
2021 SCSG
GI SYMPOSIUM

Functional GI Abstracts

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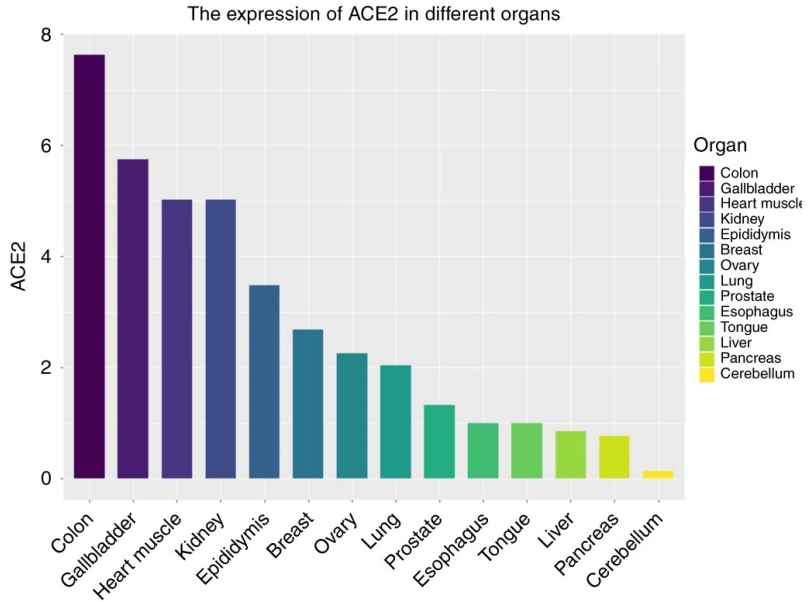
Disclosures

- Bausch Health
  - Speaker, Research Grant
- Gemelli Biotech
  - Equity
- Alnylam
  - Honorarium

Gut microbiome and COVID-19

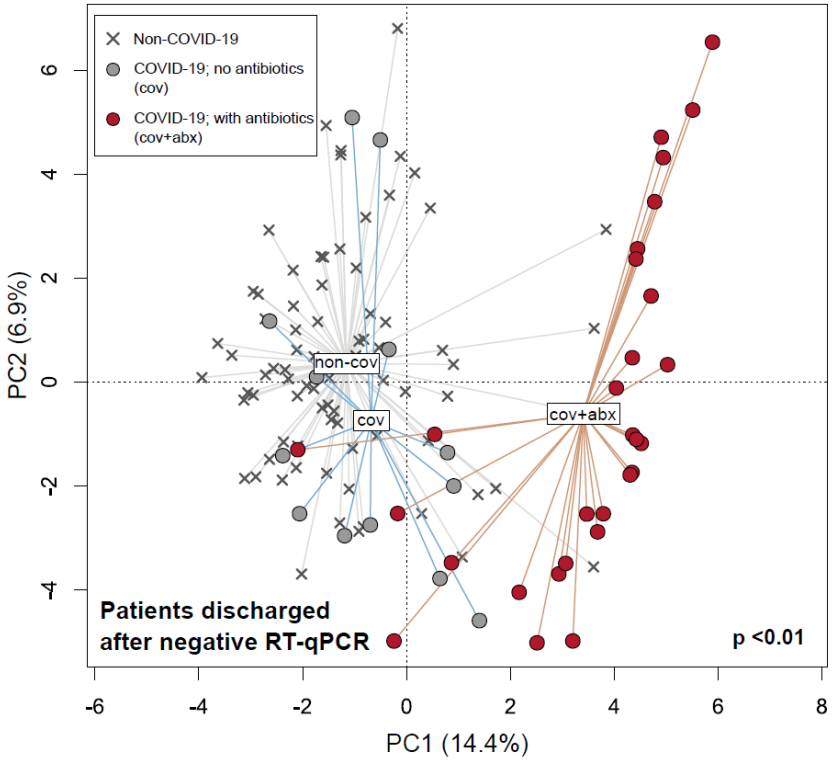
- SARS-COV-2 entry receptors (ACE-2) are heavily expressed in the GI tract
- Shedding of virus in stool is common and can outlast respiratory shedding
- Exact fecal–oral transmission route is not yet established!



