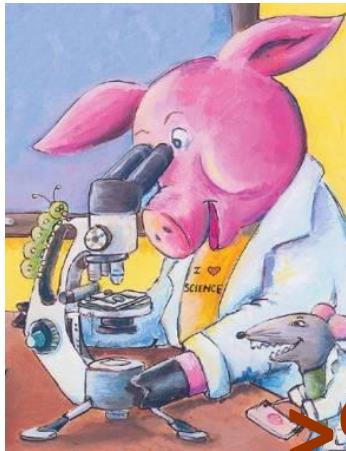
> 2 Kilograms
microbes
> 1000 species

So many microbes,
that scientists have
only named 0.5%
of them





Traditional Methods of Identification and Culturing of Microbes on Artificial Media



Identification under
Microscope



Counting colonies

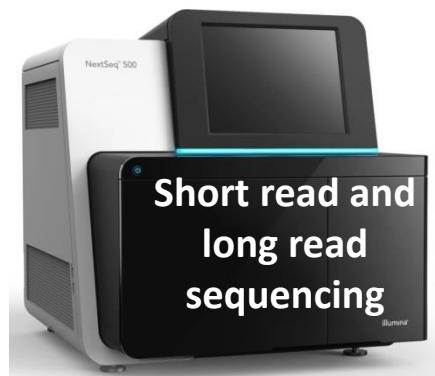
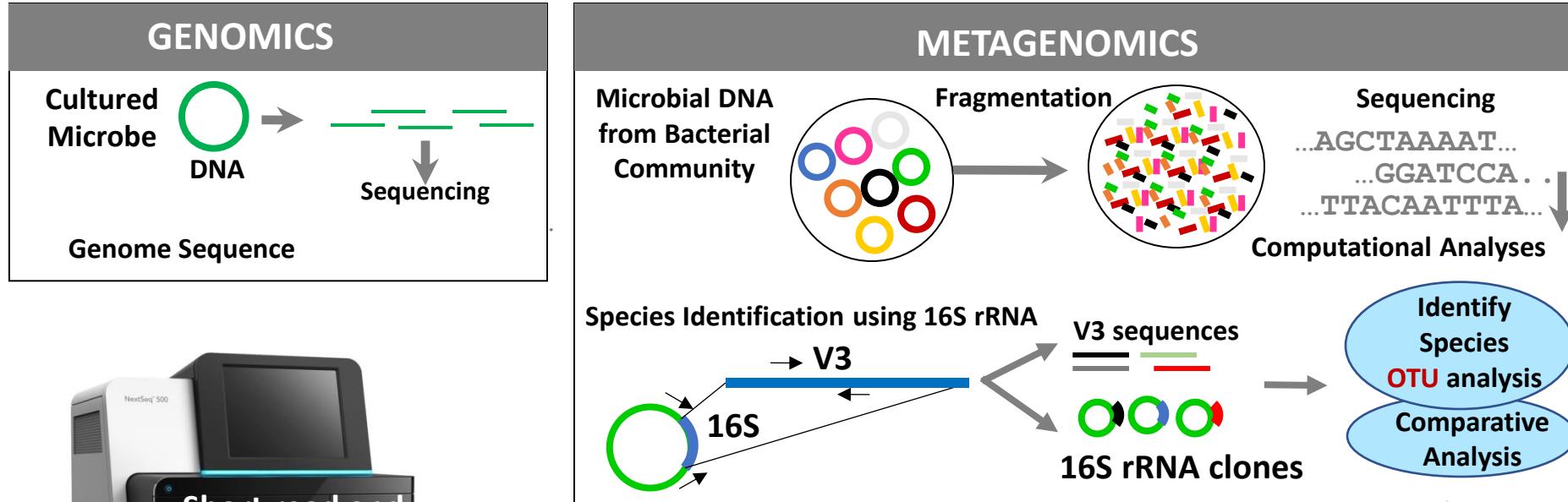


>98% Bacteria Cannot be
Cultured by Traditional
Methods

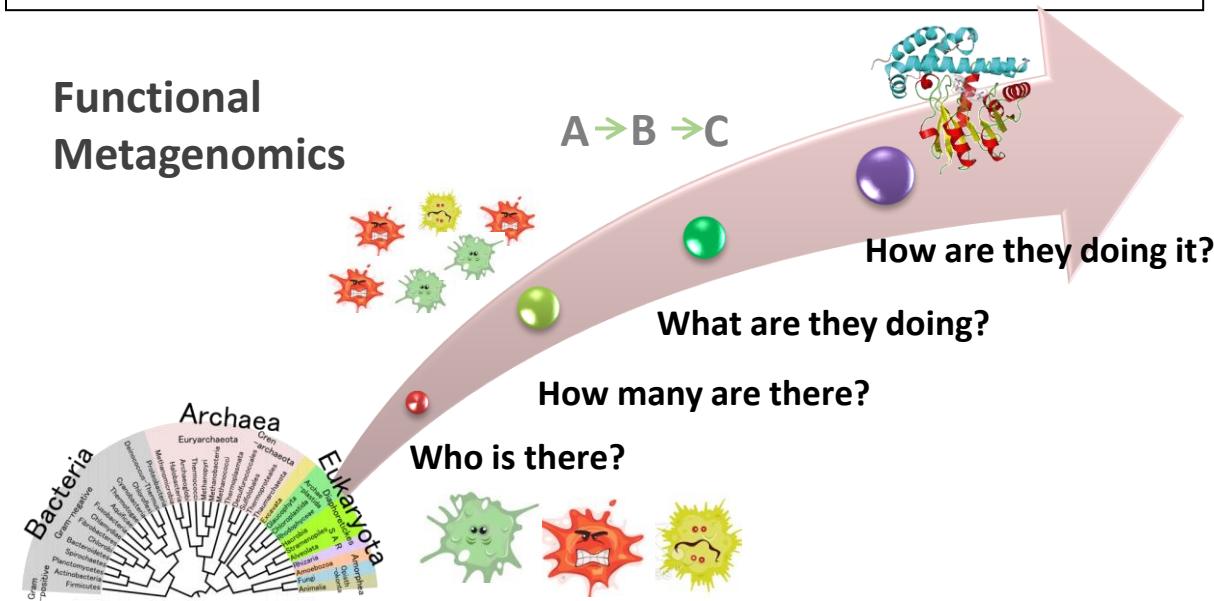


Metagenomics: Culture-independent sequencing and analysis of microbial DNA extracted directly from an environmental sample

Genomics vs Metagenomics

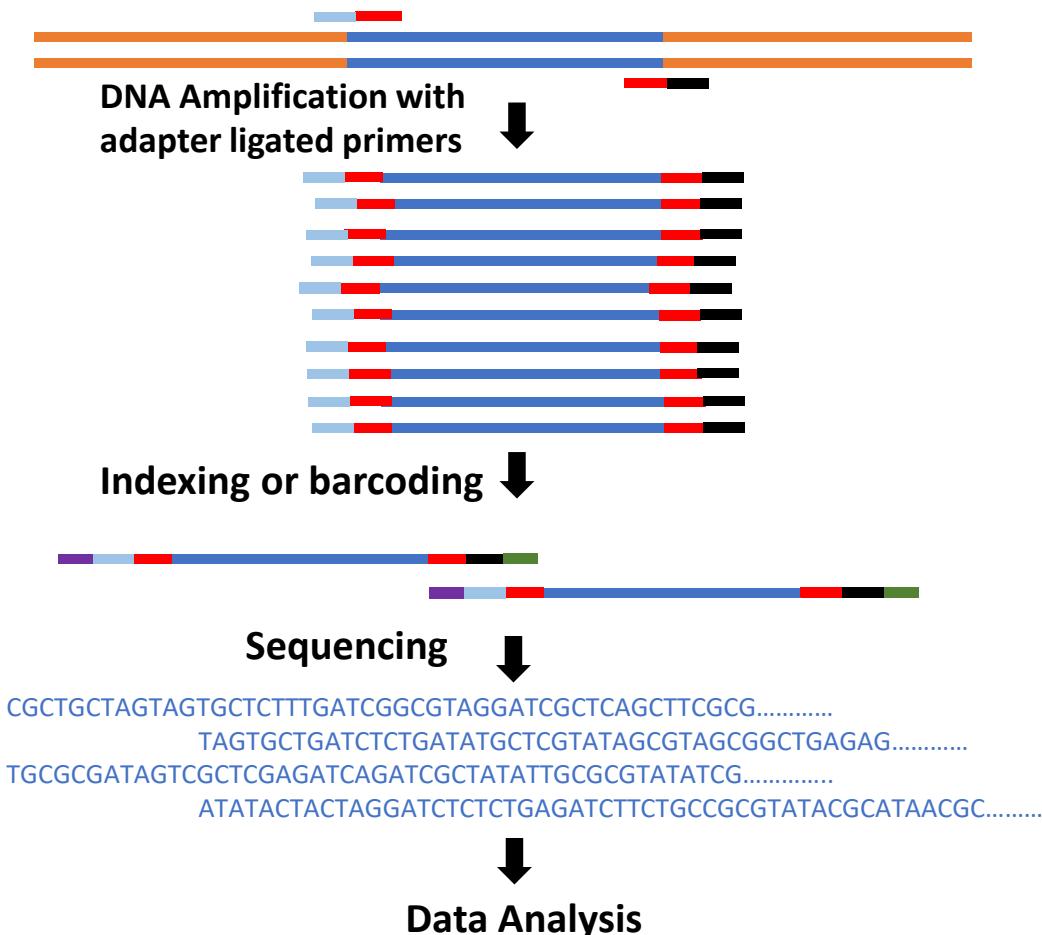


Functional Metagenomics

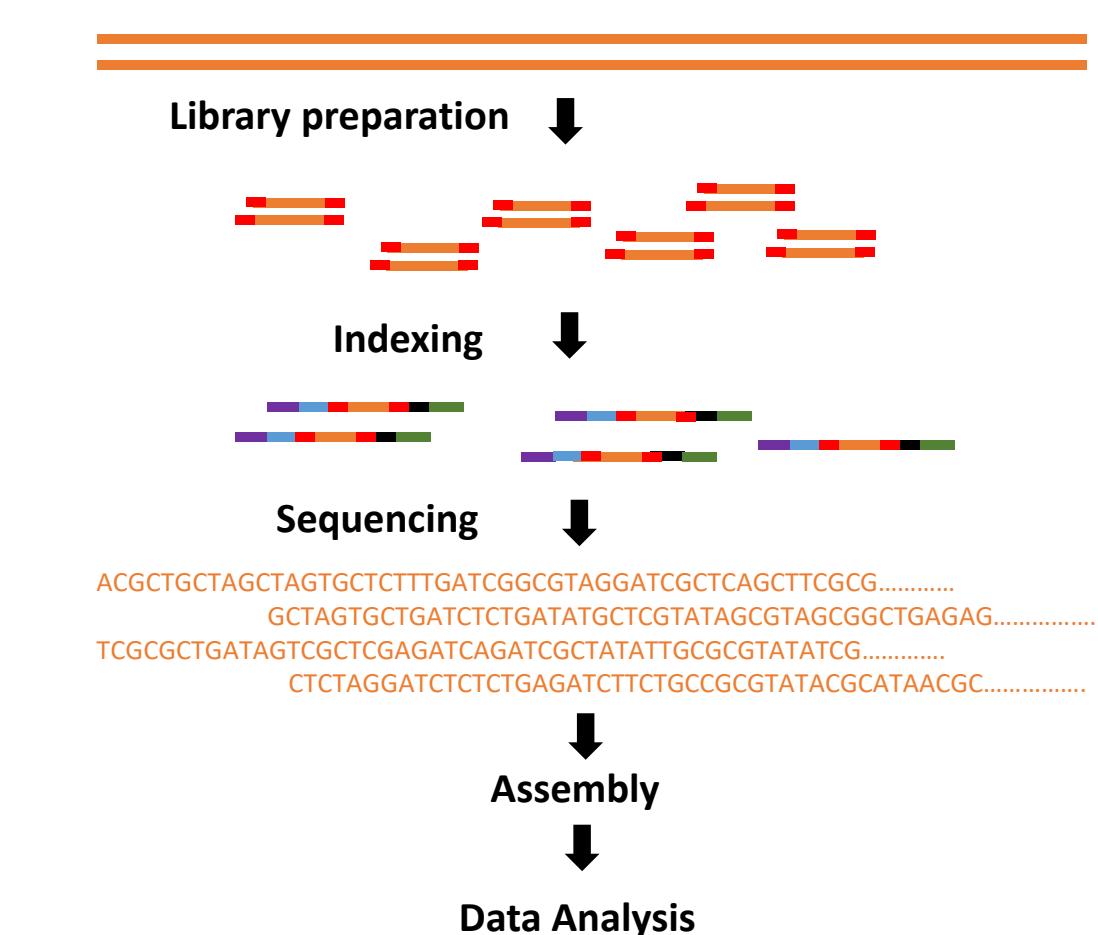


Metagenomic Sequencing Approaches for Taxonomic and Functional Analysis

Amplicon Based Sequencing (16S rDNA or Targeted Sequencing)



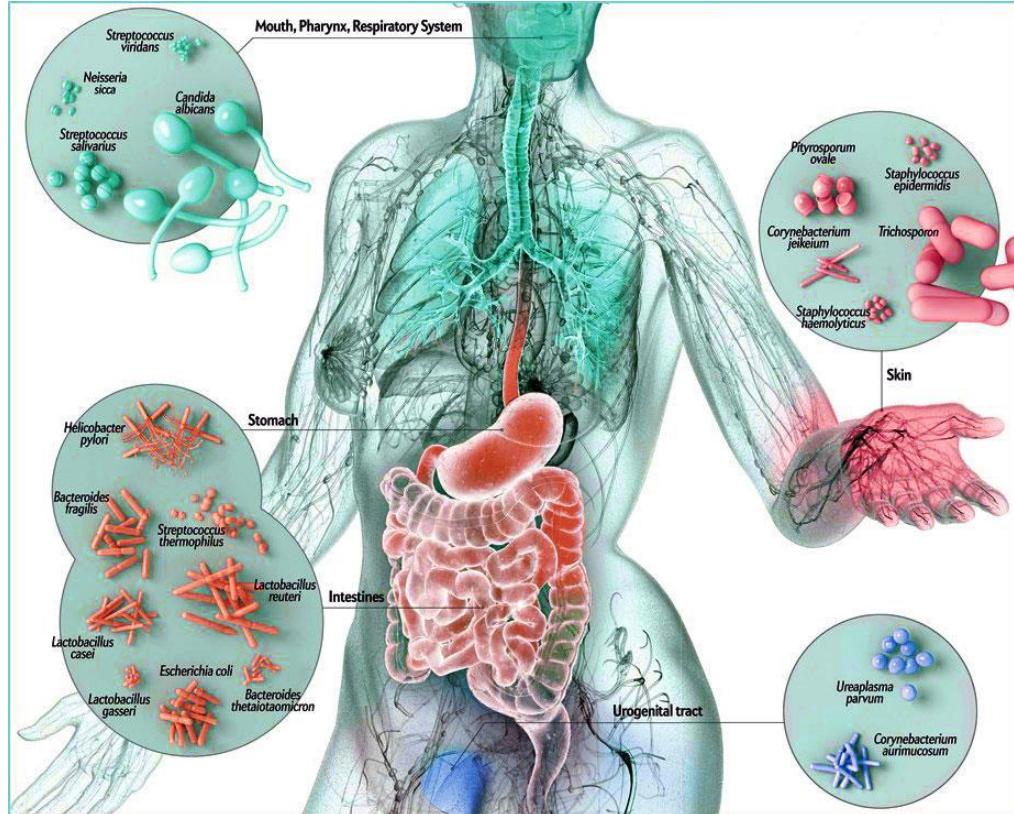
Whole Genome Sequencing (Shotgun Metagenomic or Untargeted Sequencing)



The Human Microbiome : Our Second Genome

Number of human cells = $\sim 3.0 \cdot 10^{13}$

Number of bacterial cells = $\sim 3.8 \cdot 10^{13}$



Metagenomics: Culture-independent sequencing and analysis of microbial DNA extracted directly from an environmental sample

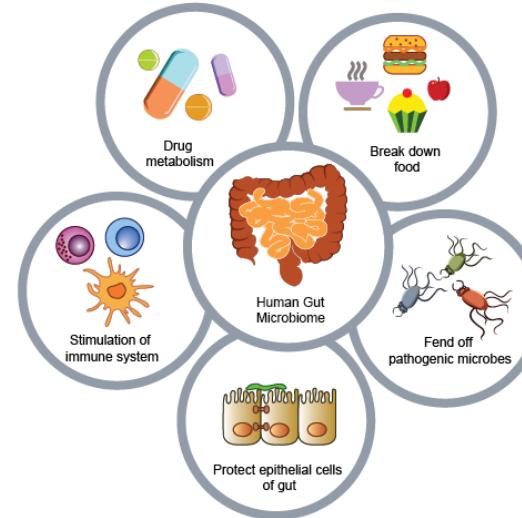
Les Dethlefsen et al. 2007, *Nature*

Ilseung Cho et al. 2012, *Nat Rev Genet*

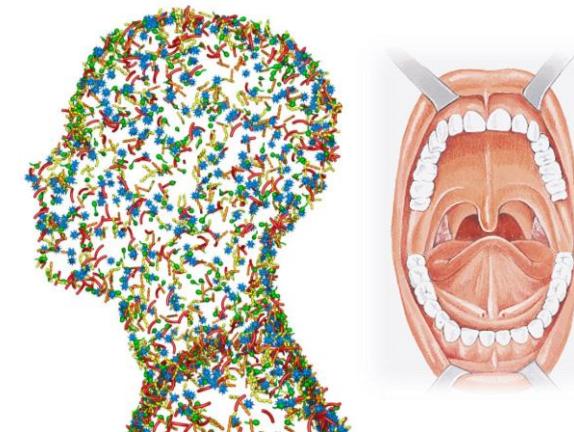
Ron Sender, et al. 2016, *PLOS Biology*

Images taken from published studies and google images are sincerely acknowledged

In the gut:
~2 Kilograms and
~1000 species of
bacteria
'Gut feeling'



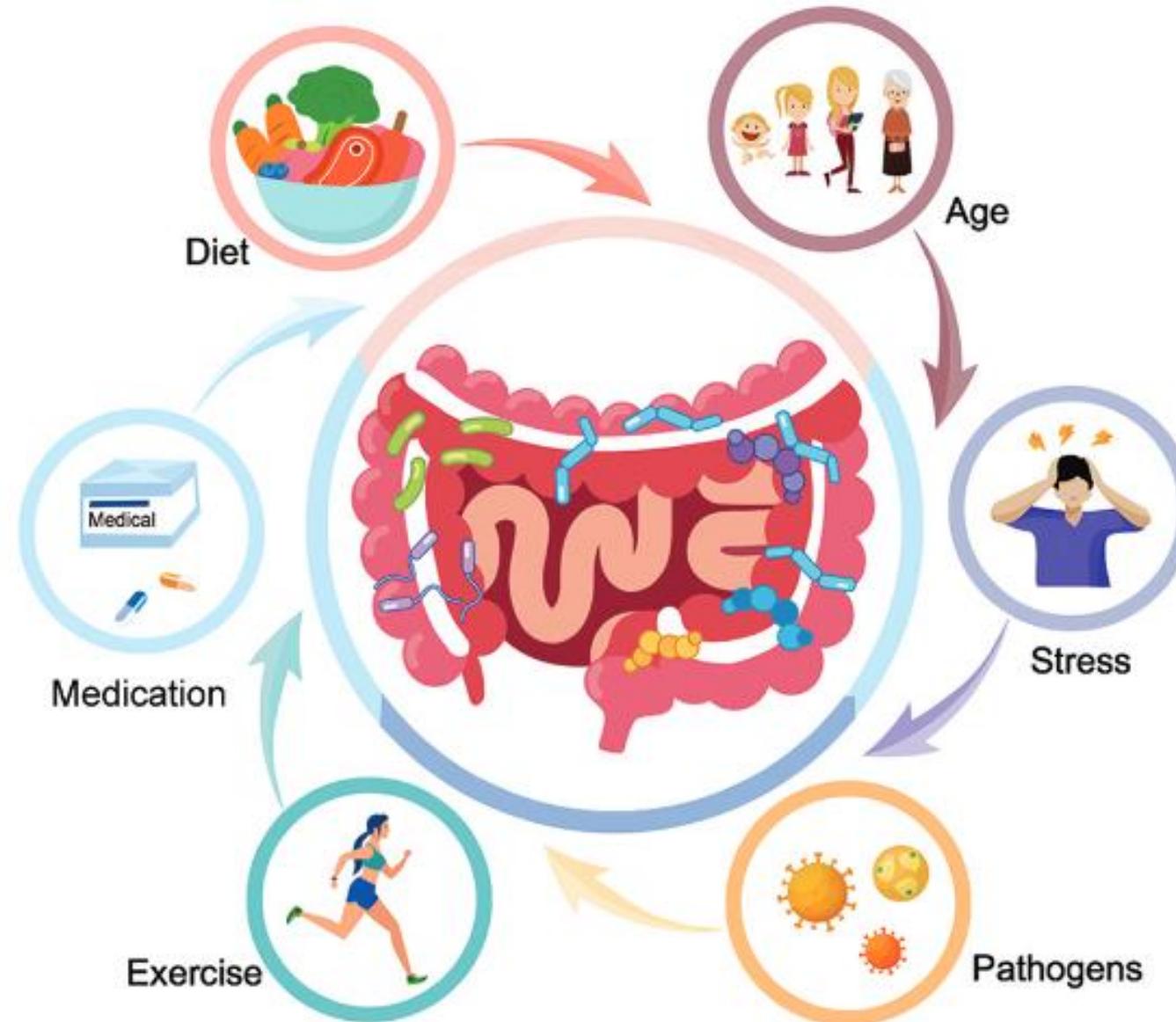
Human Skin:
Most exposed organ,
~1200 species of
bacteria, fungi,
viruses



Oral Cavity:
~700 species of
bacteria

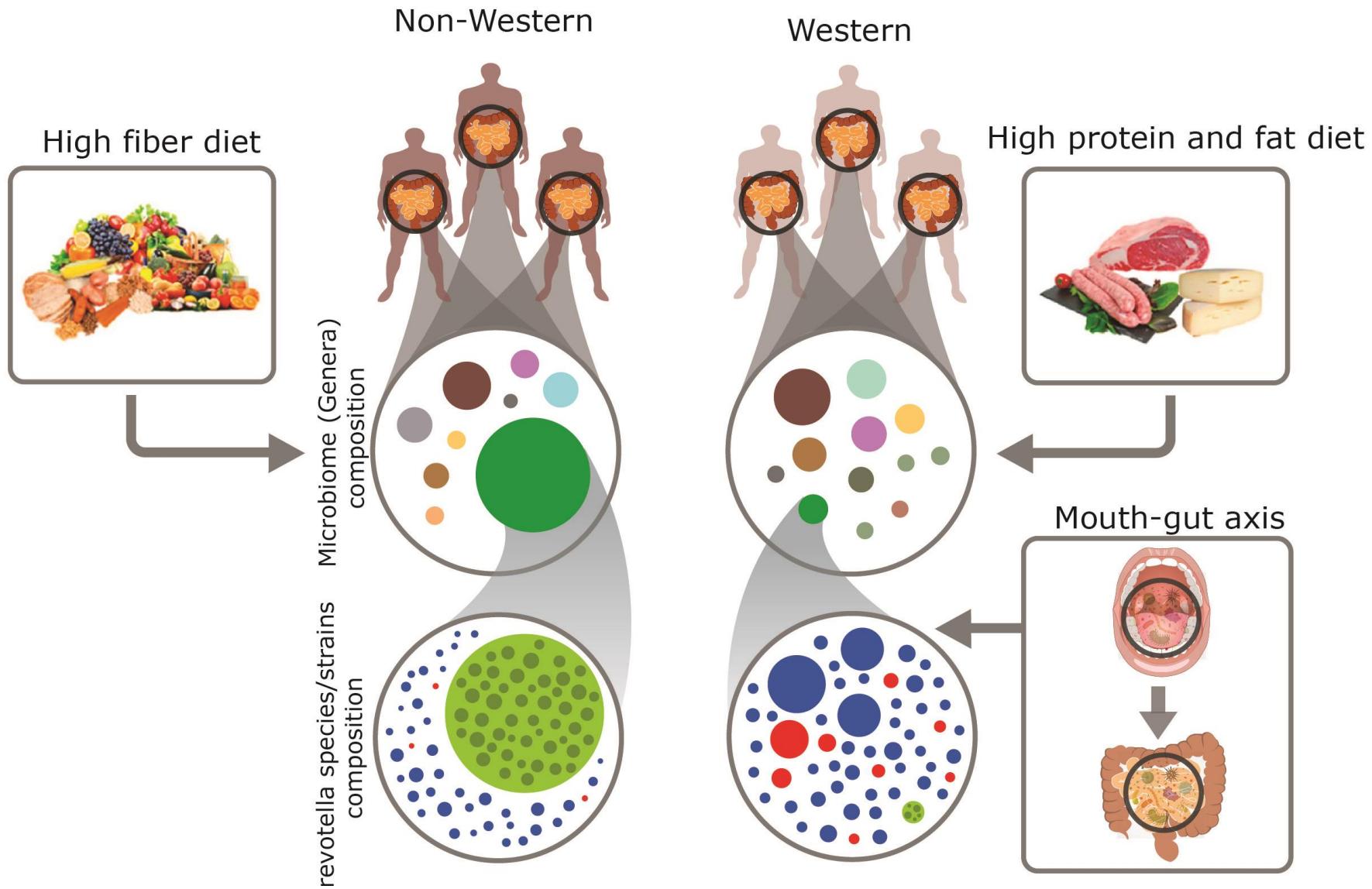


What factors Shapes or Changes our Microbiome

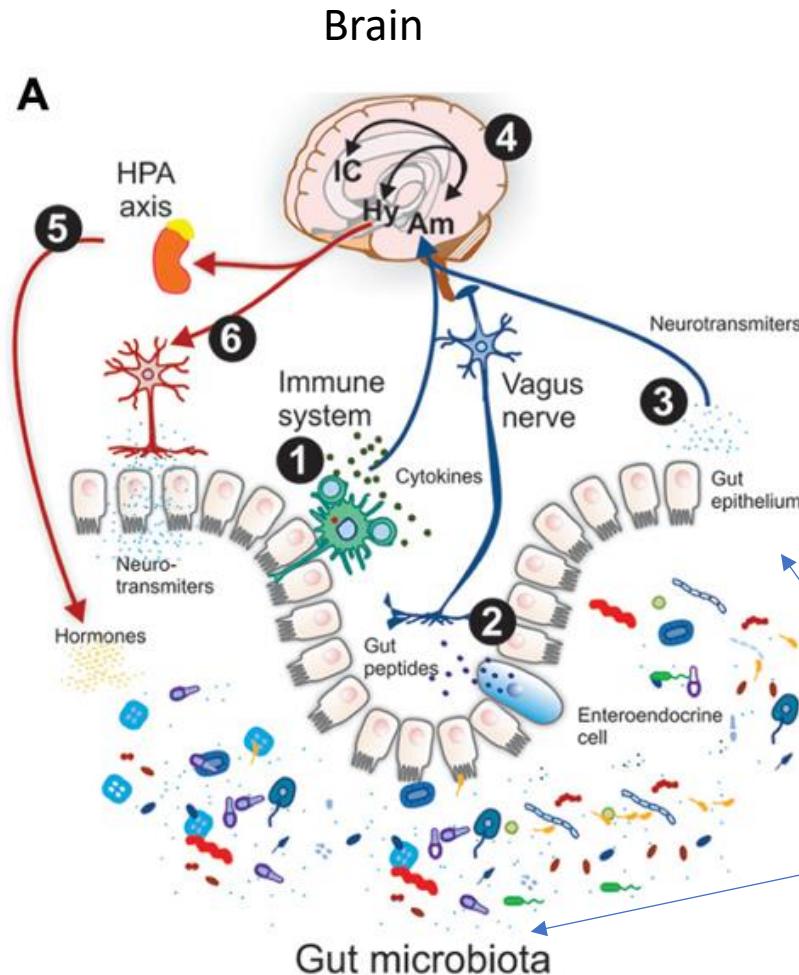




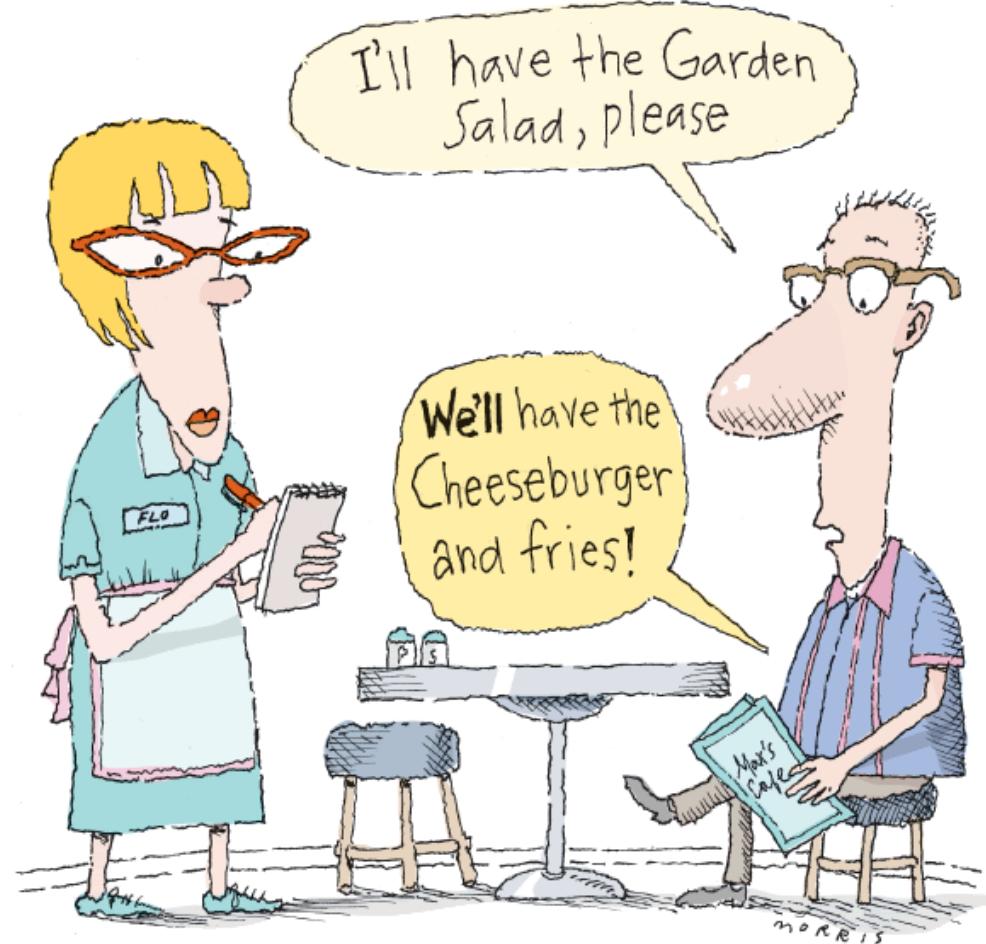
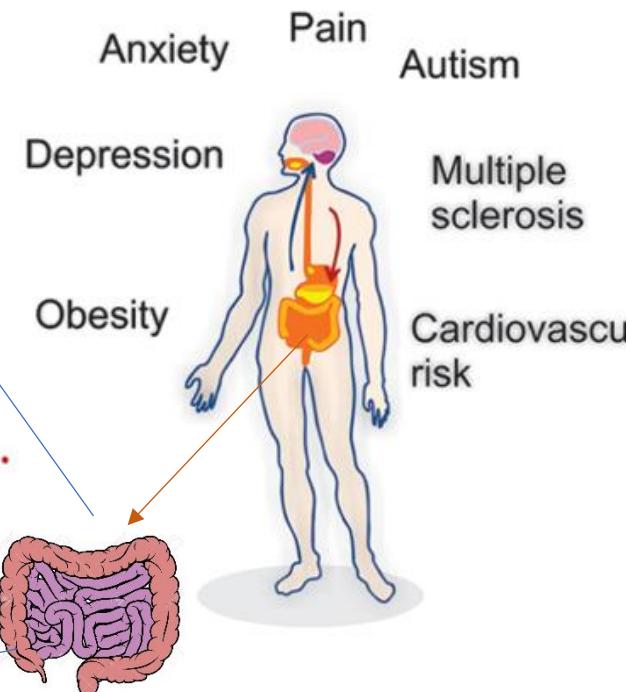
Impact of diet on gut microbiome in different populations



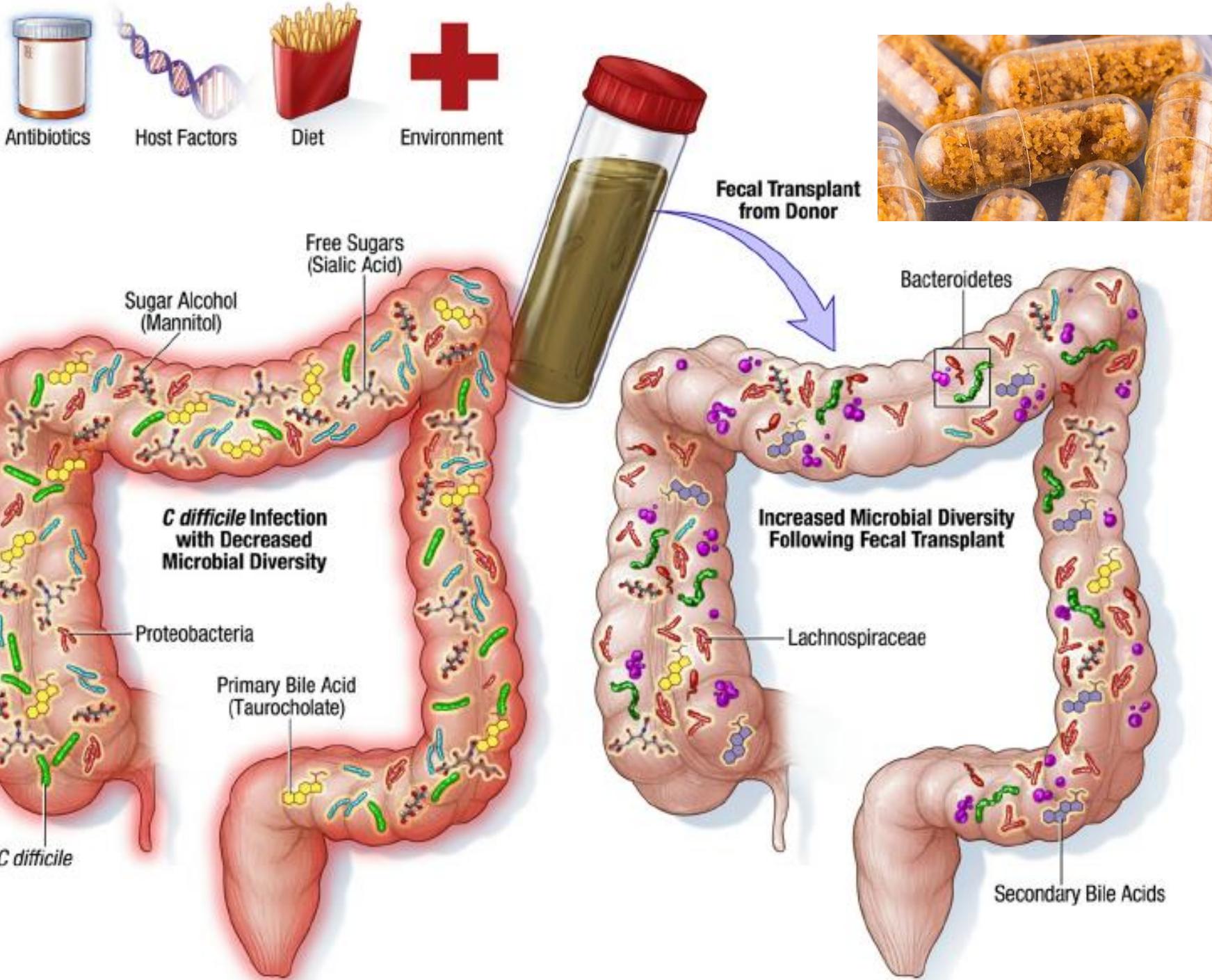
The Gut-Brain Axis: My Gut Feeling

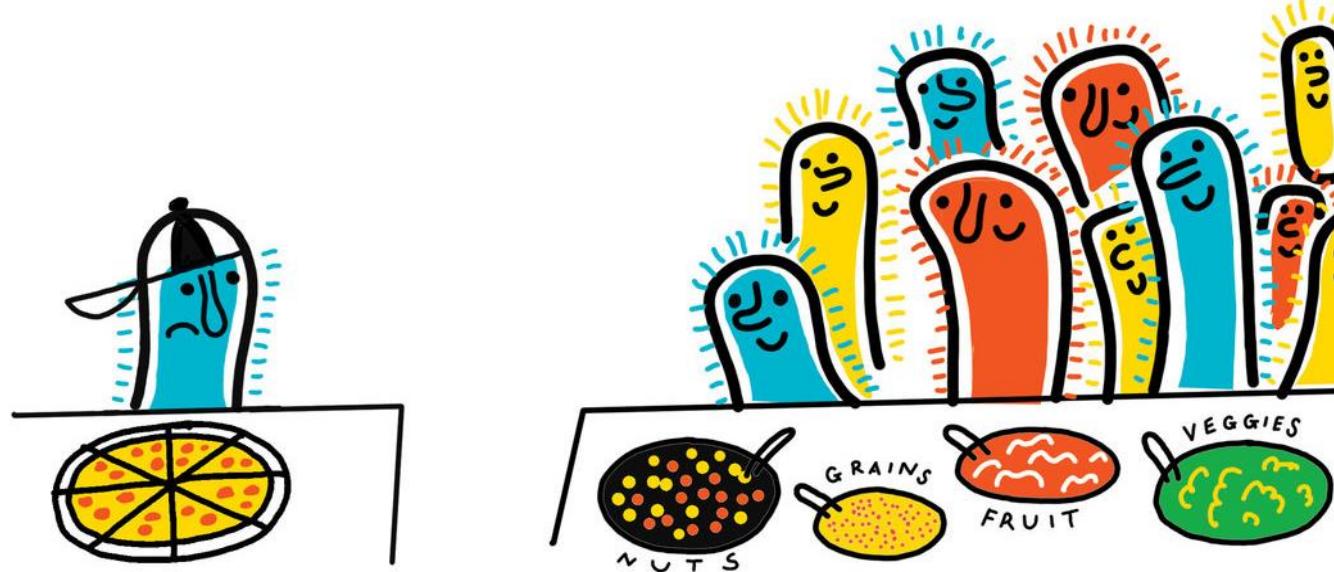
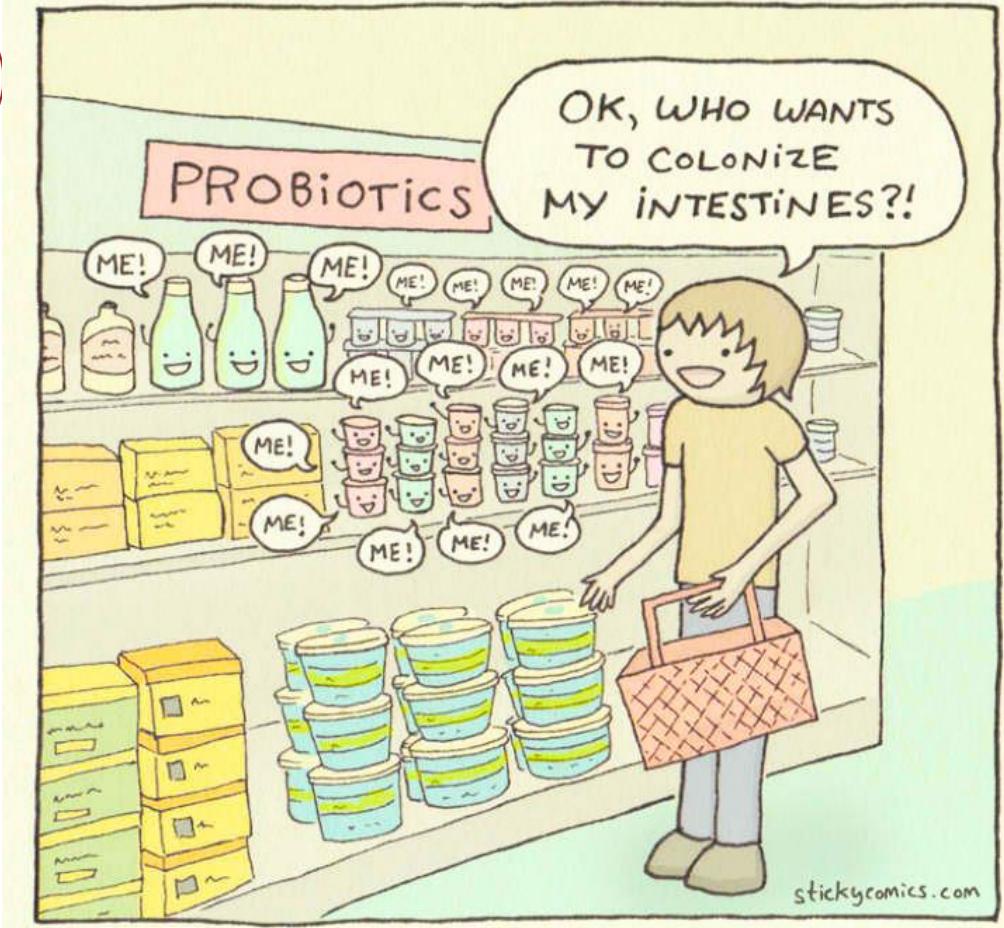


