

EVOLUTION OF MICROBIAL COMMUNITIES IN AEROBIC GRANULAR SLUDGE DURING CHANGES OF THE WASTEWATER COMPOSITION

Aline Adler, Valérie Berclaz,
Marie Horisberger, Julien Maillard and
Christof Holliger





Microbial processes for wastewater treatment

Activated sludge

- Conventional microbial process in wastewater treatment plants
- Flocular structures, settle slowly



After 1 minute settling

Aerobic granular sludge

- Granular structures, settle fast
- Allows high sludge concentration

Space and time saving

- Suited for biological phosphorus removal
 - > chemicals saving



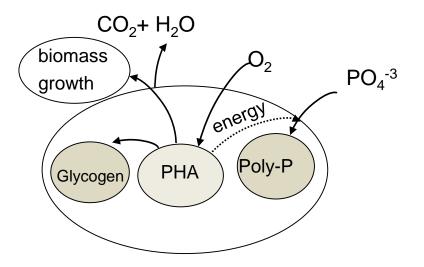
Phosphate accumulating organisms (PAO)

PAO model organism

Accumulibacter

Anaerobic VFA PO₄-3 Glycogen PHA Poly-P

Aerobic



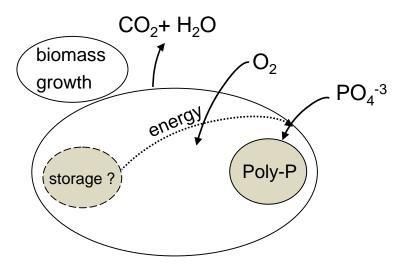
Phosphate accumulating organisms (PAO)

Fermentative PAO

Tetrasphaera

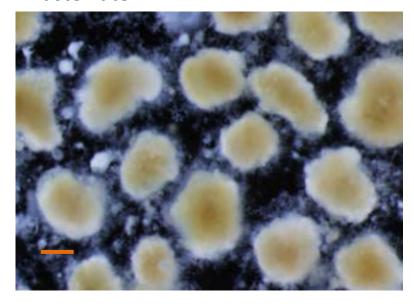
Glucose Amino acids PO₄-3 biomass growth? Poly-P energy fermentation products

Aerobic

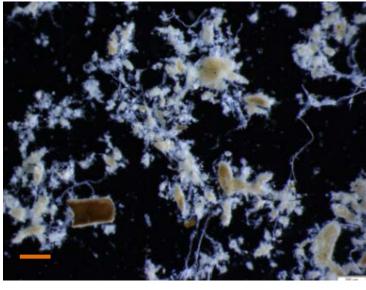


Aerobic granular sludge (AGS) for wastewater treatment

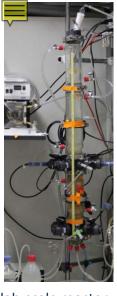
AGS fed with simple synthetic wastewater ...



... and with raw municipal wastewater



- **—** 500μm
- Eawag- LTE
- Are fermentable or polymeric compounds responsible for this difference?
- How do they impact the settling characteristics,
 - the nutrient removal,
 - the microbial communities of the AGS?



