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Ressources naturelles
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SNC Research Updates from Natural Resources Canada

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2024 Swiss Needle Cast Cooperative Annual Meeting
December 12th, 2024



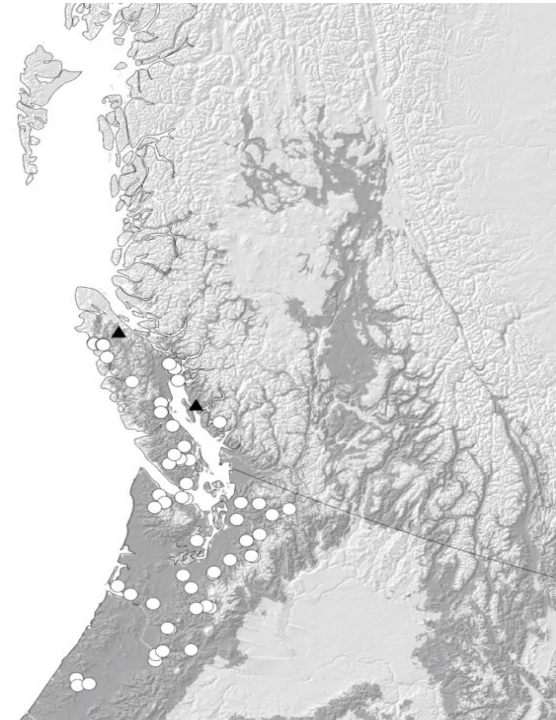
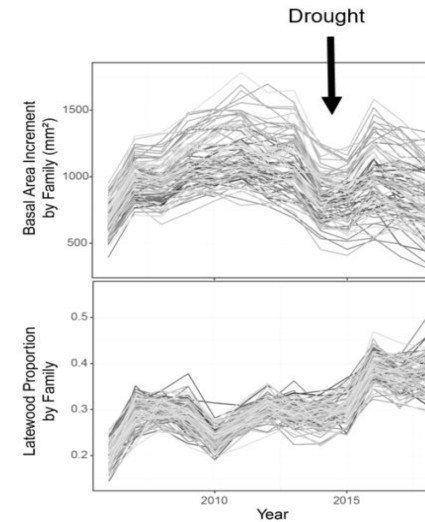
Goals

Genomics of Douglas-fir Resilience to new Environmental Disturbances (GenDRED)-GRDI project (CFS/NRCAN) 2024-28.

1 – Molecular bases of Douglas-fir tolerance to drought (genotype x phenotype [tree rings] association) - 2024-25