B



Fecal Microbiome Transplant





We ARE
WHAT WE eat

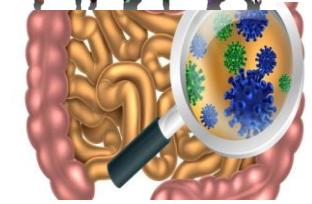
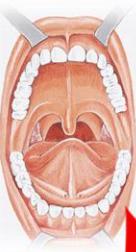


Images and some text taken from Google Search



The Human Microbiome : Exploring Our Second Genome

Oral Microbiome
Smokeless tobacco
and Cancer



Gut Microbiome
Role of diet



Colorectal Cancer

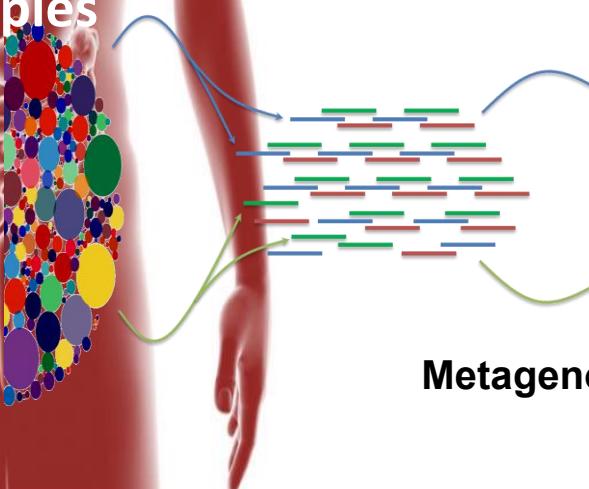


Vitiligo

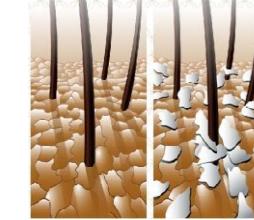
Drug metabolism



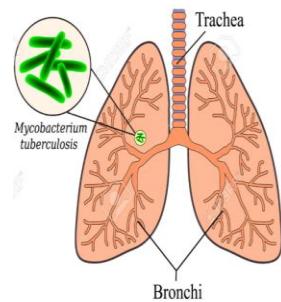
Indian
Microbiome
Data
generated
from more
than 2000
samples



Scalp Microbiome

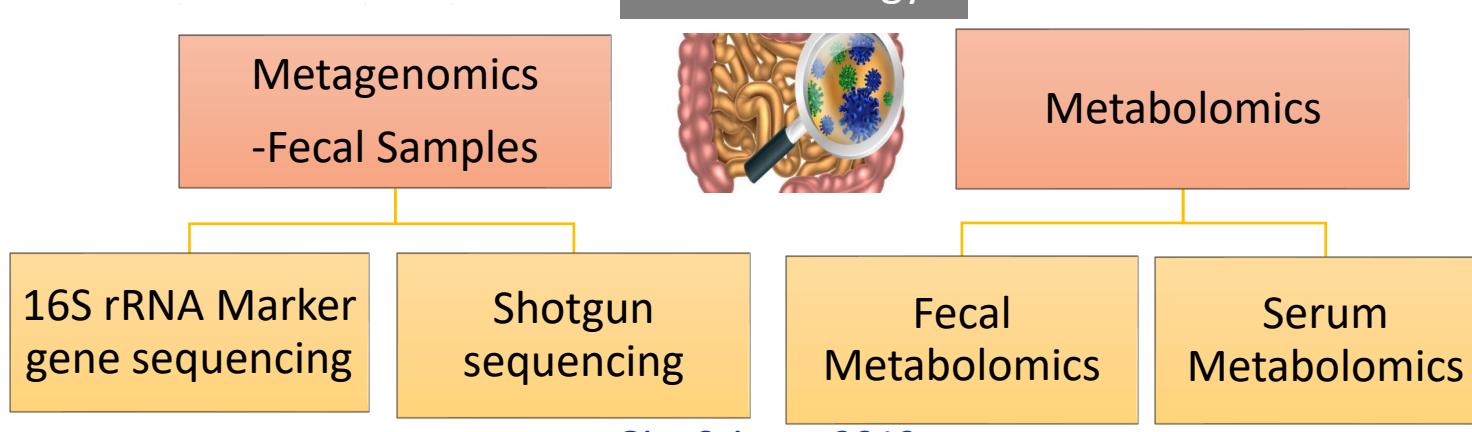
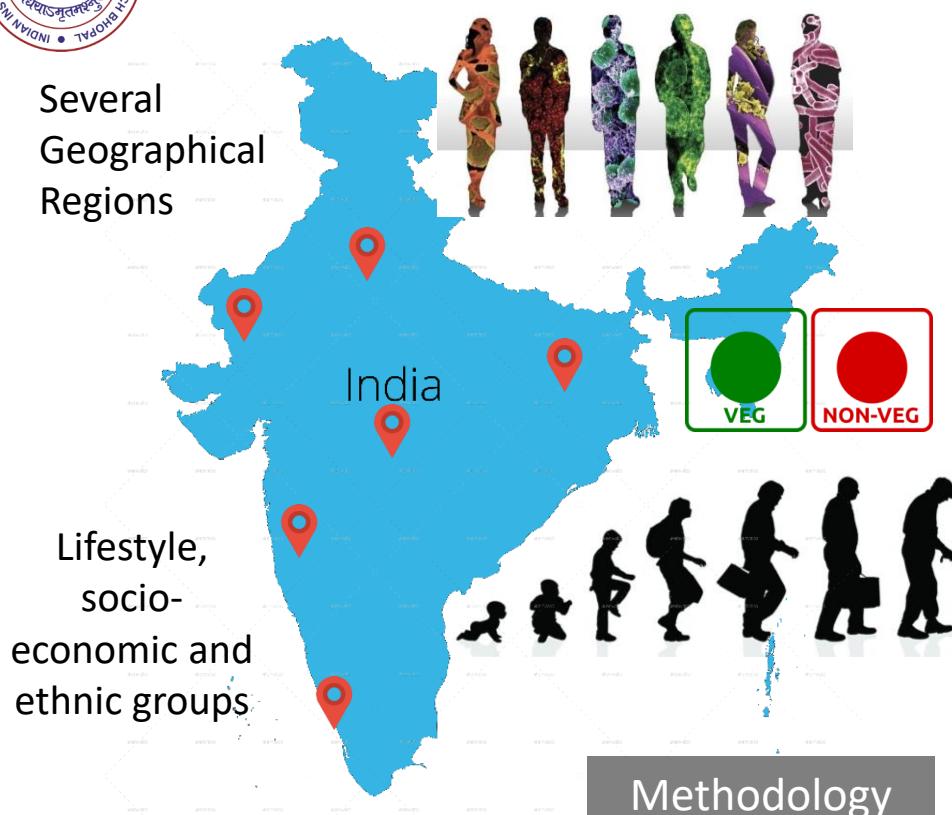


Tuberculosis



Metagenomes to Novel Genomes

Gut Microbiome across India, Diets, Populations: Role in Health and Disease



RESEARCH

GigaScience, 8, 2019, 1–20

doi: 10.1093/gigascience/giz004

Advance Access Publication Date: 30 January 2019
Research

The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches

D.B. Dhakan^{1,†}, A. Maji^{1,†}, A.K. Sharma¹, R. Saxena¹, J. Pulikkann², T. Grace^{2,3}, A. Gomez⁴, J. Scaria⁵, K.R. Amato⁶ and V.K. Sharma ^{ID 1,*}



Role of *P. copri* in Indian gut and carbohydrate metabolism

- Prevotella Genome Database (PGD) containing 2,204 genomes/bins
- Prevotella Gene Catalogue (PGC) containing ~2.9 million genes



RESEARCH

The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches

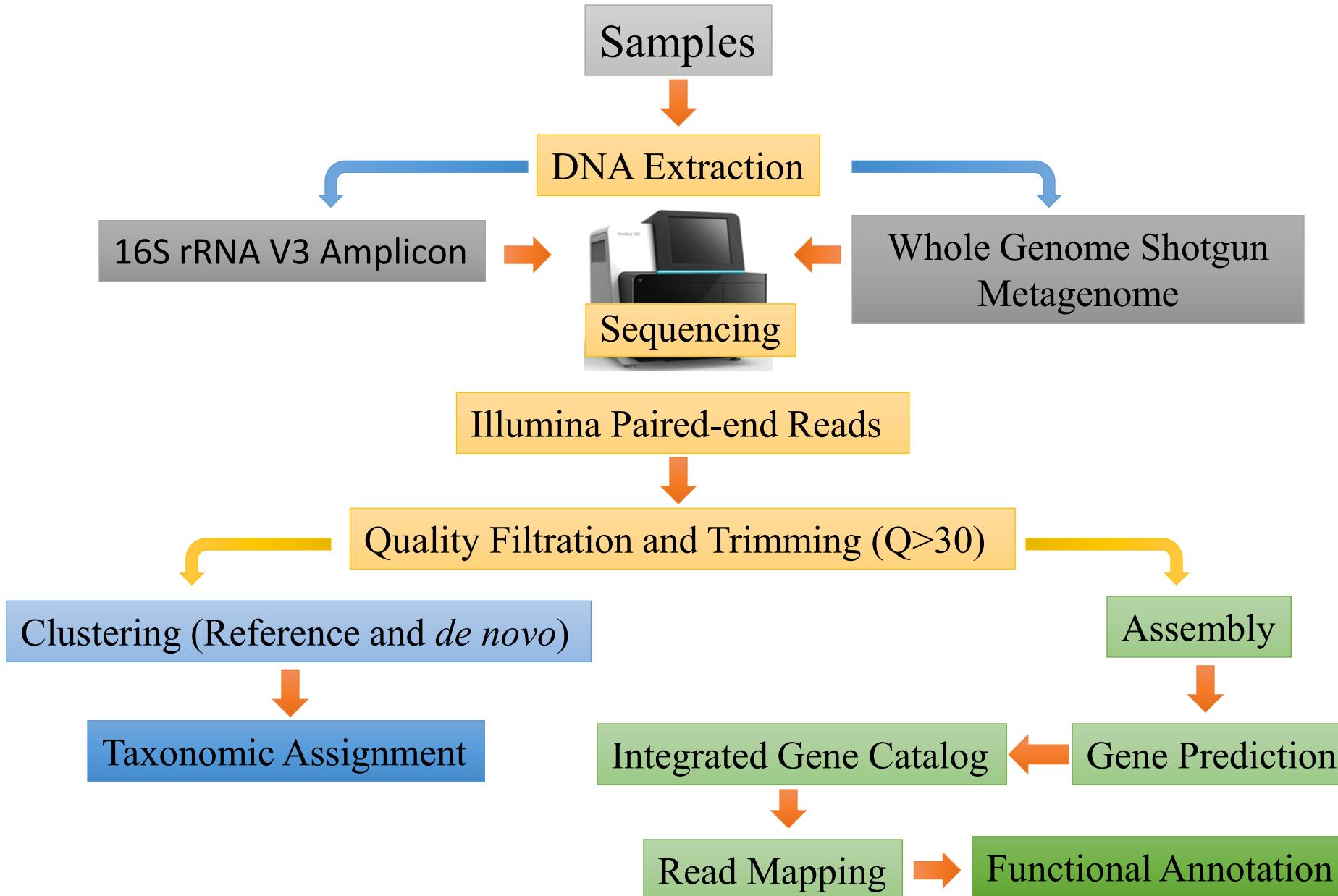
D.B. Dhakan^{1,†}, A. Maji^{1,†}, A.K. Sharma¹, R. Saxena¹, J. Pulikkan², T. Grace^{2,3}, A. Gomez⁴, J. Scaria⁵, K.R. Amato⁶ and V.K. Sharma  ^{1,*}

Abstract

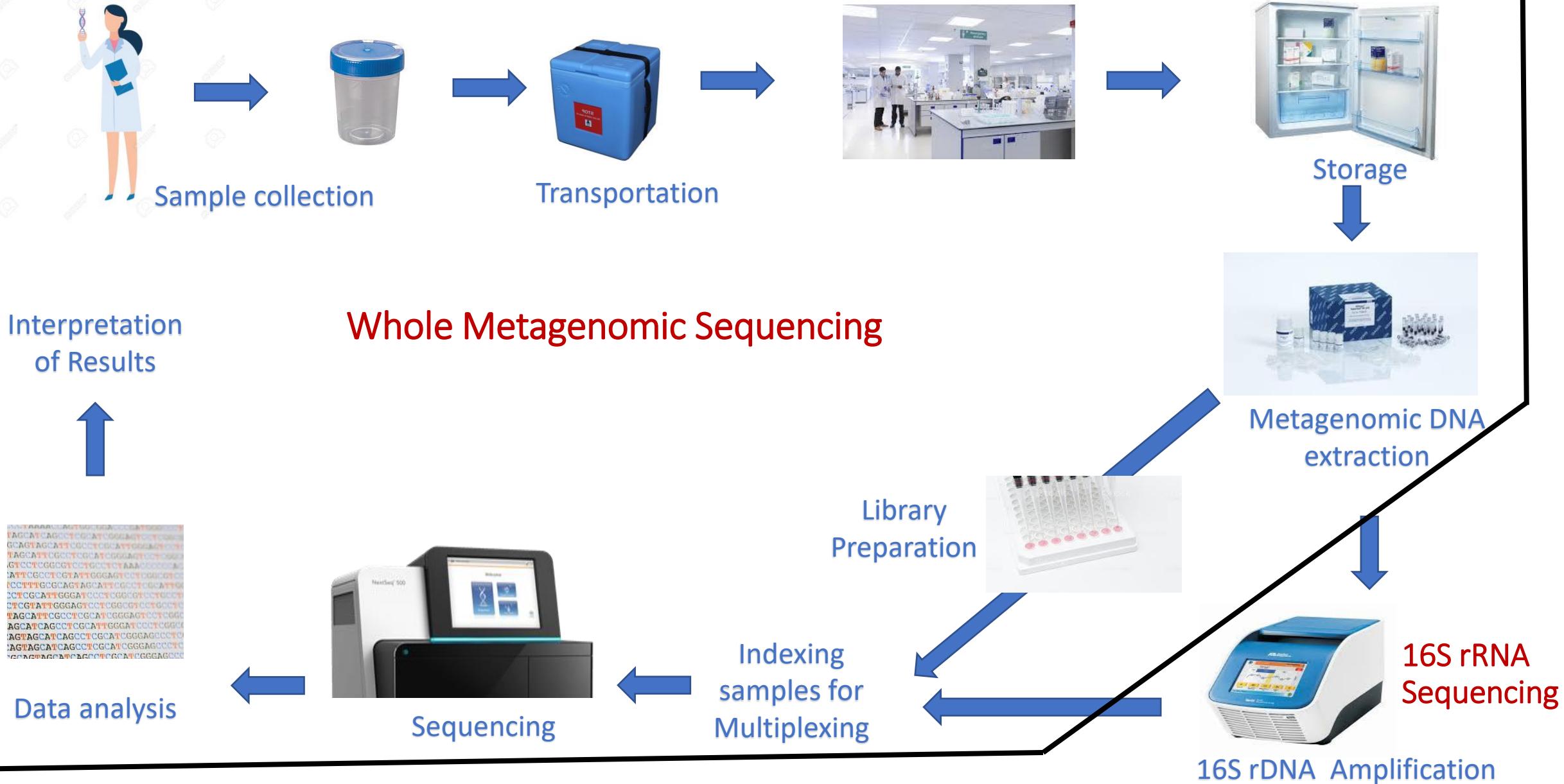
Background: Metagenomic studies carried out in the past decade have led to an enhanced understanding of the gut microbiome in human health; however, the Indian gut microbiome has not been well explored. We analyzed the gut microbiome of 110 healthy individuals from two distinct locations (North-Central and Southern) in India using multi-omics approaches, including 16S rRNA gene amplicon sequencing, whole-genome shotgun metagenomic sequencing, and metabolomic profiling of fecal and serum samples. **Results:** The gene catalogue established in this study emphasizes the uniqueness of the Indian gut microbiome in comparison to other populations. The gut microbiome of the cohort from North-Central India, which was primarily consuming a plant-based diet, was found to be associated with *Prevotella* and also showed an enrichment of branched chain amino acid (BCAA) and lipopolysaccharide biosynthesis pathways. In contrast, the gut microbiome of the cohort from Southern India, which was consuming an omnivorous diet, showed associations with *Bacteroides*, *Ruminococcus*, and *Faecalibacterium* and had an enrichment of short chain fatty acid biosynthesis pathway and BCAA transporters. This corroborated well with the metabolomics results, which showed higher concentration of BCAs in the serum metabolome of the North-Central cohort and an association with *Prevotella*. In contrast, the concentration of BCAs was found to be higher in the fecal metabolome of the Southern-India cohort and showed a positive correlation with the higher abundance of BCAA transporters. **Conclusions:** The study reveals the unique composition of the Indian gut microbiome, establishes the Indian gut microbial gene catalogue, and compares it with the gut microbiome of



Strategy



Sample workflow for metagenomic sample sequencing



What is metadata and what should be collected for a given project?



Sequencing Statistics

Sample Details	Amplicon	Metagenome
Total no. of samples	110	110
Average no. of reads per sample	1 million	4 million
Average data per sample	700 Mbp	1.5 Gbp
Total no. of reads generated	78 Million	500 Million
Total data generated	44 Gbp	150 Gbp
Read length	150x2 bp	150x2 bp

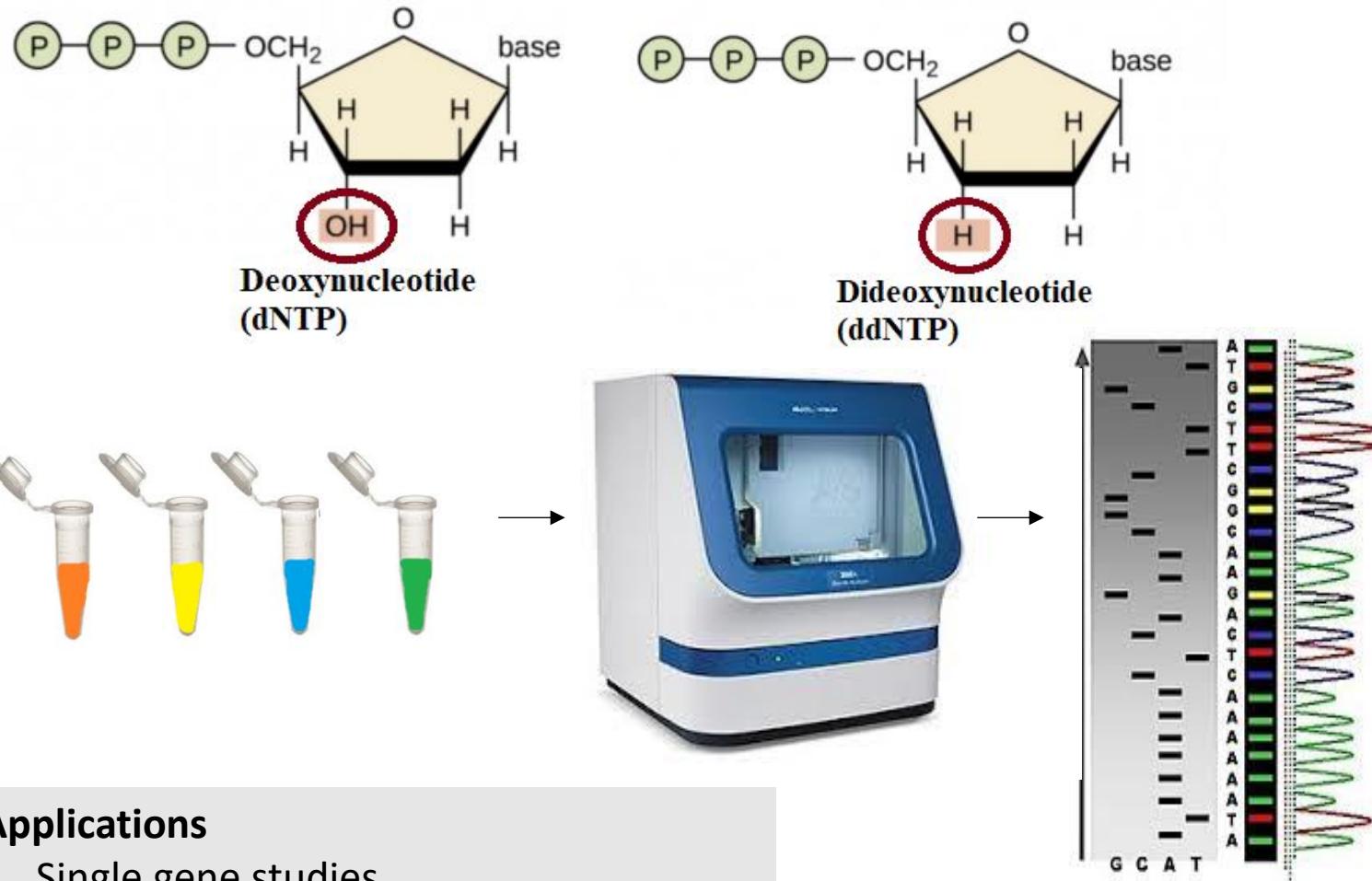
Which Sequencing technology should be used?

Sanger Sequencing

Features

- It requires PCR
- Known as dideoxy method or chain termination method
- Need of capillary electrophoresis
- Each reaction includes DNA template, primers, DNA polymerase, deoxynucleotides (dNTPs) and dideoxy nucleotides (ddNTPs)
- Total four reactions: one with each type of ddNTPs
- Modern sanger method uses fluorescent labelled ddNTPs
- Longer read length 400-900 bp
- 0.3% error rate
- Human Genome Project completed with this

Kchouk, M., et al. (2017). *Biology and Medicine*, 9(3).



Applications

- Single gene studies
- Genotyping
- Next-generation sequencing (NGS) validation

Disadvantages

- Low throughput
- Tedious method

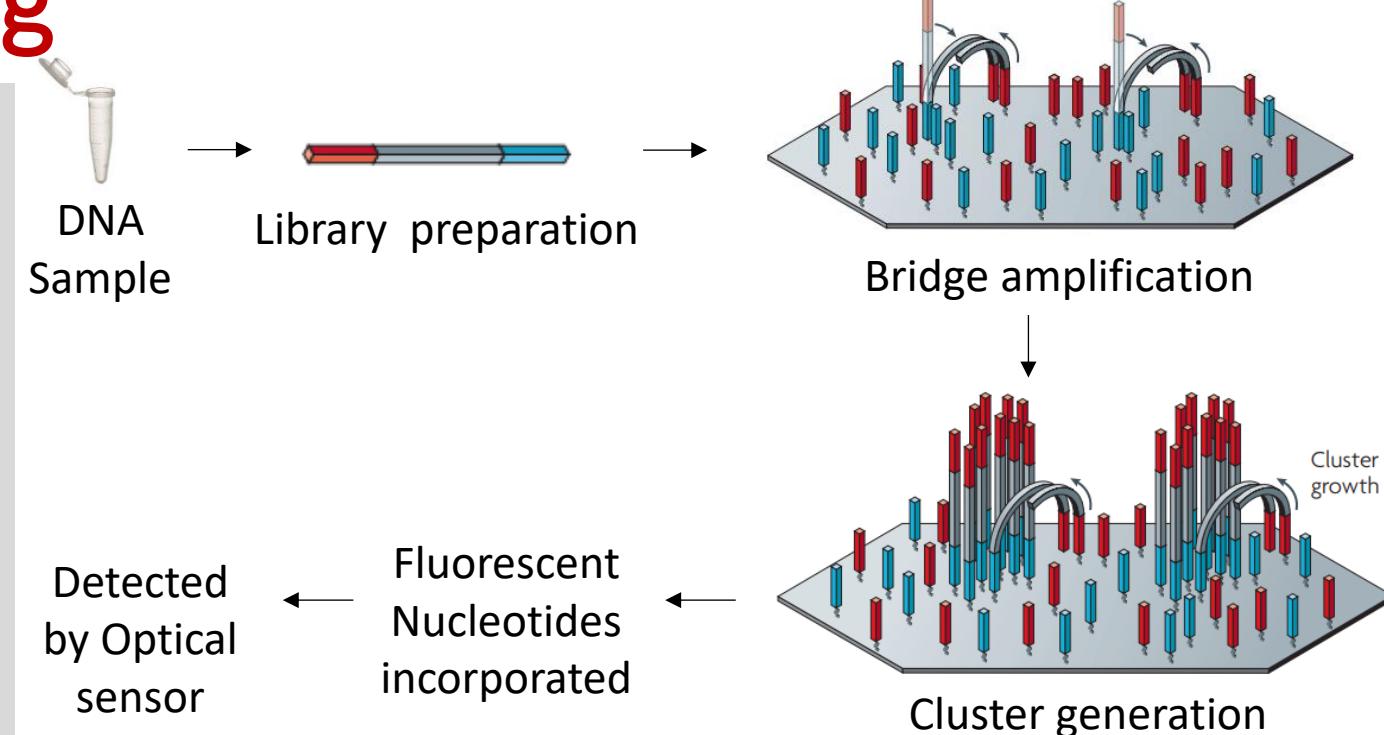


Illumina Sequencing

illumina®

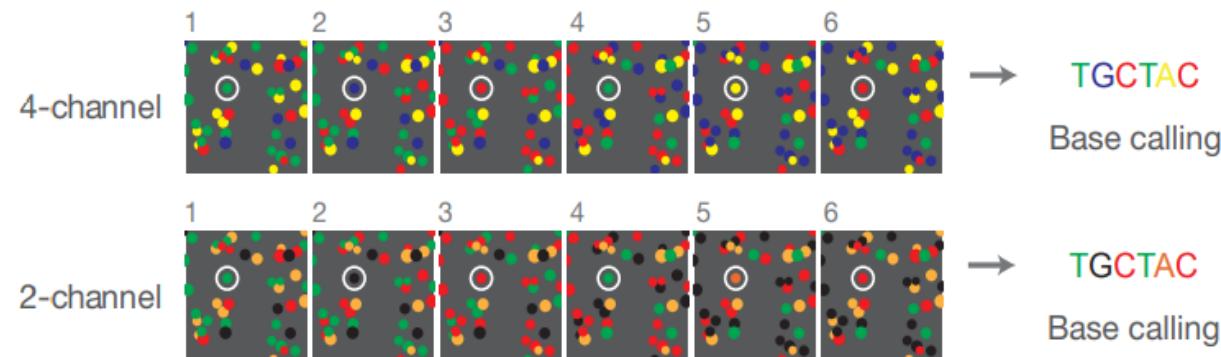
Features

- Sequencing by synthesis technology
- Needs optical system for recognition of incorporated bases
- Fluorescent nucleotides required
- Read length 150-300 bp
- Two channel and four channel technology
- Two channel uses 2 colours red and green and need 2 images to detect the incorporated base
- Indicated as Red-C, Green-T, both-A and no colour- G
- Cluster generation by bridge amplification



Advantages

- Highest throughput
- Lowest per-base cost
- Most library preparation protocols are compatible
- 0.1% error rate



Metzker, M. L. (2010). *Nature reviews genetics*, 11(1), 31-46.

Illumina sequencers for various sequencing applications



iSeq 100

- Read length: 2x 150 bp
- Output: 1.2 Gb data and 4 M reads per run
- Applications: Target resequencing, bacterial and viral sequencing



MiniSeq

- Read length: 2x 150 bp
- Output: 1.65- 7.5 Gb data and 7-25 M reads per run
- Applications: Target resequencing, whole small-genomes up to 50 and targeted gene expression profiling



NextSeq series

- Read length: 2x 150 bp
- Output: 16.25- 120 Gb data and 130-400 M reads per run
- Applications: whole genome sequencing, exome sequencing and gene expression profiling



MiSeq series

- Read length: 2x 300 bp
- Output: 250 Mb- 15 Gb data and 1-25 M reads per run
- Applications: Small whole genome, targeted sequencing, ChIP-seq, 16S metagenomic sequencing, etc.



HiSeq 2500

- Read length: 2x250 bp
- Output: 9 Gb-1 Tb data and 300M-4 B reads per run
- Applications: De novo, whole genome, exome and whole transcriptome sequencing, etc. with large scale sequencing

NovaSeq 6000

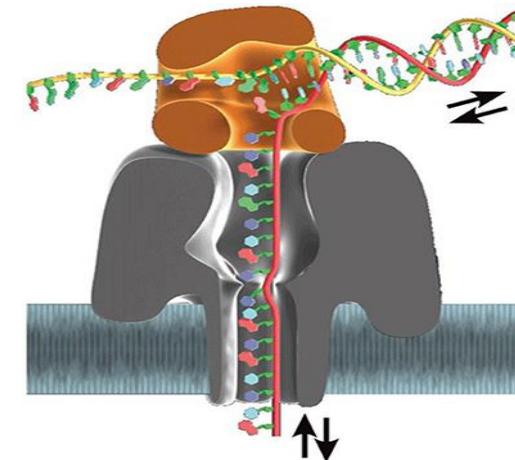
- Read length: 2x 250 bp
- Output: 4800-6000 Gb data and 32-40 billion reads per run
- Applications: WGS, whole exome, whole transcriptome, etc. with large scale sequencing



Nanopore Sequencing



- Sequences 400 bases per sec
- Protein pores embedded in membrane
- Disruption in the ionic current measured on passing of each nucleotide
- Real-time data streaming
- Eliminates PCR bias
- Allows the identification of base modifications alongside nucleotide sequence
- Quick sample preparation
- Output data is in standard FASTQ and FAST5 formats suitable for analysis
- Sequencers- MinION, GridION and ProMethION
- In case of MinION, total pores -2048
- Total active pores divided in 4 mux



Nanopore

An ionic current passes through nanopores
↓
Nanopore device measures the changes in current as biological molecules pass through the nanopore
↓
Change in current can be used to identify that molecule



Nanopore Sequencing Technology and Available Platforms



How much metagenomic data should
be generated for a project



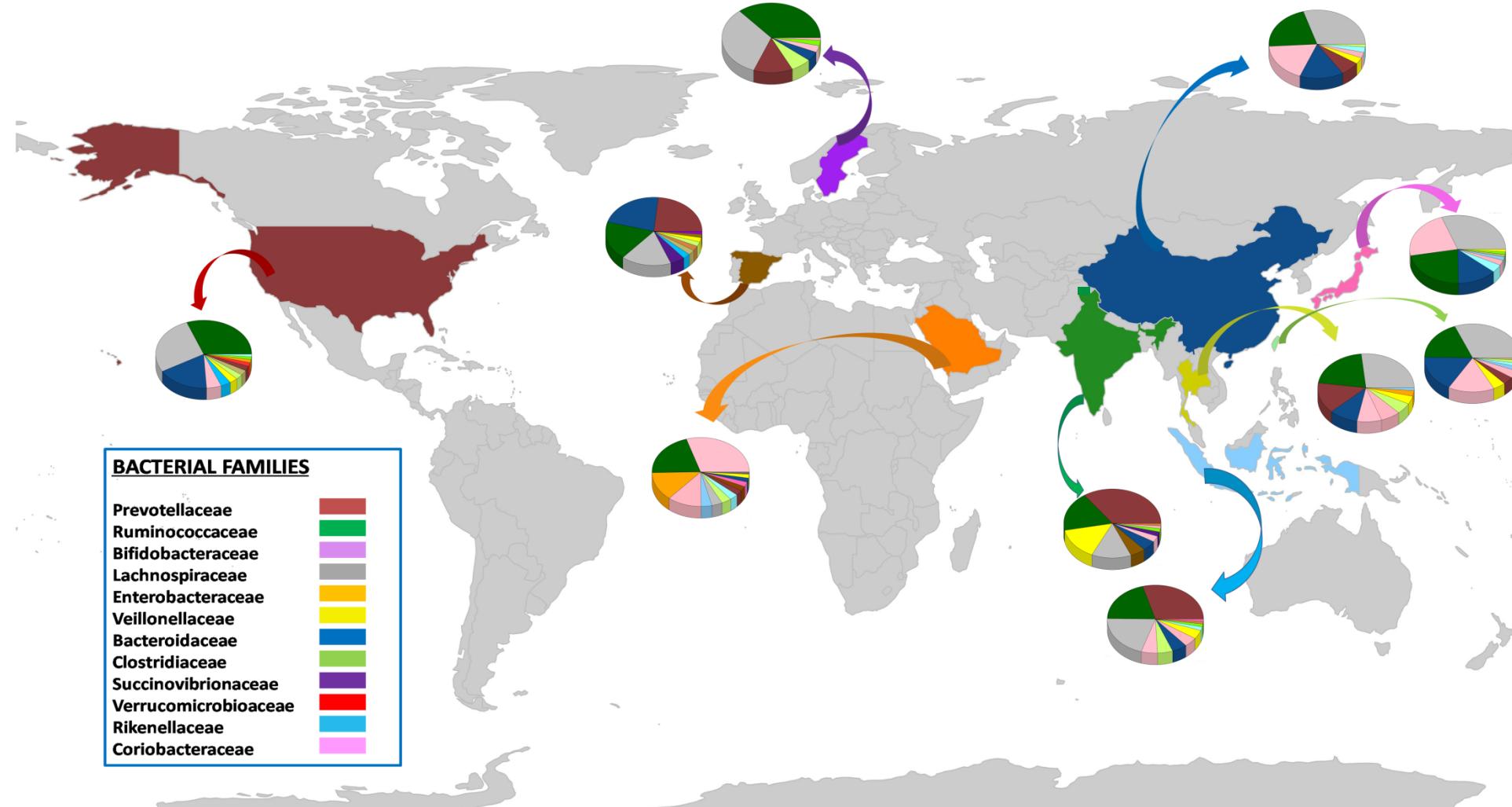
Significance of Comparative studies: Why do we need to do it and the strategy??