Progressive changes of the wastewater composition in two lab-scale reactors

lab-scale reactor

1 reactor ← 2 reactors → 1 reactor

Transition to simple monomeric wastewater

AGS fed with complex monomeric wastewater

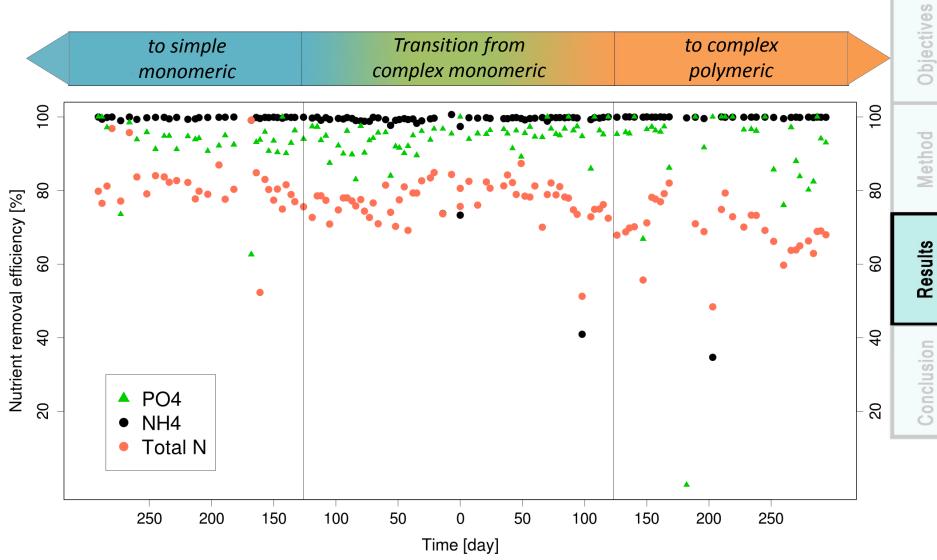
Transition to complex polymeric wastewater

VFA

VFA, glucose, amino acids

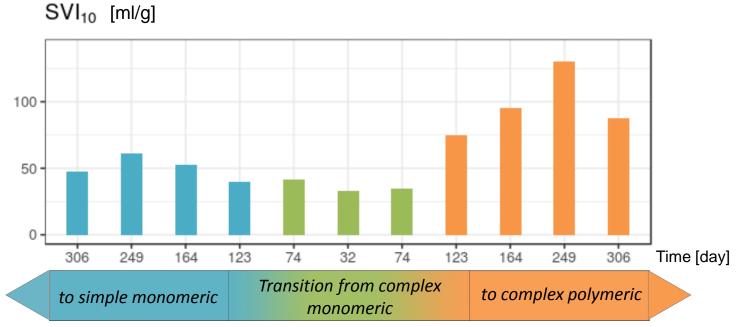
VFA, glucose, amino acids, starch, peptone

