Fungal endophytes of spotted knapweed: taxonomical, geographical and chronological analysis

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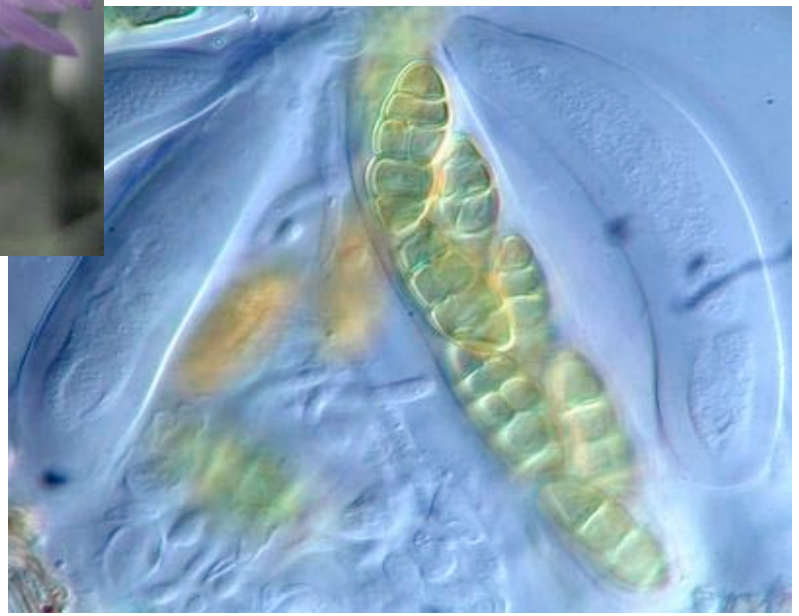

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−	**Spotted knapweed, *Centaurea stoebe***	+
Delayed flowering: *Alternaria* 123 *Fusarium* 124 Reduced number of flowers: *Alternaria* 62		Protection from seedhead weevils: *Alternaria* 62 *Epicoccum* 66
Reduced aboveground biomass and increased generalist herbivory: *Fusarium* 107		Increase of aboveground biomass: not yet investigated
Suppressed germination of *C. stoebe* itself: *Alternaria* 120 *Botrytis* 360 *Fusarium* 107 *Fusarium* 396		Suppression of germination of a competitor, assayed in the same manner as (-)-catechin: *Alternaria* 62 *Epicoccum* 66

Hypotheses of invasion and distribution of endophytes

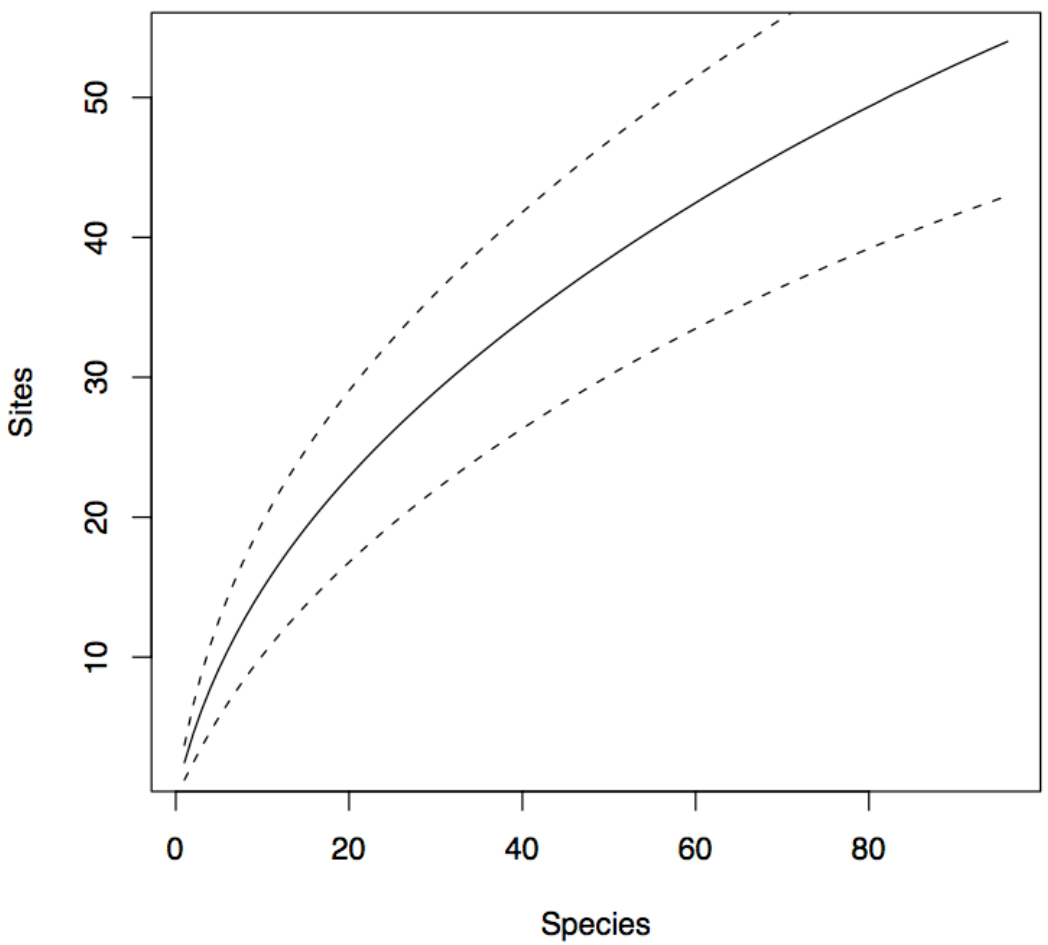
- **Enhanced Mutualism Hypothesis** – new endophytes obtained in the invaded range (IR) from native hosts (“host-jumping”)
- **Enemy Release Hypothesis** – enemies are left behind in the native range (NR) – some endophytes are cryptic pathogens
- **Novel Weapons Hypothesis** – co-introduced NR endophytes produce chemical compounds (“co-introduction”)