Indian Gut Microbiome Comparison at Global Level

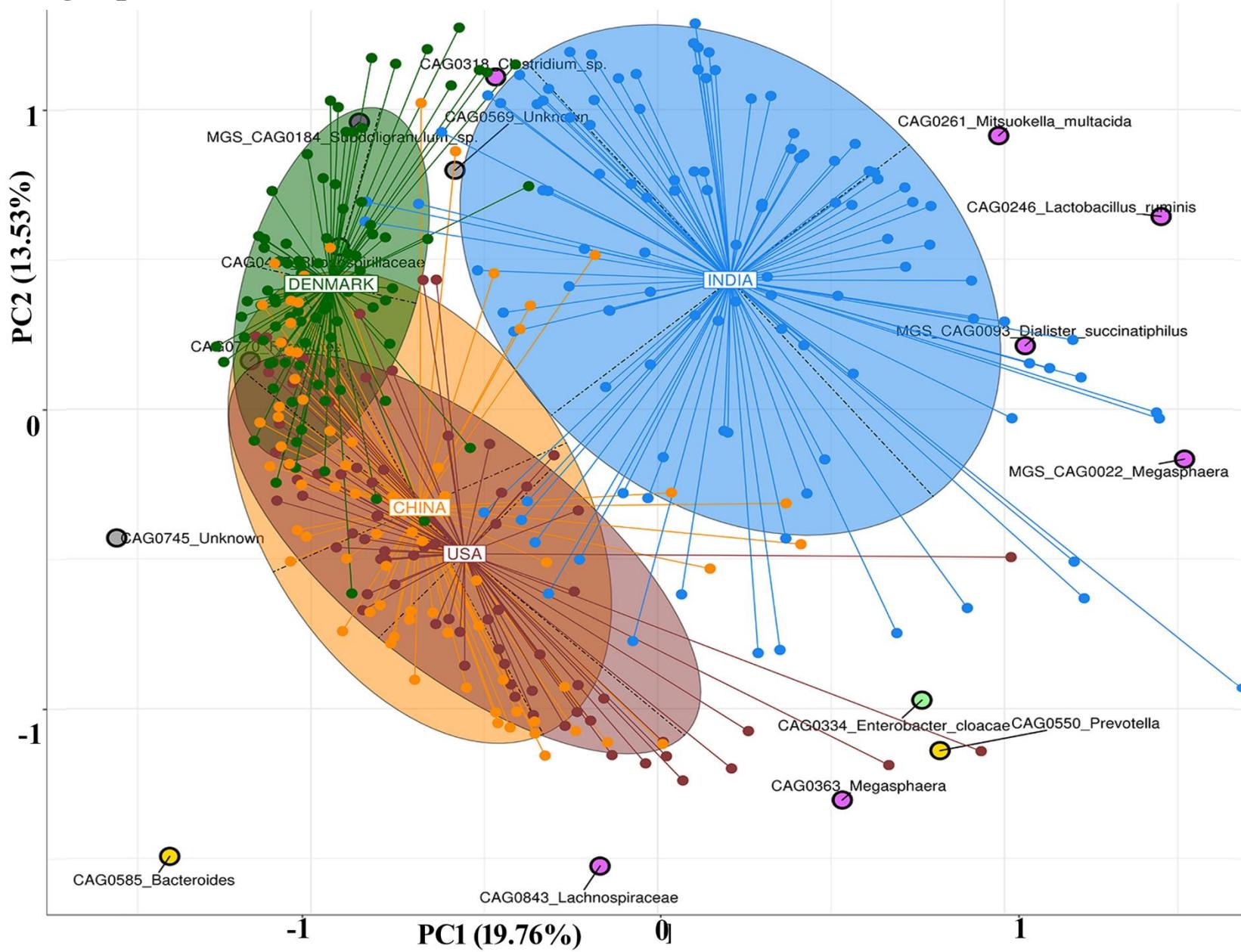
Prevotellaceae and Veillonellaceae
Bacteroidaceae and Bifidobacteraceae

↑ in Indian population
↓ in Indian population





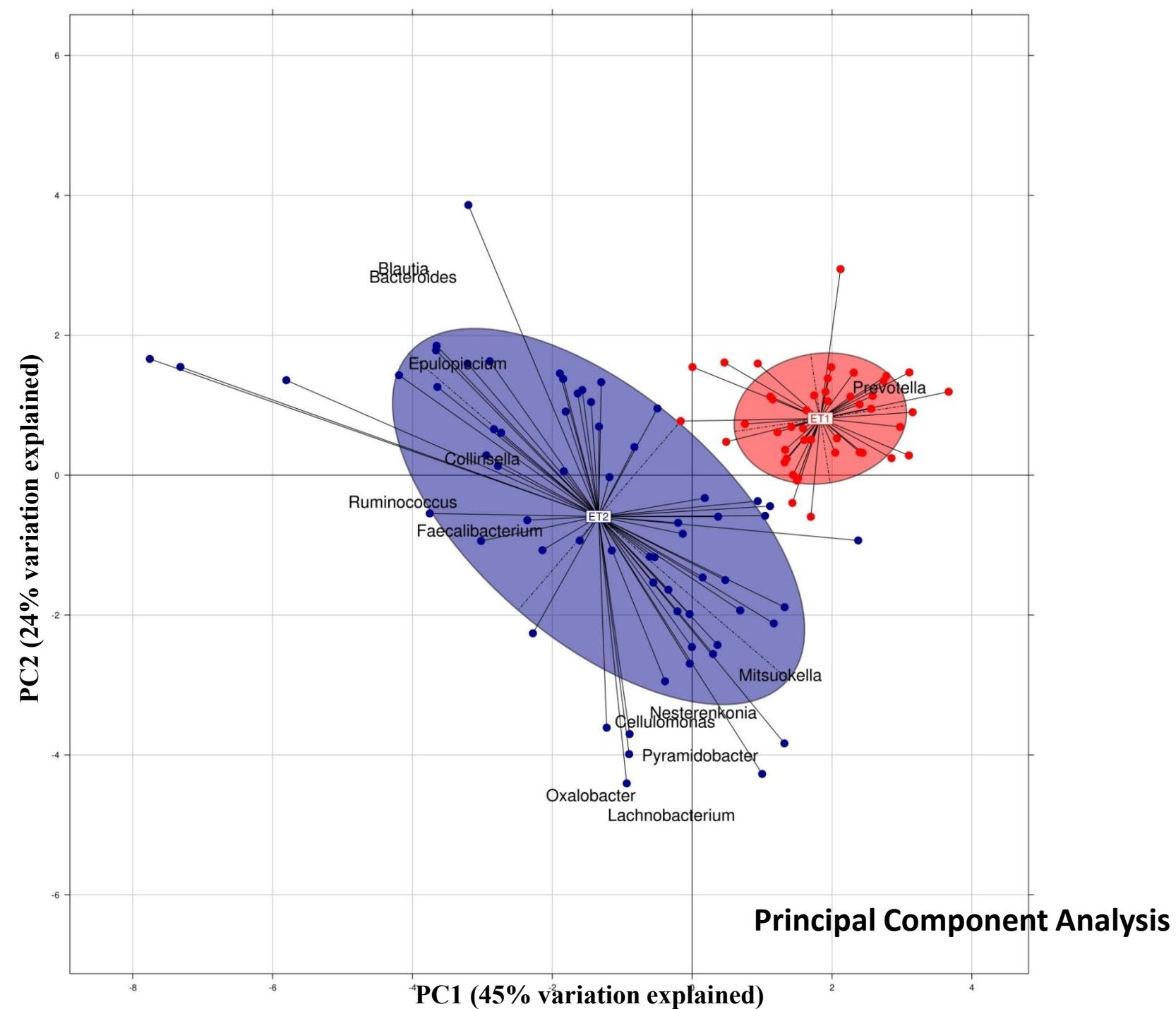
Metagenomewide association study identifies **Prevotella**, **Megasphaera**, **Lactobacillus** and **Mitsuokella** to be driver species driving separation of Indian Microbiome





Clusters identified in Indian population

Amplicon Analysis



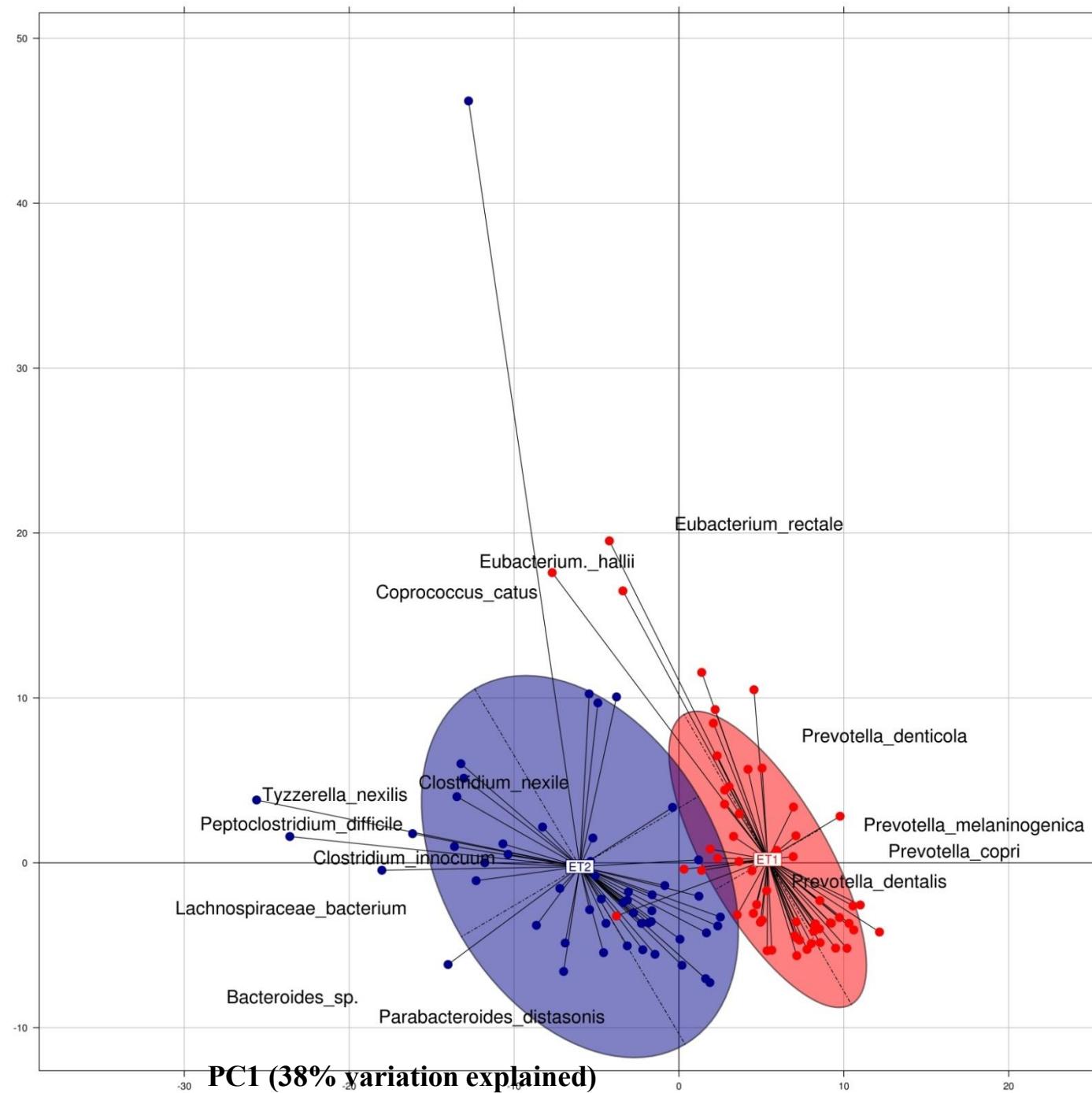
Clusters identified in Indian population

Metagenome Analysis

Principal Component Analysis

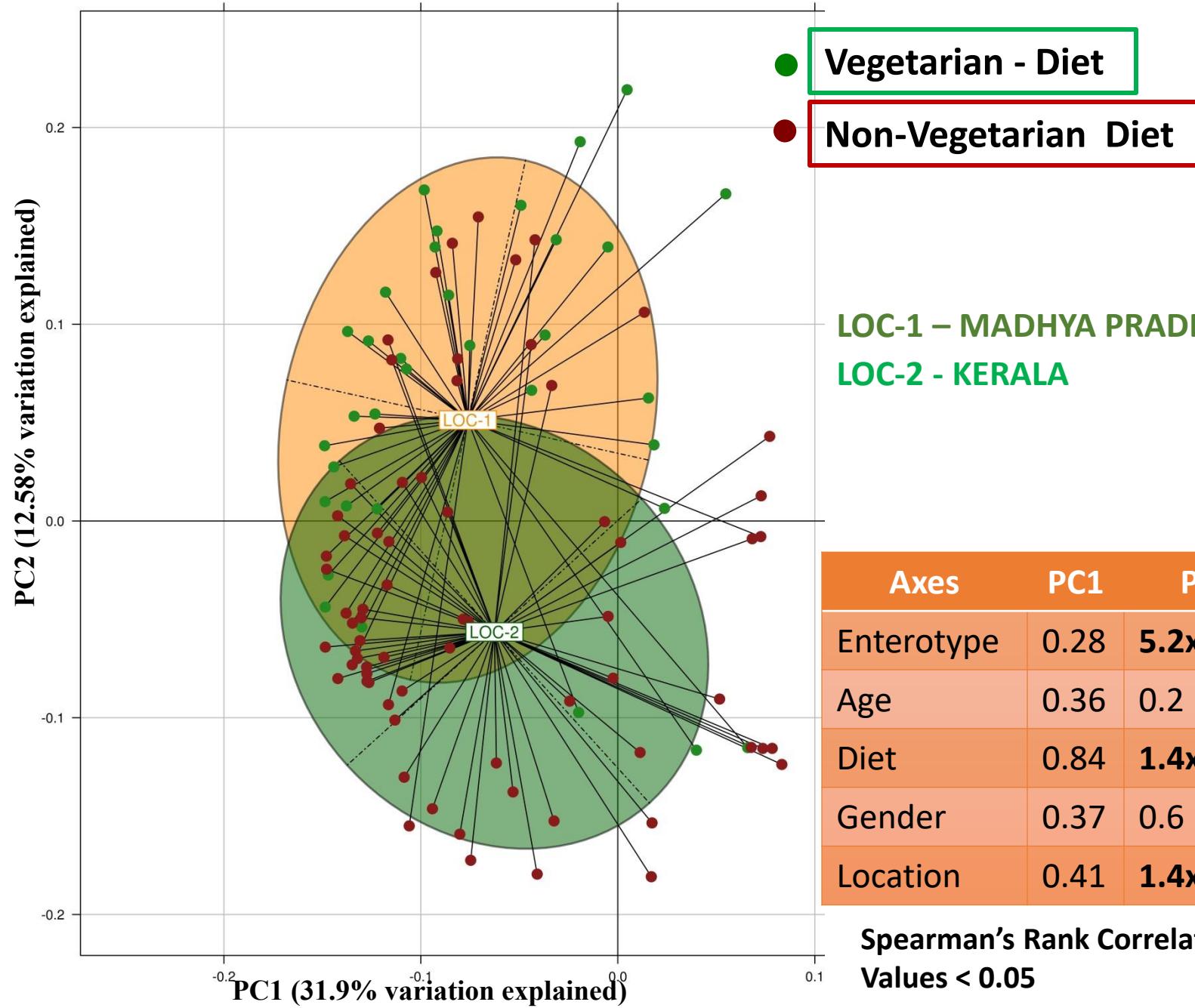
PC2 (22% variation explained)

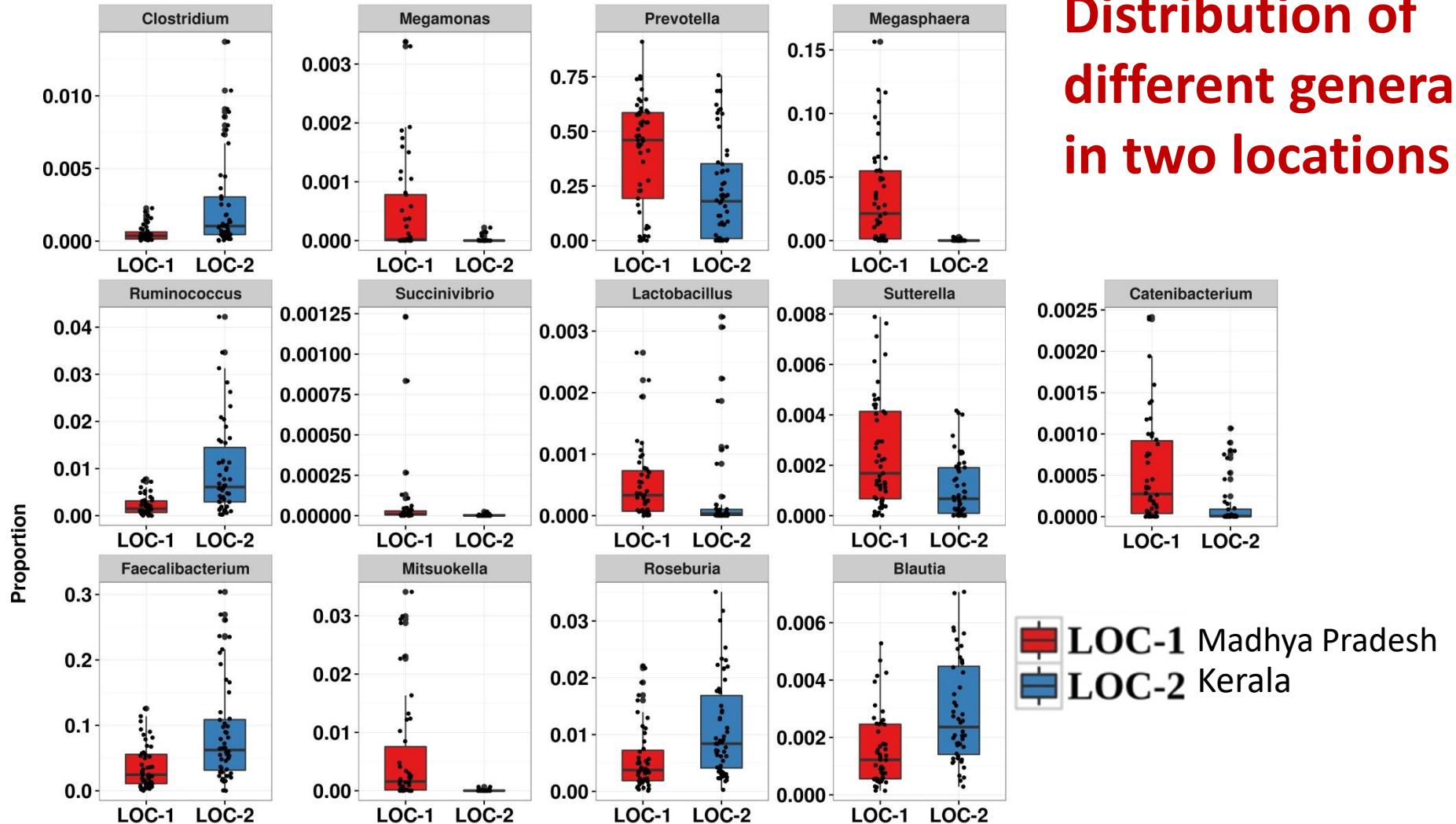
PC1 (38% variation explained)





Diet and Location explains the Clustering





Higher Abundance in MP

Megamonas, Prevotella, Megasphaera, Lactobacillus, Mitsuokella and Catenibacterium

Higher Abundance in Kerala

Clostridium, Ruminococcus, Faecalibacterium, Roseburia and Blautia

Wilcoxon Rank sum test (P < 0.05)

Distribution of different genera in two locations

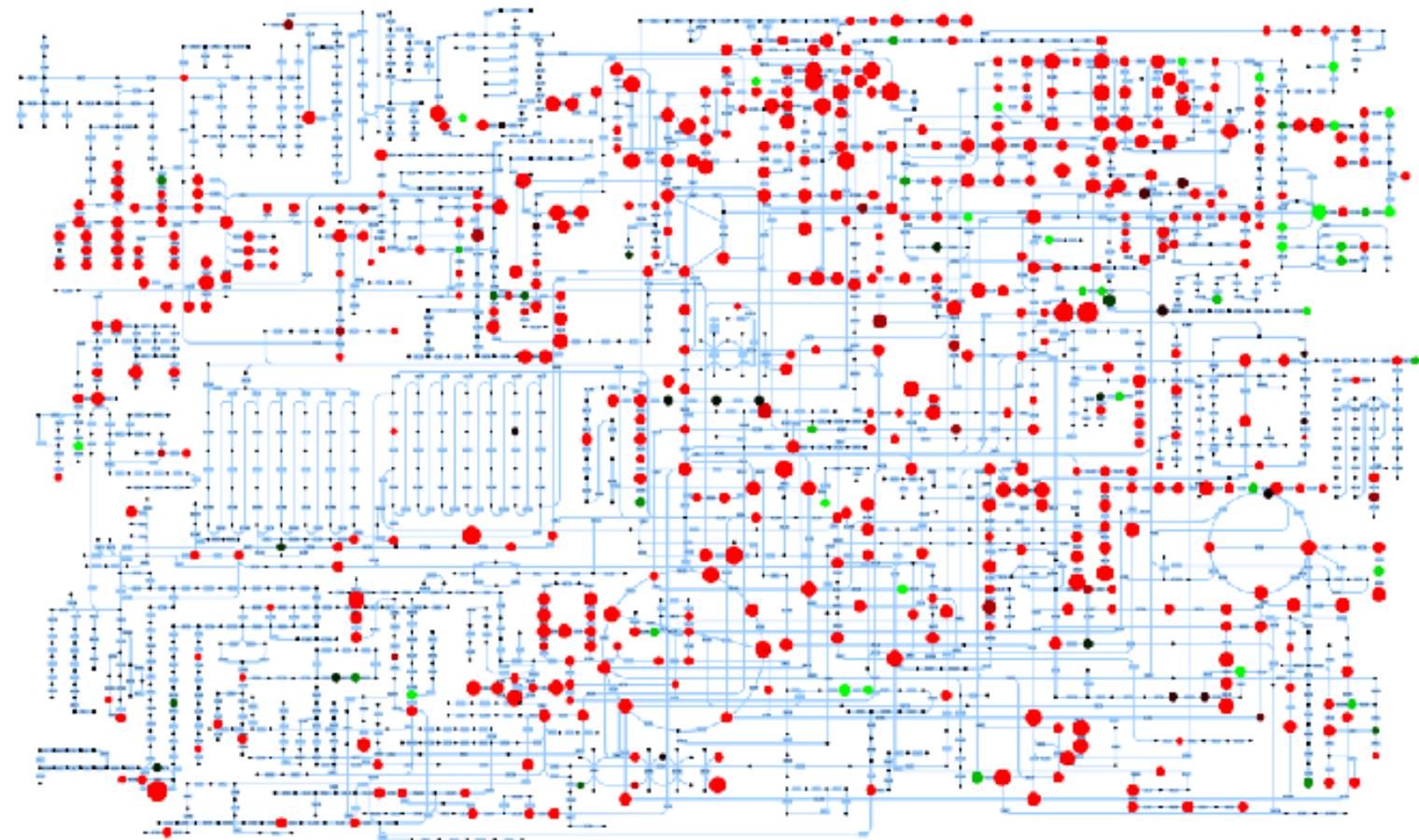
Significance of metabolome data

Microbial functions and metabolites associated with microbiome

- To decipher the microbial functions that play important role in well being of an individual.
- Identification of microbial metabolites that are the final end products of microbial metabolism.

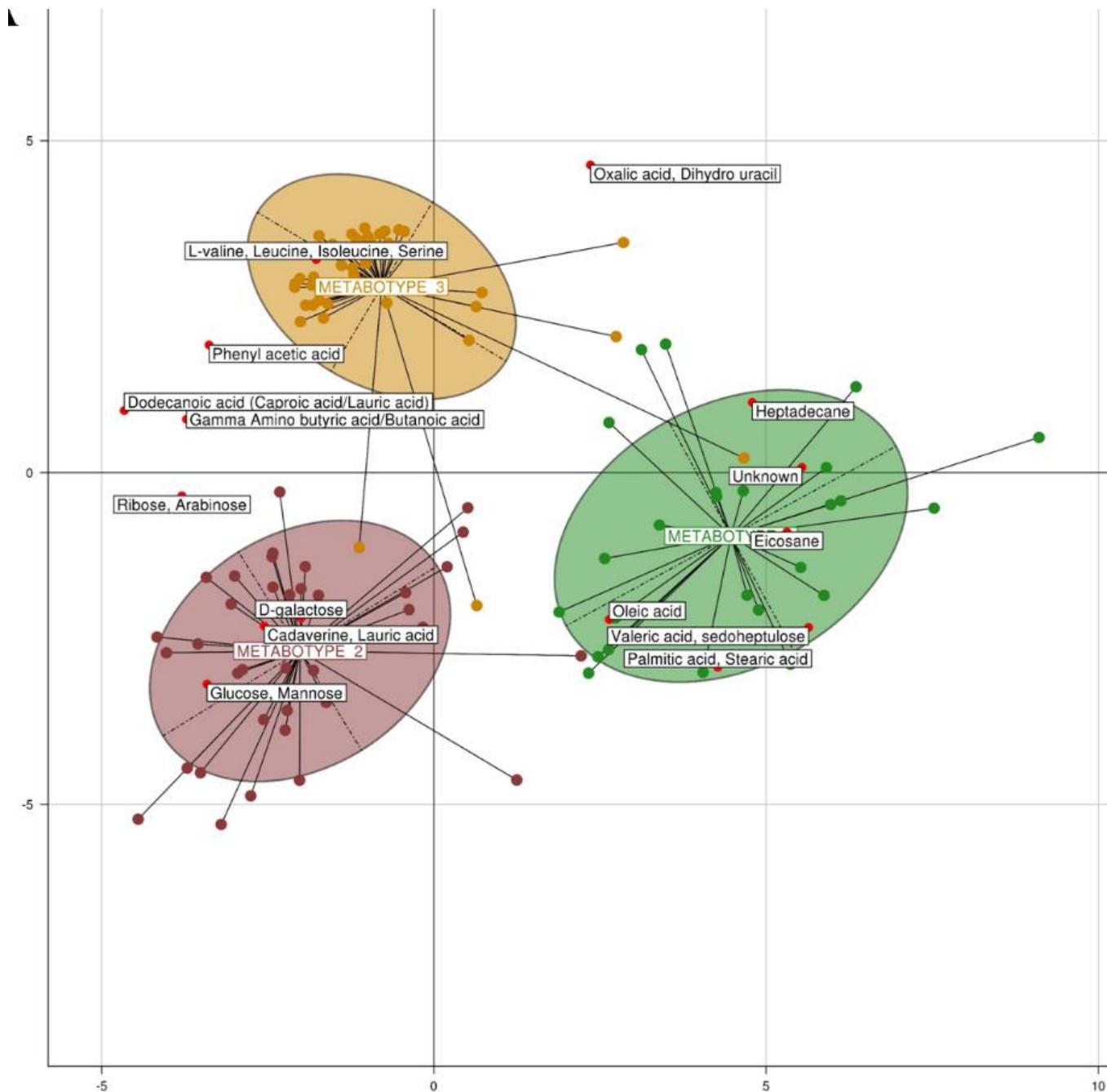
**GC-MS analysis of
stool samples and
serum samples**

**Whole Genome
Shotgun
sequencing of DNA
extracted from
stool samples**





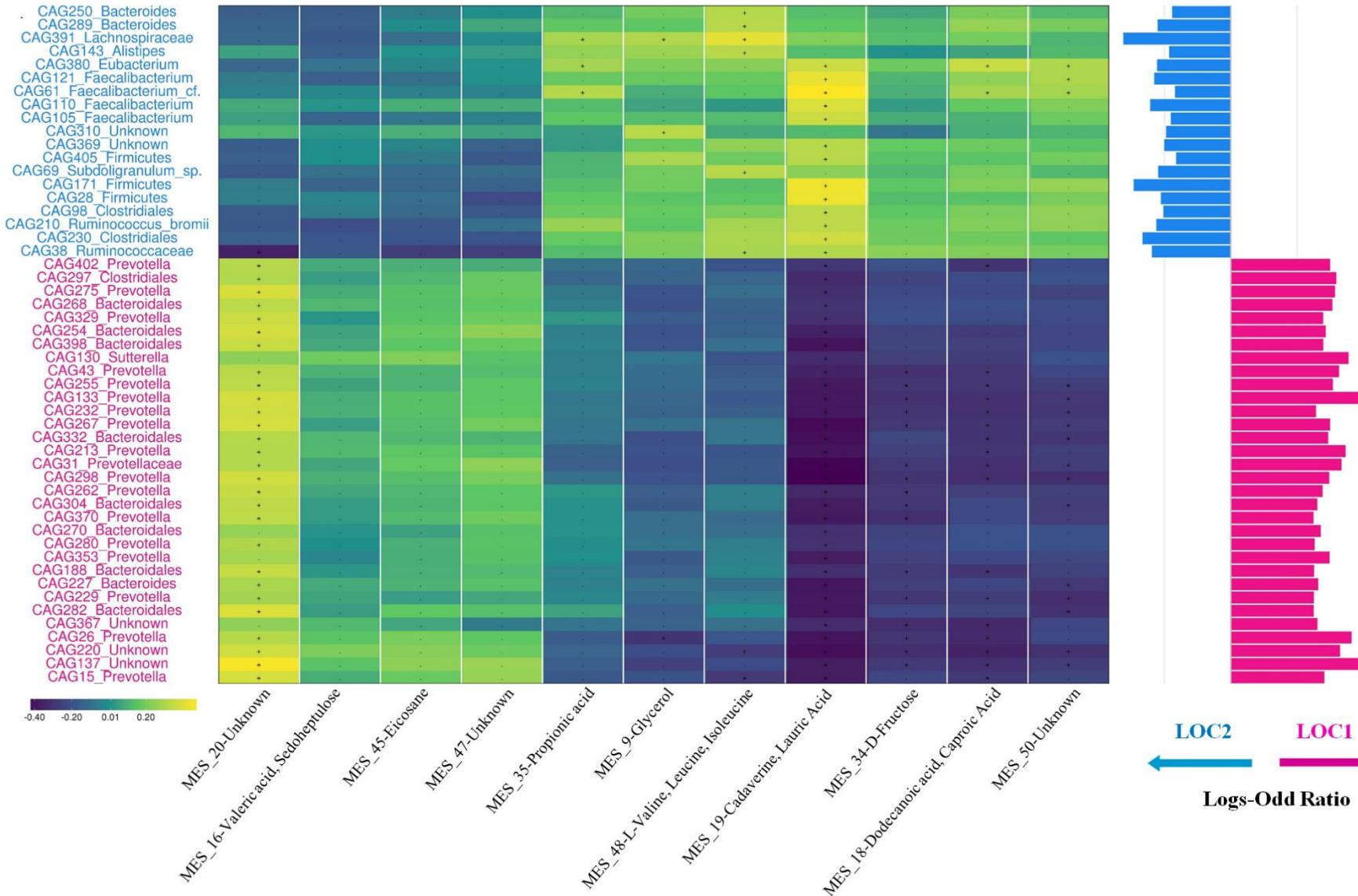
Metabolomic analysis identified three clusters (Metabotypes) in Indian population



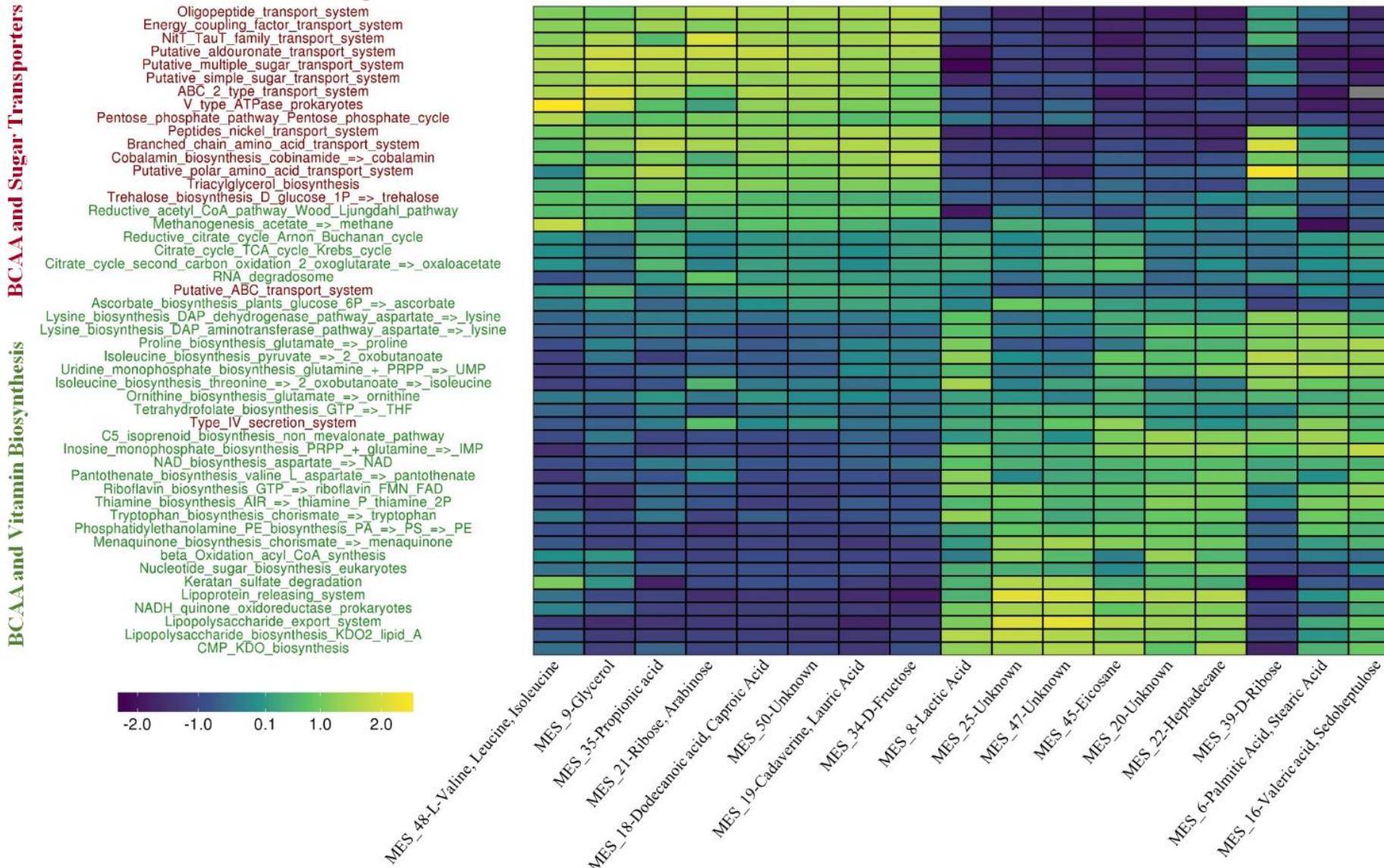
Axis	Variable	P-Value
PC1	Location	0.002068
PC1	Diet	0.036232
PC1	Age	0.854485
PC1	Gender	0.677398
PC2	Location	0.339138
PC2	Diet	0.000156
PC2	Age	0.194227
PC2	Gender	0.657895



