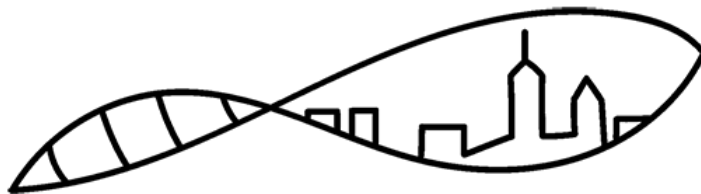


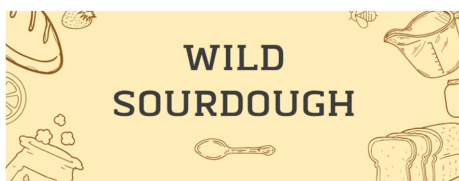
REMNET



RESEARCH EXPERIENCES IN MICROBIOMES NETWORK NEWSLETTER

AUG. 2020, ISSUE 6

WELCOME TO FALL 2020



A Science of Sourdough Project

Capture wild microbes and turn them into bread – for science!

To make your own sourdough starter, all you need is flour, water, and a little bit of time. Whether you are here because your favorite bakery is currently closed and you need your bread fix, or because you are eager to help make even the smallest progress in our understanding of the microbial world, we are glad you are here! Regardless, we hope you will follow-along, make your own sourdough starter captured from wild microbes, and share your experience.

The microbial world is still full of mysteries. Some of the answers might be lurking in your kitchen. We know more about the deep sea than we do about some of the bacteria and fungi that are most important to us, partially because they can be so difficult to study. The microbial communities in sourdough are comparatively easy to grow and study, so understanding sourdough can help us untangle some of the mysteries of the microbial world.

JOURNAL OF MICROBIOLOGY & BIOLOGY EDUCATION, May 2015, p. 85-86
DOI: <https://doi.org/10.1128/jmb.1161.859>

Tips & Tools



Increase the Visibility of Microbial Growth in a Winogradsky Column by Substituting Diatomaceous Earth for Sediment

Thomas G. Benoit
Department of Biology, McMurry University, Abilene, TX 79697

INTRODUCTION

Constructing a traditional Winogradsky sediment column is a staple ecology exercise in undergraduate microbiology labs. The column is easy to make and it provides a visual learning experience as chromogenic microbial communities develop during incubation. It is an excellent tool for teaching students about microbial diversity and metabolism, nutrient cycling, and ecological succession (2).

A difficulty with the traditional Winogradsky column, however, is that the development of microbial communities is hard to follow because the dark sediment matrix mutes their colors. Often the colors are not discernible until the column nears maturity. This tends to hamper student engagement due to the perceived long wait for something to happen.

The solution for this is to change the color of the column matrix. To this end, students in my teaching labs substitute diatomaceous earth (DE) for sediment. A DE column is made by mixing a suspension of sediment microbes with DE to form

Before beginning, obtain a 250-mL tissue culture flask to use as the column container.

Preparation

1. **Collect the sample.** Collect a sample of submerged sediment and water along the edge of a body of fresh water. The sample should be collected into a clean, wide-mouth container that can be sealed tightly. It is important to avoid collecting more than a minimum of the black subsurface sediment layer because it contains dense populations of sulfate-reducing bacteria. If they are too concentrated in the inoculum, they may rapidly take over the column with H_2S production and turn it black, a condition from which the column may not recover. Approximately 100 mL of sediment and 400 mL of water should be collected and used within 24 hours.

And it begins!

For many of us the challenge of engaging students with microbiology, safely, in their homes remains a difficult one but not impossible. We at REMNet are trying a variety of different approaches to teach students about microbiology, many of which are very easy to do, not very expensive but very exciting to perform for students. They are also accessible to their families, roommates and friends and may generate pretty interesting conversations about microbes!

The great yeast shortage of 2020 was solved by folks engaging with sourdough starters. Why not make use of the fantastic resources of the Dunn lab and have your students generate their own starters and to monitor them over time and record their data in online notebooks such as Benchling.

Another possibility is to have your students find mud and set up Winogradsky columns. There is a wealth of resources online for this and you again have your students record the column over time and document it in their notebooks.

