

*Li Deng & Christian Griebler*



# Diversity and functionality of groundwater viral communities

Institute of Groundwater Ecology

# Why study viruses?

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## Microbial biodiversity in groundwater ecosystems

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"The greatest diversity of living organisms on our planet is found within the microbes. They are ubiquitous and abundant. Invisible to the human eye, microbes are generally responsible for processes of global relevance and the turnover of energy and matter."

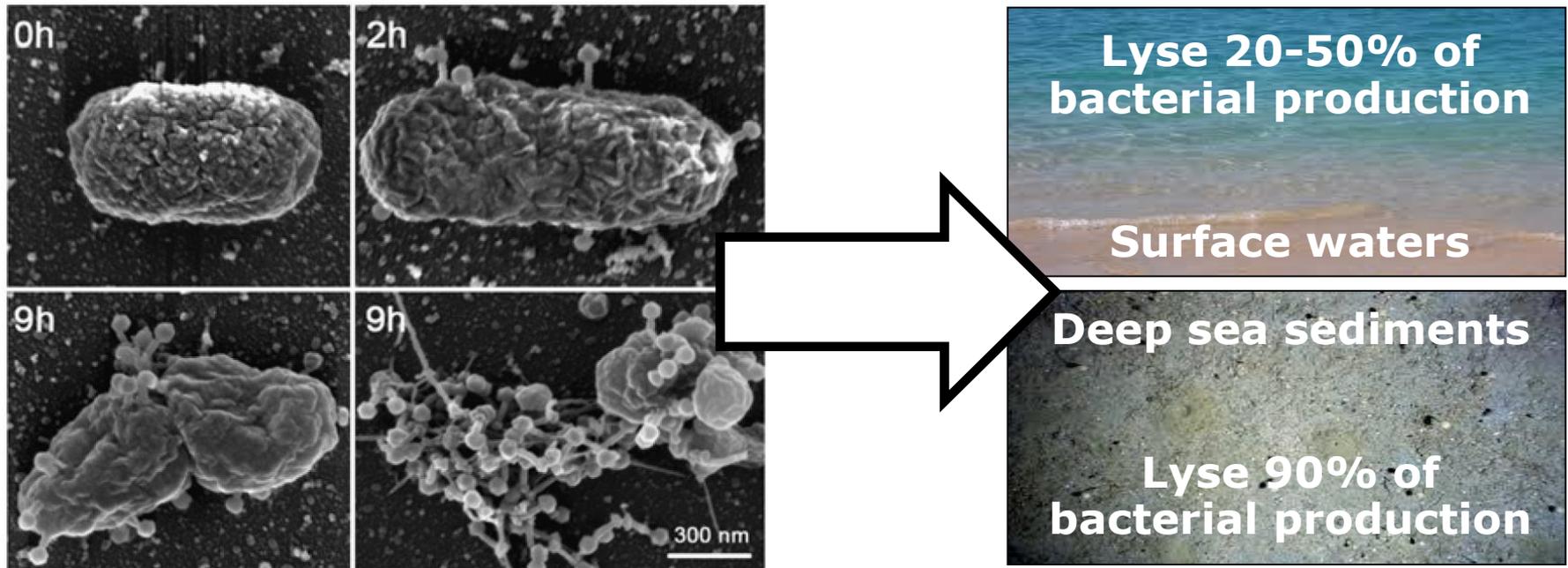
# Viruses: globally important player

**1. Small and abundant - 20-200 nm,  $10^{31}$  tailed phages, 10:1 VBR**

*Breitbart et al., 2007; Danovaro, 2008; Fuhrman et al., 1993, 1999, 2000; Mann et al, 2003; Lindell et al., 2004, 2005, 2007; Sharon et al., 2007; Sullivan et al., 2005, 2006; Suttle 2005, 2008; Williamson et al., 2008.*

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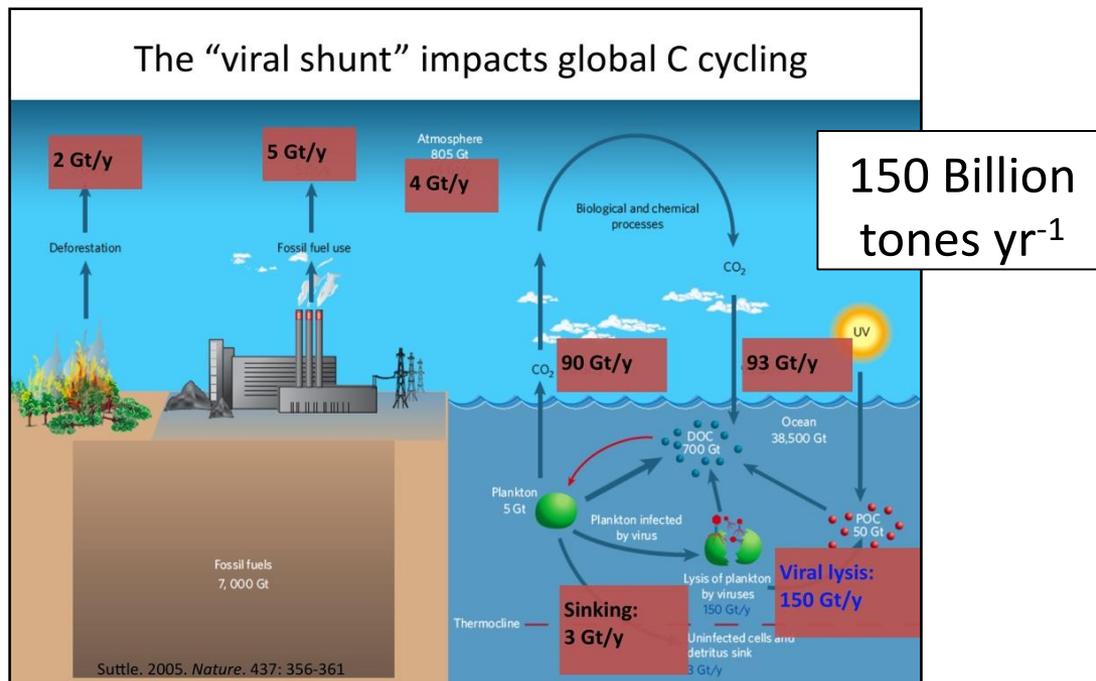
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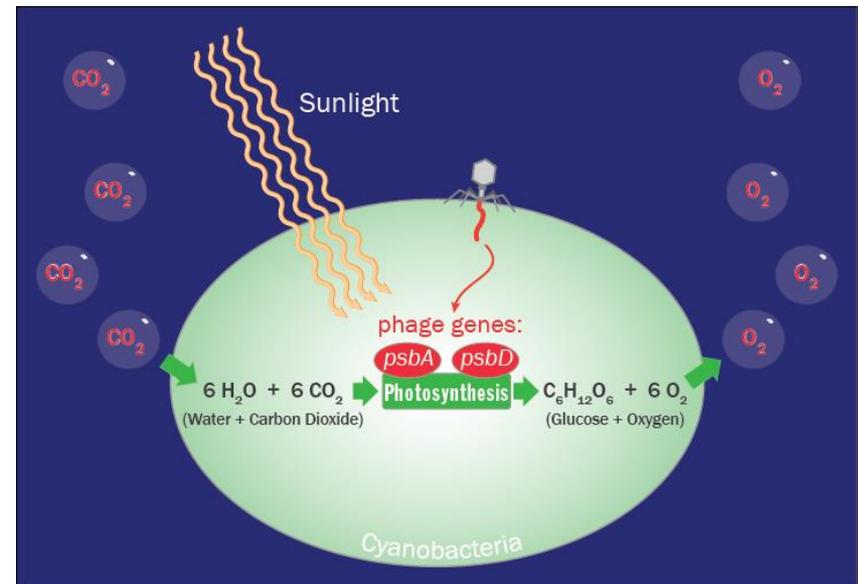


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# Viruses: globally important player

1. Small and abundant - 20-200 nm,  $10^{31}$  tailed phages, 10:1 VBR
2. Viruses infect and kill their hosts
3. They recycle carbon and nutrients – viral shunt
4. Viruses carry and make use of host genetic information

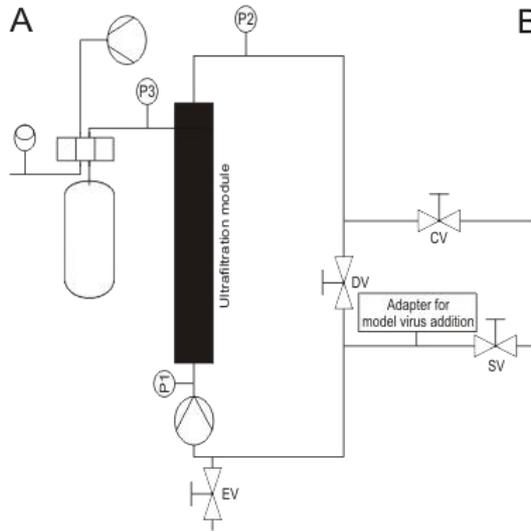
- Core **photosynthesis** genes are found in viral genomes, “used” during infection
- ‘Viral’ version of **phosphate** stress, **nitrogen** fixation, **sulfur** oxidation, **vitamin** biosynthesis, **antibiotic** resistance genes ...



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# How do we study viruses in groundwater?

