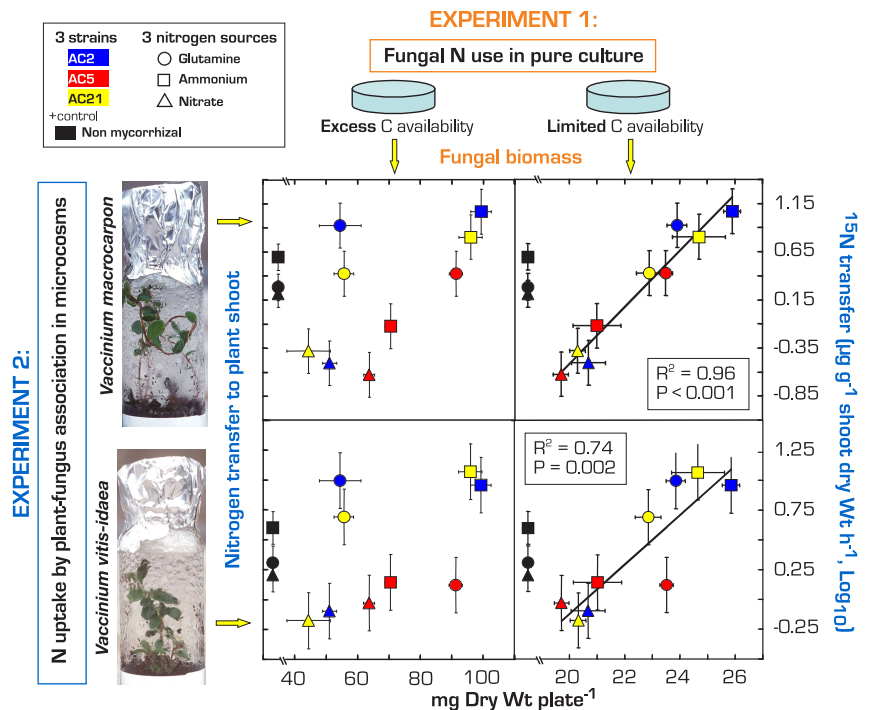


## INTRODUCTION

- The *Hymenoscyphus ericae* aggregate (*Meliniomyces* species + *Cadophora finlandica* + *Rhizoscyphus ericae*) may play a major role in soil C and nutrients cycling world-wide. Its genetic diversity is now being unravelled, but its functional diversity is still under-explored.
- Fungi of the *H. ericae* aggregate can form either ectomycorrhizal (EcM) and/or ericoid mycorrhizal (ErM) association.
- This poster presents our recent and on-going work on the link between genetic/functional diversity of these fungi and functioning of the plant-fungus association.

## STUDY 1: Nitrogen transfer to host plant is linked with fungal genetic/functional diversity

- Experiment 1:** Three closely related fungal strains (same ITS-PCR-RFLP pattern) were screened for significant variations in their ability to use different N sources in liquid culture, with either excess or limited C availability.
- Experiment 2:** *Vaccinium* seedlings were inoculated with one of these three strains, supplied with one of the N sources used in experiment 1. N transfer to plant shoot during 48 h was assessed using <sup>15</sup>N - labelling.
- There was a direct **quantitative** relationship between the rate of **N transfer to plant shoot in microcosm** and **fungal N use under limited C availability in pure culture**, irrespectively of plant host species.
- Our results highlight the need to assess C:N balance of the fungal growth media in mycorrhizal physiological studies.
- Our results clearly demonstrate that relatively **small genetic** diversity at the fungal level may **impact on the functioning** of the plant-fungus symbiosis.



## STUDY 2: Is the ability of fungi to form both ErM and EcM symbiotic associations a wide-spread characteristic within the *Hymenoscyphus ericae* aggregate?

- The aims of this study are to:
  - identify fungal genotypes co-occurring in neighbouring EcM and ErM roots
  - assess the mycorrhizal status of these genotypes.
- We are currently developing molecular markers to trace individual fungal genotypes in the field, using polymorphism in the intergenic spacer region of the rDNA (IGS-tRFLP), Single Nucleotide Polymorphism (SNPs) and/or Microsatellites (SSRs).
- The experimental approach we have initiated is summarised in the diagram below.

