



İnsan Mikrobiyomu ve Biyoterapi ÇG

Mikrobiyota Çalışmalarının Standardize Edilmesinin Önemi ve Klinik Pratikteki Kullanım Alanları

İzmir Katip Çelebi Üniversitesi Tıp Fakültesi Atatürk EAH

Dr. Yeşim TOK

Sonbaharda tuzlu ve kuru gıdaları tamamı ile bırak. Ağzına koyma. Bunlar insanda her cins illetlerin meydana gelmesine sebep olur; peynir olsun, balık olsun, tuzda yatmış her nesne kötüdür.

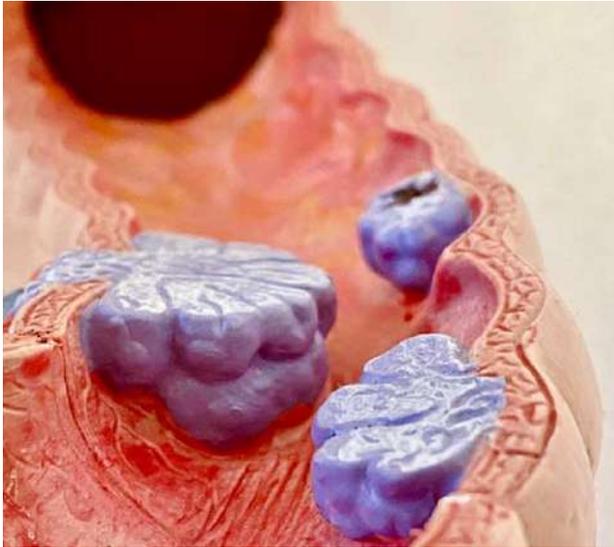
İlkbaharda çok tatlı yemekten kendini ziyadesiyle koru. Çünkü tatlının kanın üzerinde fena neticeler veren tesiri vardır. Tatlılar iki türüdür. Ballı ve hamurlu. Ballı olanlar ağızda eriyip mideye giderse sindirime yardımcı olur.

İbn-i Sina



Influence of the microbiota on vaccine effectiveness

Yanet Valdez¹, Eric M. Brown^{1,2}, and B. Brett Finlay^{1,2,3}



- Günümüzde mikrobiyomdaki değişiklikler ile otizmden kansere kadar geniş bir yelpazedeki klinik durumlar arasındaki ilişkileri belirlemek için epidemiyoloji ve modeller kullanılmış, mikrobiyal ve immünolojik mekanizmalar ortaya konmuştur.

- Omics çağında, mikrobiyom çalışmaları; ağız boşluğu ve bağırsağın kültüre dayalı araştırmalarından insan vücudunun tüm ekolojik ortamlarından mikrobiyal biyokimyanın moleküler profillerine doğru genişlemiştir.



İnsan mikrobiyom arařtırmaları bir dizi řařırtıcı bulgu ve devamında soruları ortaya ıkarmıřtır:

- Her insan, yıllarca devam eden ya da nispeten hızlı deęiřimler gsterebilen, byk lde bireysel mikrobiyal suřları tařıyor gibi grnmektedir.
- Mikrobiyal eřitlilięin, genellikle baęırsakta daha fazla olması beklenir, ancak bu farklılık disbiyotik durumlarla da iliřkili olabilir.
- Mikrobiyom, kadın reme sisteminde zellikle gebelikte advers olaylarda, GIS'te enflamatuar barsak hastalıęı ve diyabette bozulabilir, ancak iliřkili klinik durumların temelleri henz keřfedilememiřtir.



microbiota × **Search**

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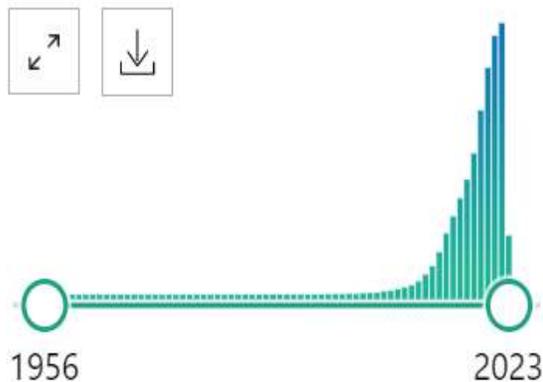
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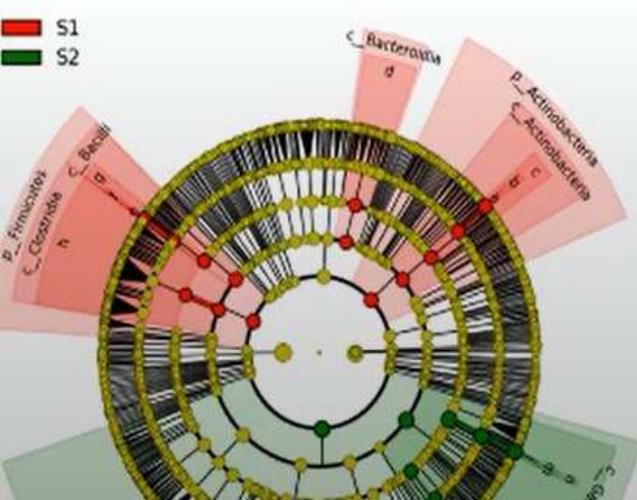
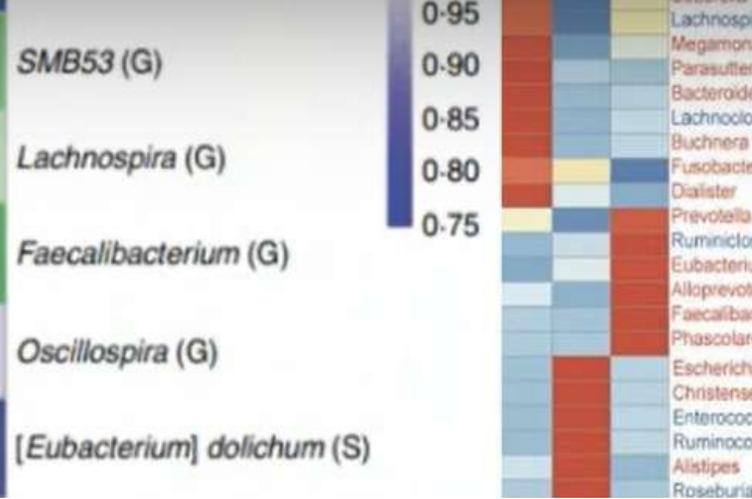
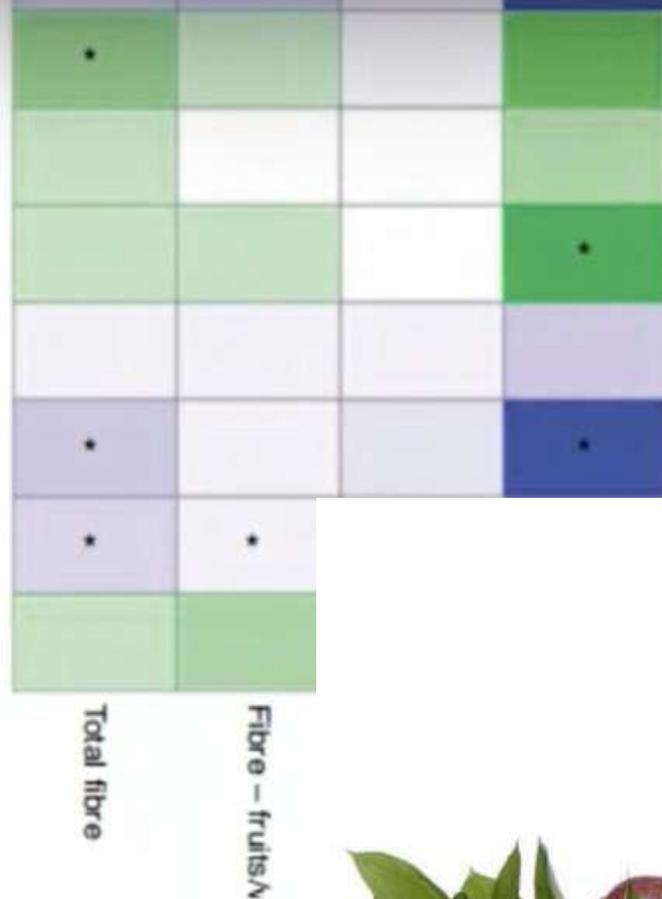
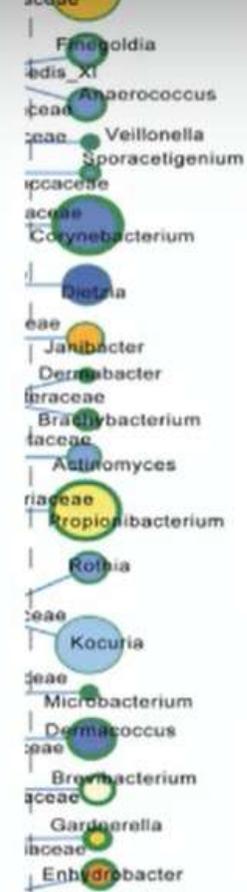
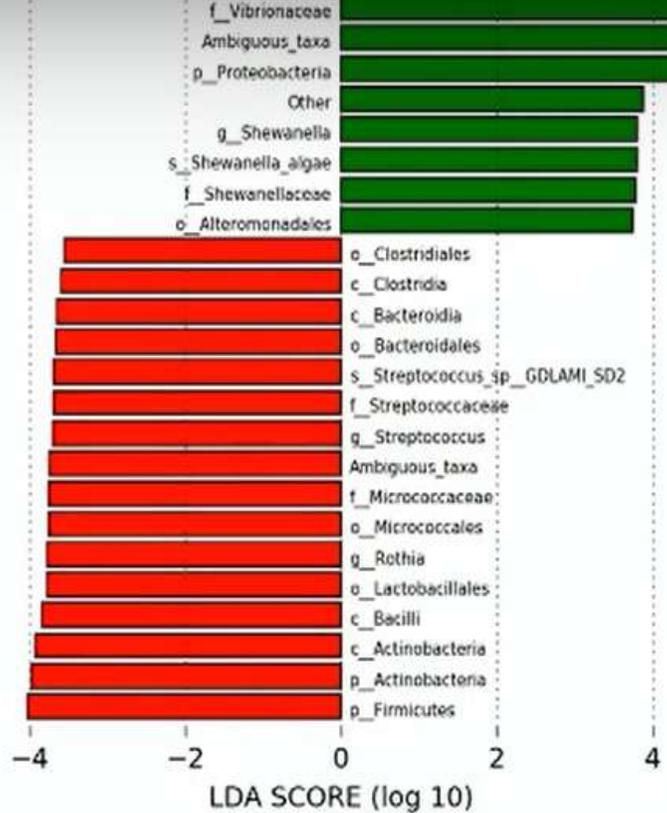
114,658 results