Evolution of nutrient removal efficiency



Introduction

Evolution of the settling properties

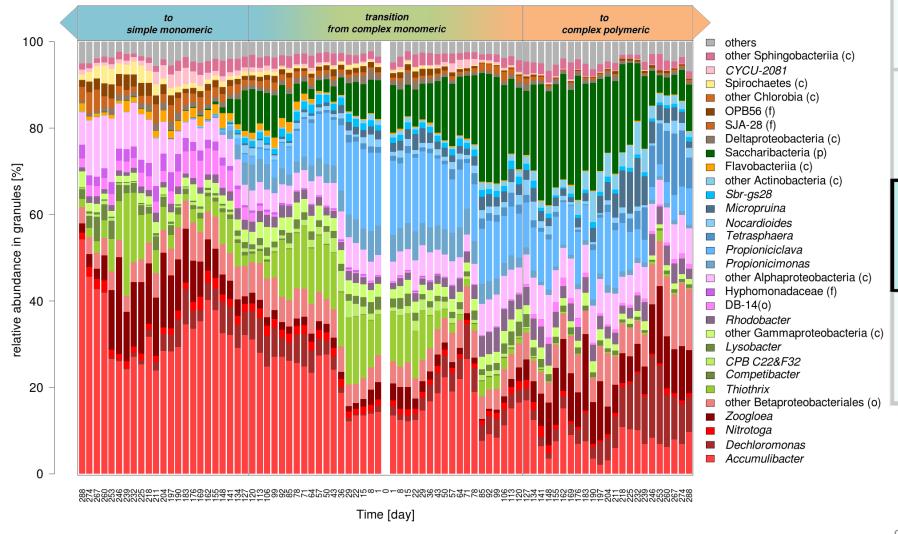




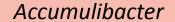




Evolution of the structure of the bacterial communities

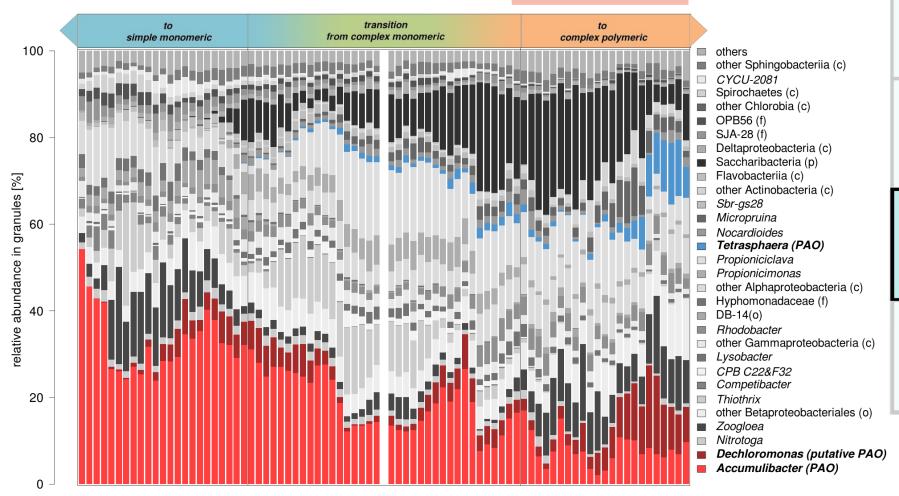


phosphate accumulating organisms (PAO)



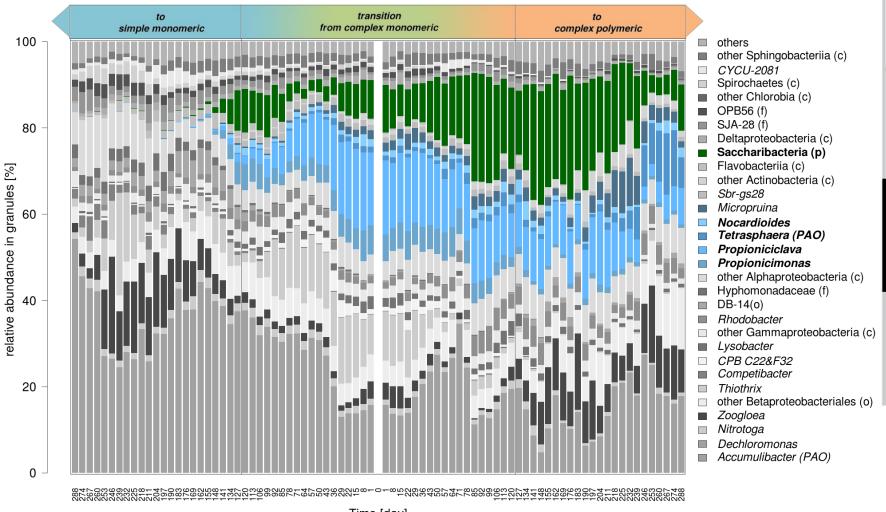
Tetrasphaera

Accumulibacter

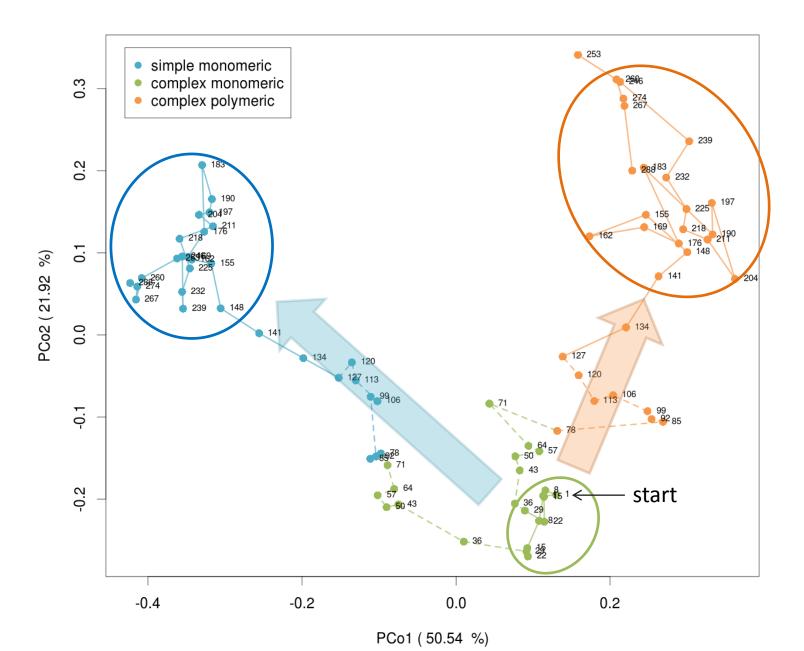


Time [day]

fermenting bacteria



Overall evolution of the microbial communities



Conclusions

 The AGS settleability and the nutrient removal performances were good with the simple and the complex monomeric wastewaters.