Guo M et al. Nature Rev. 2021
Xu H et al. International Journal of Oral Science. 2020

Gut microbiome and COVID-19

- COVID-19 patients commonly have GI symptoms (diarrhea, N/V,…)
- Gut microbiome is significantly altered in COVID-19 pts
- Microbiome changes may persist beyond recovery



Yeoh et al. Gut. 2021

The gut microbiome of COVID-19 recovered patients returns to uninfected status in a minority-dominated United States cohort

Rachel C. Newsome[1], Josee Gauthier[1], Maria C. Hernandez[1], George E. Abraham[2], Tanya O. Robinson[2], Haley B. Williams[2], Meredith Sloan[2], Anna Owings[2], Hannah Laird[2], Taylor Christian[2], Yilianys Pride[2], Kenneth J. Wilson[2], Mohammad Hasan,[2] Adam Parker[2], Michal Senitko[2], Sarah C. Glover[2], Raad Z. Gharaibeh[1], and Christian Jobin[1]

[1]University of Florida College of Medicine, Gainesville, FL, [2]University of Mississippi Medical Center, Jackson, MS

- Prospectively collected stool via rectal swab from:
  - 50 COVID-19 pts in ICU
  - 9 recovered COVID-19 pts
  - 34 non-COVID pulmonary inpatients

	COVID		COVID recovered		Non-COVID	
	Number	Percent or SD	Number	Percent or SD	Number	Percent or SD
Number of participants	50	100%	9	100%	34	100%
Age, mean years	62.3	13.4	46.7	16.1	55.0	15.8
Sex: Male	28	56%	4	44%	14	41%
Sex: Female	22	44%	5	56%	20	59%
Race, Caucasian	11	22%	4	44%	14	41%
Race, Black	35	70%	4	44%	20	59%
Race, Hispanic	1	2%	1	11%	0	0%
Race, Choctaw	3	6%	0	0%	0	0%
BMI, mean	33.6	9.8	31.5	7.6	26.6	7.9

The gut microbiome of COVID-19 recovered patients returns to uninfected status in a minority-dominated United States cohort

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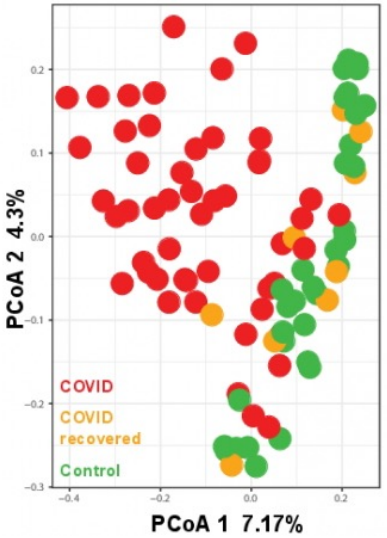
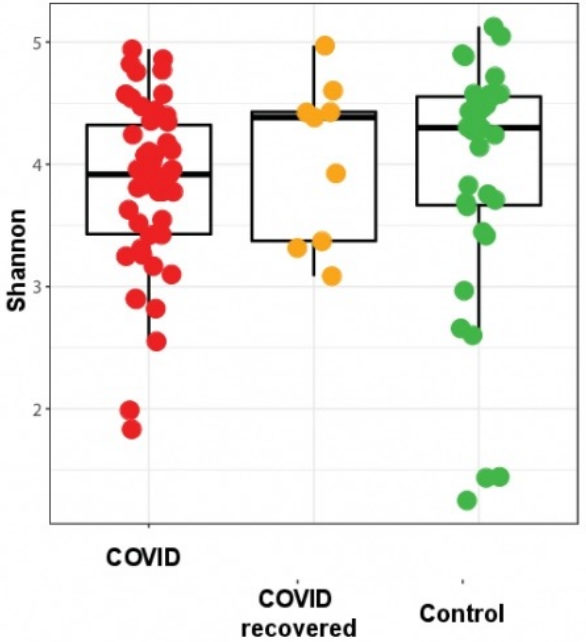
- COVID pts have different gut microbiome composition than covid recovered and controls
- COVID-recovered pts showed similar diversity as hospitalized non-covid pts
- COVID patients showed higher relative abundance of Campylobacter and Klebsiella