Page 1 of 11,466

RESULTS BY YEAR



- Cancer and the microbiota.**
1 Garrett WS.
Cite Science. 2015 Apr 3;348(6230):80-6. doi: 10.1126/science.aaa4972.
PMID: 25838377 [Free PMC article.](#) [Review.](#)
Share A host's **microbiota** may increase, diminish, or have no effect at all on cancer susceptibility. Assigning causal roles in cancer to specific microbes and **microbiotas**, unraveling host-**microbiota** interactions with environmental factors in carcinogenesis, ...



- a: g_Rothia
- b: f_Micrococcaceae
- c: o_Micrococcales
- d: o_Bacteroidales
- e: g_Streptococcus
- f: f_Streptococcaceae
- g: o_Lactobacillales
- h: o_Clostridiales
- i: g_Shewanella
- j: f_Shewanellaceae
- k: o_Alteromonadales
- l: g_Vibrio
- m: f_Vibrionaceae
- n: o_Vibrionales

- Sv129-LF
- Sv129-HF
- Sv129-HFI
- BL8-LF
- BL8-HF
- BL8-HFI





RESEARCH ARTICLE

Novel Systems Biology Techniques



January/February 2020 Volume 5 Issue 1 e00547-19

Toward Standards in Clinical Microbiota Studies: Comparison of Three DNA Extraction Methods and Two Bioinformatic Pipelines

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^bExperimental Bacteriology, Department of Medical Microbiology, Leiden University Medical Center, Leiden, The Netherlands

- **Çoklu dondurup-çözme işlemleri**
- **In-house ekstraksiyon**, DNA ekstraksiyonu yöntemlerinin performans değişkenliği
- **Çoklu negatif kontrollerin** dahil edilmesi çok önemlidir.
- Primer seçimi (varsa değişken gen bölgesi, 16 s rRNA gen bölgesi)
- Dizileme stratejisinin (shot-gun veya ampikon dizileme)
- Elde edilen ham veri **okuma sayısı, derinliği ve kapsayıcılık**
- Metatranskriptomik, metaproteomik veya metabolomik yapıyorsa
- Biyoinformatik ve istatistik yöntemler tanımlanmalı karıştırıcı faktörler için **kullanılan regresyon modelleri açıklanmalıdır**



HHS Public Access

Author manuscript

Cell Host Microbe. Author manuscript; available in PMC 2016 November 15.

Published in final edited form as:

Cell Host Microbe. 2014 September 10; 16(3): 276–289. doi:10.1016/j.chom.2014.08.014.

The Integrative Human Microbiome Project: Dynamic Analysis of Microbiome-Host Or Health and Disease

PERSPECTIVE

30 MAY 2019 | V OL 569 | NA T U R E | 641

OPEN

The Integrative HMP (iHMP)

<https://doi.org/10.1038/s41586-019-1238-8>

Abstract

Much has been learned about communities, but we still know the host, and how the host responds. The Integrative Human Microbiome Project (iHMP, <http://hmp2.cdc.gov>) study these interactions by analyzing disease-specific cohorts and their properties. These data sets will be used for analyses on the interactions between the microbiome-associated human disease, and type 2 diabetes, and how these interactions are to be collected, integrated, and analyzed.

The Integrative Human Microbiome Project

The Integrative HMP (iHMP) Research Network Consortium*

The NIH Human Microbiome Project (HMP) has been carried out over ten years and two phases to provide resources, methods, and discoveries that link interactions between humans and their microbiomes to health-related outcomes. The recently completed second phase, the Integrative Human Microbiome Project, comprised studies of dynamic changes in the microbiome and host under three conditions: pregnancy and preterm birth; inflammatory bowel diseases; and stressors that affect individuals with prediabetes. The associated research begins to elucidate mechanisms of host-microbiome interactions under these conditions, provides unique data resources (at the HMP Data Coordination Center), and represents a paradigm for future multi-omic studies of the human microbiome.

hmpdacc.org

NIH Human Microbiome Project

Characterization of the microbiomes of healthy human subjects at five major body sites, using 16S and metagenomic shotgun sequencing.

Enter HMP1

Characterization of microbiome and human host from three cohorts of microbiome-associated conditions, using multiple 'omics technologies.

Enter IHMP

Enter HMP Integrated Portal

Virginia Commonwealth University

VAGINAL MICROBIOME CONSORTIUM

Home About Projects Team Publications Resources Contact

iHMP

NIH Integrative Human Microbiome Project

Overview Membership Publications Resources Data Outreach Login

home > resources > tools and technology

Tools and Technology

Tools > Protocols

Shared protocols used by, or developed as part of the iHMP will be provided here as they become available. Please see the three iHMP project sites for project-specific protocols:

- Pregnancy and Preterm Birth
- Onset of Inflammatory Bowel Disease (IBD)
- Onset of Type 2 Diabetes