Response to drought in genetic field trials

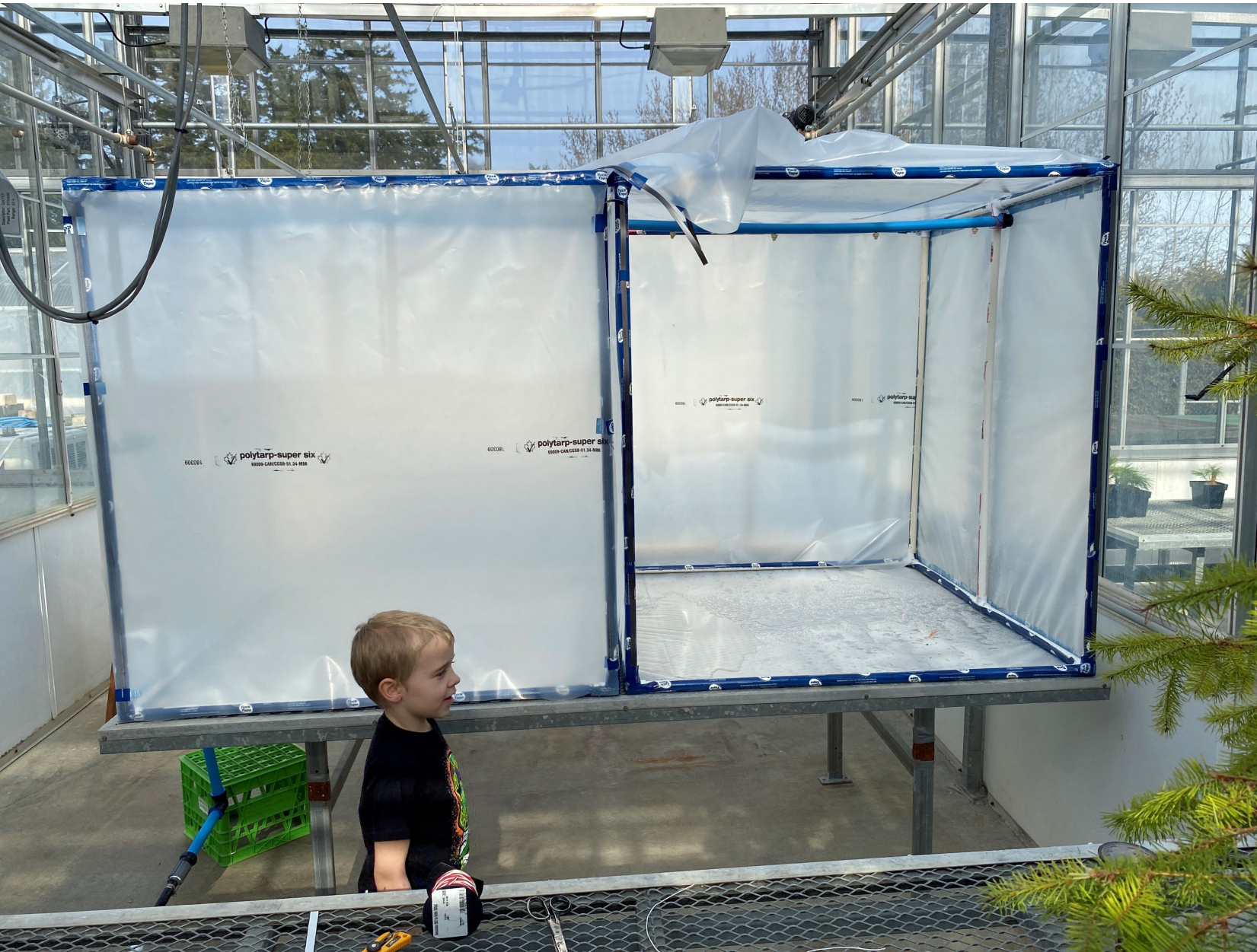


2 - ID of the molecular basis of Douglas-fir X SNC compatible interaction (2025-26)

- **KEY = Controlled inoculations with SNC**
- Transcriptomics, proteomics and metabolomics approaches

3 – Modulation of SNC needle colonization by drought (2027-28)

