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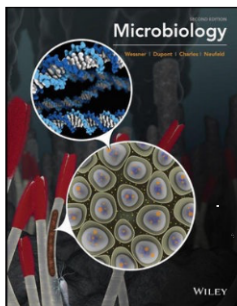
Bioeconomy Research and Innovation Forum
Guelph, Oct 24, 2016

UNIVERSITY OF
WATERLOO



living growing evolving
biology

WATERLOO
SCIENCE



Waterloo facts



Canada's most innovative university by the numbers

Our people

- 1957: University of Waterloo opens with 74 students
- Today: **31,380 undergraduate, 5,290 graduate students**
- 15 per cent international undergraduate, 36 per cent international graduate students
- 1,139 full-time faculty, 322 international faculty
- Degrees granted: **5,778 Bachelors degrees, 1,723 Masters, 303 PhDs** (2014)

WATERLOO'S **UNIQUE ATTRIBUTES**

Entrepreneurship

Entrepreneurship isn't just a thing you do. It's a way you think. That's the difference at Waterloo. We're not simply renting space to local startups and calling it an ecosystem: we're forming alumni and organizations who spearhead disruptive innovation.

Research with impact

Sustaining a research-rich environment is key to opening and optimizing the minds of our learners. Waterloo balances broad-based research intensity with special focus areas in a handful of "frontier disciplines."

Creator-owns intellectual property (IP) policy

You create it, you own it. That's the deal at Waterloo. This incentive has magnetized our campus, helping us attract some of the world's most entrepreneurial researchers and students.

Co-operative education

Experiential learning means relevant skills, financial gains, and professional growth for students and employers. More than that, our highly respected faculty work with a deep pedagogical system that transforms learners into thoughtful, insightful leaders.

Deep connections with business and industry

Waterloo was established by our founders as a platform for talent development, scholarship, and industry partnership. That broad-based connection to our community and to industry remains fundamental to the Waterloo model.

COMBINED, THESE ELEMENTS CREATE HIGHER EDUCATION WITHOUT EQUAL.