HMP Home Studies Data Cart 0 Apps

Samples Files Hide Filters

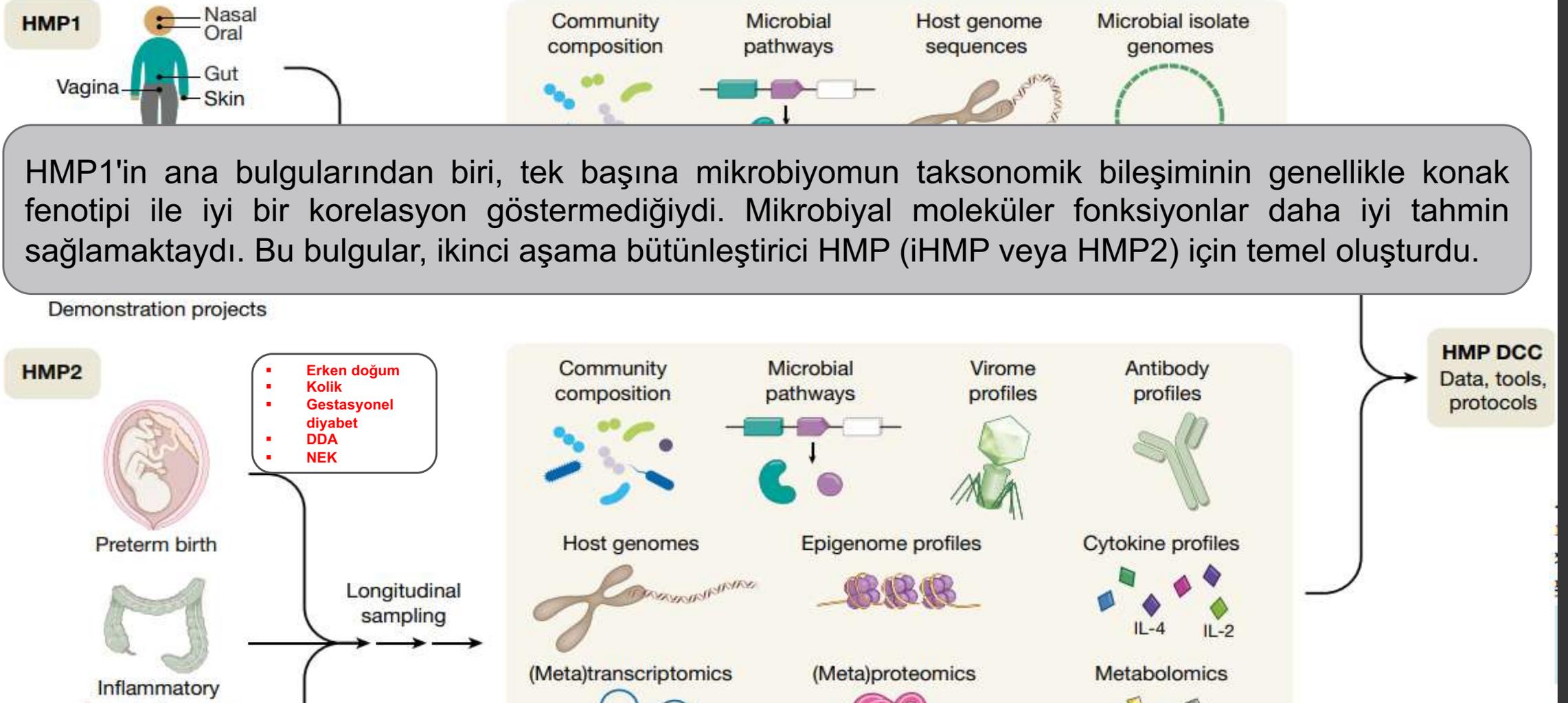
Clear Study Name IS MOMS-PI Advanced

Summary Samples (11,001) Files (39,770)

Files

Showing 1 - 20 of 39,770 Files

Access	File Name	Data Category	Data Format	Size
open	https://downloads.hmpdacc.org/iHMP/ptb/cytokine/host/analysis/EP575820_K10_MP1P.CytokineProfile.txt	abundance_matrix	CSV	373 B
open	https://downloads.hmpdacc.org/iHMP/ptb/cytokine/host/analysis/EP575820_K40_MVAX.CytokineProfile.txt	abundance_matrix	CSV	383 B
open	https://downloads.hmpdacc.org/iHMP/ptb/genome/microbiome/16s/raw/EP575820_K40_MCKD.rareseqset.tar	16s_raw_seq_set	FASTQ	30.69 MB
open	https://downloads.hmpdacc.org/iHMP/ptb/genome/microbiome/16s/raw/EP575820_K70_BCKD.rareseqset.tar	16s_raw_seq_set	FASTQ	123 KB



HMP1'in ana bulgularından biri, tek başına mikrobiyomun taksonomik bileşiminin genellikle konak fenotipi ile iyi bir korelasyon göstermediğiydi. Mikrobiyal moleküler fonksiyonlar daha iyi tahmin sağlamaktaydı. Bu bulgular, ikinci aşama bütünleştirici HMP (iHMP veya HMP2) için temel oluşturdu.

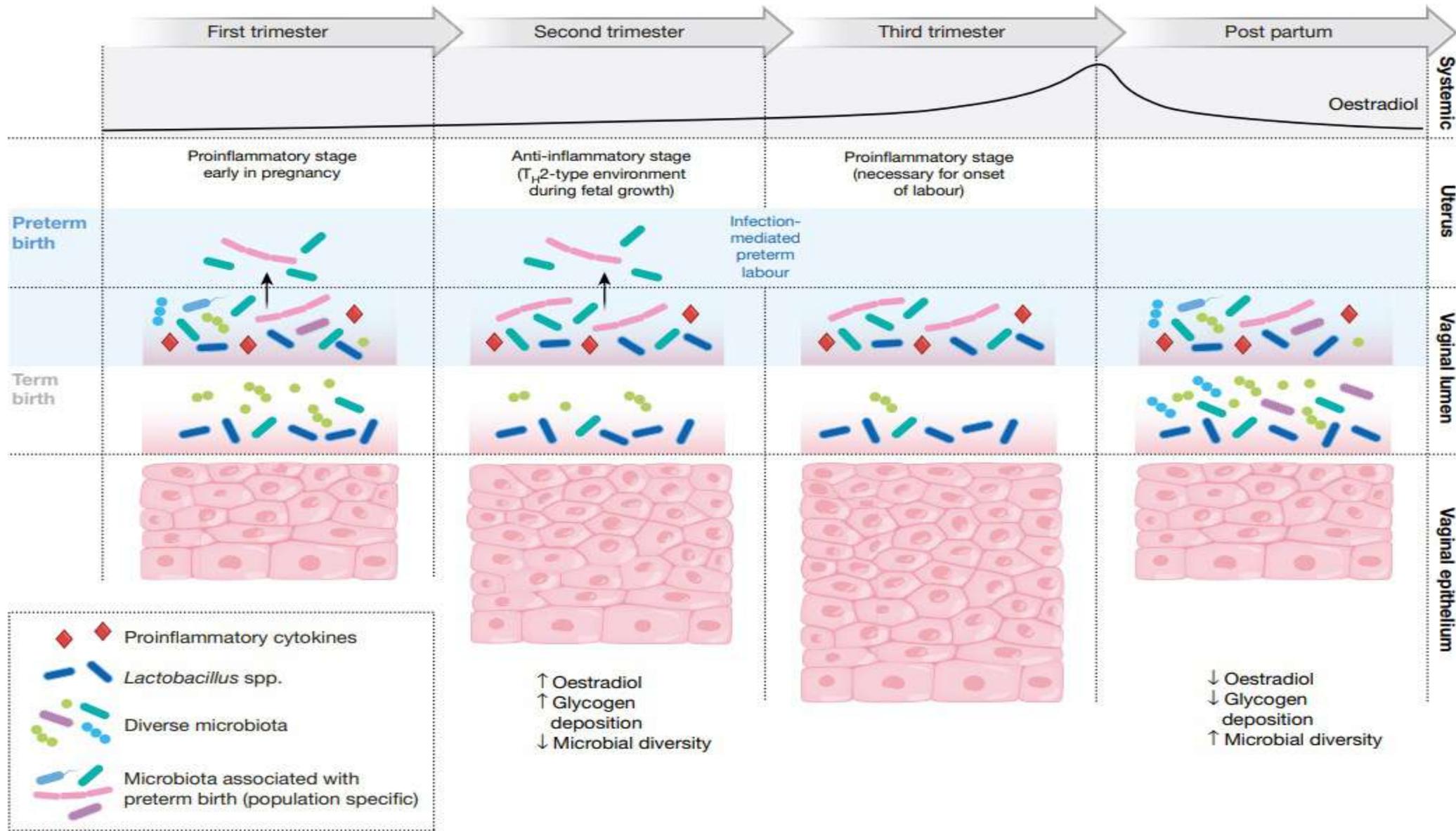
Spesifik klinik durumları ele almak üzere longitudinal iHMP; bağışıklık, metabolizma ve dinamik moleküler aktivite de dahil olmak üzere **konak-mikrobiyom etkileşimini** keşfetmek ve zamanla konak-mikrop etkileşimlerinin daha bütünsel bir görünümünü elde etmek için tasarlanmıştır.