Life cycle of knapweed endophytes (hypothesis)

Sampling

- 61 knapweed populations sampled, plus 10 populations of native North American plants (*Saussurea americana*, *Cirsium brevifolium*, *Festuca idahoensis* etc.)
- 5 plants and 100 achenes per sample
- Endophytes isolated from achenes – 2291 isolates
- Isolates grouped in 288 morphological groups (strains)
- Each group has been sequenced (ITS and “Alt a 1”), 102 haplotypes obtained

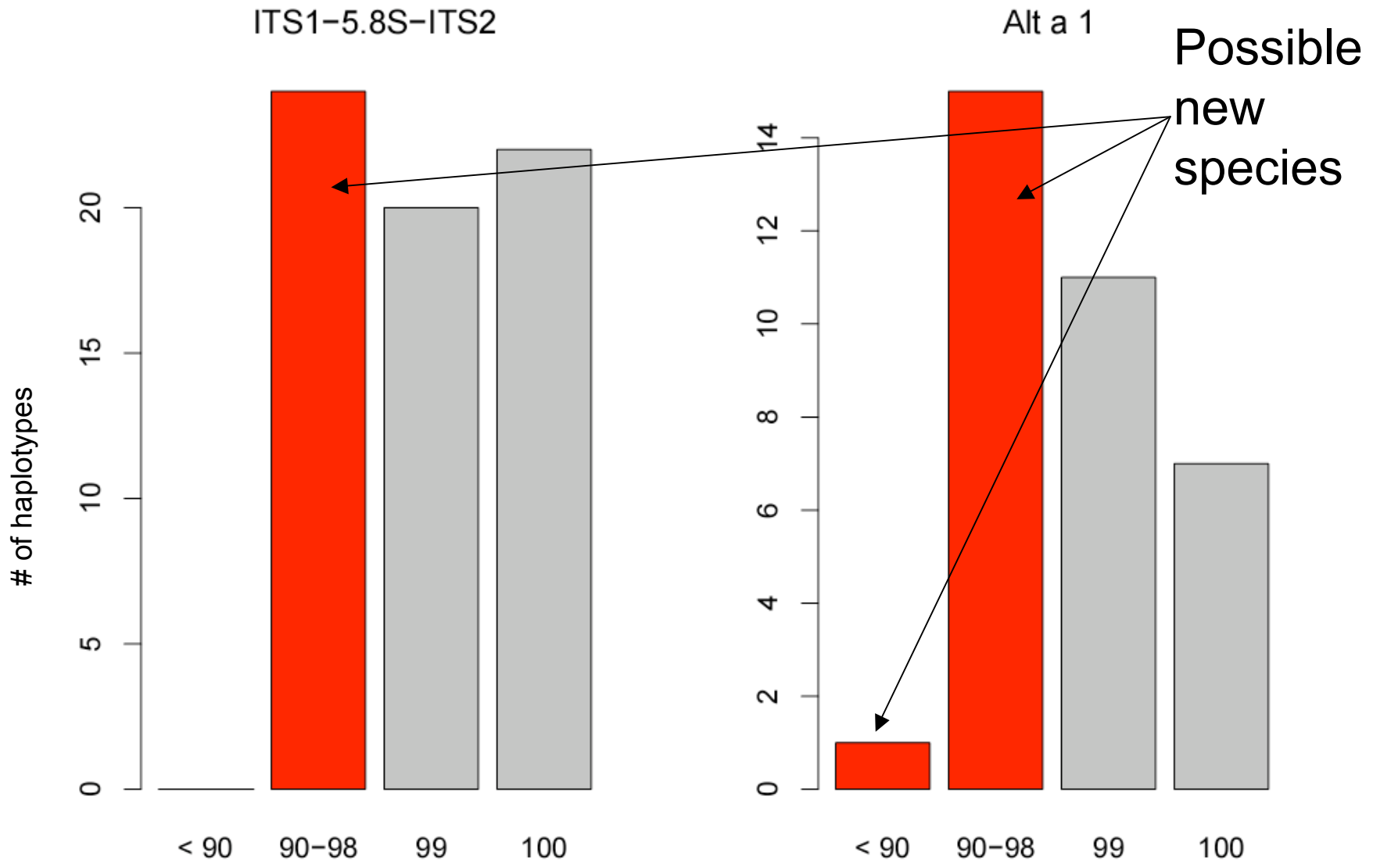
Accumulation curves