CENTRE FOR BIOENGINEERING AND BIOTECHNOLOGY



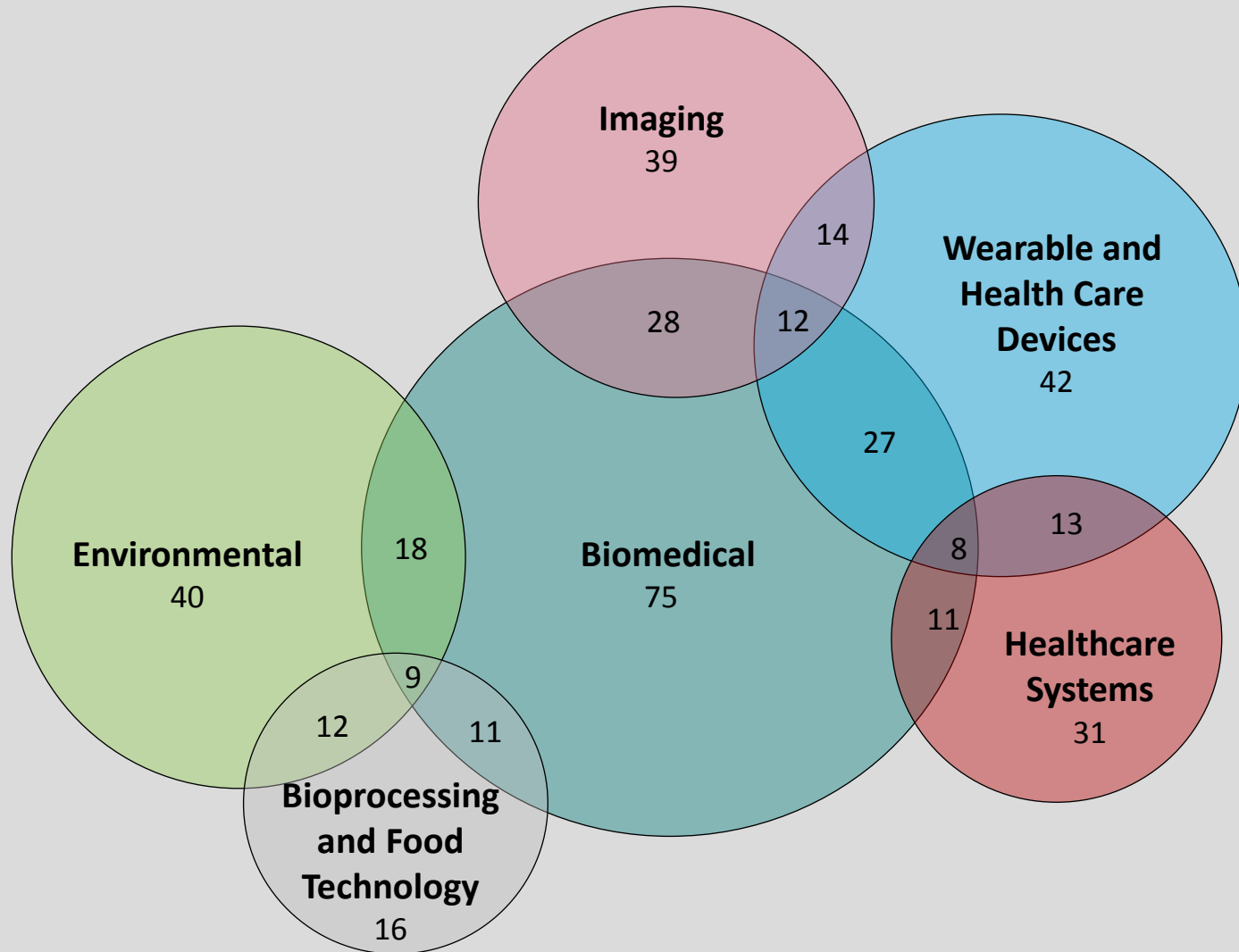
MISSION

CBB's mission is to facilitate strategic multidisciplinary research that applies technology to life sciences, human health, the environment and industrial challenges.

Senate approved: Nov 2011
Renewal: Nov 2016



TRANSDISCIPLINARY RESEARCH



IMPACT: THE FIRST 4 YEARS AT A GLANCE

- Faculty membership: 86 to 150
- Attract new research funding (CBB records)
 - » 75 proposals submitted, 32% funded
- 18 seminars, 5 distinguished lectures, 4 workshops, 3 academic-industry networking forums, 2 conferences, 2 AGM
- 82% of CBB members engaged in CBB's overall activities
 - » 162 company connections
 - » 58 external industry, and 63 internal academic networking activities
 - » 62 external industry, and 106 internal requests for CBB assistance



WATERLOO CENTRE FOR MICROBIAL RESEARCH (PROPOSED)

- >40 investigators from five faculties
- Promotion of interdisciplinary microbial research
- Application areas
 - » Health
 - » Agriculture
 - » Food
 - » Natural Resources
 - » Environment
 - » Synthetic Biology
- Planned Waterloo MicroBiome Innovation Facility



Metagenomics and Enzyme Function Research Program

Trevor Charles

Construction and screening of metagenomic libraries for gene discovery and genome engineering for bioplastics production

Chris Backhouse

Design and construction of lab-on-chip and microfluidic devices for in vivo and in vitro screening of metagenomic libraries

Andrew Doxey

Development of computational methods for comparative genomics and application to enzyme discovery

Moira Glerum

Metagenomic library construction geared towards eukaryal organisms, using microfluidics and lab-on-a-chip technologies for screening in yeast

Todd Holyoak

Biochemical analysis of novel enzymes, with focus on structure, mechanism, inhibition and allostery

Laura Hug

Methods for accessing genomes of uncultivated clades, diversity & function of microbial communities in contaminated sites

Kesen Ma

Application of functional metagenomics to extreme environments, with focus on thermostable dehydrogenases and alcohol metabolism

Brendan McConkey

Development and implementation of metaproteomics methods, and prediction of enzyme function from metagenomic sequence

Kirsten Müller

Application of functional metagenomics methods to algal organisms and studies of algal microbiome

Josh Neufeld

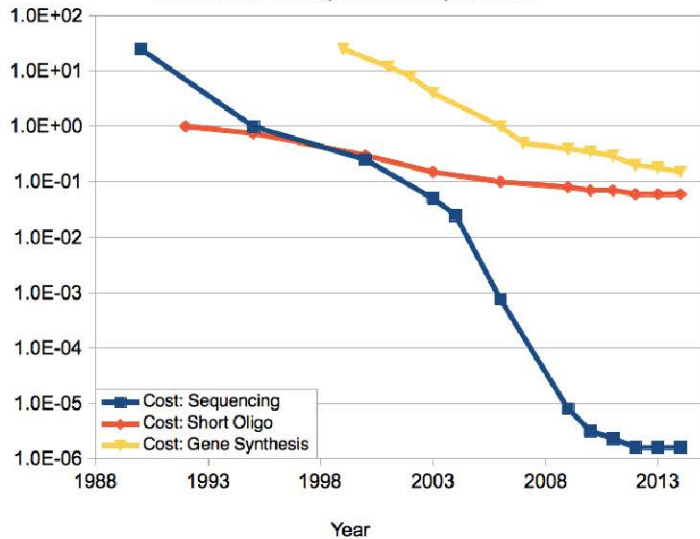
The development and implementation of methods for enriching members of the rare biosphere in metagenomic libraries

David Rose

Experimental structure determination of new protein families identified by functional metagenomic screening, with emphasis on glycosidases

Price Per Base of DNA Sequencing and Synthesis

Rob Carlson, February 2014, www.synthesis.cc



Synthetic Biology and iGEM

259 teams from
around the world,
2,700 participants



Simple
sgRNA
Exchange

Cas9 PAM
Flexibility

CRISPR
Plant
Defense

Re-engineering CRISPR-Cas9 with functional applications in eukaryotic systems

CRISPR-Cas9 is an exciting tool for synthetic biologists because it can target and edit genomes with unprecedented specificity. Our team is attempting to re-engineer CRISPR to make it more flexible and easier to use.

