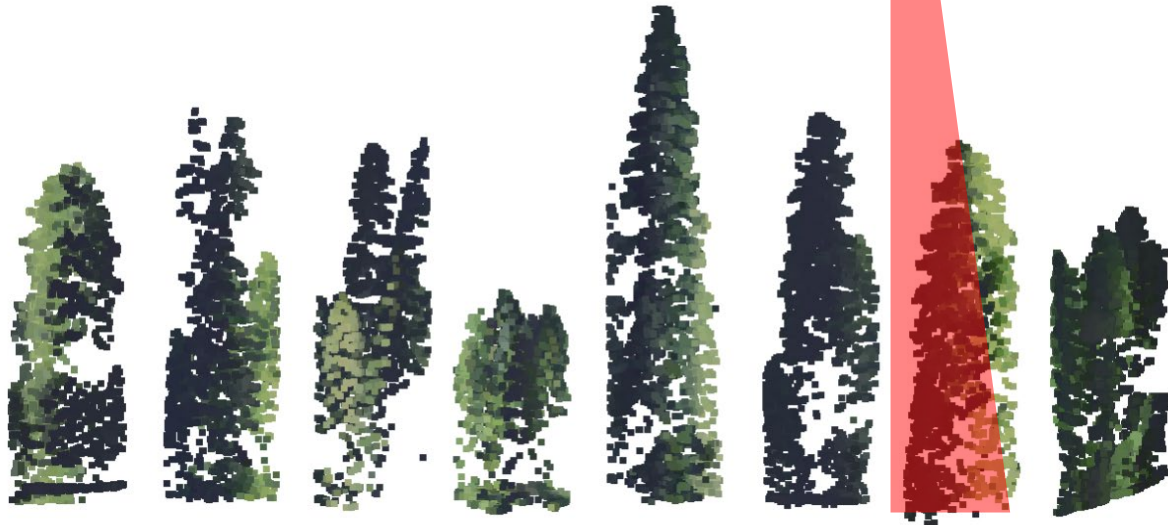


**Crown closure affects endophytic leaf
mycobiome dynamics
over time in
Pseudotsuga menziesii var. *menziesii***

Kyle A. Gervers
Daniel C. Thomas
Bitty A. Roy
Joseph W. Spatafora
Posy E. Busby



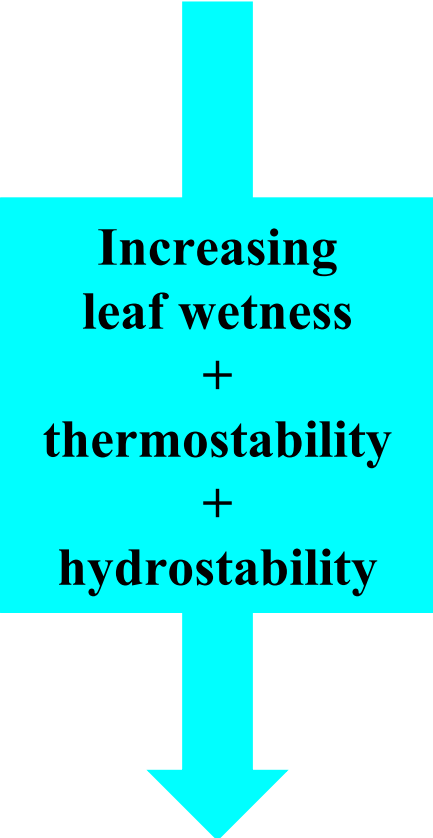
Overview

- Needle communities of old-growth canopies
- Interpreting results...
- Improving amplicon sequencing to achieve improved inference from common garden studies

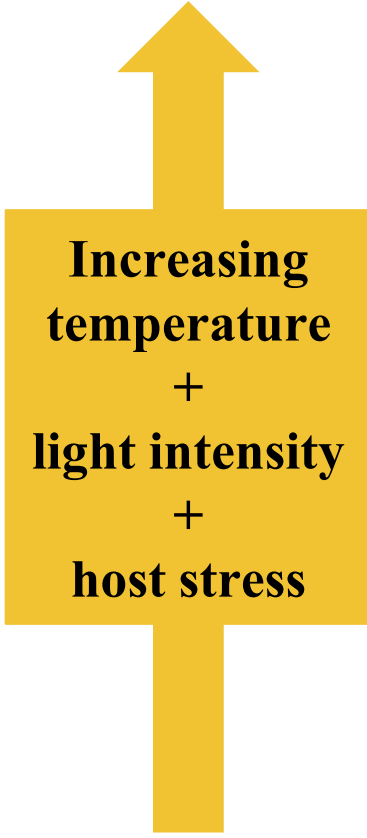


Tom Iraci





**Increasing
leaf wetness
+
thermostability
+
hydrostability**



**Increasing
temperature
+
light intensity
+
host stress**

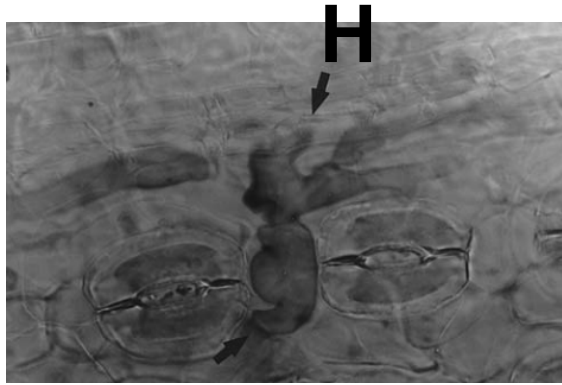
A1

More
exposure
over time

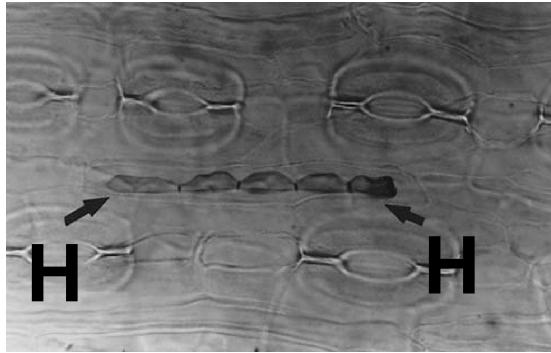
A4



Illustration by Nancy Babay



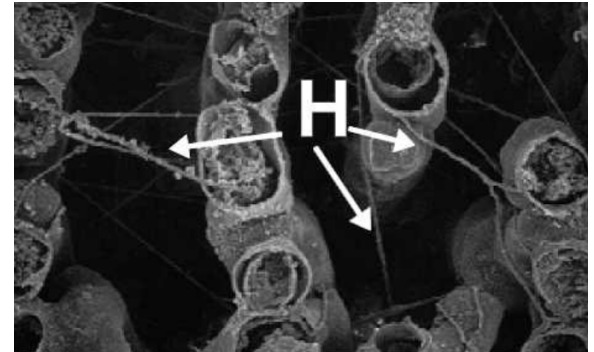
Phyllosticta spp.



Rhabdocline parkeri

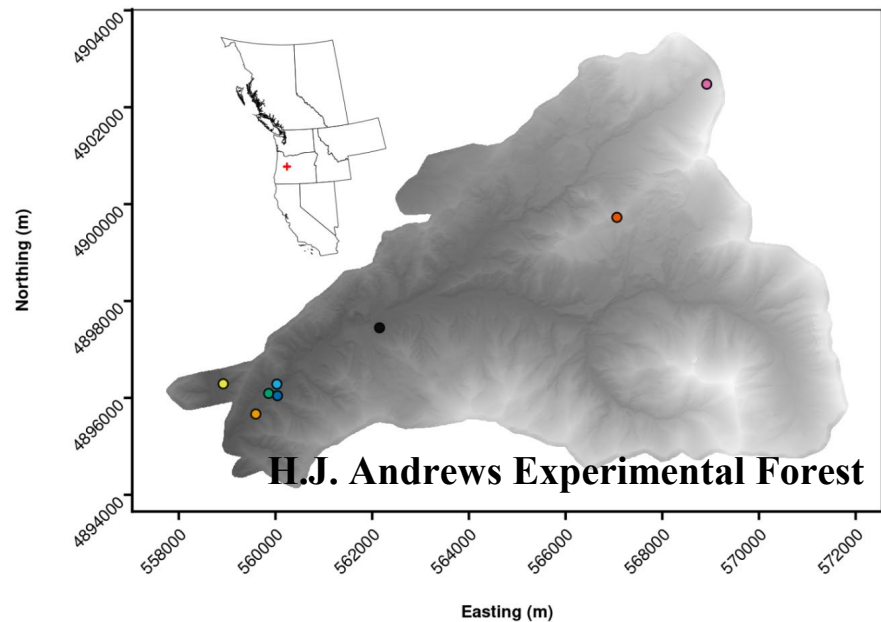


Nothophaeocryptopus gaeumannii



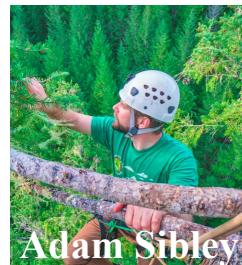
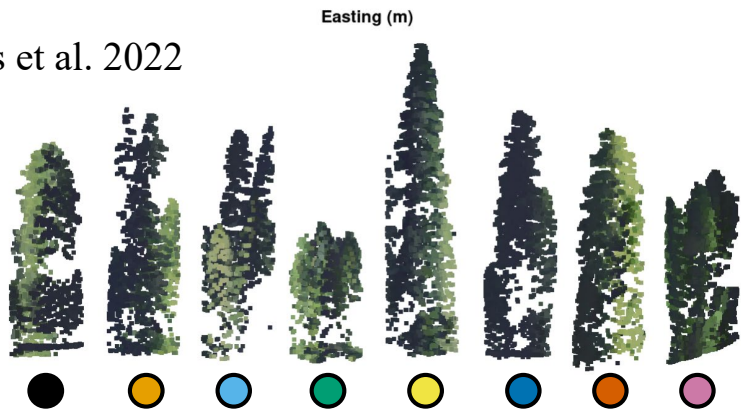
H = Hyphae

