Studies on Microbiota and Health

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Translational Health Science and Technology Institute

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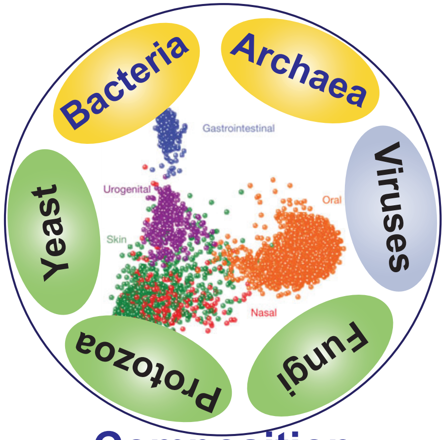
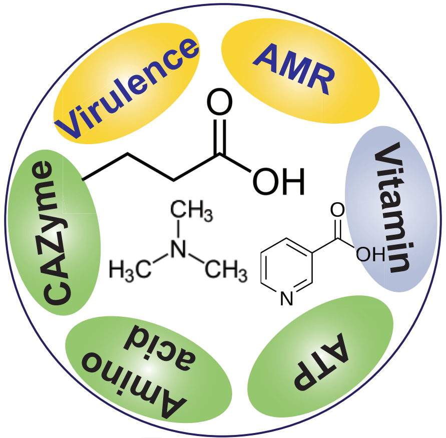
Human Microbiome Research Activities

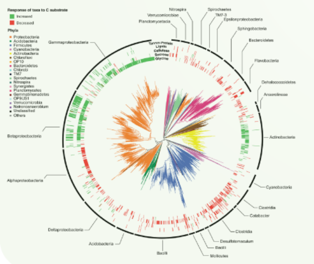


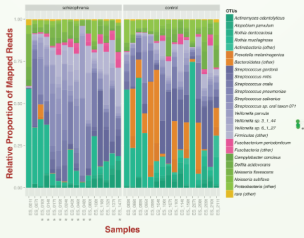
Composition



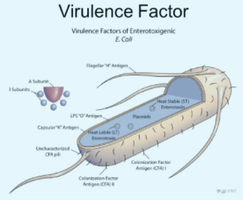
Functions

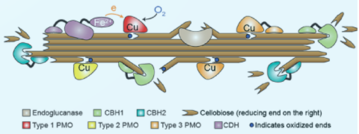
Diversity Abundance Network





Virulence AMR CAZyme





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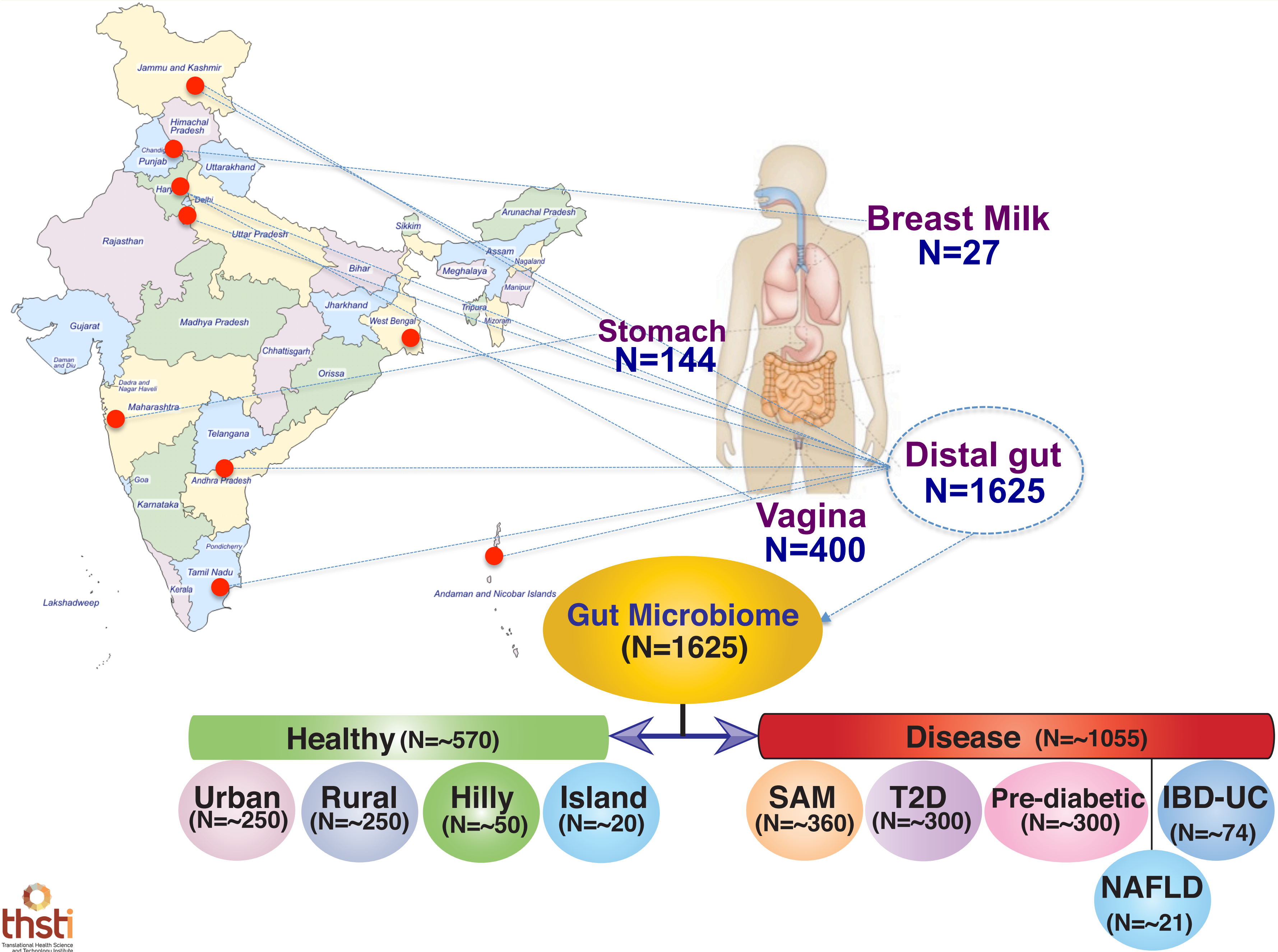
Microbiome of the Indian Population (N=2196)



Breast Milk
N=27

Stomach
N=144

Distal gut
N=1625

Vagina
N=400

Gut Microbiome
(N=1625)

Healthy (N=~570)

- **Urban (N=~250)**
- **Rural (N=~250)**
- **Hilly (N=~50)**
- **Island (N=~20)**

Disease (N=~1055)

- **SAM (N=~360)**
- **T2D (N=~300)**
- **Pre-diabetic (N=~300)**
- **IBD-UC (N=~74)**
- **NAFLD (N=~21)**