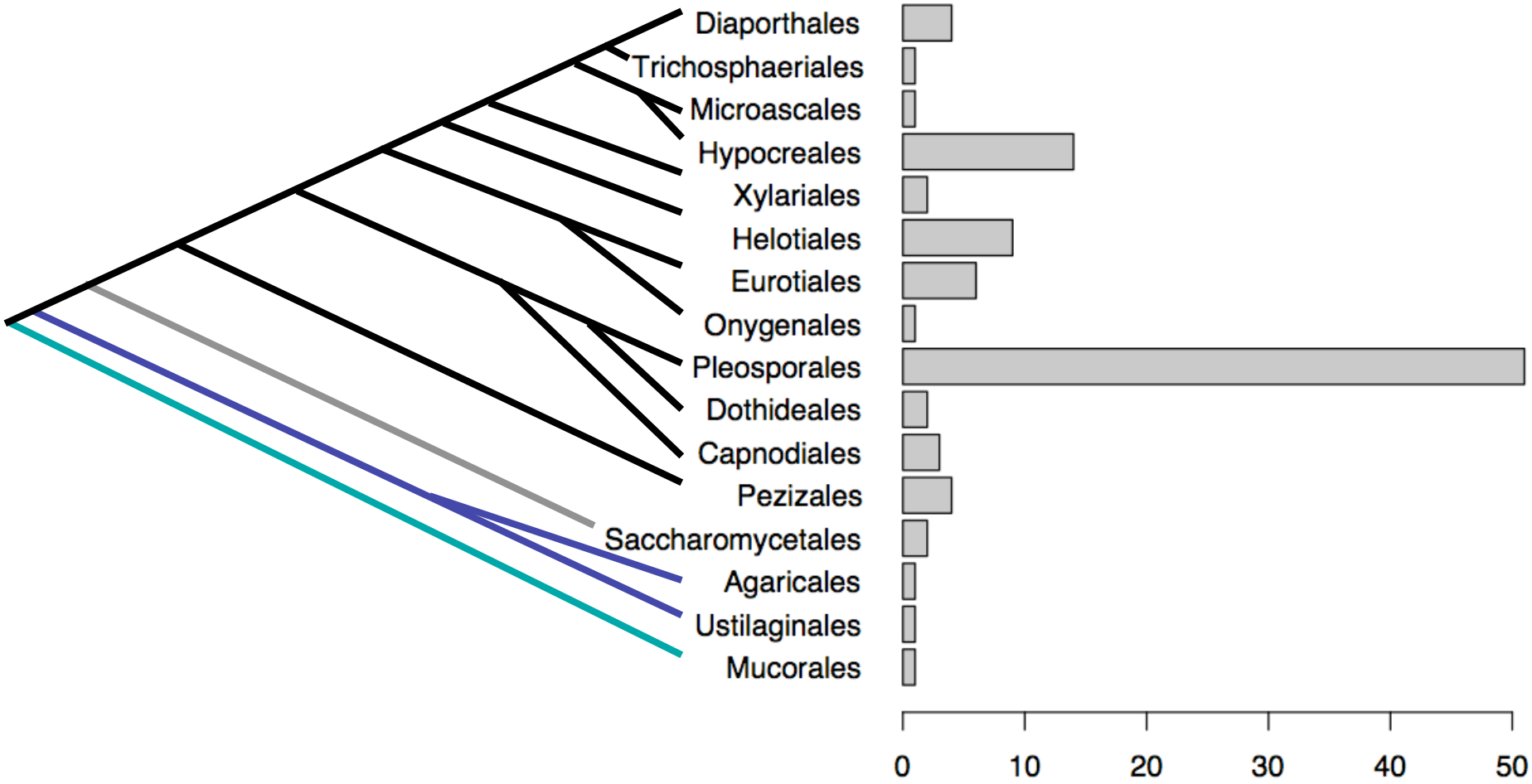
They are not asymptotic:

- The most frequent haplotypes should be analyzed;
- For ordinations, occurrence (instead of abundance) is more useful;
- For similarities between communities is better to use accumulation-based indexes (like Chao index)

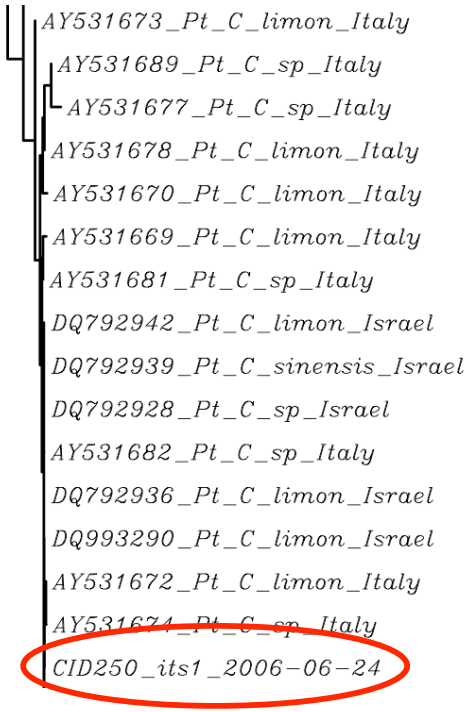
BLAST identity and new species



Taxonomic and phylogenetic structure



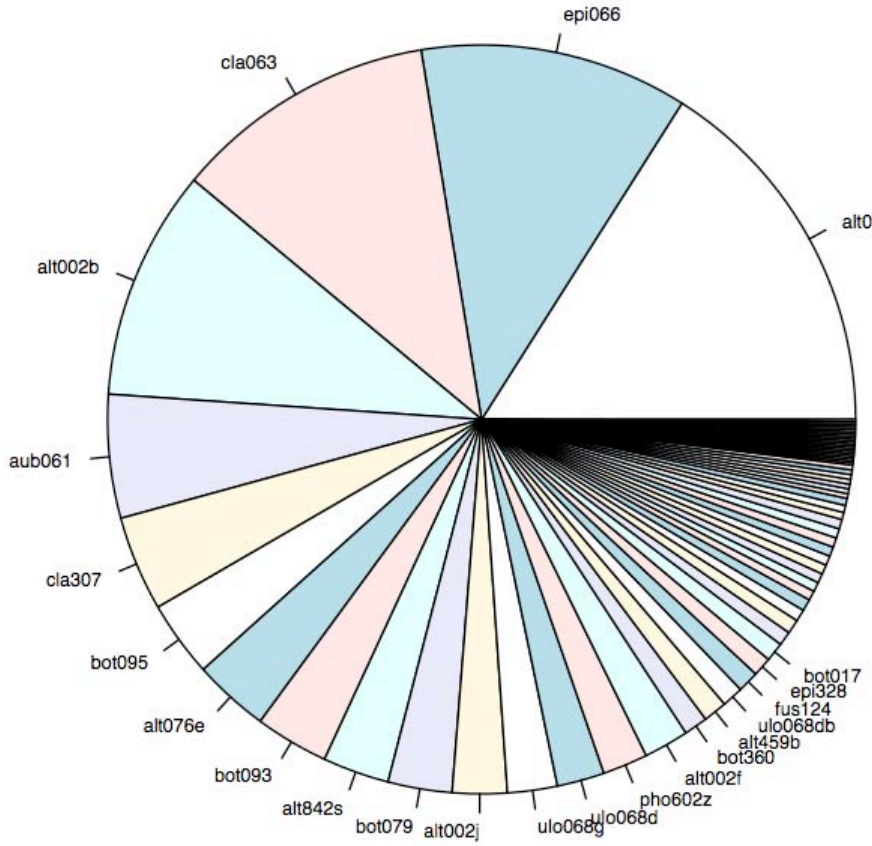
The case of putative co-introduction: *Phoma tracheiphila*