**Do needle communities from exposed crowns
differ from closed crown communities?**

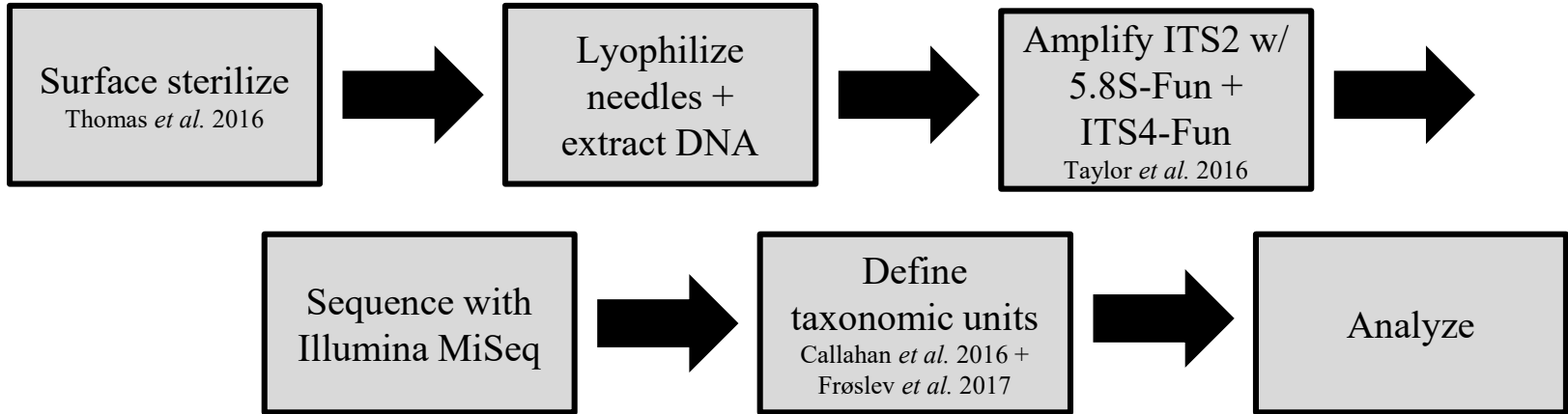


- 8 trees climbed
- 4 needle ages
- Crown sampled at consistent intervals

Gervers et al. 2022



Metabarcoding/HTS/NGS workflow

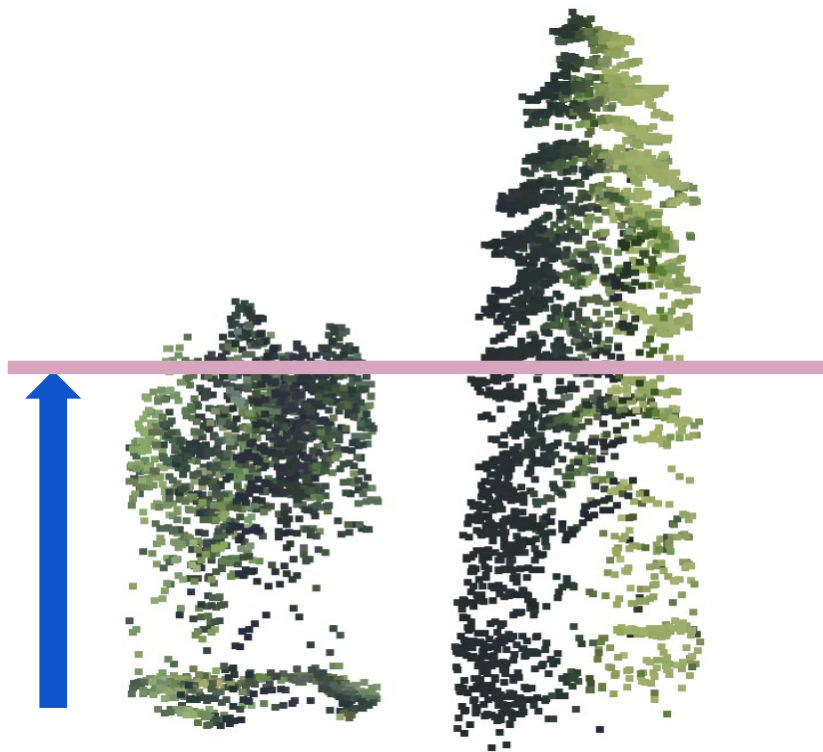


How do we quantify exposure?

Height

Crown closure

Height



How do we quantify crown closure?