- With the introduction of polymeric compounds, a significant proportion of flocs appeared and the Nremoval decreased.
- Accumulibacter was the predominant PAO with the simple wastewater. With the fermentable and polymeric compounds, the guild of PAO was more diverse.



Acknowledgments



LBE - EPFL

Marie Horisberger

Valérie Berclaz

Idriss Hendaoui

Emmy Oppliger

David Scheibler

Romain Savary

Dylan Van Tuan Magnin

Emmanuelle Rohrbach

Stéphane Marquis

Marc Deront

Julien Maillard

Christof Holliger

DPE - Eawag

Manuel Layer

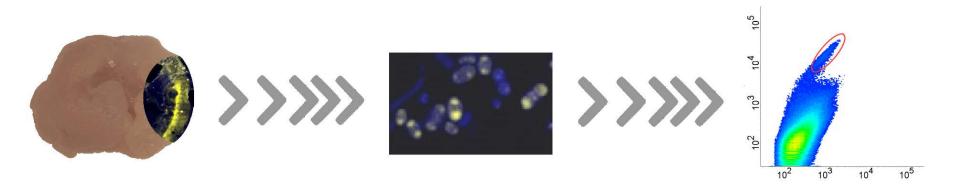
Nicolas Derlon

Eberhard Morgenroth

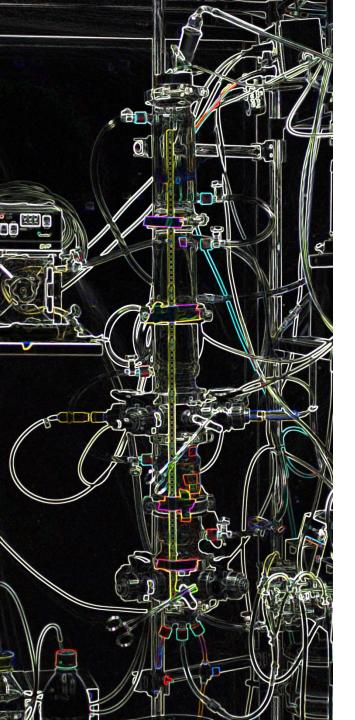


Arnaud Gelb

Identification of microorganisms in aerobic granular sludge actively involved in biological phosphorus removal



Poster n°51



Thank you for your attention!

