

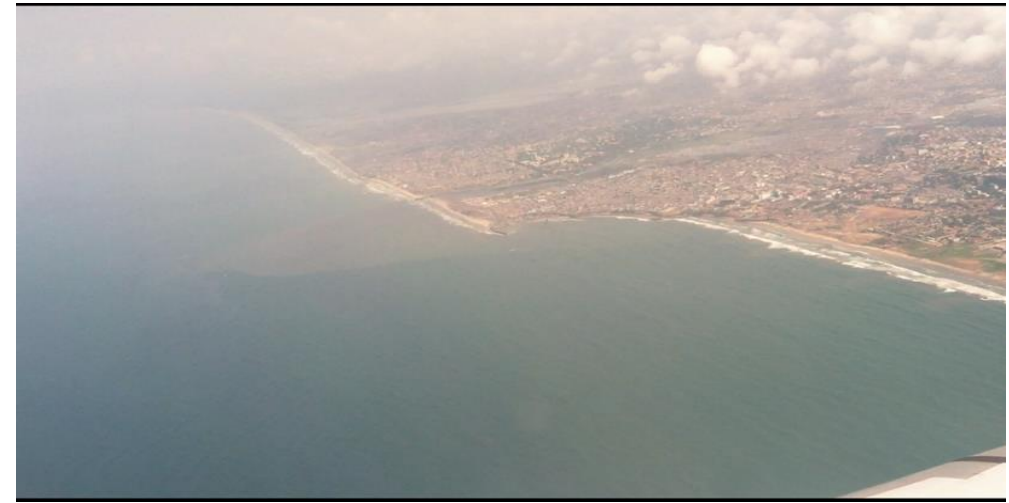
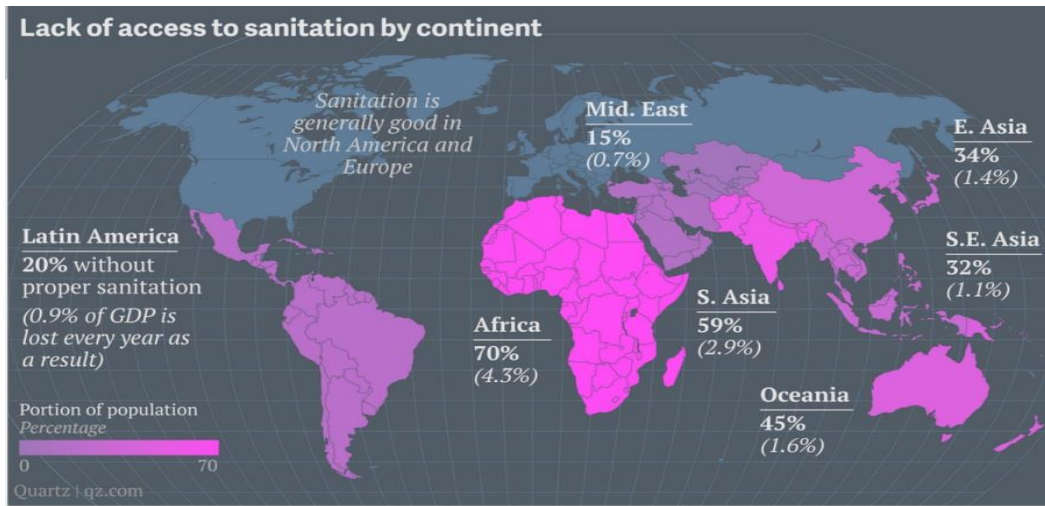


Fecal Sludge Biorefineries based on a Volatile Fatty Acid Platform

Kartik Chandran
Columbia University

FSM4, Chennai
February 20th, 2017





Lack of adequate sanitation is a global challenge



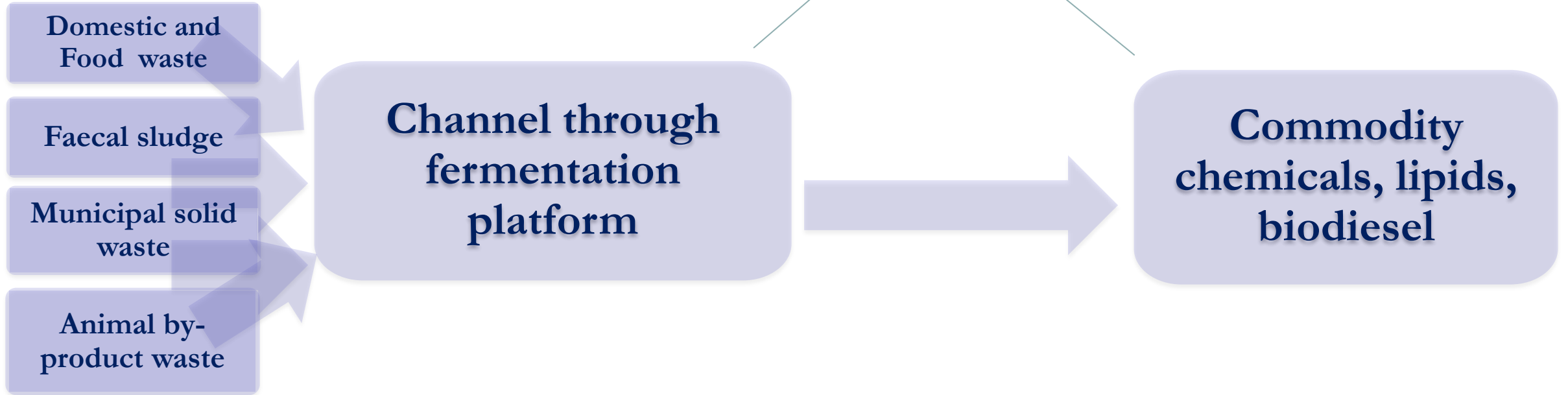
Often limited by access to reliable energy inputs and chemicals

	Energy consumed annually (tera tons oe)	Energy consumed annually for water (assuming 3%, tera tons oe)
USA	2.4	0.07
Ghana	0.01	?

Is it possible to link sanitation with higher value chain biofuels and commodity chemicals?



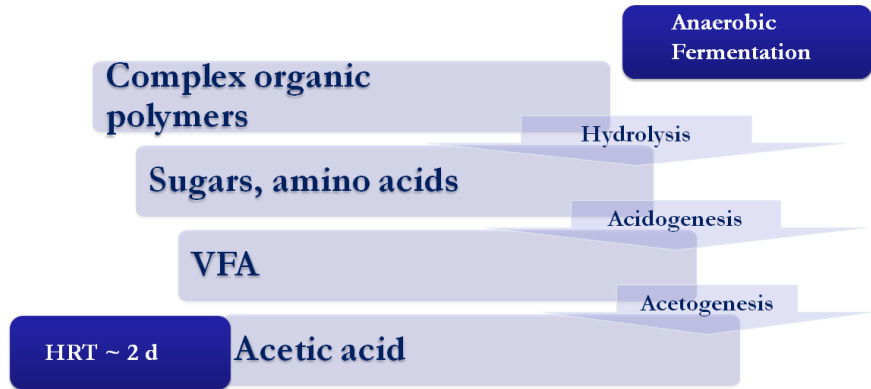
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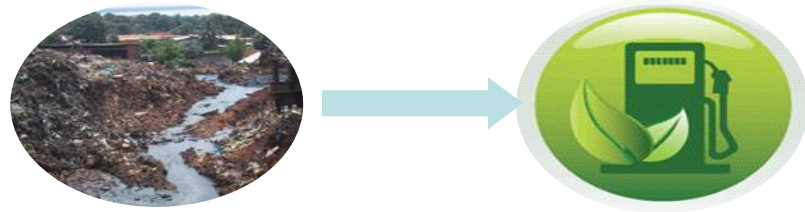
BILL & MELINDA
GATES *foundation*