Light Detection and Ranging

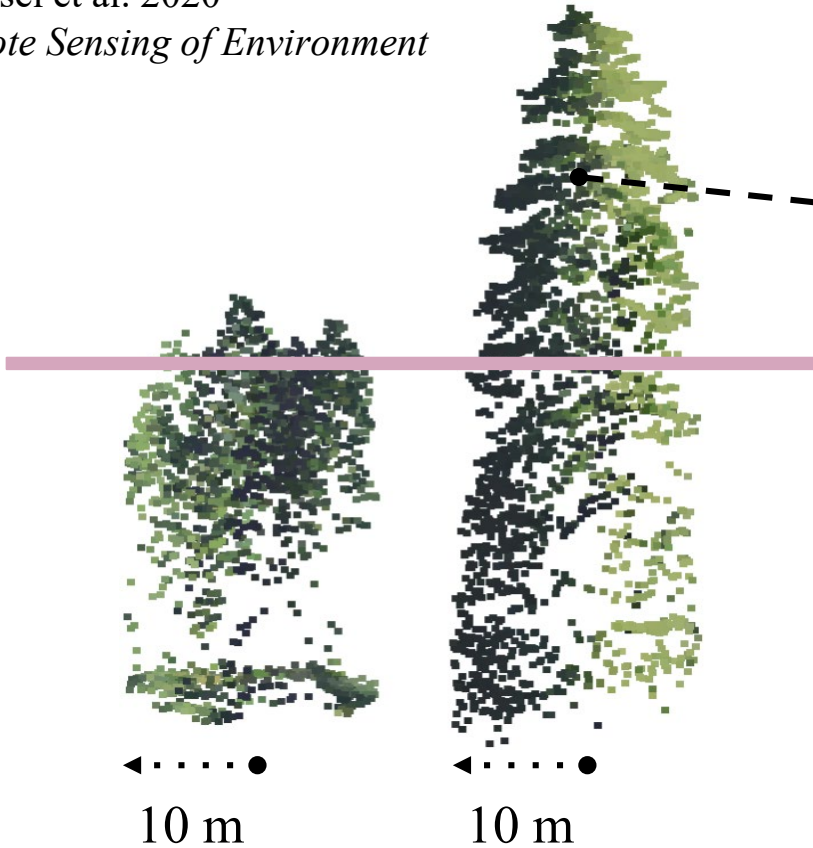


Roussel et al. 2020
Remote Sensing of Environment

Crown closure index

=

Points above
sampled height

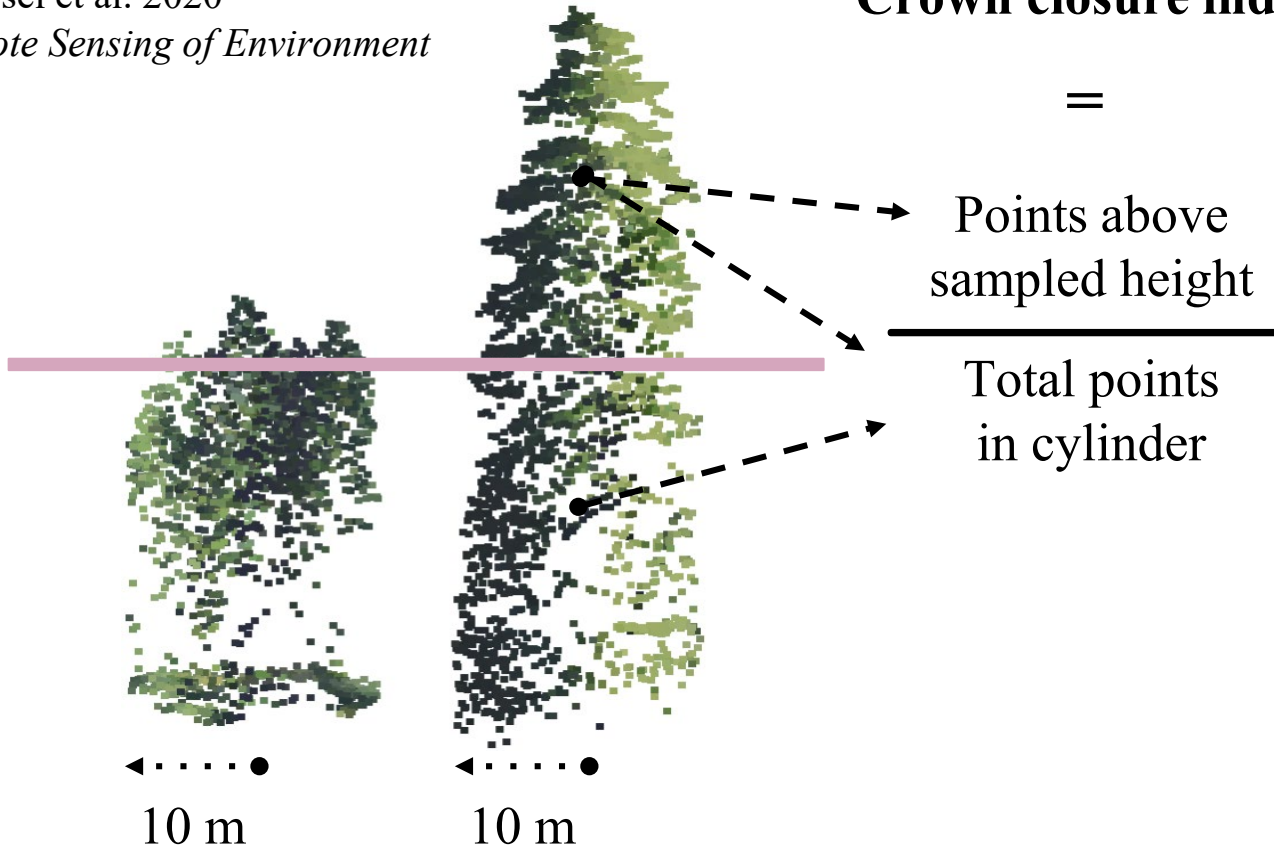




Roussel et al. 2020
Remote Sensing of Environment

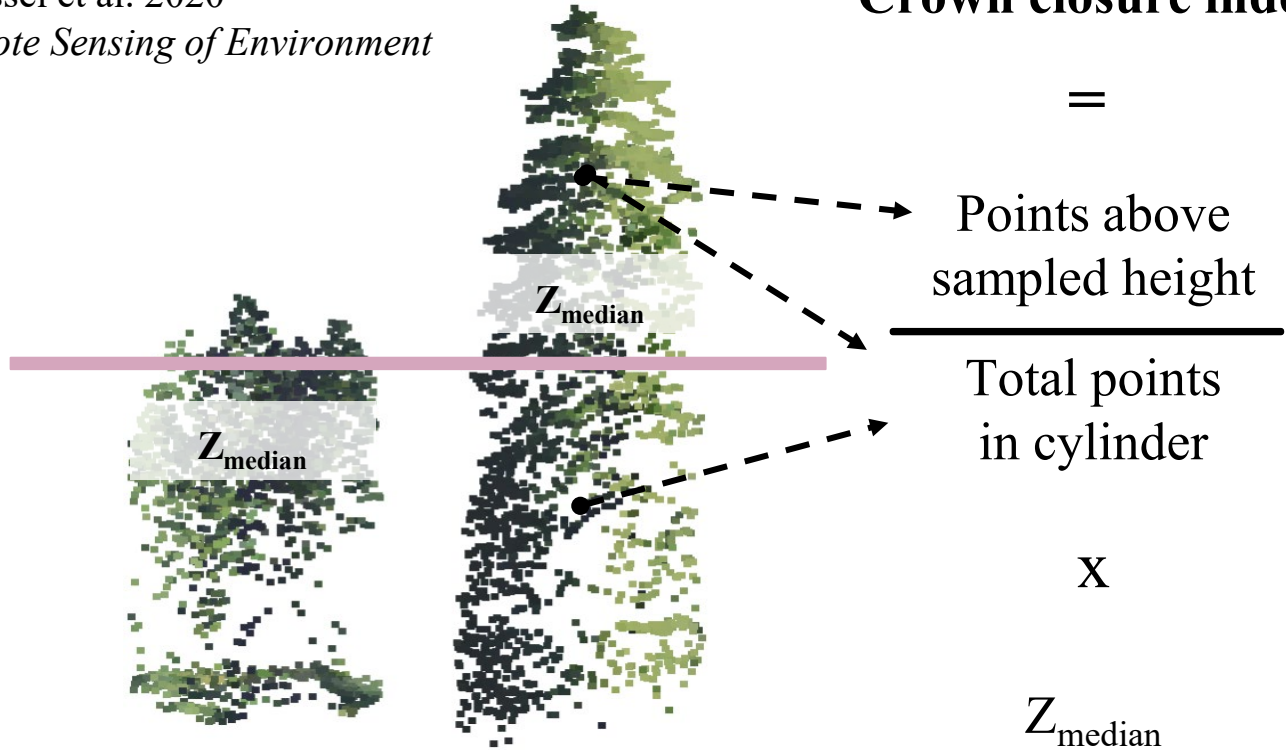
Crown closure index

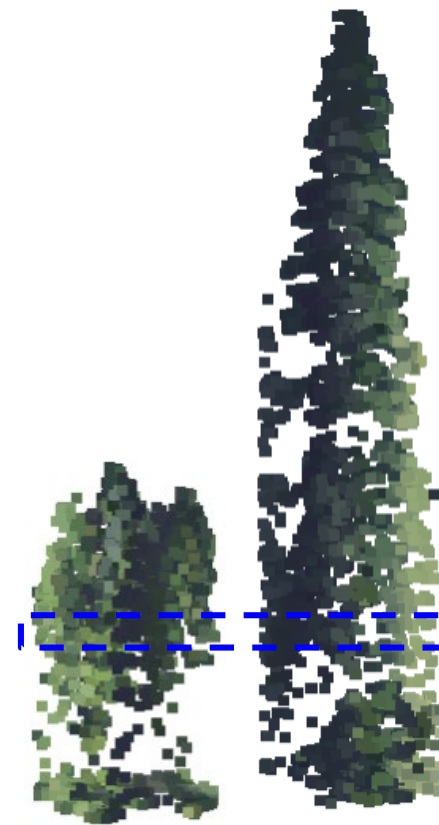
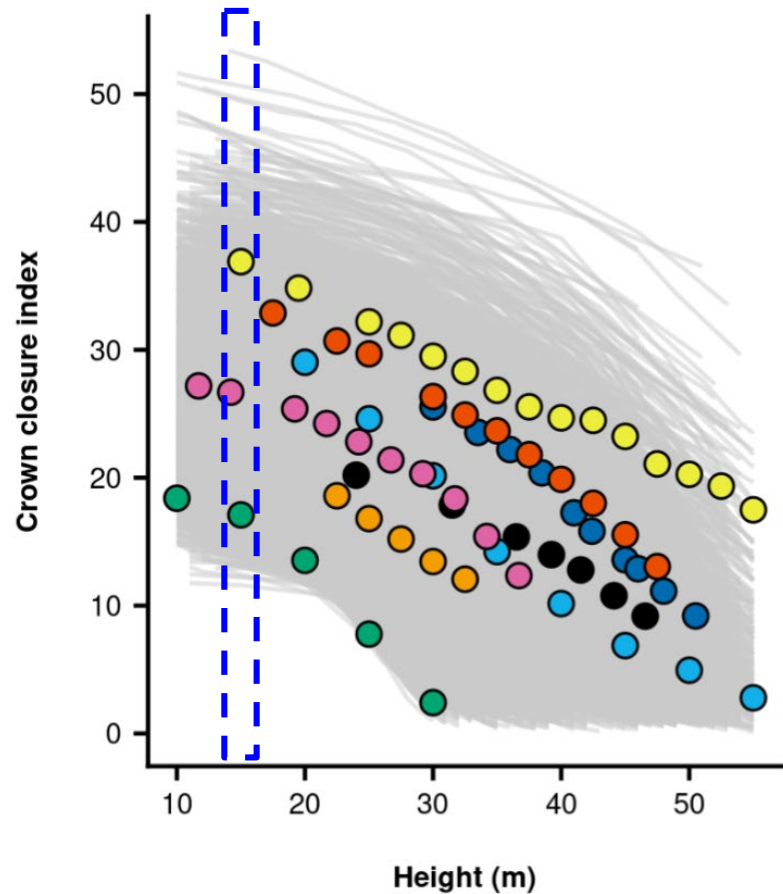
=