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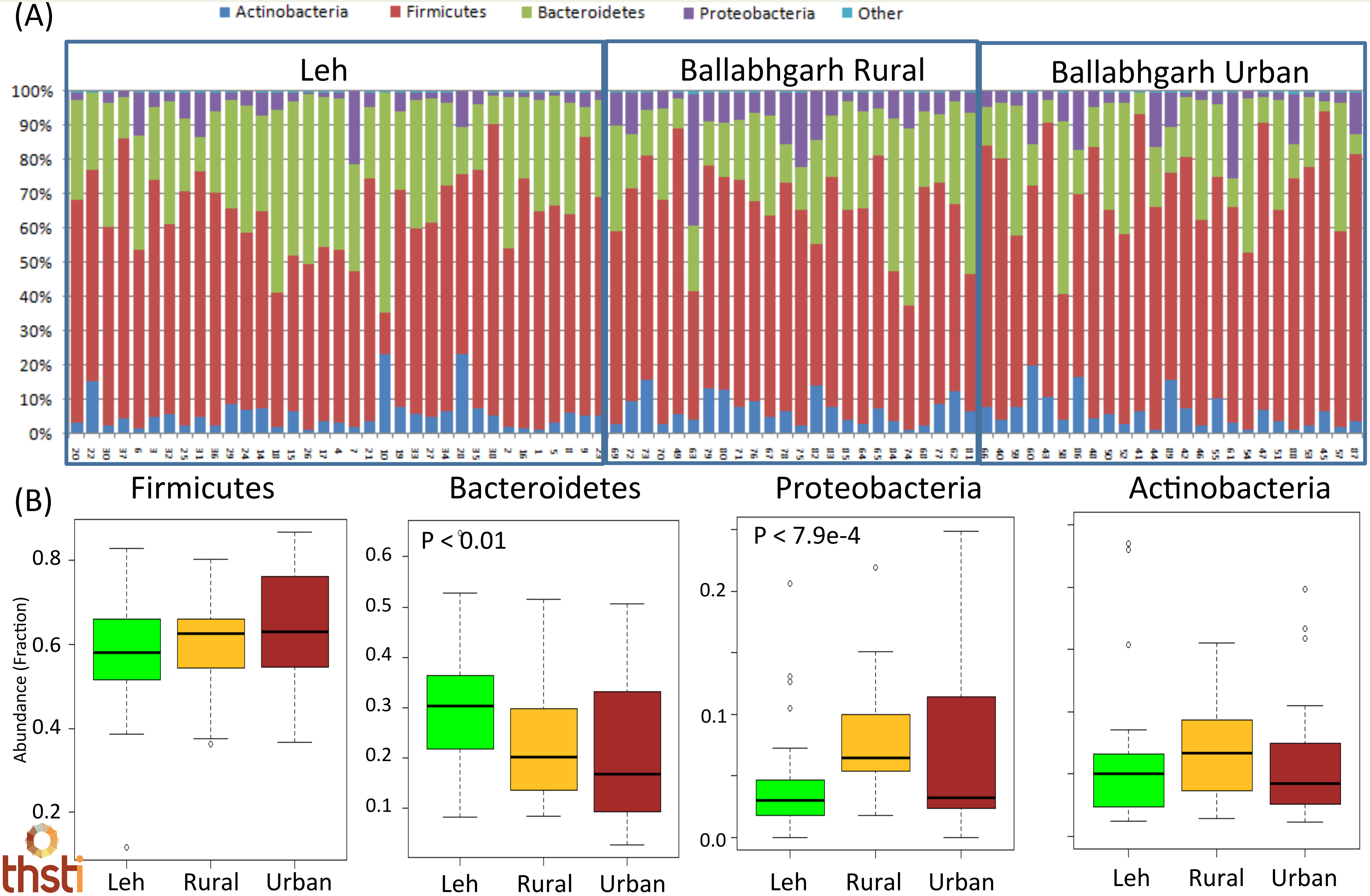
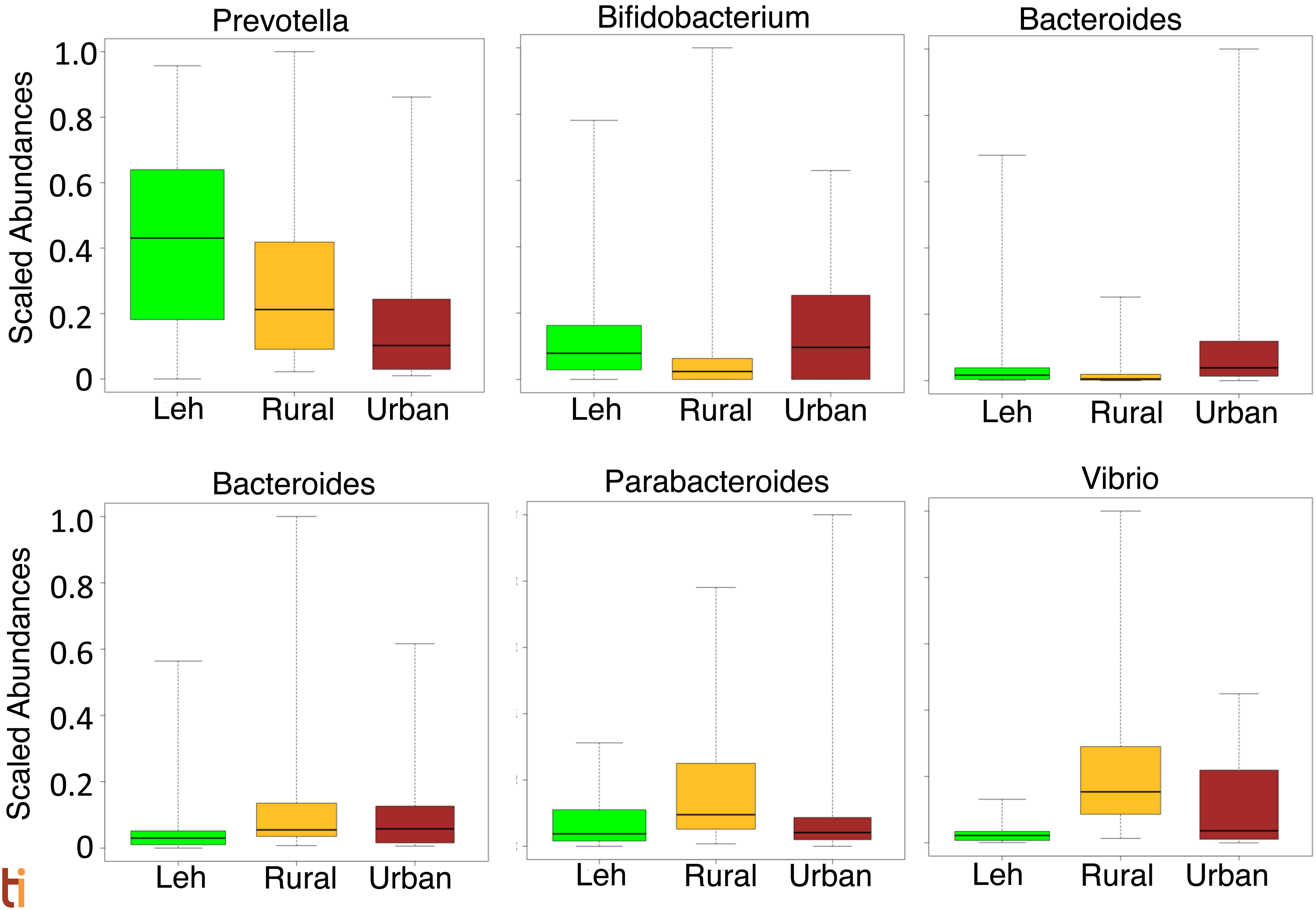
Gut Microbiome of the Healthy Adult Indians