# Collection of viral-size particles from groundwater



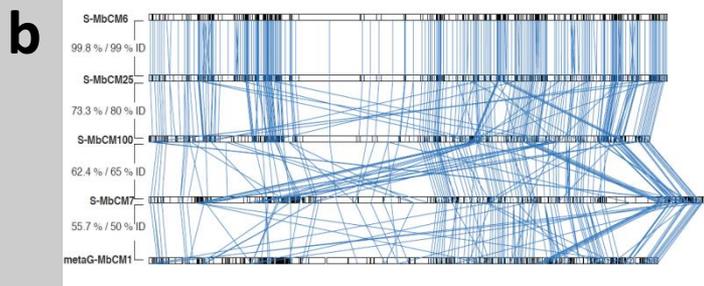
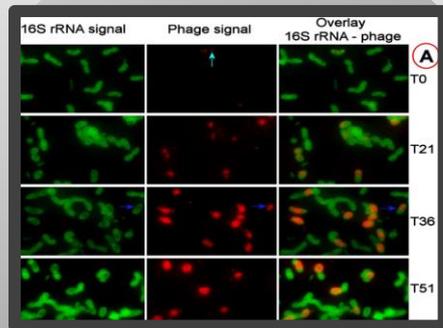
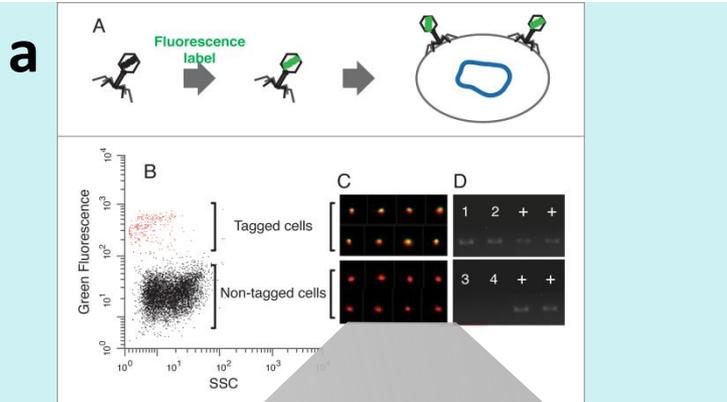
monolithic affinity filtration column

Michael Seidel & Co, TUM

- Concentration of viruses from groundwater by either precipitation with iron-chloride or via nanofiltration (few liters to 30 m<sup>3</sup>)
- Isolation of both DNA, purification, amplification, and deep sequencing (454 Roche, Illumina, Ion Torrent)



# The phage/virus tool box



## a. “Viral-Tagging”

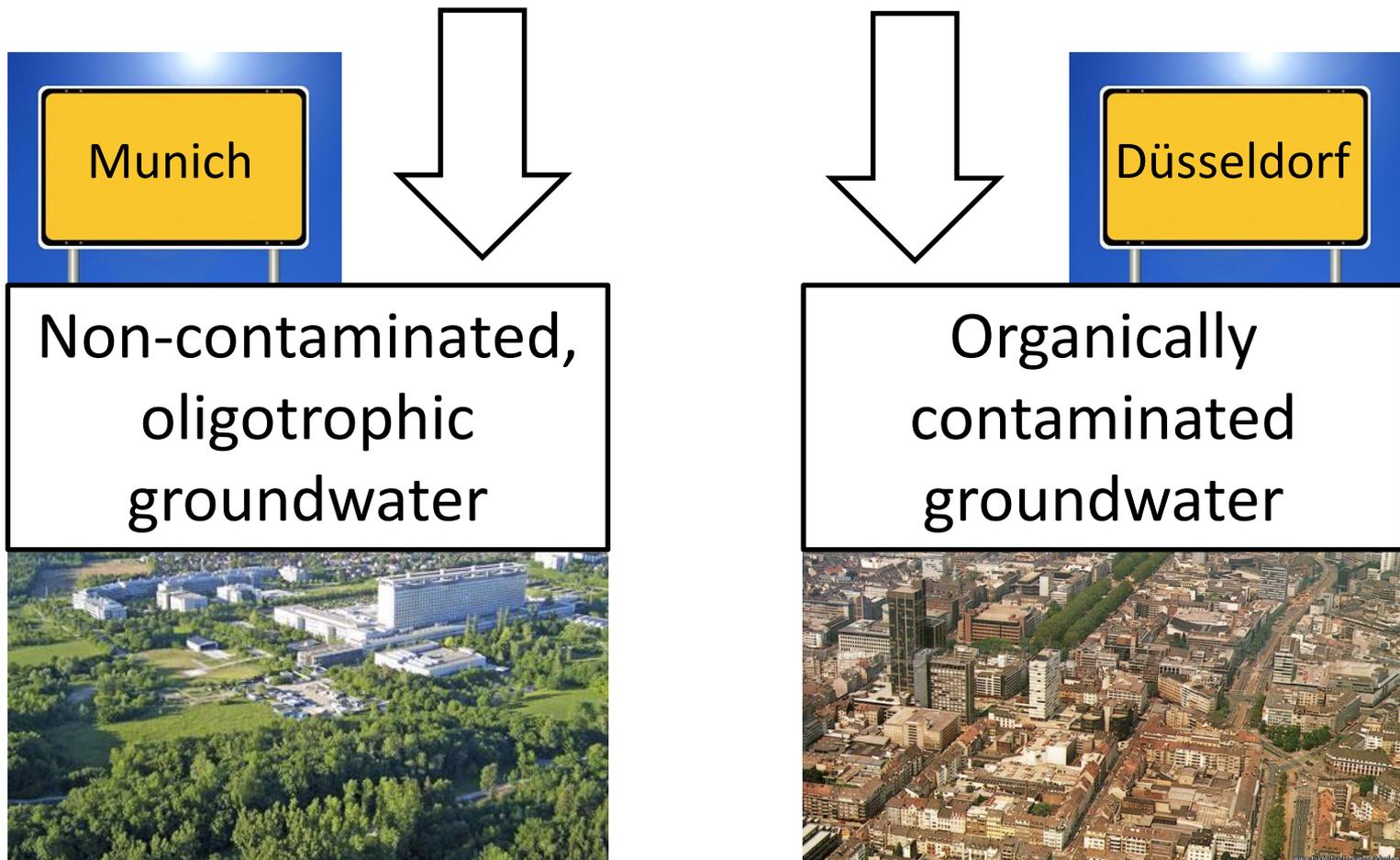
- Link of a virus to its host *In situ*
- Keep the host-virus linkage
- Simplify the viral community (for easier assembly) for deep explorations of genes

## b. “Viral metagenomics & PC analysis”

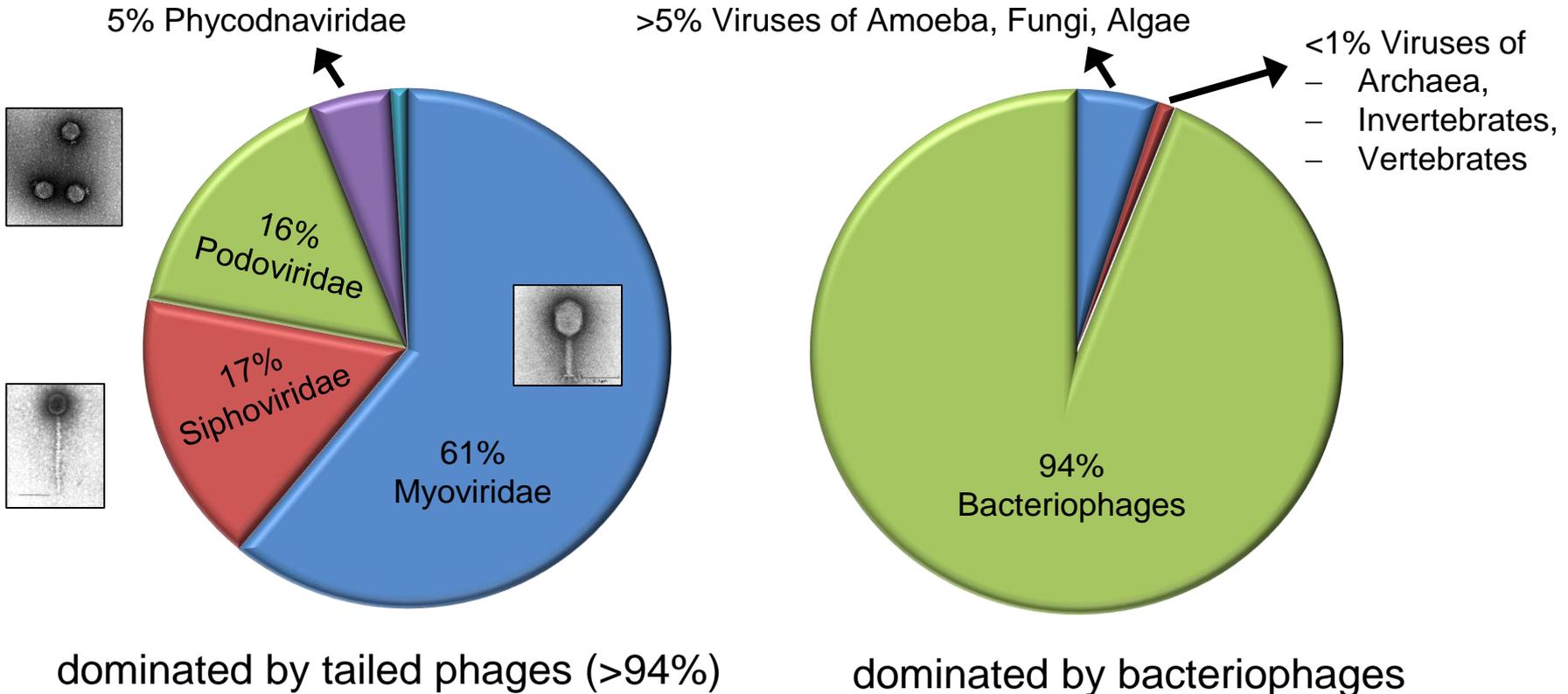
- Exploration of viral diversity
- Horizontal gene transfer (HGT)
- Auxilliary metabolic genes (AMG)