Microbiome Computational and Functional Analysis

Petrenko et al. *BMC Biology* (2015) 13:92
DOI 10.1186/s12915-015-0195-4



SOFTWARE

Open Access

MetAnnotate: function-specific taxonomic profiling and comparison of metagenomes



Pavel Petrenko, Briallen Lobb, Daniel A. Kurtz, Josh D. Neufeld and Andrew C. Doxey*

OPEN

The ISME Journal (2015) 9, 461–471
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www.nature.com/ismej



ORIGINAL ARTICLE

Aquatic metagenomes implicate *Thaumarchaeota* in global cobalamin production

Andrew C Doxey, Daniel A Kurtz, Michael DJ Lynch, Laura A Sauder and Josh D Neufeld
Department of Biology, University of Waterloo, Waterloo, Ontario, Canada

Nature Reviews Microbiology | AOP, published online 2 March 2015; doi:10.1038/nrmicro3400

REVIEWS

Lam and Charles *Microbiome* (2015) 3:22
DOI 10.1186/s40168-015-0086-5



Microbiome

RESEARCH

Open Access

Strong spurious transcription likely contributes to DNA insert bias in typical metagenomic clone libraries



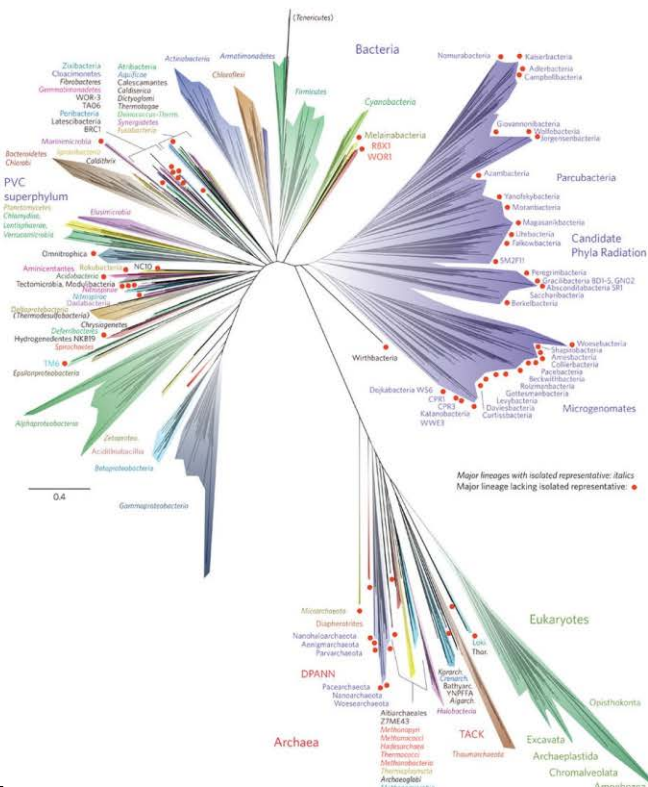
Kathy N. Lam and Trevor C. Charles*

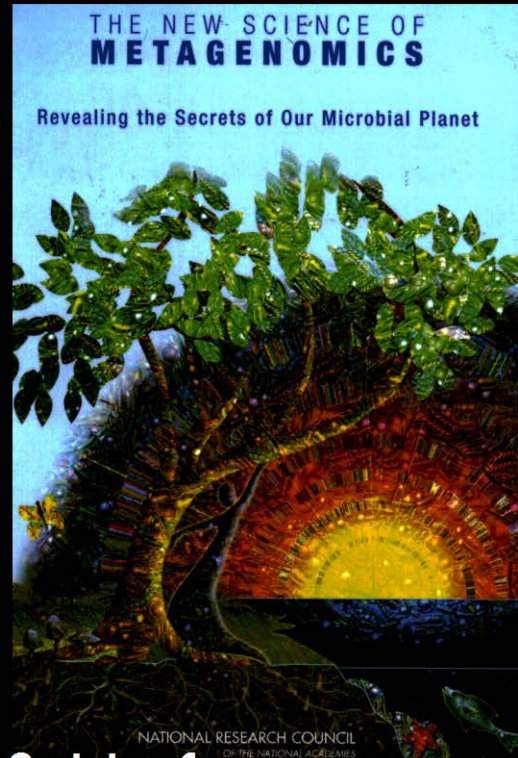
Ecology and exploration of the rare biosphere

Michael D. J. Lynch and Josh D. Neufeld

A new view of the tree of life

Laura A. Hug^{1†}, Brett J. Baker², Karthik Anantharaman¹, Christopher T. Brown³, Alexander J. Probst¹, Cindy J. Castelle¹, Cristina N. Butterfield¹, Alex W. Hernsdorf³, Yuki Amano⁴, Kotaro Ise⁴, Yohey Suzuki⁵, Natasha Dudek⁶, David A. Relman^{7,8}, Kari M. Finstad⁹, Ronald Amundson⁹, Brian C. Thomas¹ and Jillian F. Banfield^{1,9★}





“The emerging field of metagenomics presents the greatest opportunity - perhaps since the invention of the microscope - to revolutionize understanding of the living world.”