Roussel et al. 2020
Remote Sensing of Environment



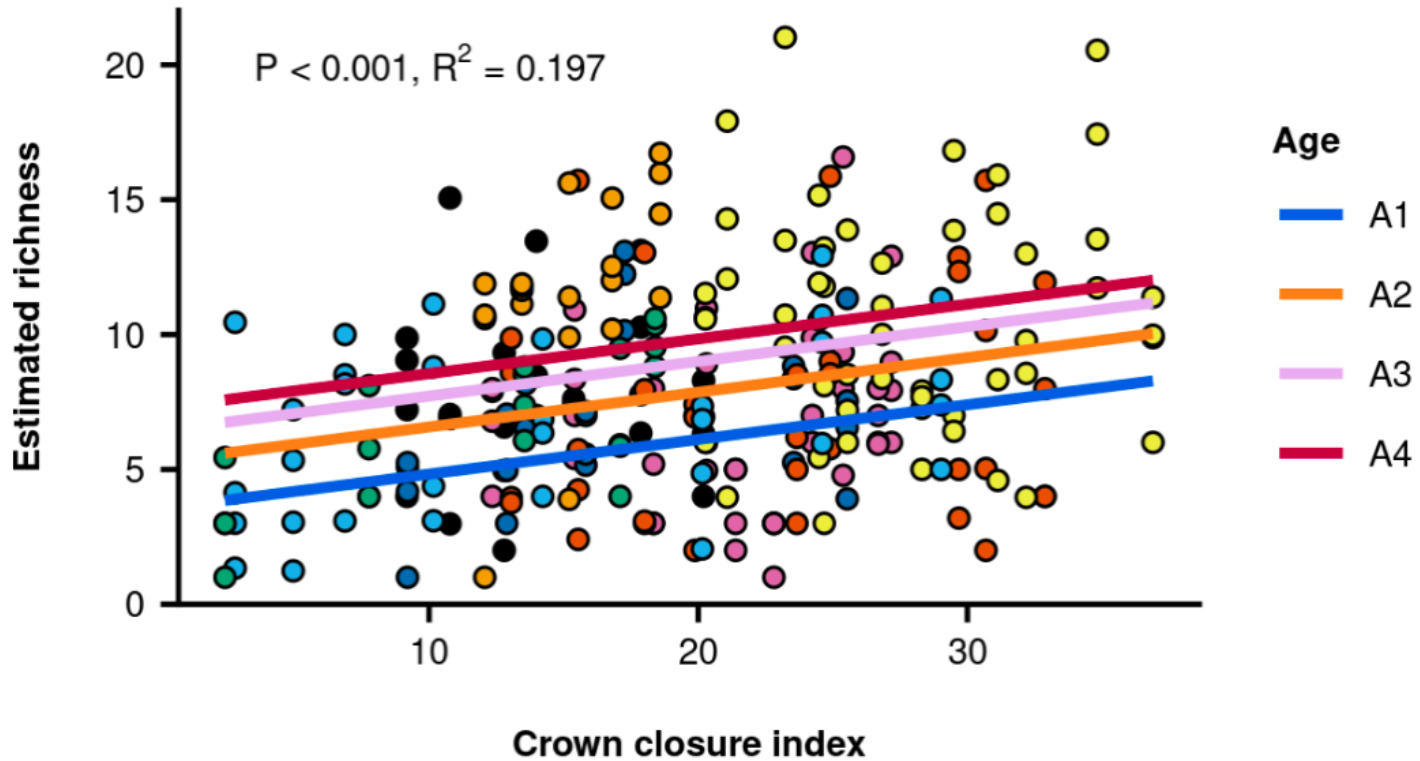


35.8m

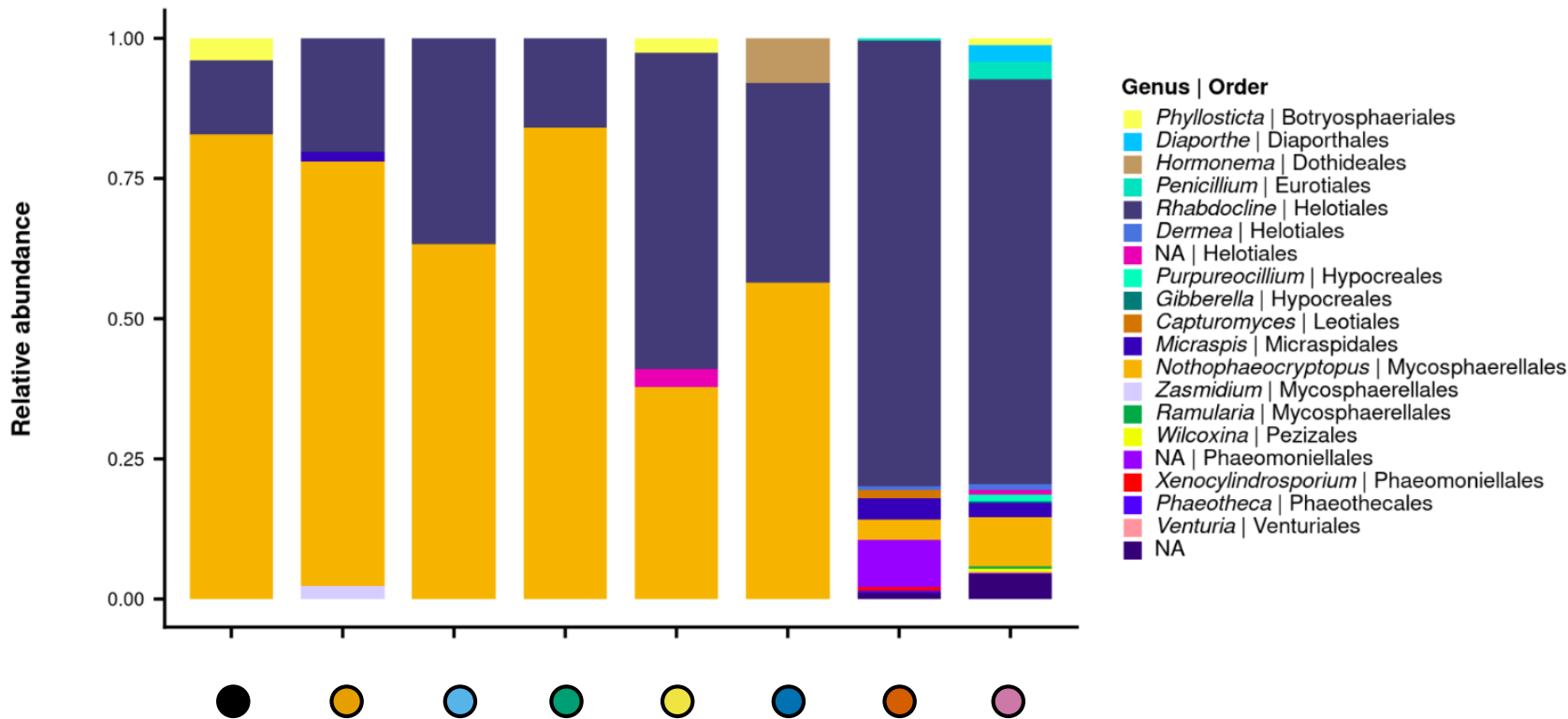


90.1m

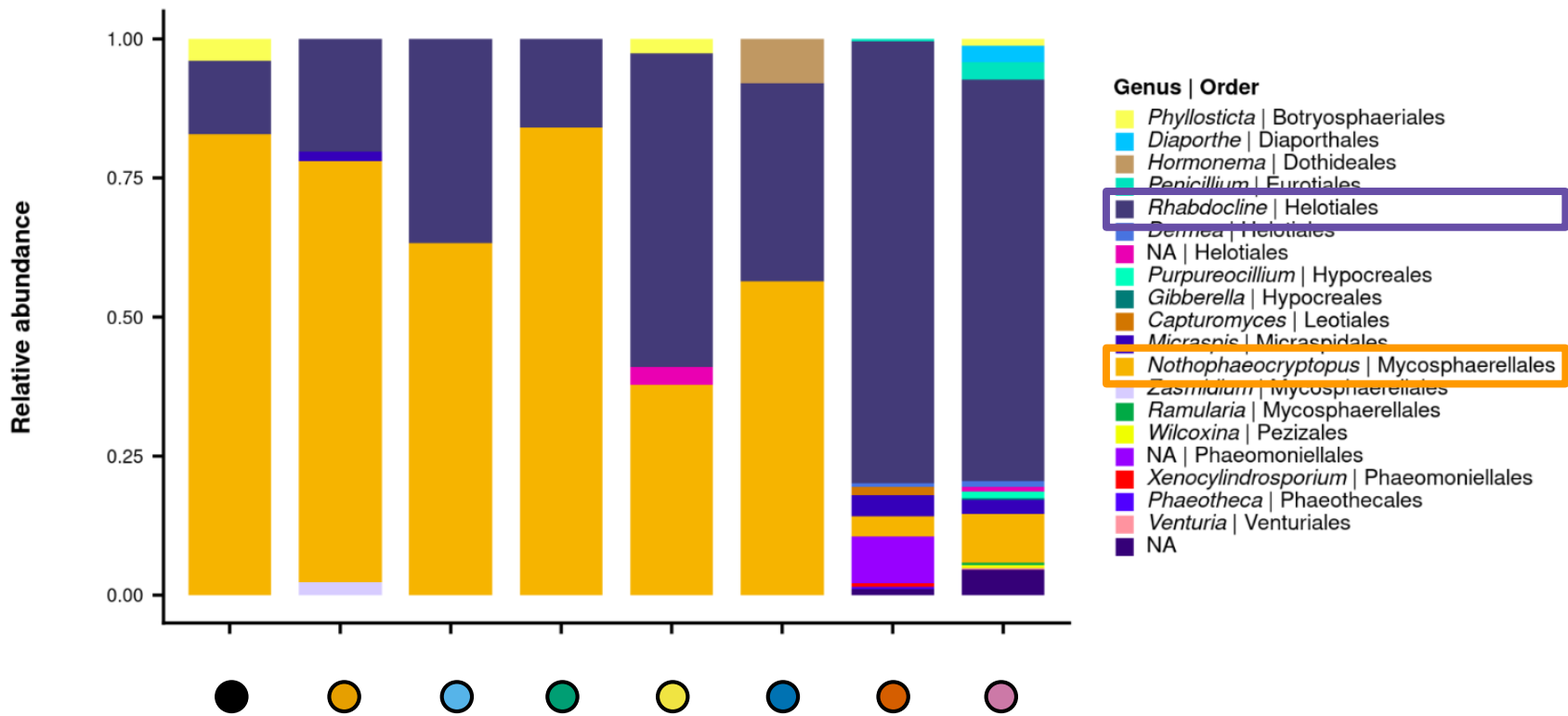
Do communities from exposed crowns differ from closed crown communities?