# Aim of our research

- Shed light to the diversity and role (functions) of viruses in groundwater ecosystems

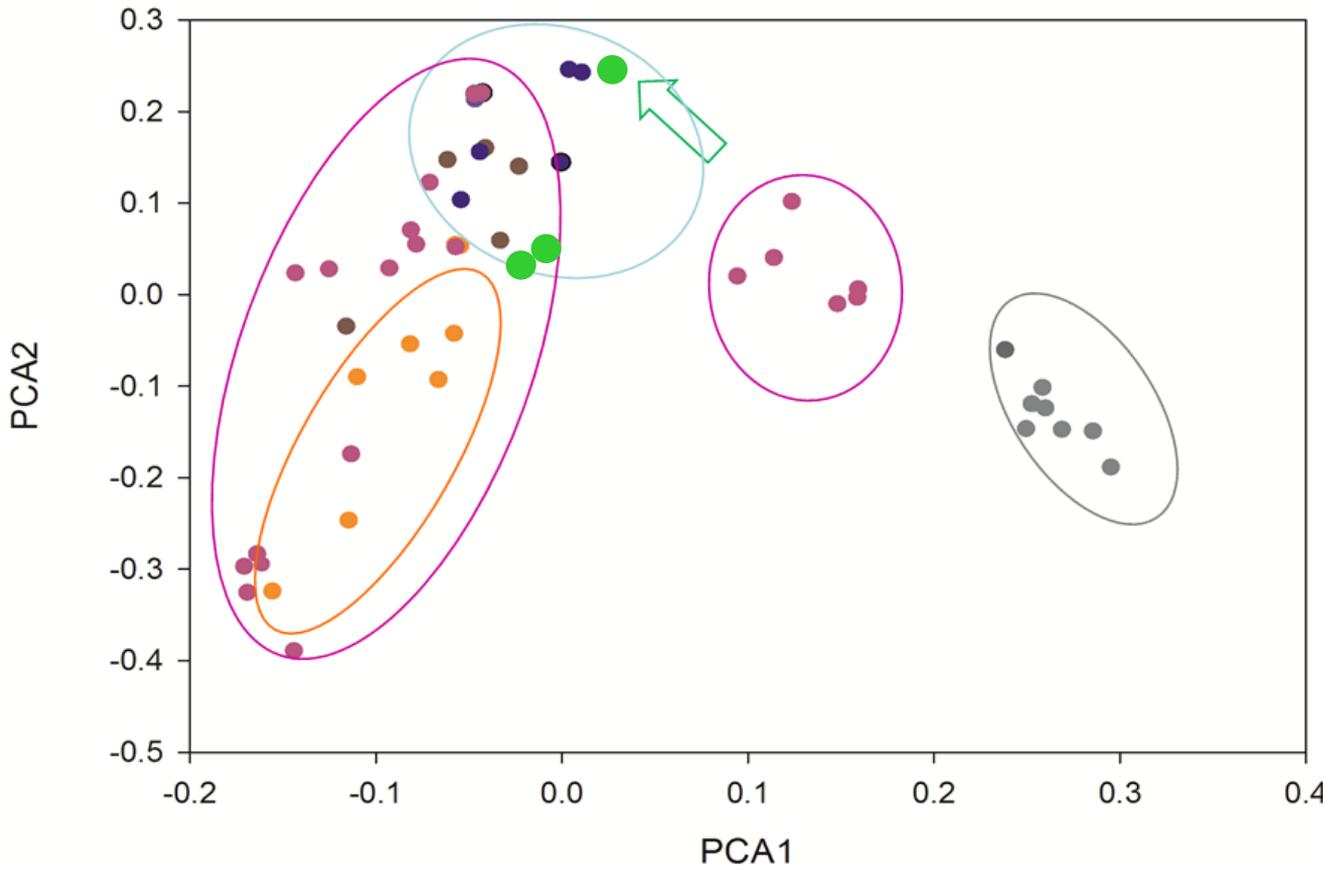


# The 1<sup>st</sup> viral metagenome from oligotrophic groundwater



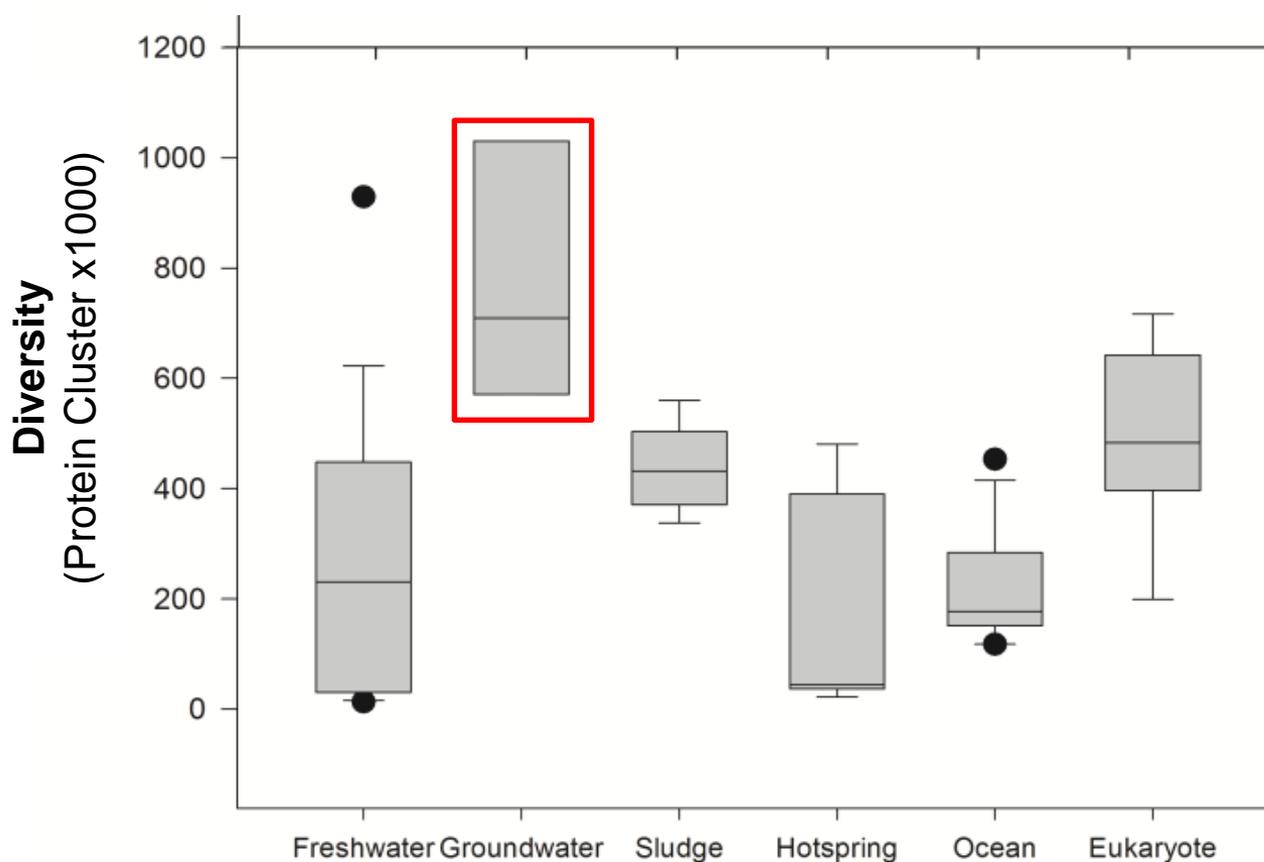


# Viral communities across aquatic habitats



- Green:** Groundwater
- Blue:** Freshwater
- Brown:** Hypersaline wat.
- Purple:** Marine systems
- Orange:** Hot springs
- Gray:** Fish associated in freshwater