National Academies Committee on Metagenomics March 2007



Canadian MetaMicroBiome Library

[Background](#) [Publications](#) [Researchers](#) [Samples](#) [Contact](#)

Microbial communities harbor immense genetic diversity with enormous promise for applications in bioproduct synthesis and green chemistry. Metagenomic libraries provide a window into this largely untapped reservoir of nucleic acid diversity. Individual libraries have been generated from a variety of terrestrial and aquatic environments but access to this reservoir is limited because the metagenomic libraries are typically project-specific and maintained in isolation. In an effort to enable the sharing of genetic material from environmental samples for the benefit of the scientific community, we are establishing the Canadian MetaMicroBiome Library (CM²BL).

The CM²BL is a publicly accessible collection of libraries of environmental DNA initiated with soil samples collected from across Canada spanning multiple biomes and ecozones. The CM²BL will be characterized by DNA sequencing techniques and screens for industrially relevant enzymes to determine the taxonomic, genetic, and metabolic diversity of each sample. Phenotypic screening of metagenomic libraries provides access to truly novel functions that would otherwise be missed by sequence-based surveys of bulk community DNA or metagenomic libraries.



“Open Resource Metagenomics”
Jointly managed with Josh Neufeld
Metagenomic libraries are freely available
<http://cm2bl.org>





Arctic Tundra, Daring Lake (NT)



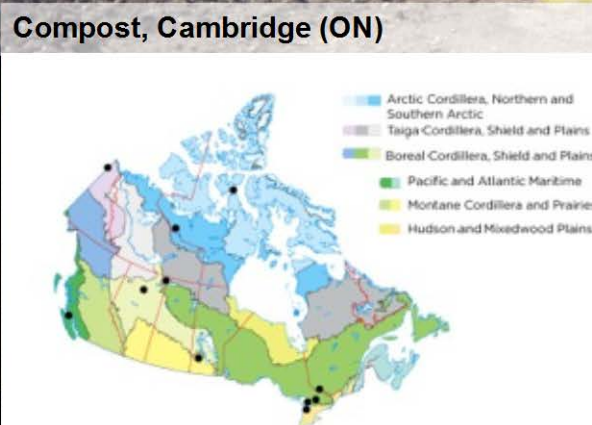
Compost, Cambridge (ON)



Swamp, Mt. St. Hilaire (QC)



Agricultural soil (soybean), Elmira (ON)



Northern peatlands, Old Crow (YT)



Tar Sand, Athabasca river (AB)



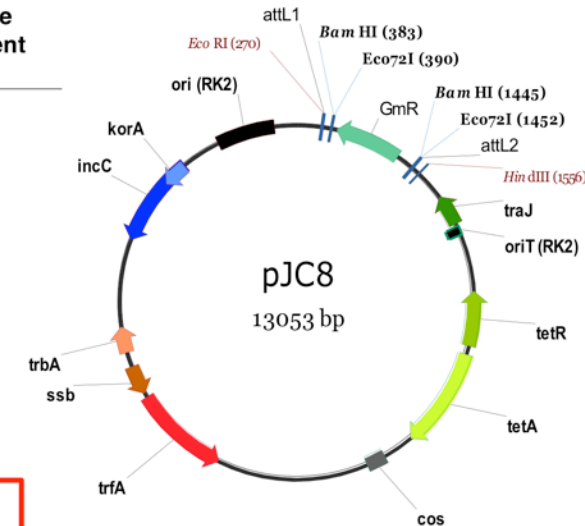
Boreal coniferous forest (AB)