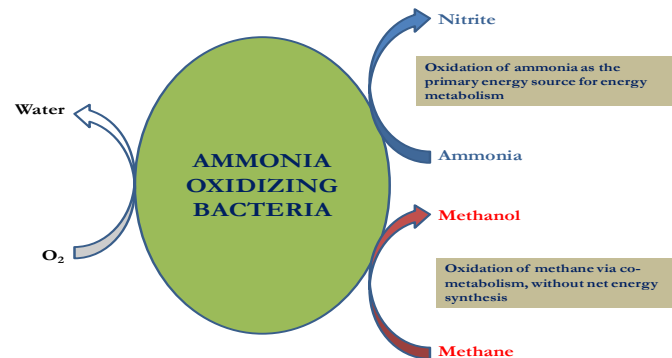
This presentation focuses on



Foundation for resource recovery through anaerobic C-conversions



Options for carbon recovery to fuels and chemicals



Resource efficient options for wastewater treatment and sanitation



**Anaerobic
Digestion**

**Complex organic
polymers**

Hydrolysis

Sugars, amino acids

Acidogenesis

VFA

Acetogenesis

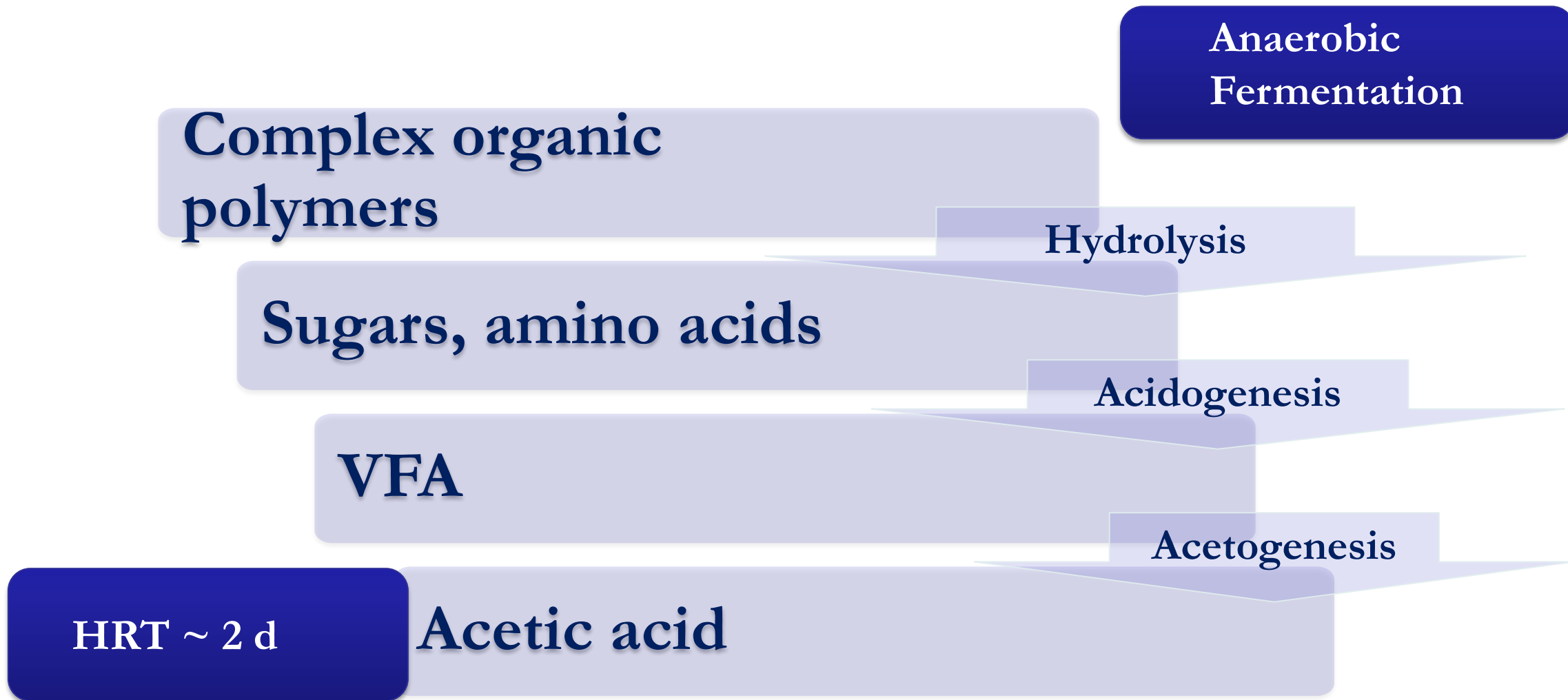
Acetic acid

Methanogenesis

