

Metabarcoding of Plant Microbiomes I: Foundations, Methods, and Applications

We invite researchers and students to join the first in a series of training schools dedicated to metabarcoding and metagenomics of plant microbiomes. This training school provides an opportunity to gain the knowledge about metabarcoding and its applications.

Experienced lecturers will guide you through experimental design, choice of phylogenetic markers, and sequencing technologies, with special attention to methodological challenges unique to plant microbiome analysis, such as chloroplast and mitochondrial contamination.

Participants will gain an overview of basic bioinformatics tools and pipelines for data analysis.

**Three-session online training
on Tuesday afternoons:**

- 20 May 2025
- 27 May 2025
- 3 June 2025

The Zoom link will be sent to registered participants.

Contact: juraj.medo@uniag.sk

Final program

Tuesday 20 May 2025

What you need to know before starting metabarcoding experiment

13:00-14:00

Why to choose amplicon sequencing in plant microbiome research

Caroline de Tender (*Ghent University, Belgium*)

14:00-15:00

Experimental design / survey sampling plan, replications and appropriate controls

Matthias Noll (*University of Applied Sciences Coburg, Germany*)

15:00 -16:00

Phylogenetic markers for microbiome research 16S, ITS, and others

Tomáš Větrovský (*The Czech Academy of Sciences, Prague, Czech republic*)

Tuesday 27 May 2025

How to prepare samples for sequencing

13:00-14:00

Available technologies for amplicon sequencing Illumina, ONT, and others

Joel Pothier (*Zurich University of Applied Sciences, Wädenswil Switzerland*)

14:00-15:00

Library preparation possibilities, common errors and how to avoid them

Kristine Bohmann (*Globe Institute, University of Copenhagen, Denmark*)

15:00 -16:00

Methodological problems of plant microbiome analysis and how to deal with them

Juraj Medo (*Slovak University of Agriculture in Nitra, Slovakia*) Benjamin Dubois (*Walloon Agricultural Research Centre, Belgium*)

Tuesday 3 June 2025

Bioinformatics tools showcase

13:00-14:00

Necessary bioinformatics - traditional pipelines and other possibilities

Juraj Medo (*Slovak University of Agriculture in Nitra, Slovakia*)

14:00-15:00

SEED2 a user-friendly platform for amplicon high-throughput sequencing data analyses

Tomáš Větrovský (*The Czech Academy of Sciences, Prague, Czech republic*)

15:00 -16:00

PRONAME: a user-friendly pipeline to process long-read nanopore metabarcoding data in plant microbiome research

Benjamin Dubois (*Walloon Agricultural Research Centre, Belgium*)

Each topic will consist of 45 min lecture and 15 min discussion