16S rRNA gene survey	Sequence-based analysis of 16S ribosomal RNA gene in total DNA extracts; the data are used to develop microbial community compositional profiles.
Whole metagenome shotgun sequences	Sequence-based analysis of all genes in total DNA extracts; the data are used to develop microbial community compositional, functional, and genomic profiles.
Whole metatranscriptome shotgun sequences	Sequence-based analysis of RNA transcripts in a microbial community by converting RNA in total RNA extracts to complementary DNA and sequencing the cDNA.
Whole virome shotgun sequences	Sequence-based analysis of all virus genes and genomes used to develop viral community profiles. These sequence data are derived from two approaches, either by first isolating viral-sized particles from a sample and then sequencing this fraction, or by sequencing the DNA (or cDNA from RNA) extract and computationally determining DNA and RNA viral sequences in the metagenome.
Bacterial isolates	Isolation and cultivation of a specific bacterium in a mixed community through the use of selective media or enrichment techniques to preferentially grow one bacterium of interest.
Single-cell genome sequences	Physical separation or physical enrichment of a single microbial cell from a mixed population of cells. Sequence-based analysis of the single cell's genome is conducted using a DNA random priming method to first increase the total DNA concentration in the cell and subsequently sequence this amplified DNA.
Single-cell RNA sequences	Sequence-based analysis of RNA transcripts in a cell by converting RNA in total RNA extracts to complementary DNA and sequencing the cDNA.
LC-MS/MS peptide profiles	Analysis of individual peptides in a mixture of proteins by a combination of liquid chromatography and mass spectroscopy after enzymatic digestion of the protein mixture. To derive the microbiome metaproteome, data from the companion metagenome is used along with KEGG and other protein databases to verify the microbial proteins in the total protein mixture. To derive the host proteins, a similar approach is used based on search against the human genome.
Human subject whole genome sequences	Analysis of the sequence of the host genome using high-throughput DNA sequencing.
Whole exome sequences	Analysis of the protein coding regions of the host genome, which is generally done through sequence analysis.
Whole transcriptome sequences	Sequence-based analysis of RNA transcripts in host tissue using polyA tail separation of eukaryotic transcripts from a mixture of transcripts, converting the RNA to complementary DNA and sequencing the cDNA.
Cytokines	Circulating immune system glycoproteins in blood, plasma, or other bodily fluids are measured through an ELISA assay; data are used as a marker for systemic inflammation.
DNA methylation profiles	Measurement of methylated regions of the host genome. This method uses a combination of restriction enzymes and a reduced representation bisulfite sequencing (RRBS) method to enrich for regions of the genome with cytosine-guanine pairs; these regions are then screened for methylated bases.
Fecal calprotectin proteins	Fecal calprotectin is a protein found in stool, the concentration of which is measured through a standardized immunoassay method and is used to evaluate levels of intestinal inflammation.
Serology	Measurement of antibodies for specific pathogens or protein markers conducted with serum through an ELISA assay.
Human subject contaminating genome sequences	Sequence from total nucleotide extracts from most microbially focused sample types yields a combination of host and microbial sequence data. A computational filtering step, using human genome reference sequence, will separate microbiome from human sequences.
Interactomes	Analysis of protein-protein interactions between members of the microbiota or between the microbiota and the host.
Intestinal epithelial cell profiles	Functional or sequence-based readouts of phenotypes for cell lines derived from primary epithelial cells from individual hosts.
Metabolomes	Measure of metabolomic profiles using untargeted and targeted LC-MS methods.
Lipidomes	Measure of lipid profiles using 2D UPLC-ESI-MS/MS (ultra performance liquid chromatography combined with electrospray ionization tandem mass spectroscopy) with an initial focus on AA

Source of Property	Property Derived from Primary Data	Primary Data from Biospecimen	Biospecimen from Preterm Birth Cohort	Biospecimen from IBD Cohort	Biospecimen from Prediabetic Cohort	Repository for Primary Data
Microbiome	microbial community composition	16S rRNA gene survey	cervical ^a , vaginal ^a , rectal, buccal, fetal membranes, placenta, amniotic fluid from women; buccal, rectal, stool, meconium, respiratory secretions from neonate	stool	anterior nares, stool	SRA
	microbial community composition	whole metagenome shotgun sequences	vaginal ^a	stool	anterior nares, stool	SRA
	predictions of microbial genes, metabolic pathways	whole metagenome shotgun sequences	vaginal ^a	stool	anterior nares, stool	SRA
	RNA transcript profiles	whole metatranscriptome shotgun sequences	vaginal ^a	stool	anterior nares, stool	SRA
	microbiome metaproteome profiles	LC-MS/MS peptide profiles	–	stool	stool	EBI PRIDE and/or Peptide Atlas
	viral community composition	whole virome shotgun sequences	–	stool	anterior nares, stool	SRA
	bacterial cultures	bacterial isolates	cervical ^a , vaginal ^a , rectal, buccal, stool from mothers or neonates	–	–	ATCC/BEI
	bacterial whole genome sequences	bacterial isolates	cervical ^a , vaginal ^a , rectal, buccal, stool from mothers or neonates	–	–	SRA
	bacterial whole genome sequences	bacterial single-cell sequences	–	stool	–	SRA
	single-cell bacterial RNA transcript profiles	single-cell bacterial transcript sequences	–	stool	–	SRA

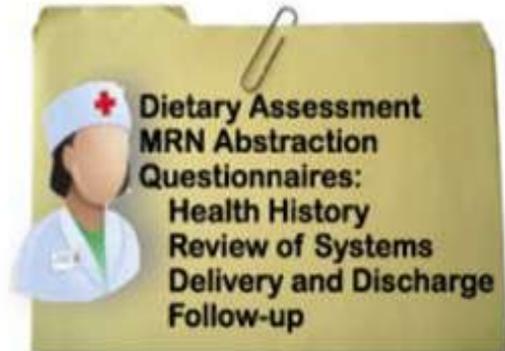
Source of Property	Property Derived from Primary Data	Primary Data from Biospecimen	Biospecimen from Preterm Birth Cohort	Biospecimen from IBD Cohort	Biospecimen from Prediabetic Cohort	Repository for Primary Data
Host	subject exome/whole genome	subject genome sequences	blood (future ^b) from mothers and neonates	blood	blood	dbGaP/SRA
	RNA transcript profiles	whole transcriptome sequences	vaginal ^a	colon biopsy	PBMCs	dbGaP/SRA and GEO
	subject protein profiles	LC-MS/MS peptide profiles	–	stool	PBMCs, serum (future)	EBI PRIDE and/or Peptide Atlas
	systemic inflammation levels	cytokine profiles	vaginal ^a , buccal from mothers or neonates	blood	plasma	Study DB
	intestinal epithelial cell cultures	intestinal epithelial cell isolates	–	colon biopsy	–	–
	subject DNA methylation profiles	reduced representation bisulfite sequencing (RRBS) profiles	–	blood	PBMC (future)	SRA
	intestinal inflammation levels	fecal calprotectin protein concentrations	–	stool	–	Study DB
	serum antibody composition and levels	serology	–	blood	–	Study DB
	subject contaminating genome sequences	human sequence from unfiltered total microbial community sequences	vaginal ^a	stool	stool	dbGaP/SRA
	subject profiles for cohort	subject phenotypes, clinical metadata, medical panels	collected on each subject in the study	collected on each subject in the study	collected on each subject in the study	dbGaP
Global (host and microbiome)	protein-protein interaction network between host and microbiome	yeast two-hybrid binary protein complexes	vaginal ^a	–	–	EBI IntAct
	pathway-level crosstalk between host and gut microbiome	intestinal epithelial cell profiling response to bacterial metabolites	–	colon biopsy	–	dbGaP/SRA and GEO
	global metabolite profiles	untargeted and targeted LC-MS metabolomic profiles	–	stool	urine, plasma	Metabolomics Workbench
	global lipid profiles	untargeted and targeted LC-MS metabolomic profiles	vaginal ^a	stool	urine, serum	Metabolomics Workbench

Vajinal Mikrobiyom, Gebelik ve Erken Doğum



Subjects

- Etnisite
- Yaş
- * Sağlık özgeçmiş
- Diet
- Alışkanlıklar



Sample Collection

Prenatal 3-5

- | | | | | | |
|---------|---|------------------------|----------|---|---|
| Buccal | M | B | Cervix | M | |
| Nostril | M | B | Rectum | M | B |
| Chest | M | B | Placenta | B | |
| Palm | M | B | Stool | B | |
| Vagina | M | Cord blood | B | | |
| | | Amniotic fluid | B | | |
| | | Antecubital fossa | M | | |
| | | Blood - plasma | M | | |
| | | Blood - whole blood | M | | |
| | | Blood - buffy coat | M | | |
| | | Respiratory secretions | B | | |
| | | Membranes | B | | |

