



Exploring enigmatic Gracilibacteria and exceptions to the genetic code

Gracilibacteria are a group of underexplored and so far uncultured bacteria, that are characterized by small and streamlined genomes. They were predicted to possess limited metabolic abilities and to lead a symbiotic lifestyle, although the search for host organisms is still ongoing. Gracilibacteria have evolved to use an alternative genetic code, in which the common stop codon UGA encodes the amino acid glycine. This codon reassignment could have been enabled by their low GC content, which might be an adaptation to ecosystem constraints. Originally described from marine habitats, such as hydrothermal vents in the Pacific Ocean, Gracilibacteria have since been detected in drinking, ground and waste water, and are likely also present in the human body.

The overall goal of this study is the characterization and genomic re-evaluation of the enigmatic Gracilibacteria lineage. You will propose a new type species, infer metabolic abilities and the evolutionary history, assess biogeography and explore potential host organisms.

Experimental Design

- 1) Assessing the biogeography distribution of Gracilibacteria (~2 weeks)
- 2) Recovering metagenome-assembled genomes (MAGs) from existing sequencing data (~4 weeks)
- 3) Inferring genome phylogeny of Gracilibacteria and related lineages (~4 weeks)
- 4) Proposing a new type species (1 week)
- 5) Reconstructing the metabolic potential of Gracilibacteria (~8-12 weeks)
- 6) Comparing Co-occurrence network to find possible hosts (~4 weeks)
- 7) Preparing a manuscript summarizing the project's finding

Optional tasks, depending on the candidate's progress and interests:

- 8) Exploring viruses targeting Gracilibacteria
- 9) Attempting to culture Gracilibacteria and their potential hosts



Main Objective and Methods

- 1) Bioinformatic analysis of metagenomic samples (read QC, assembly, binning, and read mapping, on the command line; gene annotation & metabolic reconstruction; phylogeny; co-occurrence networks)

Starting date: **March 2025.**

Prerequisites:

- SE/UE Structure and Function (by Rinke, Dutkiewicz), or equivalent expertise in metagenomics.
- Team player who can also work independently
- Fluent English, since all meetings in our group are in English

Inquire by emailing Prof. Chris Rinke (<https://lfuonline.uibk.ac.at/public/people.vcard?id=440284&search=1>).