Gut microbiome and COVID-19

- Somewhat discordant with data from Hong Kong, stool microbiome appears to recover in COVID pts in the US!
- Promising but larger studies with longer follow-up are needed
- GI symptoms in “long COVID” patients are yet to be fully defined

Demographic and clinical factors associated with severe abdominal bloating in FGIDs:
Gardiner CP, Sing P, Ballou S, Hassan R, Yu V, Lembo A, Nee J, Iturrino J

- Bloating is seen in 16% of the general population and up to 70% of FGIDs
- Complex and multifactorial pathophysiology

Demographic and clinical factors associated with severe abdominal bloating in FGIDs

Gardiner CP, Sing P, Ballou S, Hassan R, Yu V, Lembo A, Nee J, Iturrino J

- 612 (78% female, age 44±16.5) consecutive new patients were recruited from a single center.
- Rome IV criteria used for diagnosis of FGID
- PAGISYM was used for assessment of bloating severity for two weeks prior to recruitment

Demographic and clinical factors associated with severe abdominal bloating

Gardiner CP, Sing P, Ballou S, Hassan R, Yu V, Lembo A, Nee J, Iturrino J

- Bloating severity was mild, moderate and severe in 38%, 35% and 27%, respectively
- Multivariate analysis showed bloating severity is associated with
  - Younger age
  - Presence of functional dyspepsia
  - Presence of functional constipation
  - Abdominal pain severity and somatization score
- Severity of anxiety, depression and sleep disturbance were not associated with bloating severity

Bloating is associated with many organic diseases

- Commonly missed DDx of bloating:
  - Anatomical (enterocele, hypermobile Ehlers-Danlos syndrome)
  - Motility (Pseudoobstruction, gastroparesis, rapid gastric emptying, intraabdominal adhesions/bands)
  - Microbiome (SIBO, Small intestinal fungal overgrowth, probiotics, post-FMT)
  - Miscellaneous (POTS, mast cell activation syndrome)

Pichetshote N, Rezaie A.
Current Treatment Options Gastro. 2020

PREVENTING HEMORRHOIDS AND FISSURES OF PREGNANCY: RESULTS OF THE RANDOMIZED CONTROLLED TRIAL

T. Poskus[1], Z. Sabonyte Balsaitiene[1], M. Smigelskaite[1], G. Barkauskaite[1], E. Jasiunas[2], M. Jakubauskas[1], L. Jakubauskiene[1], K. Strupas[1], G. Drasutiene[1].

[1]*Vilniaus universitetas, Vilnius, Vilnius, Lithuania*; [2]*Vilniaus Universiteto ligonines Santariskiu klinikos, Vilnius, Lithuania*

- Incidence of hemorrhoids during pregnancy is 15-40%
- Pathophysiology: Increased circulating blood volume, increased intraabdominal pressure, relaxation of venous smooth muscles by progesterone, and constipation

Shin GH et al. AJG. 2015

Hemorrhoids in pregnancy

- Aim: To assess effectiveness of dietary and behavior recommendations for prevention of hemorrhoids during pregnancy
- Single-blind Multicenter trial: During the first trimester 260 women were randomized 1:1 to dietary/behavior recommendations or standard care
- Endpoint: Reduction in postpartum rate of hemorrhoids

Poskus T et al. DDW. 2021

Dietary/behavior recommendations

- Dietary:
  - Consume at least 1.5 liters of fluid
  - Consume a tablespoon of bran and 2-5 prunes daily
  - Consume ~300g of fruits and 500g vegetables and 30g nuts
- Behavior
  - Exercise 30-60 minutes daily
  - Spend less than 3 minutes on the commode
  - Washing after bowel movements