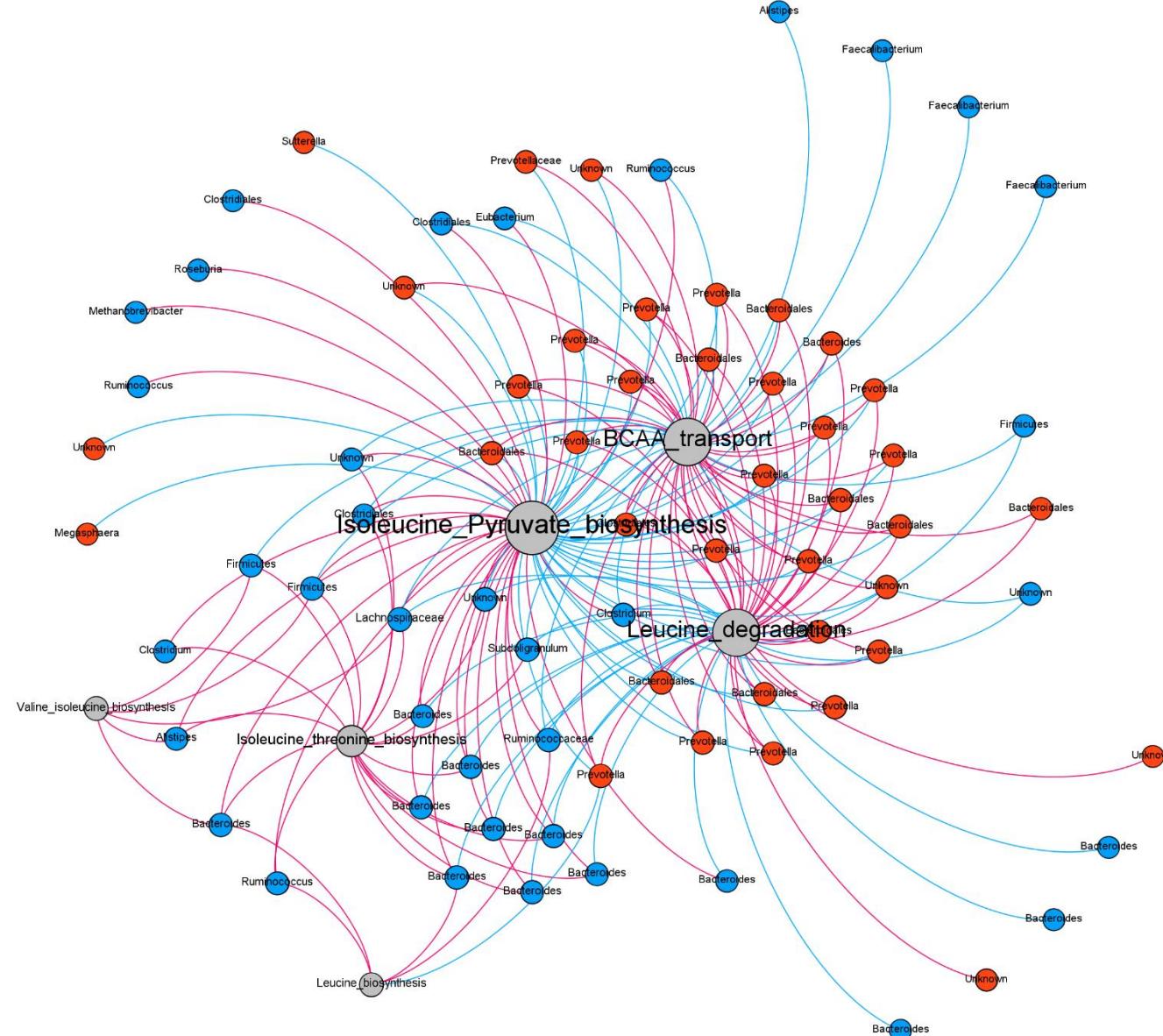
Association of metabolites with Metagenomic species identified Prevotella associated with Metabotype-1 and Bacteroides with Metabotype-2



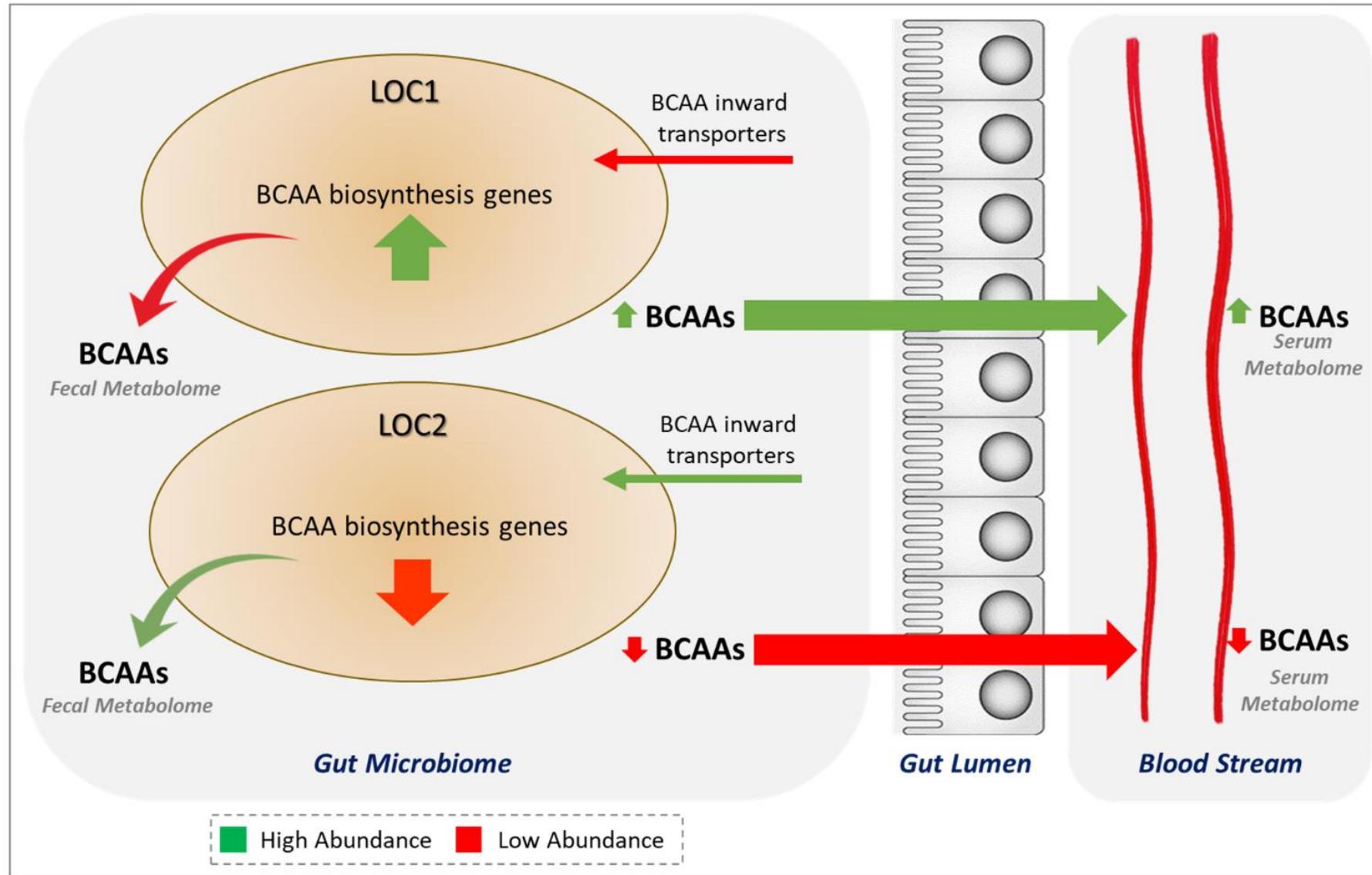
Pathways for BCAA biosynthesis were negatively correlated to BCAA levels in serum whereas transporters showed positive correlation



Prevotella regulated BCAA biosynthesis through threonine independent pathway



The dynamics of Branched chain amino acids and their metabolism in gut microbiome were found differentially abundant in LOC-1 and LOC-2 with their transporters and biosynthetic pathways playing major roles.



Conclusions

- Prevotella and Megaphaera drive the unique composition of Indian gut microbiome which makes it different from other populations across globe.
- Indian populations differ significantly between two locations within India.
- Prevotella dominated the Vegetarian population whereas, Bacteroides dominated the Non-Vegetarian population
- The diet and location play important role in guiding the metabolomics structure in gut of Indian population.
- BCAA transporters and BCAA biosynthesis pathways show differential correlations with BCAA levels in gut and serum thus playing important role in BCAA flux.
- Prevotella regulates BCAA through threonine independent BCAA biosynthesis pathway



Investigating the composition, diversity, and functional roles of *Prevotella* in the human gut

Dataset

- 586 healthy samples from western and non-western populations
- Largest Indian cohort comprising of 200 samples
- 189 Inflammatory Bowel Disease samples from western populations.

npj Biofilms and Microbiomes

www.nature.com/npjbiofilms

ARTICLE

OPEN

Check for updates

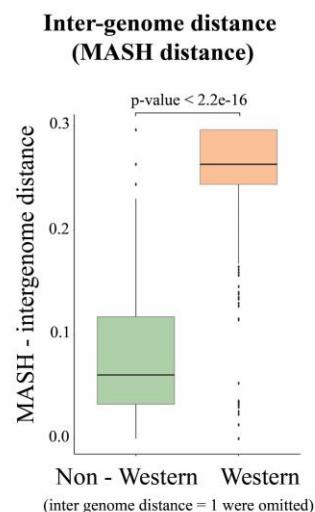
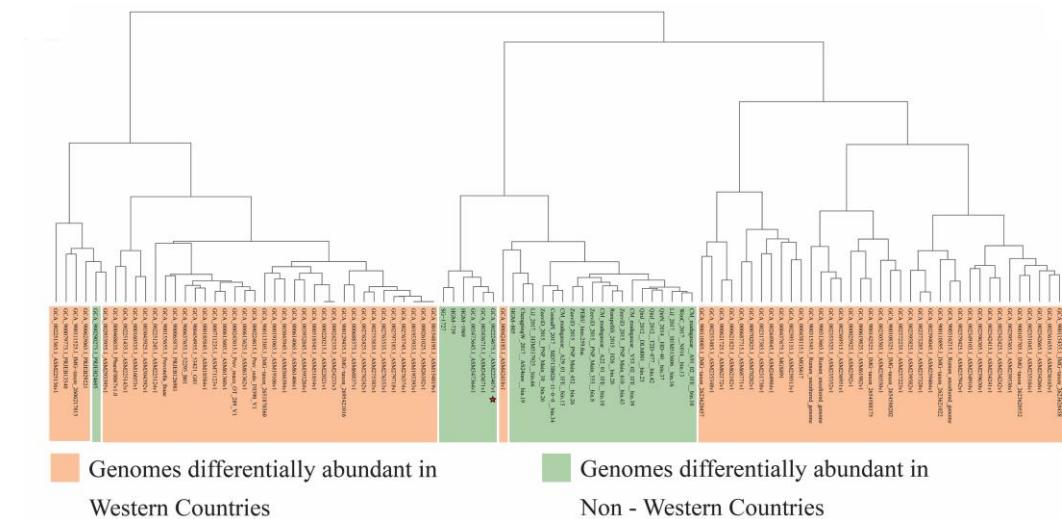
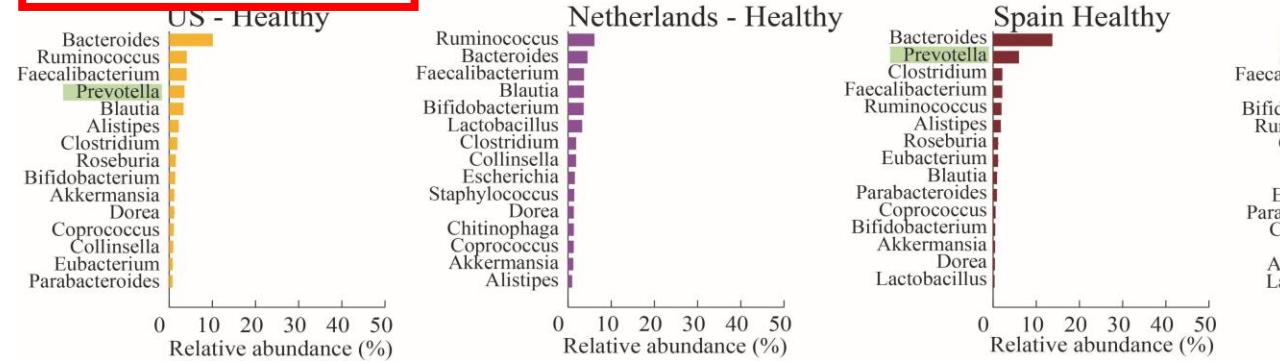
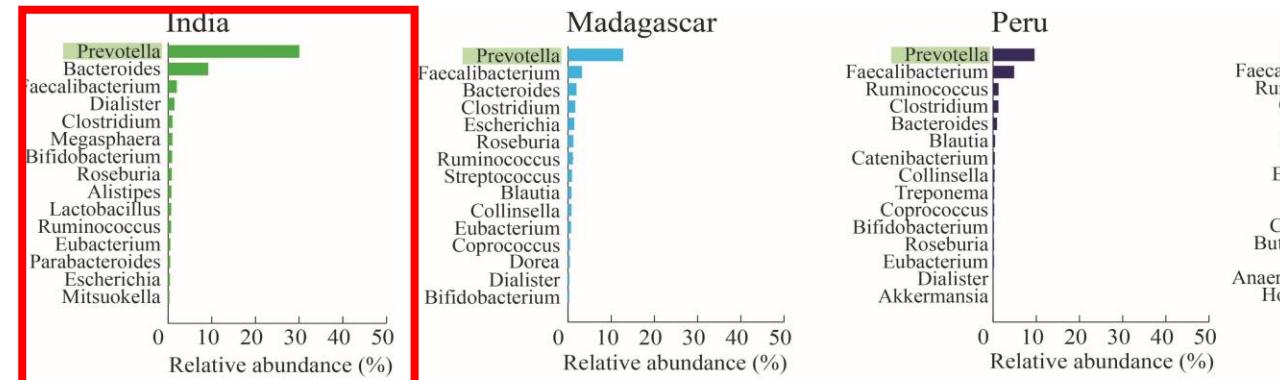
Western and non-western gut microbiomes reveal new roles of *Prevotella* in carbohydrate metabolism and mouth–gut axis

Vishnu Prasoodanan P. K.¹, Ashok K. Sharma^{1,2}, Shruti Mahajan¹, Darshan B. Dhakan^{1,3}, Abhijit Maji^{1,4}, Joy Scaria^{1,4} and Vineet K. Sharma¹

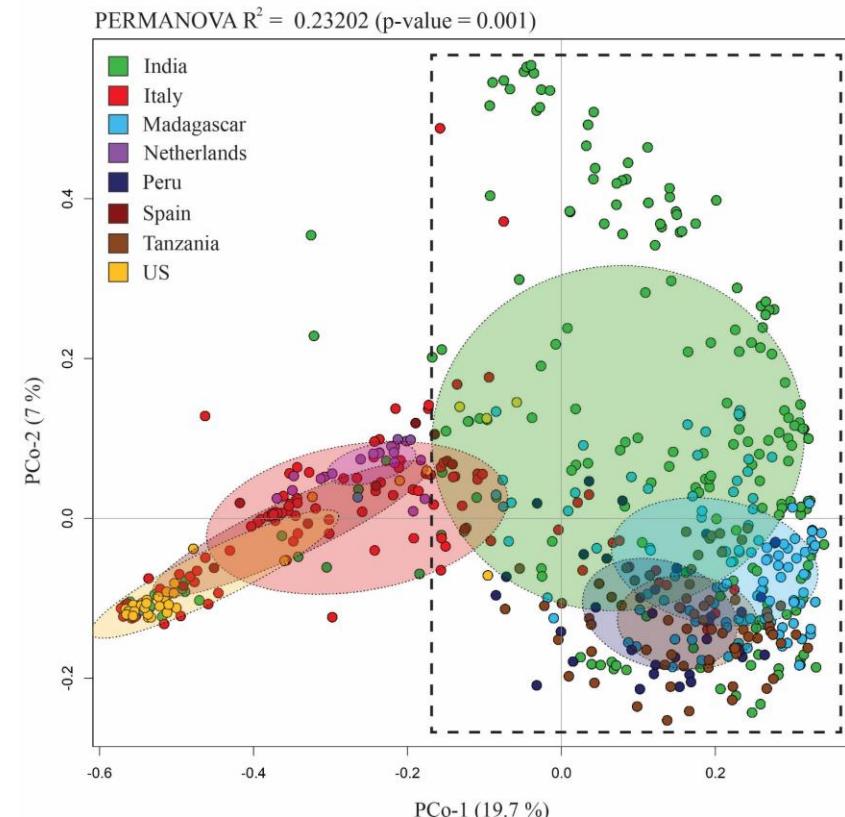
The abundance and diversity of host-associated *Prevotella* species have a profound impact on human health. To investigate the composition, diversity, and functional roles of *Prevotella* in the human gut, a population-wide analysis was carried out on 586 healthy samples from western and non-western populations including the largest Indian cohort comprising of 200 samples, and 189 Inflammatory Bowel Disease samples from western populations. A higher abundance and diversity of *Prevotella copri* species enriched in complex plant polysaccharides metabolizing enzymes, particularly pullulanase containing polysaccharide-utilization-loci (PUL), were found in Indian and non-western populations. A higher diversity of oral inflammations-associated *Prevotella* species and an enrichment of virulence factors and antibiotic resistance genes in the gut microbiome of western populations speculates an existence of a mouth-gut axis. The study revealed the landscape of *Prevotella* composition in the human gut microbiome and its impact on health in western and non-western populations.

npj Biofilms and Microbiomes (2021)7:77; <https://doi.org/10.1038/s41522-021-00248-x>

Differential Distribution of *Prevotella* sp in Indian- Non-western and Western Gut Microbiome

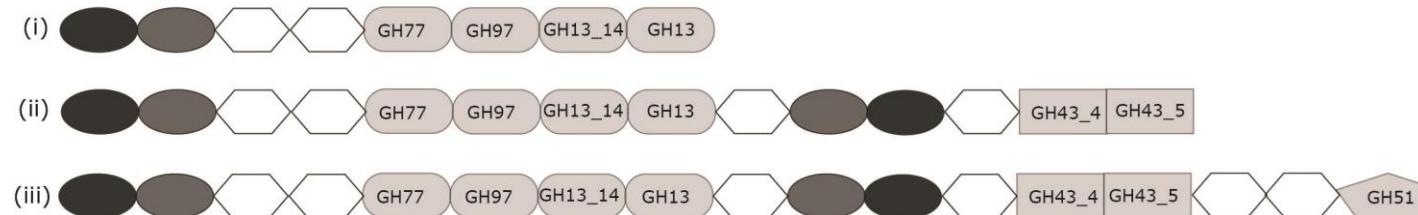


- 102 *Prevotella* genomes/bins were differentially abundant between western and non-western populations.
- 26 *Prevotella* genomes/bins were differentially abundant in non-western population and 76 genomes/bins were differentially abundant in western population

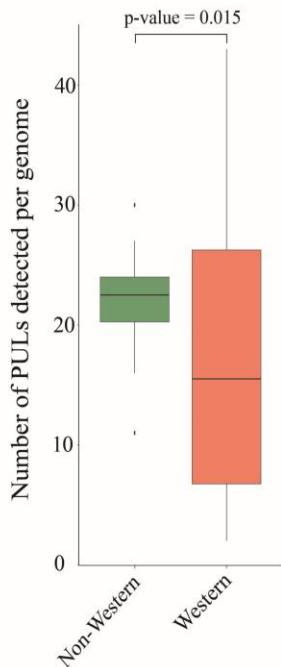


P. copri performs plant-polysaccharide metabolism in Non-western Gut Microbiome

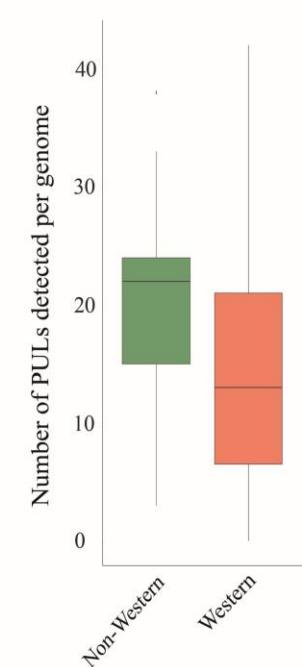
- 37,389 Polysaccharide Utilization Loci (PULs) in 2,204 genomes from PGD
- 2,197 *Prevotella* genomes were predicted to have at least one PUL



[A] Number of PULs in *Prevotella* genomes differentially abundant in Western and Non-Western populations



[B] Number of PULs in 50 *Prevotella* genomes that showed highest abundance in Western and Non-Western populations



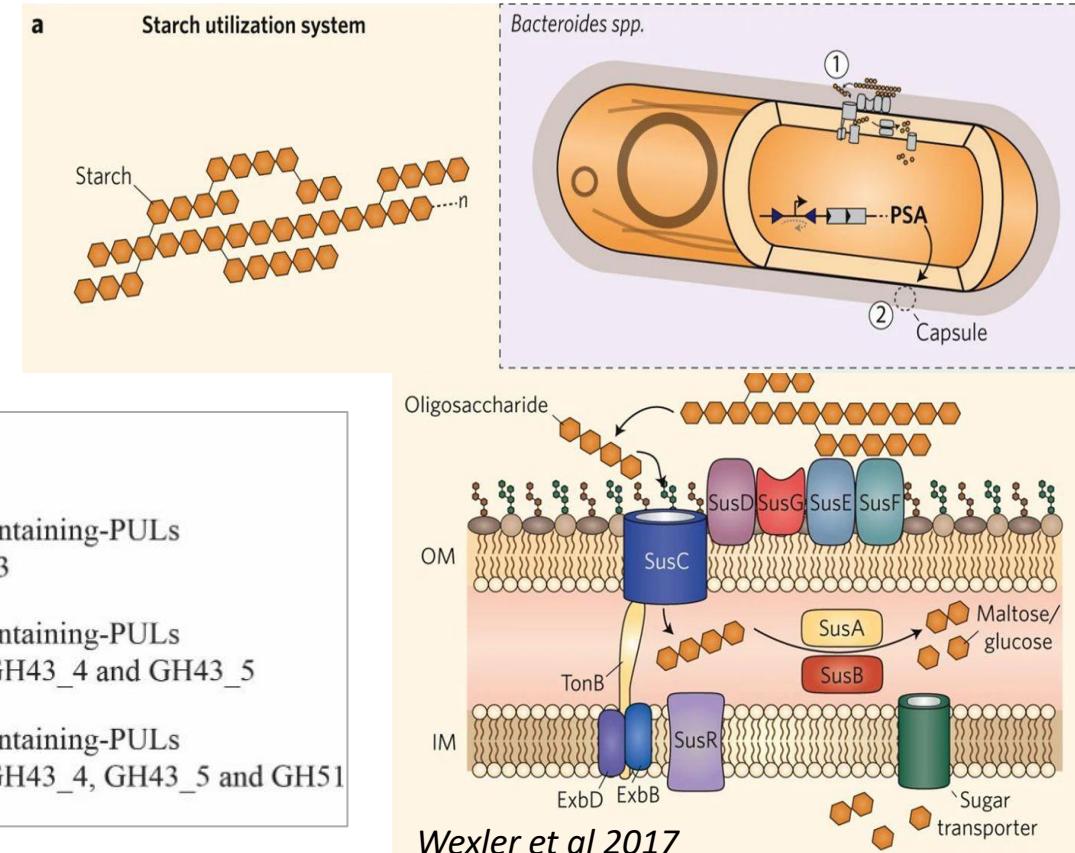
1023 *P. copri* genomes

782 *P. copri* genomes with pullulanase-containing-PULs having GH77, GH97, GH13_14 and GH13

569 *P. copri* genomes with pullulanase-containing-PULs having GH77, GH97, GH13_14, GH13, GH43_4 and GH43_5

168 *P. copri* genomes with pullulanase-containing-PULs having GH77, GH97, GH13_14, GH13, GH43_4, GH43_5 and GH51

37 CAZy families and subfamilies were identified as differentially abundant in *Prevotella* species in the Indian population compared to other healthy populations



Wexler et al 2017

Ability of Bacteroidetes species to recognize and metabolize plant and host derived polysaccharides

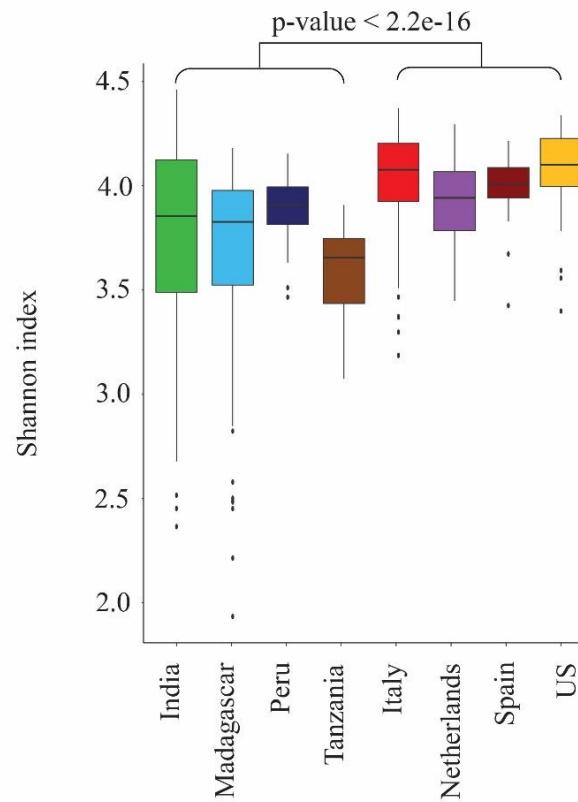
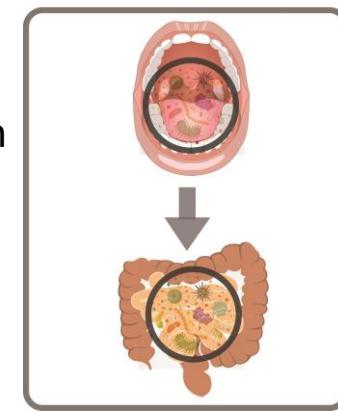
Gut *Prevotella* possibly originates from Oral *Prevotella* in Western Population gut microbiomes



- ❖ 30 *Prevotella* sp were Differentially abundant between Healthy and IBD
- ❖ Eight of these were significantly abundant in IBD, of which Seven were common in US and Netherlands IBD datasets
- ❖ Seven *Prevotella* genomes identified as differentially abundant in IBD populations

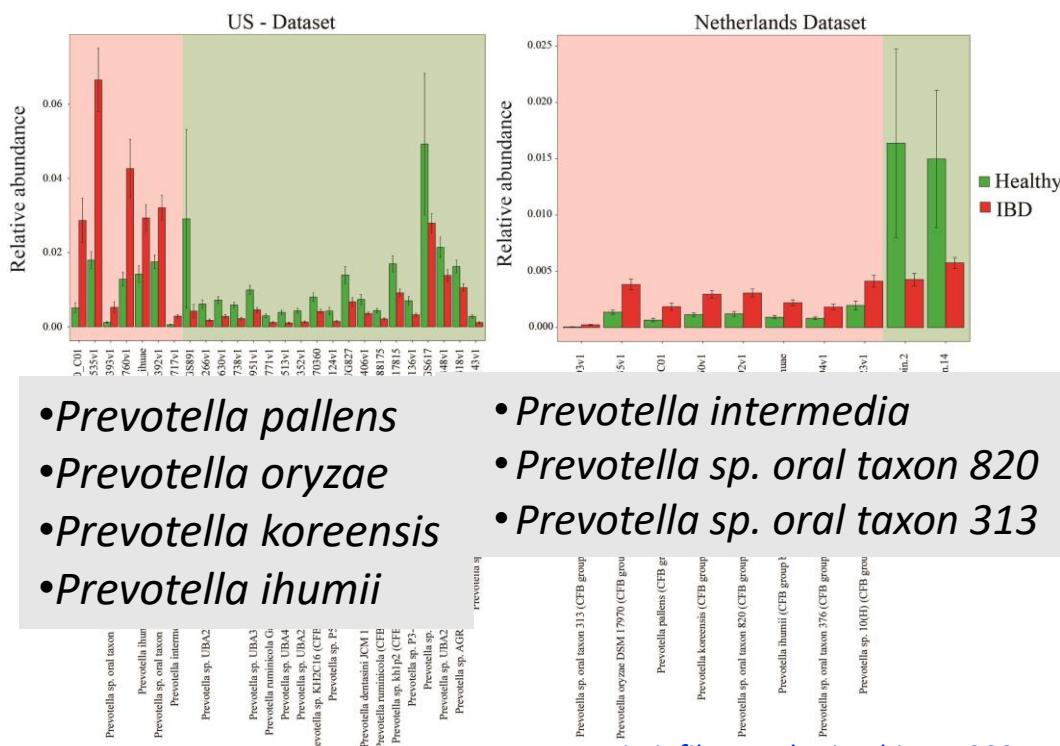
- ❖ In IBD patients, ingested oral bacteria help in disease pathogenesis by translocating to the lower digestive tract
- ❖ In colorectal cancer patients, a higher enrichment of oral species *P. intermedia* and *P. nigrescens* has been observed
- ❖ Gut inflammation disrupts colonization resistance mediated by healthy gut microbiota helping oral pathogens to ectopically colonize the gut

Mouth-gut axis



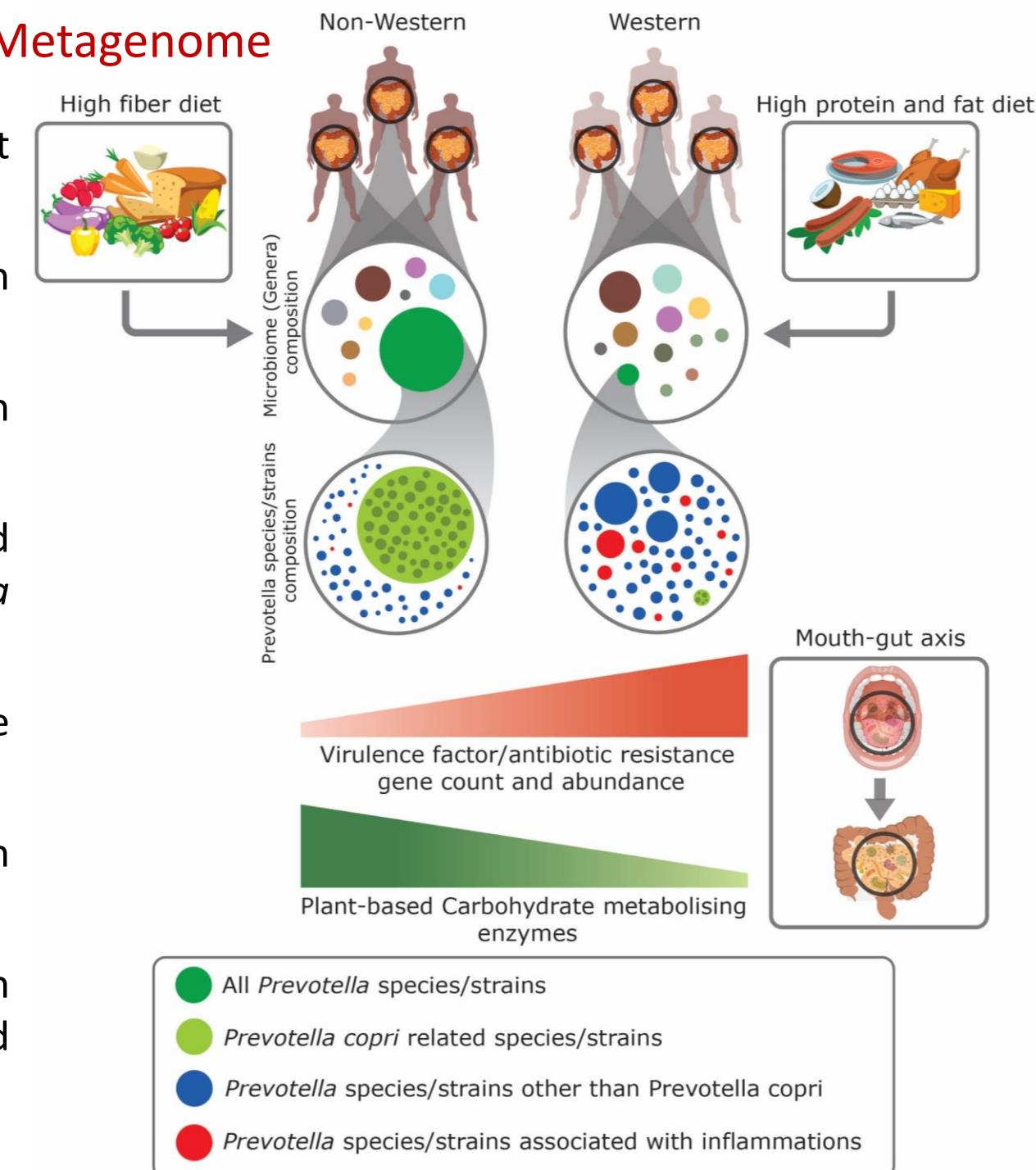
Virulence factors and Antibiotic Resistance Genes in *Prevotella*

Antibiotic resistance genes encoding proteins involved in the inactivation of antibiotics were the most abundant in *Prevotella* genomes, followed by those involved in antibiotic efflux, antibiotic target alteration, and target protection in western populations



Insights from The Unique Indian Gut Metagenome

- Largest gut metagenomic study of healthy cohort samples from various parts of India
- Prevotella* emerged as most abundant genus in Indian gut
- Indian and non-western populations showed high relatedness noted in *P. copri* clade composition analysis
- Significantly higher abundance of plant-based carbohydrate metabolizing enzymes in *Prevotella* genomes in non-western populations including India
- Several novel strains and subspecies of *P. copri* are observed in non-western populations
- Higher genetic diversity in *Prevotella* sp. in western populations
- Differentially abundant *Prevotella* sp. in western populations are present in their oral microbiome and are associated with oral inflammatory conditions



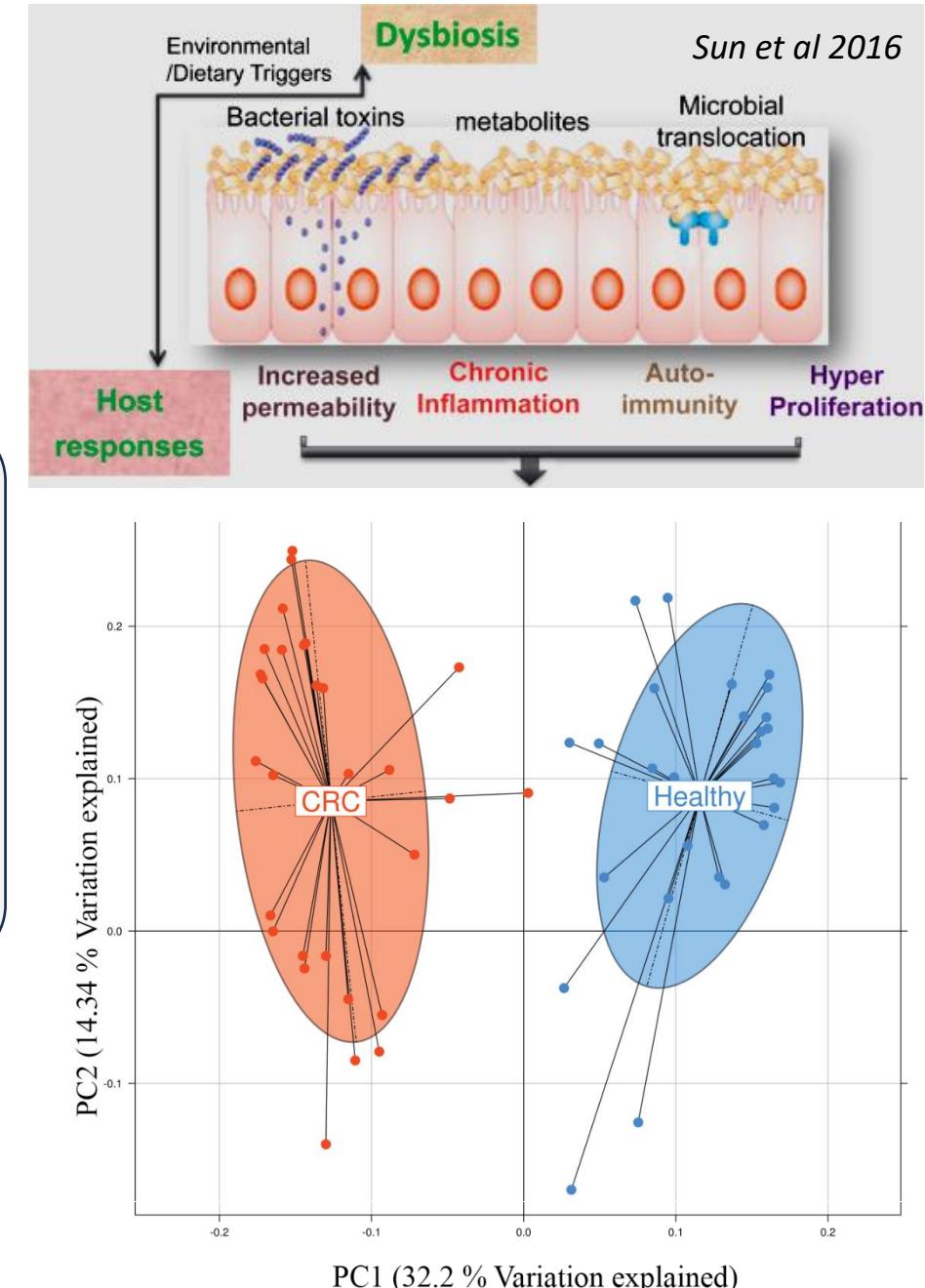
Colorectal Cancer Gut Microbiome: Biomarkers, new Bacterium associated with CRC, Diagnosis

- 3rd most common cancer and 2nd leading cause of cancer deaths
- Surprisingly lower in India, attributed to **high flavonoids consumption and plant-fibre based diets**
- Colorectal cancer risk on the rise in India: Due to western lifestyle