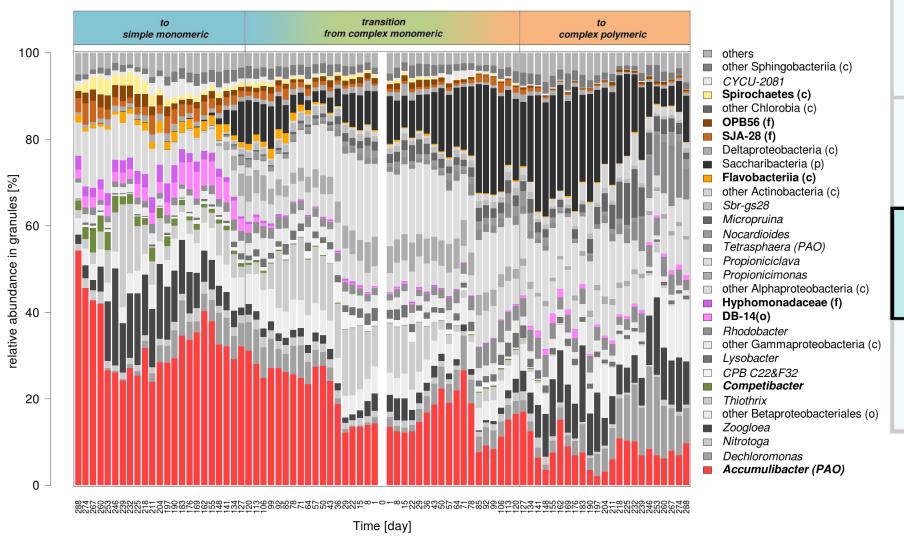
Synthetic wastewater compositions

Medium	COD [mgO2/L]	VFA	Glucose and amino acids	Starch and peptones
Simple monomeric	450	100 %	-	-
Complex monomeric	600	33 %	66 %	-
Complex polymeric	600	33 %	33 %	33 %

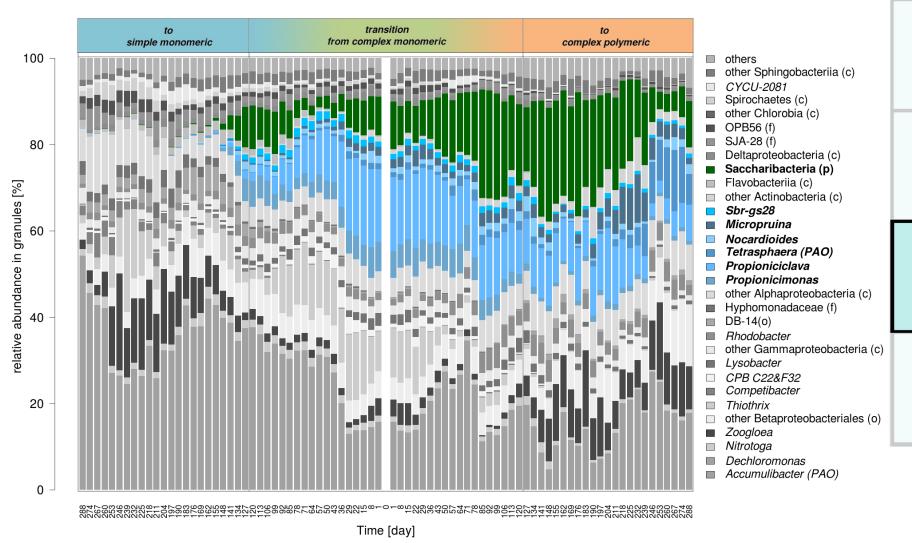
Phosphorus: 22 [mg/L]

Nitrogen: 56 [mg/L]

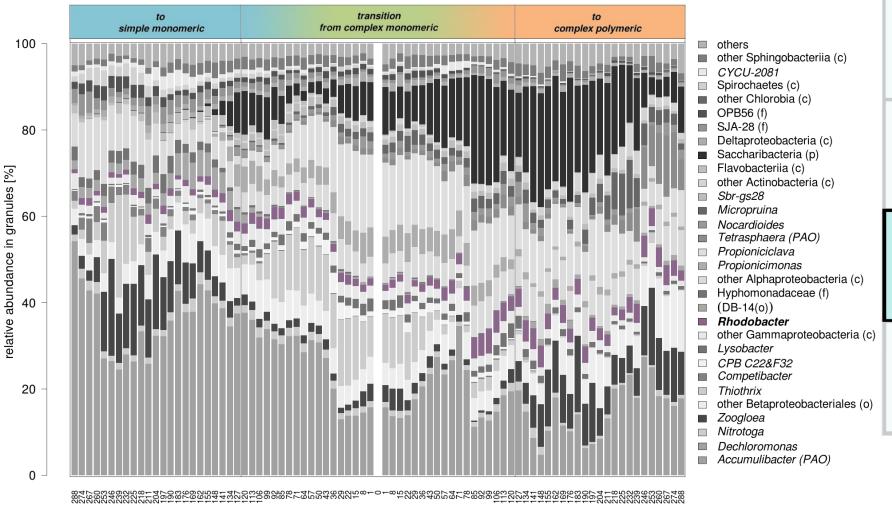
Some taxa are found in higher abundance with the simple wastewater



