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#### ACS Scholar Adunoluwa Obisesan

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"The ACS Scholars Program provided me with monetary support as well as a valuable network of peers and mentors who have transformed my life and will help me in my future endeavors. The program enabled me to achieve more than I could have ever dreamed. Thank you so much!"

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He longent name Jung to ta S. un molectinistip untrities University for compare In Brh.D. in engigent chemitry from the larger site primerity of hard results with postoccours experience an Planc's laboratories in L. plak. CA has pays divide of the Postoch Section of the American Chemical Society and the Society Section of hard endoced and the consequence Career exploration and development for purgers and an and an encouraging career exploration and development for purgers

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#### A synthetic microbiota designed through meta-analysis provides insight to community function in *Clostridioides difficile* resistance

Jordan Bisanz PhD Biochemistry and Molecular Biology One Health Microbiome Center Pennsylvania State University



### **Challenges in translating microbiome science**

- 1. What defines a healthy microbial community?
- 2. Does a singular healthy microbiota exist?
- 3. What are the mechanisms that drive health?
- 4. How can we design functional microbial communities?

Proposed solution: meta-analysis



### **Microbiome meta-analysis**

- >10 years of high throughput microbiome data in public repositories
- Not all of it is useful, but it allows for studying the human microbiome across populations and disease states
- MAGs have become an incredibly powerful tool for microbiome research
- Is there more we can learn from this data in aggregate?



### **Clostridioides difficile**

- Opportunistic pathogen causing spectrum of disease
- Normally suppressed by healthy gut microbiome and triggered by antibiotics
- Treatment frequently followed by recurrent infection
- ~½ million annual infections in US and on the rise costing billions
- Fecal transplant has proven effective but has limitations



### **Fecal transplant alternatives**

- Fecal transplants are highly efficacious but:
  - May carry MDR pathogens
  - May have undesirable off-target effects
  - Rely on human donors -> intrinsically irreproducible composition
- Can we rationally design a synthetic fecal microbiome transplant (sFMT) alternative?
  - But what organism(s) should we put in it?



# I. Design of Synthetic Communities

### C. difficile meta-analysis





Susan Tian BMMB Grad Student

Goal: Identify the organisms most robustly anticorrelated with *C. difficile* colonization

## Altered community composition with *C. difficile*



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#### **Random Forest model training**



- Accurate predictions of *C. difficile* colonization in external validation studies (AUROC=0.81±0.2)
- ~200 features (organisms) with predictive ability

### **Predictive taxa**

- Predictive taxa are enriched for negative predictors
- Predictive taxa cover a broad phylogenetic range
- *Clostridium scindens*, a known inhibitor of *C. difficile* is not predictive of *C. difficile* colonization *in vivo*



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### Identifying taxa for synthetic community

- Features anti-correlated with *C. difficile* are correlated with each other:
  - Evidence that they will form a stable community?
- We constructed:
  - sFMT1: 37 pure culture strains anti correlated with *C. difficile*
  - sFMT1+Cs: sFMT1 with C. scindens
  - ProCd: 25 pure culture strains positively associated with *C. difficile*



# II. Characterizing Community Assembly and Function

#### **Characterization in serial culture**



• sFMT forms a stable community in vitro



• sFMT colonization kinetics mimic a human fecal transplant

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#### In vivo vs in vitro



- · There are "waves" of succession during colonization similar to humans
- In vivo community composition and temporal dynamics are distinct from in vitro

- Metagenomic methods • needed to differentiate strains for higher sensitivity and specificity
- Developed StrainR2: normalization based on effective unique genome size
- FPKM (Fragments per kilobase per million reads mapped)
- FUKM (Fragments per unique thousand hashed k-mers per million reads mapped)





Kerim Hebe CS/BMB Undergrad

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CS/Biology Faculty



### Intraspecies competition



What are the determinants of competitive exclusion in vivo? •

#### sFMT metabolism in vivo



- SCFAs are derived from bacterial metabolism of non-digestible carbohydrates among other sources
- sFMT1 replicates metabolism of human-derived fecal transplant (hFMT)

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### sFMT bile acid transformation



 sFMT1 replicates many biotransformations observed in a complex human sample and addition of *C. scindens* leads to 7a-dehydroxylation

#### An unexpected observation





- 3-oxoLCA is a potent antiinflammatory molecule acting on Th17 cells
- 3-oxoLCA is also an inhibitor of *C. difficile*
- How could 3-oxoLCA be produced in the absence of *C. scindens*?

### III. Measuring resistance to *C. difficile* infection

### C. difficile exclusion in vitro



- sFMT1 and hFMT reduce *C. difficile* abundance by orders of magnitude
- ProCD (organisms positively correlated with *C. difficile*) has no significant effect

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### **Gnotobiotic infection model**



· Colonization reduces disease severity and virulence factor expression

### IV. Determining sFMT Mechanism(s) of Action



• Proline fermentation is an important pathway for *C. difficile in vivo,* could sFMT1 members be competing for proline?