First Comprehensive Metagenomic and Metabolomic study from India

- Indian Samples from early to late stages of cancer
- Compared CRC GM and metabolome with healthy gut
- Confirmed the association of known bacterial taxa with CRC
- Constructed gene catalogue and metabolome for colorectal cancer
- Microbiome dysbiosis : reduction in pathways related to the biosynthesis of six out of the nine essential amino acids in CRC
- Comparison with Austrian and Chinese CRC and ML-based identification of Cohort-specific biomarkers

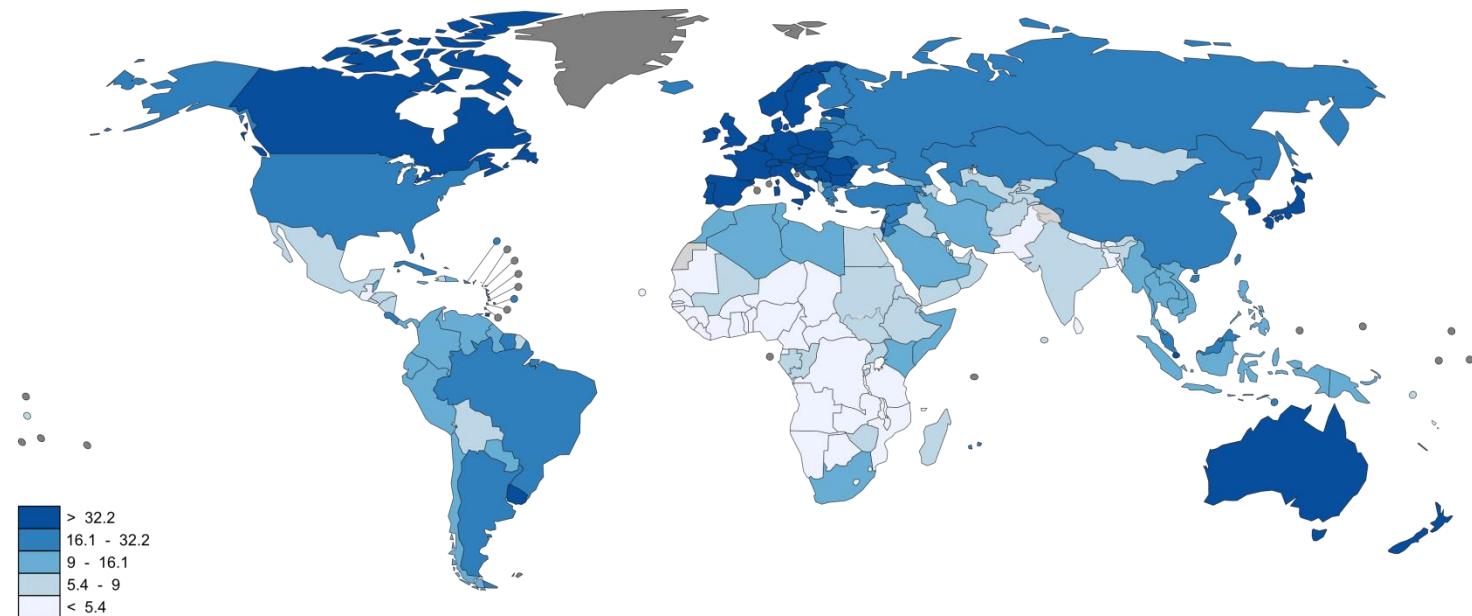
- Found a new bacterium *Flavonifractor plautii* associated with CRC
- 33 gene markers
- 20 taxonomic markers



Development of PCR, NGS and AI/ML based methods for non-invasive diagnosis of CRC, in progress

Colorectal Cancer Statistics

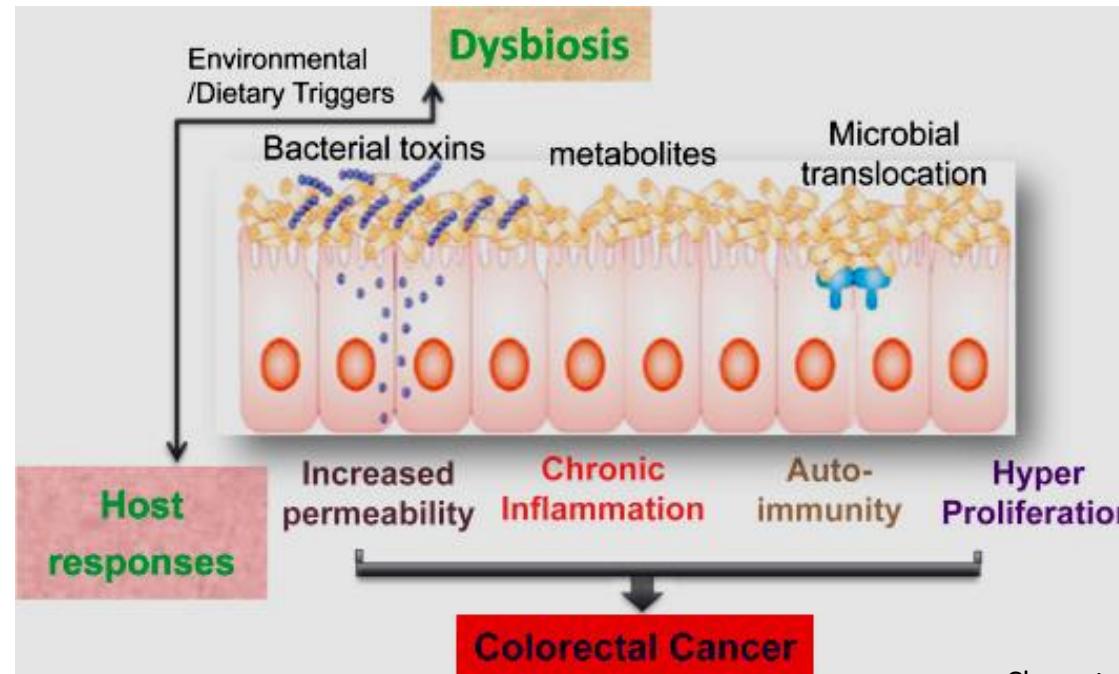
- **3rd most common cancer** in both males and females and the **2nd leading cause of cancer deaths**
 - Expected to **increase by 60%** to more than 2.2 million new cases and 1.1 million deaths by 2030.

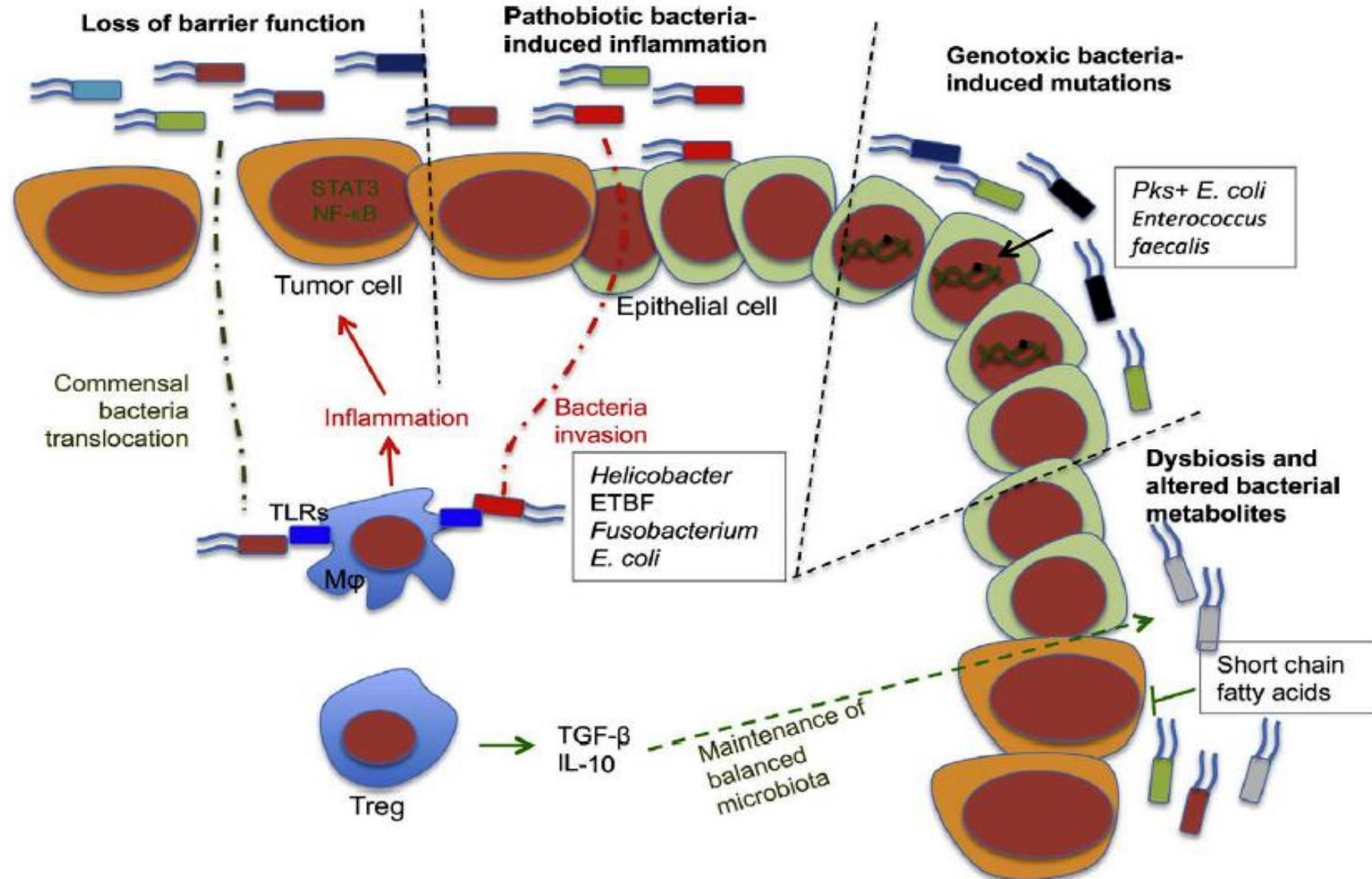


- Surprisingly lower in India but **on the rise** : Adoption of **western lifestyle**, Lack of **early detection** techniques
 - **Diet** has major influence on colorectal cancer risk
 - **Polyphenol-rich diet**: Associated with reduced inflammation and oxidative stress

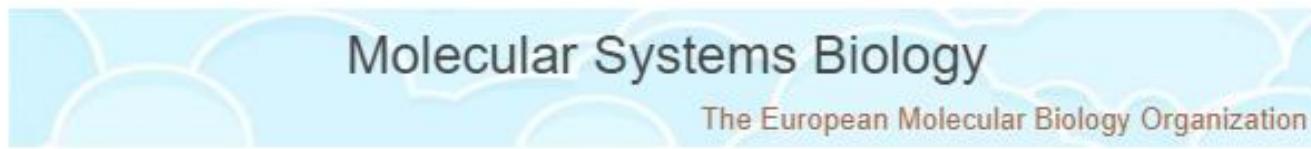
Role of microbiome in CRC

- Dysbiosis in the gut promotes chronic inflammatory conditions and the production of carcinogenic metabolites
- Inflammation in the gut induces carcinogenic mutagenesis and promotes colorectal cancer initiation
- Bacteria promotes CRC development by exploiting tumour surface barrier effects following cancer initiation



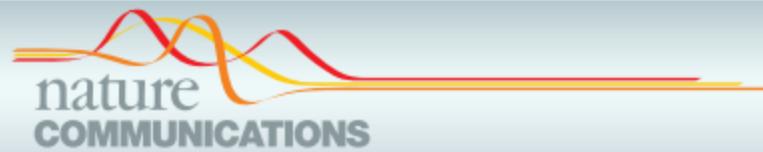


Metagenomic Studies before our work



Potential of fecal microbiota for early-stage detection of colorectal cancer

France 2014



Gut microbiome development along the colorectal adenoma-carcinoma sequence

Austria 2015

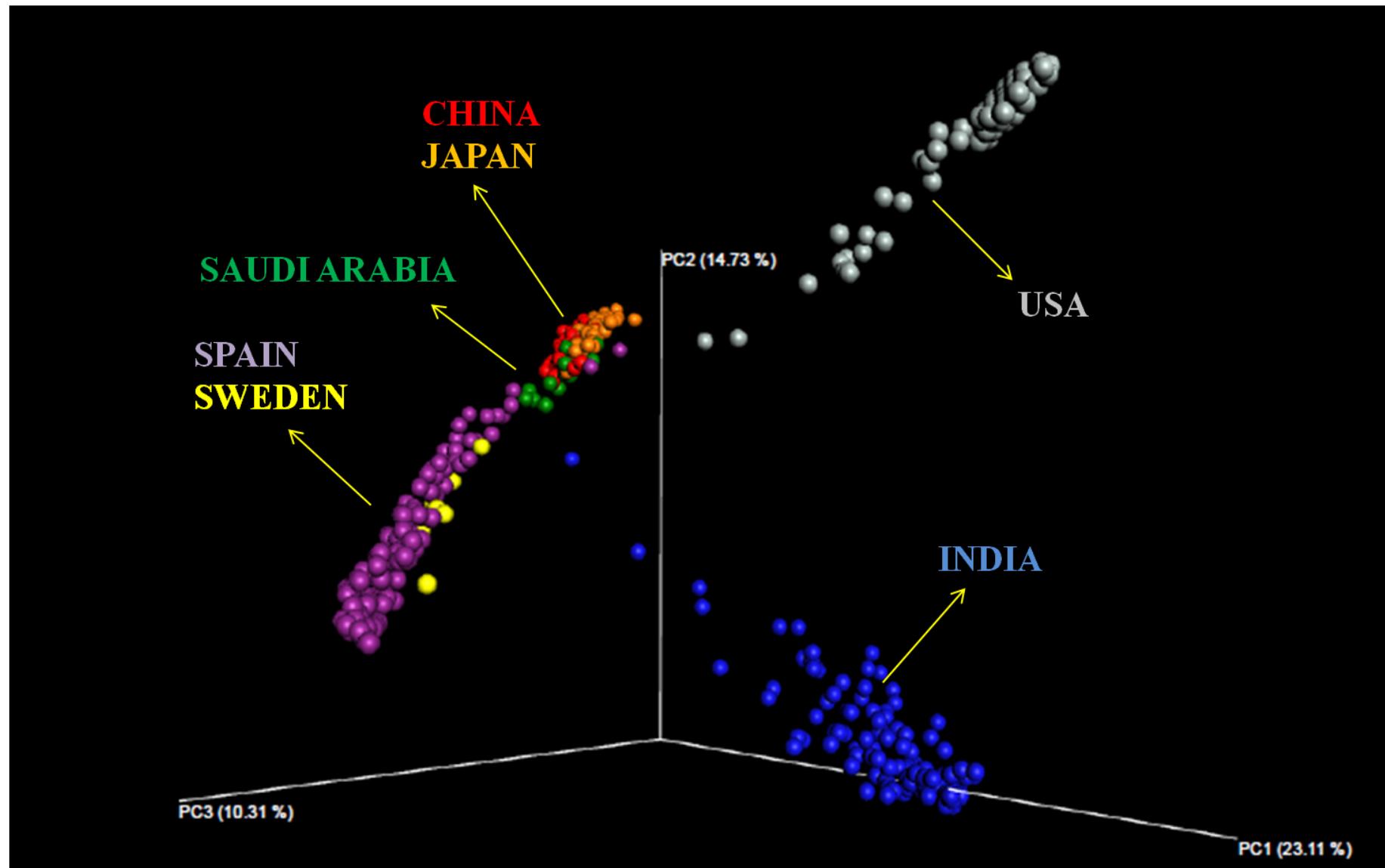
Gut microbiota

ORIGINAL ARTICLE

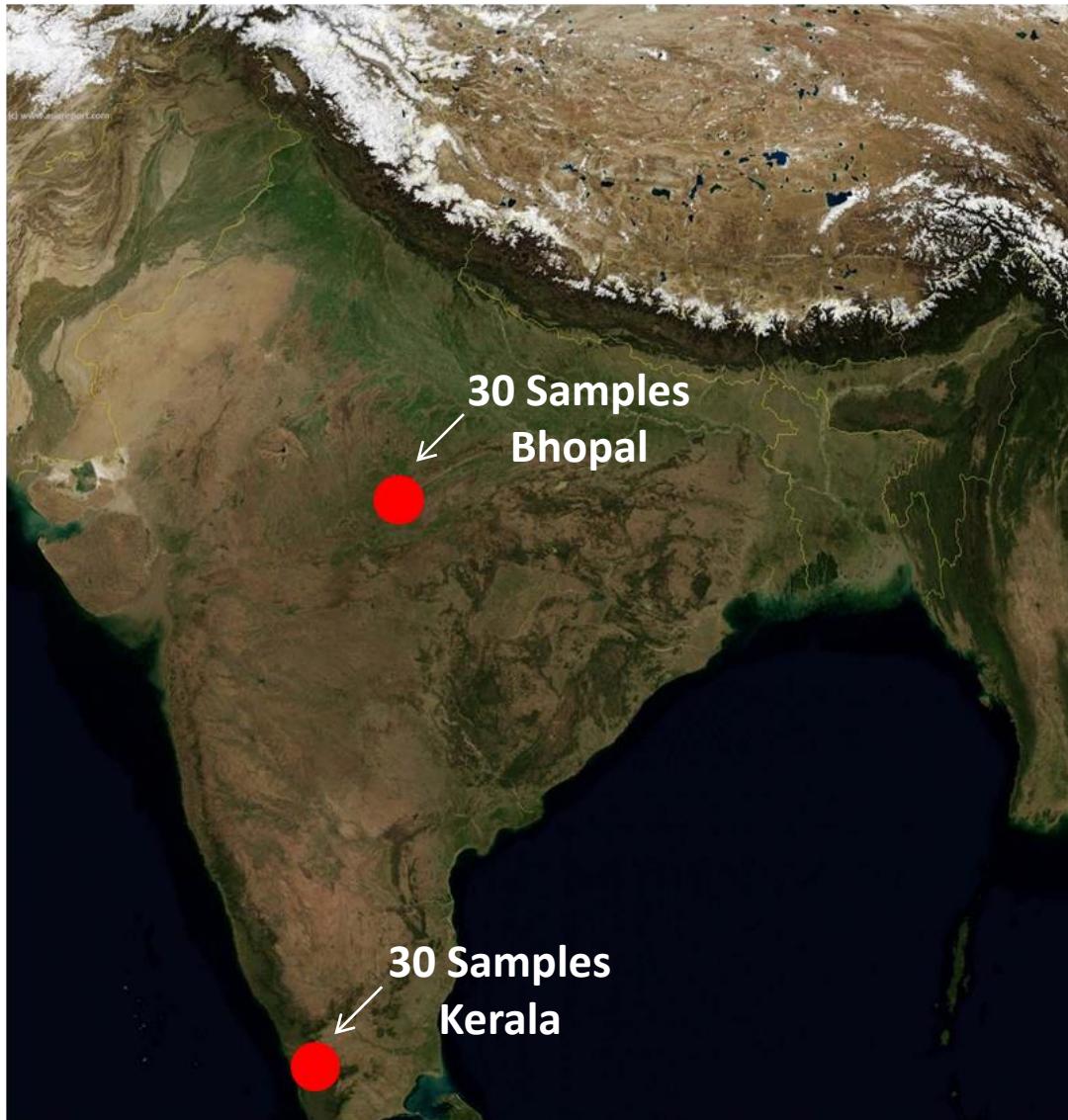
Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer

China 2016

CRC - Indian Perspective



Sample Collection



**Sample Size : 60 Individuals
(30 Cases, 30 Controls)**

Sample Type : Fecal

Sequencing : 10.7 ± 5.1 M reads/sample

Sample Inclusion Criteria:

- ✓ Colonoscopy
- ✓ FOBT Test
- ✓ TNM Staging

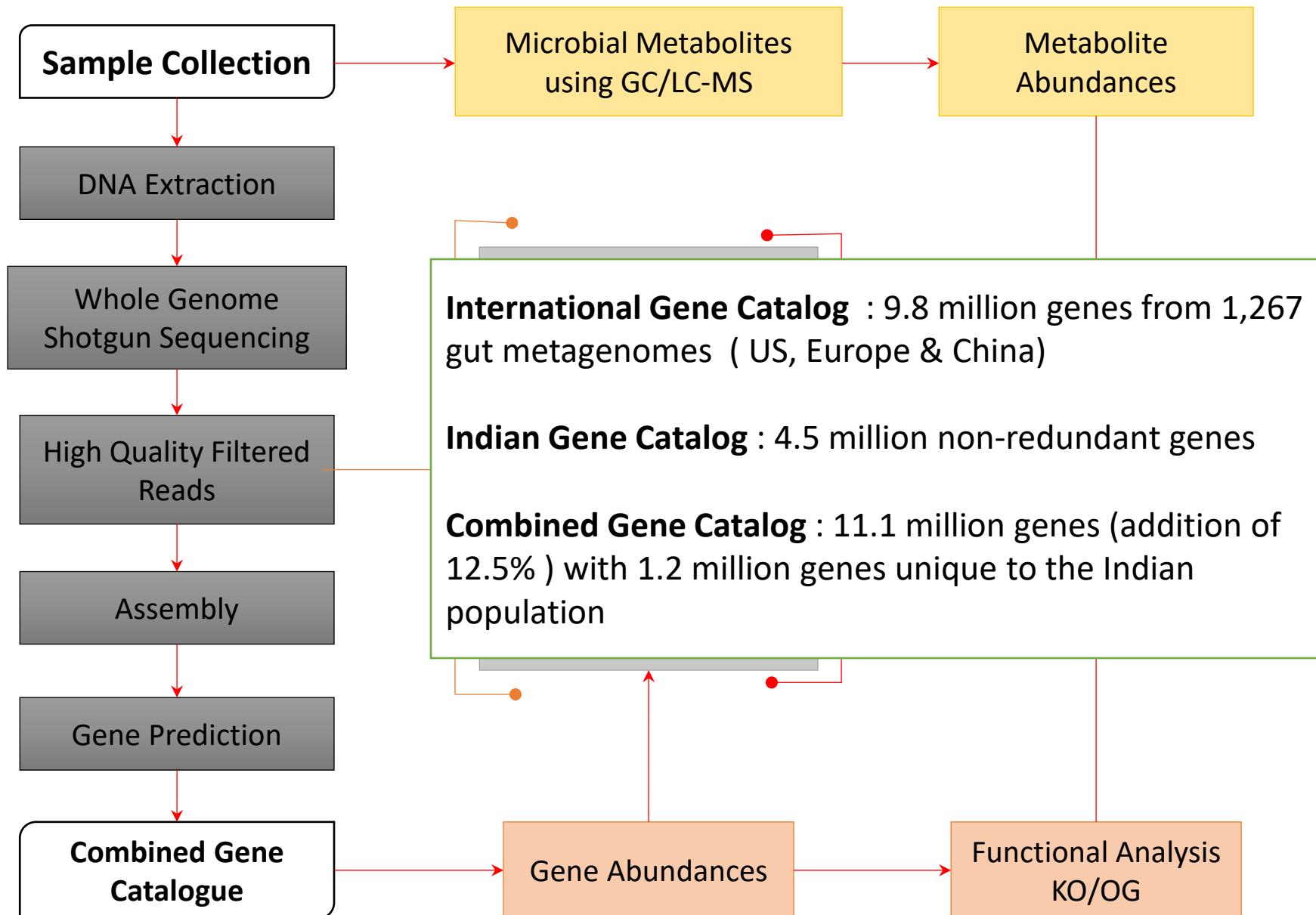
Sample Exclusion Criteria:

- ✓ Previous history of diseases
- ✓ Use of Antibiotics

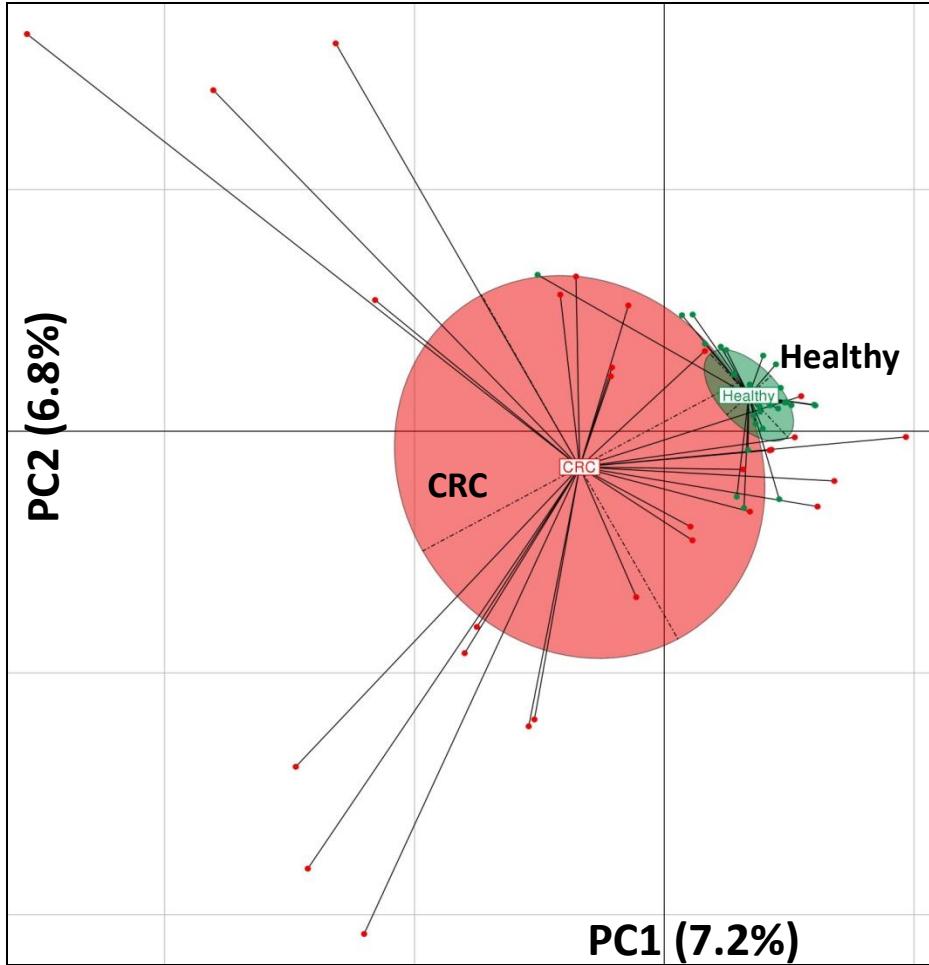
Metadata :

- ✓ Age : Middle, Old
- ✓ Gender : M, F
- ✓ BMI : Under, Ideal, Over
- ✓ Location : Bhopal, Kerala

Flowchart of the Methodology



Correlation with Metadata



Principal Component Analysis

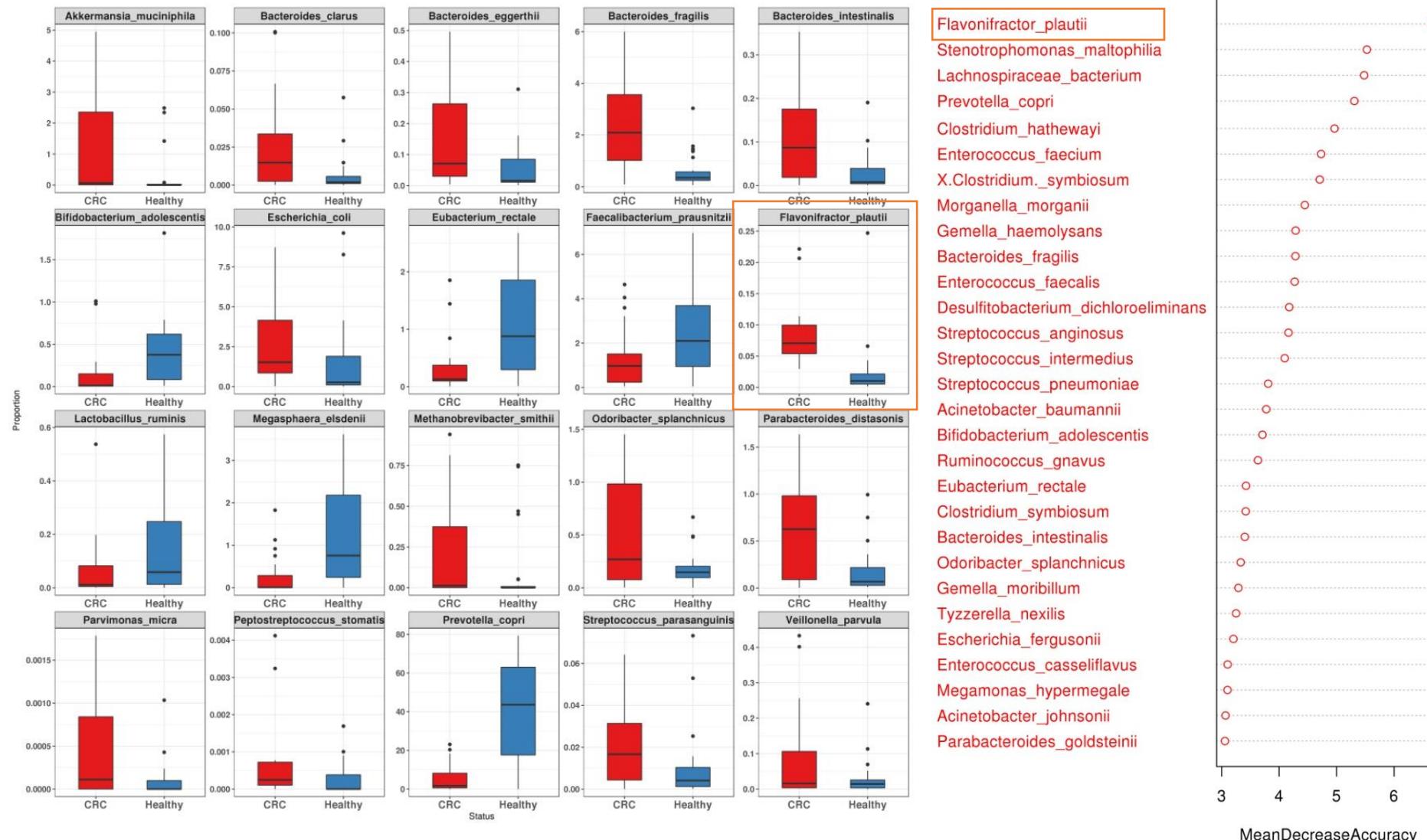
- PC1 with Health Status (q-value < 10^{-15})
- PC2 with Location (q-value = 0.0004)

PERMANOVA Analysis

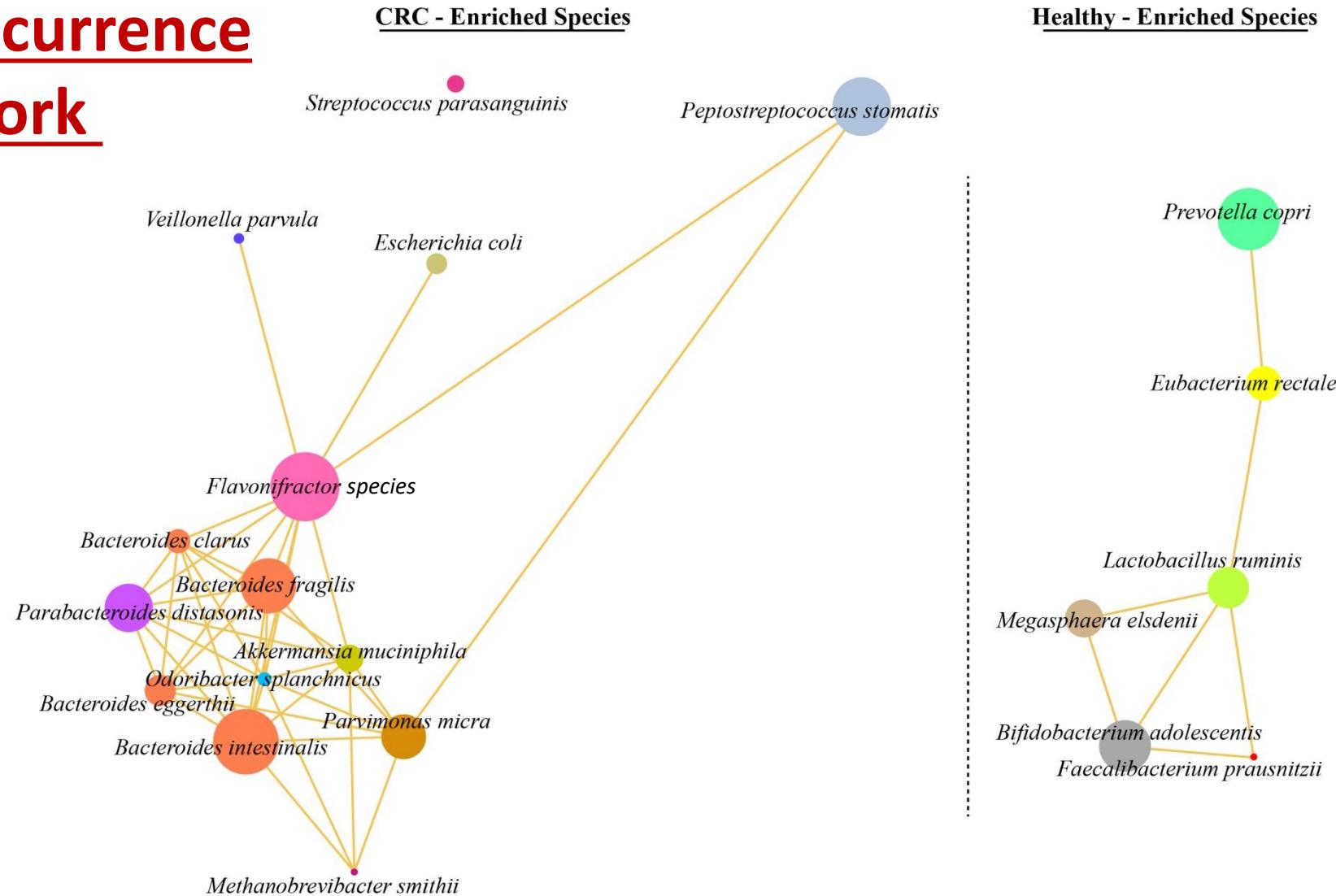
- Health status explained maximum variation (q-value=0.004) followed by Location

Taxonomic Biomarkers Identification

Species that were significantly higher in all three strategies (HMP-NCBI species, MGS species and any one the clade marker based approach i.e. mOTUs or Metaphlan) were considered



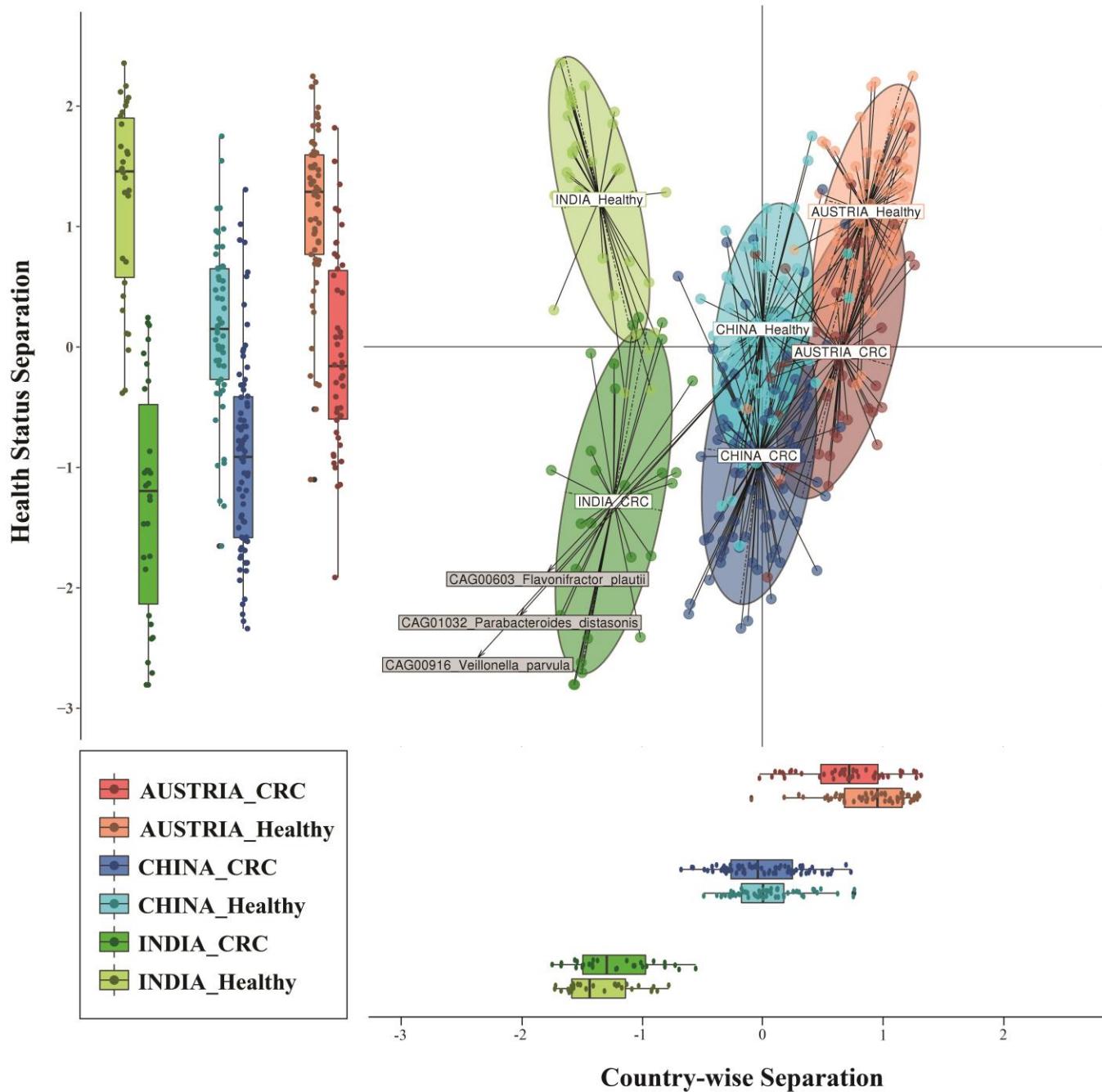
Co-occurrence Network



Bacteroides	Odoribacter	Parvimonas	Akkermansia	Parabacteroides	Flavonifractor
Veillonella	Streptococcus	Peptostreptococcus	Bifidobacterium	Megasphaera	Faecalibacterium
Escherichia	Lactobacillus	Eubacterium	Prevotella		

Global Patterns

- db-RDA analysis constrained for population and health status
- Country-wise difference is higher as compared to health status
- The difference in the CRC vs. Healthy is higher in India as compared to other countries
- *Flavonifractor* species along with 2 other bacteria is separating Indian CRC patients





Flavonifractor Species and Flavonoid degradation

- *Flavonifractor* can degrade flavonoids by cleaving the C-ring of the flavonoid molecules
- Flavonoids are important constituents of human diet; comprised of polyphenolic secondary metabolites with **broad-spectrum pharmacological activities**
- Accumulating evidence in prevention of cancer, cardiovascular disease, type-2 diabetes, and cognitive dysfunction
- Could therapeutically target the intestinal microbiome by promoting beneficial bacteria and inhibiting potentially pathogenic species
- Several common Indian foods such as:
 - High amount - tea, coffee, apple, guava, terminalia bark, fenugreek seeds, mustard seeds, cinnamon, red chili powder, cloves, turmeric, and pulses.
 - Medium amount - Indian gooseberry, omum, cardamom, cumin, betel leaf and **brandy**.
 - Small but significant amounts - kidney beans, soyabeans, grapes, ginger, coriander powder, bajra and brinjal



INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY, July 1991, p. 355-357
0020-7713/91/030355-03\$02.00/0
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Vol. 41, No. 3

Clostridium orbiscindens sp. nov., a Human Intestinal Bacterium Capable of Cleaving the Flavonoid C-Ring

J. WINTER,¹ M. R. POPOFF,² P. GRIMONT,³ AND V. D. BOKKENHEUSER^{1*}

Department of Pathology, St. Luke's-Roosevelt Hospital Center, New York, New York 10025,¹ and Unite des Anaerobies,² and Unite des Enterobacteries, Institut National de la Sante et de la Recherche Medicale, Unite 199,³ Institute Pasteur, 75724 Paris Cedex 15, France

Clostridium orbiscindens sp. nov. is an obligate anaerobe that is capable of cleaving the C-3-C-4 bond of the natural anticarcinogen quercetin. The metabolic products, 3,4-dihydroxyphenylacetic acid and presumably phloroglucinol, are not known to possess anticarcinogen properties. This organism was isolated from human feces. On sheep blood agar plates *C. orbiscindens* forms minute, irregular, convex, gray or white, shiny, smooth, nonhemolytic colonies. It is beta-hemolytic on rabbit blood agar. The motile peritrichous rods are gram variable. Subpolar spores are common. Cultures are resistant to 80°C for 10 min. Capsules are absent. This asaccharolytic organism does not metabolize esculin, urea, meat, gelatin, casein, or nitrate. The G+C content is 56 to 57 mol %. DNA hybridization experiments did not reveal relatedness to phenotypically similar *Clostridium* strains. Strain 265 (= ATCC 49531) is the type strain.