2023 Inoculations - Pilot

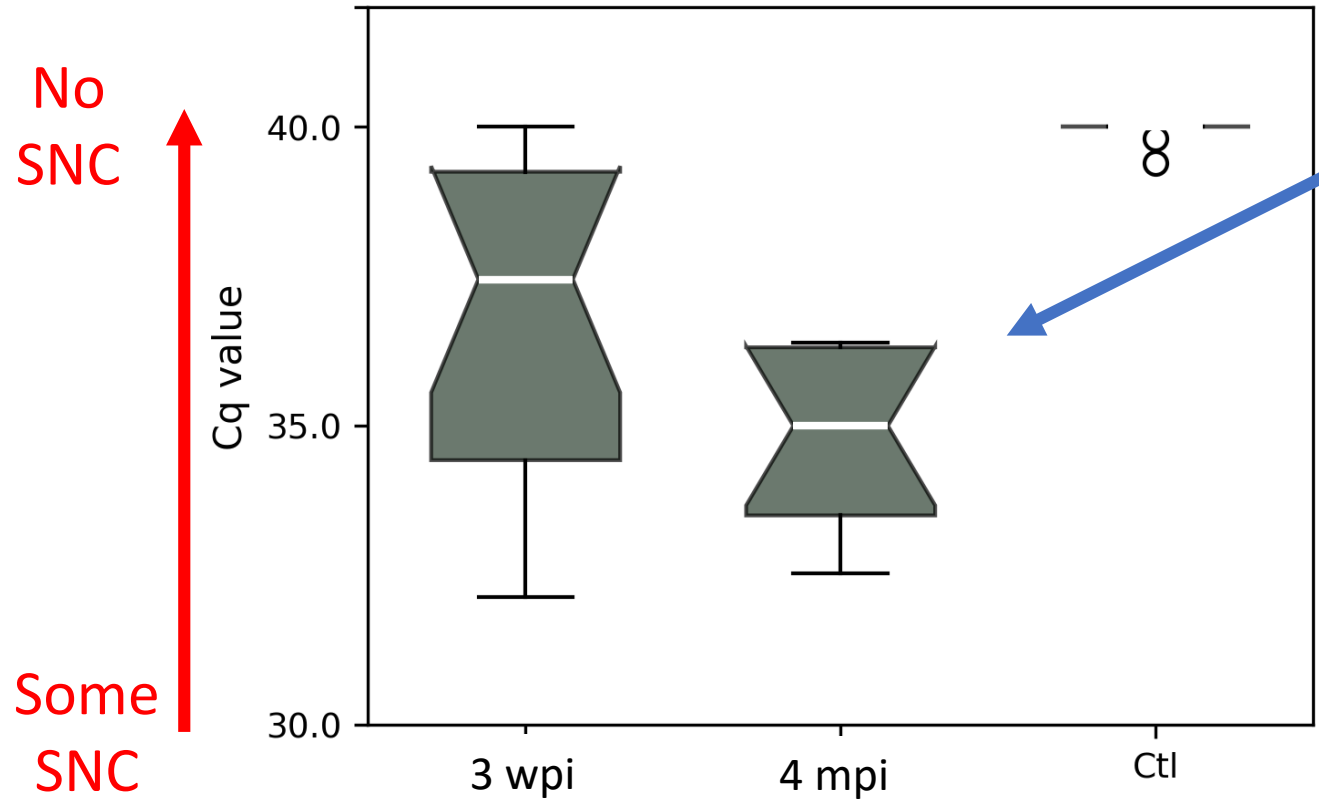
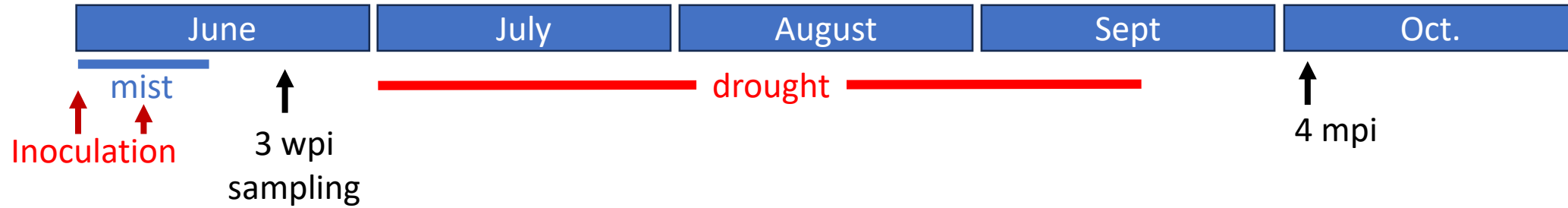


Sprayed fragmented mycelium (adjusted to 20gr/L in 0.05% water agar)

Mist chambers >80% humidity, 20°C ($\pm 3^{\circ}\text{C}$)