Greater closure and needle age are associated with richer communities

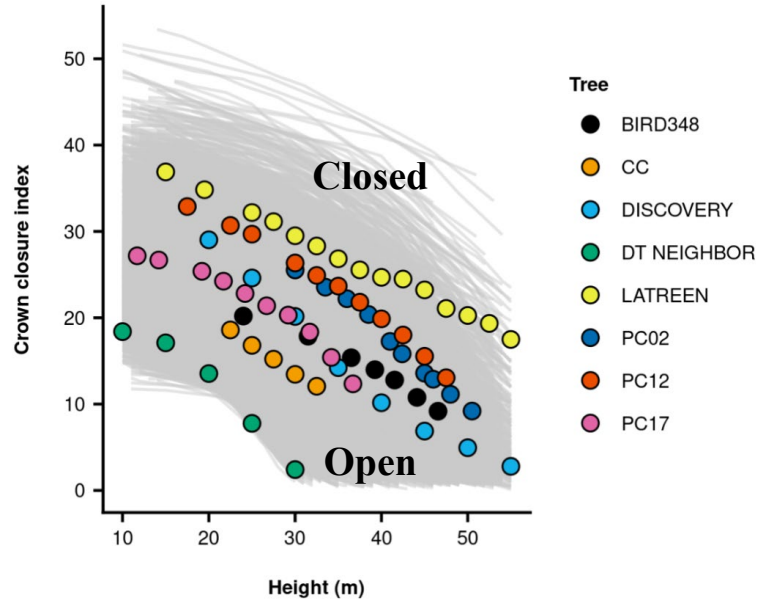


218 OTUs across 256 samples



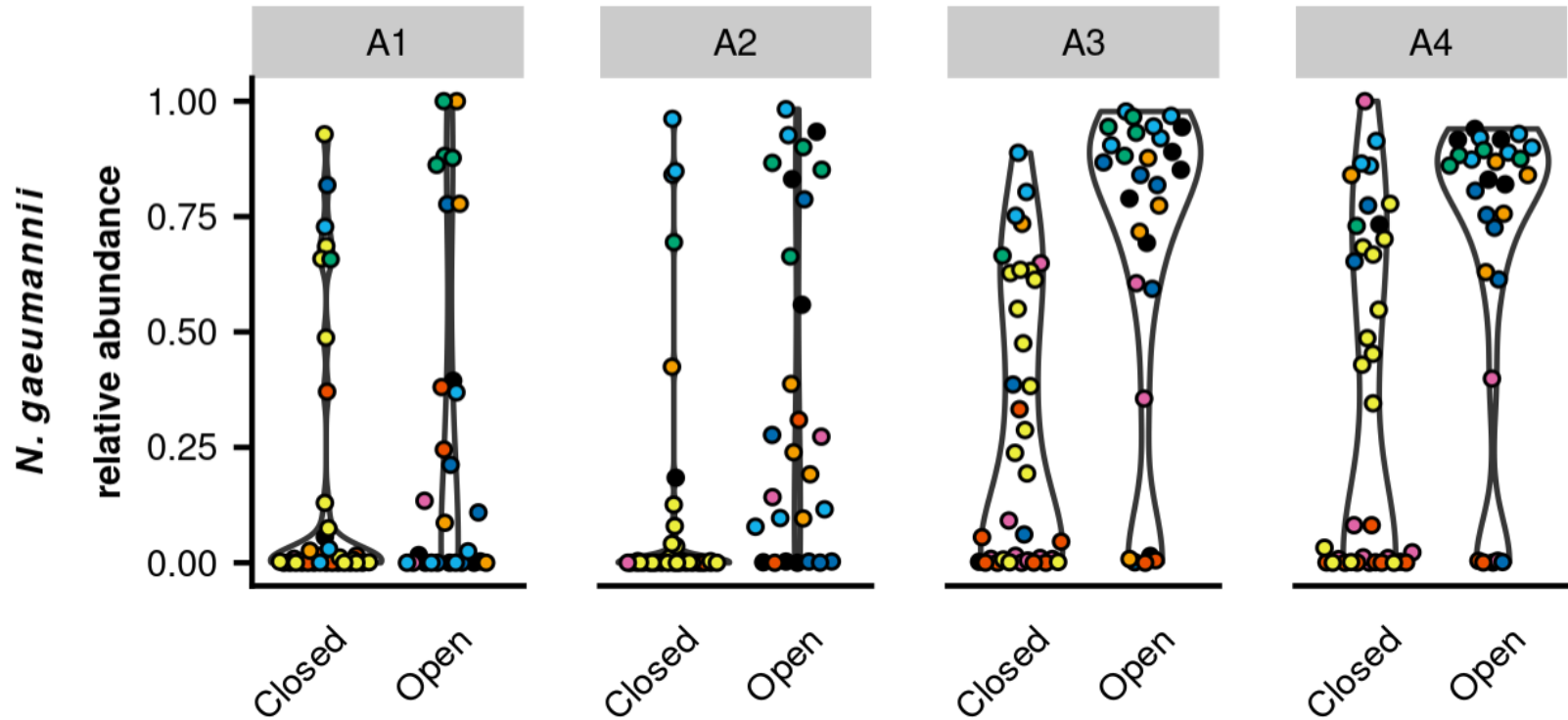
**OTUs assigned to *N. gaeumannii* (OTU.1) +
R. parkeri (OTU.2, OTU.3, OTU.6)**

Dominant taxa have **divergent** niches

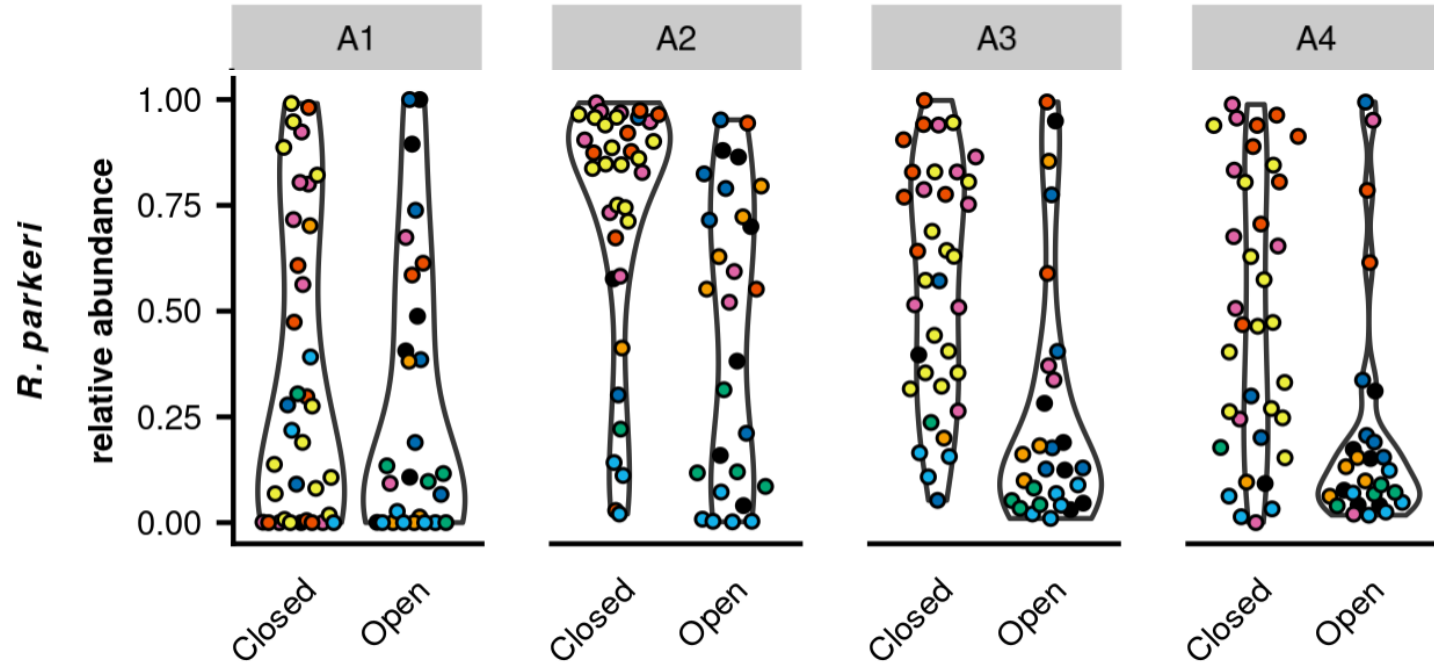


OTU	Taxon	Group	IV	P
OTU.1	<i>N. gaumannii</i>	Open	0.629	0.006
OTU.2	<i>Rhabdocline parkeri</i>	Closed	0.488	0.009
OTU.3	<i>Rhabdocline parkeri</i>	Closed	0.482	0.022
OTU.10	Dermateaceae sp.	Closed	0.414	0.006
OTU.16	Dothideomycetes sp.	Closed	0.361	0.006
OTU.73	Phaeomoniellaceae sp.	Closed	0.173	0.006

P values were obtained after 999 permutations and corrected for the false discovery rate using the Benjamini-Hochberg method.