During investigations of flavonoid metabolism by the human intestinal flora, we isolated four bacterial strains that are capable of cleaving the C-ring of the aglycone quercetin (15). Quercetin has been shown to inhibit leukemia, breast cancer, and skin cancer in rodents (6, 11, 12, 17); its effect on natural or induced colorectal cancer has not been determined. If this compound inhibits colorectal cancer, then the C-ring-cleaving bacteria abrogate a naturally occurring anti-carcinogenic compound. The purpose of this study was to examine the characteristics of the C-ring-cleaving bacteria, which do not belong to a previously described bacterial species.

Identification of C-ring-cleaving bacteria. (i) **Microbiological characteristics.** Colonial morphology was determined from growth on sheep blood agar plates. Cell morphology, motility, and Gram-staining properties were determined by microscopically examining broth cultures that were incubated for 18 to 24 h.

(ii) **Phenotypic characteristics.** Biochemical characteristics and fermentation products were determined after 3 days of incubation (8). Antibiotic susceptibility was tested by using broth disk methods (8, 14).

(iii) **Electron microscopy.** Young bacterial cells of a pure culture of C-ring-cleaving bacteria were harvested from sheep blood agar plates, centrifuged at 7,000 × g for 15 min,

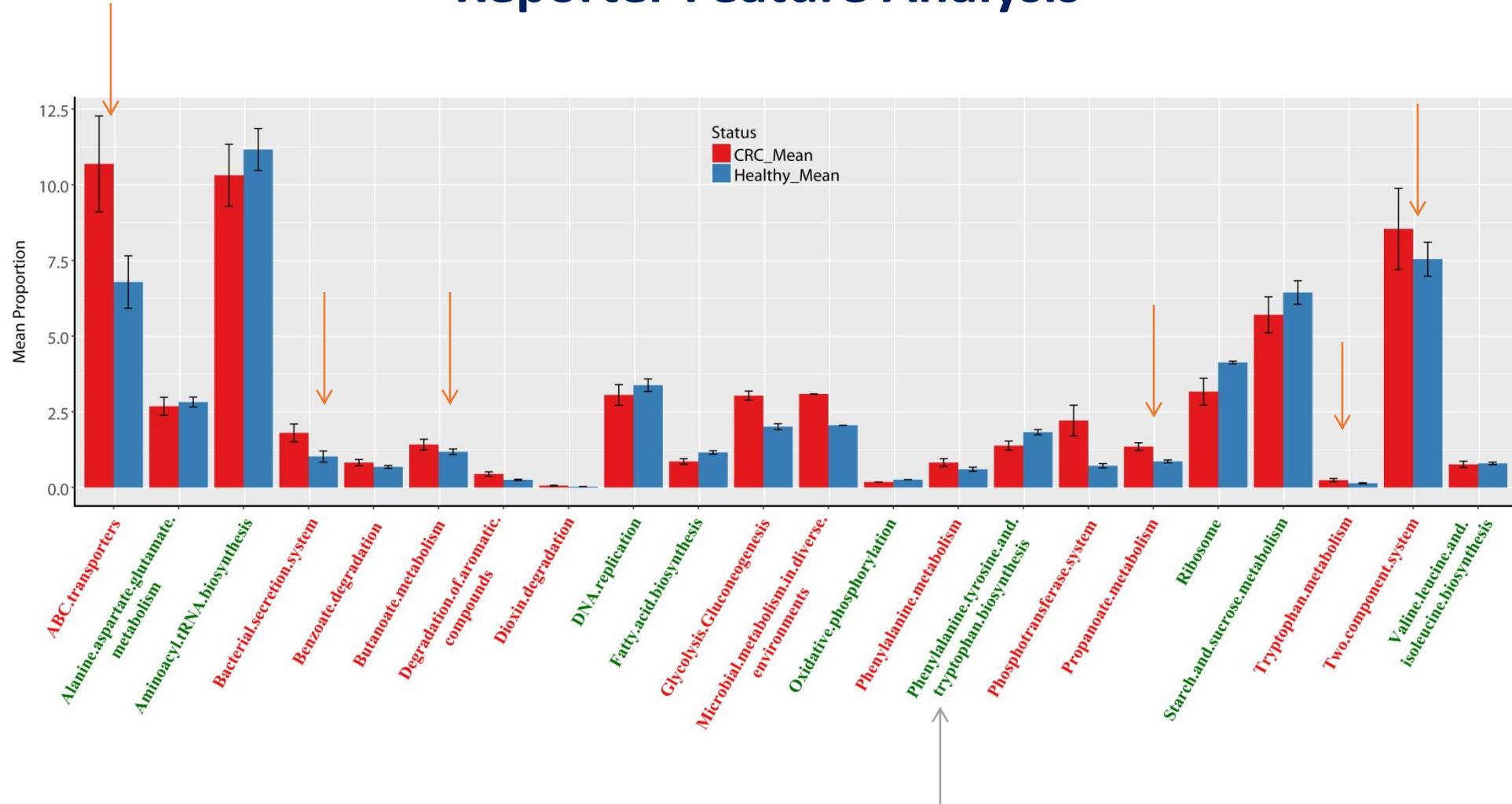


Our Hypothesis

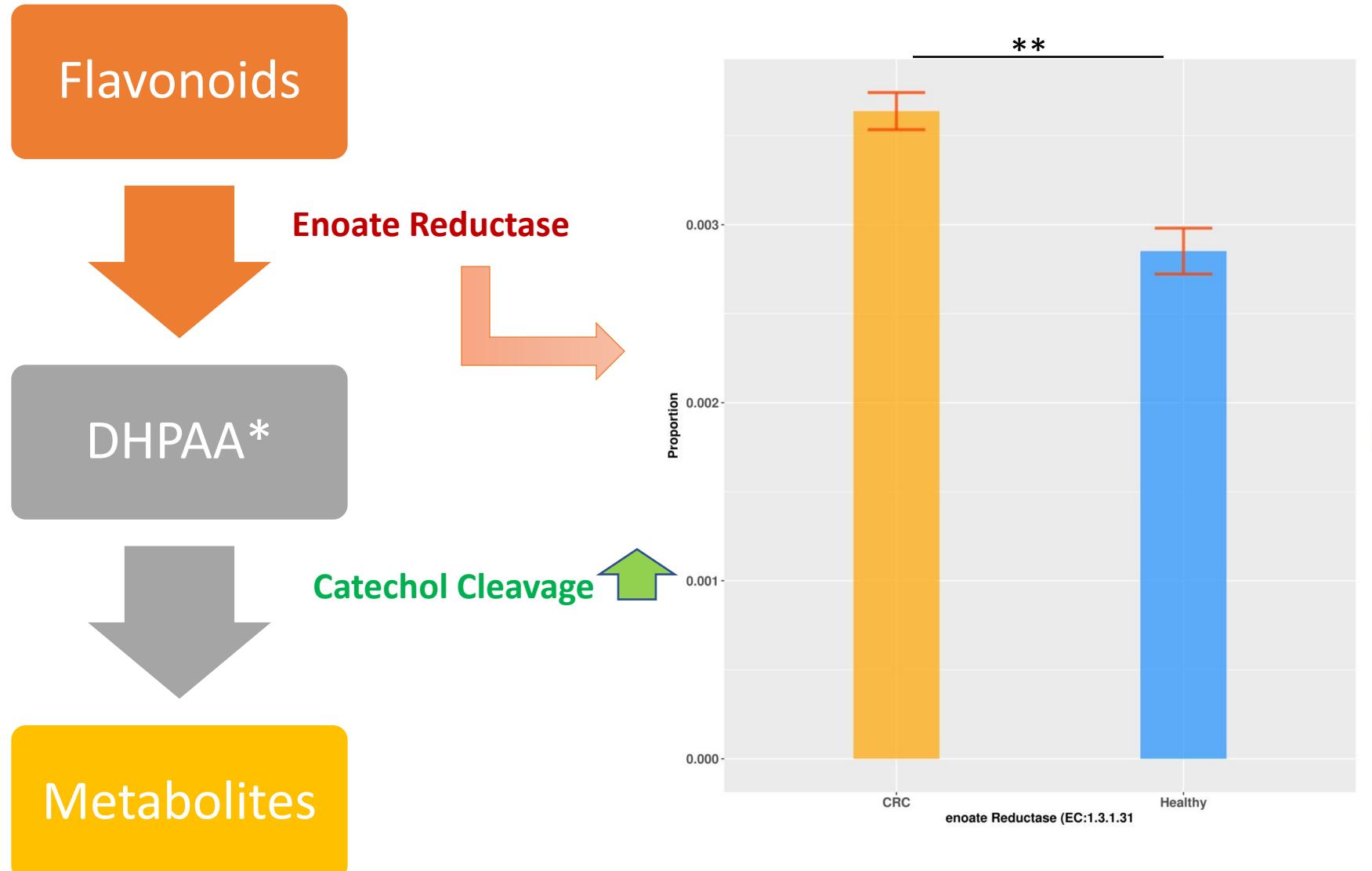
- Low risk of Colorectal cancer in India is attributed to high amount of flavonoids consumption
- We hypothesise that the degradation of beneficial flavonoids might be playing an important role in cancer progression in Indian cohort
- Bacteroides species along with Flavonifractor species are playing a major role in cancer progression in Indian patients
- The high association between the 20 taxonomic marker species indicates that the dysbiosis in CRC-associated gut microbiome is mediated by several species.

Differential Abundance of Pathways

Reporter Feature Analysis



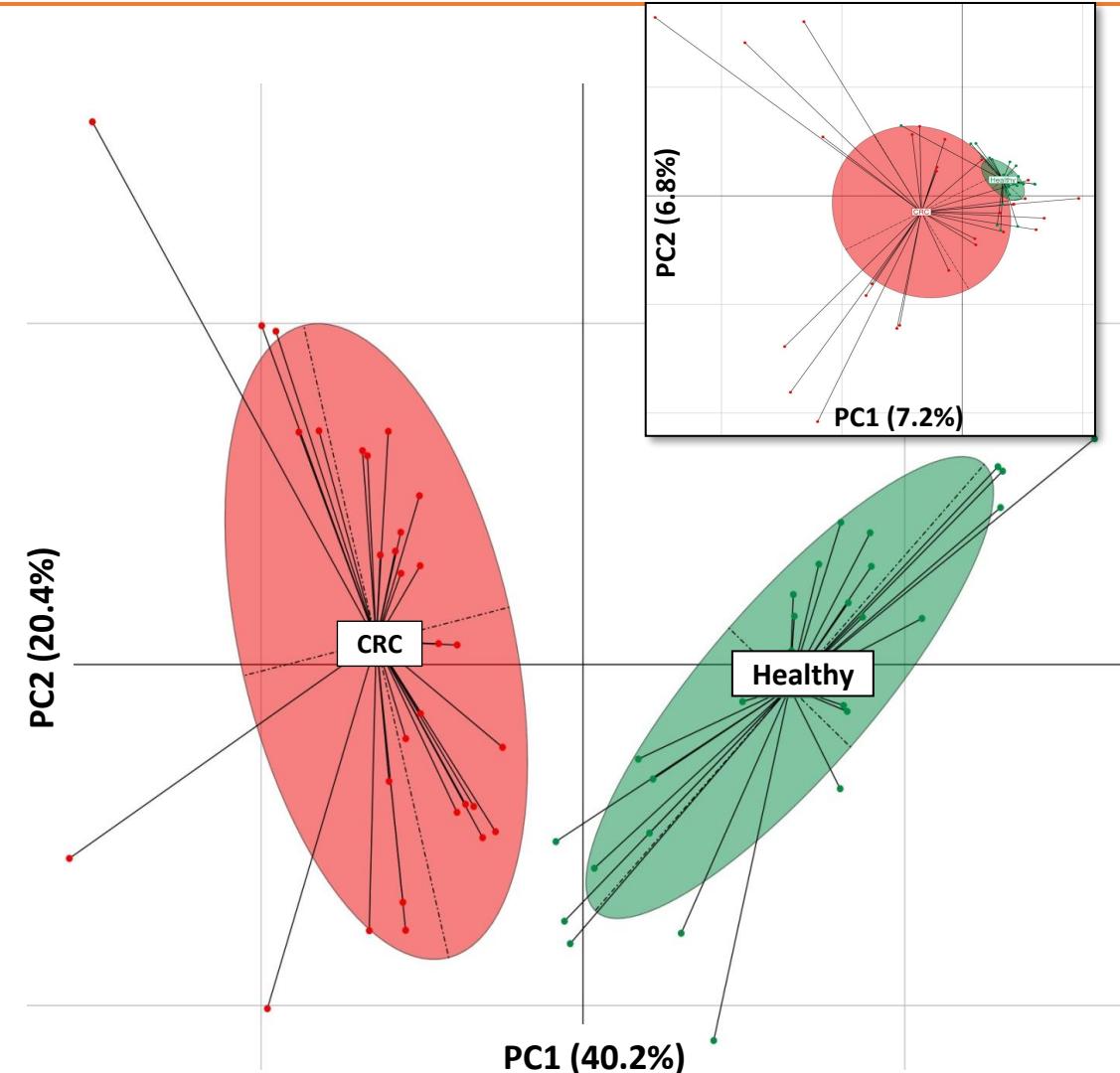
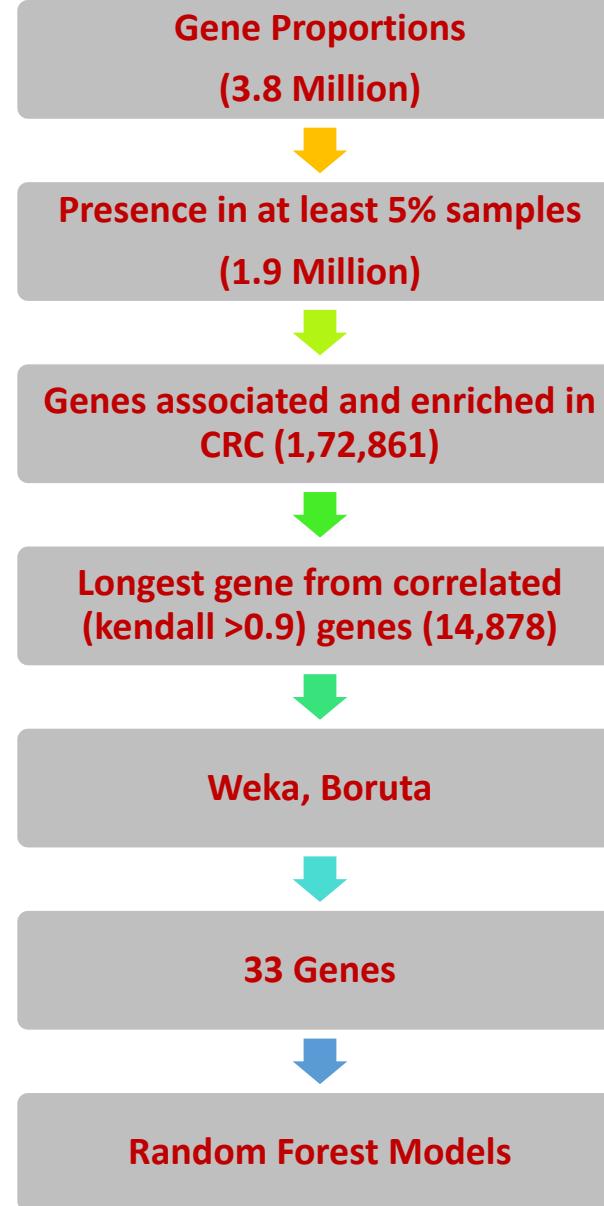
Flavonoid Degradation



*3,4-dihydroxyphenylacetic acid

** P-value = 0.045

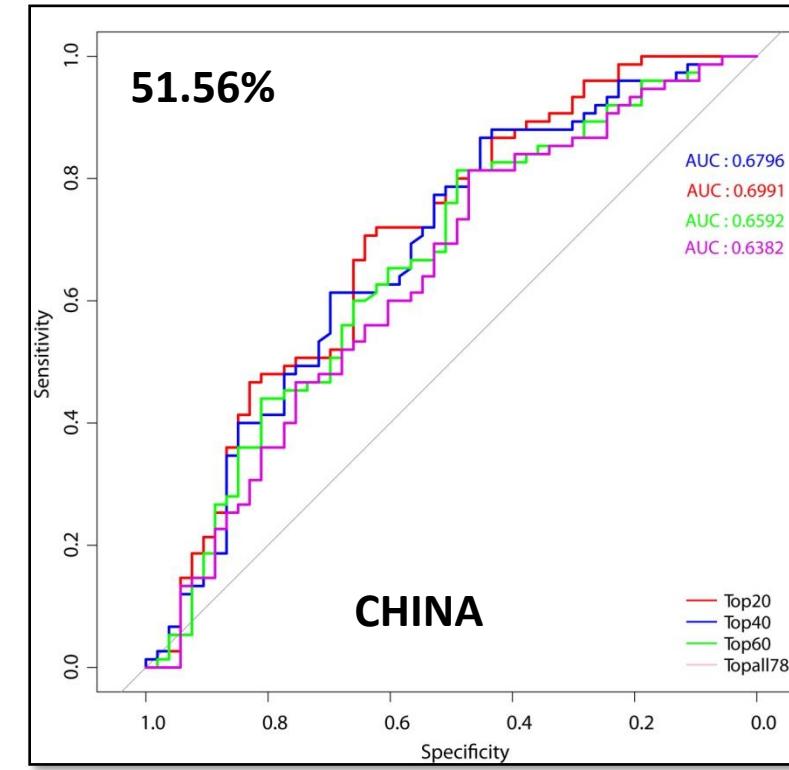
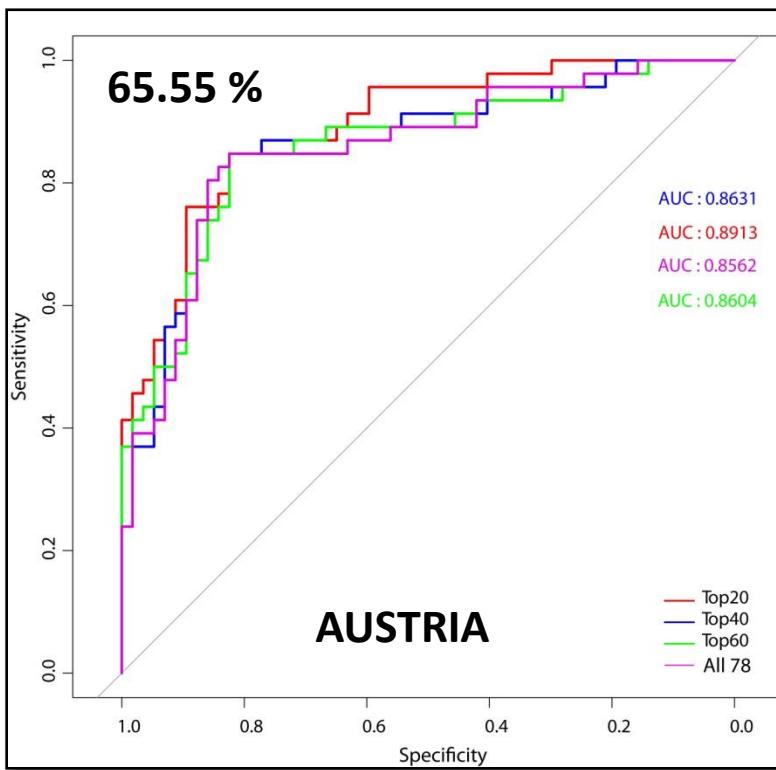
Genetic Biomarkers Identification



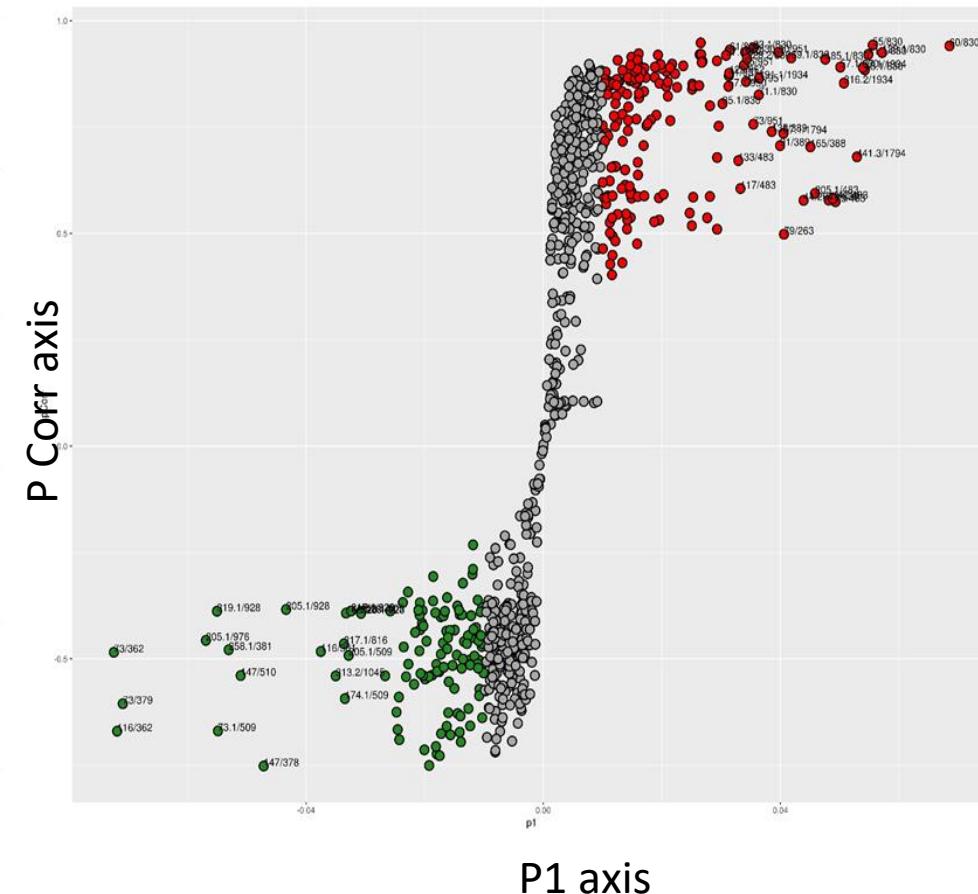
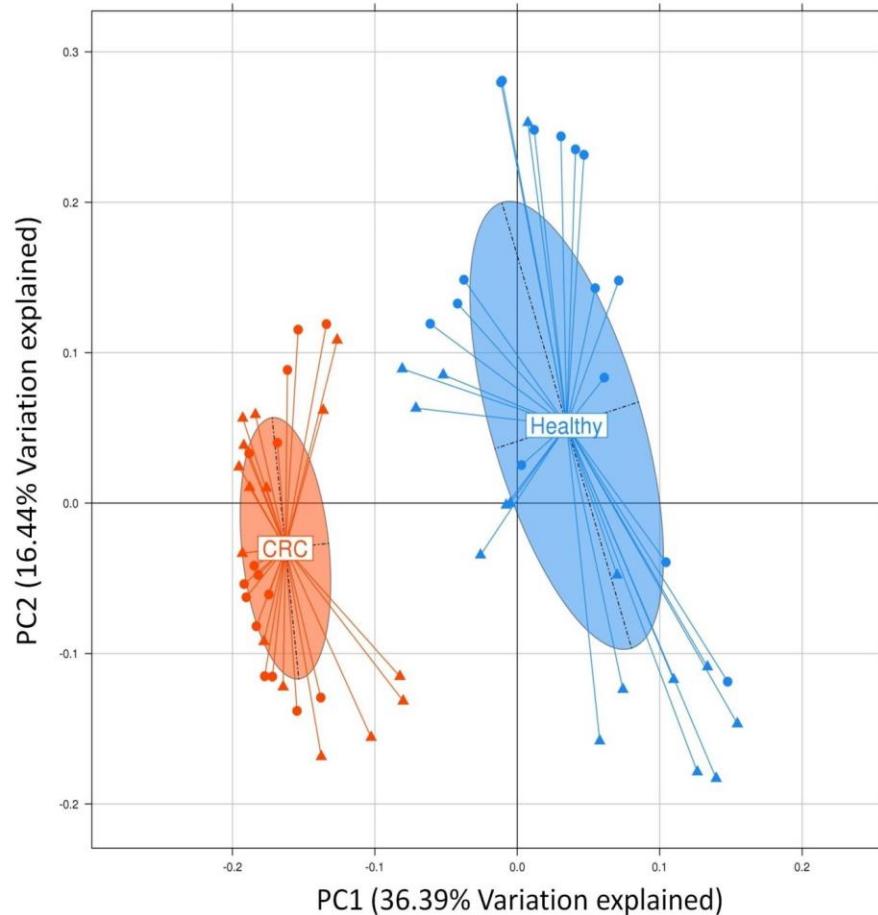
First 3 PCs highly associated only with the health status
Adjusted p-values: PC1 = 7.5×10^{-10} , PC2 = 1.97×10^{-8} , PC3 = 0.0005

Are these Markers Global ??

- An accuracy of **91.77% (11 out of 12 correct)** on cohort B
- We tested our markers on other countries datasets : Austria and China



CRC Associated Metabolome

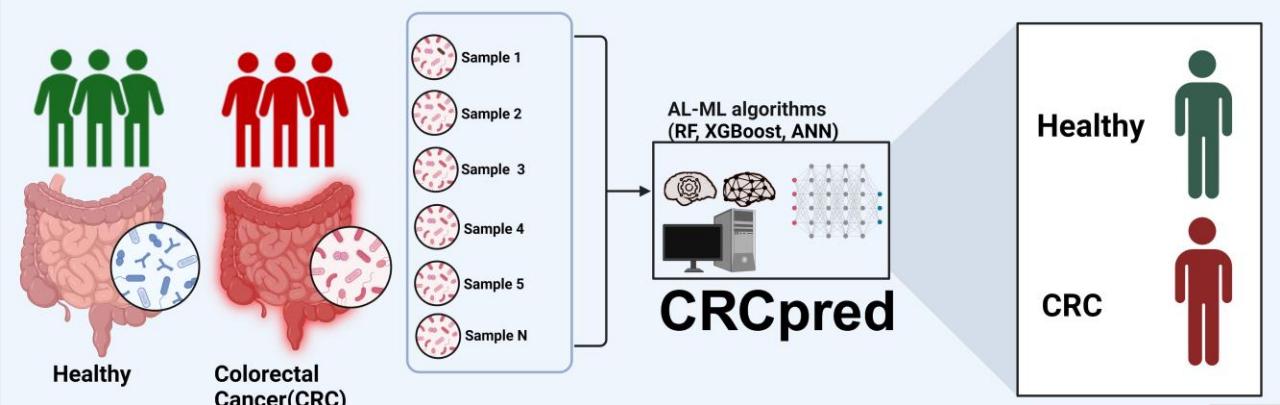


Conclusions

- Significant differences in CRC associated gut at each level : Species, Genes and Metabolites
- Metabolomics results are showing very strong patterns, however, they lack annotation
- Indian gut is very less studied and we show some unique patterns in CRC associated with Indian gut
- Microbial markers show tremendous potential to augment or replace current non-invasive tests for the diagnosis of CRC
- A combination of microbial markers and clinical characteristics can provide cheap and best classification accuracies

Future Directions

- Validation of gene markers identified: qPCR
- Testing these markers on large sets
- Correlation between Metabolomic and Metagenomic data.



CRCpred

AIML based tool to predict the healthy and CRC status of a metagenomic dataset using microbial species abundance

Flavonifractor plautii: New bacterium proposed to be associated with CRC, highly cited now and validated by several researchers

- Consortium of CRC marker species

In progress

- Pipeline for NGS data analysis
- AIML based diagnostic prediction tool
- qPCR based diagnostic kit

For early, accurate, rapid and non invasive diagnosis of colorectal cancer

INSTITUTE OF SCIENCE EDUCATION AND RESEARCH
 IIT ROORKEE
 ROORKEE, UTTARAKHAND - 247667

METABIOSYS
PREDICTION OF HEALTHY AND CRC STATUS BASED UPON GUT MICROBIOME SPECIES ABUNDANCE

Upload microbial abundance profile for Input

Note: The tutorial to generate input microbial abundance profile is given in tutorial section

No file chosen
 Upload Sample File

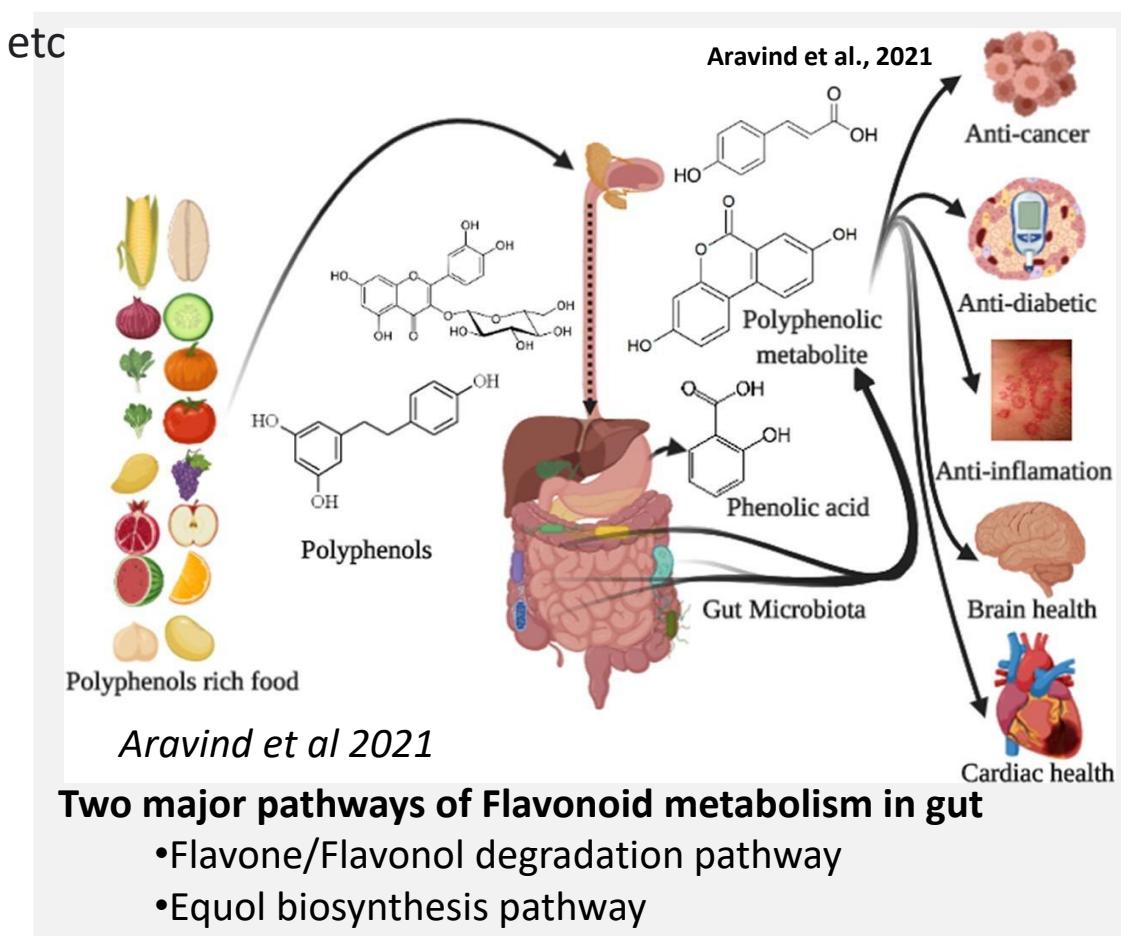
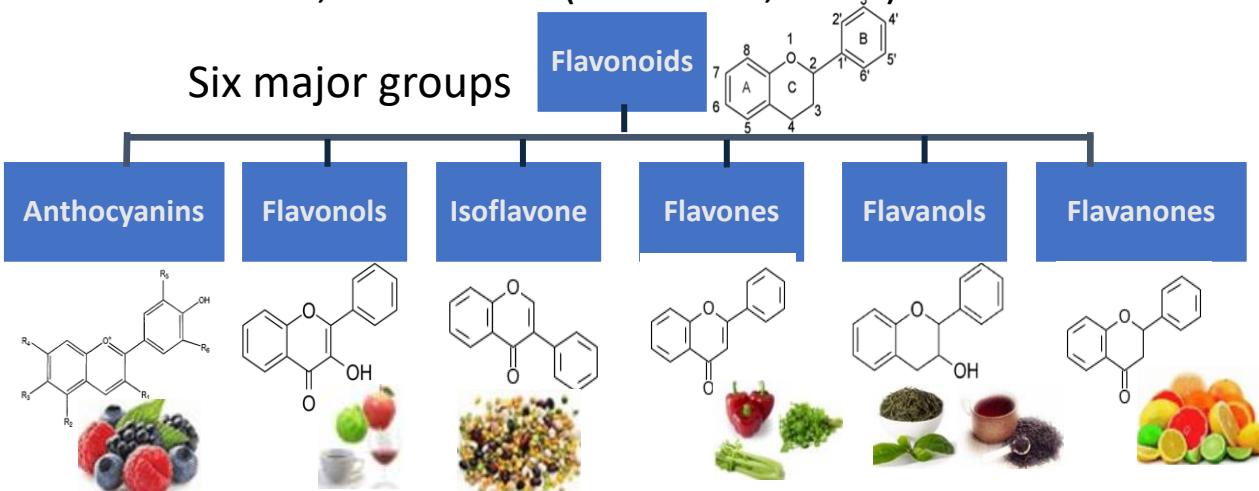
Model for Health Status Prediction