Methane

HRT > 10 d

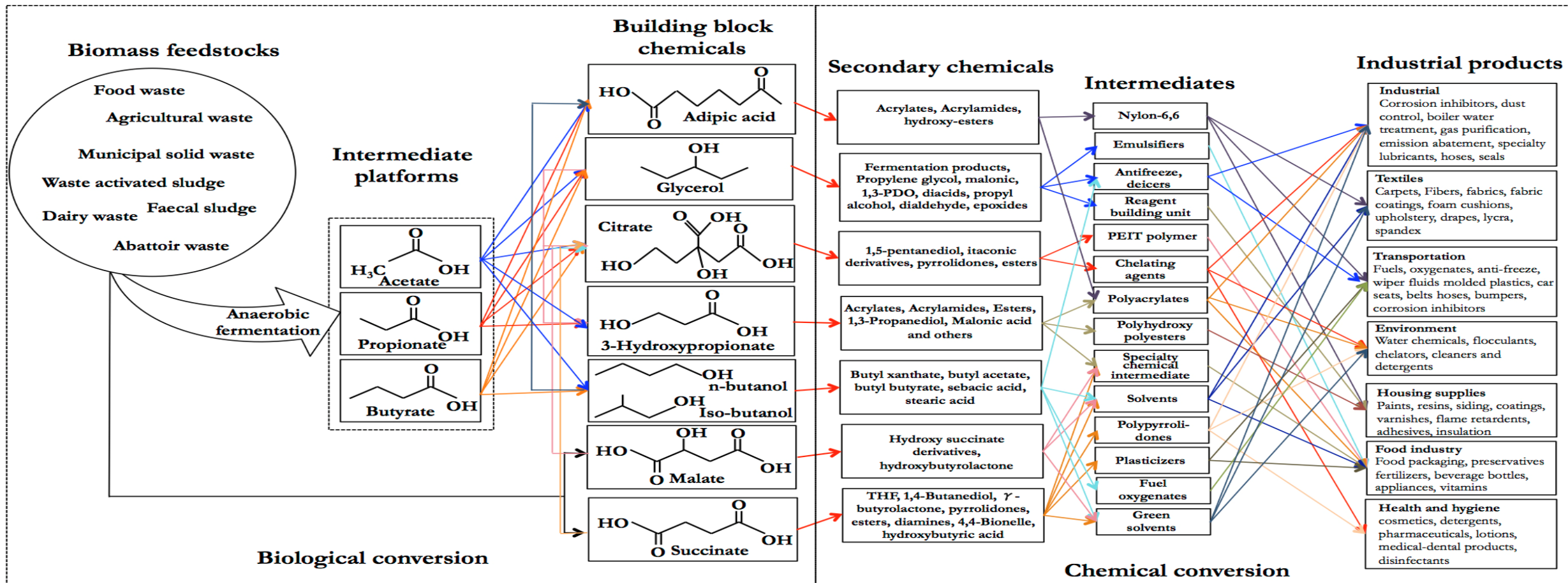




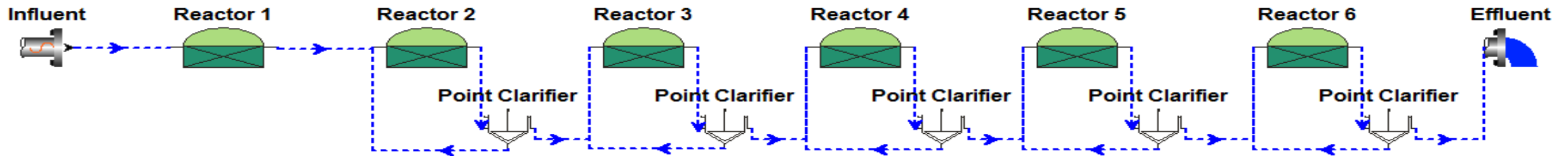
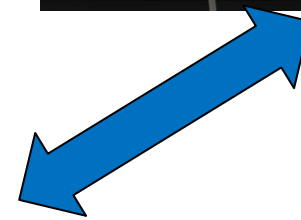
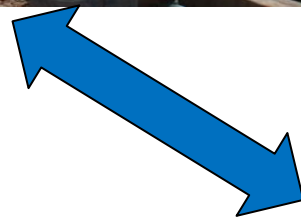
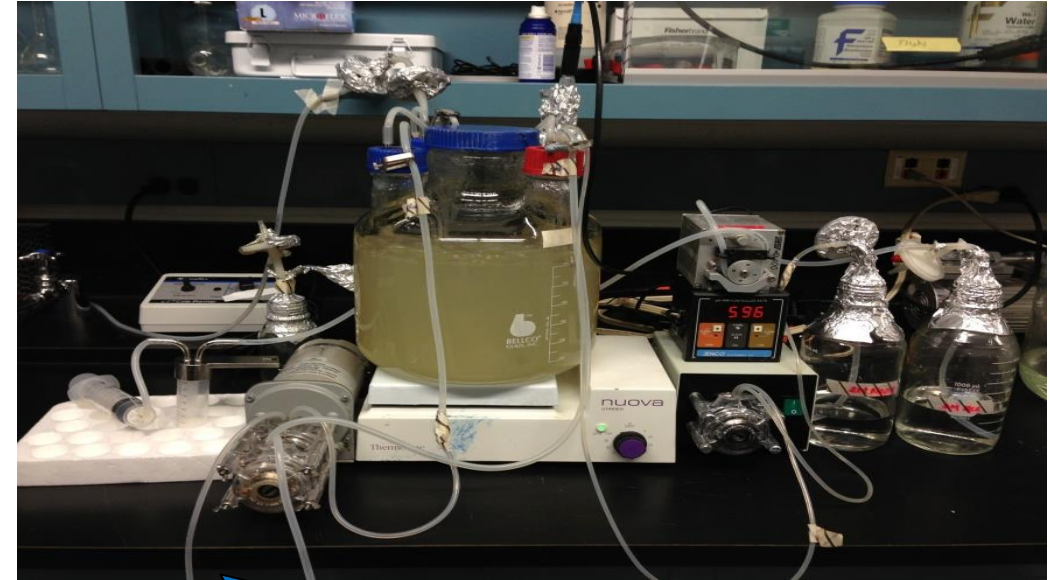
- Fermentation is more advantageous than just anaerobic digestion
- Fermentation can be incorporated into existing digestion processes



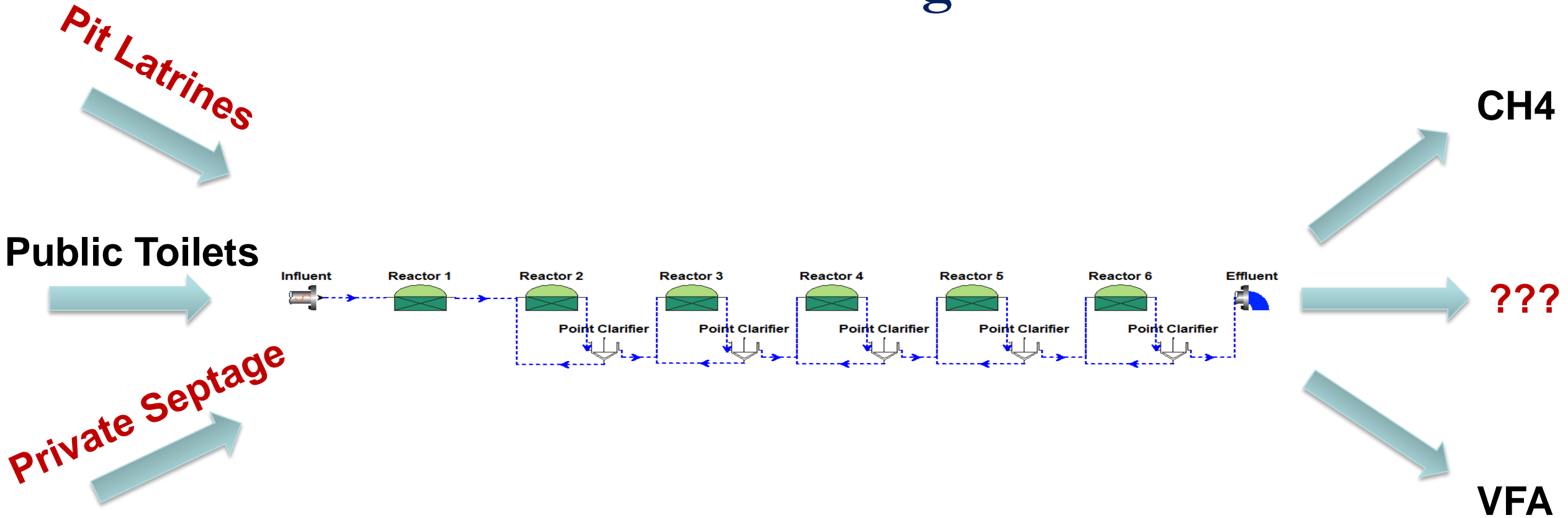
Fermentation as a platform for resource recovery