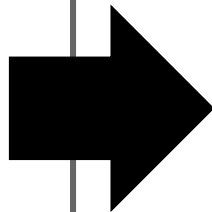
***N. gaeumannii* dominates open exposures as needles age**



***R. parkeri* initially dominates closed exposures**

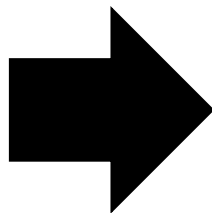
Hansen et al. 2000
Manter et al. 2003
Manter et al. 2005
Shaw et al. 2014
Lan et al. 2019
Ritóková et al. 2021
Lan et al. 2022

(apologies if I missed someone!)



Needles/trees in **southern aspects/upper crowns/unshaded treatments** experience more severe SNC and/or higher *N. gaeumannii* biomass

Gervers et al. 2022



Needles with less **crown closure** have relatively more *N. gaeumannii* reads than other endophytic fungi



Why might *Nothophaeocryptopus gaeumannii* dominate open exposures?

Why might this be?



N. gaeumannii **preempts** other fungi
in open crowns

Other fungi (e.g. *R. parkeri*)
exclude *N. gaeumannii* in closed
crowns

N. gaeumannii **accesses nutrients**
and/or grows better than other
fungi in open crowns

N. gaeumannii **survives** better than
other fungi in the hostile
environment of open crowns

N. gaeumannii **antagonizes** other
fungi more in open crowns



MINI-SYMPOSIUM ON JUNE 2021 HEAT DOME FOLIAGE SCORCH



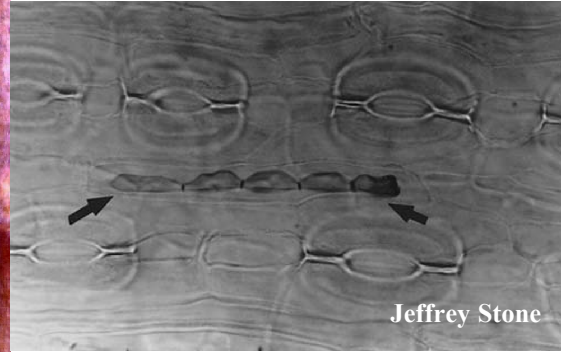
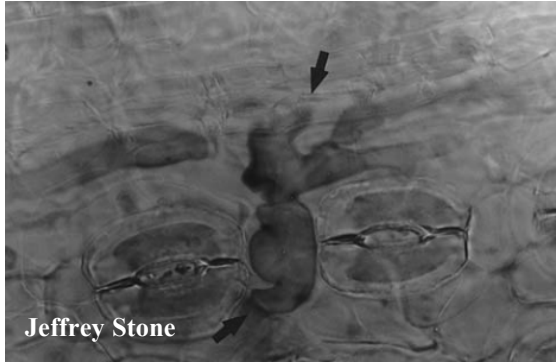
Gabriela Ritóková



Dave Shaw

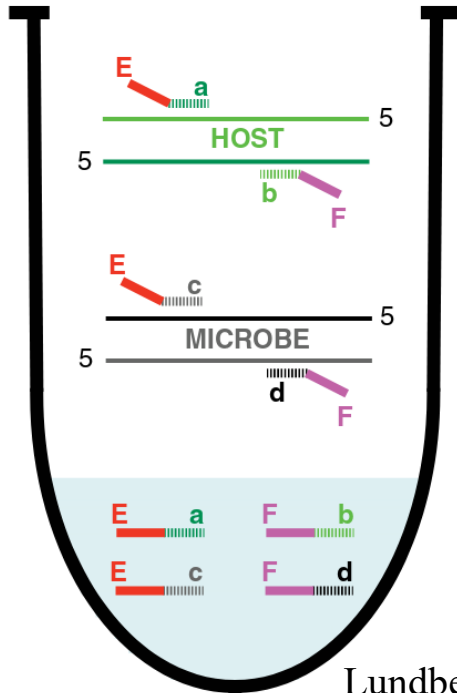
Proposed research by Chris Still + Posy Busby et al.

Please ask me more about these mechanisms!
(I've got bonus slides...)



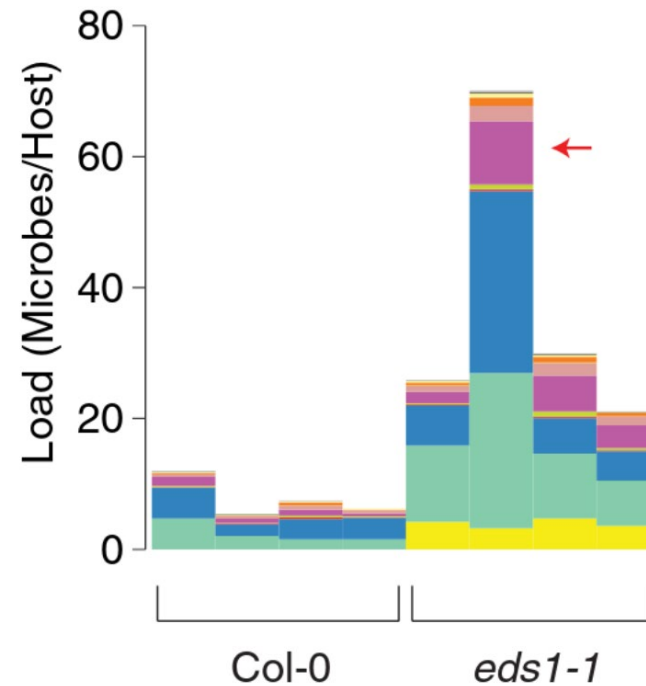
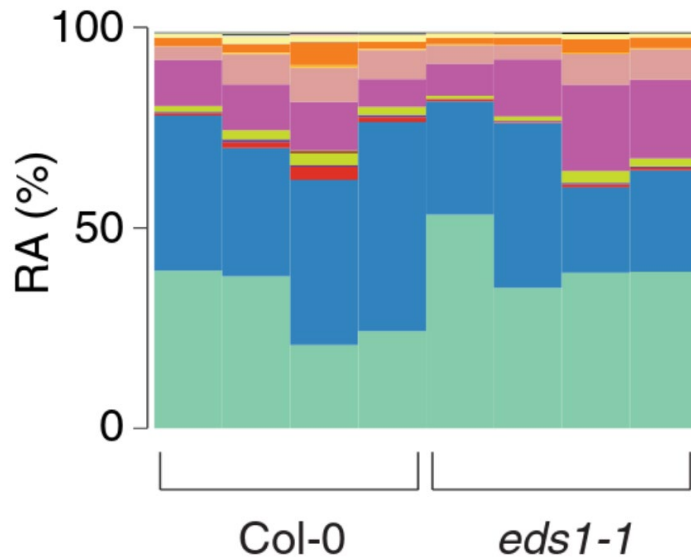
How can we improve our sequence-based analyses of needle fungi communities?