A consensus of ANN, RF, and XGBoost classifier is used to predict health status

[Deepika et al, 2025](#)

Landscape of Flavonoid Metabolism in Gut: Western vs Non-western & Healthy vs Diseased

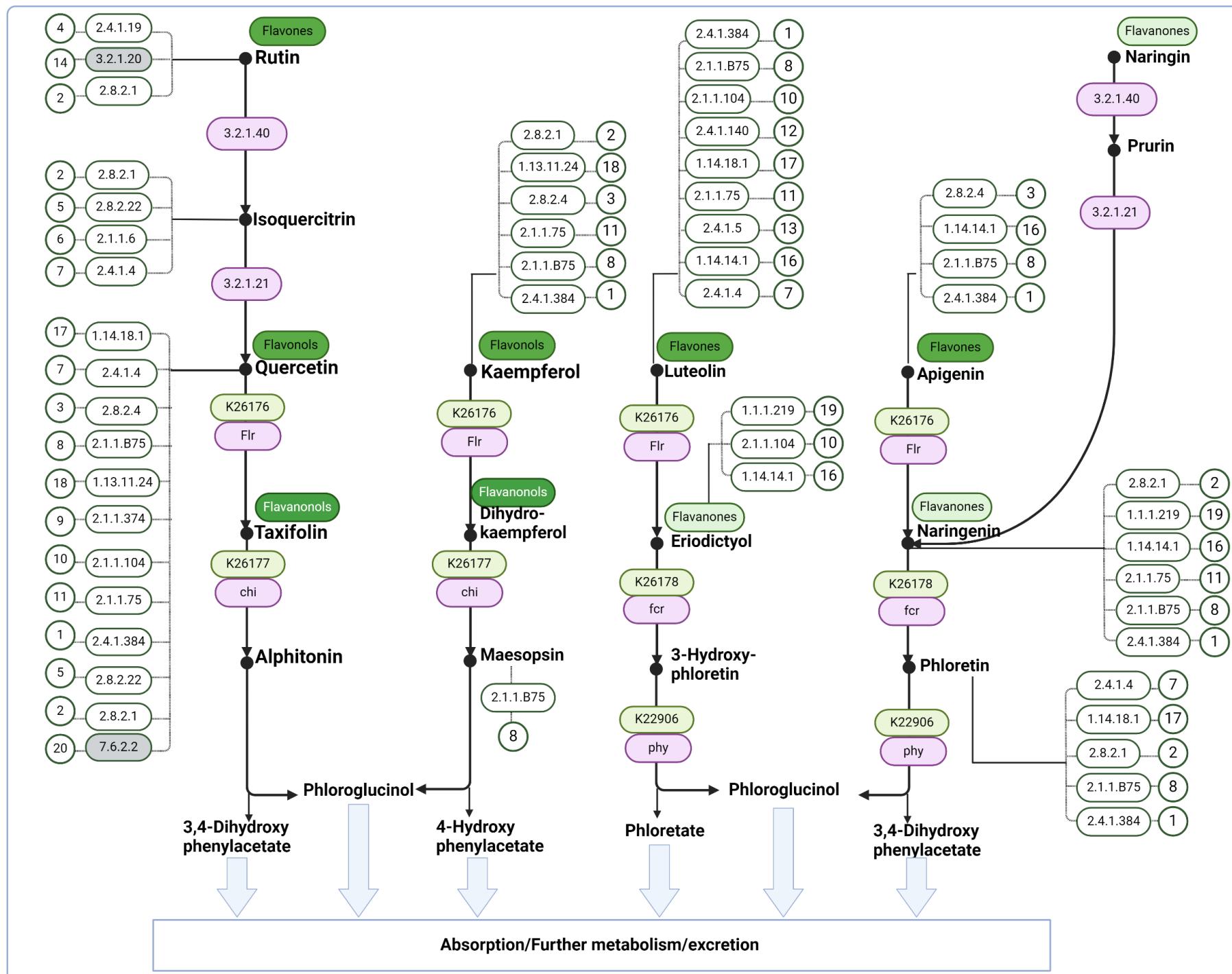
- Plant secondary metabolites in fruits, vegetables, tea, wine etc
- Present in commonly consumed **Indian foods**
 - High flavonoid content (> 100 mg/100 gm) in tea, coffee, guava, fenugreek, mustard, cinnamon, red chili, cloves, turmeric
 - Medium levels (50-100 mg) in Indian gooseberry, omum, cumin, cardamom (Nair et al., 1998)



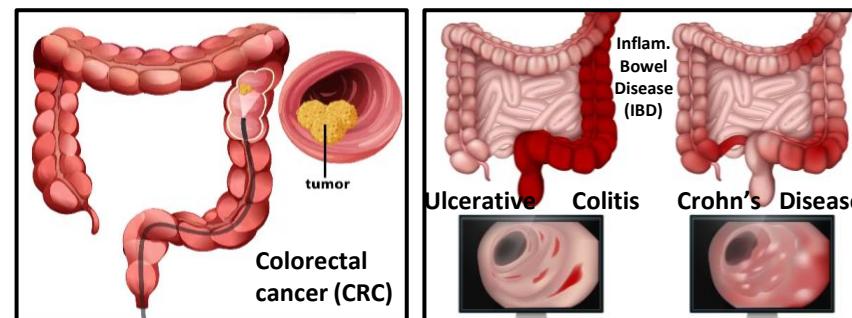
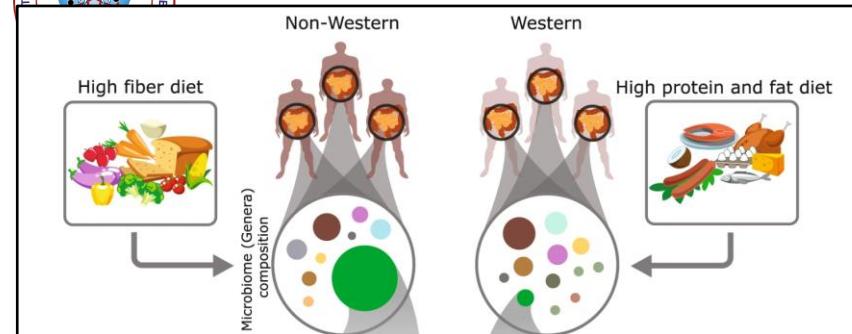
- Only few flavonoid-modifying bacteria and enzymes reported so far, need to identify across populations
- We identified ~ 7,000 bacterial protein sequences belonging to 37 EC numbers
- More than 25 ECs were not previously reported in bacteria-mediated flavonoid metabolism in gut
- >4,700 species and MAGs with at least one homolog for potential flavonoid metabolizing protein sequences
- Two key bacterial species play a prominent role on Flavonoid metabolism

Flavone/Flavonol Degradation Pathway

Reconstruction of the Flavone/Flavonol degradation pathway using information of newly identified EC numbers and species data



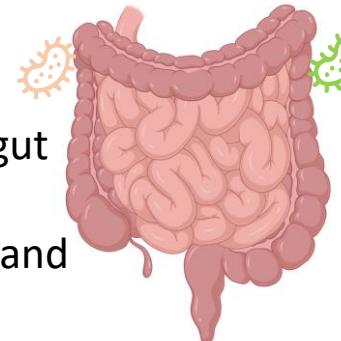
Variation in Flavonoid Metabolism across Populations And Disease



Country	Healthy	Disease
Austria	63	93 CRC (47 Adenoma, 46 carcinoma)
China	43	75 CRC
India	30	30 CRC
US	34	107 IBD (54 CD, 53 UC)
Netherlands	22	43 IBD (23 UC, 20 CD)
Tanzania	27	NA
Peru	36	NA
Madagascar	111	NA
Italy	73	NA

Flavonifractor plautii

- Common inhabitant of human gut
- C-ring cleavage
- Enzymes involved: Phy, Chi, Flr, and Fcr
- Studies have linked *F. plautii* to less healthy dietary patterns



Eubacterium ramulus

- Common inhabitant of human gut
- C-ring cleavage
- Enzymes involved: Phy, Chi, Fcr
- Highly prevalent in the human intestine, reaching cell counts of 107 to 109 per g fecal dry weight (Simmering et al., 1999)

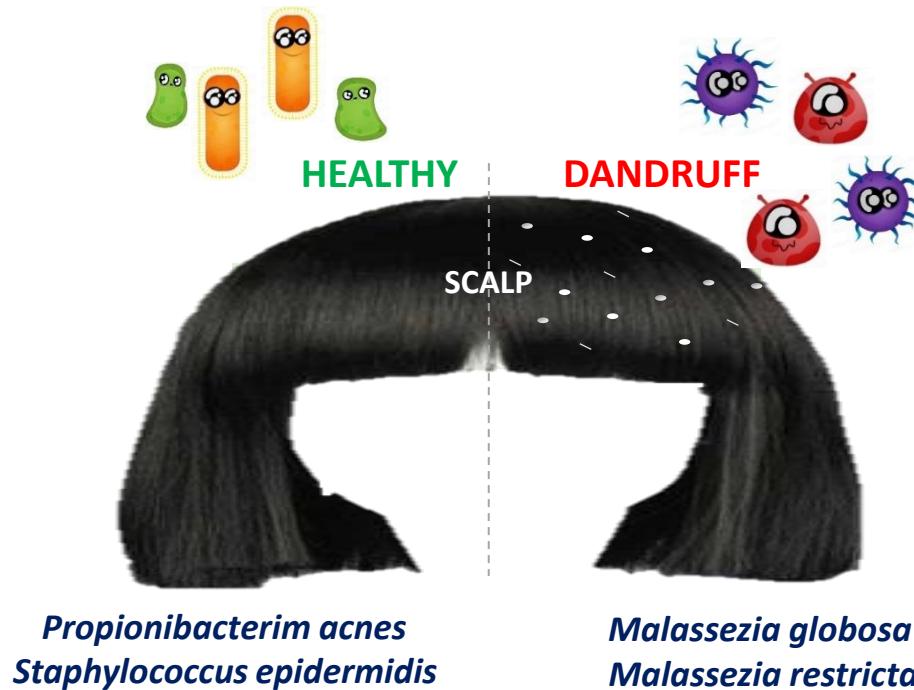
Enzymes/Genome	Western vs Non-western	IBD vs. Healthy	CRC vs. Healthy
Phy, Chi, Flr, and Fcr of <i>F. plautii</i>	↑ in healthy Western	↑ in IBD compared to healthy	↑ in CRC compared to healthy
<i>F. plautii</i>	↑ in healthy Western	↑ in IBD compared to healthy	↑ in CRC compared to healthy
Fcr, PHY, and CHI in <i>E. ramulus</i>	↓ in Indian population	↑ in healthy compared to IBD	
<i>E. ramulus</i>	↓ in Indian population	↑ in healthy compared to IBD	

Images taken from published studies and google images are sincerely acknowledged



Some example studies form our group

Scalp Microbiome: The Global Scenario



Scalp Microbiome of Different Populations in the World



Phylogenetic marker (16S/ITS) based studies

Scalp Microbiome of Indian Population



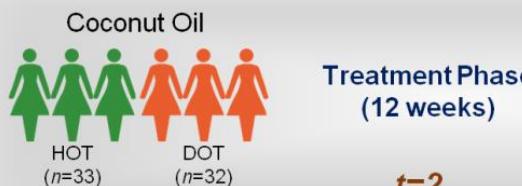
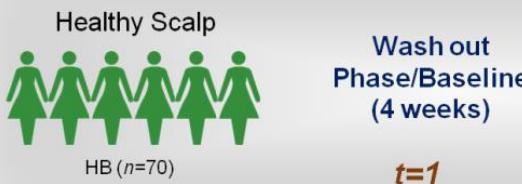
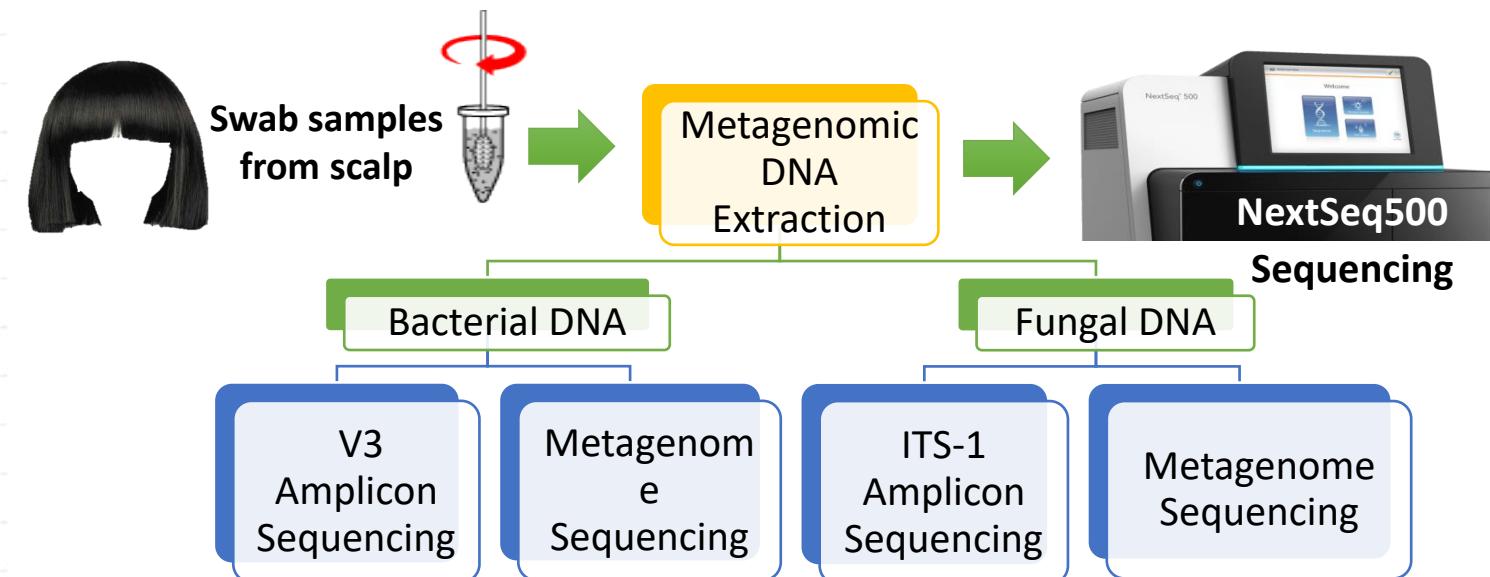
Yet Unknown

Elucidating Healthy and Dandruff Scalp Metagenome : Largest Study in the World



L'ORÉAL

Cohort : Women
Sample: ~ 1400



Major Constituents	Proportion(%)
Lauric Acid	46.3
Myristic Acid	15.6
Palmitic Acid	8.3

Anti-Fungal and Anti-Bacterial Activity

Common practices to maintain scalp health



And



Core Microbial Species, Individual Variations, Role on Scalp and Dandruff

Bacterial Species

Staphylococcus epidermidis



Propionibacterium acnes



Malassezia restricta



Uncultured Malassezia

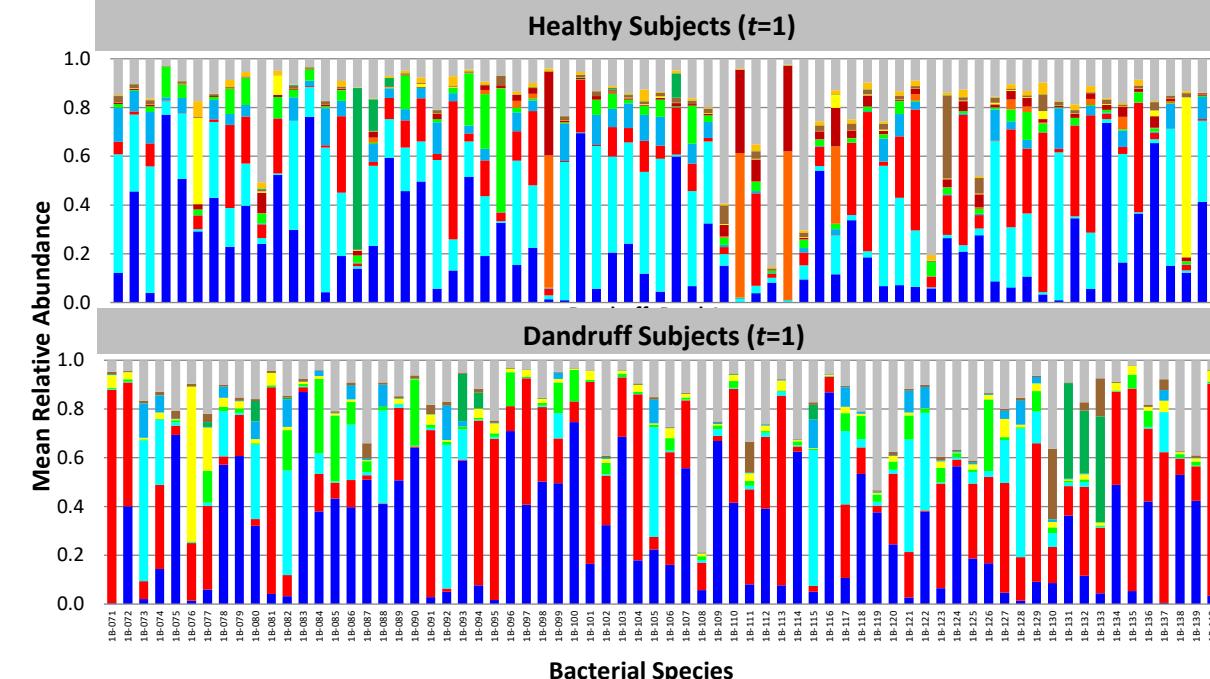


Malassezia globosa

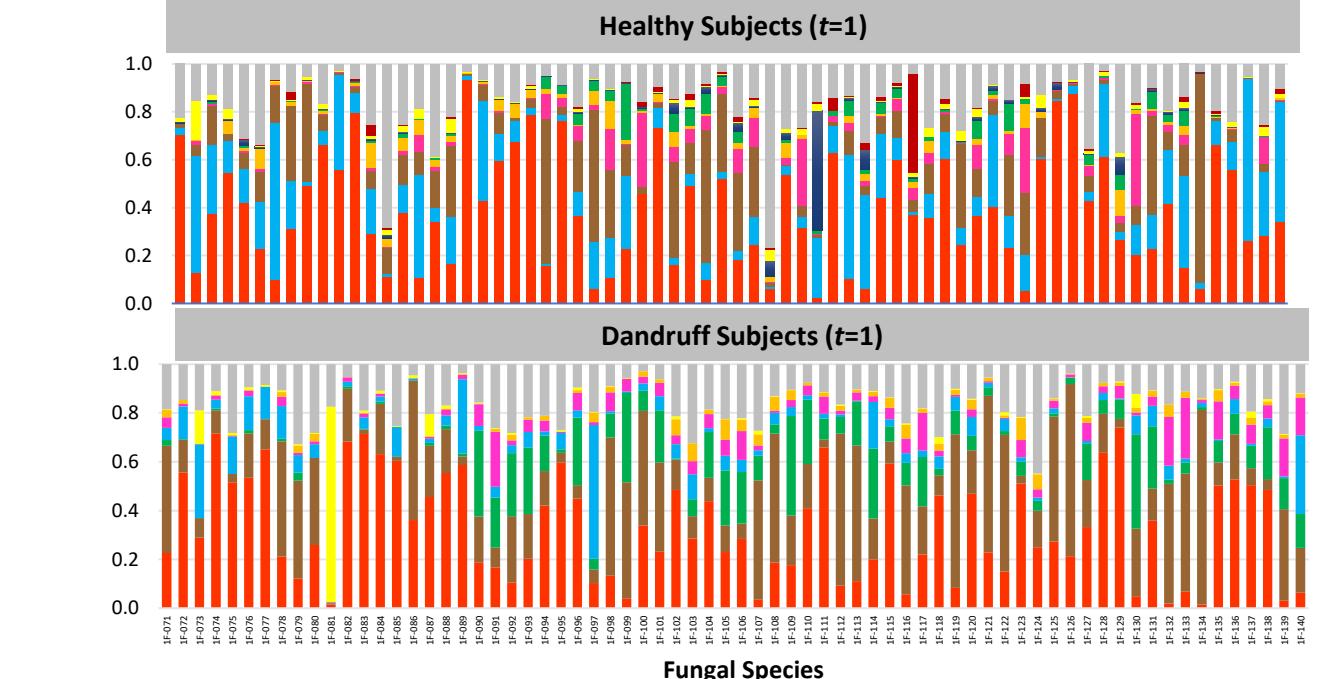
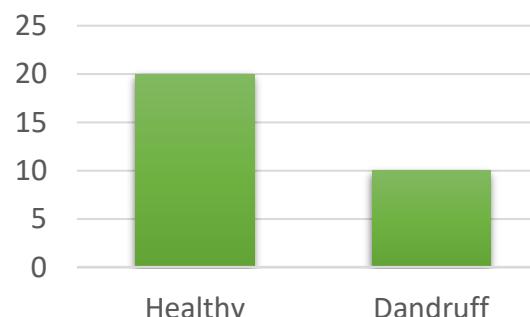


Malassezia sp.

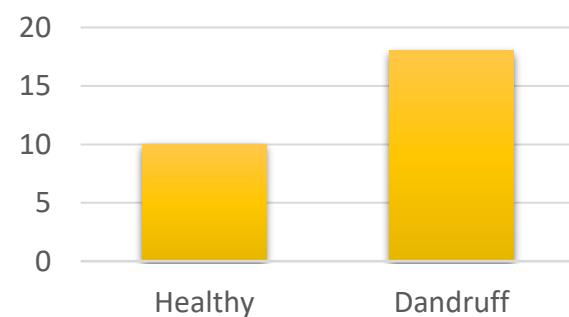
Fungal Species



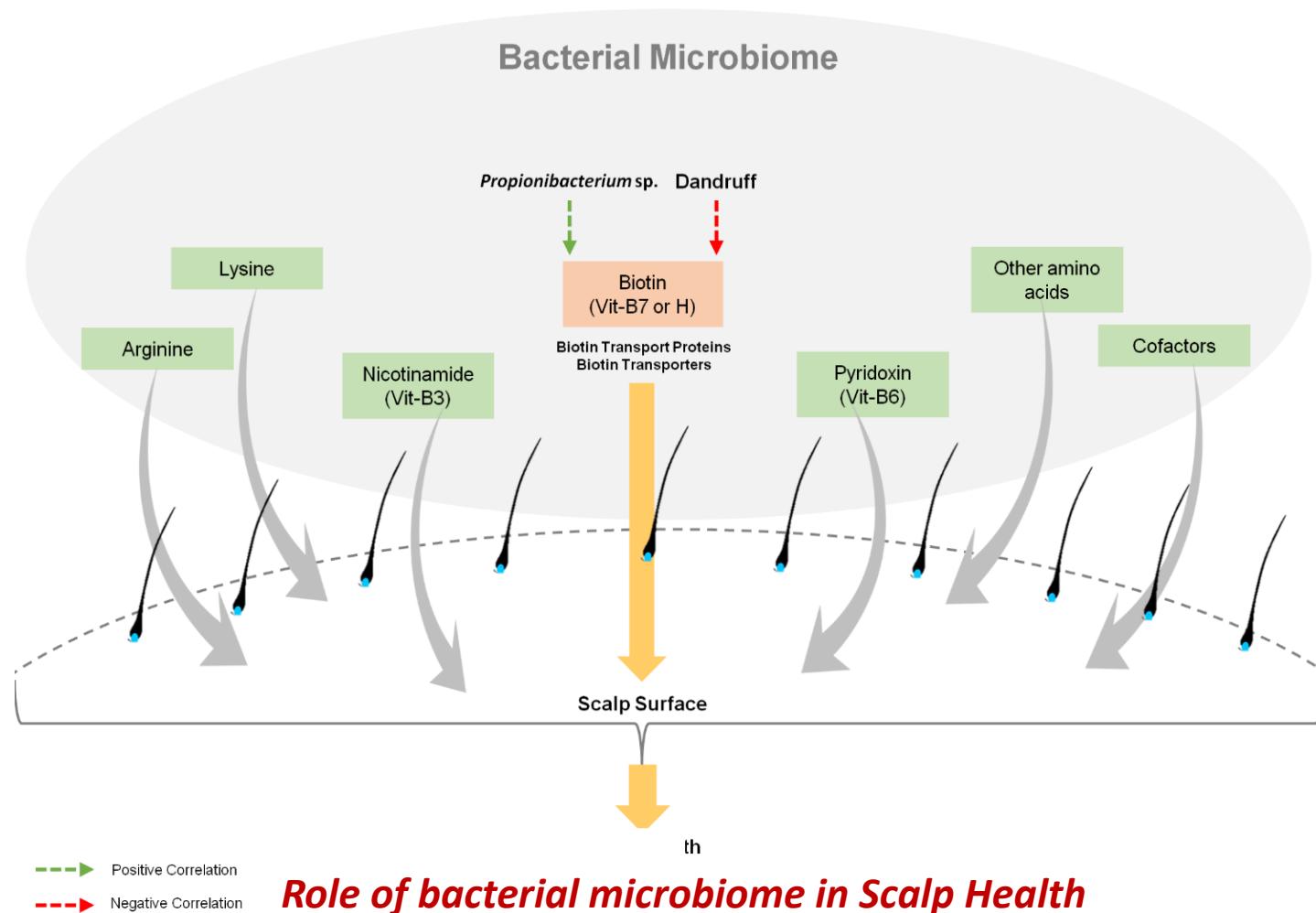
P. acnes : S. epidermidis



M. restricta : M. globosa



The bacterial microbiome supplies host with nutrients essential for a healthy scalp



Key Conclusions and Outcomes

- **The Indian scalp microbiome:** Distinct distribution than other world populations
- **Unknown/Uncultured *Malassezia* sp. in dandruff :** A unique revelation in Indian population
- **Bacterial Microbiome:** Actively involved in maintaining scalp nutrient homoeostasis
- **Understanding the population specific scalp microbiome:** Efficient anti-dandruff therapies
- **Coconut oil:** Appears to be effective in maintaining a healthy scalp flora

Further enrichment of scalp-health associated pathways related to the metabolism of essential nutrients, such as amino acids, biotin and other B-vitamins in the healthy scalp, after the treatment with coconut oil

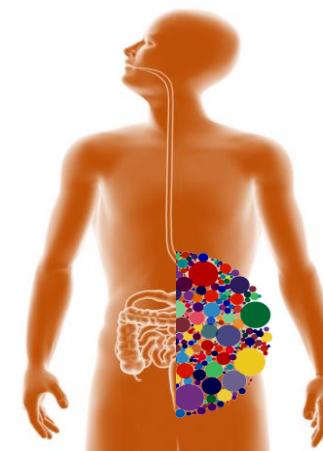
Microbiome and Exosome: AI to Predict the Microbial Biotransformations



Oral Drugs



Prebiotics



Gut microbiome

Human
microbiome

- >10,000 microbial species,
- >3 Million microbial enzymes,
- >20,000 Enzymatic reactions



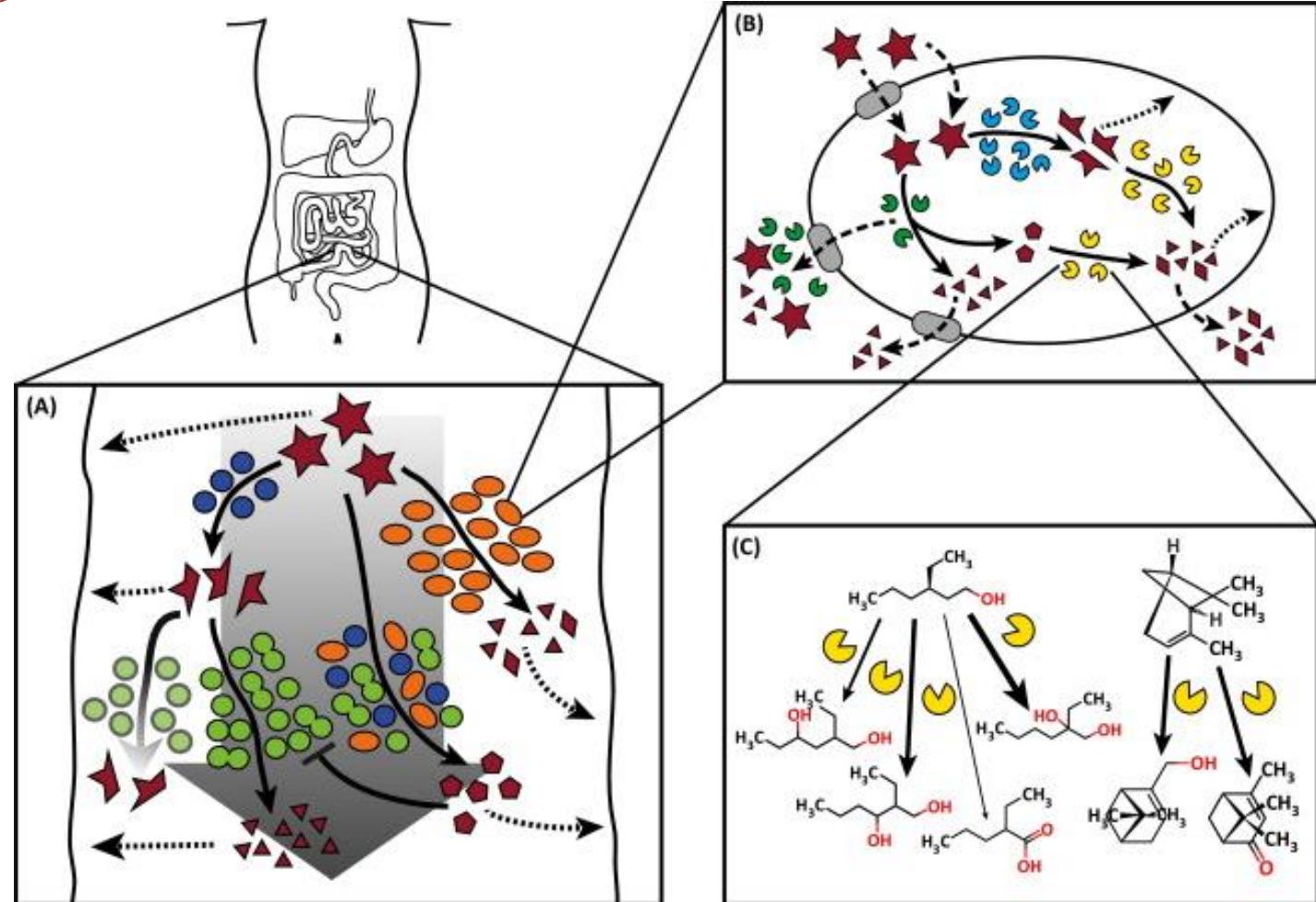
Cosmetics etc



Skin and Scalp microbiome

Have you ever wondered how the external molecules/xenobiotics that we come across in our daily lives are metabolized our invisible second genome:- The microbiome

A Cascade of Drug/Xenobiotic Metabolic reactions by Gut Microbiome



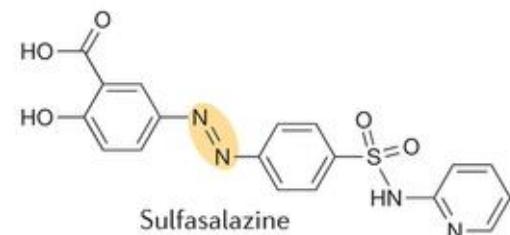
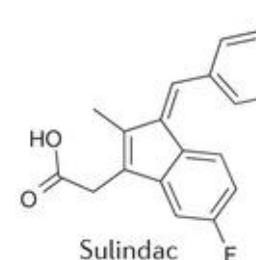
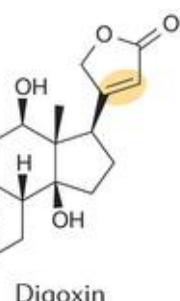
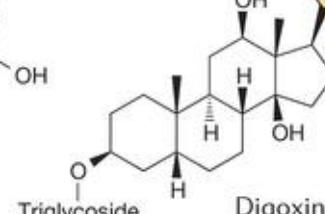
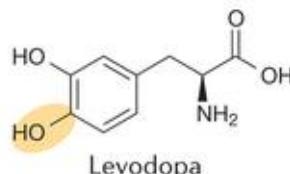
Key:

- Orally administered xenobiotic
- Degradation intermediates
- Gut microbes

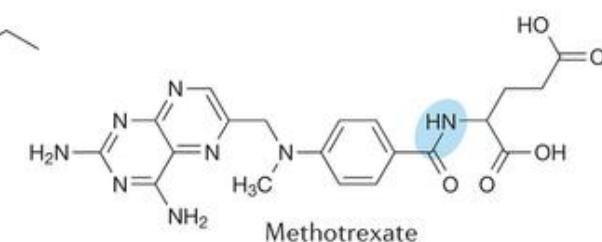
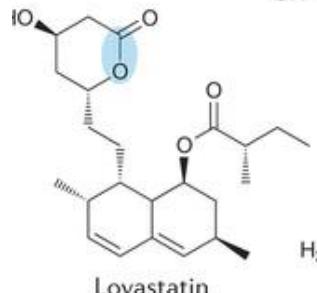
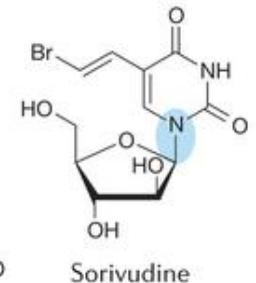
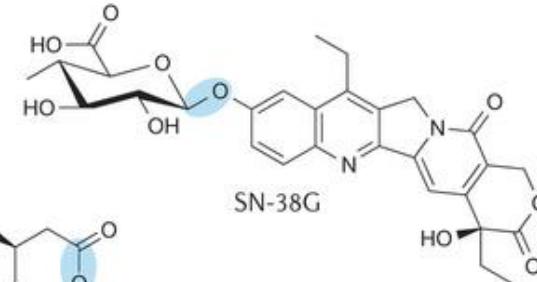
..... ➤ Absorption into organism
 ➡ Biotransformation
 —➡ Inhibition of growth

Metabolic enzymes
 Transport protein
 —➡ Transport reaction

a Reduction



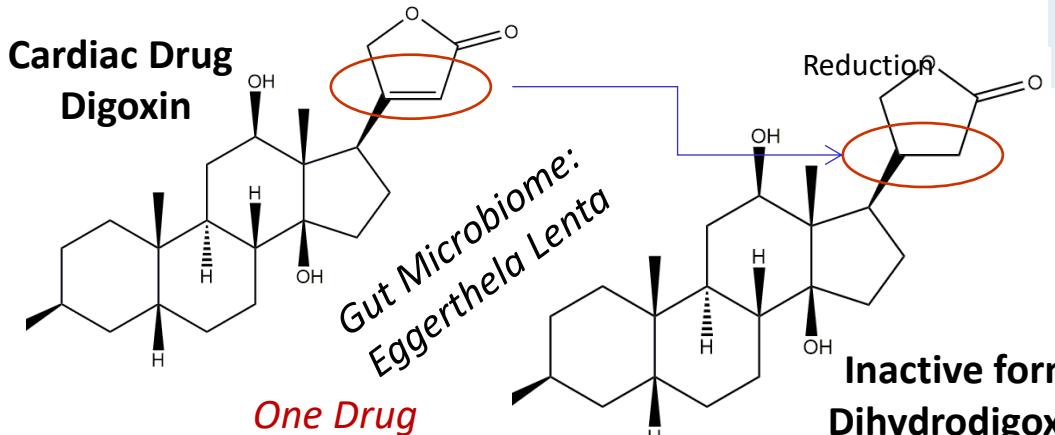
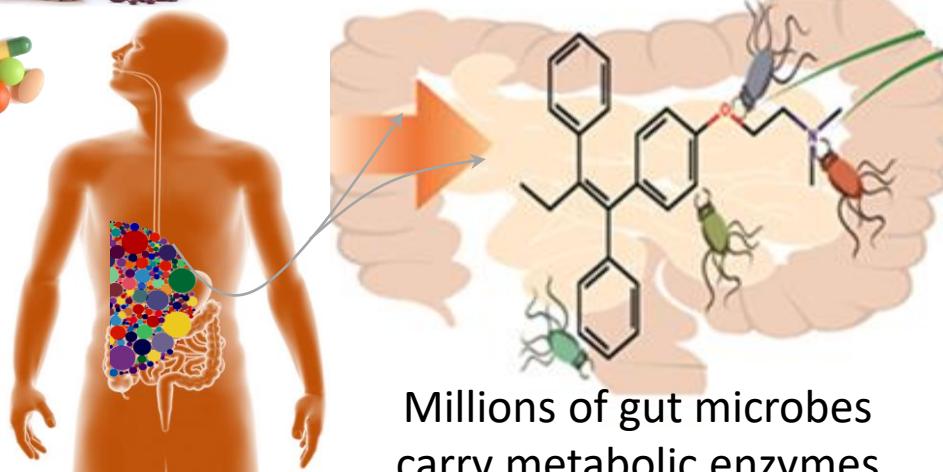
b Hydrolysis