Sprayed every two hours (9am-8pm) for 5 min (nozzle) during 2 weeks

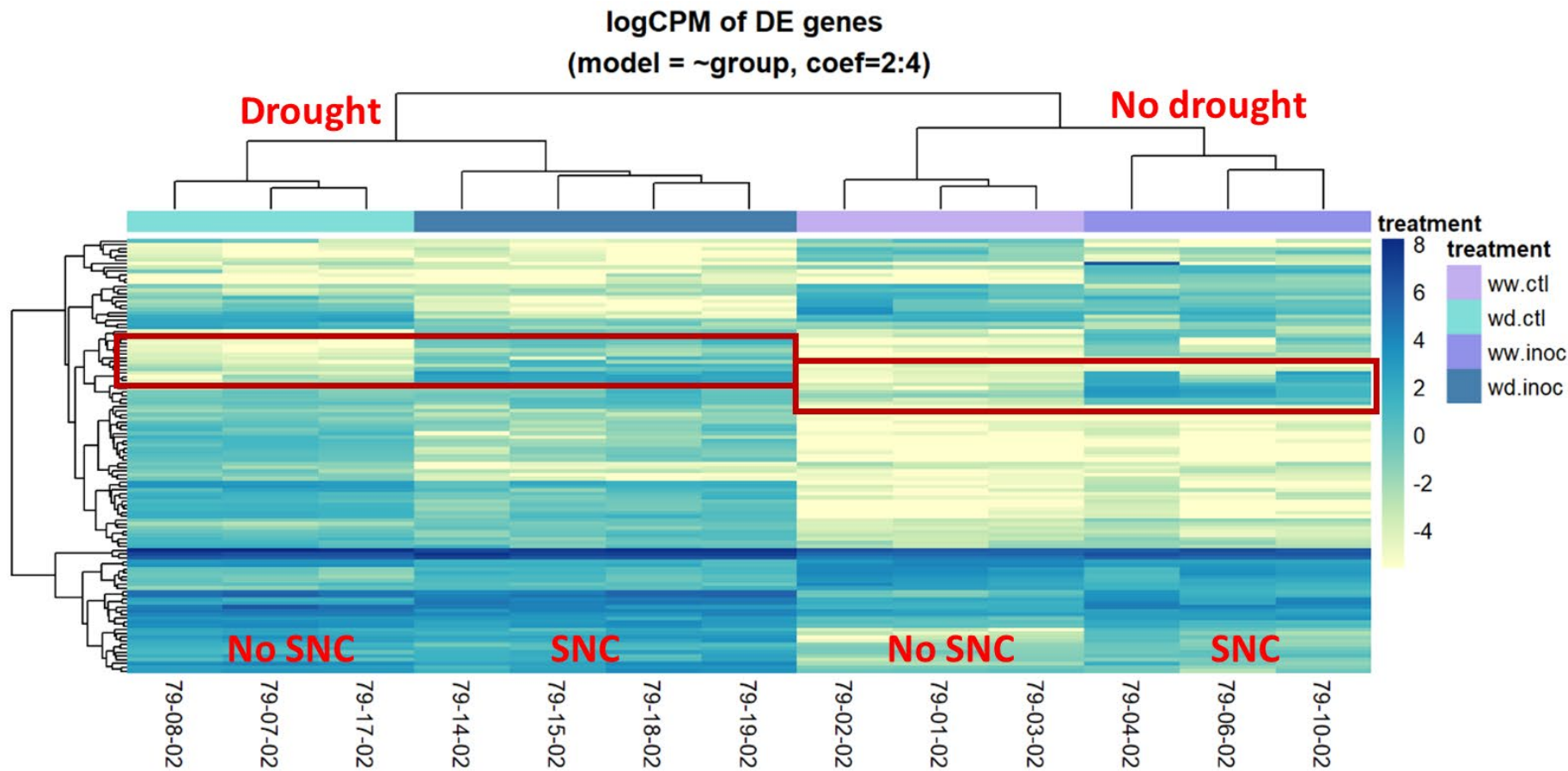
Tracking SNC colonization by real-time PCR



0.1 to 0.5% or RNAseq reads map on SNC genome

- Limited SNC biomass and transcript
- Strong variability between needles

Df RNAseq 4 months after inoculation



- Lineage 2
- Differential gene expression at 3 wpi & 4 mpi in Douglas-fir
- Drought vs. ctl
- SNC vs. ctl

We find some genes differentially expressed between SNC and Ctl treatments
Meaning that... that SNC induces a response in Douglas-fir

Next steps

2025 => SNC inoculation. no drought treatment.