CM²BL Metagenomic Libraries in pJC8 IncP cosmid vector



J. Cheng

| DNA source (Library ID) | Bulk Density (g/cm ³) | Total Carbon (% dry) | Total Nitrogen (% dry) | pH | Number of clones | Average insert (kb) | Microbial genome equivalent |
|--|-----------------------------------|----------------------|------------------------|-----|------------------|---------------------|-----------------------------|
| Arctic Tundra (1AT-A) | 0.21 | 46.9 | 1.42 | 3.9 | 178,100 | 27.1 | 1,026 |
| Arctic Tundra (2ATN-A) | 1.05 | 3.74 | 0.25 | 6.7 | 62,260 | 31.1 | 412 |
| Oil sand 1 (4TS-A) | 1.23 | 2.11 | 0.11 | 7.6 | 73,000 | 37.4 | 581 |
| Boreal coniferous forest (5BF-A) | 1.16 | 1.14 | 0.08 | 4.6 | 56,370 | 29.7 | 356 |
| Temperate deciduous forest (6TD-A) | 1.10 | 3.56 | 0.26 | 6.4 | 2,306,580 | 40.2 | 19,728 |
| Temperate rainforest (7TR-A) | 0.62 | 10.80 | 0.35 | 4.9 | 68,200 | 33.7 | 469 |
| Wetland soil (9WLM-A) | 0.26 | 43.30 | 1.22 | 5.5 | 64,470 | 19.7 | 270 |
| Soybean field (10AS-A) | 1.10 | 2.44 | 0.22 | 7.6 | 760,000 | 37.5 | 6,064 |
| Wheat field (11AW-A) | 1.10 | 1.85 | 0.19 | 7.4 | 8,806,400 | 41.2 | 77,196 |
| Corn field (12AC-A) | 1.67 | ND | ND | 7.8 | 79,060 | 33.4 | 561 |
| Compost (13CO-A) | 0.86 | 11.70 | 0.92 | 8.0 | 42,000 | 34.2 | 305 |
| Oil sand 2 (19TS-A) | 1.12 | 2.76 | 0.07 | 6.0 | 149,880 | 33.8 | 1,078 |
| Community garden (20CG-A) | 0.87 | 10.0 | 0.63 | 7.6 | 118,300 | 36.9 | 929 |
| ¹³ C-cellulose pooled soils (SIP-A) | N/A | N/A | N/A | N/A | 83,000 | 31.2 | 550 |
| Human gut (CLGM-A) | N/A | N/A | N/A | N/A | 42,000 | 28.1 | 250 |

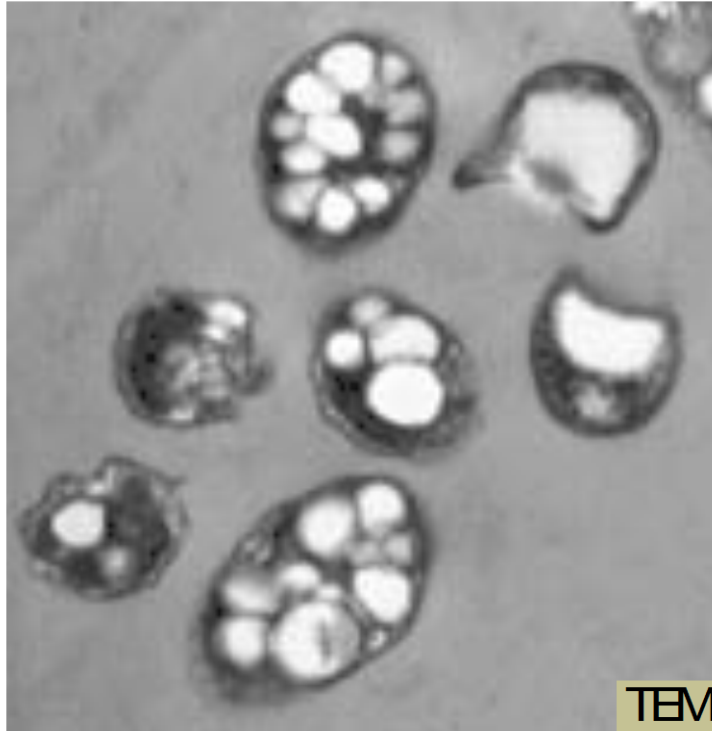


Key Features of pJC8 cosmid:

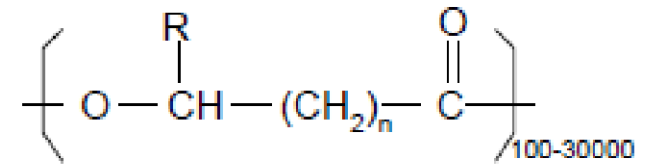
- IncP, supporting replication in Proteobacteria
- oriT for triparental conjugation
- Blunt-end cloning site
- Tc^r for selection
- Gateway® entry att sites flanking insert