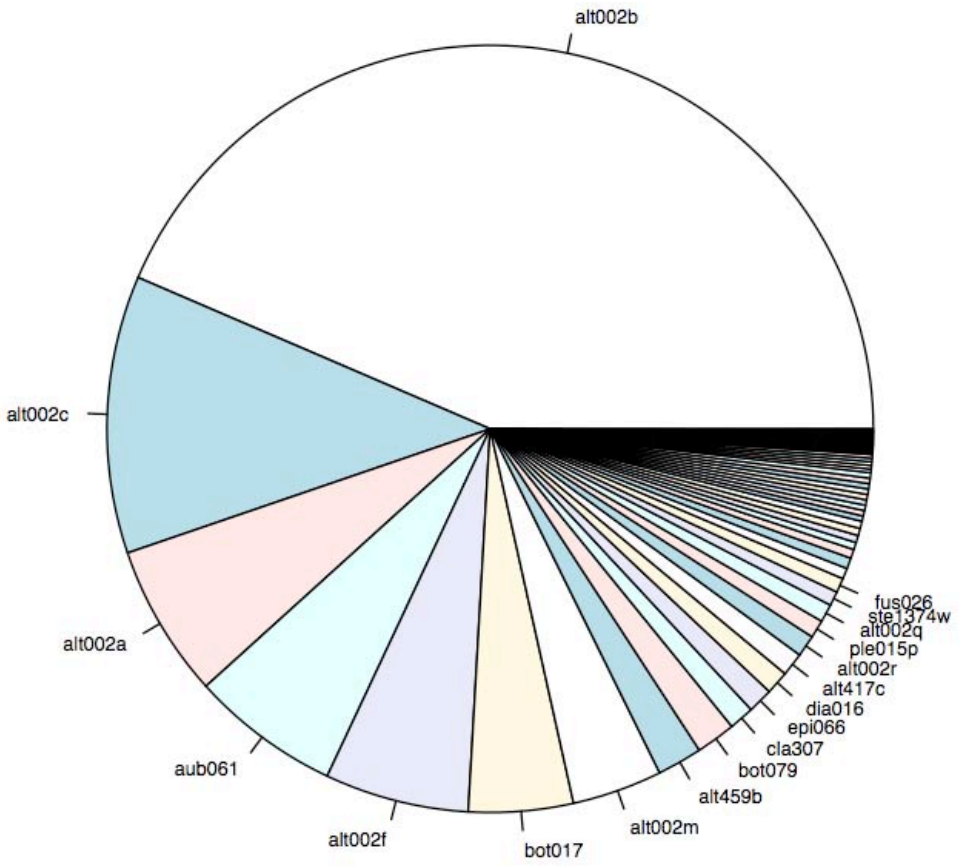
The endophyte **pho250** (South Germany) has 99% identity with GenBank sequences of *Phoma tracheiphila*, very dangerous pathogen of *Citrus* trees

SUDDEN DIEBACK CAUSED BY MAL SECCO.