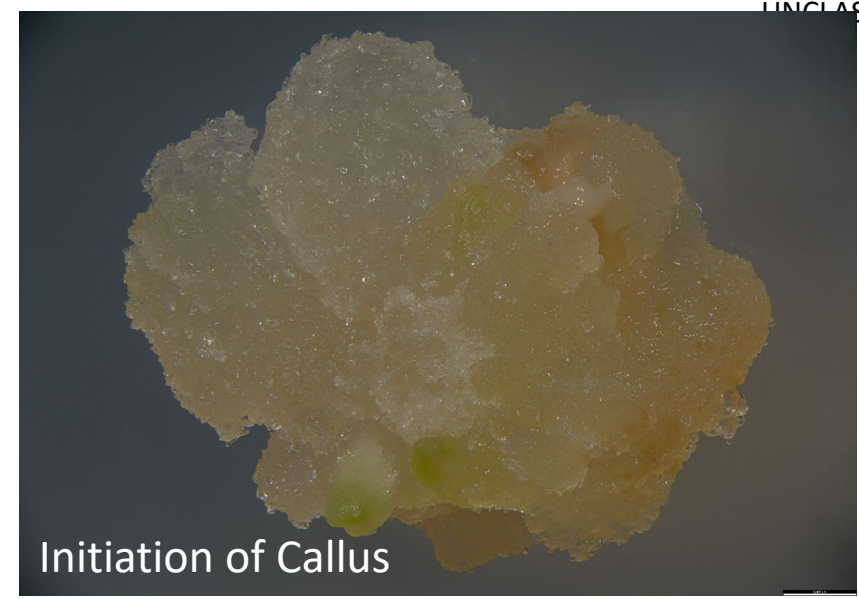
L1c and L2. RNAseq, proteomics and metabolomics (Orbitrap LC-MS)

2026 and after. SNC inoculation + summer drought



Next steps: increase our inoculation capacity

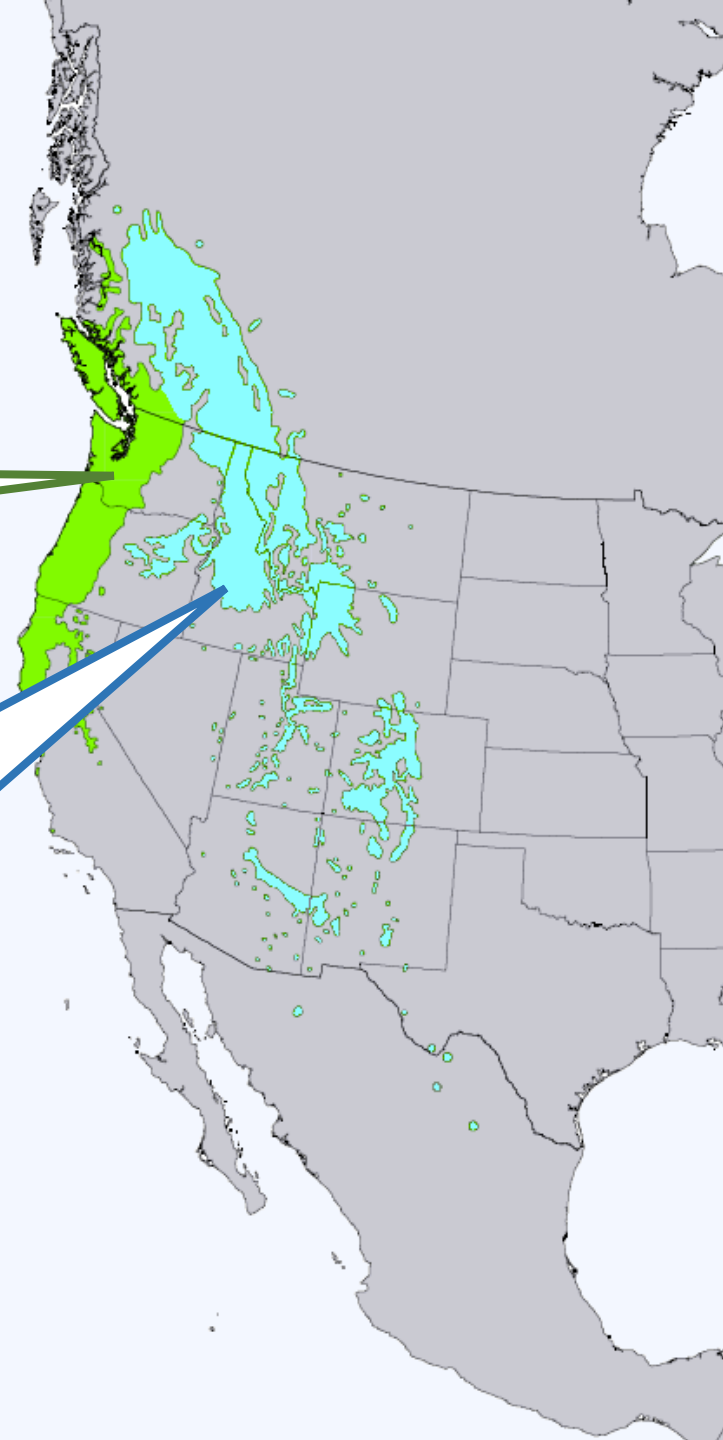
- So far... 1 inoculation per year
- Generate Fdc material by somatic embryogenesis (Amin Aminul, PFC)
- Transformation of *N. gaeumannii* L1C and L2 with mCherry (fluor. microscopy) – P. Tanguay (LFC, Quebec)