- | | |
|----------------|---|
| Vagina | M |
| Blood - plasma | M |
| Amniotic fluid | B |

- | | | |
|------------------------|---|---|
| Vagina | M | |
| Cheek | M | B |
| Respiratory secretions | B | |

- | | |
|----------------|---|
| Vagina | M |
| Amniotic fluid | B |
| Membranes | B |



Assays

Illumina MiSeq
RDP Classifier
STIRRUPS/OTU

Microbes: 16S rRNA gene profiling

30,400 samples

Microbes: Bacterial cultivation / seq

30,400 samples

Host: Lipidomic profiling

Microbes

8000 samples

Host: Cytokine assays

8000 samples

HUMAnN pipeline
ASGARD tool

Microbes: Metatranscriptome

Host

60 samples

Microbes: Interactome maps

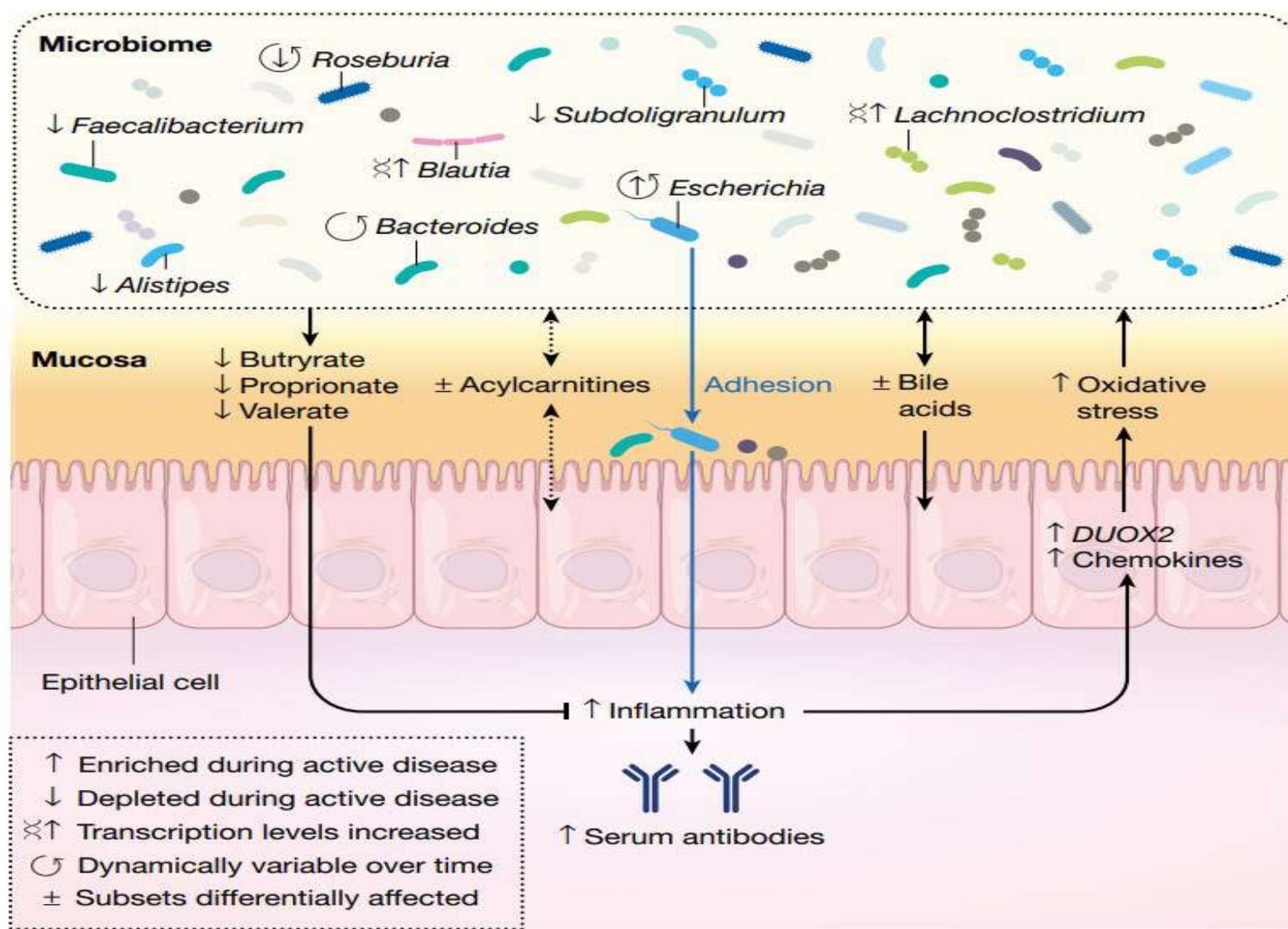
Host

pilot study

Microbes: Metagenome

Host

60 samples

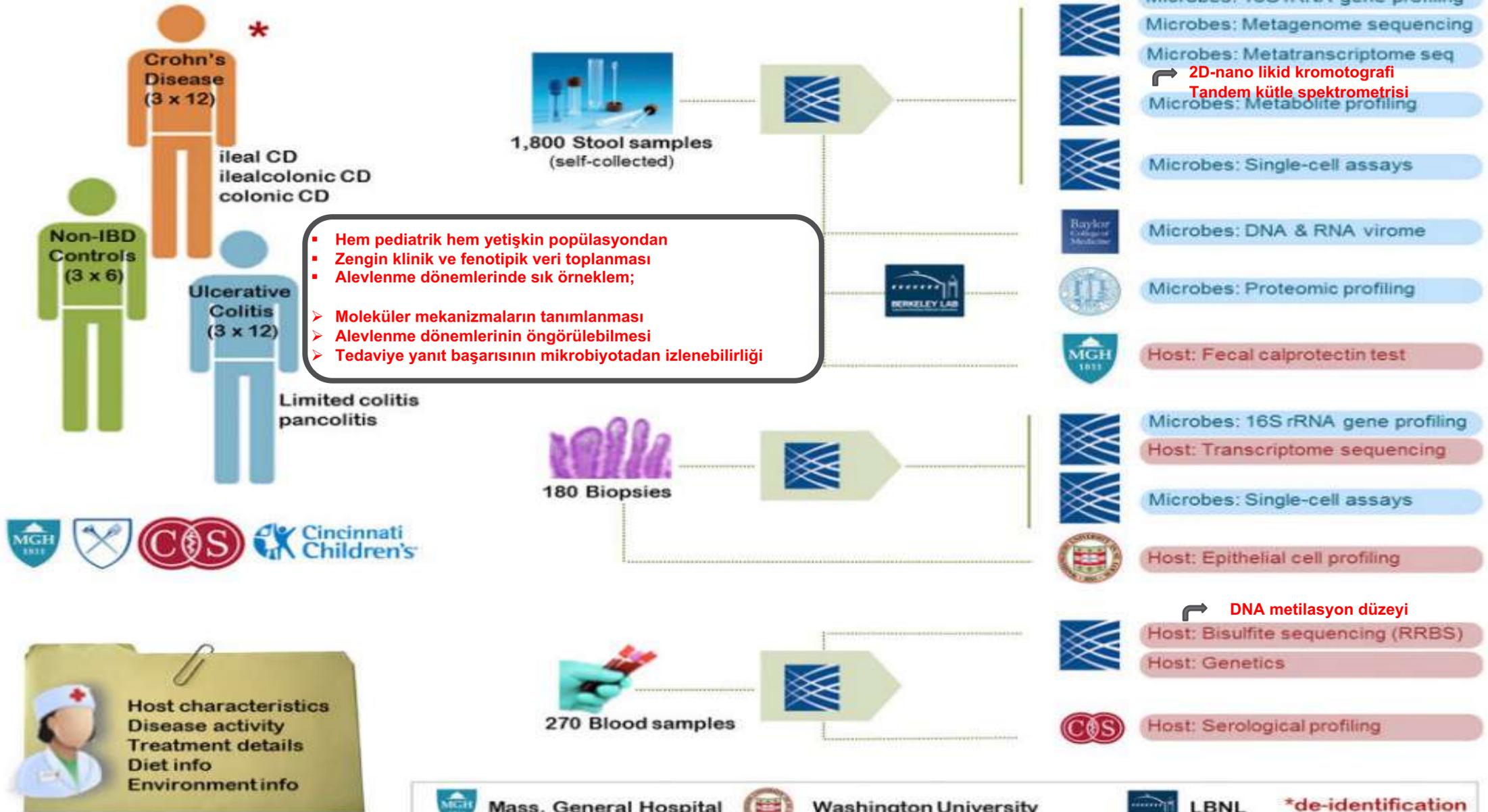


- Crohn hastalığı ve ülseratif kolit dahil olmak üzere IBH, batılılaşma, kentleşme, beslenme modellerindeki değişimler, antimikrobiyal maruziyet ve konak-mikrobiyom homeostazını etkileyebilecek daha pek çok faktörlerin etkisiyle son 50 yılda artan insidansla dünya çapında milyonlarca kişiyi etkilemektedir.