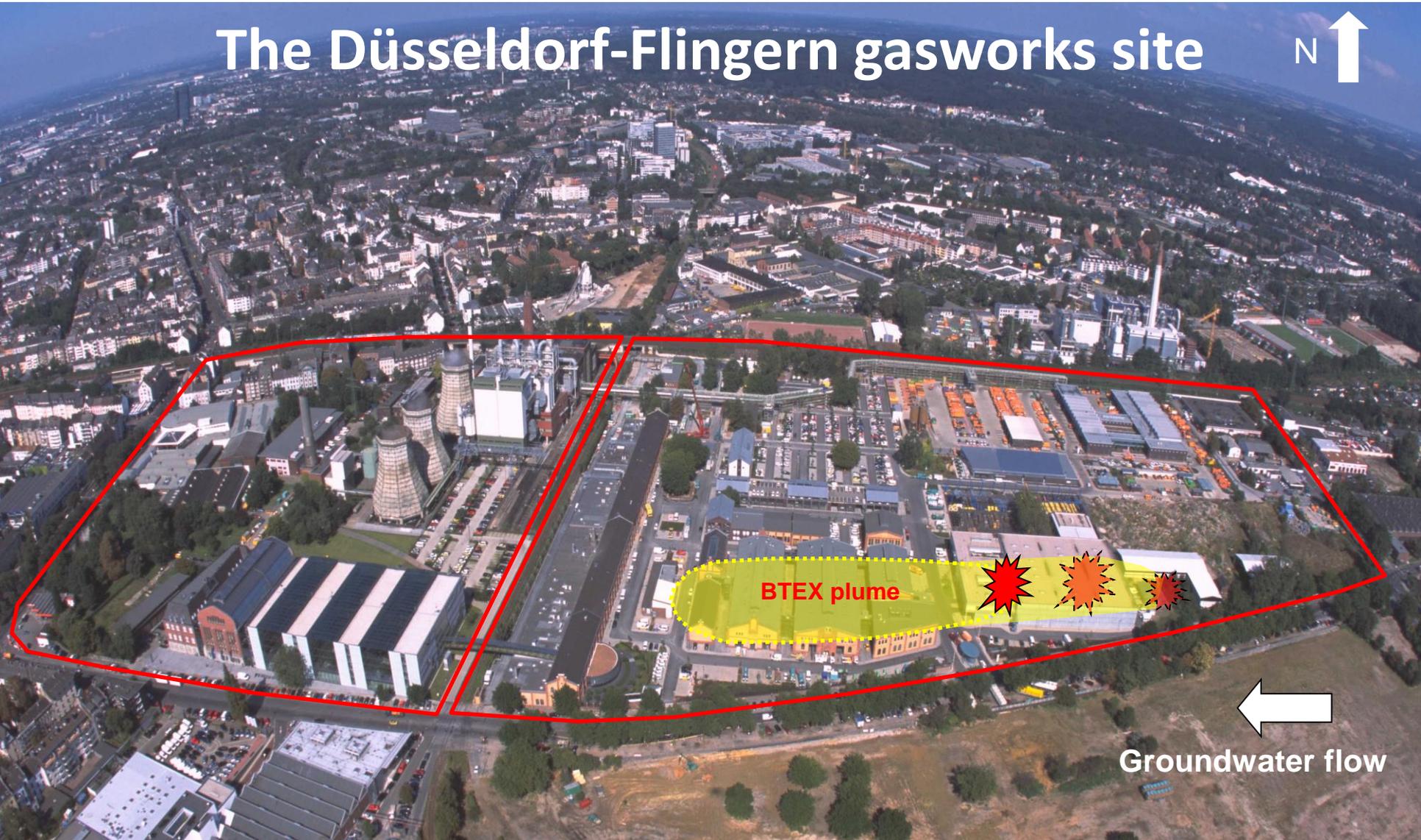
# Viral communities across aquatic habitats



- The cluster richness of each viral assembly, however, was significantly different between each other.
- The highest diversity being observed in our groundwater sample.

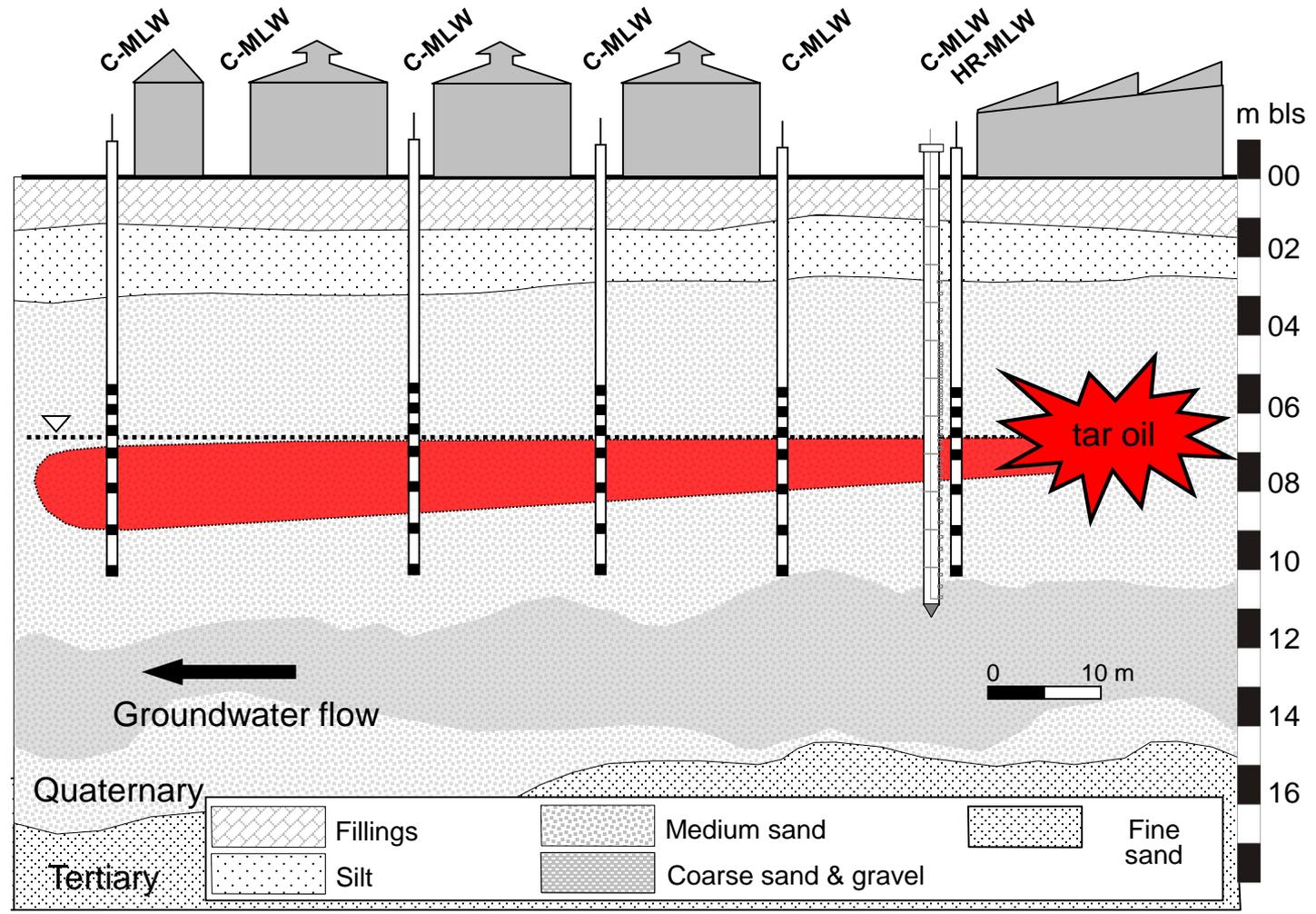
# Is there different viruses in contaminated groundwater ?

The Düsseldorf-Flingern gasworks site



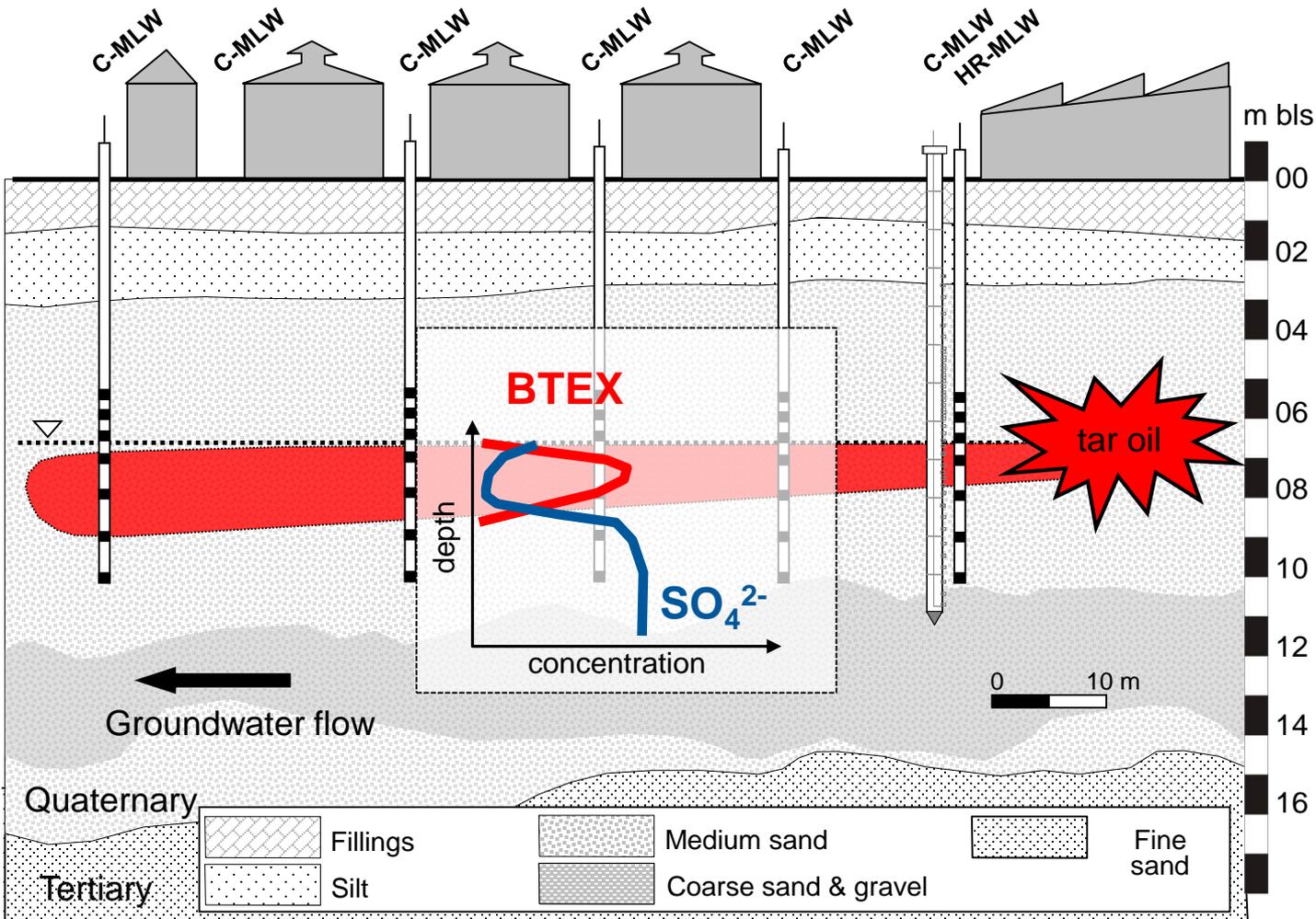
# What happened in the Düsseldorf-Flingern aquifer?

