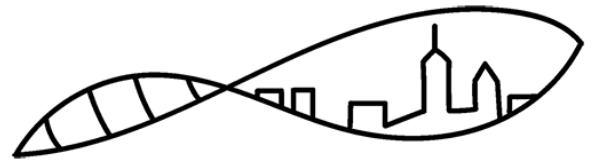


REMNET



RESEARCH EXPERIENCES IN MICROBIOMES NETWORK
NEWSLETTER

APRIL, 2020, ISSUE 2

GREETINGS REMNET COMMUNITY



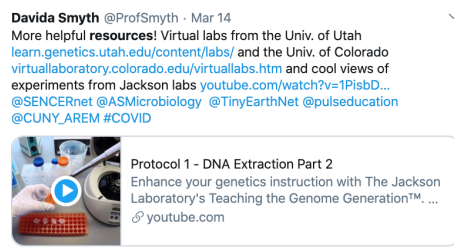
Theo practicing social distancing

Well we're almost there. Summer is approaching and now the planning begins in earnest for fall. Will we be back in our labs or will we be online once more? For many of us we are in a holding position until May 15th or later. As we go through our stay-at-home orders, this is a time to reflect on what's important in our lives and to think about how we teach, work with our colleagues and navigate our research. We're all in this together.

The scientific community has made giant leaps forward in the last weeks in the battle against this virus and it's been wonderful to see how we've all come together to help however we could. From sewing masks, to donating gloves, sharing online resources and kits to volunteering our expertise. It's been nice to see folks getting creative with their time at home, spending time with family, playing games, going for walks and working less (hopefully!)



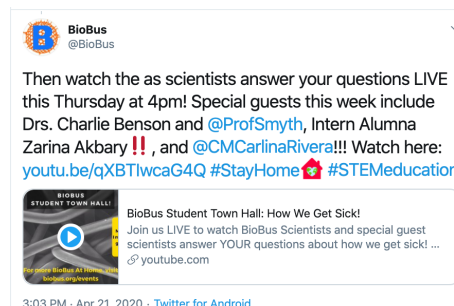
We've donated PPE



We've shared our resources



We've sowed masks



We've answered kiddies questions on "How we get sick!"

UPCOMING EVENTS:

ASCB TEACHING TOMORROW'S

SCIENTISTS: 5/30/20

REGISTRATION ENDS 5/27/20

(FREE BUT LIMITED TO 200 ZOOM PARTICIPANTS)

ASMCUE: 7/9/20-7/12/20

REGISTRATION ENDS 7/1/20

BIOQUEST: 7/27/20-8/7/20

WILL BE HELD AS AN ONLINE WORKSHOP

REGISTRATION OPEN NOW

SABER: TBA

ONLINE WEBINARS WILL BE HELD

SENCER SSI: 7/30/20-8/2/20

WILL BE HELD AS AN ONLINE MEETING

PROPOSAL DEADLINE 6/15/20

ESA MID-ATLANTIC:

POSTPONED UNTIL 10/16/20-10/18/20

REGISTRATION ENDS 9/25/20

AAAS is seeking proposals for

"UNDERSTANDING DYNAMIC ECOSYSTEMS"

Proposal deadline 7/14/20



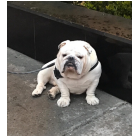
WHAT'S BEEN HAPPENING



Empty NYC Subways



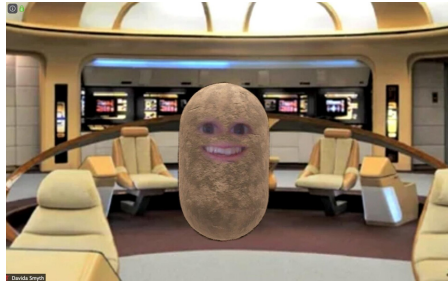
We've been missing each other



We've encountered internet celebrities in real life @jwalterwhite



Above all else we've missed the lab and our students! Click on the image to view the video!



We've experimented with ZOOM and Snap Camera Effect

WORKING GROUPS

We've identified some of our working group co-chairs. Thanks for stepping up folks!

Veronica Segarra and Philips Akinwole have agreed to be co-chairs of the Wet-Bench Working group. They'll be joined by Mangala Tawde and Sarah Rosario as co-chairs of the Dissemination working group.

If you've not signed up to be in a working group and would like to get involved please email us at ugmicronet@gmail.com



Veronica Segarra, co-chair of the Wet-Bench working group

THANKS VERONICA!

OPPORTUNITIES

There are Grant Opportunities

NSF and the DOD have put forth calls for proposals supported COVID crisis related projects.

Call For Papers

SENCER has put out a call for submissions to the Summer 2020 issue of Science Education and Civic Engagement: An International Journal - "Teaching Through COVID". We invite submissions of 1,000 words that describe your experiences with teaching through COVID. Possible topics include:

- Changes that you made to course content
- Adapting your teaching to online instruction
- Student reactions to learning science during a pandemic
- How your connection with SENCER has influenced your response to COVID
- The deadline for submission is June 15, 2020.