Collection of high quality metagenomic libraries suitable for screening

Polyhydroxyalkanoate Bioplastics



Courtesy Gabriela Meglei



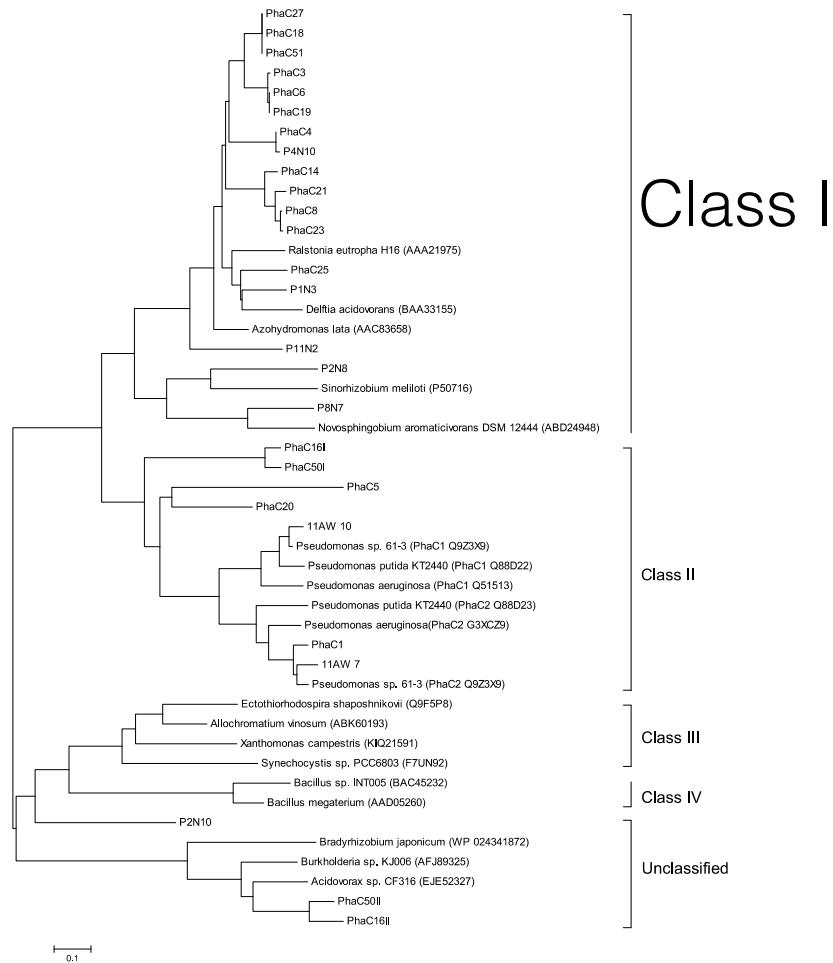
Polyesters, >150 different monomers

Wide range of properties

Thermoplastic and elastomeric

short chain length (scl) 3-5 C

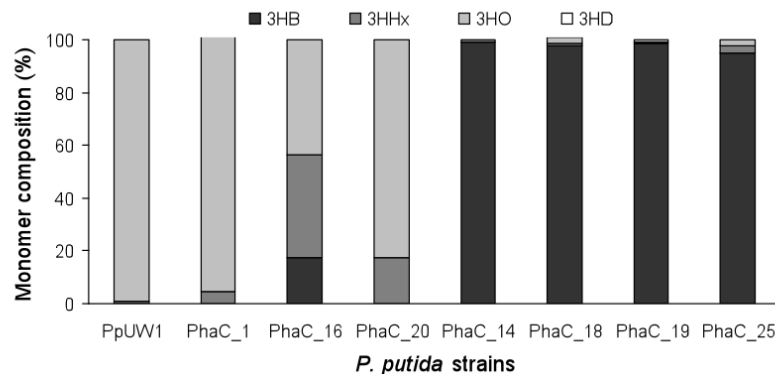
medium chain length (mcl) 6-14 C



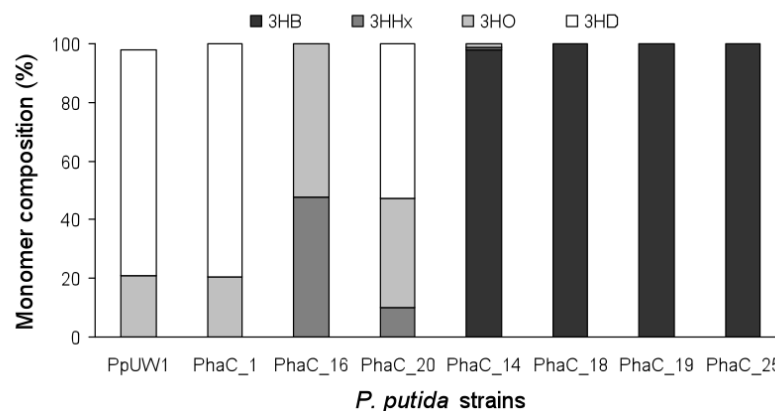