### **Designing** $\triangle$ **Stickland functional knockout**



- Stickland fermenting strains predicted on basis of possessing proline reductase homologs (Nstrains=8)
- Verified in vitro using NMR

### **Testing** \Delta Stickland functional knockout



- Compared 3 groups:
  - original sFMT1 (N=37 strains)
  - sStickland1 (N=8 strains predicted to reduce proline)
  - sFMT1∆Stickland1 (N=29 strains [37-8])
- NMR confirms functional knockout in vivo



### But can we refine further?

### Reducing sStickland1 complexity

- Validated Stickland fermentation within sStickland1 members *in vitro*
- 2 strains of Dorea longicatena and Peptostreptococcus anaerobius demonstrate most convincing activity
- Contrasted:
  - Germ-free
  - sFMT1 (37 strains)
  - sStickland2 = JEB00029 + JEB000254
  - sFMT1∆Stickland2 = sFMT1 sStickland 2



### **Reducing sStickland1 complexity**

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  - sFMT1∆Stickland2 = sFMT1 sStickland 2



#### **Translational targets**

- Predictive power not driven by differential abundance, but differential presence
- These two species are found in ~20% of individuals without *C. difficile* while largely absent in carriers
- Could these be key predictors of susceptibility and/or potential therapeutic targets?



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### Conclusions

- Meta-analysis allowed the design of a functional synthetic community
- *C. scindens* may be dispensable for *C. difficile* resistance in a complex community, but strains which conduct Stickland fermentation of proline are necessary and sufficient
- Limitation of proline availability may be key to microbial suppression of *C. difficile*



#### Conclusions

- Synthetic microbiomes are tractable tools • for mechanistic study coupling big data with experimental opportunities
- Synthetic fecal transplants and ٠ derivatives thereof (sFMT) may have potential for clinical translation



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### **Microbiome Mechanics: Building a Healthier Gut**

Peptidoglycan's Role in Gut Homeostasis



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The Gut Microbiome

- The human digestive tract is populated with bacteria (~95% of the human microbiome is located here)
- Essentially a microbial organ within a host organism
- Commensal relationship



### The Gut Microbiome

- Gut homeostasis affects our day-to-day functioning
- Two way relationship in terms of exchange of signaling molecules
- We only know of a few biologically active molecules being produced by gut microbiota



A major molecule that is now entering this small list is MDP, which happens to be a fragment of bacterial cell walls

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## Bacterial cell wall: Peptidoglycan



- Peptidoglycan (also known as sacculi) is a single LARGE molecule that surrounds the entire bacterial cell
- All bacteria are protected by this 'jacket' like structure
- Peptidoglycan is uniquely bacteria in nature (humans do not have any molecules similar to it)

Brown, L.; Wolf, J.M.; Prados-Rosales, R.; Casadevall, A. Nat Rev Microbiol, 2015, 13, 620.

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### **MDP Released by Gut Microbiota**



 Fragments (or 'bricks') from the cell wall are released by muramidases (e.g., lysozyme)



### Sensing of NOD2

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MDP is a fingerprint of bacterial presence

- It gets detected by NOD2 inside mammalian cells
- This process was thought to be defensive in nature
  - signifying an infection
  - but this concept may not capture all that MDP does....

65

### **Alternative role for NOD2?**



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Science

hibitor cancer immunotherapy

### **Potentiation of Immunity**

 Could NOD2 activation from microbiome peptidoglycan lead to better immunological state?

Enterococcus peptidoglycan remodeling promotes checkpoint in-

 Can this improved state potentiate checkpoint cancer immunotherapy?





E

### **Potentiation of Immunity**



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### **Potentiation of Immunity**



- In mice devoid of gut bacteria, the supplementation of MDP was sufficient to replicate the anti-cancer phenotype
  - · Has implications for drug design and better cancer immunotherapies

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### **Alternative role for NOD2?**



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### **Regulation of appetite**

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Bacterial sensing via neuro temperature		egulates a	ppeti	te and	d body

- Could NOD2 operate in the brain?
  - If so, what physiology could it control?



