Phylogenomic Study of the Whole Alpine Flora

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How is the Climate Changing...

an evidence: a very significant increase of the climate change induced by human activities
Consequences of climate change on mountain landscapes
Why Is the Alpine Flora Comparatively Robust against Climatic Warming?

Christian Kienzer * and Erika Hilbichunner

Abstract:

Plant species richness occurs at mid latitude, that is the temperate zone [4,10,11,14,15]. The individual and interacting influences of these changes act upon alpine plants through differences in moisture, temperature, and light, and the growing season at the level of plant meristems may vary between 6 and 14 months depending on altitude and exposure. The sun. This is also the reason why tree stature and high foliage density, alpine plants engineer a microclimate that differs greatly from free air and what trees at treeline experience [1,12].

Effects on Alpine Plant Communities

Life conditions for alpine plant communities create by climate and topography...
Phenological and elevational shifts of plants, animals and fungi under climate change in the European Alps

Yann Vitasse1*, Sylvain Urschulack1,2,3,4, Geoffrey Klein1,2, Thierry Rohnerstange2, Yannick Chattaro2, Anne Delostrate1,2, Christian Monnerat6, Martine Rebetez2,5, Christian Rixen2, Nicolas Strehbl3, Beredikt R. Schmidt2,4, Soaja Wipf2,5, Thomas Wohlgemuth2, Nigel Gilles Yoccoz1 and Jonathan Leitner2,5

Novel competitors shape species’ responses to climate change

John M. Alexander1, Jeffrey M. Dixon2 & Jonathan M. Leitner2

Effects on Alpine Plant Communities

Phenological and elevational shifts under climate change, depending on dispersal capacity and leading to new species composition (competition)
How to preserve it?

understanding how plant communities are assembled (functional or phylogenetic diversity) is a paramount..
OriginAlps/Phylo[Alps/Norway] projects

understanding the evolutionary and ecologic assembly of the whole artico-alpine flora
A Genome Skimming Approach

Whole genome sequencing at very low coverage sufficient to capture organelle genomes.
homogenizes the nucleotide composition of the IRs among abundant

Presentation of Non-identical IRs

automatically scans the other side of the region when deciding

complementing this region would bisect the gene – Chloroplot
gene is extending beyond a region – and hence, reverse

panel.

Zheng et al.
schemes and interesting genomic indices.

FIGURE

e presence of IRs is nearly a universal feature of the chloroplast

Goulding et al., 1996). Since concerted evolution

en assembled

ten times

duction
cient

e identity (%)

rbcL

90%

matK

89%

ITS2

96%

sequences using the manual function.

is acting over the IRs, this is the proper methodological procedure,

identical (embedded in OGDRaw assume that IR sequences are completely

arising from sequencing errors, which has accidentally slipped

undetected, which can lead to erroneous interpretations. For

assembly, read processing, and quality assessment are o

Non-identical IR copies frequently arising from poor genome

In the case of

aware IR detection method would help reduce such error rates.

that errors might slip the attention of researchers, and an error-

mtDNA genomes

Lohse et al., 2013

Comparative analyses showed that the identity

was 92.267, and

90% for all three markers in 1034 of 1036 genera in 160 families, and only Boraginaceae

differences (Table 1). In addition, the reassembled

recovered coding genes from both tissue sources (121 for silica gel dried and 118 for herbarium

specimens mainly from the European Alps and the Carpathians. Overall, we were able to assemble

of 2051 herbarium specimens from Norway

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Abstract:

Genome skimming has the potential for generating large data sets for DNA barcoding and

rDNA recovery of coding genes from both tissue sources (121 for silica gel dried and 118 for herbarium

wider biodiversity genomic studies, particularly via the assembly and annotation of full chloroplast

type. It is therefore an e

and work well across most of the land plant families and genera we tested, independently of material

rate was

90%

63%

96%

89%

70%

68%

40%

84%

88%

83%

84%

84%

86%

88%

90%

92%

92%

94%

96%

97%

99%

Bioinformatic Challenges I

new computational tool need to overcome complex plastid structure, mtDNA assembly

and organelle transfers issues using traditional assembler
Bioinformatic Challenges I

development of ORTHOSKIM pipeline to perform in silico sequence capture
(Pouchon et al. accepted.)

available on Github: https://github.com/cpouchon/ORTHOSKIM
example of ORTHOSKIM capture and phylogenetic application
**Bioinformatic Challenges II**

high resource and computational time requirements

luke23: 20 CPUs, 128 Gb
luke49: 24 CPUs, 128 Gb

median assembly time: 1h:5m:0s (24 CPUs)/library

expected time for all libraries: 6943h:38m:30s ~ 290 days

phylogenetic inference time: 154h:3m:1s (24 CPUs) ~ 1 week
A First Phylogeny of a Whole Biogeographic Area

6986 taxa - 4,775 full cpDNA + 2,211 ORTHOSKIM) - 84 genes (79 CDS, 4 rRNA, trnL-UAA) - 62,049 Nt (49,660 informative; 9.05% missing)
Where is it Going?

more data, more taxa and more complex models (phylogeny and dating): utopia vs reality (Dahu)?
Thank you

in behalf of the PhyloAlps consortium