Overall Approach - Faecal Sludge to Chemical Products and Biodiesel



FS Fermentation and Digestion Model

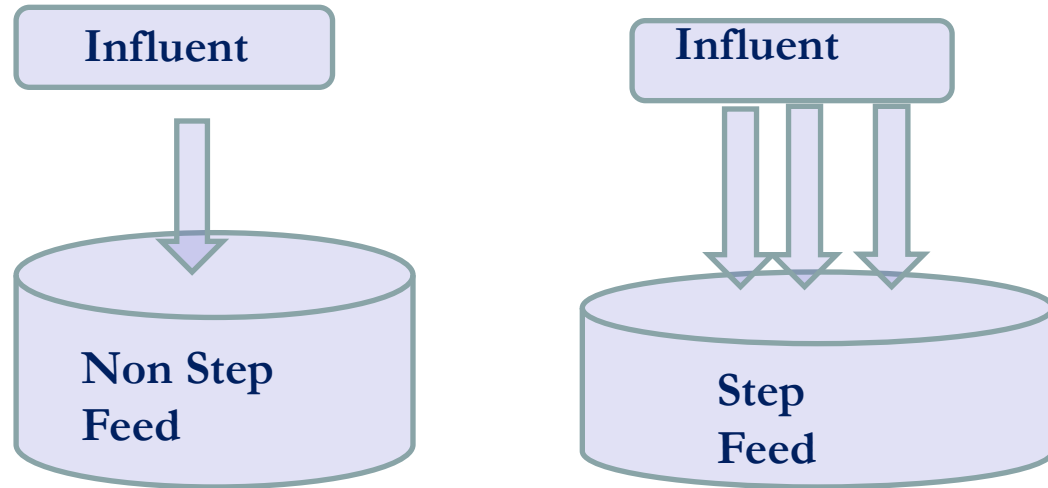


This model can be extended (and modified) for other fecal sludge processing operations



Microbial pathways involved in VFA production

1. Continuous lab-scale systems fed with food waste
2. Impact of reactor configuration on process and microbiology



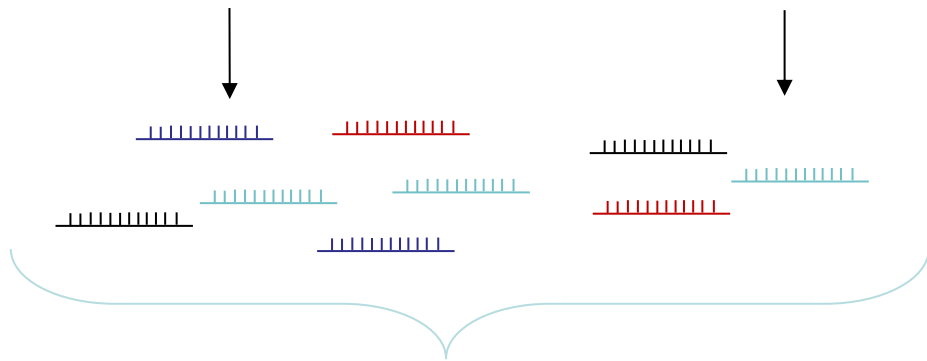
Near identical performance (VFA yield, speciation obtained from both syste designs



Library Preparation/Sequencing

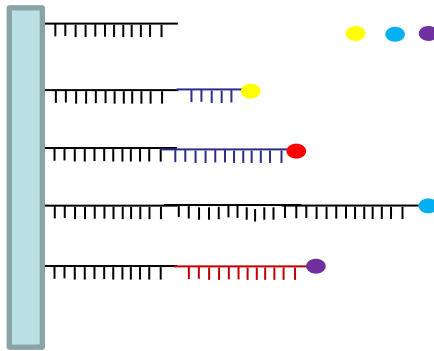


Mixed microbial community DNA

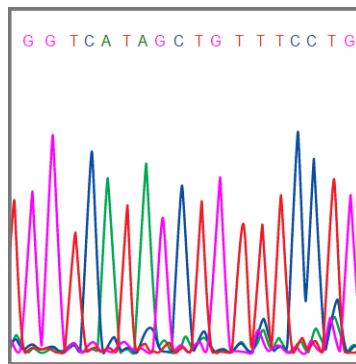


Oligos

A T C G



Illumina® Flow Cell



Bioinformatics

```
ATGCTGAANTGCGATCTATGCTGNATGC
GTCANGTGACGGGTGACGTAGNCCGTAATGCA
ATNCAGTCGTAGACTAGCNTAGCCGTTTTACGATC
```

Raw sequences

```
GTCANGTGACGGGTGACGTAGNCCGTAATGCA
ATNCAGTCGTAGACTAGCNTAGCCGTTTTACGATC
```

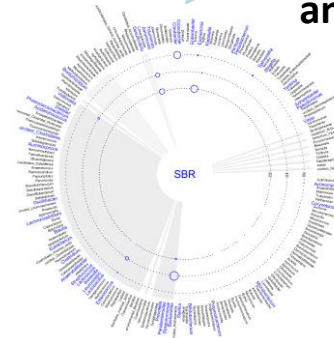
Trimming/Quality Control
(by size, # ambiguous bases, homopolymeric regions)

```
GTCANGTGACGGGTGA
CAGTCCACATGCCACTACGTACGTATGCATG
```

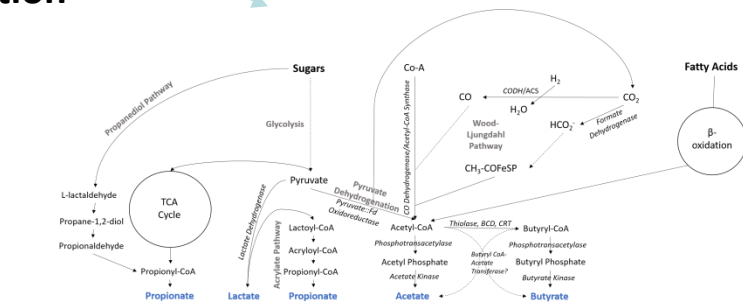
Alignment to Reference Database
(Protein Coding Sequences)

Note: Coding regions of in-house annotated anammox species and recently published anammox and comammox species were manually appended to NCBI non-redundant (nr) protein database (ver. 123)

Data Processing and Visualization



Community Structure: Which organisms are contributing to the reactor's potential protein products?



Functional Potential: Which potential functional pathways is each sample capable of producing, and which organisms are likely to produce these proteins?



Notwithstanding identical process performance, microbial populations entirely different