A really simple experiment that will allow you to tackle hand-washing was pioneered by some Idaho school teachers and has recently been covered online and in social media. Using simple slices of bread and having your students touch them before and after hand-washing is a great way to demonstrate the utility of soap and water and you can combine this with citizen science and outreach activities.

Lastly check out all of what the journal Nature has to offer on the microbiome [here](#).

UPCOMING EVENTS:

MACUB: TBD in October

VINCENT RANCANIELLO WILL BE THE GUEST SPEAKER!

ESA MID-ATLANTIC:

POSTPONED UNTIL 10/16/20-10/18/20
REGISTRATION ENDS 9/25/20

SACNAS: 10/19/20-10/24/20

ONLINE
REGISTRATION OPEN NOW

ASM: 10/23/20-10/26/20

CONFERENCE ON NEXT GENERATION SEQUENCING
LAST CHANCE REGISTRATION BY OCT 26TH

AACU: 11/5/20-11/7/20

TRANSFORMING STEM HIGHER EDUCATION

ABRCMS: 11/9/20-11/13/20

ONLINE
REGISTRATIONS OPENS 9/8/20

LIVING

Disgusting classroom experiment proves you really should wash your hands

By Hannah Sparks

December 18, 2019 | 1:58pm | Updated



Jaralee Annice Metcalf / Facebook



COVID AND THE MICROBIOME?

If you're looking for ways to bring the Pandemic into your microbiology and microbiome related courses, consider having your students review the emerging literature that is suggesting linkages between outcomes and the microbiome. Gu et al. (2020) have shown that the gut microbial signature of patients with COVID-19 differed from that of H1N1 patients and healthy controls, suggesting the potential value of the gut microbiota as a possible diagnostic biomarker and therapeutic target for COVID-19. Another small study of 30 COVID patients described alterations in the fungal microbiome, with enrichment of fungal pathogens from the genera *Candida* and *Aspergillus*, during hospitalization as compared with controls.

Alterations of the Gut Microbiota in Patients With Coronavirus Disease 2019 or H1N1 Influenza

Sitao Gu,^{1*} Yufei Chen,^{1*} Zhengjie Wu,^{1*} Yanbo Chen,^{1*} Haimo Guo,^{1*} Longxian Lu,^{1*} Feifei Guo,^{1*} Xuesu Zhang,² Rui Luo,^{1*} Chenjie Huang,^{1*} Haifeng Lu,^{1*} Beiven Zheng,^{1*} Jiaying Zheng,^{1*} Ren Yan,^{1*} Hua Zhang,^{1*} Haiyong Jiang,^{1*} Qiaomai Xu,^{1*} Jing Guo,^{1*} Yiwon Gong,^{1*} Lingling Tang,^{1*} and Lanjuan Li^{1,3*}

¹State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, National Clinical Research Center for Infectious Diseases, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, China, ²Department of Infectious Diseases, Shaoxing Hospital, affiliated to Shaoxing International Medical College, Zhejiang Shaoxing University, Hangzhou, China, and ³Department of Parasitology, First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, China

Background. Coronavirus disease 2019 (COVID-19) is an emerging serious global health problem. Gastrointestinal symptoms are common in COVID-19 patients, and severe acute respiratory syndrome coronavirus 2 RNA has been detected in stool specimens. However, the relationship between the gut microbiome and disease remains to be established.

Methods. We conducted a cross-sectional study of 30 patients with COVID-19, 24 patients with influenza A (H1N1), and 30 matched healthy controls (HCs) to identify differences in the gut microbiota by 16S ribosomal RNA gene V3–V4 region sequencing.

Results. Compared with HCs, COVID-19 patients had significantly reduced bacterial diversity; a significantly higher relative abundance of opportunistic pathogens, such as *Streptococcus*, *Rotifera*, *Verrucomicrobia*, and *Actinomyces*; and a lower relative abundance of beneficial symbionts. Five biomarkers showed high accuracy for distinguishing COVID-19 patients from HCs with an area under the curve (AUC) up to 0.89. Patients with H1N1 displayed lower diversity and different overall microbial composition compared with COVID-19 patients. Seven biomarkers were selected to distinguish the 2 cohorts (AUC = 0.94).

Conclusions. The gut microbial signature of patients with COVID-19 was different from that of H1N1 patients and HCs. Our study suggests the potential value of the gut microbiota as a diagnostic biomarker and therapeutic target for COVID-19, but further validation is needed.