2006



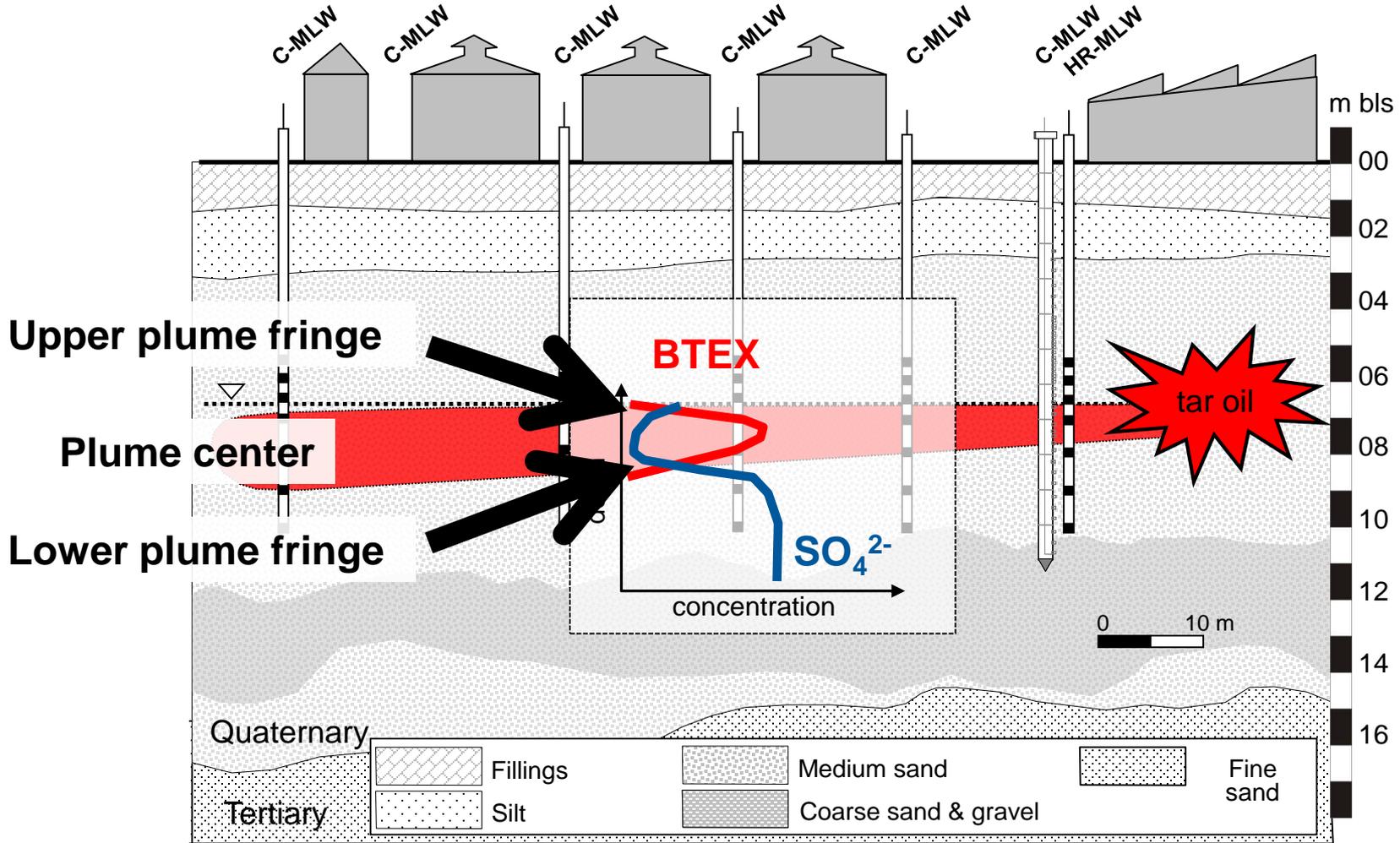
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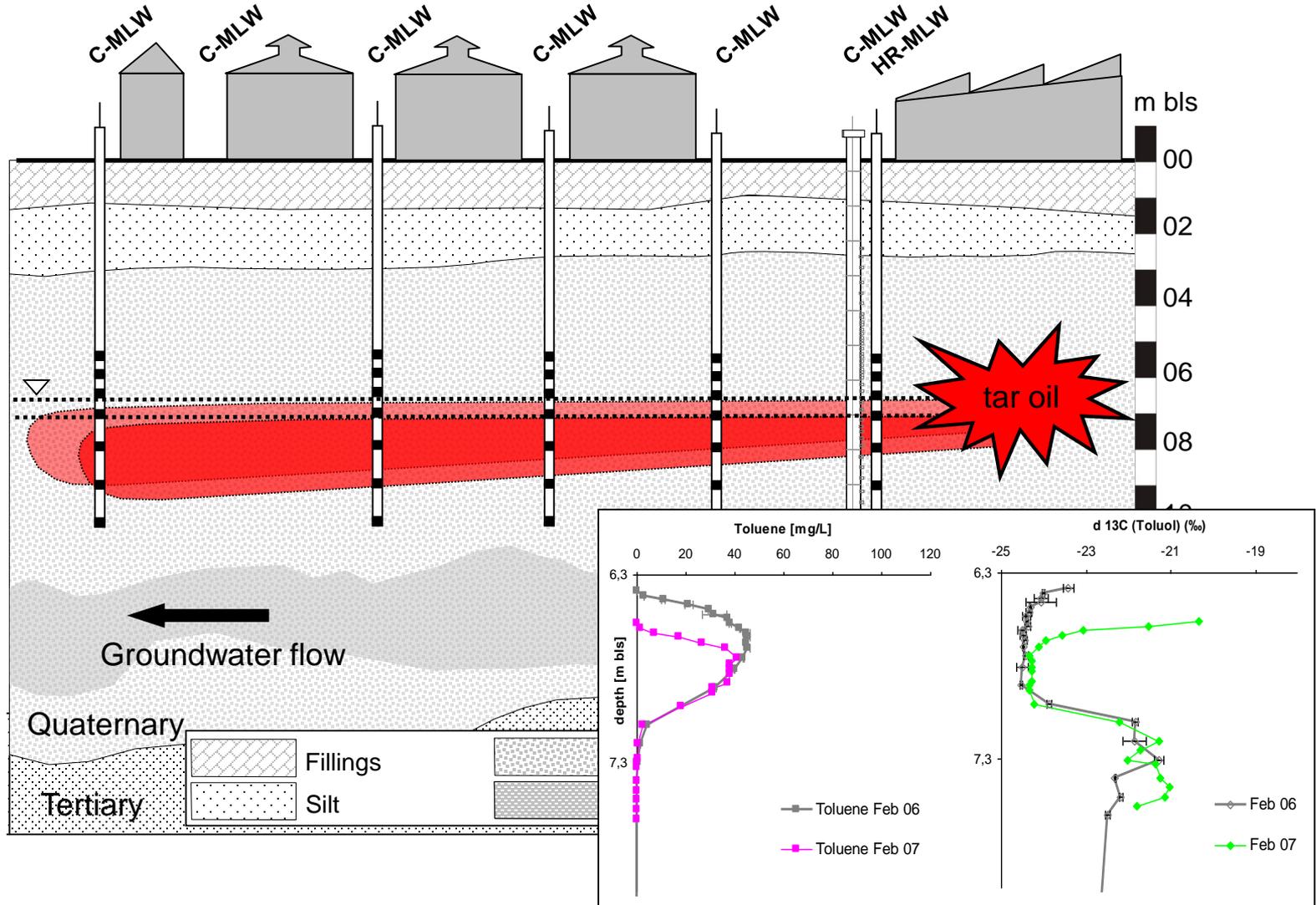
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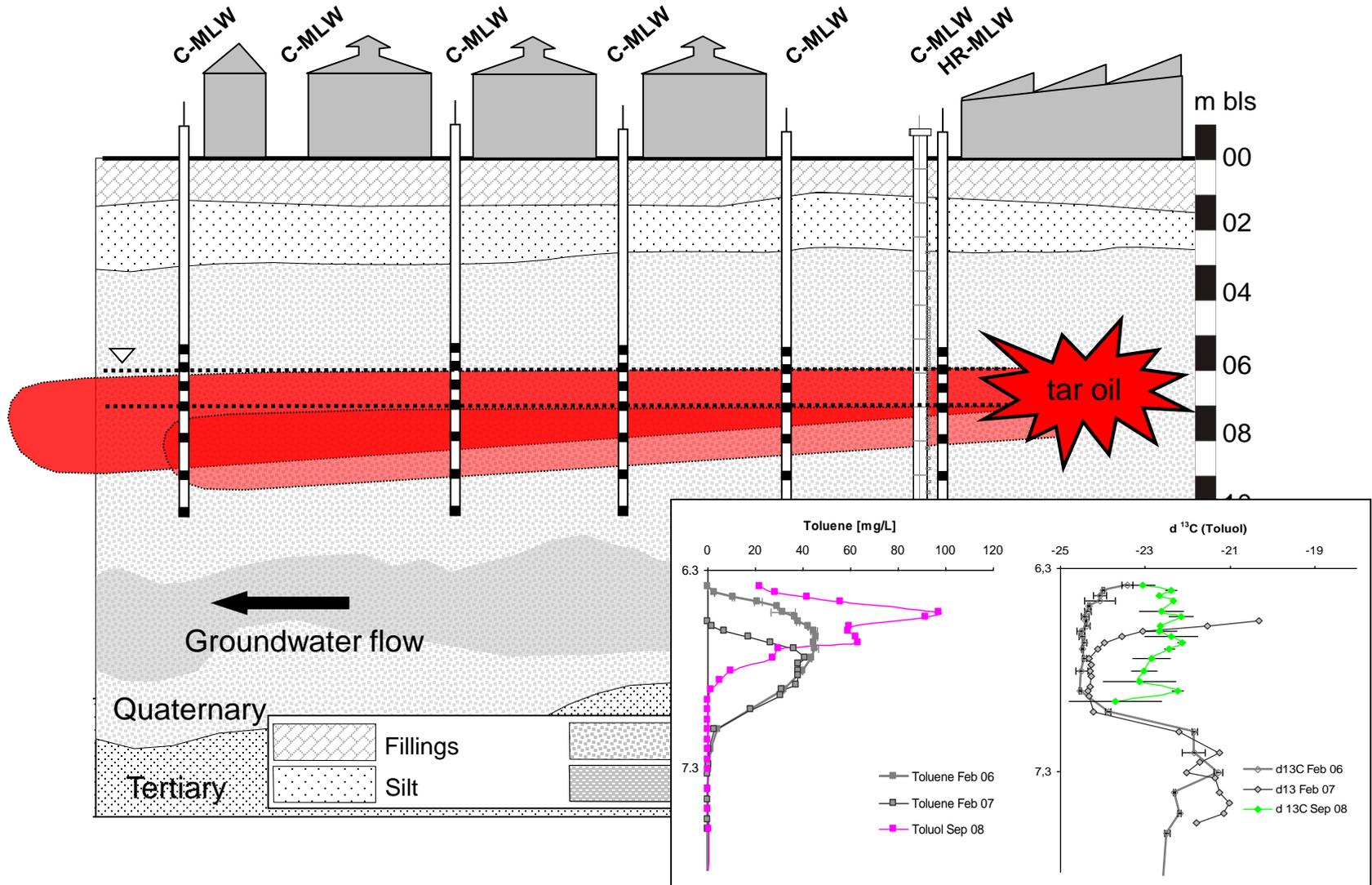
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2006 to 2007