Poskus T et al. DDW. 2021

Results

- Hemorrhoids were seen in 40.8% of control group as compared to 15.4% in the intervention group ($p < 0.01$)
- There was no difference in maternofetal outcomes

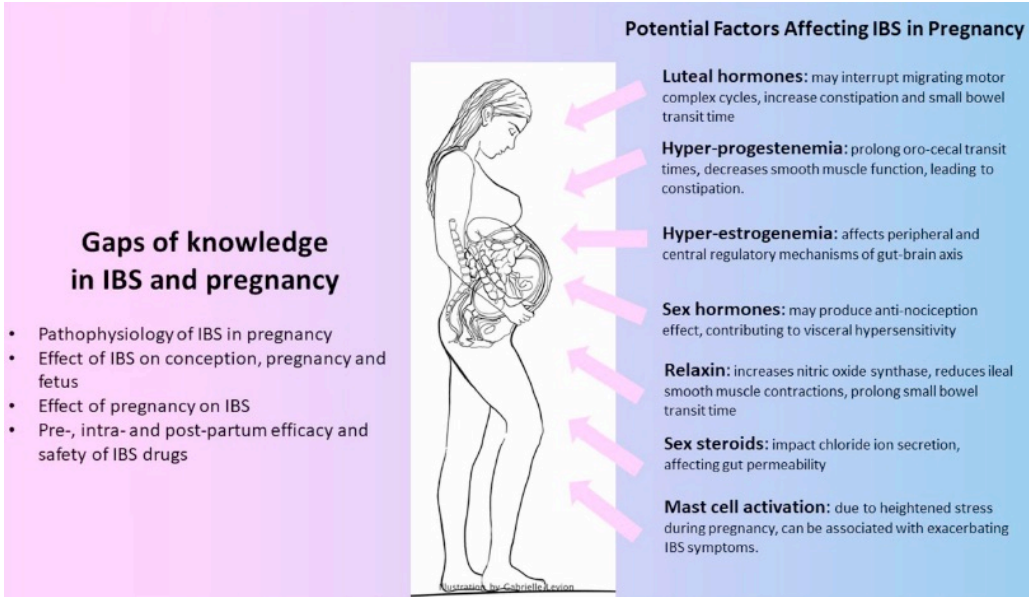
Poskus T et al. DDW. 2021

Irritable Bowel Syndrome in Pregnancy

Sarvee Moosavi, MD[1], Mark Pimentel, MD[2,3,4], Melissa S. Wong, MD[5] and Ali Rezaie, MD, MSc[2,3,4]

Am J Gastroenterol 2021;116:480–490. https://doi.org/10.14309/ajg.0000000000001124

- Review on management of IBS-D, IBS-C and IBS-M in pregnancy



Gut microbiome samples – does stool represent right?

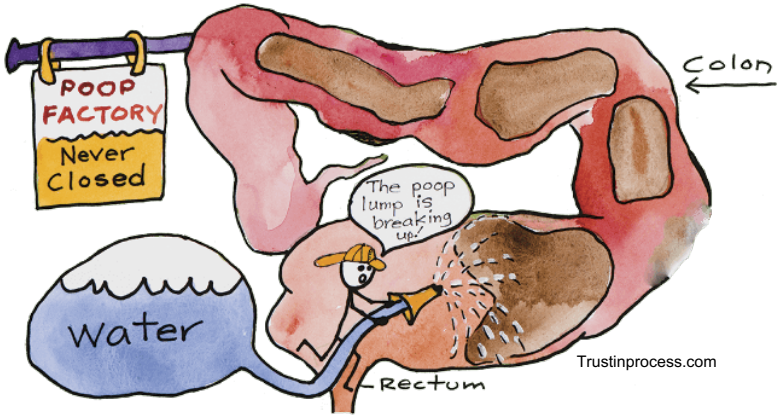
Orly Levitan[1], Dawn B. Burleson[1], Peter McCaffrey[2], Lanying Ma[2], Ayin Vala[2], David A. Johnson[3]

[1]Hygieacare Inc., Norfolk, VA, USA [2]VastBiome, San Carlos, CA, USA [3]Eastern VA Medical School, Norfolk VA, USA

