Comparing microbiome studies across diseases reveals patterns of microbial dysbiosis

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Contents

1 Abstract

In spite of the recent increase in research on the human microbiome, there is not a clear consensus on the relationship between the human gut microbiome and disease. Many researchers have found associations between gut microbial communities and individual diseases, but combining results from different studies about the same disease often yields conflicting results. To date, no one has performed a comprehensive comparison of gut microbiome studies across all disease states using standardized processing and analysis methods. Here, we

show that collecting and re-processing gut microbiome datasets across multiple diseases and conditions identifies a shared microbial response to disease as well as microbial associations unique to specific diseases. Our work provides an important contribution toward synthesizing existing knowledge on the gut microbiome and moving the field toward mechanistically-motivated hypotheses and physiologically-relevant associations.

2 Introduction

other stuff

3 Results

3.1 Collection of 16S gut microbiome case-control datasets

3.2 Within-disease meta-analyses reveals consistent, but not distinct, microbial markers of disease

Sean: edit away! Possibly make this four different sections for each of the diseases with more than 3 studies?

3.3 Cross-disease comparison of microbes associated with health and disease reveals microbes consistently associated with health and disease

Shared microbial response to disease

Cross-disease comparison identifies a shared microbial response to disease

3.4 General markers of dysbiosis are indicative only of certain diseases and conditions

General dysbiosis is not generalizable across studies

Alpha diversity

BF ratio?

4 Discussion

5 Methods

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Dataset ID	Year	Disease(s)	N control	N case	Median reads per sample	Sequencer	16S Region	Ref.
asd_kb	2013	ASD	20	19	1345	454	V2-V3	[1]
asd_son	2015	ASD	44	59	4777	Miseq	V1-V2	[2]
cdi_schu	2014	CDI	243	93	3557	454	V3-V5	[3]
cdi_vincent	2013	CDI	18	17	5518	454	V1-V3	[4]
cdi_young	2014	CDI	18	27	16516	Miseq	V4	[5]
crc_baxter	2016	CRC	122	120	9476	Miseq	V4	[6]
crc_xiang	2012	CRC	22	21	1152	454	V1-V3	[7]
crc_zackular	2014	CRC	58	30	54269	MiSeq	V4	[8]
crc_zeller	2014	CRC	75	41	120612	MiSeq	V4	[9]
crc_zhao	2012	CRC	54	44	161	454	V3	[10]
crc_zhu	2013	CRC	18	12	1835	454	V3	[11]
edd_singh	2015	EDD	82	222	2573	454	V3-V5	[12]
hiv_dinh	2015	HIV	15	21	3248	454	V3-V5	[13]
ibd_alm	2012	UC, CD	24	66	1303	454	V3-V5	[14]
ibd_eng	2009	UC, CD	32	32	2658	454	V5-V6	[15]
ibd_gevers	2014	CD	16	146	9773	Miseq	V4	[16]
ibd_hut	2012	UC, CD	27	186	995	454	V3-V5	[17]
mhe_zhang	2013	CIRR, MHE	25	46	487	454	V1-V2	[18]
nash_baker	2013	NASH, OB	16	47	9904	454		[19]
nash_chan	2013	NASH	22	32	1743	454	V1-V2	[20]
ob_escobar	2014	OW, OB	10	20	1126	454	V1-V3	[21]
ob_goodrich	2014	OW, OB	451	528	27364	Miseq	V4	[22]
ob_gord	2009	OW, OB	61	219	1569	454	V2	[23]
ob_ross	2015	OB	26	37	1583	454	V1-V3	[24]
ob_zup	2012	OB	167	117	1392	454	V1-V3	[25]
par_schep	2015	PAR	74	74	2351	454	V1-V3	[26]
t1d_alkanani	2015	T1D	23	89	9117	MiSeq	V4	[27]
t1d_mejia	2014	T1D	8	21	4702	454	V3-V5	[28]

Table 1: Datasets currently collected and processed through standardized pipeline. Disease labels: ASD = Austism spectrum disorder, CDI = *Clostridium difficile* infection, CRC = colorectal cancer, EDD = enteric diarrheal disease, UC = Ulcerative colitis, CD = Crohn's disease, CIRR = Liver cirrhosis, MHE = minimal hepatic encephalopathy, NASH = non-alcoholic steatohepatitis, OW = overweight, OB = obese, PAR = Parkinson's disease, T1D = Type I Diabetes.

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