Subjects

Sample Collection

Assays



- Hem pediatrik hem yetişkin popülasyondan
- Zengin klinik ve fenotipik veri toplanması
- Alevlenme dönemlerinde sık örneklem;
- Moleküler mekanizmaların tanımlanması
- Alevlenme dönemlerinin öngörülebilmesi
- Tedaviye yanıt başarısının mikrobiyotadan izlenebilirliği

2D-nano likid kromatografi
Tandem kütle spektrometrisi

DNA metilasyon düzeyi

Kan, dışkı ve nazal bölgeden 2-3 ayda bir örneklem (stres durumlarında daha sık)

Differential responses to weight gain, respiratory viral infections and host-microbial networks

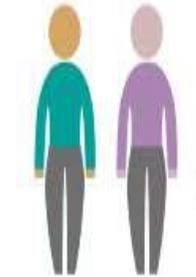
Insulin sensitive (IS)

- Responsive to respiratory viral infections
- Acute phase response pathway
- Cytokine production
- Altered nasal microbial ecology

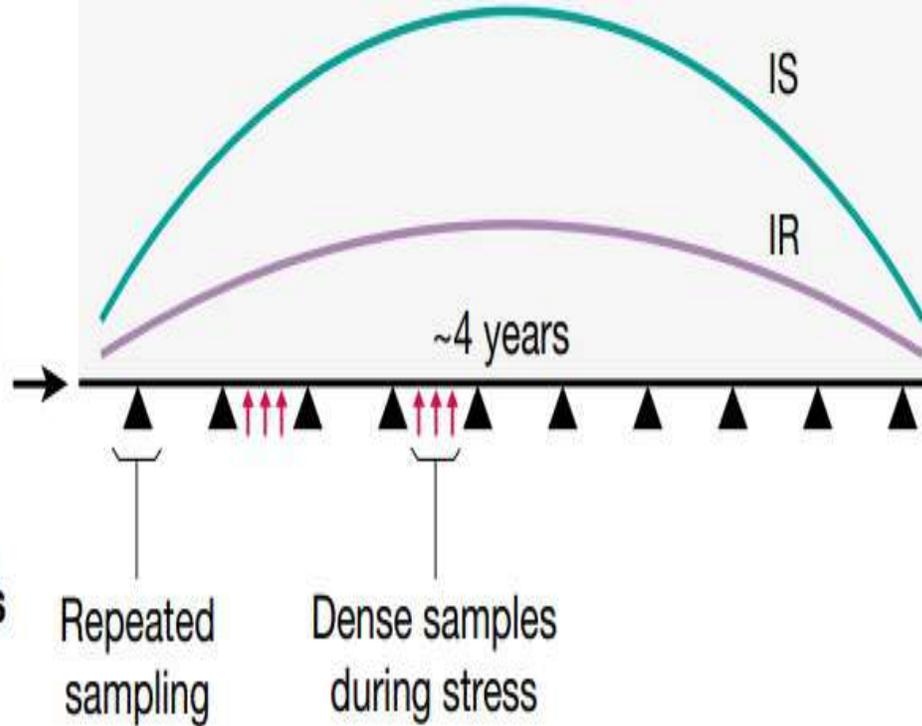


Insulin resistant (IR)

- Reduced response to respiratory viral infections
- More chronic inflammation
- Altered lipid metabolism
- ↑ *Blautia*, ↓ *Odoribacter*



106 individuals



Host features

- Proteomics } Plasma
- **Metabolomics** } Plasma
- Exomes } PBMC
- Transcriptomes } PBMC
- Clinic profiles } PBMC
- Weight } PBMC



Multivariate data analysis

Microbial features

- 16S sequencing
- Metagenomics



Subjects

Sample Collection

Assays

Pre-diabetes *



Stool samples



Nasal Swabs

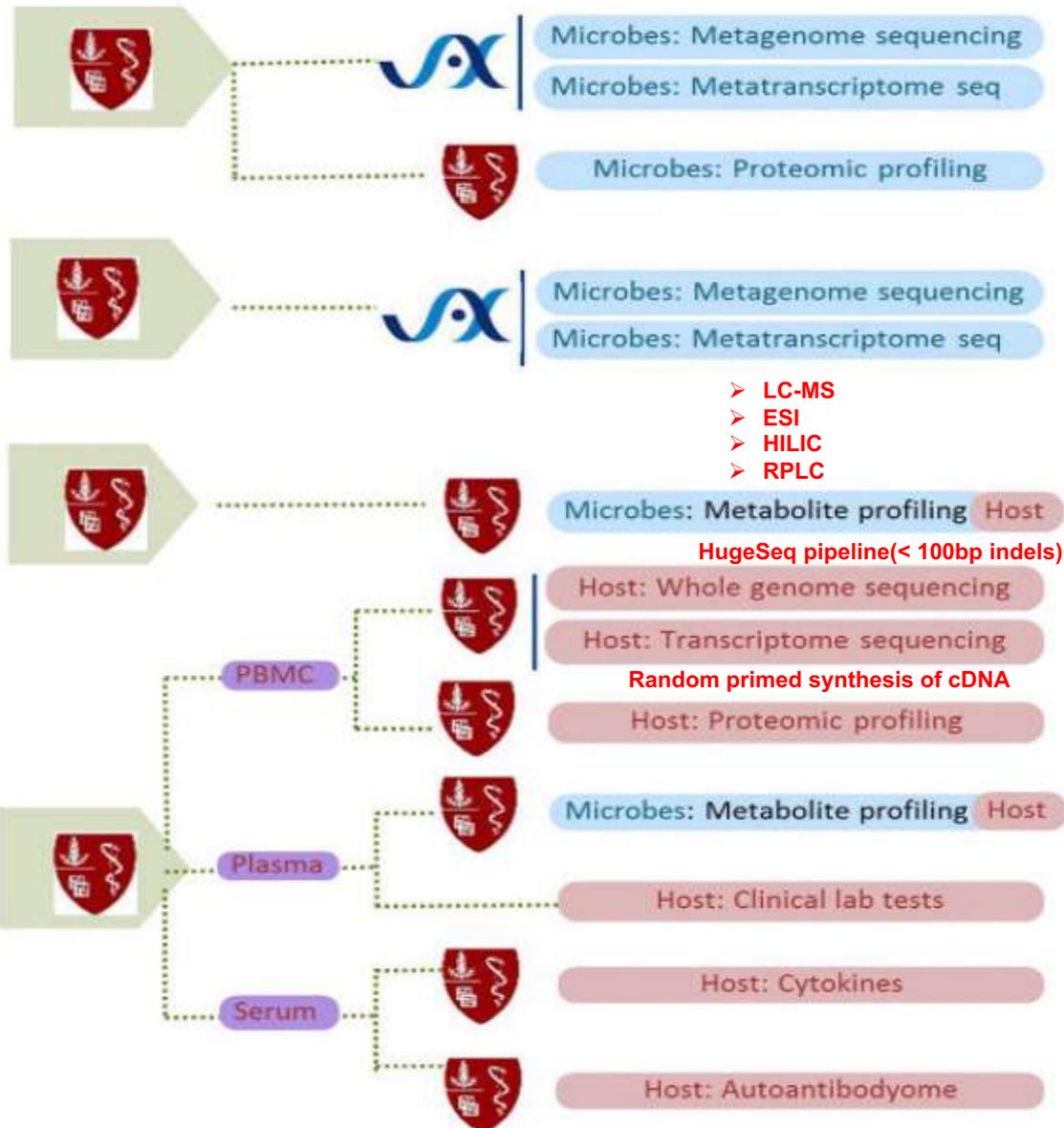


Urine samples



Blood samples

Host characteristics
Activity level
Stress questionnaires
Diet info
Environment info



SRA

SRA

Search

Advanced

Help



SRA - Now available on the cloud

Sequence Read Archive (SRA) data, available through multiple cloud providers and NCBI servers, is the largest publicly available repository of high throughput sequencing data. The archive accepts data from all branches of life as well as metagenomic and environmental surveys. SRA stores raw sequencing data and alignment information to enhance reproducibility.

metabolomicsworkbench.org

ibdmdb.org/cb/browser/Data%20Generation%20Protocols



(Home) » Data Generation Protocols

Containers

- Clinical Protocols
- Sample Handling Pro...
- Data Generation Pro...

