

Data obtention

Sampling of Flora Alpina

Collection of leaves
(preserved in silica-gel)
+ herbarium specimens

4500 taxa
(60% done)



Sequencing

10 cpDNA regions
(different variability levels)



Phylogenetic reconstruction

Alignment

4 algorithms (ClustalW2, MAFFT, Muscle, Kalign)

Quality assessment & selection (MUMSA)

Removal of ambiguous sites (trimal)

Concatenation of matrices (FASconCAT)

TGAACCTGAGT
TGAACTTGAGT
TGAACCTGACT
TGA-CCTTAGT
TG--CCTTAGT

Phylogenetic inference

Supermatrix + Supertree constraint

Maximum-Likelihood (RAxML)

Bayesian inference (BEAST)



Diversification analyses

Molecular dating

Relaxed molecular clock:

- autocorrelated model (r8s)
- uncorrelated model (BEAST)



Niche evolution

Rate

Tempo (ancient vs. recent)

Mode (gradual vs. punctual)