Cohort	Age (yrs)	Average Sequence Length (bp)	Reads per sample
Leh (N=35)	35.7 ± 1.8	604.9 ± 1.4	16157 ± 1494
Ballabhgarh Urban (N=24)	34.0 ± 1.4	645.9 ± 9.1	28858 ± 6832
Ballabhgarh Rural (N=25)	36.0 ± 1.7	686.4 ± 4.7	21789 ± 481

People living in the Leh region have minimal pathobionts in their distal gut



Differential abundances of the prominent bacterial genera across the three regions



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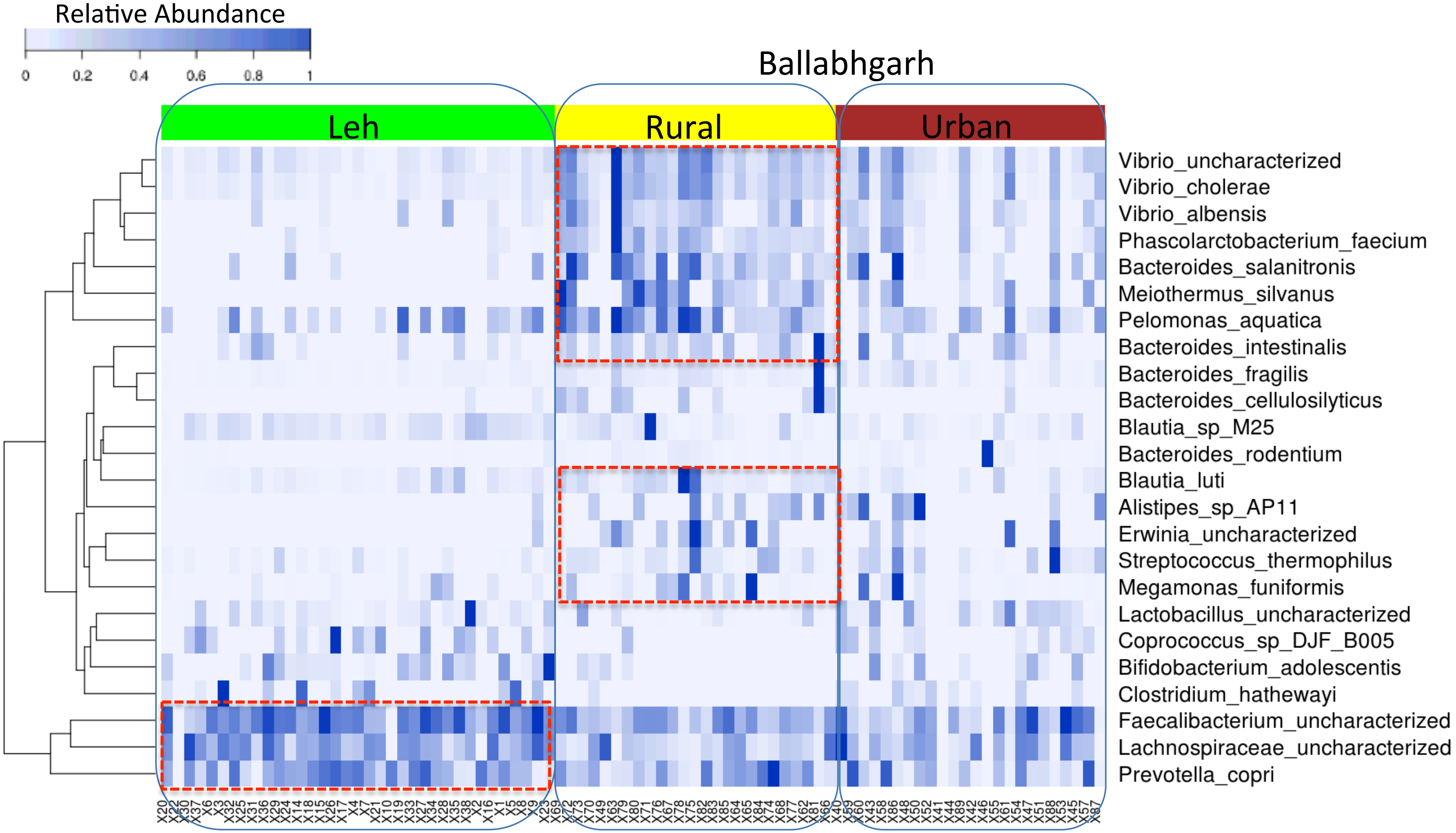
Gut of the Leh People is Enriched with anti-inflammatory microbiota