Some taxa are found in higher abundance with the complex wastewater

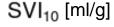


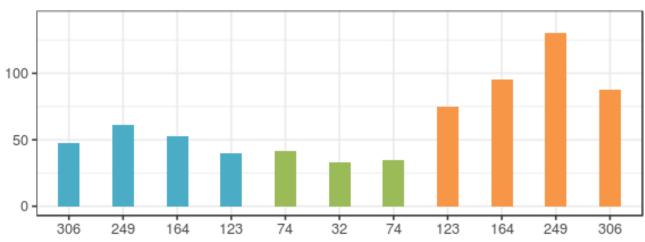
Rhodobacter was found in higher abundance with the polymeric wastewater



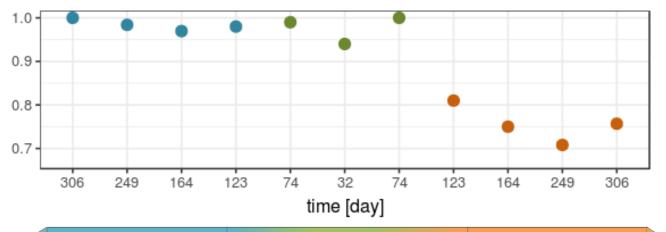
Time [day]

Sludge volume index (SVI)





ratio SVI₁₀/SVI₃₀



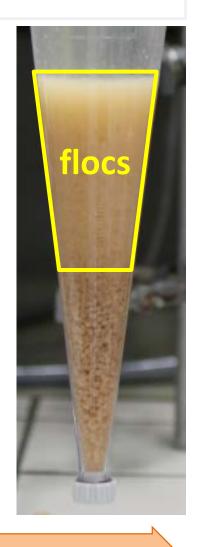
to simple monomeric

Transition from complex monomeric to complex polymeric

Evolution of the settling capability of the AGS





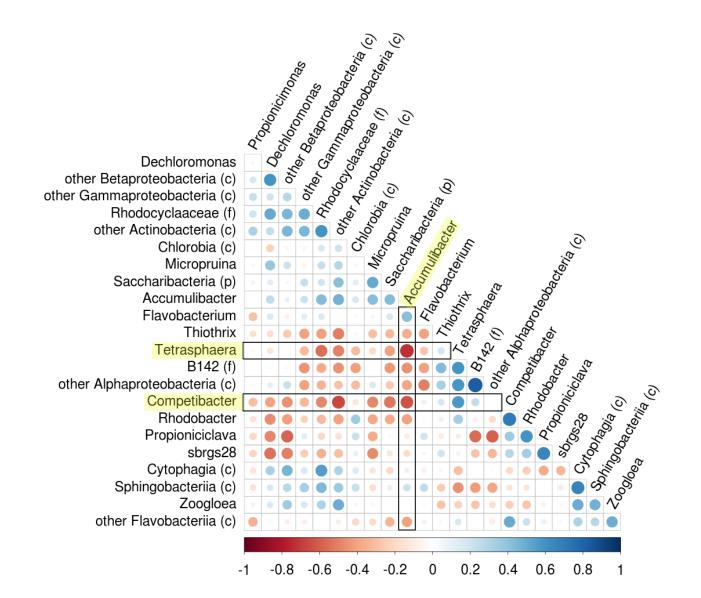


Transition to **simple monomeric**

Complex monomeric

Transition to complex polymeric

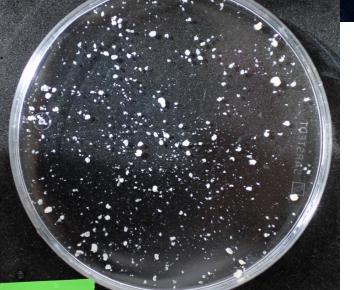
Correlation between the relative abundance of main taxa with complex monomeric wastewater