- High volume colonic irrigation or *"Colonic" has been considered for:*
  - *Alternative therapy for constipation*
  - *Preparation for colonoscopy*

Parekh et al. J Clin Gastro Hep 2018
Harish K et al. J Gastrointest Dig Syst 2016

- *Several other techniques/devices widely available in California with unfounded claims of "detoxification"*



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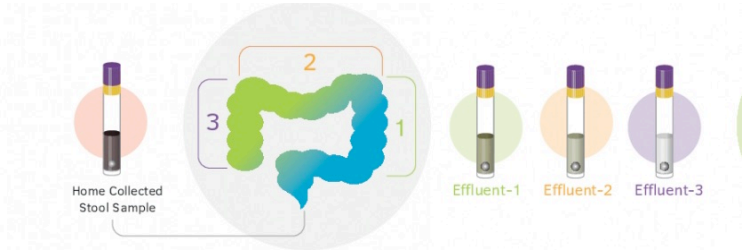
- *20 subjects underwent high volume colonic irrigation before colonoscopy*
- *Stool samples were collected prior to irrigation*
- *Three serial stool samples were collected during colonic for metagenomic sequencing*



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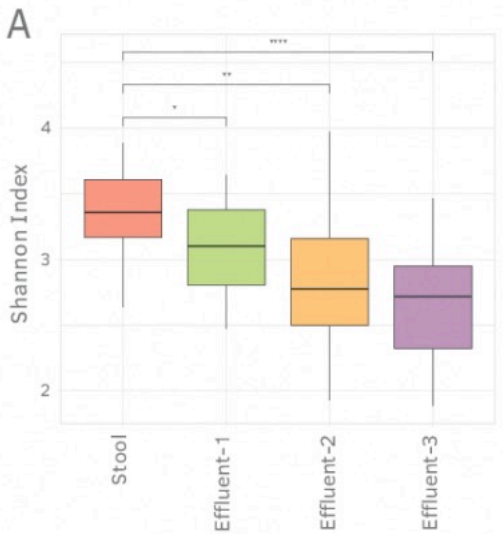
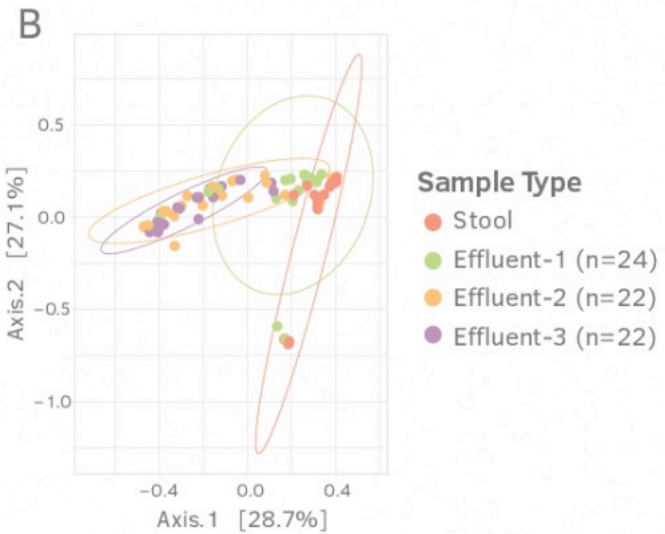
There was drastic difference in microbiome alpha diversity of each sample

There was drastic difference in microbiome beta diversity





Conclusion

- Unclear each sample represents which part of the colon, but the study highlights that stool is an unreliable medium for global assessment of microbiome