Comparison of diversity between two ranges

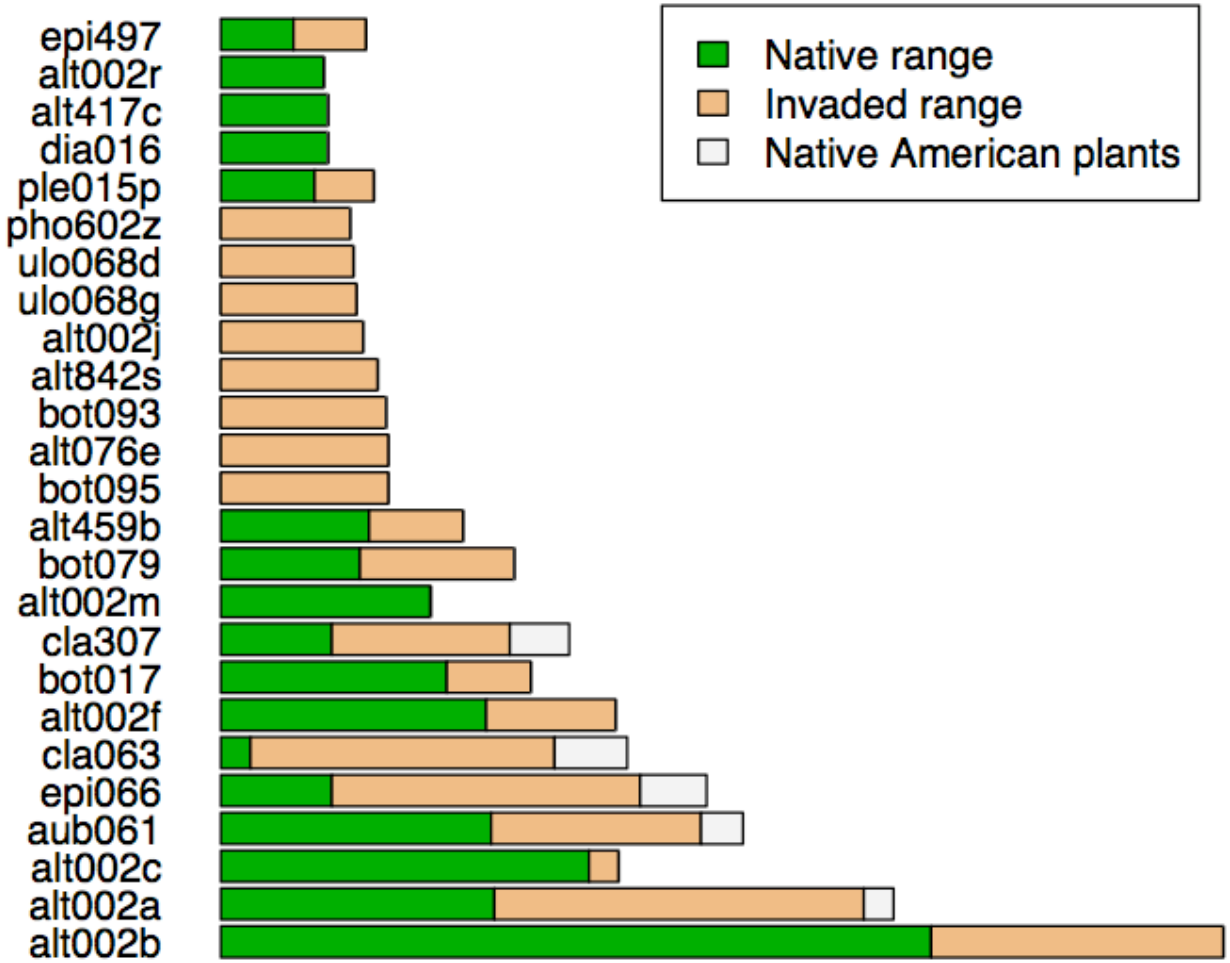


Invaded range
(N. America)

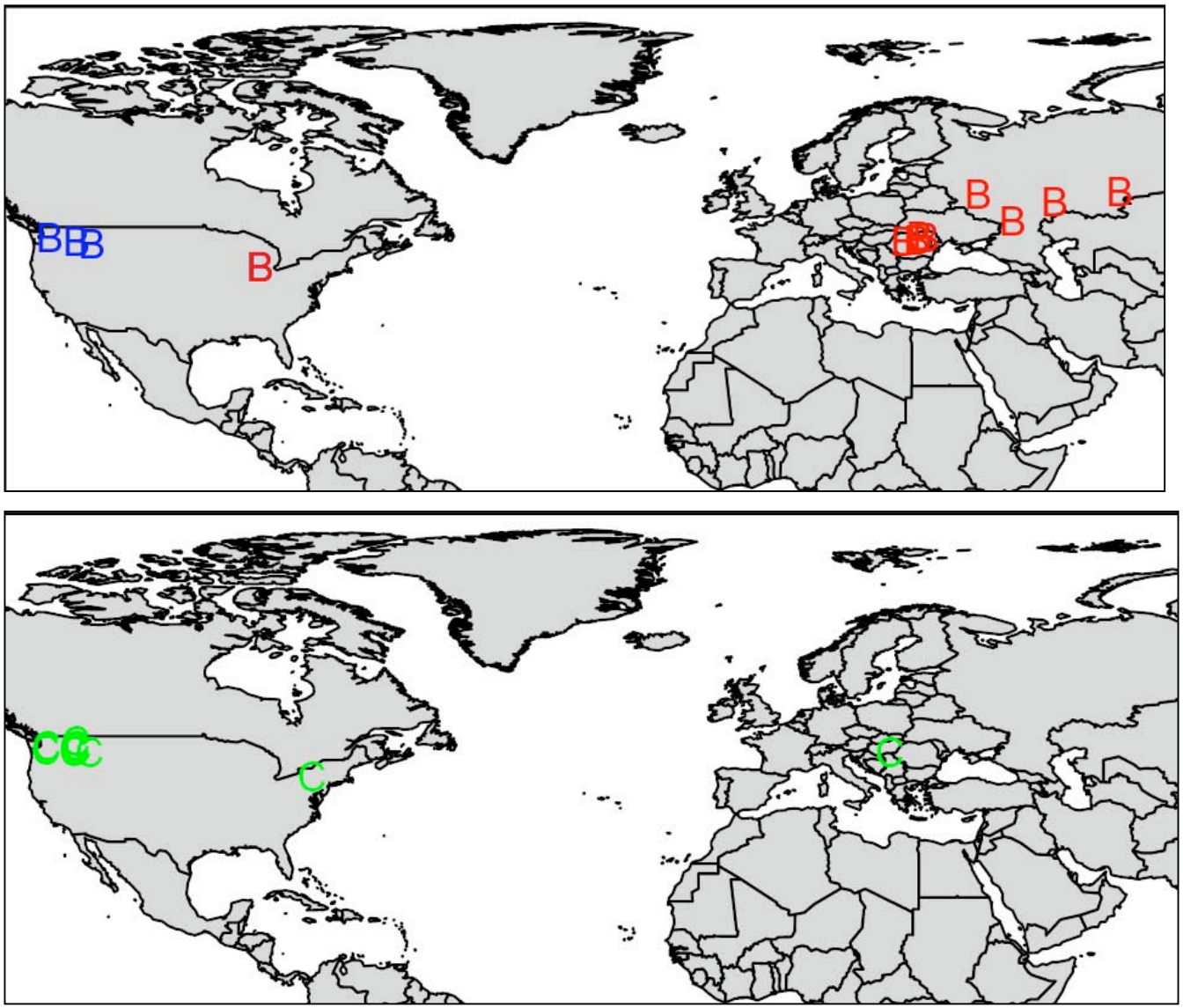


Native range
(Europe)