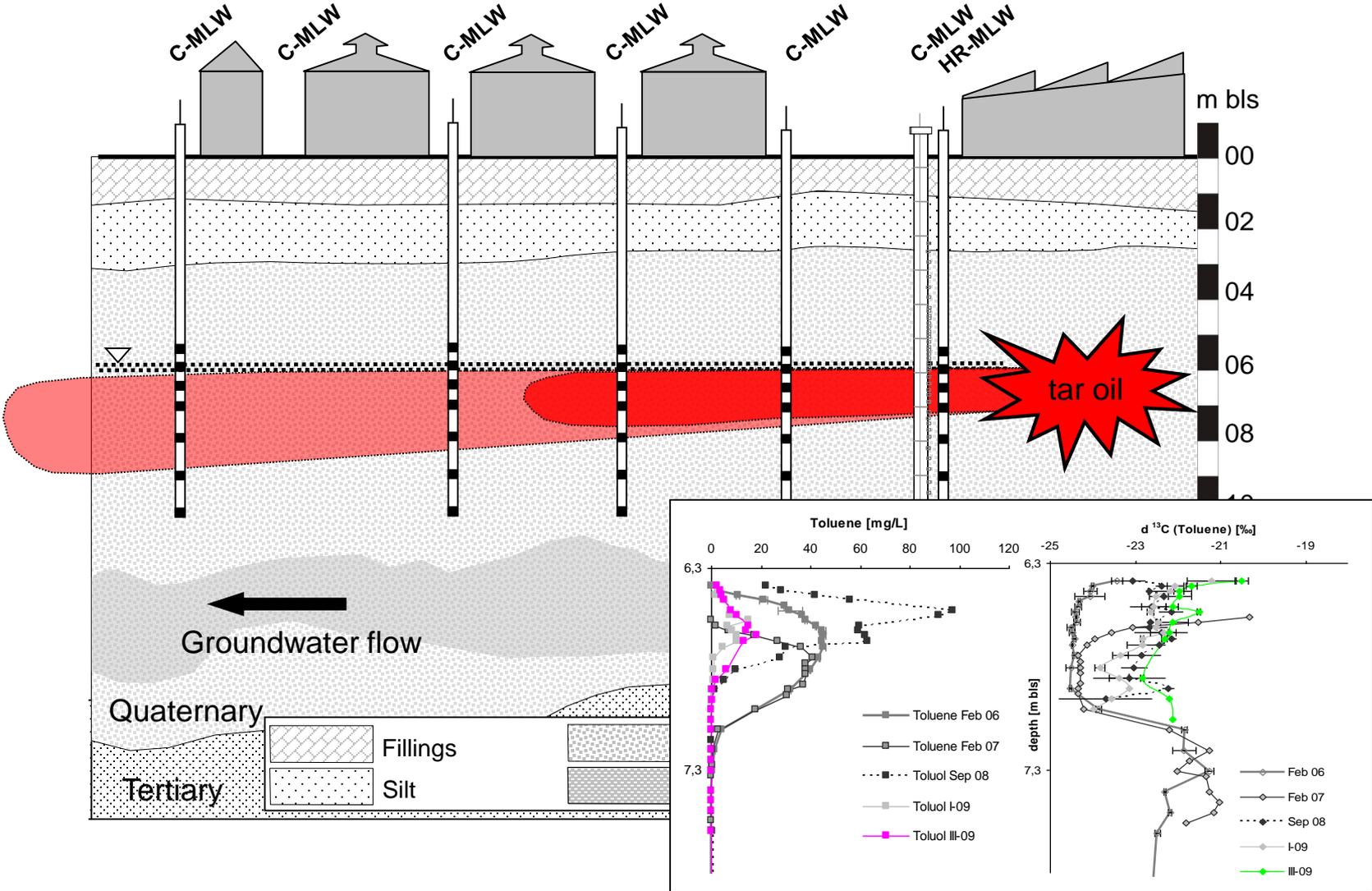
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2007 to 2008

