Université de Neuchâtel
Institut de biologie

IBIOL

EXTERNAL SEMINAR

21 MAY 2026

12:15-13:15

ROOM F200

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Phylogenomics for biodiversity assessment of regional flora in Switzerland

Accurate knowledge of phylogenetic relationships and divergence time among plant species composing a regional flora is crucial for understanding the origin of the biodiversity patterns we observe today. Unfortunately, resources available for reconstructing regional phylogenies are still largely incomplete and poorly resolved at the species level. To overcome this limitation, we developed a workflow to assemble a phylogenetic dataset for a regional flora using Angiosperms353 target-enrichment and high-throughput genome sequencing. To test our method, we sampled tissues from freshly collected plants and herbarium specimens representing 96% of the angiosperm diversity of the Geneva canton in Switzerland (1'098 species). Our result provides a more resolved and complete tree than the synthetic phylogenies currently available. We will see how this new genomic reference can be useful for guiding the necessary nomenclatural changes in the Swiss flora and how this type of genomic data opens perspectives for fine-scale biodiversity and conservation research that integrate evolutionary history.