Amplify **plant** and **fungal** sequences

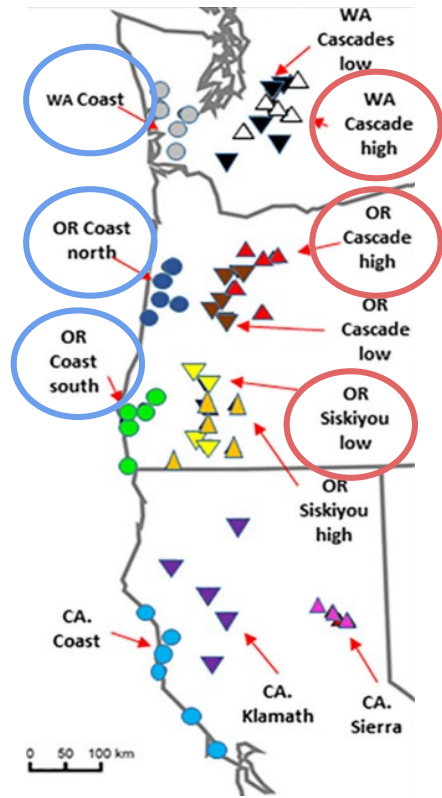


Lundberg et al. 2021

$$\begin{aligned} &\text{Fungal load} \\ &= \\ &\text{fungal sequences} \\ &\div \\ &\text{plant sequences} \end{aligned}$$



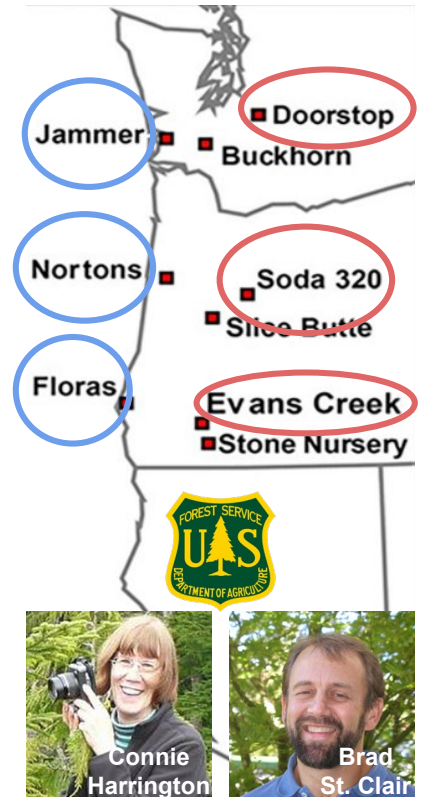
Load reveals a much stronger genotype effect!



Natural Populations

DFSSMT

6 sites
6 seed regions
30 populations
2nd-year needles
3 sampling years
>4000 samples



Common Gardens

**Please ask me if you want to know more about
how this technique works!**

Acknowledgements



Oregon State
University



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Busby Lab

Austen Apigo, Abbey Neat Maria-

Jose Romero Jimenez

Kim Syring, Melissa Vergara,

Jessie Zimmerman

Questions?

Comments?

References

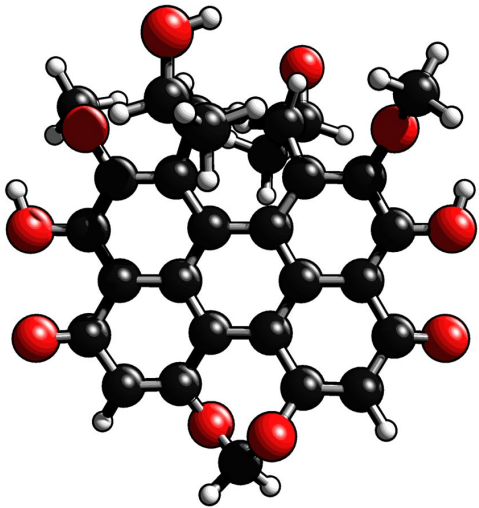
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Bonus slides!

The systematic position of *Phaeocryptopus gaeumannii*

2007

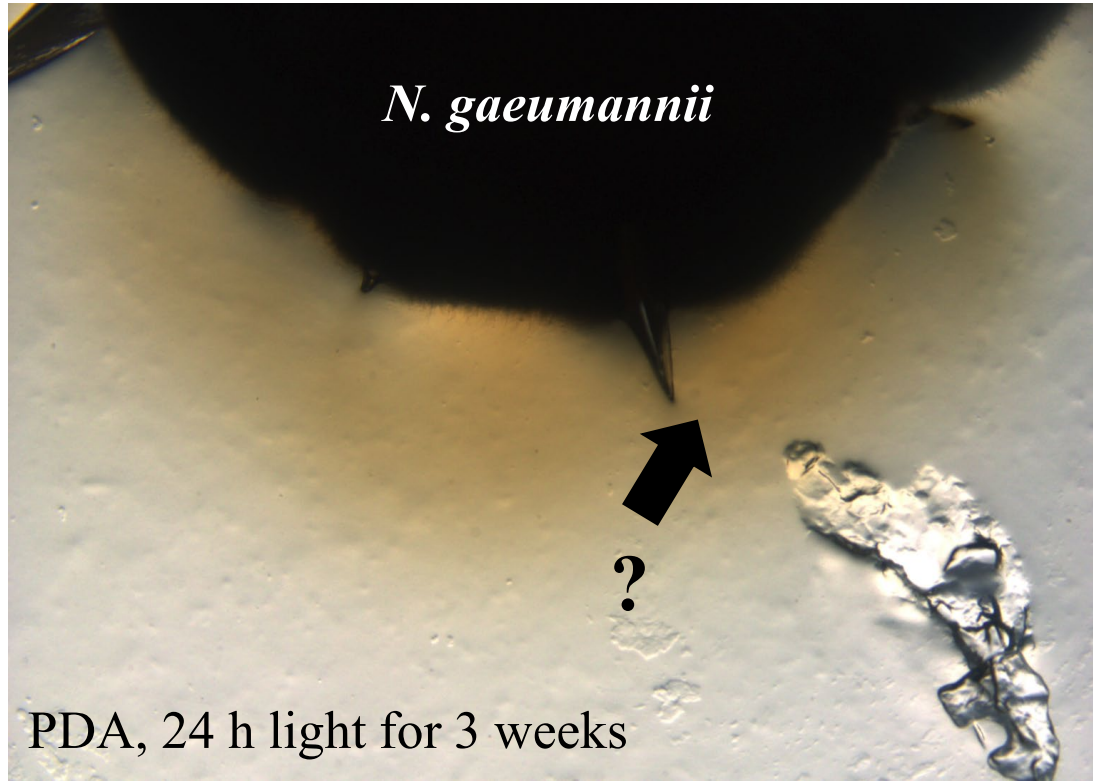
Loretta M. Winton, Jeffrey K. Stone, Everett M. Hansen & R.A. Shoemaker



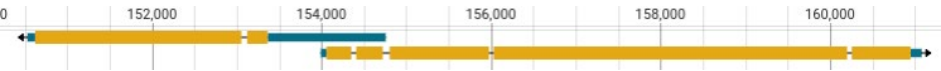
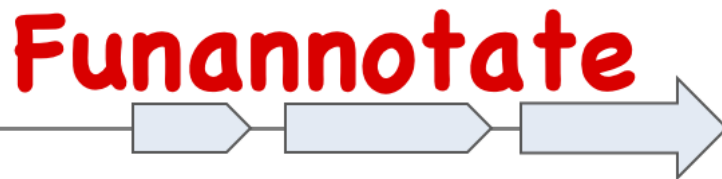
A light-activated phytotoxin

“Isolates of *P. gaeumannii* also have been observed to produce **diffusing red pigments in culture** (Winton and Stone unpubl.).

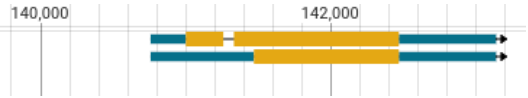
...the possibility that this pigment might be a **cercosporin-like substance** that might play a role in the pathology of Swiss needle cast disease must be considered.”



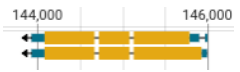
Support for an earlier hypothesis...