On the fungus side: One species, three genetic lineages

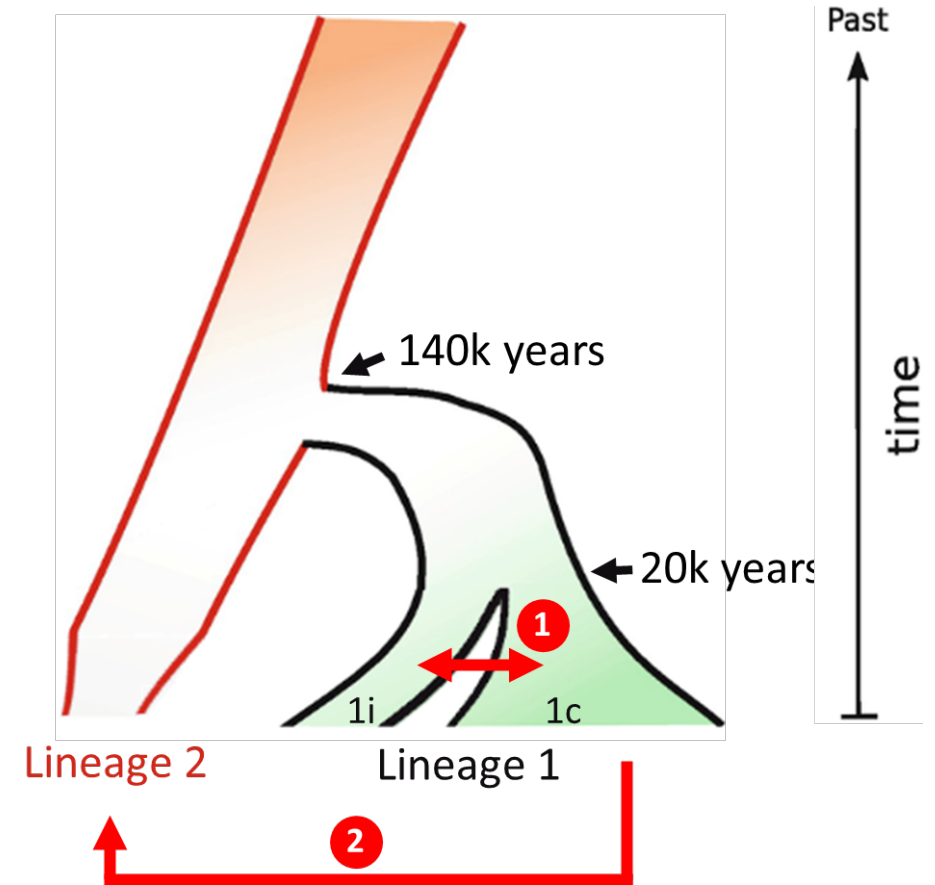
Coastal Douglas-fir
(*P. menziesii* var. *menziesii*)
Lineage 1c and Lineage 2

Rocky Mountains Douglas-fir
(*P. menziesii* var. *glauca*)
Lineage 1i



Genomics of *Nothophaeocryptopus gaeumannii*

Feau & al. Speciation in the genetic lineages of the Swiss needle cast pathogen, *Nothophaeocryptopus gaeumannii* is challenged by introgression through secondary contact. In prep. for Mol. Ecol.