Endemic and cosmopolitan haplotypes

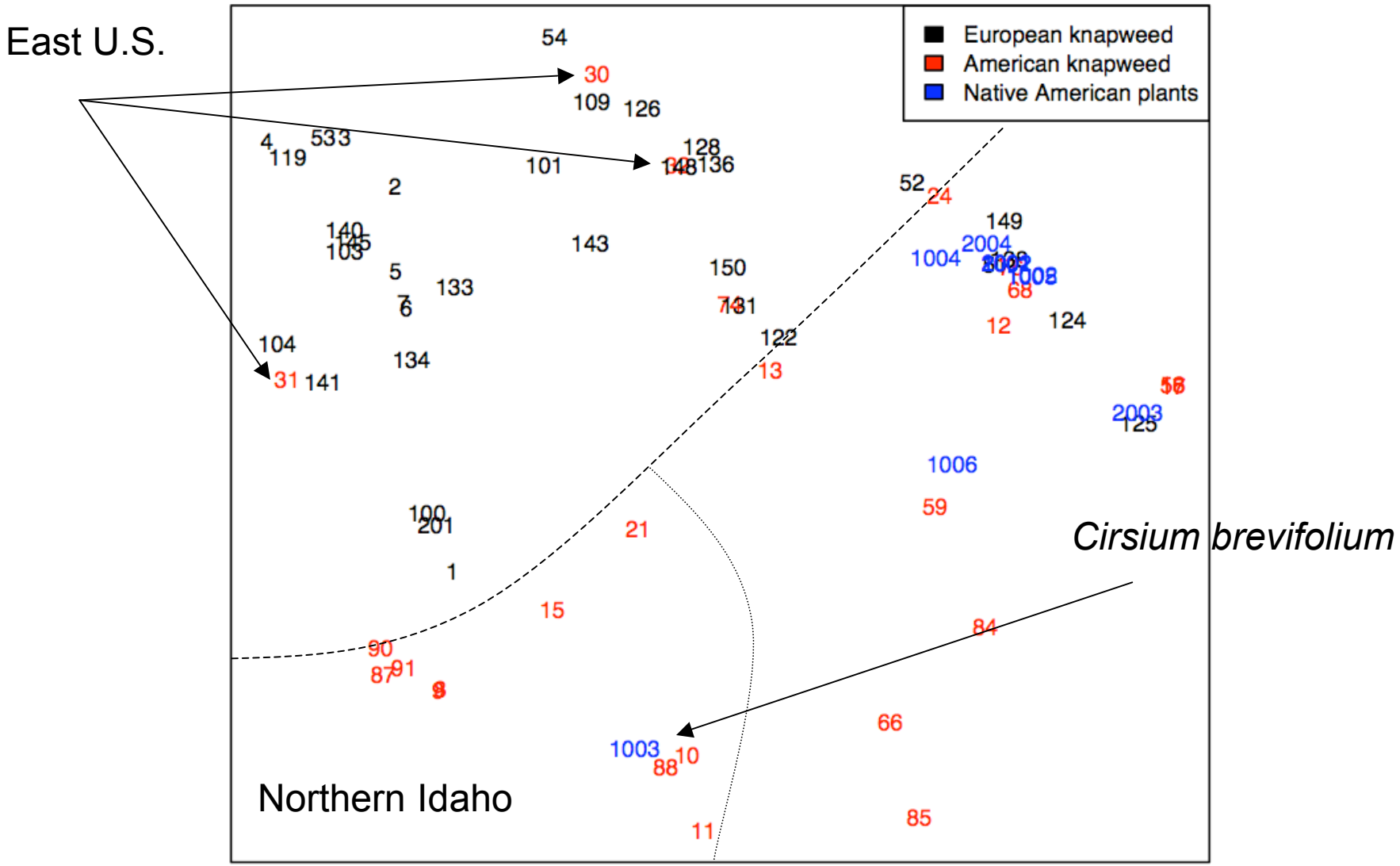


Distribution of *Botrytis* 017/095 and *Cladosporium* 063



Ordination of communities

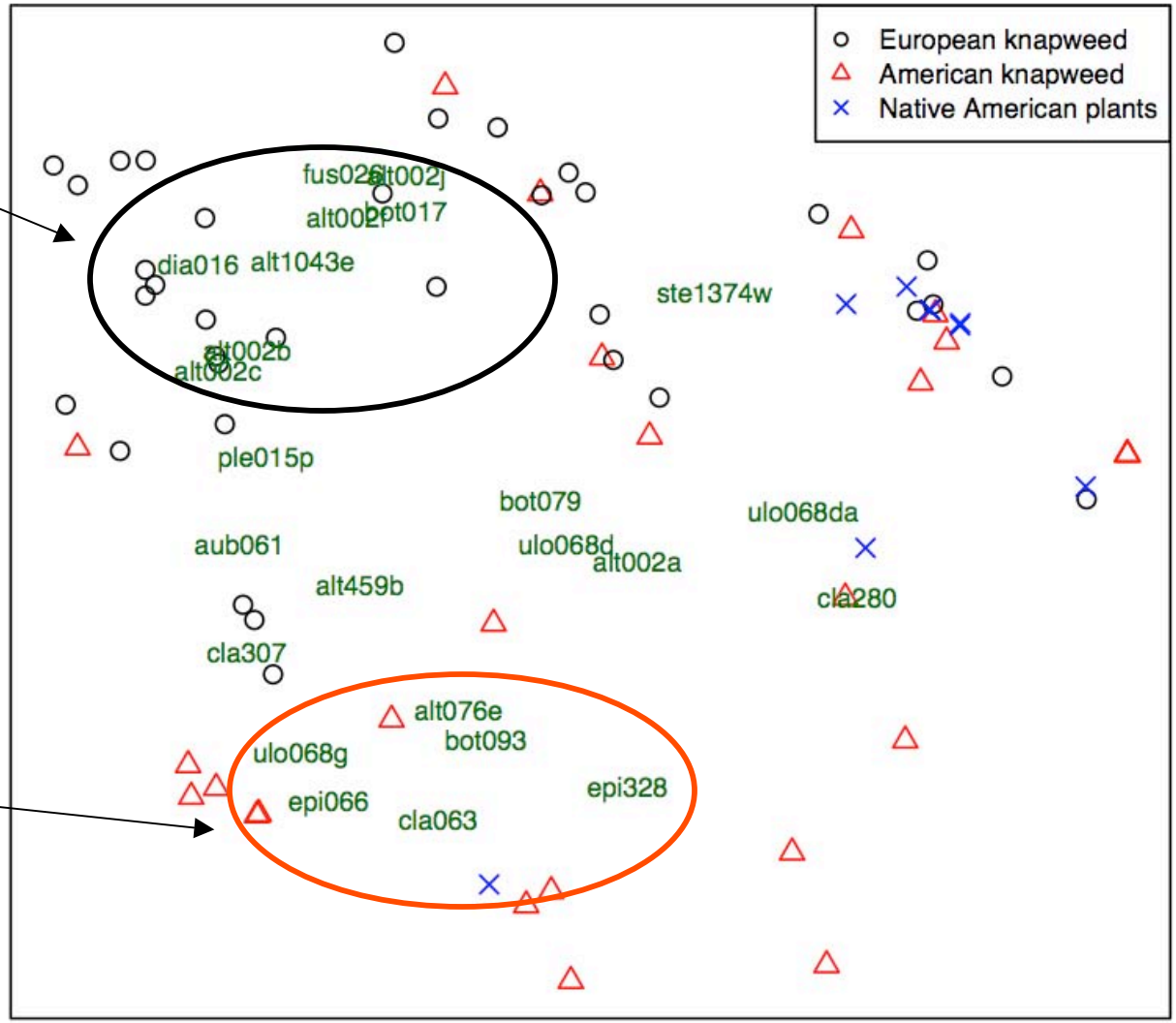
Principal coordinates analysis (PCO) based on **Chao similarity** indexes