gnment using MEGA6

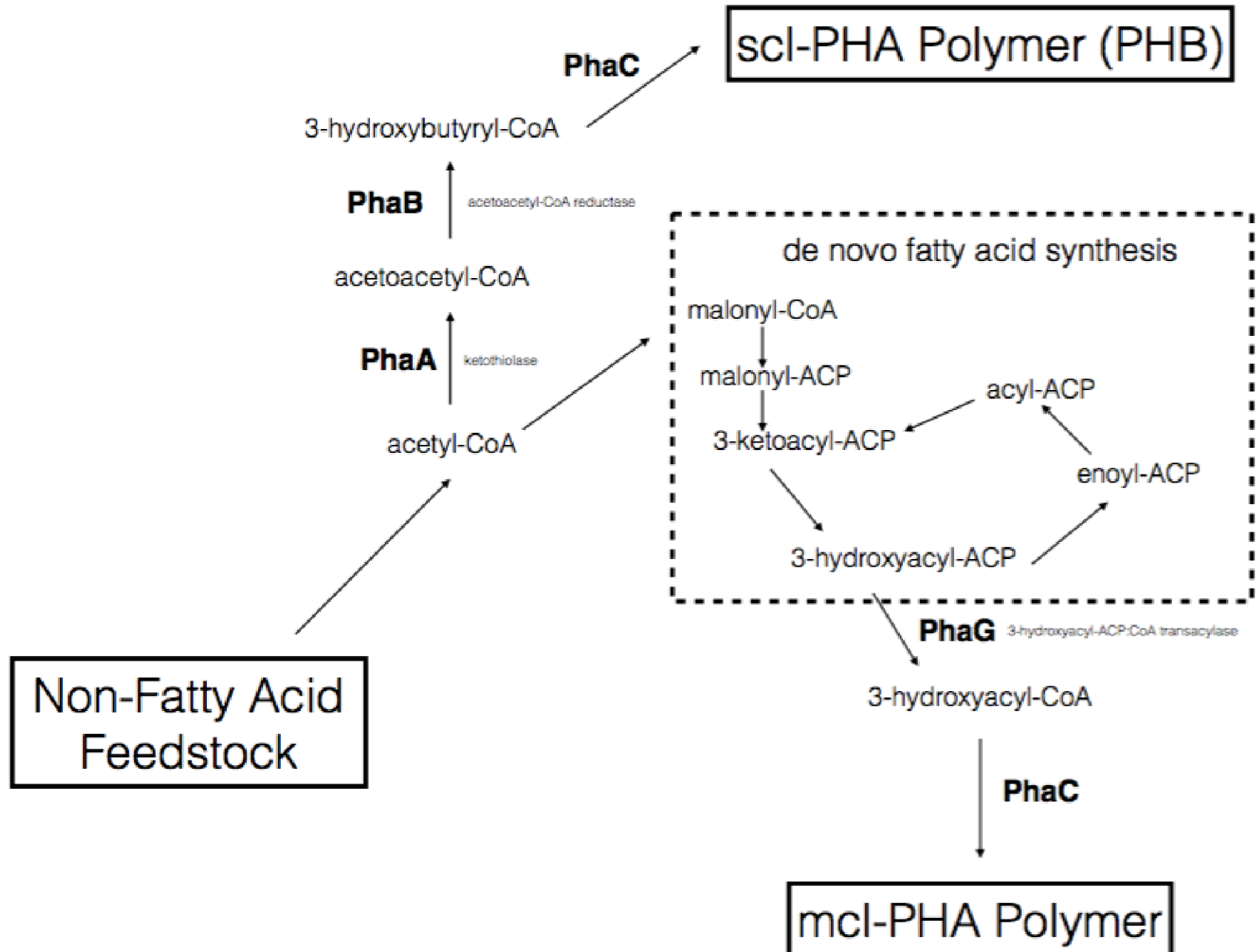
Composition of PHA in *Pseudomonas putida* containing metagenomic clones

A. Na octanoate

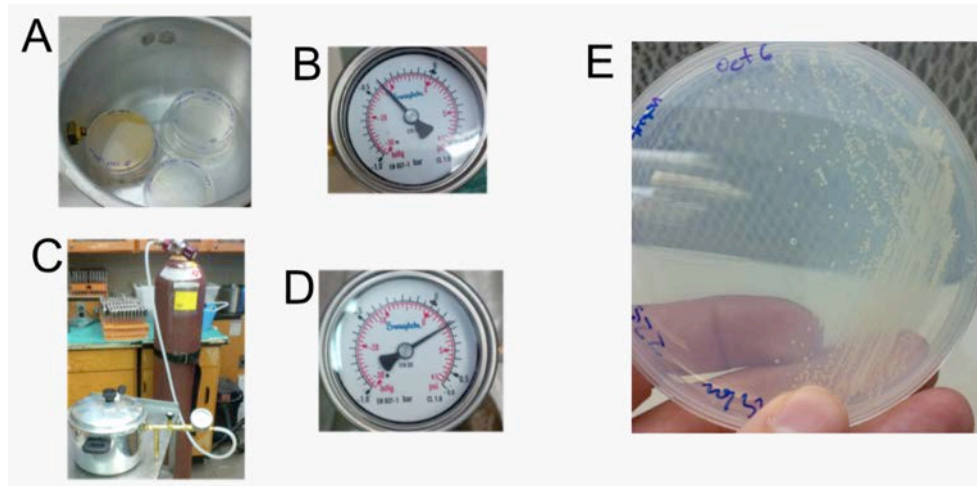


B. Gluconic acid





METHANE TO BIOPRODUCTS



See poster: Heil, Matysiakiewicz, Charles

Goal: Genome engineering to achieve mcl-PHA production in *Methylosinus trichosporium*, a methane utilizing member of the Rhizobiales

METAGENOM BIO INC.