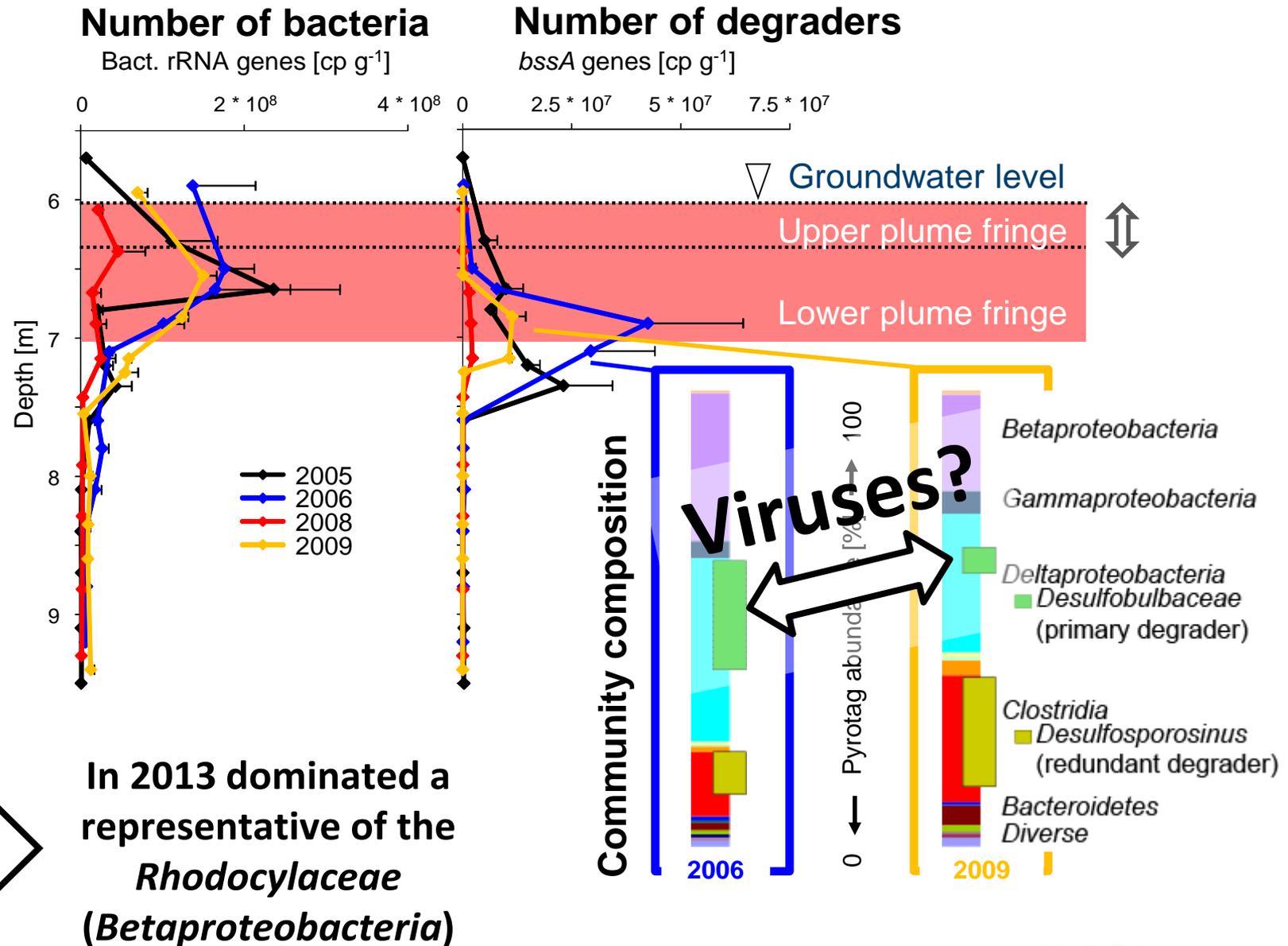


# What happened in the Düsseldorf-Flingern aquifer?

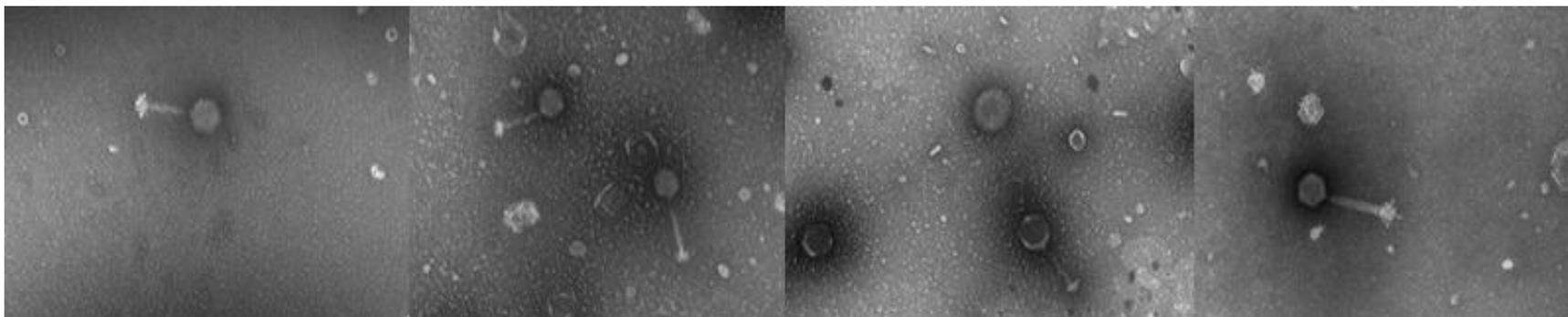
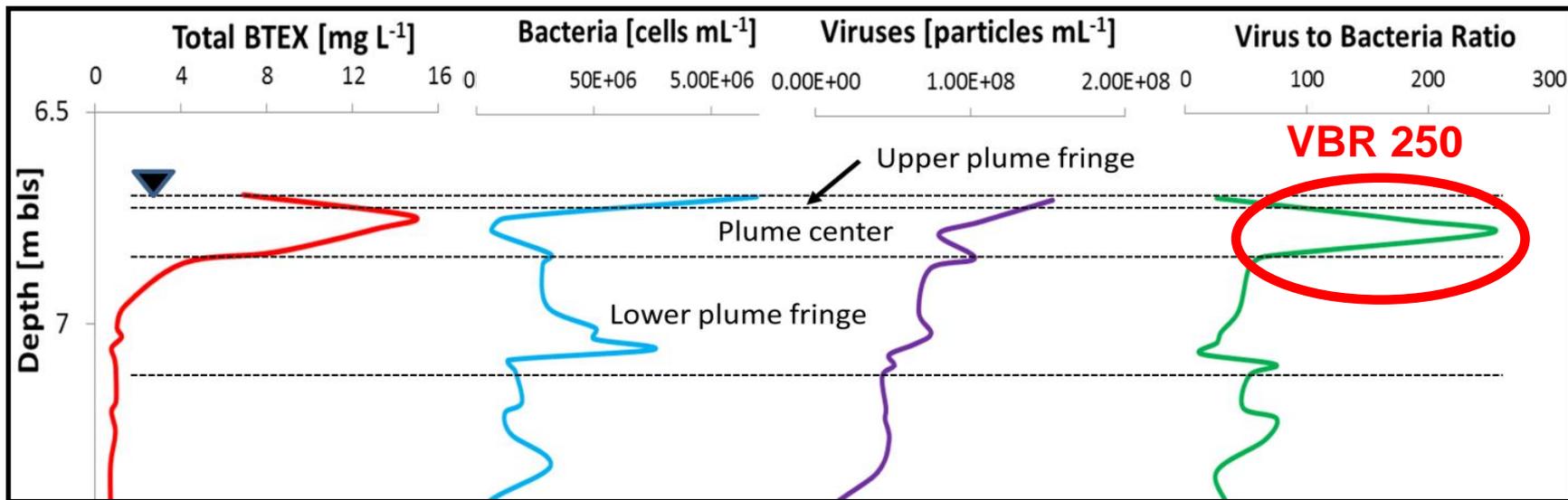
2008 to 2009



# Do abiotic dynamics translate into microbiomes?

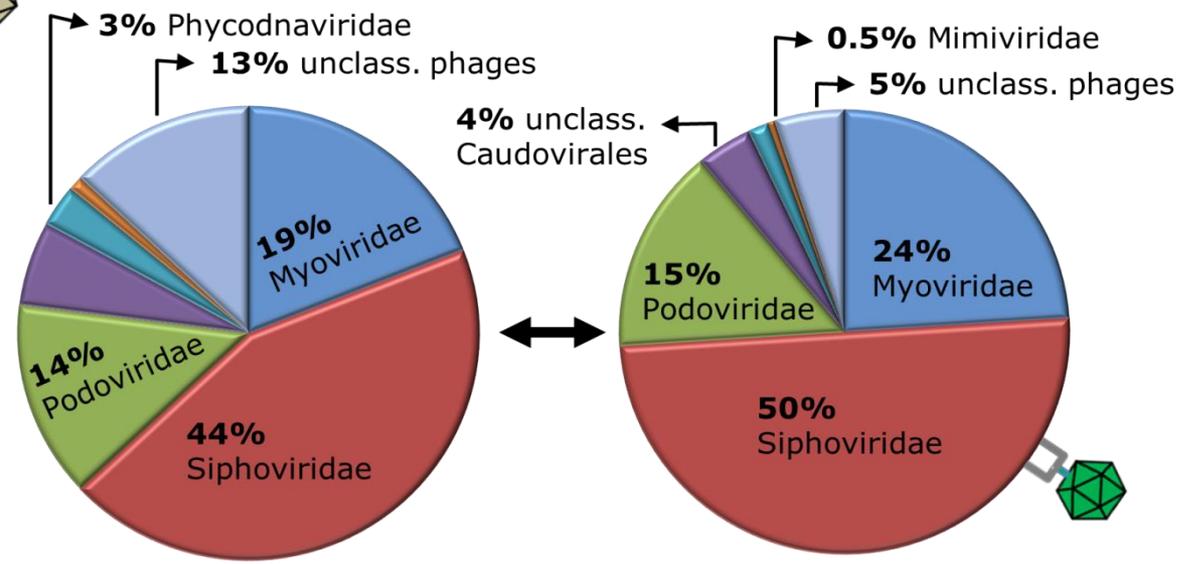
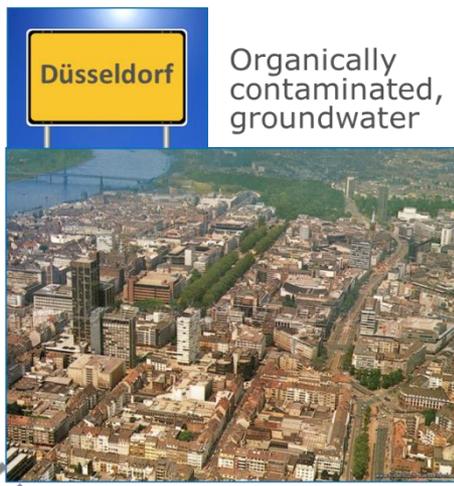
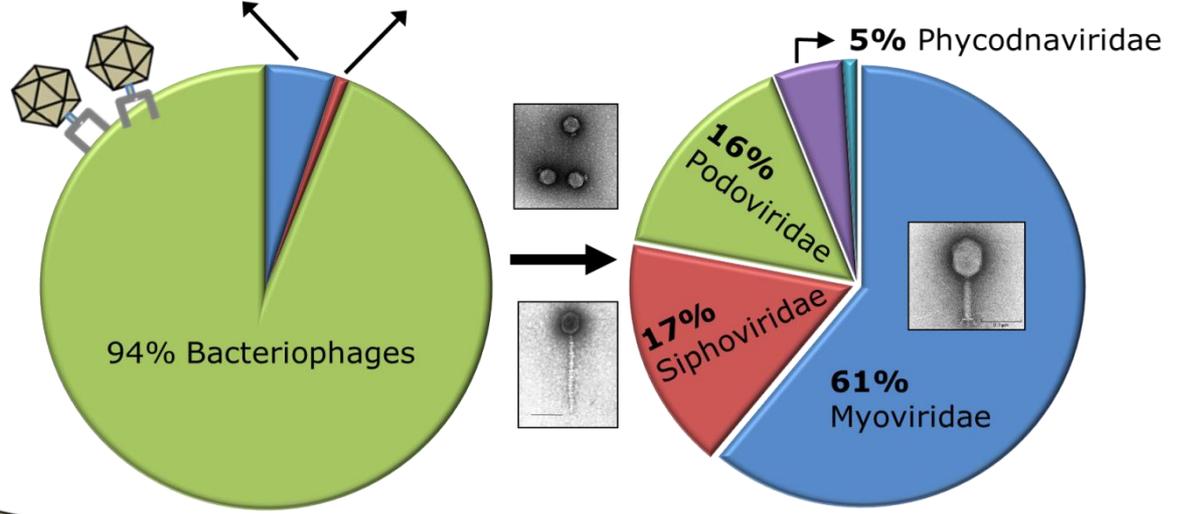
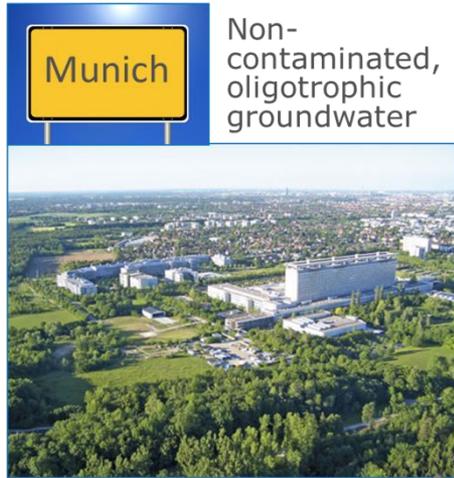