Comparative genomics in L1c, L2 and L1i



GENOME SEQUENCES
February 2024 Volume 13 Issue 2 e01008-23
<https://doi.org/10.1128/mra.01008-23>

Genome sequences of three genetic lineages of the fungus *Nothophaeocryptopus gaeumannii*, the causal agent of Swiss needle cast on Douglas-fir trees

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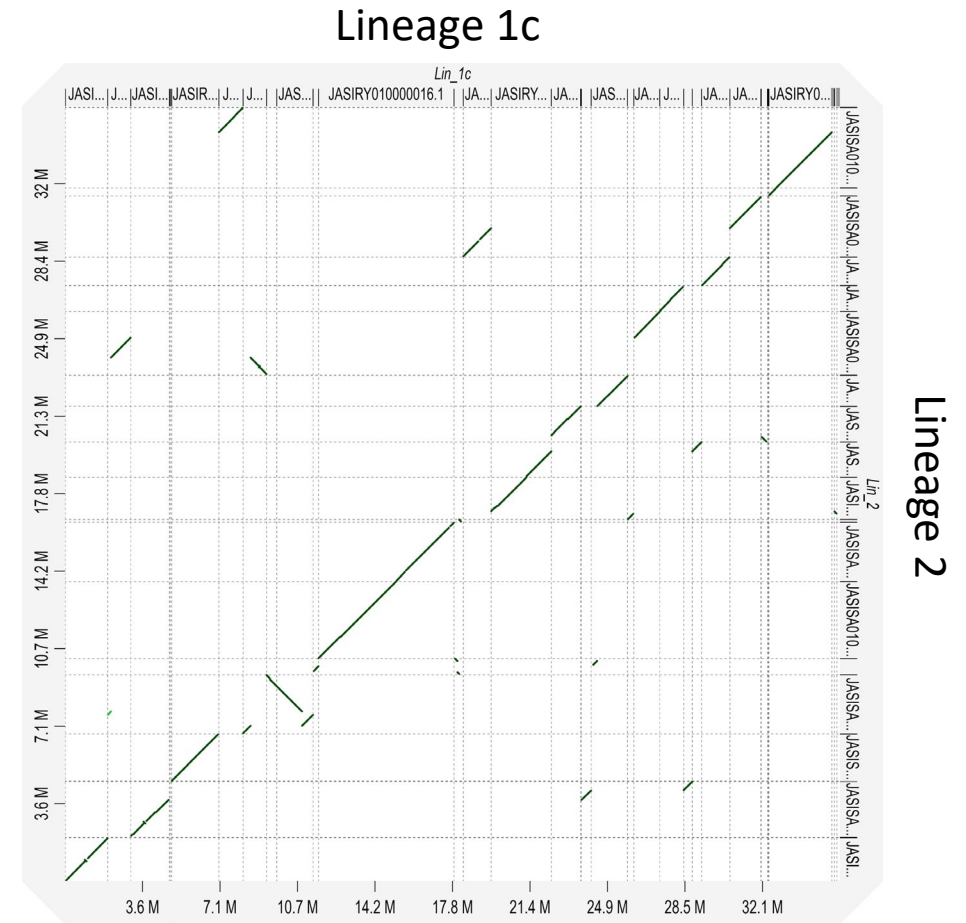
³Département des Sciences du Bois, Université du Québec, Québec, Canada

Here, we present the genome sequences of three genetic lineages of *Nothophaeocryptopus gaeumannii*, the causal agent of Swiss needle cast, a foliar disease of Douglas-fir trees with a wide distribution range.

KEYWORDS fungal pathogen, comparative genomics, phylogenetics, Swiss needle cast

TABLE 1 Origin and general features of the genome sequences of Lineage 1c, 1i, and 2 of *Nothophaeocryptopus gaeumannii* isolated from Douglas-fir (Table view)