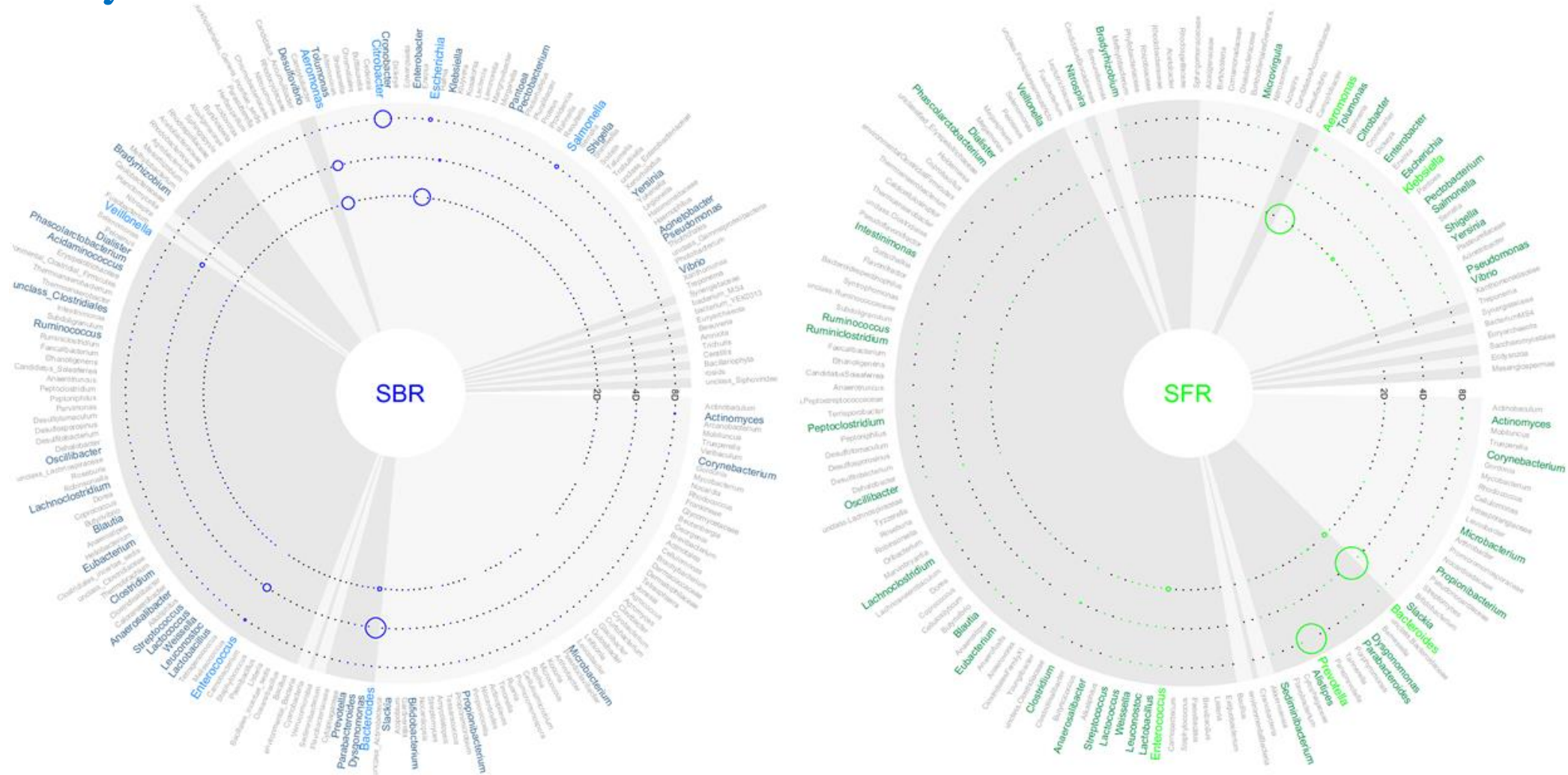
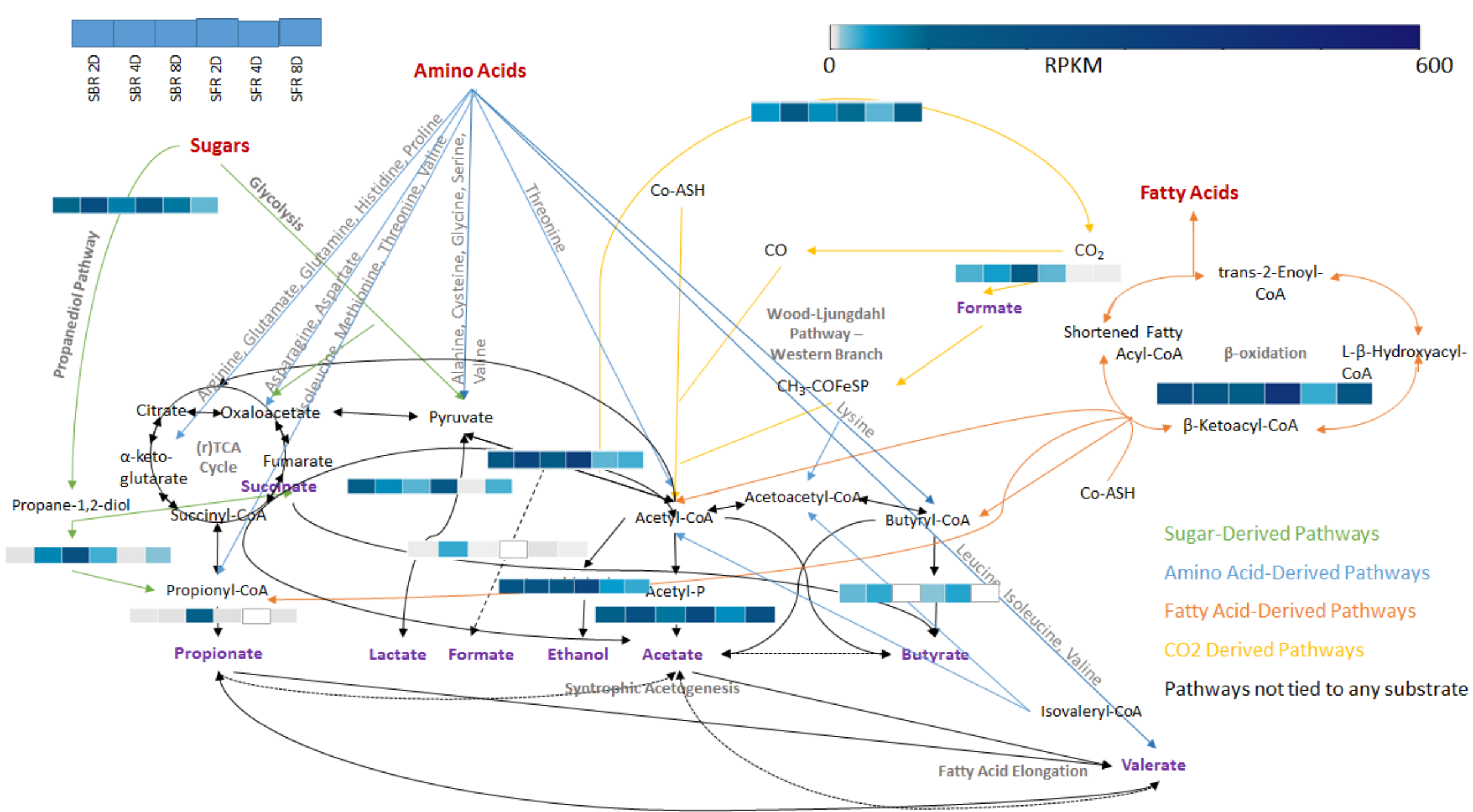


Figure 1. Comparison of microbial community profiles in both SBR and SFR at 8d, 4d, and 2d HRT; genera included have been assigned ≥ 50 reads per million (RPM) for at least one HRT; dark blue or green color indicates assignment of $\geq 1,000$ RPM; light blue or green color indicates assignment of $\geq 50,000$ RPM; dot size scaled to RPM values; shading reflects phylum-level relationships