Complex monomeric

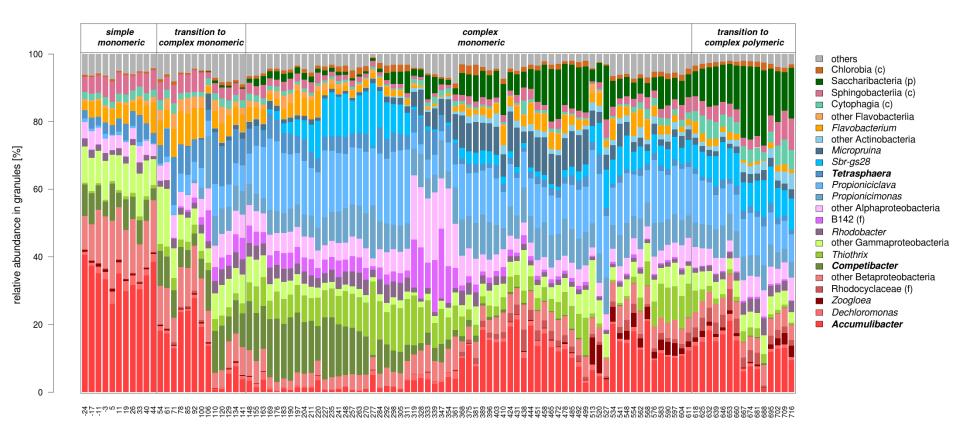


Complex polymeric

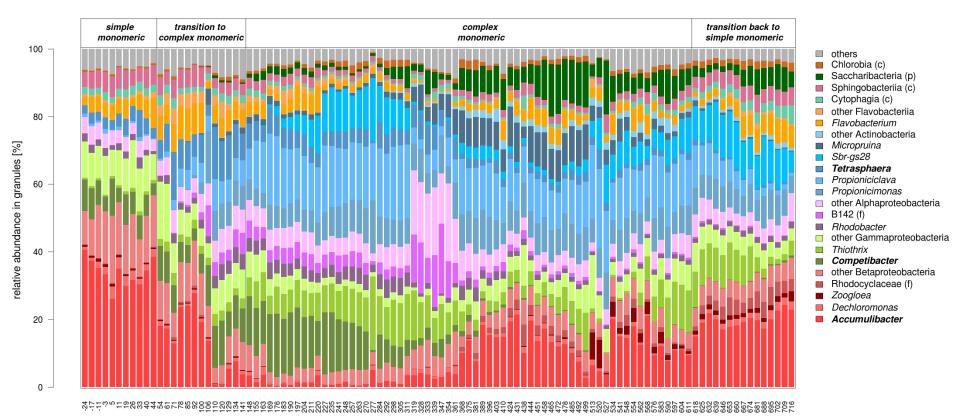


Simple

monomeric

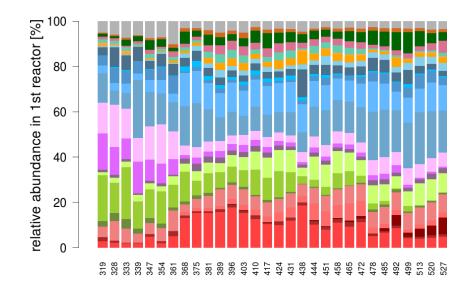


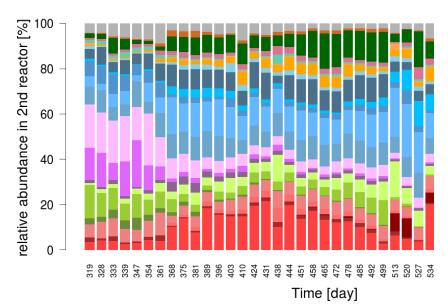
Time [day]



Time [day]

Microbial communities evolution in two reactor fed with complex monomeric wastewater





- others
- Chlorobia (c)
- Saccharibacteria (p)
- Sphingobacteriia (c)
- Cytophagia (c)
- other Flavobacteriia
- Flavobacterium
- other Actinobacteria
- Micropruina
- Sbr-gs28
- Tetrasphaera
- Propioniciclava
- Propionicimonas
- other Alphaproteobacteria
- B142 (f)
- Rhodobacter
- other Gammaproteobacteria
- Thiothrix
- Competibacter
- other Betaproteobacteria
- Rhodocyclaceae (f)
- Zoogloea
- Dechloromonas
- Accumulibacter