# Viruses in a petroleum hydrocarbon contaminated aquifer



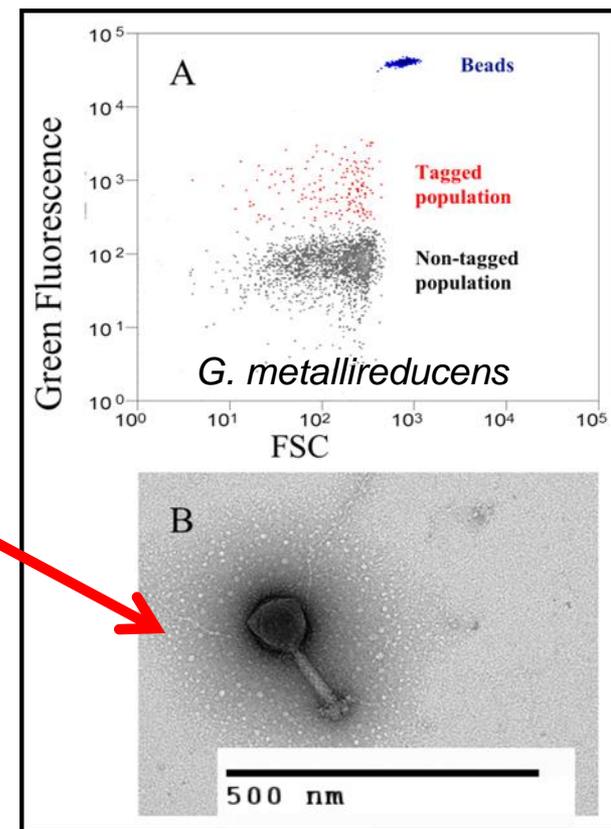
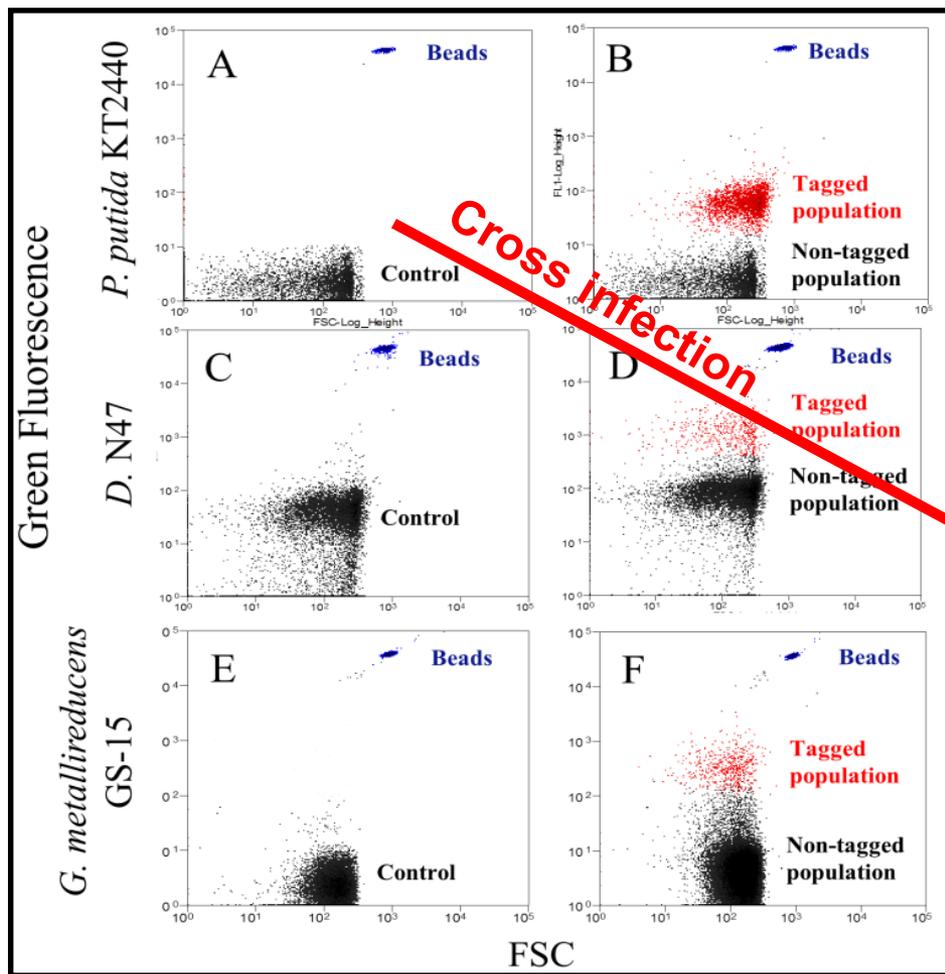
# Virus diversity in groundwater ecosystems

>5% Viruses of Amoeba, Fungi, Algae      <1% Viruses of Archaea, Invertebrates, Vertebrates



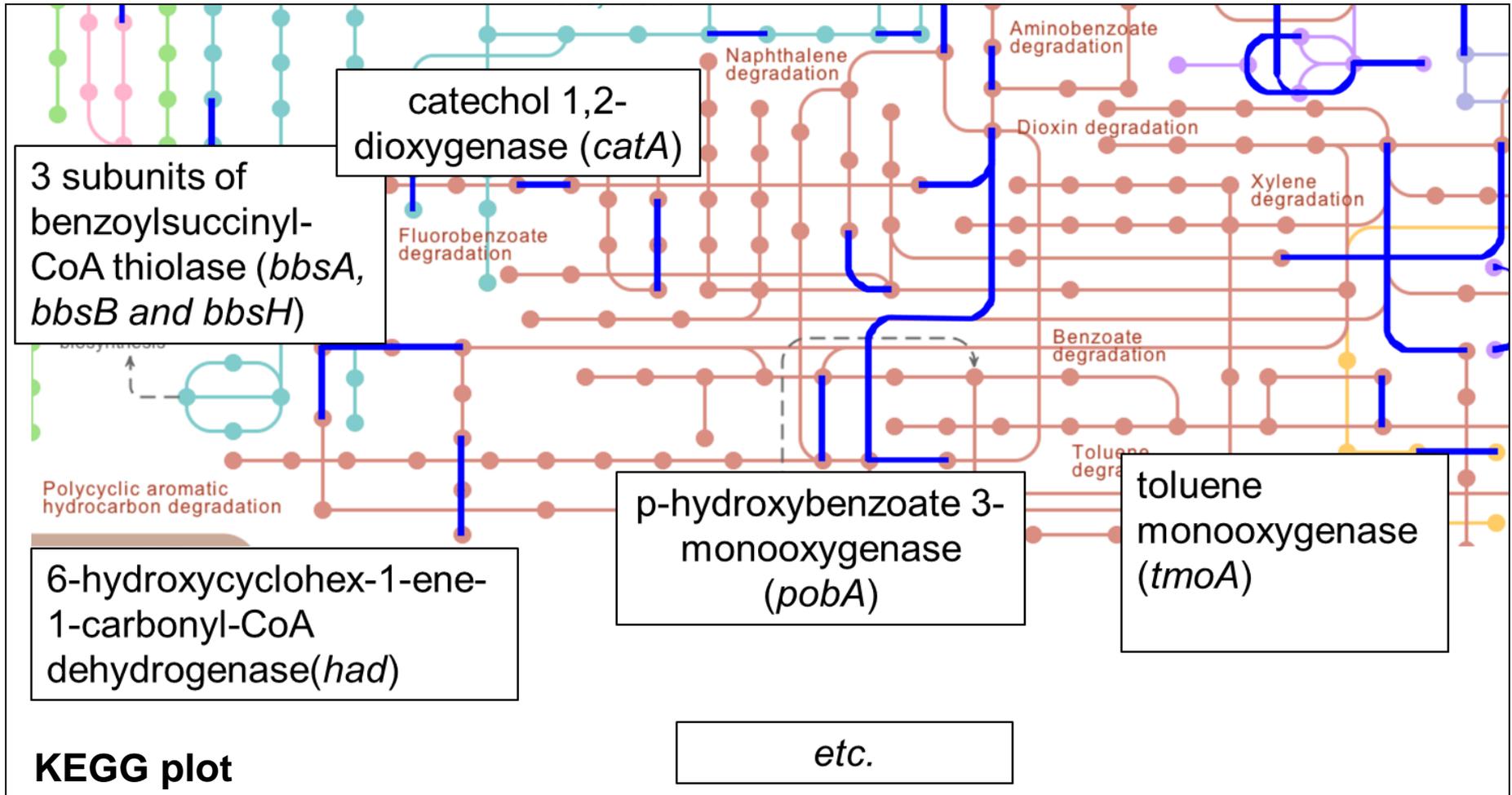
Non-tagged community vs. tagged community

# Viruses in a petroleum hydrocarbon contaminated aquifer



Deng & Griebler, unpubl results

# Bacterial degradation related genes in the virus fraction of a simplified microbial community



# What comes next?

- Detailed study of the role of viruses in microbial aerobic/anaerobic contaminant biodegradation
- Groundwater viral metagenomes from different types of aquifers including different biogeographical regions

# Thank you for your attention!

## We acknowledge

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