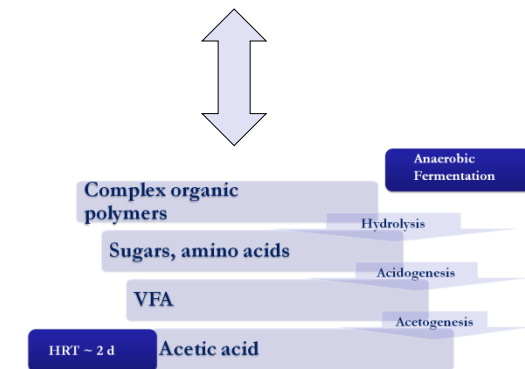
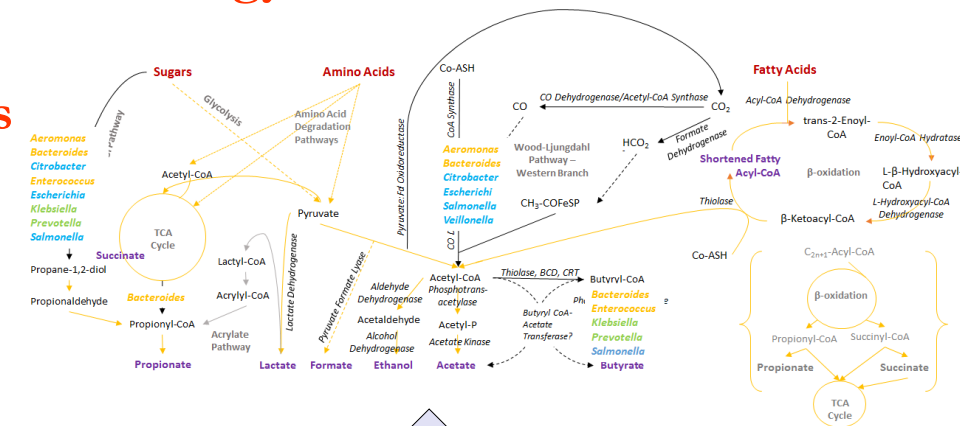


Significance

- As we attempt to move away from ‘digestion’ or ‘fermentation’ towards carbon recovery and biorefining, we need more structured information
- It becomes beneficial to link
 - Process configurations and operating conditions with microbial ecology, metabolic function
 - and in turn with product yield and speciation

– Feedstocks (can import or mine added ones) with products

- Not needed for every case
 - Synthesized approaches needed to enhance translation



Conversion of VFA to Lipids

- Different COD sources

- VFA from food waste fermentation
- Synthetic VFA
- Glucose

- Different initial VFA concentrations

6:1:3 acetate,
propionate,
butyrate. 2 day
HRT

- Different initial N concentrations

- Excess N: COD:N = 5:1
- Limiting N: COD:N = 25:1, 50:1, 125:1, 250:1
- Stoichiometric COD:N supply = 33:1