Images taken from published studies and google images, sincerely acknowledged



Promiscuous Metabolism of Xenobiotics by Human Gut Microbiome

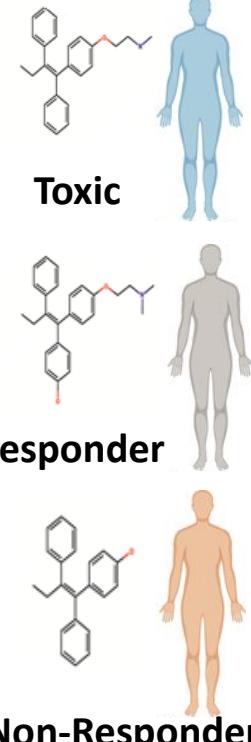
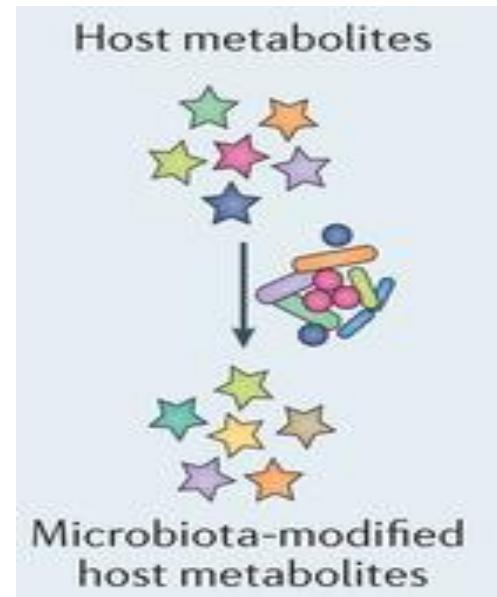
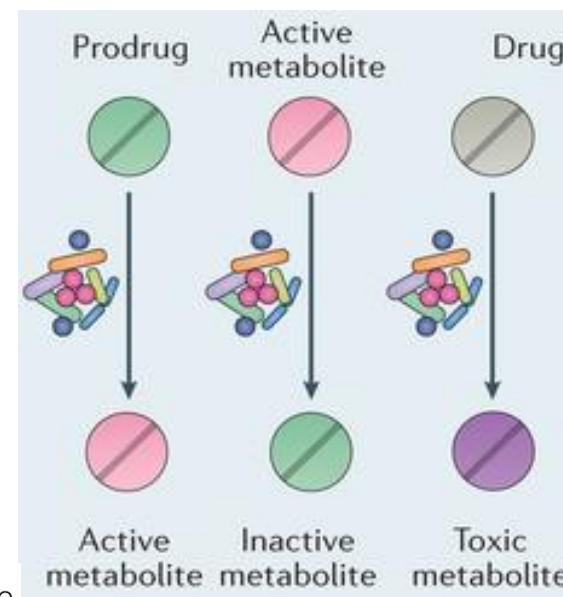


Two top papers: Science 1984 → Science 2014
Identification took Two Decades

Need To Identify

- Microbe
- Metabolic Enzyme
- Site of Metabolism
- Population-specific variability

Promiscuous Xenobiotic Metabolism by Microbes



- *Metabolism of nutraceuticals and drug Inefficacy is a major issue in different populations*
- *Drug discovery and biometabolite proposition is a very costly and time consuming process*

GutBug

A method to detect the promiscuous metabolism of an oral xenobiotic molecule
Save time, cost, better designing of the product for population specificity

Performance of GutBug and DrugBug using hybrid features and optimised models

Validation on test sets	Hybrid Fingerprint									
	RF model without-upsampling dataset					RF model with-upsampling dataset				
	TPR	TNR	PPV	ACC	MCC	TPR	TNR	PPV	ACC	MCC
CV-10 FOLD	52.83	92.63	60.32	89.33	0.49	91.58	98.32	91.46	97.19	0.89
Splitting and Testing	60.84	92.71	49.05	88.94	0.46	87.02	97.49	87.25	95.75	0.84
Blind Set	55.52	94.17	66.15	92.14	0.54	67.41	94	63.19	91.18	0.59

TPR = True Positive Rate or Sensitivity, FPR = False Positive Rate or Specificity, PPV = Positive Predictive Value or Precision, ACC = Accuracy and MCC = Matthews correlation coefficient

Validation Set: Diverse molecules selected including xenobiotics and bioactive dietary substrates

Biotic molecules:

1. Inulin
2. Daidzein
3. Chalcone
4. Quercetin
5. Curcumin
6. Lactulose
7. 2'-fucosyllactose
8. Lacto-N-neo-tetraose
9. Lactosucrose

Xenobiotic molecules:

1. Nicardipine
2. Capecitabine
3. Risperidone
4. Sulfasalazine
5. Spironolactone
6. Misoprostol
7. Digoxin
8. Hydrocortisone
9. Omeprazole

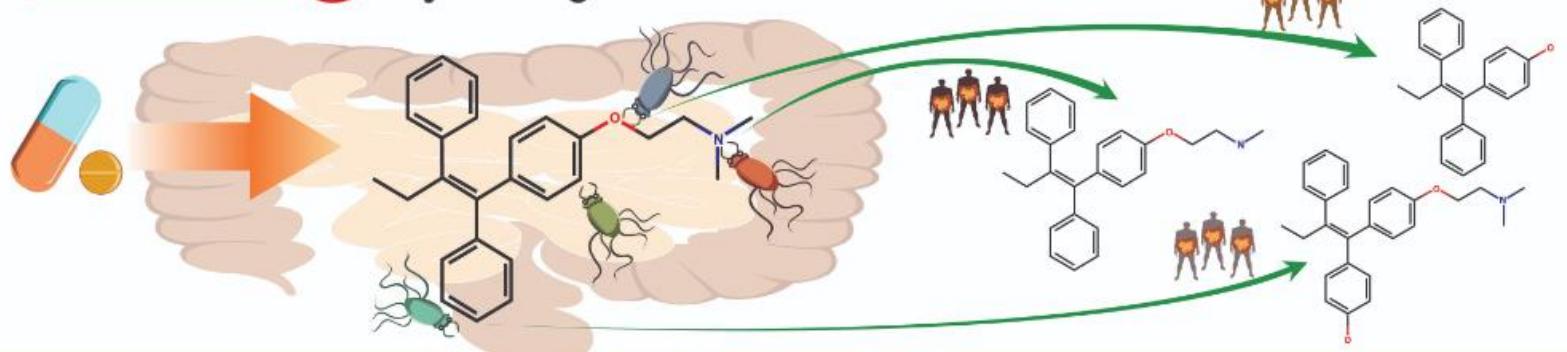
- Includes essential drugs, dietary molecules, nutraceutical products, prebiotics etc.
- GutBug predicts known metabolic reactions as well as new reactions.
- Previously unknown enzymes and gut bacterial species identified for many molecules (Misoprostol, Lactosucrose, Loperamide)
- Additional reactions predicted: logically correct as per the functional groups
- Predicted known enzymes and species



A step closer to the goal of personalized diet and medicines

GutBug

AI based tool for prediction of biotic and xenobiotic biotransformation by human gut bacteria



Upload File or provide Pubchem ID for Input Molecule

No file chosen

Upload Sample File

Please enter PubChem ID here

Model for Reaction Class Prediction

A consensus of ANN and Random Forest models will be taken to predict the final reaction class

Probability Threshold

The probability threshold of 0.5 was used for the reaction class prediction

Submit

First tool to predict the potential enzymes and human gut bacteria for the metabolism of a given xenobiotic molecule

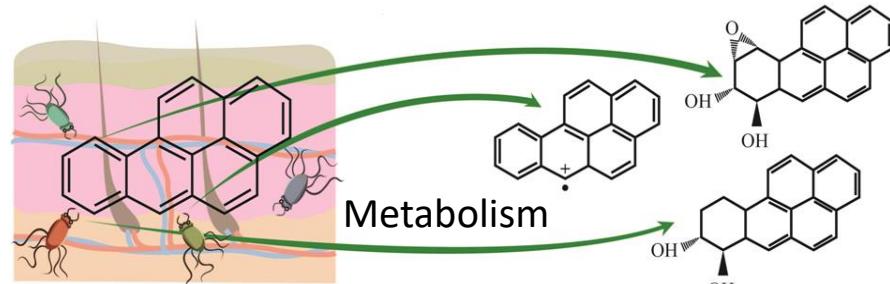
Can predict the individual-specific and population-specific metabolism and bioavailability of a xenobiotic molecule

Results will help in population specific drug-design, develop co-therapies including diet, nutraceuticals, prebiotics, probiotics, antimicrobials



Predict Metabolism of Biotic and Xenobiotic Molecules by Skin Microbiome using AIML approach

Skin microbiome: Body site-specific variation, >1000 bacterial species, large diverse pool of enzymes other than host genome



- Change in pharmacological activity of molecule (efficacy, bioavailability, etc.)
- Adverse physiological effect: Toxicity of molecule

Important outcomes of this undesired metabolism

METABIOSYS

HOME PREDICTION ALGORITHM TEAM

SkinBug | A Tool to Predict Metabolism of Biotic and Xenobiotic Molecules by Skin Microbiome

Upload File or provide Pubchem ID for Input Molecule

Choose File No file chosen Upload Sample File

Molecule CID * (example: 123456, 1983, 60838)

Model for Reaction Class Prediction

A consensus of ANN and Random Forest SRC model will be taken to predict the final reaction class

Probability Threshold

The probability threshold of 0.5 was used for the reaction class prediction

Submit

Prediction by SkinBug

- Skin Microbe, Skin site, Metabolic Enzyme for Biotransformation
- Metabolic reaction, Reaction center and Resultant Metabolites
- **ADMET** properties (Toxicity) for the resultant metabolites
- Population-specific xenobiotic metabolism

Validation of SkinBug

- Validation on 50-100 selected xenobiotics commonly used and environmental pollutants (exposome)
- Computational validation: MD simulations
- Experimental validation: Gene knockout and Metabolomics

A user friendly web server was developed and is available at

<http://metagenomics.iiserb.ac.in/skinbug>

iScience, 2021

Datasets and Performance

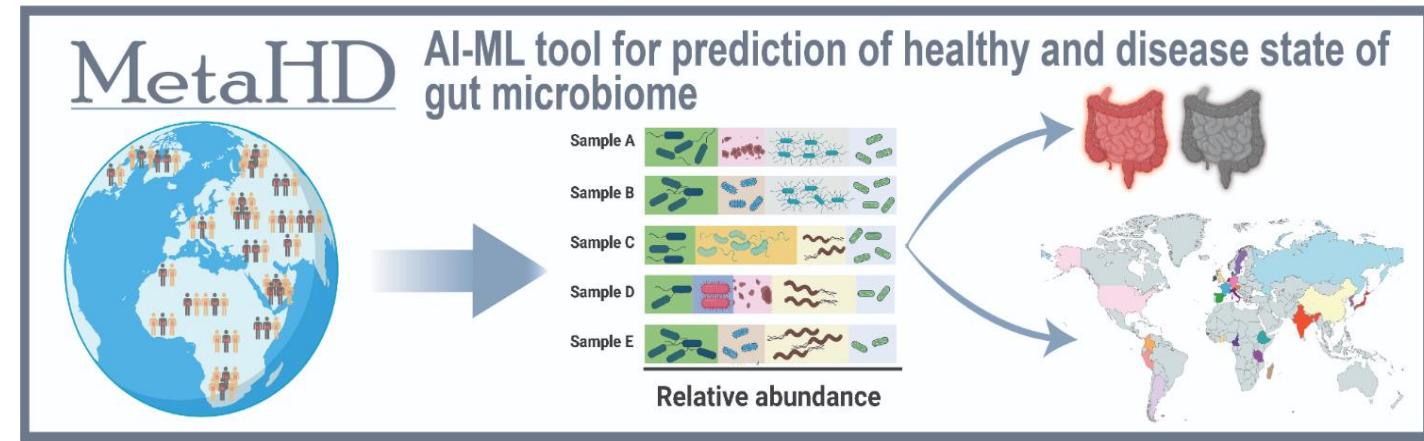


METABIOSYS

HOME PREDICTION ALGORITHM TEAM



- 11,270 publicly available metagenomic samples from 65 studies, 29 diseases and 27 populations.
- Health status prediction accuracy : 0.81
- Population prediction accuracy : 0.96



In progress

- AIML models for all diseases and dysbiosis associated with gut microbiome
- Proof of concept is applicable for any dysbiosis in any metagenome including human or other environment

Upload microbial abundance profile for Input

Note: The tutorial to generate input microbial abundance profile is given in tutorial section

No file chosen

Upload Sample File

Model for Health Status and Population Prediction

A consensus of ANN and XGBoost classifier is used to predict health status and XGBoost classifier is used to predict population

Submit

XenoBug: Prediction of Xenobiotic Metabolism by Environmental bacteria



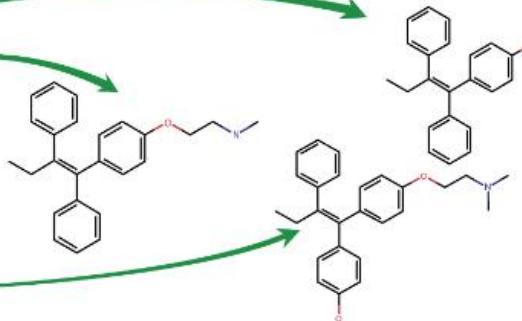
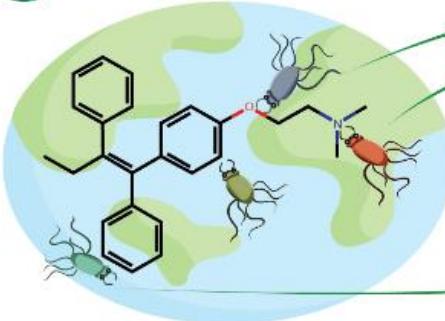
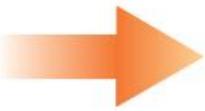
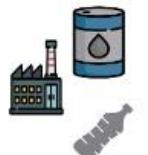
METABIOSYS

HOME PREDICTION ALGORITHM TEAM



XenoBug

AI based tool predicting degradation of environmental pollutants by environmental bacteria



Upload File or provide Pubchem ID for Input Molecule

No file chosen

Upload Sample File

Please enter PubChem ID here

Model for Reaction Class Prediction

A consensus of ANN and Random Forest models will be taken to predict the final reaction class

Probability Threshold

The probability threshold of 0.5 was used for the reaction class prediction

Submit

NAR Genomics and
Bioinformatics, 2025



Sequencing of Eukaryotic Genomes of National and International Importance

First ever genome sequencing of important eukaryotes in the world

National Bird, National animal, National tree, and proposed National herb, medicinal, commercial plants

Banyan Tree



Peepal Tree



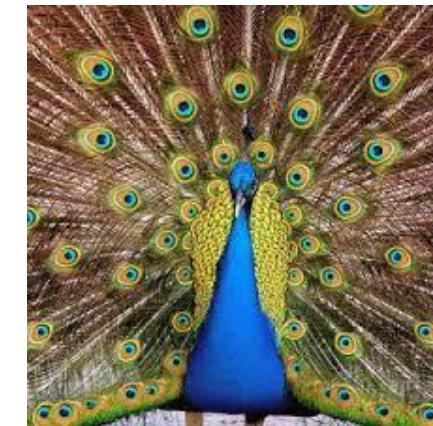
Water Hyacinth



Bag worm



Peacock



National
Bird of India

Turmeric



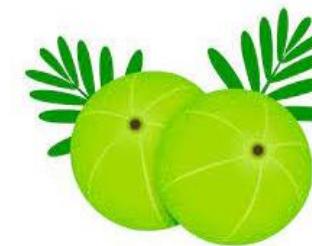
Aloe vera



Giloy



Amla



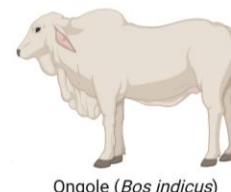
Custard apple



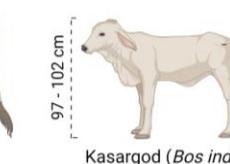
Jamun



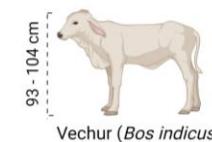
Several more are in progress now



Ongole (*Bos indicus*)



Kasargod (*Bos indicus*)



Vechur (*Bos indicus*)

First Genomes of Four Indian cow breeds (*Bos indicus*) including the World's Smallest Cow

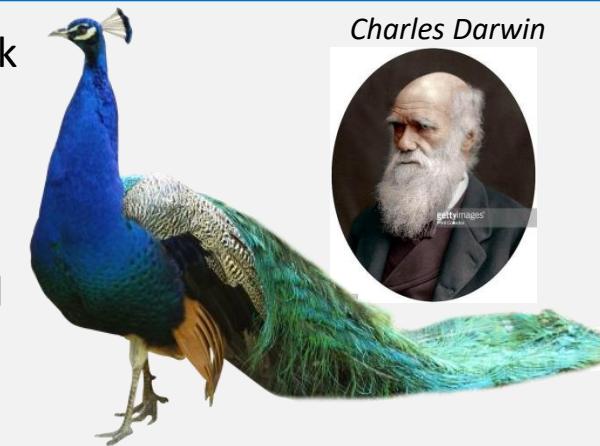


First genome sequencing of Indian Tiger (National Animal) from India

Genome Sequencing of Peacock (*Pavo cristatus*): The National Bird of India



- First ever Sequencing of Peacock in the World
- Schedule-I conservation: Highly protected
- Elaborate eyespots, ornamental plumage
- One of the largest flying birds



Charles Darwin

The sight of the peacock's tail makes me sick

Key Research Findings

- 444x Illumina short read, 81x linked read, 7.6x Nanopore long read data
- Hybrid genome assembly approach using both short and long read data
- Genome Size : 1.13 GB, 69 pseudochromosomes
- Genes 25,681, tRNAs: 290, snoRNAs: 236, and miRNAs: 540
- Two declines around 4,000 million and 450,000 years ago.
- 429 genes showed multiple signs of adaptive evolution
- Adaptive evolution of neuronal and skeletal muscle developmental genes
- Genomic clues for peacock feathers
- Robust immune system



Comparative genomics with green peafowl (*Pavo muticus*)

- 42% more coding genes in *Pavo cristatus* (blue peafowl)
- Higher number of unique gene clusters, segmental duplicated genes and expanded gene families in blue peafowl
- Better evolution in neuronal and developmental pathways in blue peafowl
- Evolutionary advantage of blue peafowl over green peafowl

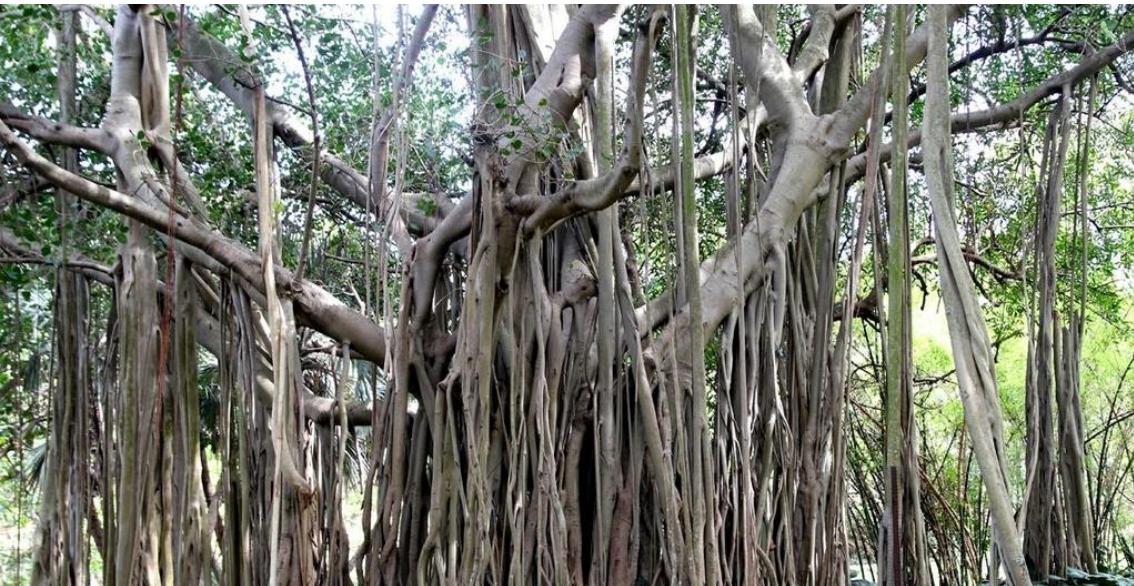


Pavo muticus

Genome sequencing is crucial for

Species revival in case of decline, Tackle pathogenic attacks, Better strategies for their breeding, Management and conservation of our national bird

Genome sequencing of *Ficus benghalensis*: National tree of India



- Indian Banyan tree
- Draft genome assembly: 392.89 Mbp, N50: 486.9 Kbp
- 25,016 coding genes, %GC: 34.54, repeats: 51.36%
- Hybrid assembly approach using 10x Genomics linked reads and Nanopore long reads
- Constructed phylogenetic tree with 46 other plant species to determine their position
- Genes responsible for the longevity of these plant were found to be evolved

Genome sequencing of *Ficus religiosa*: Most sacred and ancient tree of India



- Peepal tree
- Draft genome: 332.97 Mbp, N50: 553.4 Kbp
- 23,929 coding genes, %GC: 34.31, repeats: 45.88%

First ever Turmeric genome sequencing

Hybrid sequencing and assembly approach

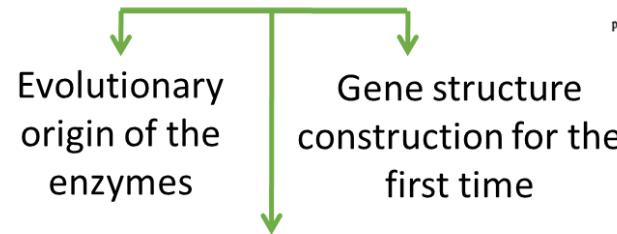


10x Genomics linked reads (82X coverage)

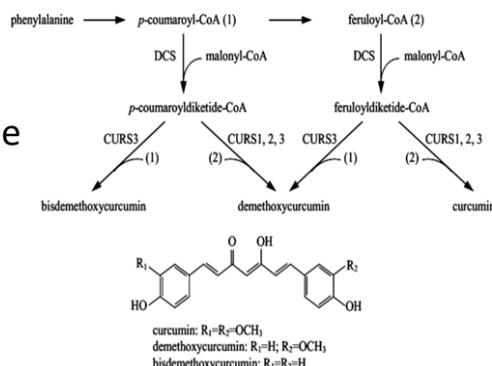
Oxford Nanopore long reads (41X coverage)

- Genome size - 1.02 Gbp, N50 - 100.6 Kbp
- Complexity - High heterozygosity (4.83%), 70% repeats, triploid
- Reference quality assembly, BUSCO (>92%), 50,401 genes
- For the first time, transcriptome sequencing from leaf tissue

Elucidation of curcuminoid biosynthesis pathway



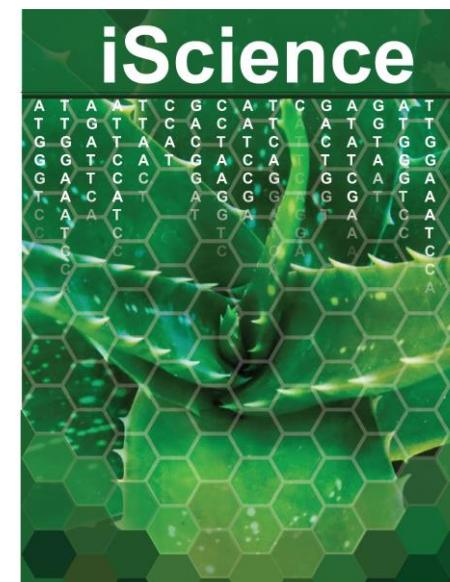
Adaptive evolution, gene family expansion/contraction of the enzymes



Communications Biology, 2021

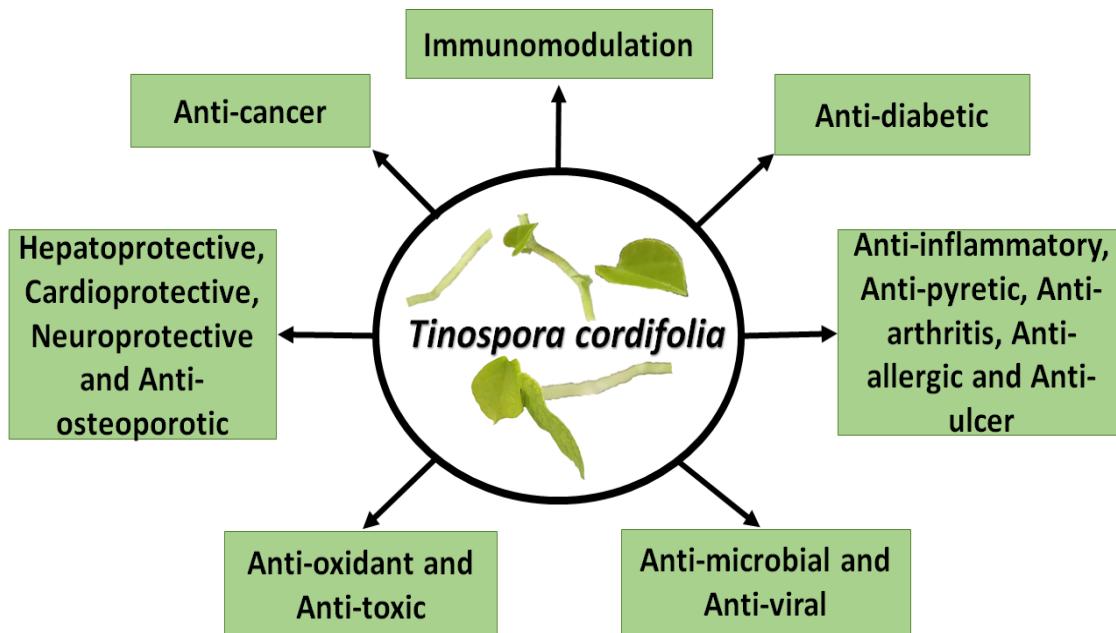
First Genome Sequence of Aloe vera

- First genome from Asphodelaceae plant family
- Largest angiosperm genome sequenced till date
- Gigantic genome : 16 Gbp (>5 times human genome)
- Largest genome sequenced using Oxford nanopore technology at the time of publication
- Hybrid approach of sequencing and assembly
- Molecular basis of drought tolerance capabilities
- Unique medicinal properties adds to our traditional medical knowledge of Ayurveda



iScience, 2021

First Genome Sequence of Giloy (*Tinospora cordifolia*) : A medicinal herb



- First genome sequenced from plant family Menispermaceae
- Hybrid genomic assembly approach using 10X Genomics linked-reads and Nanopore long reads
- Estimated genome size: 1.13 Gbp
- Draft genome assembly had 1.01 Gbp with N50 of 50.2 Kbp and 56,342 scaffolds
- 34.7 Gbp transcriptome from Leaf
- 19,474 genes, %GC: 35.12, Repeats: 75.15%
- Resolved phylogenetic position of Giloy by comprehensive genome-wide phylogenetic analysis with 36 other plant species

A high-quality genome assembly of *Annona squamosa* (custard apple)

OXFORD
ACADEMIC

Journals

Books

DNA Research

JOURNAL ARTICLE

A high-quality genome assembly of *Annona squamosa* (custard apple) provides functional insights into an emerging fruit crop

 Save

 Related Papers

 Chat with paper

Manohar S Bisht, Shruti Mahajan, Abhisek Chakraborty, Vineet K Sharma 

DNA Research, Volume 32, Issue 3, June 2025, dsaf007,

<https://doi.org/10.1093/dnarecs/dsaf007>



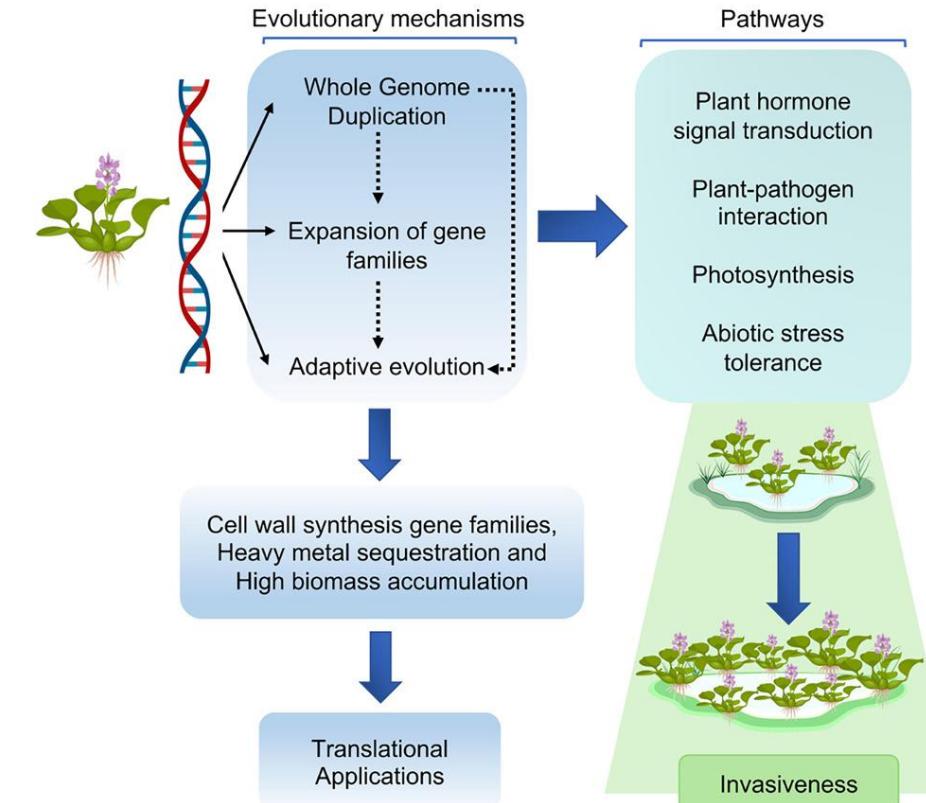
- *Annona squamosa*, also known as custard apple, is an emerging fruit crop with medicinal significance
- Extracts from custard apple roots, bark, leaves, and fruit exhibit diverse ethnomedicinal properties, including anticancer, antioxidant, etc.
- The genome has an N50 value of 93.2 Mb assembled into seven pseudochromosomes
- The demographic history showed a continuous decline in the effective population size of *A. squamosa*
- Comparative analysis with other magnoliids revealed the adaptative evolution in the genes of flavonoid biosynthesis pathway, amino sugar, nucleotide sugar and sucrose metabolism, conferring medicinal value and enhanced hexose sugar accumulation

Genome sequencing of world's most noxious weed – water hyacinth



iScience, 2024

- Hybrid genomic assembly approach
- Genome size of 1.2Gbp with tetraploid nature
- N50 : ~2Mbp
- BUSCO: 95%
- Transcriptome data from three different tissues

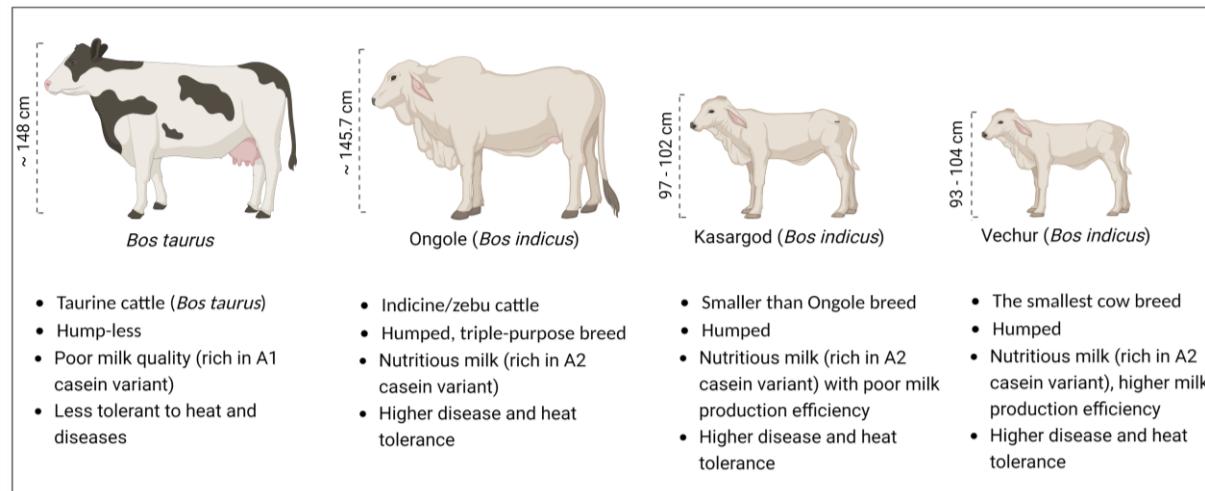


Genomic insights into pathways contributing to the invasiveness and translational potential of water hyacinth

- ✓ Plant-pathogen interaction (**Invasiveness**)
- ✓ Hormone signalling (**Invasiveness**)
- ✓ Abiotic stress tolerance (**Invasiveness**)
- ✓ Heavy metals sequestration (**phytoremediation potential**)
- ✓ Photosynthesis (**Biofuel production** and **Carbon sequestration**)
- ✓ Cell wall biosynthesis (**Biofuel production** and **Paper production**)

First Genomes of Four Indian cow breeds (*Bos indicus*) including the World's Smallest Cow

Indian cow breeds are known for their adaptability, highly nutritious milk, disease tolerance



- Constructed - reference-based genome assemblies, *de novo* genome assemblies (~3 Gbp), mitochondrial genome assemblies (~16.5 Kbp), 18S rRNA marker gene sequences
- Identified the bovine genes related to distinct phenotypic characteristics and other biological processes for this species compared to *B. taurus*, which are plausibly responsible for providing better adaptive traits

First Genome of Royal Bengal Tiger from India

Sequencing Stats

Tiger	Data
Amur	83x, 203 Gb
Bengal	27x, 67 Gb



Bandhu (Van vihar)

- Developed 'SeqBug' pipeline for assembly correction
 - Validated of assembly errors using sequencing of Bengal tiger genome
 - Single nucleotide substitution errors in Tiger genome assembly
 - Assembly errors affect evolutionary analysis and bias interpretations
- Multiple signs of adaptations in 955 genes in tiger**
- ✓ Enriched for developmental and neuronal genes
 - ✓ Evolution in NOTCH signaling pathway

Why do banyan and peepal trees live so long?

Sequencing identifies genes responsible for longevity

RESEARCH HIGHLIGHT | 11 February 2023

Genome of the world's smallest cow decoded

The study also identifies gene variations between important Indian cow breeds

RESEARCH HIGHLIGHT | 28 October 2021

Genome of turmeric plant decoded

Scientists identify the genes that give turmeric its medicinal and disease-defying properties

RESEARCH HIGHLIGHT | 13 March 2021

Aloe vera genome decoded

RESEARCH HIGHLIGHT | 12 September 2023

Gene expansion has given blue peafowls an evolutionary edge

Green peafowls have lost genes because of human disturbance and habitat loss

NEWS | 22 April 2019

Diets shape your gut microbes

RESEARCH HIGHLIGHT | 05 October 2018

Peacock genome sequencing to aid conservation

RESEARCH HIGHLIGHT | 20 November 2018

Clues to potential anti-dandruff therapies

NEWS | 03 February 2020

A bug in the gut that shoots up risk of colon cancer

RESEARCH HIGHLIGHT | 30 November 2021

Indians have abundance of specific gut bacteria which help digest fibre-rich foods

These microbes could potentially be used to develop prebiotics and probiotics to treat gut disorders

RESEARCH HIGHLIGHT | 13 September 2021

Giloy herb genome decoded

Pathways for survival mechanisms sought in plant with therapeutic value

RESEARCH HIGHLIGHT | 21 September 2023

Amla genome decoded

Now we know which genes relate to its super antioxidant properties and pathogen resistance

RESEARCH HIGHLIGHT | 10 September 2024

Genes reveal how water hyacinth invades new habitats



L'ORÉAL
PARIS



Past PhD Students (present affiliation)

- Dr. Darshan Dhakan (Assistant Professor, Nirma University)
- Dr. Ashok Sharma (Senior Scientist at Takeda, USA)
- Dr. Ankit Gupta (Team Leader at Siemens Healthineers Bengaluru)
- Dr. Rituja Saxena (Life Sciences, Merck, Bangalore)
- Dr. Parul Mittal (Data Science Scientist at L&T Infotech)
- Dr. Shubham Jaiswal (Data Scientist, Gold Medallist)
- Dr. Vishnu Prasoodanan (Postdoc, Sweden, Best thesis)
- Dr. Shruti Mahajan (Postdoc in Poland)
- Dr. Abhisek Chakraborty (Postdoc in Germany)
- Dr. Aditya Malwe (Postdoc Denmark)
- Dr. Sudhir Kumar

Past PostDocs

- Dr. Abhijit Maji
- Dr. Sudheer Gupta
- Dr. Sanjiv Kumar

Thank you !!



Present PhD Students

- | | |
|-----------------|-----------------------|
| • Deepika | • Martin Abraham |
| • Manohar Bisht | • Vanshika Srivastava |
| • Mitali Singh | • Bayasis Sharma |
| • Usha Longwani | • Siddhant Mahato |
| • Muskaan | • Sonal Sharma |