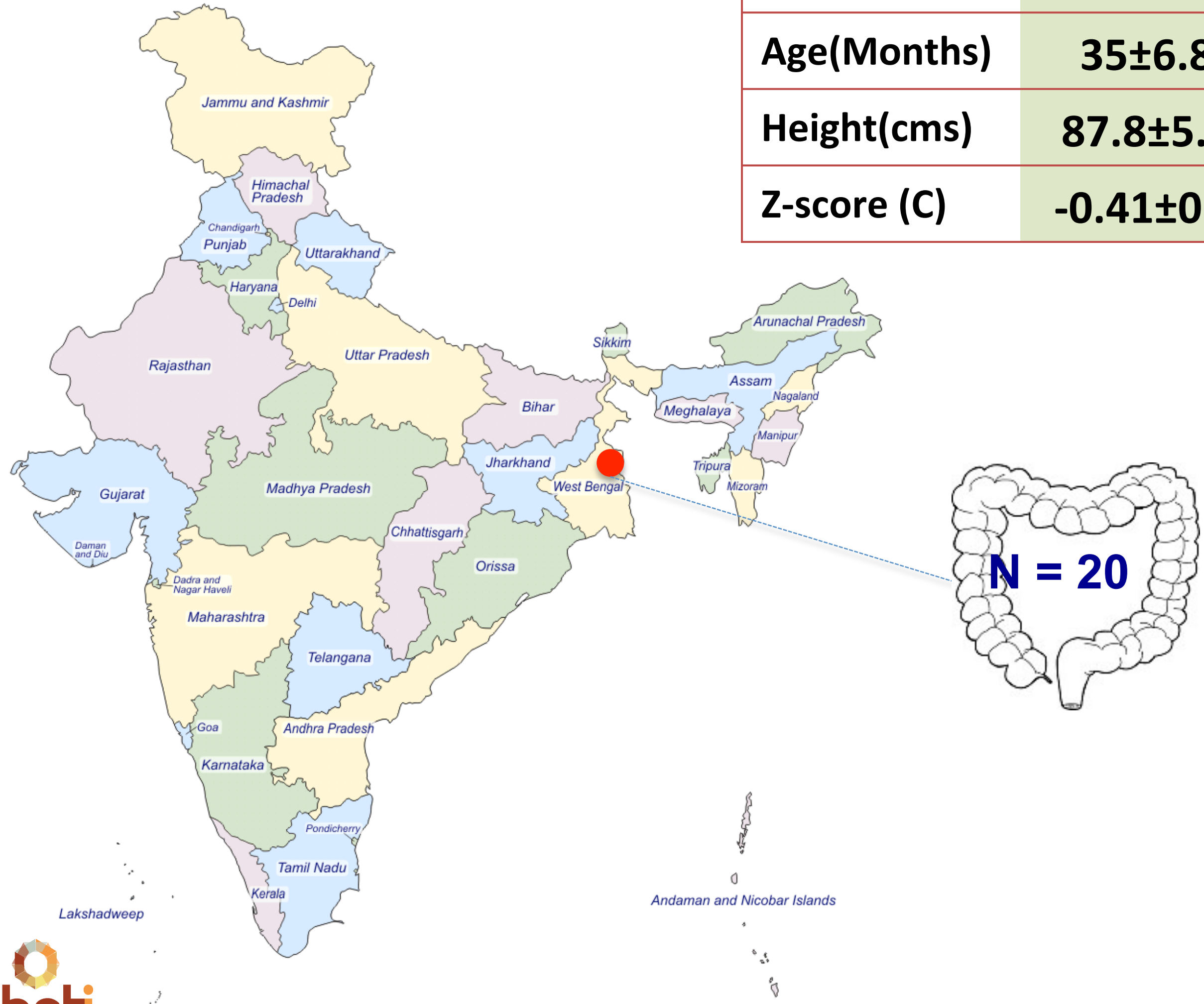


Das *et al.* 2018

OPEN ACCESS Freely available online
PLOS ONE 2014

Gut Microbiomes of Indian Children of Varying Nutritional Status

	AH	BL	SM
Sub. #	6	6	8
Age(Months)	35±6.8	39±3.7	51±6.1
Height(cms)	87.8±5.4	86.4±2.9	88.7±2.1
Z-score (C)	-0.41±0.5	-7.93±0.3	-10.47±0.34



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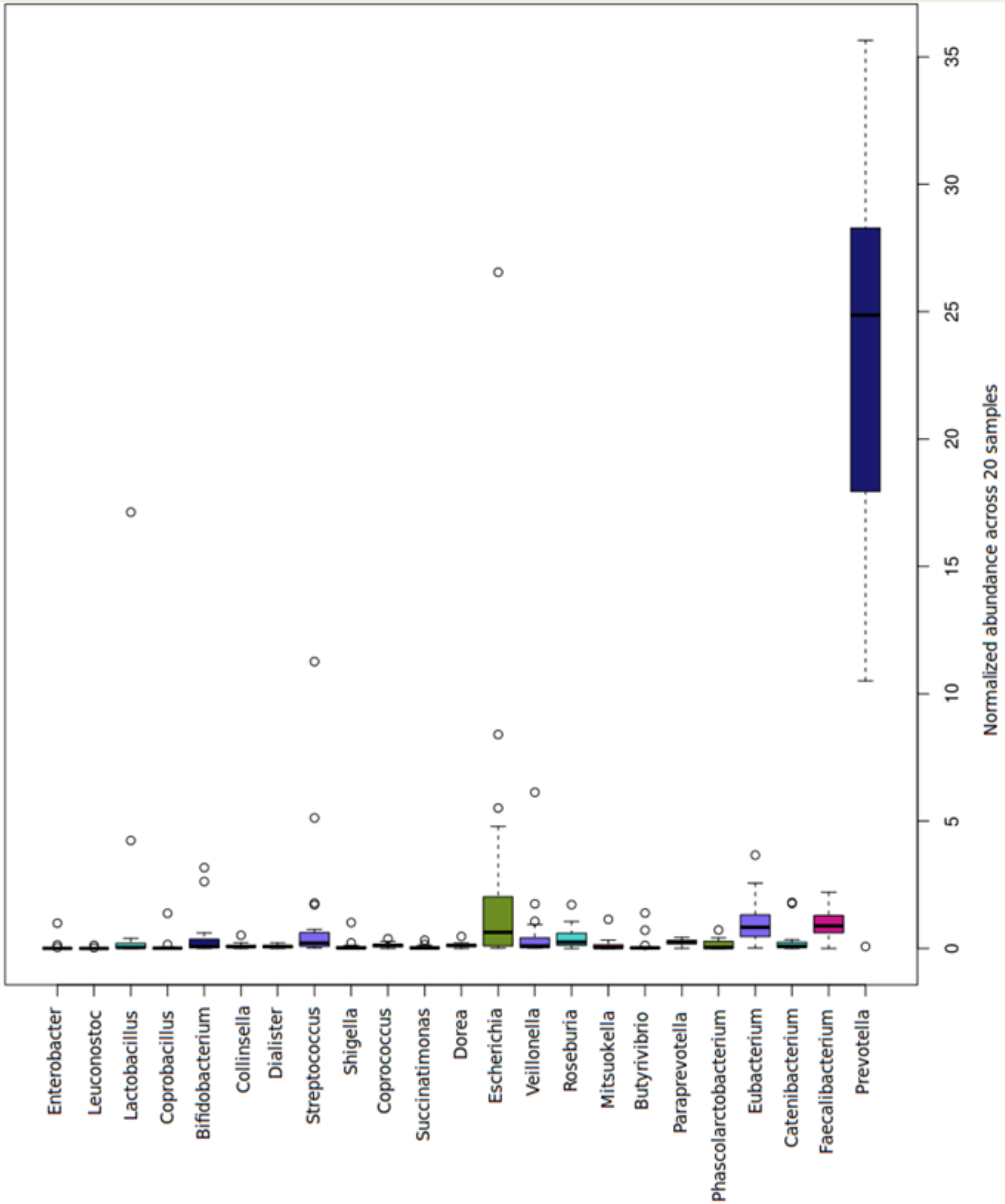
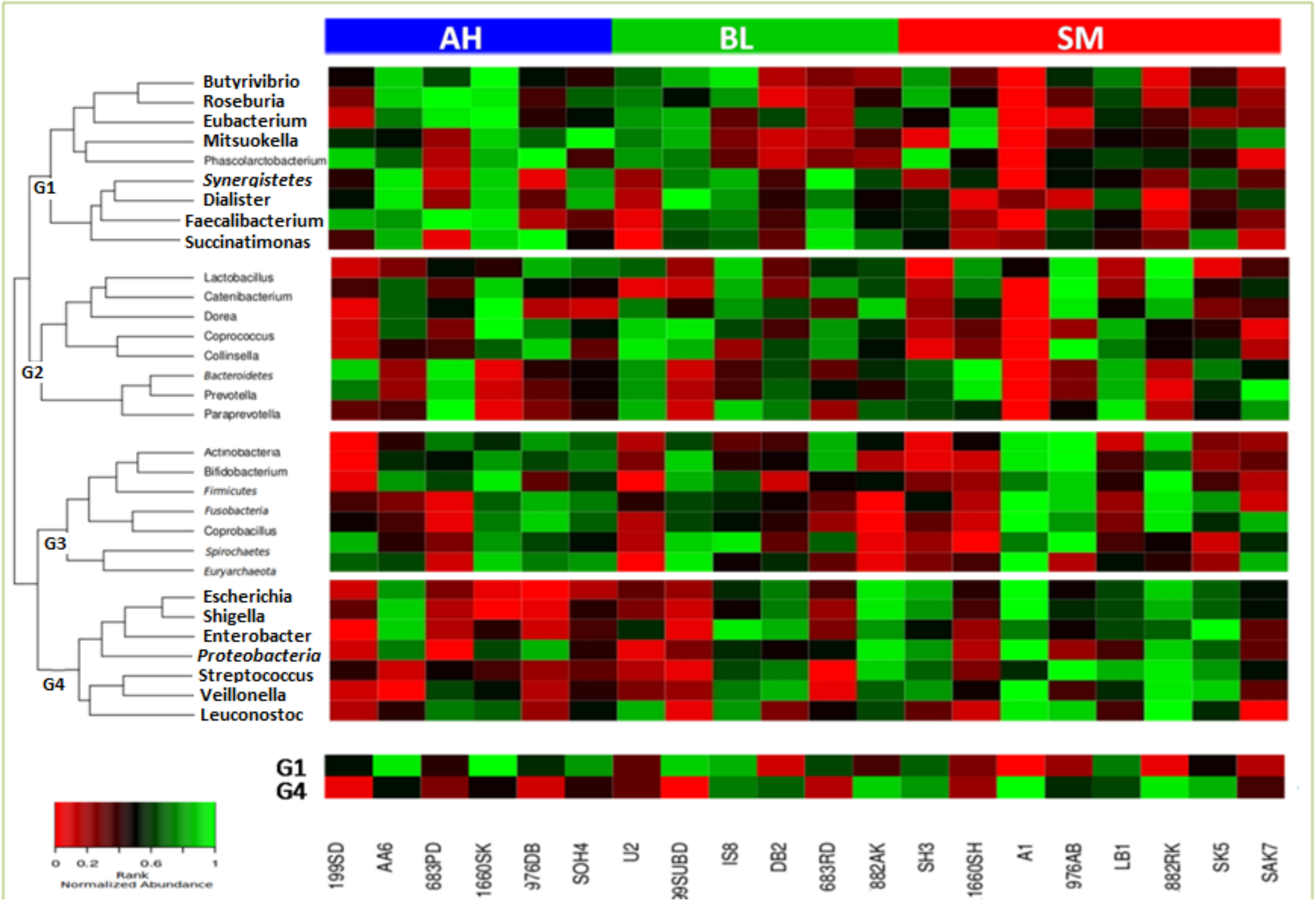
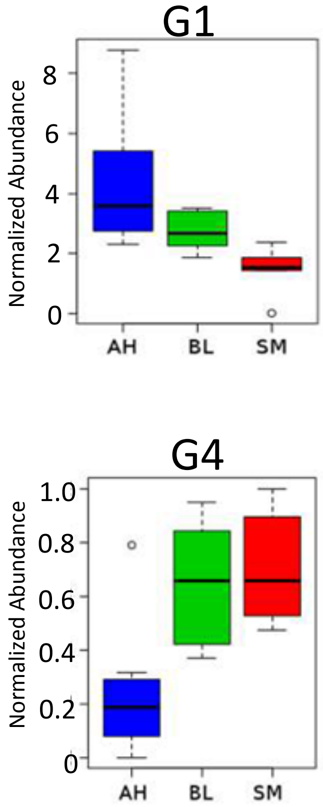
Core Microbiota of Indian Children with varying nutritional status