Fungal haplotypes that characterize communities

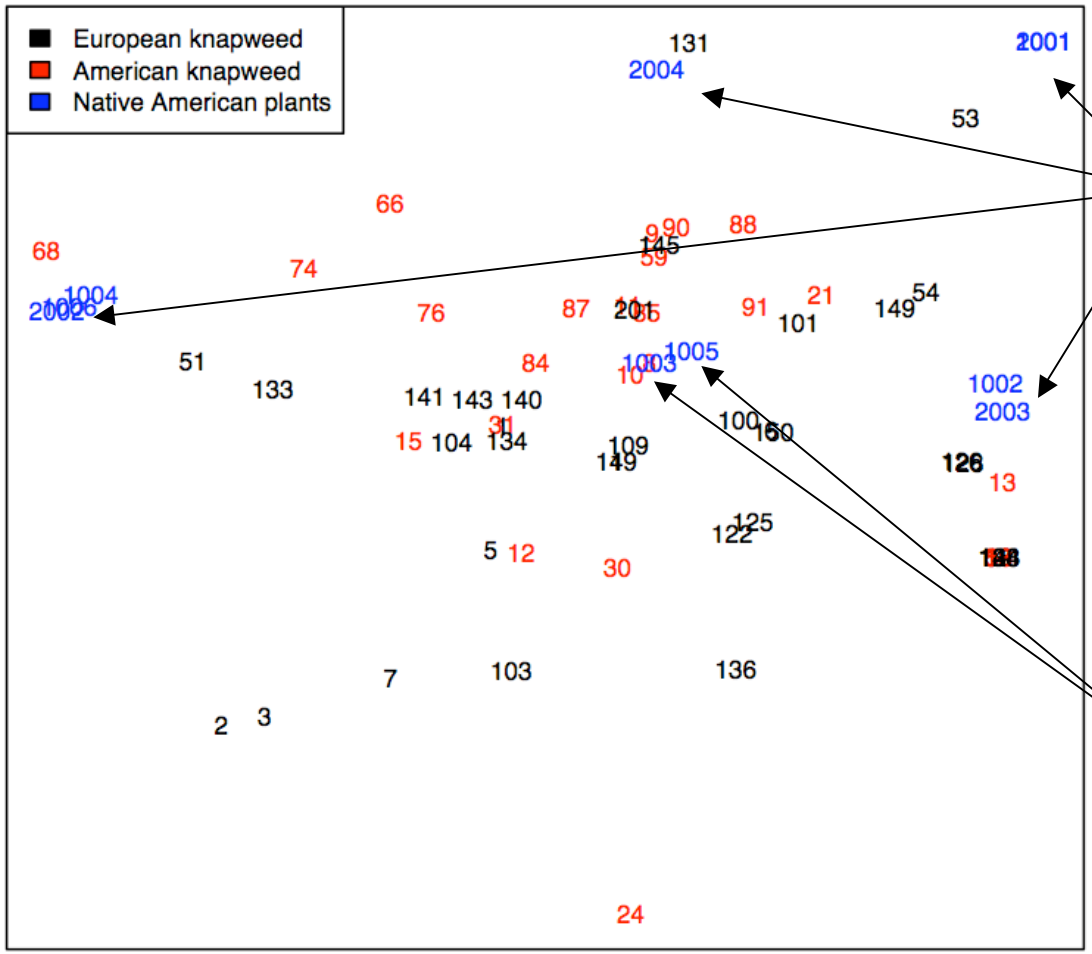
Species are common for NR

Species are common for IR



Phylogenetic ordination via Phylocom (Web et al., 2007)