Lipid content
of *C. albidus*



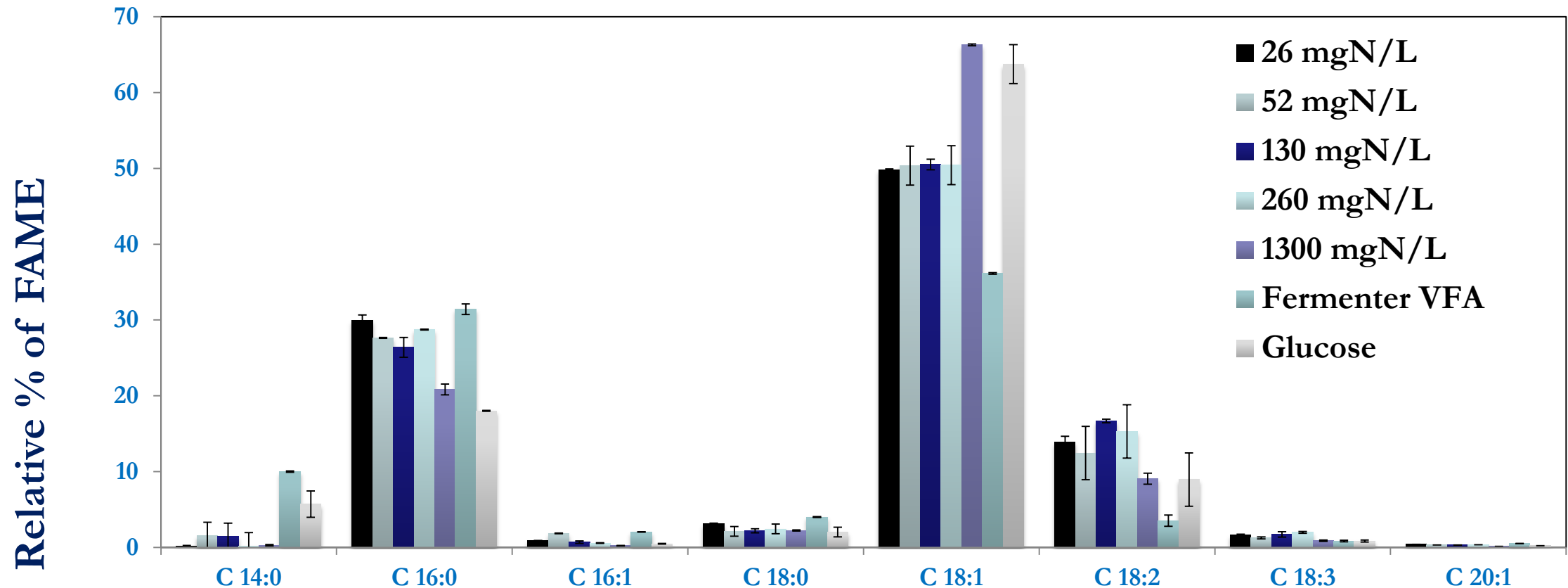
Batch reactor



Chemostat



Lipid Composition



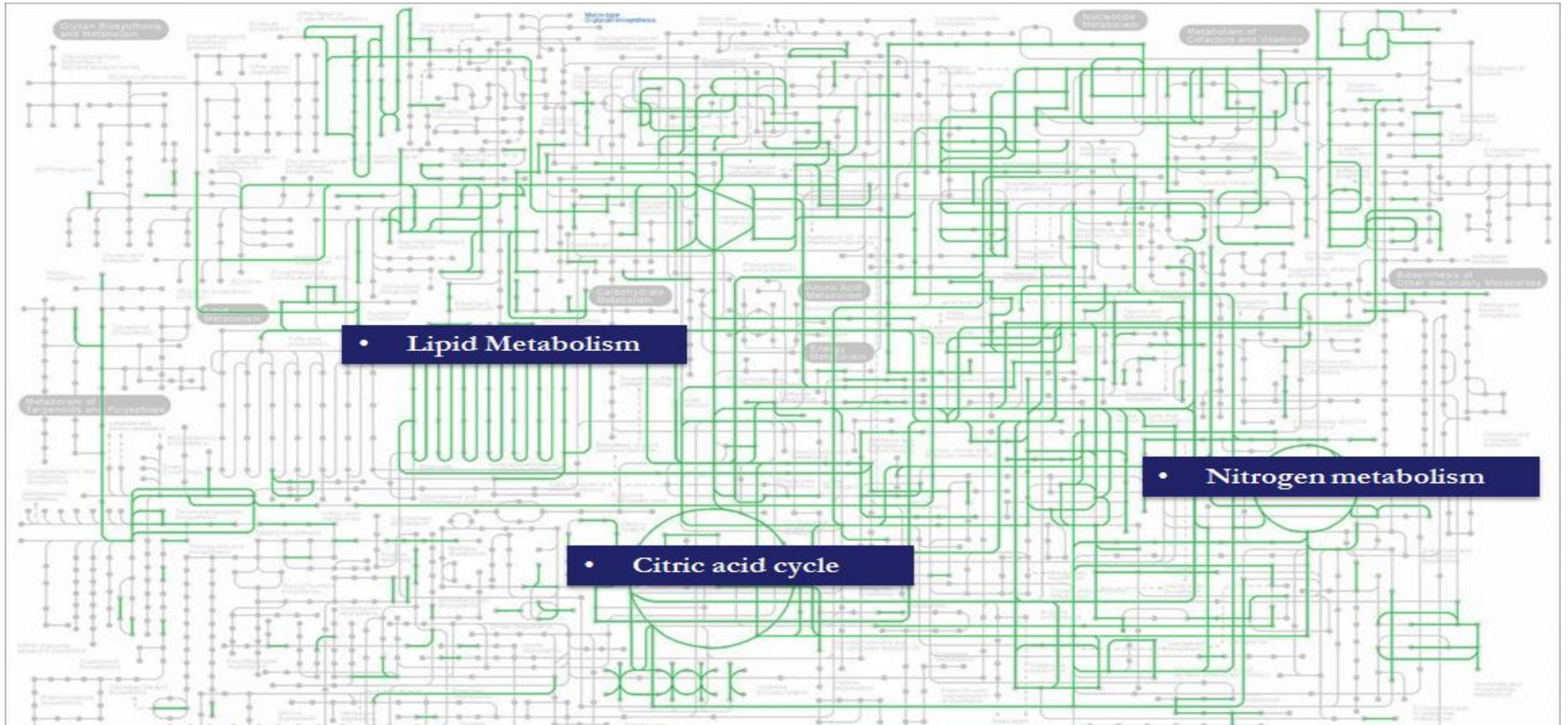
Major fatty acids accumulated are palmitic (C16:0), oleic (C18:1), and linoleic acid (C18:2)

Similar to soybean oil and jatropha oil, which are used as feedstock for biodiesel production in the US and the EU

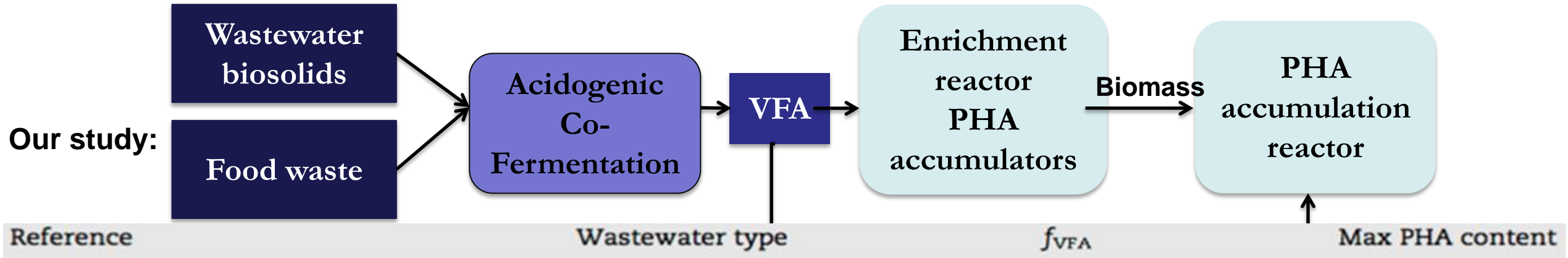


What else can *C. albicans* accumulate (or do)?

Under what conditions?

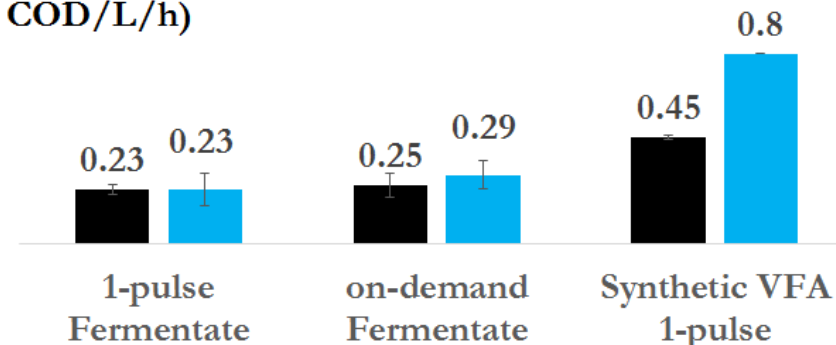


Conversion of VFA to Bioplastics

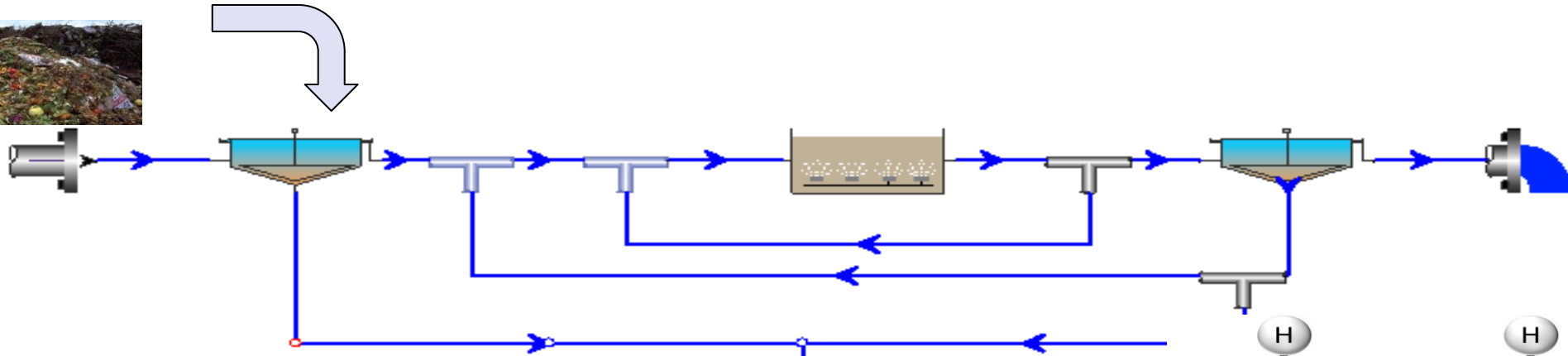


PHA accumulation (gPHA/gVSS)

Rate of sCOD consumption (g-COD/L/h)



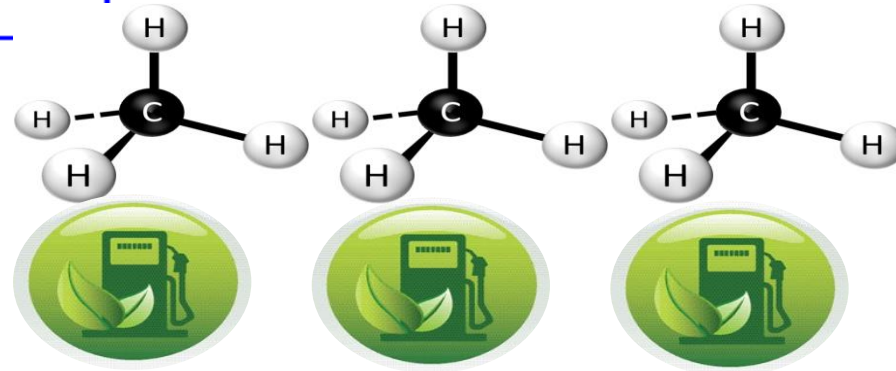
Water Quality-Energy Implications



- Another version of carbon refining

- Separation of N-P and C
- Converting the carbon to the appropriate form for meeting WQ objectives