CTB3 CTB1



CTB2



CTB4

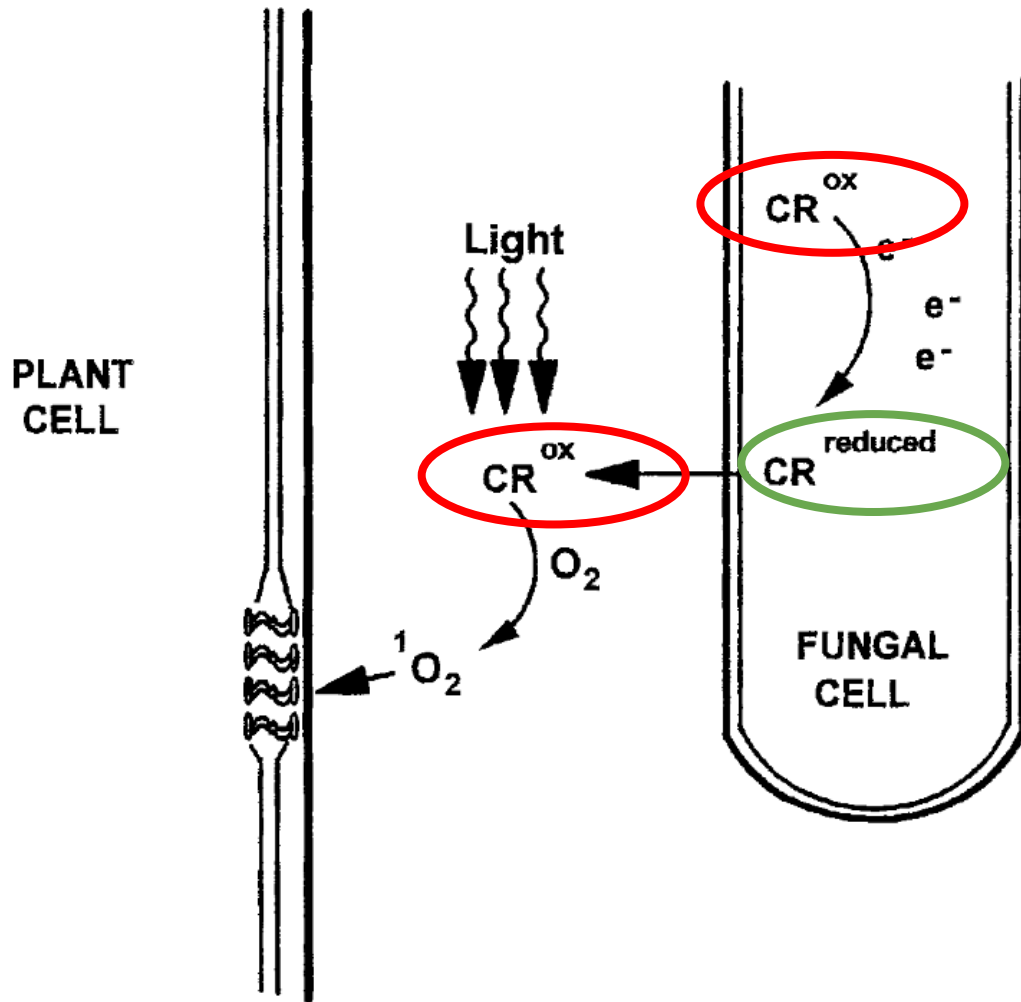


CTB5

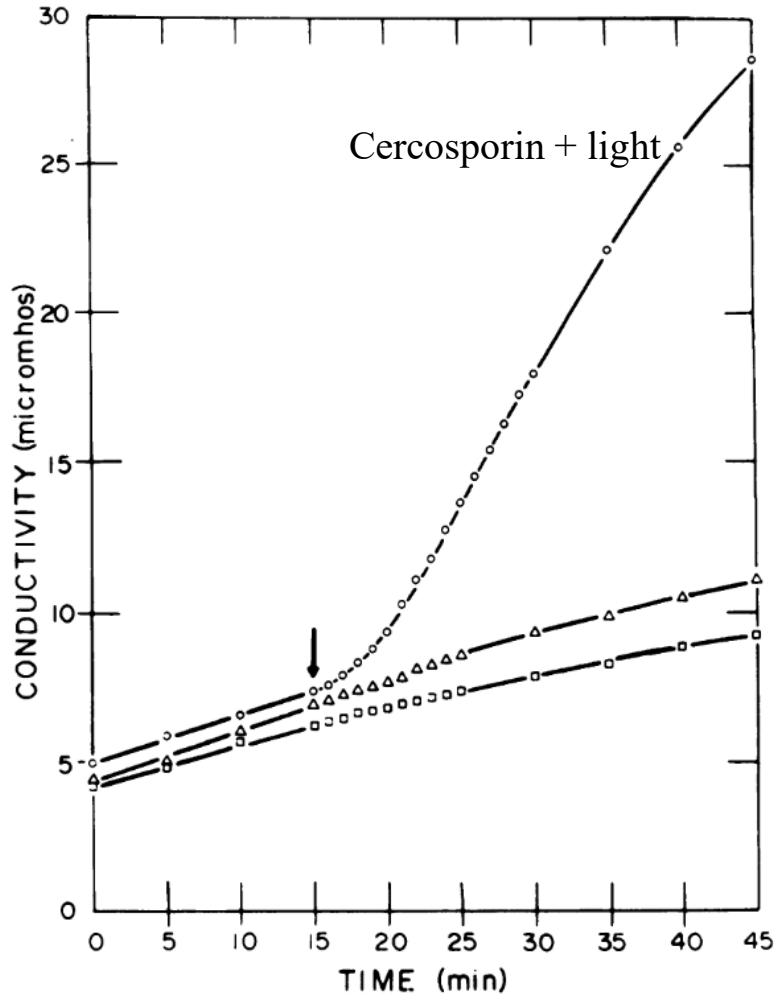
Genomic and transcriptomic evidence suggest this is a possibility

RNA-Seq data from Hess *et al.* 2016
N. gaeumannii genome (BioProject: PRJNA212511)
sequencing + assembly by TAIGA

Unpublished



Compounds like cercosporin form reactive **singlet oxygen** under high-light conditions



Cercosporin induces electrolyte leakage in plant cells when exposed to light

- Cercosporin + light
- △ Cercosporin + dark
- Water + light

Study 1

No apparent toxins involved in the development of Swiss needle cast symptoms.

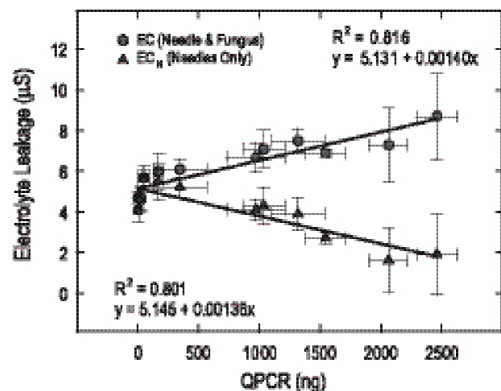
2000

Dan Manter and Katy Kavanagh.

Cooperators: Greg Filip, Jeff Stone, Wendy Sutton and Lori Winton.

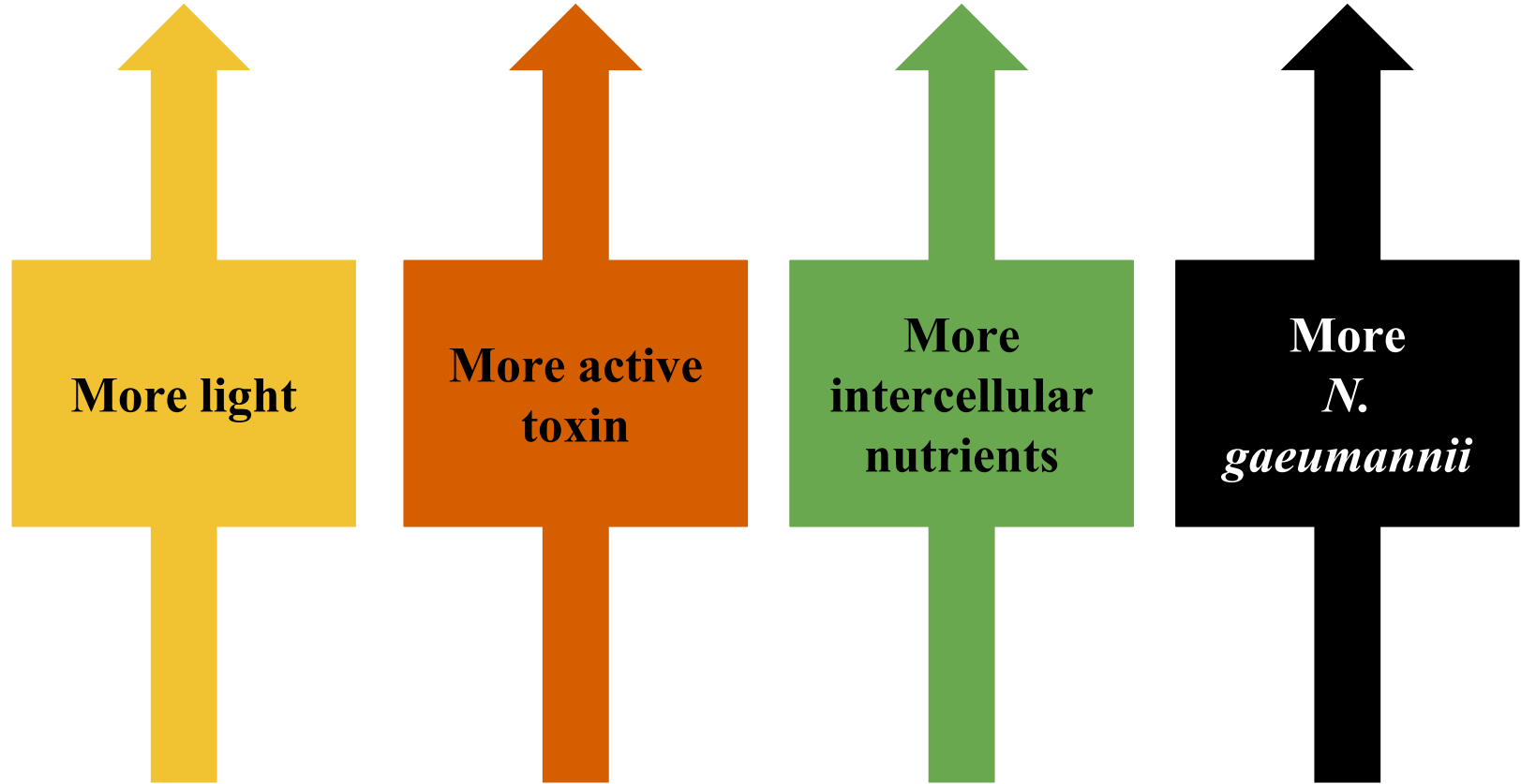
2001

Electrolyte Leakage and Nutrient Status in SNC-infected Douglas-fir



Dan Manter and Jeff Stone

Support for an earlier hypothesis...



References

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Hess, M., Wildhagen, H., Junker, L.V., Ensminger, I., 2016. Transcriptome responses to temperature, water availability and photoperiod are conserved among mature trees of two divergent Douglas-fir provenances from a coastal and an interior habitat. *BMC Genomics* 17, 682. <https://doi.org/10.1186/s12864-016-3022-6>

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<https://doi.org/10.1080/15572536.2007.11832584>