Please send your submission to the journal's Managing Editor, Marcy Dubroff, marcy.dubroff@fandm.edu

Call for Guest Editors

A search has been launched for Guest Editors for JMBE's Themed Issue: "Teaching in a Time of Crisis". The principal responsibilities of guest editors are to:

- Develop the call for papers for the issue
 - Oversee the review of a set of submissions.
- Qualifications include
- Expertise in a field related to the focus of the themed issue
 - Excellent communication and organizational skills
 - Experience having served as a reviewer or editor for JMBE or similar journals

To apply, please send a one-page letter of intent and a CV to mstotten@ung.edu. Application review will begin on May 8.

Curriculum

DOI: <https://doi.org/10.1128/jmbe.v21i1.2019>



Testing the "Grandma Hypothesis": Characterizing Skin Microbiome Diversity as a Project-Based Learning Approach to Genomics¹

Marcos Pérez-Losada^{1,2*}, Kelly M. Crandall³, and Keith A. Crandall¹

¹Computational Biology Institute, Department of Biostatistics and Bioinformatics, Milken Institute School of Public Health, George Washington University, Washington, DC 20052-0066, USA;

²CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, Vairão 4485-661, Portugal;

³Department of English, Woodgrove High School, Loudoun County Public Schools, Purcellville, VA 20132-2854, USA

The constantly evolving nature of genomics provides new challenges for students in Public Health as they try to understand how genomic information relates to health and disease. As Public Health curricula attempt to keep pace with the most recent advances in genomics, students should gain experience with analyzing genomic data and applying genomic tools to the study of health-related issues. To advance undergraduate and graduate student education and provide a more comprehensive view of genomics, we developed an educational project including both pedagogic and research components to characterize skin microbial communities (microbiomes) using targeted amplicon sequencing of their genomes (metatranscriptomics). All students completed the lab procedures, analyzed 16S rRNA genomic data (formative assessments), and wrote a five-page scientific report summarizing and discussing their results (summative assessment). Student grades for the summative assessment ranged from 31.5 to 40 (out of 40) points. They also successfully completed two practicum (problem sets) focused on microbiome sequence data and responded to 12 minute-papers related to genomic topics covered in class. In all these exercises the 2019 students outperformed 2018 students, who did not participate in this educational lab project. By fulfilling all the requirements of this project-based learning experience, students better understood the complexity of genomics and acquired a valuable set of marketable experience and skills in molecular technologies, bioinformatics and statistics (quantitative skills). Additionally, students were able to generate new valuable microbial 16S rRNA genomic data and test hypotheses about the composition and diversity of the microbes living on our skin (microbiota).



Available online at www.sciencedirect.com

ScienceDirect

Current Opinion in
Insect Science

Microbiomes as modulators of *Drosophila melanogaster* homeostasis and disease

Danielle NA Lesperance¹ and Nichole A Broderick^{1,2}

Drosophila melanogaster harbors a simple gut microbial community, or microbiome, that regulates several facets of its physiology. As a result, the host employs multiple mechanisms of maintaining control over its microbiome in an effort to promote overall organismal homeostasis. Perturbations to the balance between microbiome and host can result in states of instability or disease, making maintenance of microbial homeostasis a fundamental physiologic aspect of *D. melanogaster* biology. While the interactions between microbes and their hosts can be direct, particularly in the context of immunity and gut renewal, effects resulting from indirect interactions, such as those between microbiota members, can be equally as important. This review highlights the major ways, in which *D. melanogaster* regulates microbial homeostasis, the consequences of disruptions to homeostasis, and the different mechanisms, by which the microbiome interacts with its host.

Addresses

¹Department of Molecular and Cell Biology, University of Connecticut, Storrs, CT 06269, USA

²Institute for Systems Genomics, University of Connecticut, Storrs, CT 06296, USA

microbiota can tip the balance between states of homeostasis and instability, or disease. In this review, we highlight how an understanding of the interactions of *D. melanogaster* with its microbiome will reveal relationships between homeostasis and disease.

The microbiome is a malleable organ that modulates host physiology

D. melanogaster typically harbors simple bacterial communities containing species primarily from the *Lactobacillus* and *Acetobacter* genera [1,2]. The nature of the microbial community- including factors shaping the microbiome, its diversity and abundance, its roles in host physiology, and the ecological consideration of these associations- has been extensively reviewed elsewhere [3,4]. Some of the more well-studied contributions of the fly microbiome to physiology include impacts on innate immunity, intestinal homeostasis, reproduction, nutrition, and metabolism (Figure 1) [5*,6,7**,8,9,10**,11,12,13*,14-21,22*]. These studies have revealed the fly microbiome to be, in some ways, an additional organ that interacts with other host systems to influence overall biology. Like other



This material is based upon work supported by the National Science Foundation under grant no. 1827035