Metabolic interactions in microbial communities

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Metabolic interactions in microbial communities

Elizabeth Shank

Program in Systems Biology
Microbiology and Physiological Systems
Bacterial differentiation

Cellular heterogeneity

Metabolite production
• ~1.7% of genome
• 2.5 megaDalton enzymatic machine
• 581 Da specialized metabolite
Coculture antibiotic assay

Pathogen
Microbispora sp.
Monoculture

Coculture

Microbispora sp.
Monoculture

Coculture promotes antibiotic production
Coculture to identify cell-cell signals

Analyzed ~1,500 genomes
Identified those with unusual biosynthetic gene clusters
We selected 127 strains
Performed > 5,000 pairwise cocultures

2017, mSystems, Grubbs and Bleich et al.
Coculture to identify cell-cell signals

Monoculture  Coculture  Monoculture

Killing

Growth

Biofilm

Influenced

Influencer

2017, mSystems, Grubbs and Bleich et al.
Cellular heterogeneity
Cellular heterogeneity

Gene1

YPet

PsdpA
PsboA
PtapA

2 mm
Cellular heterogeneity

YPet

Gene1

Gene2

mTurq

YPet

mTurq

2 mm
Selected 18 genes of interest (physiology and metabolites)

∴ Built 153 dual-labeled strains

Flow cytometry

Microscopy

Imaging Mass Spectrometry

mTurq

YPet

agar

air

P_{sdp} P_{tapA}
**Interspecies signaling**

- *B. cereus* 
  - Thiocillin

- *E. coli* 
  - Enterobactin

**Intraspecies signaling**

- *P. protegens* 
  - DAPG

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2015, *PNAS*, R Bleich et al.
Transparent Soil

2 mm

IN

OUT

2020, eLife, K Sharma et al. (Accepted)
Shank Lab

Sarah Yannarell
Alexi Schoenborn
Hunter Talley
Noam Eckshtain-Levi

Eric Beaudoin
Kasia Dubiel
Vanessa Nepomuceno

Chris Anderton
David Berry
Will Chrisler
Galya Orr

We are recruiting!

Email me at Elizabeth.Shank@umassmed.edu

Collaborators

Bacterial images created with BioRender.com
Questions?