Objects

Name	Content Type	Encoding	Size (Bytes)	Date
16S_Biopsy_HMP2_Protocol.pdf	application/pdf	--	36.0 KB	Jan. 16, 2018, 9:09 p.m.
Exome_HMP2_protocol.pdf	application/pdf	--	85.4 KB	Sept. 29, 2017, 1:47 p.m.
Host_Transcriptomics_HMP2_protocol.pdf	application/pdf	--	48.5 KB	Sept. 29, 2017, 1:48 p.m.
MetabolomicsHMP2Protocol.pdf	application/pdf	--	93.3 KB	Oct. 6, 2017, 2:29 p.m.
Metagenomics_HMP2_Protocol.pdf	application/pdf	--	21.6 KB	Jan. 16, 2018, 8:55 p.m.
Metatranscriptomics_HMP2_Protocol.pdf	application/pdf	--	27.3 KB	Jan. 16, 2018, 8:55 p.m.
Proteomics_HMP2_protocol.pdf	application/pdf	--	32.9 KB	Jan. 29, 2018, 11:25 p.m.
ViromicsHMP2Protocol.pdf	application/pdf	--	87.7 KB	June 20, 2016, 6:20 p.m.
rrbs_hmp2_protocol.pdf	application/pdf	--	65.1 KB	Sept. 28, 2017, 8:22 p.m.

Welcome to the UCSD Metabolomics Workbench, a resource sponsored by the Common Fund of the NIH

National Metabolomics Data Repository

Upload and Manage Studies

Browse and Search Studies

Analyze Studies

As of 03/13/23 a total of 2422 studies have been processed by the National Metabolomics Data Repository (NMDR). There are 2125 publicly available studies and the remainder (297) will be made available subject to their embargo dates.

Recently released studies on NMDR

ST002476 - High body temperature increases gut microbe diversity and SARS-CoV-2 infection; *Mus musculus*; [Kaio](#)

ST002479 - High body temperature increases gut microbe diversity and SARS-CoV-2 infection (Hamster); *Mesocricetus*

Tweets from @MetabolomicsWB

<https://www.ncbi.nlm.nih.gov/gap/dbGaP>

<https://www.metabolomicsworkbench.org/>

"Flavones", "Flavanols",

The Integrative HMP (iHMP) Research Network Consortium

Lita M. Proctor^{1,13,14}, Heather H. Creasy^{2,13,14}, Jennifer M. Fettweis^{3,4,5,14},
Jason Lloyd-Price^{6,7,14}, Anup Mahurkar^{2,14}, Wenyu Zhou^{8,14},
Gregory A. Buck^{3,5,9*}, Michael P. Snyder^{8,10,11*}, Jerome F. Strauss III^{4,5*},
George M. Weinstock^{12*}, Owen White^{2*} & Curtis Huttenhower^{6,7,13*}

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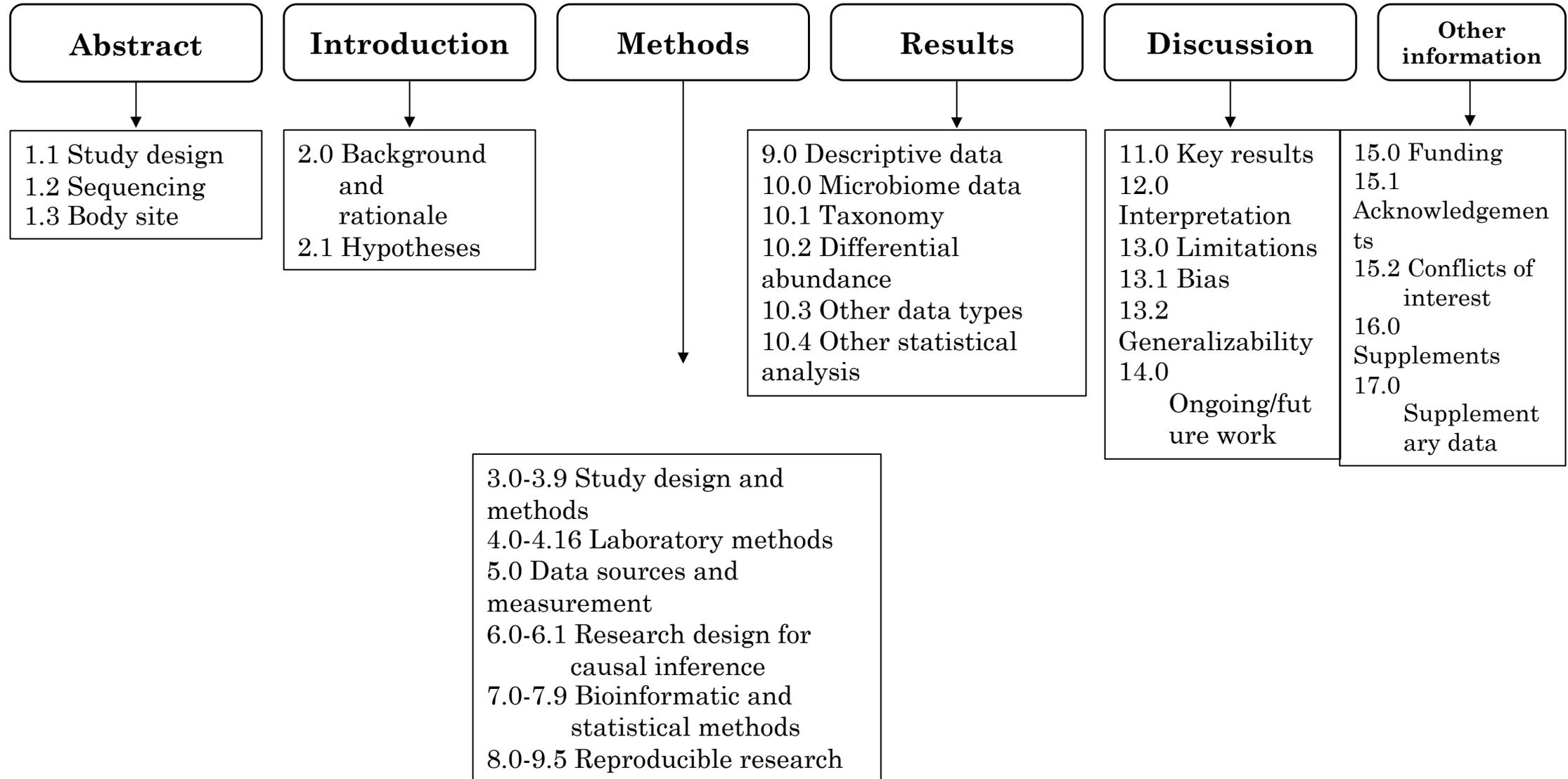
Reporting guidelines for human microbiome research: the STORMS checklist

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The particularly interdisciplinary nature of human microbiome research makes the organization and reporting of results spanning epidemiology, biology, bioinformatics, translational medicine and statistics a challenge. Commonly used reporting guidelines for observational or genetic epidemiology studies lack key features specific to microbiome studies. Therefore, a multidisciplinary group of microbiome epidemiology researchers adapted guidelines for observational and genetic studies to culture-independent human microbiome studies, and also developed new reporting elements for laboratory, bioinformatics and statistical analyses tailored to microbiome studies. The resulting tool, called 'Strengthening The Organization and Reporting of Microbiome Studies' (STORMS), is composed of a 17-item checklist organized into six sections that correspond to the typical sections of a scientific publication, presented as an editable table for inclusion in supplementary materials. The STORMS checklist provides guidance for concise and complete reporting of microbiome studies that will facilitate manuscript preparation, peer review, and reader comprehension of publications and comparative analysis of published results.