Ghosh et al. 2014

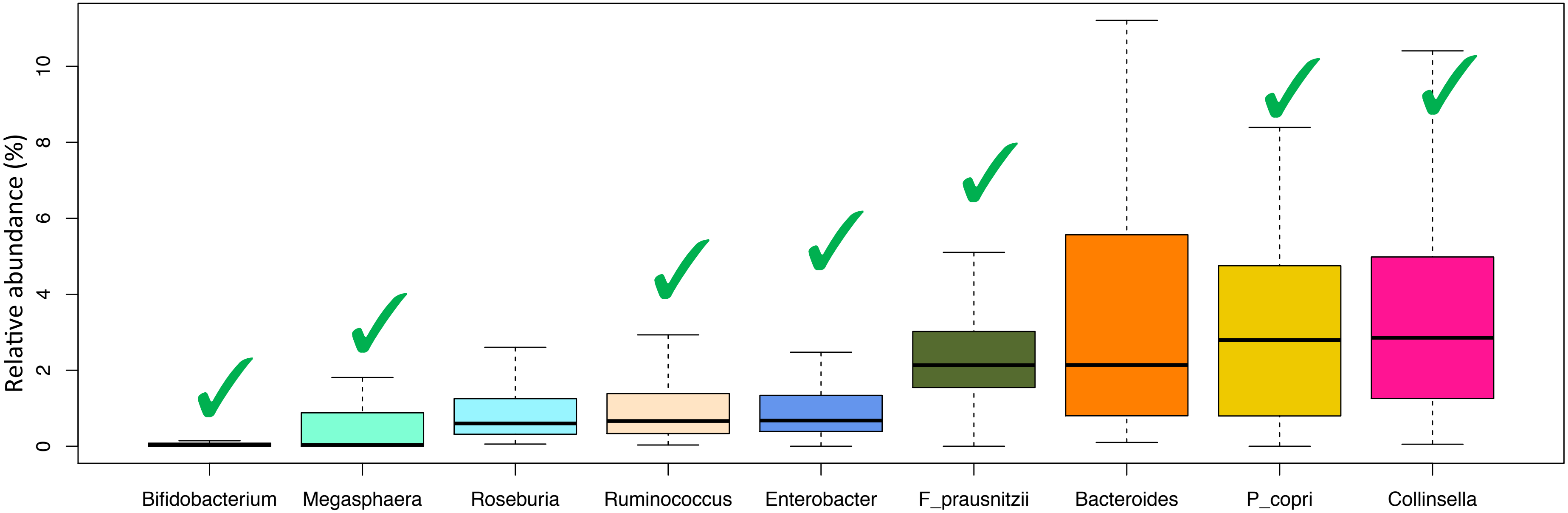
Predominance of pathogenic bacteria in the guts of malnourished children