- University of Waterloo spinoff, founded April 2014
- Focus is microbiome analysis by high throughput DNA sequencing (mining, agriculture)
- Identified greenhouse and other closed loop hydroponic systems as **new market space** with tremendous potential
- Developing *Metagenom-1*, an enhanced bioinformatics framework for microbiome analysis

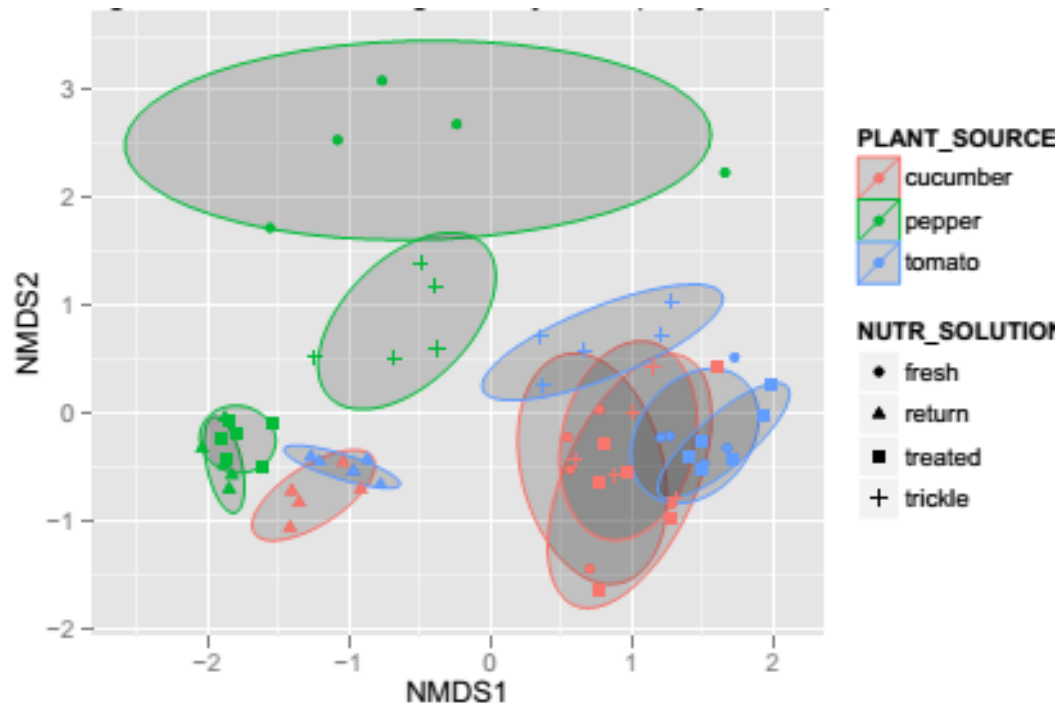


Vegetable Greenhouse Microbiome

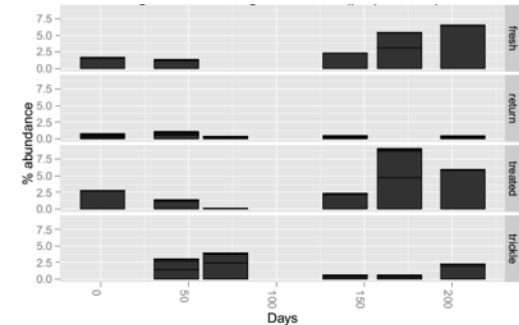


BIOINFORMATIC ANALYSIS OF GREENHOUSE FERTIGATION SYSTEM MICROBIOME

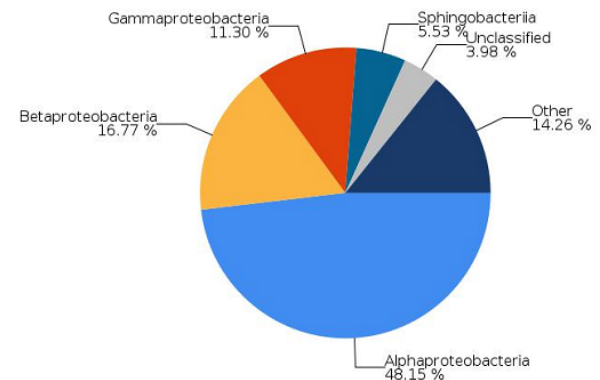
Distinct microbial communities throughout fertigation system



Detection of a specific bacteria



Phylogenetic constraint of greenhouse microbiome



Cucumber Return Nutrient Sample

You're invited to the 67th ANNUAL CSM MEETING

June 20-23, 2017
Waterloo, Ontario

@CSM2017 #CSMWATERLOO2017



UNIVERSITY OF
WATERLOO





PolyFerm Canada



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RESEARCH & INNOVATION CENTRE



**NSERC
CRSNG**

MEDRELEAF
THE MEDICAL GRADE STANDARD™



Ontario

Ministry of Agriculture,
Food and Rural Affairs



CIHR IRSC
Canadian Institutes of
Health Research
Instituts de recherche
en santé du Canada