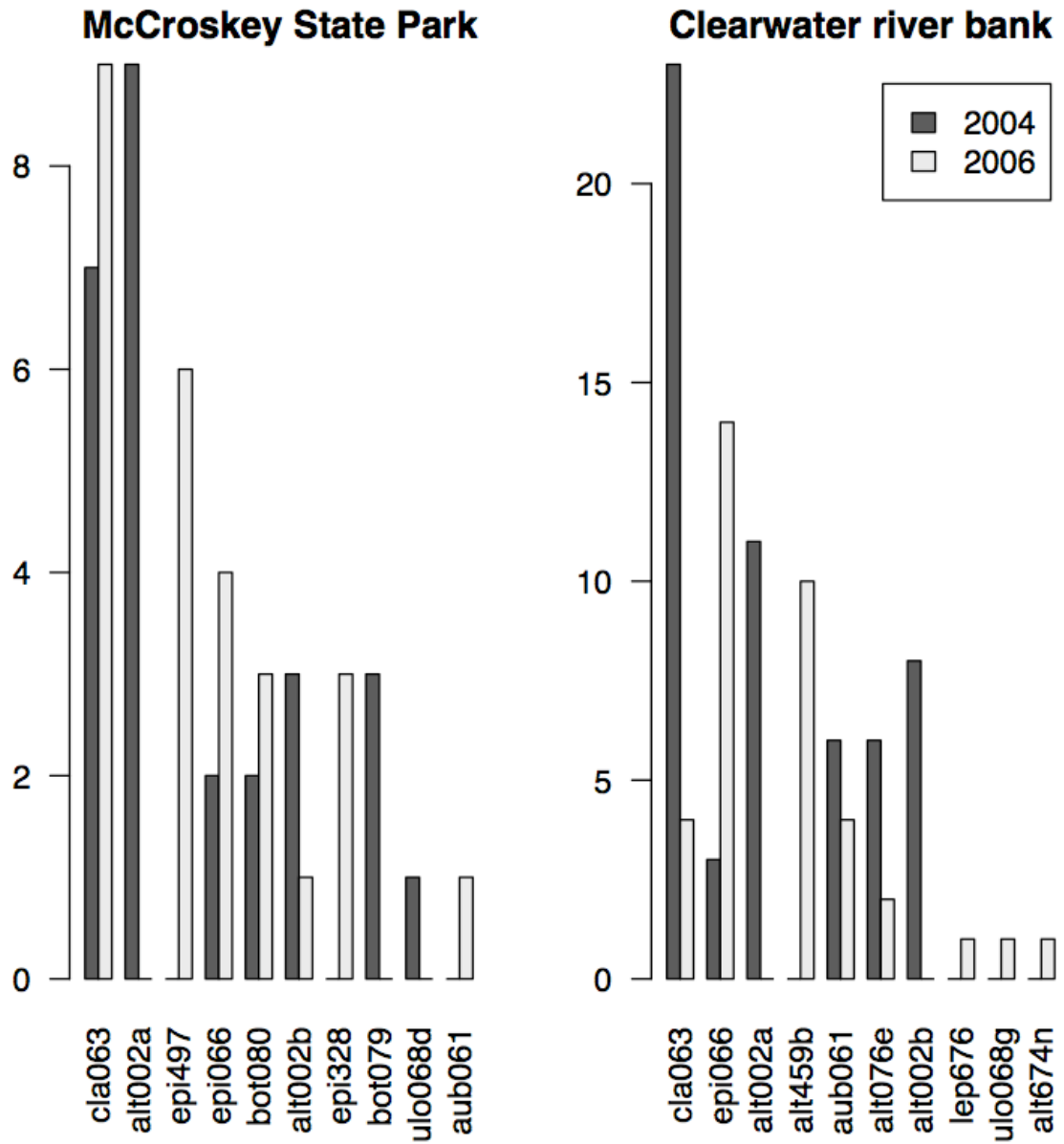
mean phylogenetic distances based on ITS MP phylogenetic tree



Fescue (*Festuca* spp.) communities

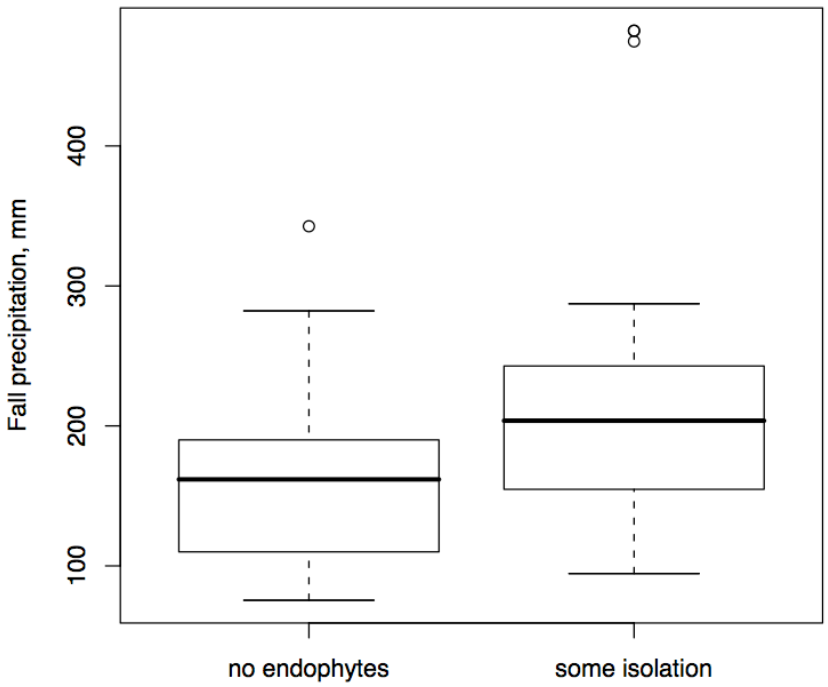
Aster jessicae and *Cirsium brevifolium* communities

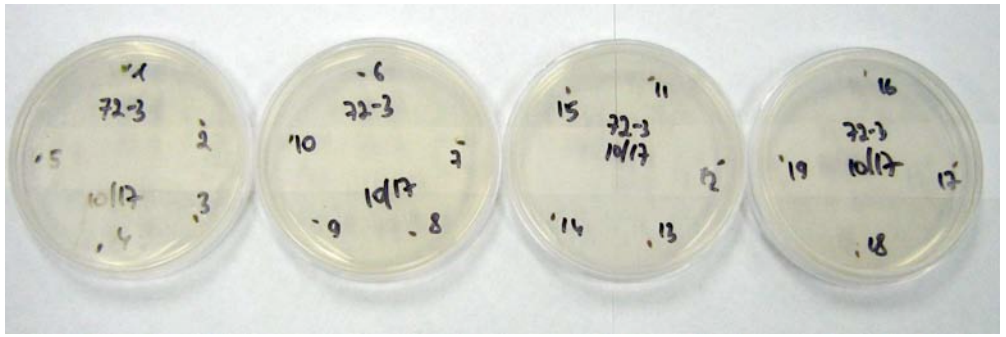
Repeated sampling



Some of most widespread fungi are repeatedly isolated whereas some *Alternaria* species are not easy to re-isolate

Diversity and climate





We have higher isolation frequencies from sites where late summer and fall (August-November) precipitation is higher

Acknowledgements

- Timothy Prather
- Cort Anderson
- Rebecca Ganley
- Sanford Eigenbrode
- Hongjian Ding
- Maryse Crawford
- The team of R project for statistical computing
- Idaho State Government

Web-site of the project:
http://uidaho.edu/~shipunov