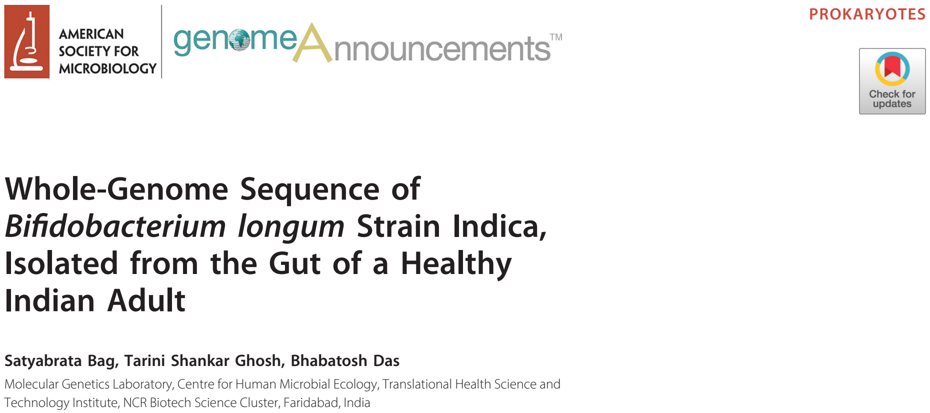




Ghosh et al. 2014

Most Dominant Microbiota in the Gut of Healthy Indians

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PROKARYOTES

Check for updates

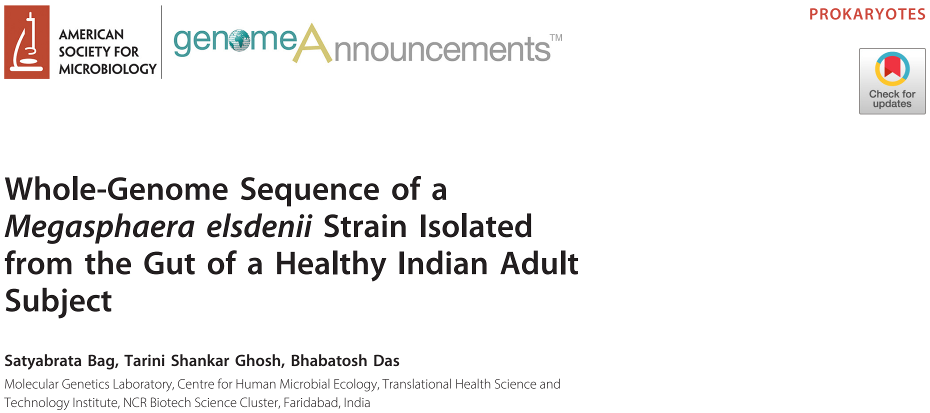
Whole-Genome Sequence of *Bifidobacterium longum* Strain Indica, Isolated from the Gut of a Healthy Indian Adult

Satyabrata Bag, Tarini Shankar Ghosh, Bhabatosh Das

Molecular Genetics Laboratory, Centre for Human Microbial Ecology, Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad, India

Complete-Genome Sequence of *Faecalibacterium prausnitzii* strain Indica isolated from the Gut of Healthy Indian Adult

Bag et al. GA (2017)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PROKARYOTES

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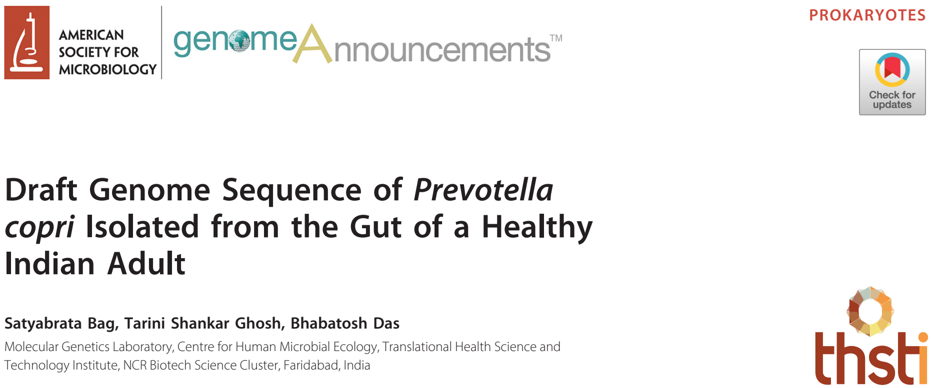
Whole-Genome Sequence of a *Megasphaera elsdenii* Strain Isolated from the Gut of a Healthy Indian Adult Subject

Satyabrata Bag, Tarini Shankar Ghosh, Bhabatosh Das

Molecular Genetics Laboratory, Centre for Human Microbial Ecology, Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad, India

Complete-Genome Sequence of *Collinsella aerofaciens* strain Indica isolated from the Gut of Healthy Indian Adult

Bag et al. GA (2017)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Draft Genome Sequence of *Prevotella copri* Isolated from the Gut of a Healthy Indian Adult

Satyabrata Bag, Tarini Shankar Ghosh, Bhabatosh Das

Molecular Genetics Laboratory, Centre for Human Microbial Ecology, Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad, India

Whole-Genome Sequence of *Enterobacter cloacae* strain Indica isolated from the Gut of Healthy Indian Adult

Bag et al. GA (2017)

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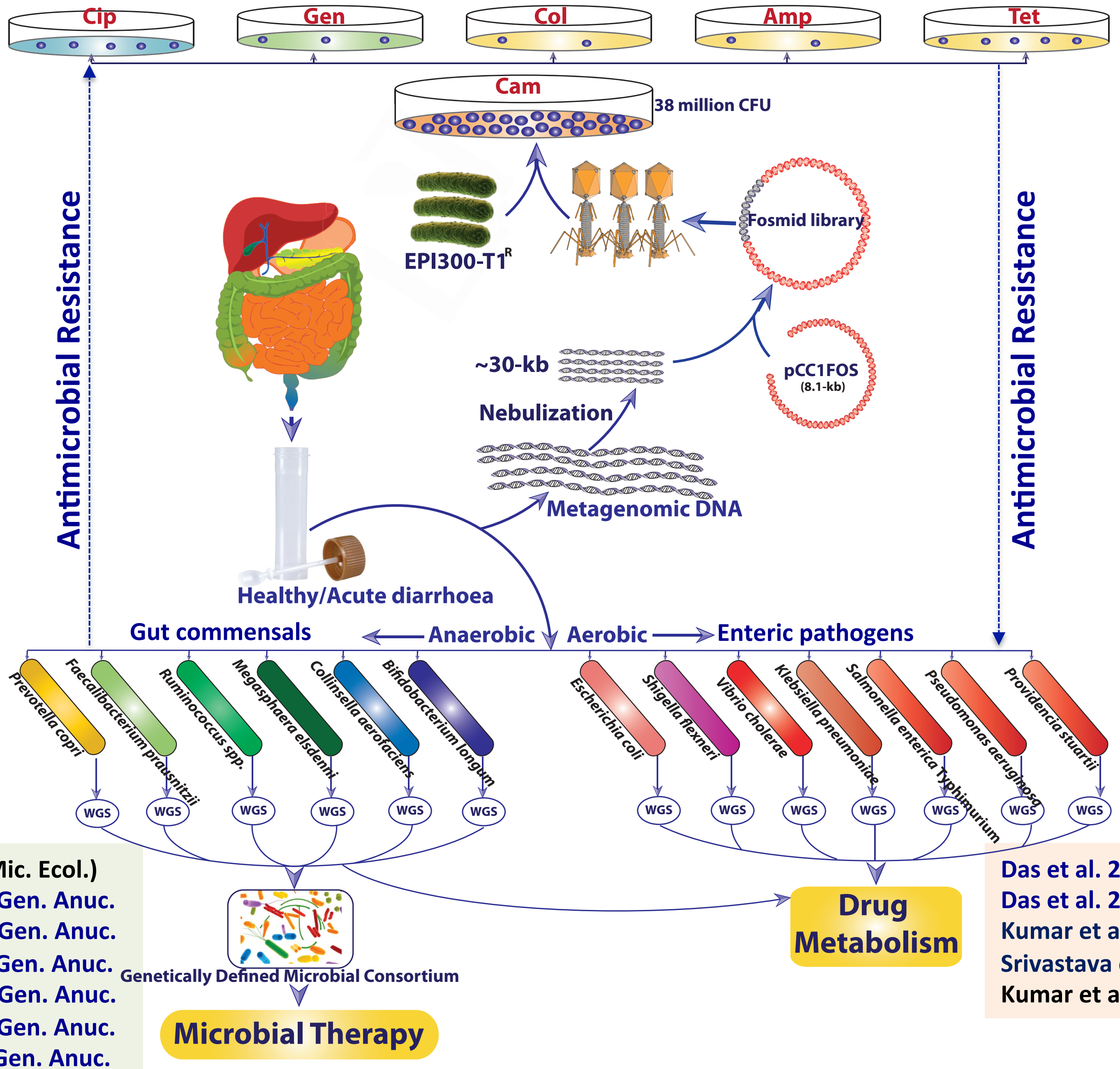
Functional Metagenomics of Gut Microbiota