Stool microbiome testing not ready for clinical use

	Reference Range	IBS	IBD	Metabolic Syndrome	Chronic Fatigue	Auto-immune	Type 2 Diabetes	High Blood Pressure	Mood Disorders
Bacteroidetes Phylum									
Bacteroides-Prevotella group		↑	↑	↑	↑	↑	↑	↑	↑
Bacteroides vulgatus		↑			↑	↑		↑	↑
Barnesiella spp.									
Odoribacter spp.									
Prevotella spp.		↑		↑	↑	↑		↑	↑
Firmicutes Phylum									
Anaerotruncus colihominis	H	↑	↑	↑	↑	↑	↑	↑	↑
Butyrivibrio crossotus									
Clostridium spp.									
Coprococcus eutactus		↑			↑	↑		↑	↑
Faecalibacterium prausnitzii		↑				↑			↑
Lactobacillus spp.									
Pseudoflavonifractor spp.	H	↑	↑	↑	↑	↑	↑	↑	↑
Roseburia spp.			↓						
Ruminococcus spp.		↑↑	↓	↓	↓	↑↑	↑↑	↑↑	↑↑
Veillonella spp.		↑	↑	↑	↑	↑	↑		↑
Actinobacteria Phylum									
Bifidobacterium spp.									
Bifidobacterium longum									
Collinsella aerofaciens		↑↑	↑↑	↓	↑↑	↑↑	↑↑	↑↑	↑↑
Proteobacteria Phylum									
Desulfovibrio piger									↑
Escherichia coli	H	↑	↑	↑	↑	↑	↑	↑	↑
Oxalobacter formigenes		↑		↑	↑				↑
Euryarchaeota Phylum									
Methanobrevibacter smithii		↑				↑			↑
Fusobacteria Phylum									
Fusobacterium spp.		↑	↑	↑	↑	↑	↑	↑	↑
Verrucomicrobia Phylum									
Akkermansia muciniphila		↓	↓	↓	↓	↓	↓	↓	↓

Commensal Bacteria (PCR)	Result CFU/g stool	Quintile Distribution 1st 2nd 3rd 4th 5th	Reference Range CFU/g stool
Bacteroidetes Phylum			
Bacteroides-Prevotella group	1.7E8		3.4E6-1.5E9
Bacteroides vulgatus	<DL		<=2.2E9
Barnesiella spp.	5.4E7		<=1.6E8
Odoribacter spp.	<DL		<=8.0E7
Prevotella spp.	6.6E6		1.4E5-1.6E7
Firmicutes Phylum			
Anaerotruncus colihominis	3.7E7 H		<=3.2E7
Butyrivibrio crossotus	3.2E4		5.5E3-5.9E5
Clostridium spp.	1.4E10		1.7E8-1.5E10
Coprococcus eutactus	4.7E6		<=1.2E8
Faecalibacterium prausnitzii	3.8E9		5.8E7-4.7E9
Lactobacillus spp.	1.1E9		8.3E6-5.2E9
Pseudoflavonifractor spp.	3.8E8 H		4.2E5-1.3E8
Roseburia spp.	4.9E8		1.3E8-1.2E10
Ruminococcus spp.	3.0E8		9.5E7-1.6E9
Veillonella spp.	4.0E6		1.2E5-5.5E7
Actinobacteria Phylum			
Bifidobacterium spp.	1.1E9		<=6.4E9
Bifidobacterium longum	3.3E7		<=7.2E8
Collinsella aerofaciens	5.3E7		1.4E7-1.9E9
Proteobacteria Phylum			
Desulfovibrio piger	<DL		<=1.8E7
Escherichia coli	9.3E7 H		9.0E4-4.6E7
Oxalobacter formigenes	<DL		<=1.5E7
Euryarchaeota Phylum			
Methanobrevibacter smithii	8.5E7		<=8.6E7
Fusobacteria Phylum			
Fusobacterium spp.	1.9E4		<=2.4E5
Verrucomicrobia Phylum			
Akkermansia muciniphila	2.7E7		>=1.2E6
Firmicutes/Bacteroidetes Ratio			
Firmicutes/Bacteroidetes (F/B Ratio)	91		12-620

Stool microbiome testing not ready for clinical use

- Stool microbiome testing has multiple limitations
  - Extremely wide range of “Normal” stool microbiome
  - Extremely wide range of stool microbiome in disease
  - Daily variability of stool microbiome
  - Variability of stool microbiome even within one BM
  - Normal ≠ Healthy
- Microbiome field moving to mucosal and small bowel microbiome