Keywords. COVID-19; H1N1; intestinal microbiota; dysbiosis; biomarker.

Journal Pre-proof

Alterations in Fecal Fungal Microbiome of Patients With COVID-19 During Time of Hospitalization until Discharge

Tao Zuo^{1,2,3*}, Hui Zhan^{1,2,3*}, Fen Zhang^{1,2,3}, Qin Liu^{1,2,3}, Eugene Y.K. Tso⁵, Grace C.Y. Lu^{3,4}, Nan Chen^{1,3}, Amy Li^{2,3}, Wenqi Lu^{1,3}, Francis K.L. Chan^{1,2,3}, Paul K.S. Chan^{1,6}, Siew C. Ng^{1,2,3*}

1. Center for Gut Microbiota Research, Faculty of Medicine, The Chinese University of Hong Kong, Shatin, Hong Kong, China
2. State Key Laboratory for digestive disease, Institute of Digestive Disease, Li Ka Shing Institute of Health Science, The Chinese University of Hong Kong,

OPPORTUNITIES

Monthly JMBE LIVE!!

Announcing a new free webinar series featuring an informal discussion with editors and authors from JMBE. Our first meeting will be Friday, September 11, 1 – 2 PM Eastern time/10–11 AM Pacific time. This meeting will feature editors of the JMBE Special Themed Issue “Teaching in a Time of Crisis” who will take your questions about preparing manuscripts for the upcoming Special Themed Issue. To learn more about the JMBE Special Themed Issue, click [here](#) (deadline is October !!).

Register in advance for the September 11 meeting with editors of JMBE’s “Teaching in a Time of Crisis”: <https://zoom.us/join/register/tJMuduupzooE9O6iK9sdxsFKsPoUmjnWzTD>.

There is no cost to attend. After registering, you will receive a confirmation email containing information about joining the meeting. Meeting will be recorded.

ASM AWARD 2021

This year’s ASM Award for Education has gone to Nichole Broderick. Many of us know Nichole for her amazing work with Tiny Earth. We are all delighted for her!



The award recognizes general excellence in microbiology education. Education is broadly defined and meant to include any and all activities that inform and motivate students about the discipline of microbiology.



FOOD FOR THOUGHT

Sourdough Hands: How Bakers And Bread Are A Microbial Match

November 12, 2018 · 11:37 AM ET

LINDSAY PATTERSON



“Our data suggests that something about baking seems to be changing the hands of the people who do the baking,” says ecologist Rob Dunn.

Rick Gayle/Getty Images



RESEARCH ARTICLE

Temporal and Spatial Distribution of the Microbial Community of Winogradsky Columns

David J Esteban*, Bledi Hysa, Casey Bartow-McKenney

Department of Biology, Vassar College, Poughkeepsie, New York, United States of America

* daesteban@vassar.edu

Abstract

Winogradsky columns are model microbial ecosystems prepared by adding pond sediment to a clear cylinder with additional supplements and incubated with light. Environmental gradients develop within the column creating diverse niches that allow enrichment of specific bacteria. The enrichment culture can be used to study soil and sediment microbial community structure and function. In this study we used a 16S rRNA gene survey to characterize the microbial community dynamics during Winogradsky column development to determine the rate and extent of change from the source sediment community. Over a period of 60 days, the microbial community changed from the founding pond sediment population: Cyanobacteria, Chloroflexi, Nitrospirae, and Planctomycetes increased in relative abundance over time, while most Proteobacteria decreased in relative abundance. A unique, light-dependent surface biofilm community formed by 60 days that was less diverse and dominated by a few highly abundant bacteria. 67–72% of the surface community was comprised of highly enriched taxa that were rare in the source pond sediment, including the Cyanobac-



OPEN ACCESS

Citation: Esteban DJ, Hysa B, Bartow-McKenney C (2015) Temporal and Spatial Distribution of the Microbial Community of Winogradsky Columns. PLOS ONE 10(8): e0134588. doi:10.1371/journal.pone.0134588

Editor: Alexander V. Alekseyenko, New York University School of Medicine, UNITED STATES

Received: January 13, 2015

Accepted: June 10, 2015