Das et al., 2018 (Mic. Ecol.)
Bag et al., 2017a, Gen. Anuc.
Bag et al., 2017b, Gen. Anuc.
Bag et al., 2017c, Gen. Anuc.
Bag et al., 2017d, Gen. Anuc.
Bag et al., 2017e, Gen. Anuc.
Bag et al., 2017f, Gen. Anuc.

Das et al. 2017, BMJ
Das et al. 2017, Vaccine
Kumar et al. 2017, Sci. Rep.
Srivastava et al. 2017, CDD
Kumar et al. 2017 (Com)

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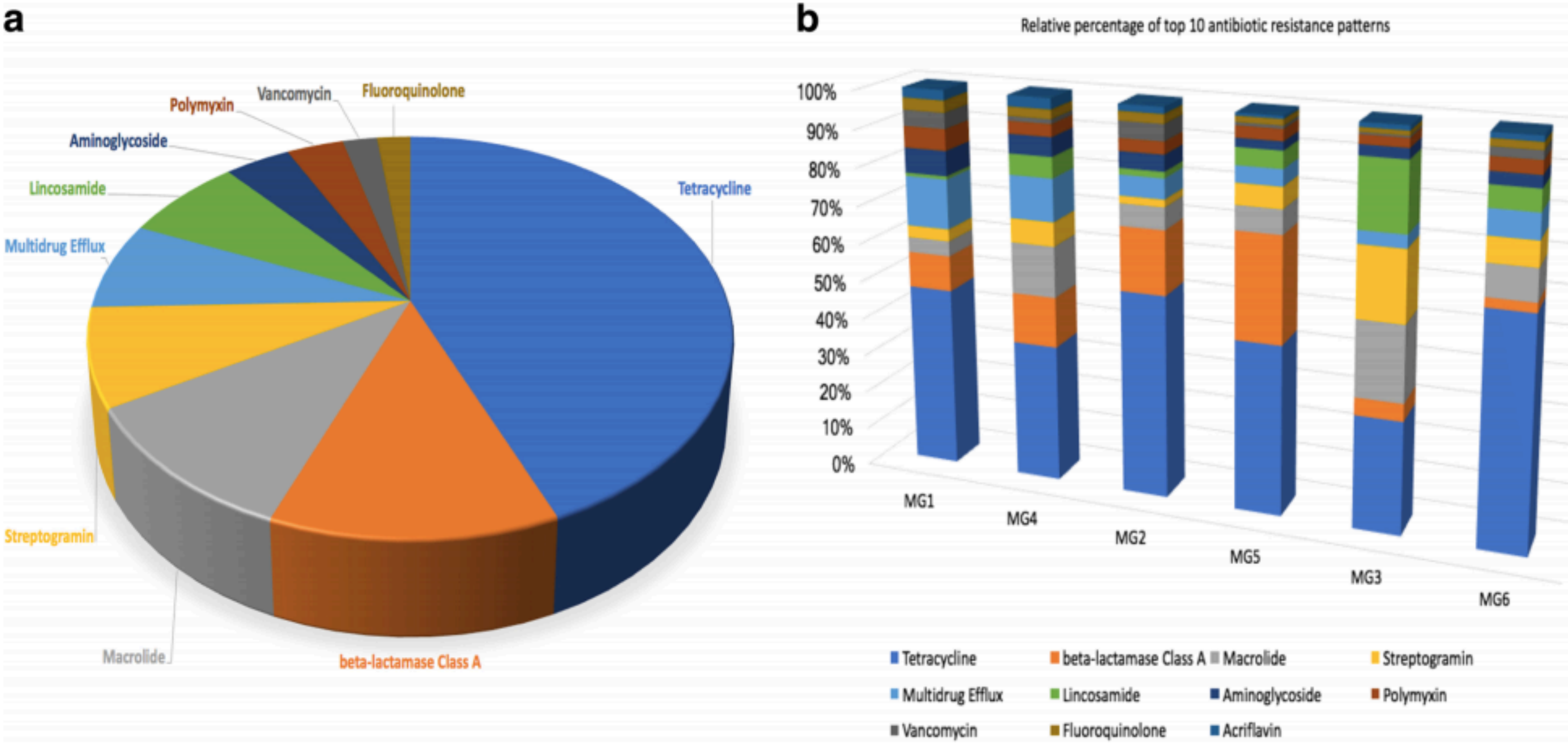
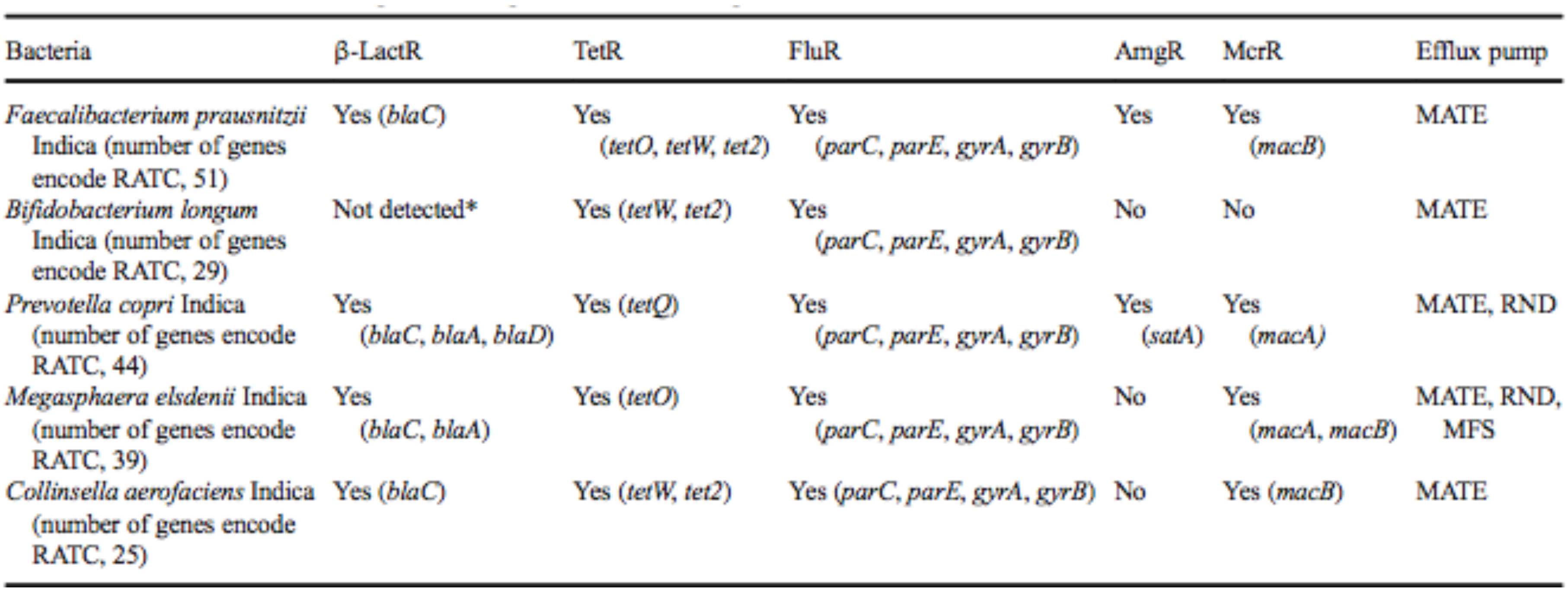
Antimicrobial Resistance Traits of Commensal Human Gut Microbiota



