Metabolic interactions in microbial communities

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Metabolic interactions in microbial communities

Elizabeth Shank

Program in Systems Biology
Microbiology and Physiological Systems
Cellular heterogeneity

Bacterial differentiation

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

Coculture antibiotic assay
Coculture promotes antibiotic production

*Microbispora* sp. Monoculture

Coculture

*Microbispora* sp. Monoculture
Coculture to identify cell-cell signals

<table>
<thead>
<tr>
<th>Monoculture</th>
<th>Coculture</th>
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<td>Killing</td>
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<td>Growth</td>
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<tr>
<td>Biofilm</td>
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- 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

Influencer

2017, *mSystems*, Grubbs and Bleich et al.
Cellular heterogeneity
Cellular heterogeneity
Selected 18 genes of interest (physiology and metabolites) 
∴ Built 153 dual-labeled strains

![Diagram with genes and labels]

Microscopy

Flow cytometry

Imaging Mass Spectrometry
Intraspecies signaling

B. cereus
Thiocillin

Interspecies signaling

E. coli
Enterobactin

DAPG

P. protegens

2011, PNAS, EA Shank et al.
2015, PNAS, R Bleich et al.
2015, JBact, M Powers et al.
2017, AEM, G Grandchamp et al.
Transparent Soil

2 mm

IN

OUT

2020, *eLife*, K Sharma et al. (Accepted)
Fungal hyphae

IN

OUT

2 mm

100 μm
Fungus + B. subtilis

Fungal hyphae
We are recruiting!

Email me at Elizabeth.Shank@umassmed.edu