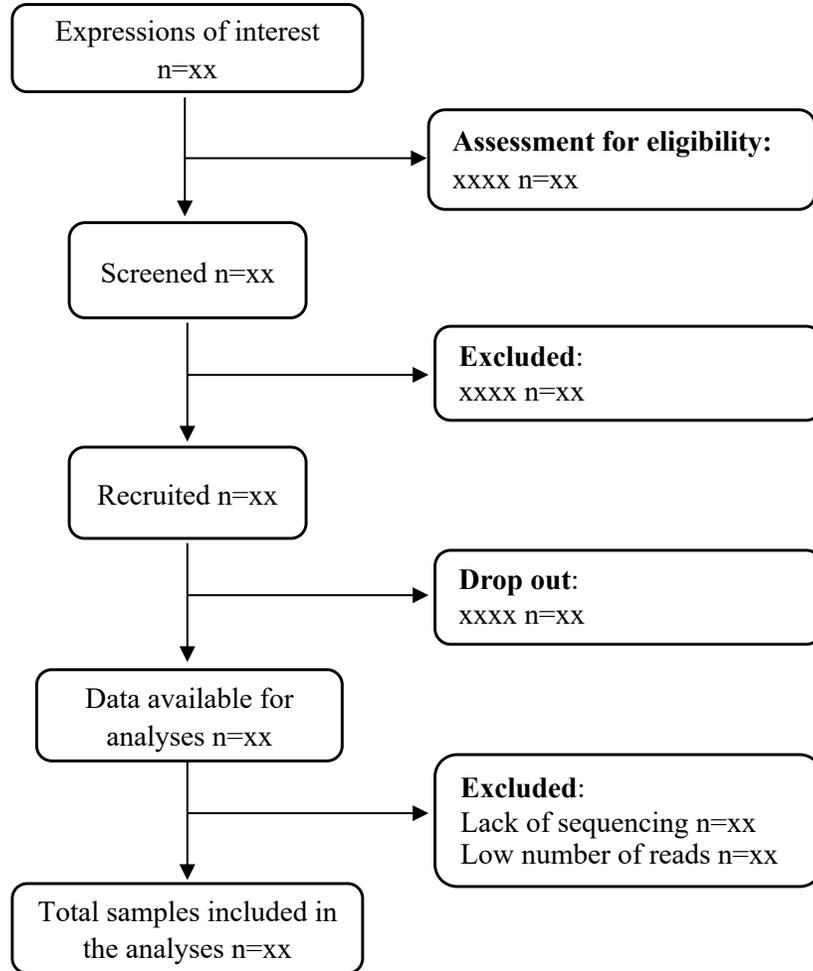
Mikrobiom çalışmalarının tasarlanması, raporlandırılması ve karşılaştırılmasında bir check-list...

Strengthening The Organizing and Reporting of Microbiome Studies (STORMS)

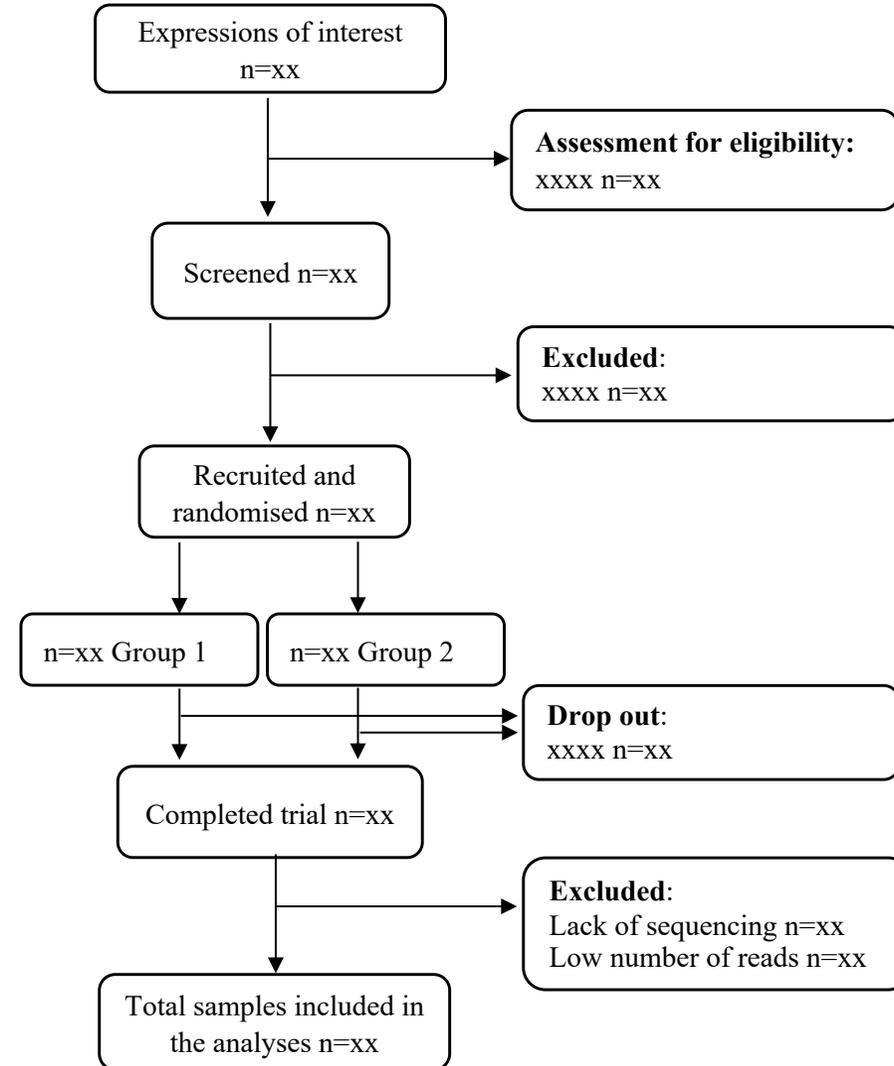


STORMS analytic sample size flowcharts (item 3.6)

Observational



Experimental



BugSigDB

A Comprehensive Database of Published Microbial Signatures

BugSigDB.org is a community-editable Semantic Mediawiki knowledge management system that simplifies and standardizes the recording, finding, and re-analysis of differential abundance results from all types of metagenomics studies. To contribute please request an account, learn how to contribute or analyze, learn more about the project, report issues, or join the user forum.

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Featured Taxon 90964	Featured Studies Study by name
Staphylococcaceae (family) <small>cellular organisms / Bacteria / Terrabacteria group / Bacillota / Bacilli / Bacillales</small>	Characteristics of the intestinal flora in patients with peripheral neuropathy associated with type 2 diabetes <small>The Journal of international medical research, 2020 Feces diabetic neuropathy, type II diabetes mellitus China</small>
BugSigDB Statistics <ul style="list-style-type: none"> • Number of studies: 20 (filter) • Number of signatures: 27 • Number of direct descendants: 16 	Effects of PM2.5 exposure during gestation on maternal gut microbiota and pregnancy outcomes <small>Chemosphere, 2020 Colon air pollution China</small>

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```

1 # install BiocManager
2 if (!require("BiocManager", quietly = TRUE))
3   install.packages("BiocManager")
4
5 # install the package
6 BiocManager::install("bugsigdb")
7
8 # load the package
9 library(bugsigdb)
10
11 # import BugSigDB data
12 bsdb <- importBugSigDB()
13
14 # inspect the resulting data frame
15 class(bsdb)
16 dim(bsdb)
17 colnames(bsdb)
18
19 # subset the data frame
20 us.obesity.feces <- subset(bsdb,
21                            'Location of subjects' == "United States of America" &
22                            Condition == "obesity" &
23                            'Body site' == "feces")
24
25 # get the signatures
26 sigs <- getSignatures(bsdb)
27 length(sigs)
28 sigs[1:3]
  
```

```

> # get the signatures
> sigs <- getSignatures(bsdb)
> class(sigs)
[1] "list"
> length(sigs)
[1] 2270
> sigs[1:3]
$`bsdb:1/1/1_adenoma:conventional-adenoma-cases_vs_controls_UP`
 [1] "91061" "1236" "1654" "1716" "1301" "162289" "189330"
 [8] "33024" "40544" "2037" "2049" "506" "186826" "1300"
 [15] "31977" "91347" "1653" "57037" "1386" "186817" ]

$`bsdb:1/1/2_adenoma:conventional-adenoma-cases_vs_controls_DOWN`
[1] "100883" "1117"

$`bsdb:1/2/1_Hyperplastic-Polyp:hyperplastic-polyp-cases_vs_controls_UP`
[1] "207244" "57037"

> |
  
```

Dinlediđiniz için teŝekkürler...