### **Regulation of appetite**

#### Science

### Bacterial sensing via neuronal Nod2 regulates appetite and body temperature

opers Archive About 🗸 (Submit n

- 508X07 + 15 Apr 2012 Vel 376, trans 6010 <u>201-10.1126/steinero.uk</u>2016
- NOD2 expression in neurons could impact feeding and temperature in female mice



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### **Regulation of appetite**

# Science Control 10 Ministry (Ministry (M

 Supplementation of MDP (peptidoglycan fragment) can modulate neuronal activity



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### **Alternative role for NOD2?**



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Science

### **Peptidoglycan Can Promote Growth**



 Peptidoglycan can be readily isolated from bacteria, including those that harbor our guts



### **NOD2 Activation Can Promote Growth**



• Probiotic with *Lactobacillus plantarum* improves intestinal NOD2 stimulation and linear growth

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### **NOD2 Activation Can Promote Growth**

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HOME > SCIENCE > VOL. 379, NO. 4634 > INCRORE-MEDIATED INTESTINAL MORE STRULATION INPROVES LINEAR GROWTH OF UNDERNOVHISHED INFANT.	for section wereing 2-2-20 <sup>10</sup> CHU 30 ur LI <sup>20/20</sup> , or PULCERO orally 5 x medi.
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	$ \begin{array}{c} \mathbf{K}  \text{if } \mathbf{K}  \text$

• Probiotic with *Lactobacillus plantarum* improves intestinal NOD2 stimulation and linear growth

### **Open Questions - NOD2 in Host Health**



- Can we visualize peptidoglycan of gut bacteria in live animals?
- Can we isolate peptidoglycan from stool samples to analyze its composition and NOD2 activation level?

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Volume 29, Issue 12, 15 December 2022, Pages 1721-1728.e5

### Goal # 1 – Live Animal Imaging

We metabolically tagged the peptidoglycan of gut bacteria in live mice with near IR fluorophores





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### Goal # 2 – Non-invasive Sacculi Isolation

We set out to isolate peptidoglycan from fecal samples to readily interrogate NOD2 signaling

- But how?
  - Fecal samples are very complex and it is not trivial to isolate bacteria/sacculi
  - We took advantage of a special property of sacculi: its resistance to SDS/heat/DNAase/RNAase/protease



Noninvasive Analysis of Peptidoglycan from Living Animals Kart L. Oku, Stee H. Koll, Saadmun S. Akmad, Judes M. Dresler, Mahendra D. Chorda, Brandon L. Jutras, Mahanie R. Rutkowski, and Marcos M. Pres\*



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### The Gut Microbiome

 Peptidoglycan from gut bacteria operates as a biologically active mediator of host health via NOD2 sensing



#### Gut Microbial Metabolism of Dietary Input Matters for Host Health

Jan Claesen







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#### The American Obesity Epidemic



Obesity is defined as a BMI over 30 Map: Elijah Wolfson for TIME • Source: N Engl J Med 2019;381:2440-50. • Created with Datawrapper



#### Obesity Increases Propensity of All-Cause Mortality

Dagfinn et al. 2016 BMJ

#### Moderate Flavonoid Consumption is Negatively Associated With Mortality



Bondonno et al. (2019) Nat Commun



#### Flavonoids are a large family of plant secondary metabolites

89

#### Gut bacterial flavonoid catabolism & cardiometabolic disease





Luke Osborn



Karlee Schultz



Sara Alqudah

**Hypothesis:** Monophenolic acids stemming from microbial flavonoid catabolism are responsible for the anti-obesogenic effect of flavonoid consumption.





Diet Informs Gut Microbial Composition

Osborn et al. (2022) PNAS

93

Berry Diets Promote Microbial Diversity





#### Targeted Mass Spec on Microbial Portal Blood Flavonoid Catabolites

#### 4-Hydroxyphenylacetic acid is correlated with improved metabolic parameters



Hoyles et al. (2018) Nat Med



#### A Single Monophenolic Acid (4-HPAA) Reprograms Global Fat Storage

Osborn et al. (2022) PNAS

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#### Non-Alcoholic Fatty Liver Disease (NAFLD)



NAFLD is often a consequence of obesity and is a risk factor for cardiometabolic disease



#### The Non-Alcoholic Fatty Liver Disease (NAFLD) Spectrum

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#### 4-HPAA Reverses High Fat Diet-Induced Steatosis





#### AMPK Regulates Liver Lipid Metabolism

101

Osborn et al. (2022) PNAS



Osborn et al. (2022) PNAS



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#### 4-HPAA Directly Activates AMPK in Primary Hepatocytes in a Dose Dependent Manner





Osborn et al. (2022) PNAS

BJ Massey



#### Identification of the initiating step in flavonol catabolism

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#### Homologs of F. plautii Catabolic Genes are Rare in Human Fecal Microbiomes



#### Conclusions

- Supplementing a HFD with flavonoid-rich elderberry extract significantly attenuated HFD-induced obesity 4-HPAA was enriched in the portal plasma of these mice
- Continuous subcutaneous delivery of 4-HPAA was sufficient to reverse HFD-induced hepatic steatosis
- This anti-steatotic effect is associated with the activation of AMP-activated protein kinase  $\alpha$  (AMPK $\alpha$ )
- In a large survey of healthy human gut metagenomes, about two percent contained homologues of all four characterized bacterial genes required to catabolize flavonols into 4-HPAA.

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#### Acknowledgements

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