Bag *et al*., 2018

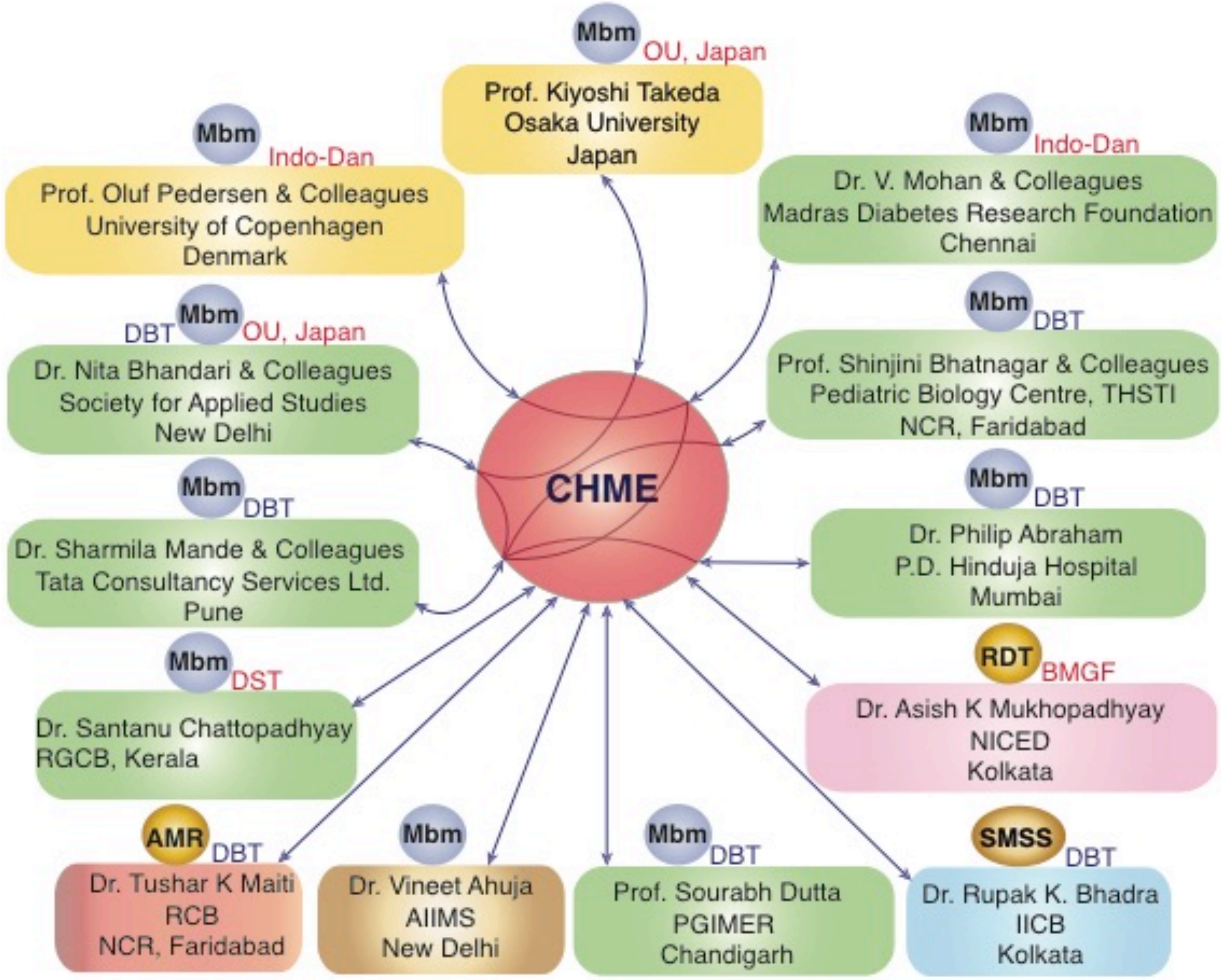
Antimicrobial resistance genes in the genome of dominant gut microbiota



Bacteria	β-LactR	TetR	FluR	AmgR	McrR	Efflux pump
Faecalibacterium prausnitzii Indica (number of genes encode RATC, 51)	Yes (*blaC*)	Yes (*tetO, tetW, tet2*)	Yes (*parC, parE, gyrA, gyrB*)	Yes	Yes (*macB*)	MATE
Bifidobacterium longum Indica (number of genes encode RATC, 29)	Not detected*	Yes (*tetW, tet2*)	Yes (*parC, parE, gyrA, gyrB*)	No	No	MATE
Prevotella copri Indica (number of genes encode RATC, 44)	Yes (*blaC, blaA, blaD*)	Yes (*tetQ*)	Yes (*parC, parE, gyrA, gyrB*)	Yes (*satA*)	Yes (*macA*)	MATE, RND
Megasphaera elsdenii Indica (number of genes encode RATC, 39)	Yes (*blaC, blaA*)	Yes (*tetO*)	Yes (*parC, parE, gyrA, gyrB*)	No	Yes (*macA, macB*)	MATE, RND, MFS
Collinsella aerofaciens Indica (number of genes encode RATC, 25)	Yes (*blaC*)	Yes (*tetW, tet2*)	Yes (*parC, parE, gyrA, gyrB*)	No	Yes (*macB*)	MATE

Bag *et al.*, 2018

Collaborators



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Thank you

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