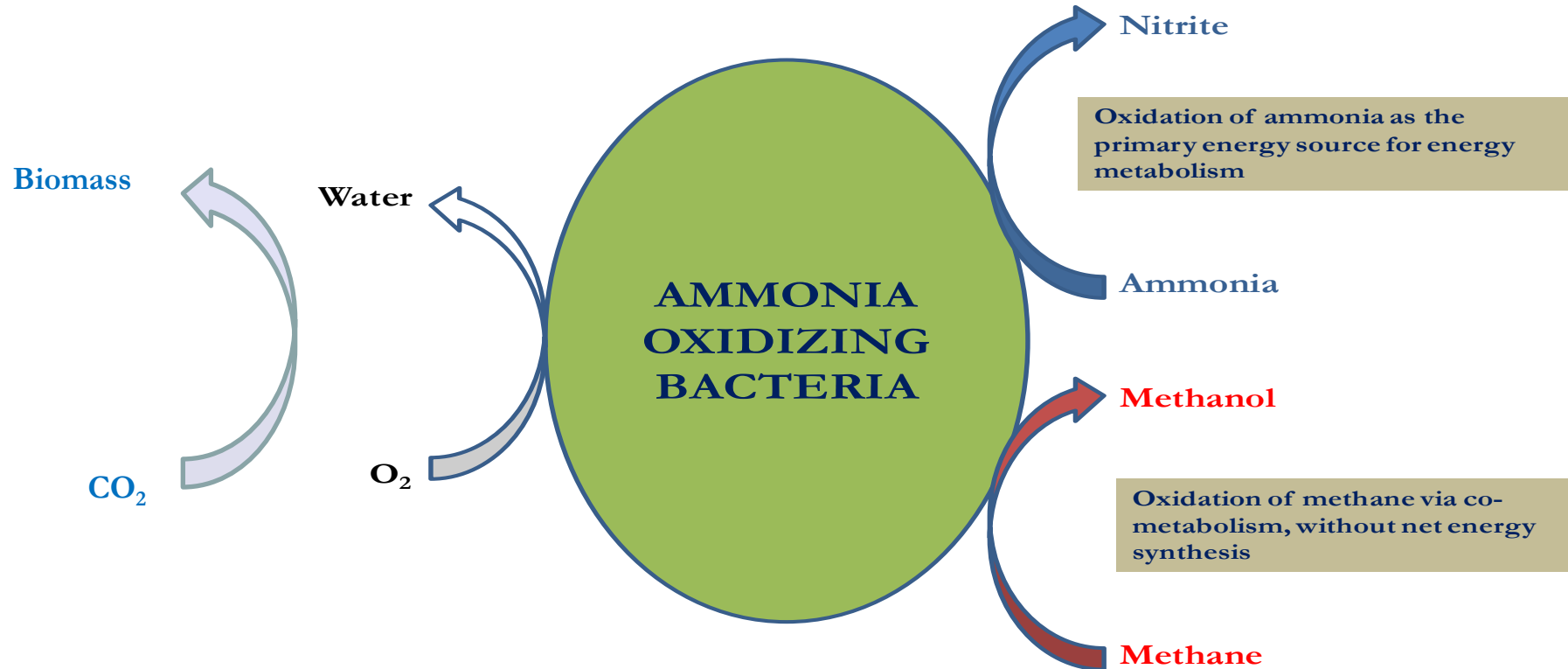
Anaerobic Digester



Org-N and NH₃
Org-N and NH₃
Org-N and NH₃



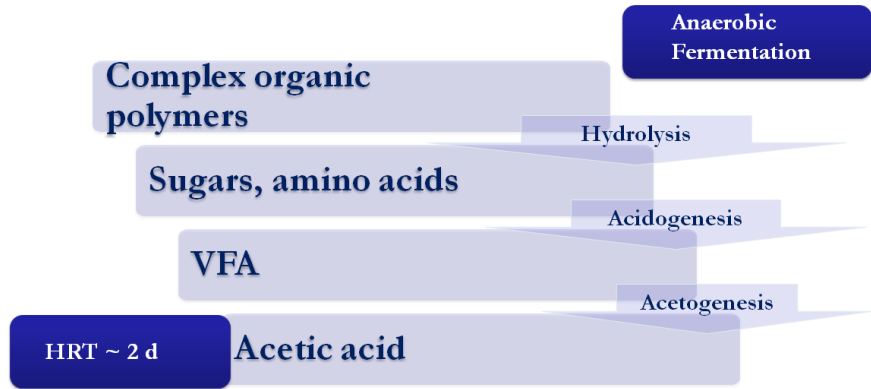
III. C. From Greenhouse Gas to Green Fuel



- Concomitant oxidation of CH_4 and CO_2 fixation
- Prospect of combining C & N cycles

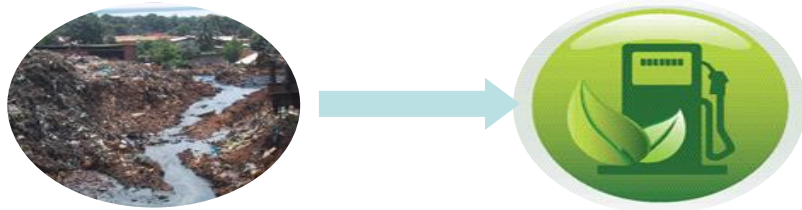


Concluding remarks



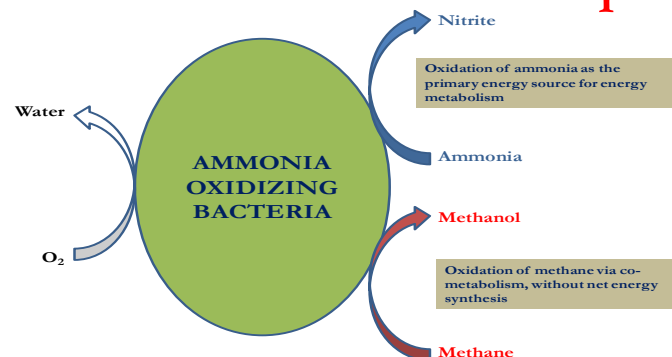
Channeling anaerobic C-conversions through SC-FA offers attractive flexible prospects for resource recovery

Detailed understanding of microbial structure and function in conjunction with reductionist approaches needed to advance implementation



Wide variety of endpoints (chemicals, fuels..) possible

Disrupting conventional agro- or fossil-based pathways



Links to other applications needed and possible

Resource efficient options for FSM and sanitation



Abstracts due: Feb 28th, 2017

2nd International Resource Recovery Conference 2017

August 5-9 | Exhibition: August 7-9
Columbia University | New York, NY
www.irrc2017.org



Water · Energy · Nutrient



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