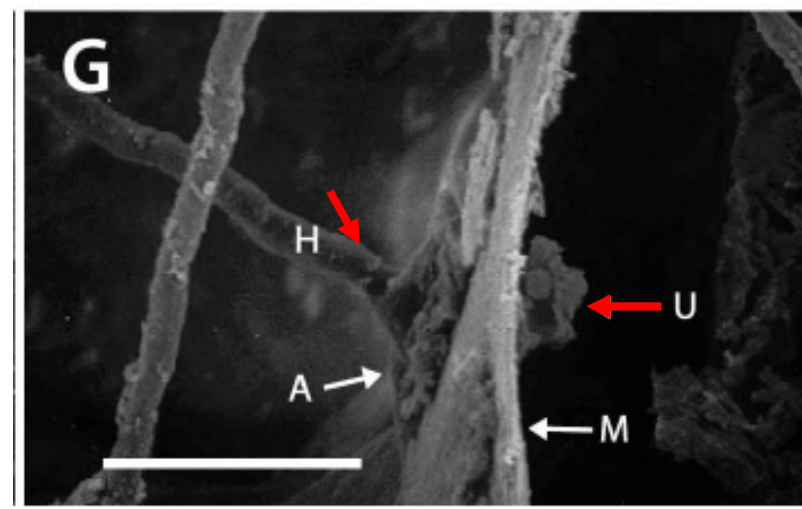
	Lineage 1c	Lineage 1i	Lineage 2
Host	<i>P. menziesii</i> var. <i>menziesii</i>	<i>P. menziesii</i> var. <i>glauca</i>	<i>P. menziesii</i> var. <i>menziesii</i>
Location	West Harrison I., BC, Can. (N49.44, W121.85)	Enderby, BC, Can. (N50.56, W119.09)	Vancouver Island, BC, Can. (N49.34, W124.51)
DAOMC ^a Identifier	252736	252735	252734
GenBank assembly	GCA_032718785.1	GCA_031771855.1	GCA_031771865.1
ON reads (SRA)	SRR26424609	SRR26369461	SRR26369462
No. of ON ^b reads (N50 [bp])	137,939 (9,224)	91,752 (10,439)	239,558 (8,712)
Illumina reads (SRA)	SRR26424608	SRR26363295	SRR26363294
No. of Illumina reads	8,016,282	8,980,234	7,094,830
Assembly size (Mb)	35.47	35.59	35.51
Coverage	20.0X	14.0X	46.0X
No. of contigs	50	61	42
N50 (Mb)	1.67	1.84	2.70
L50	7	7	6
Length longest contig (Mb)	6.23	4.10	3.67
No. of contigs > 1 Mb	17 (34.0%)	11 (18.03%)	15 (35.71%)
GC content	52.52%	52.52%	52.52%
% BUSCO (C,D,F,M) ^c	99.87% (755,2,2,1)	99.74% (753,3,3,2)	99.74% (755,2,1,2)



Strong synteny between lineages, but still some differences

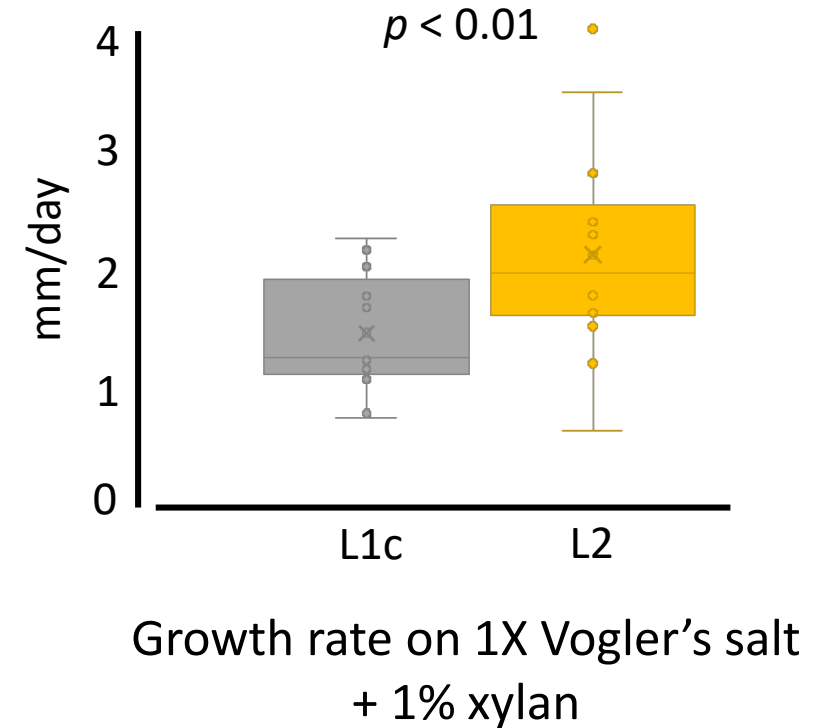
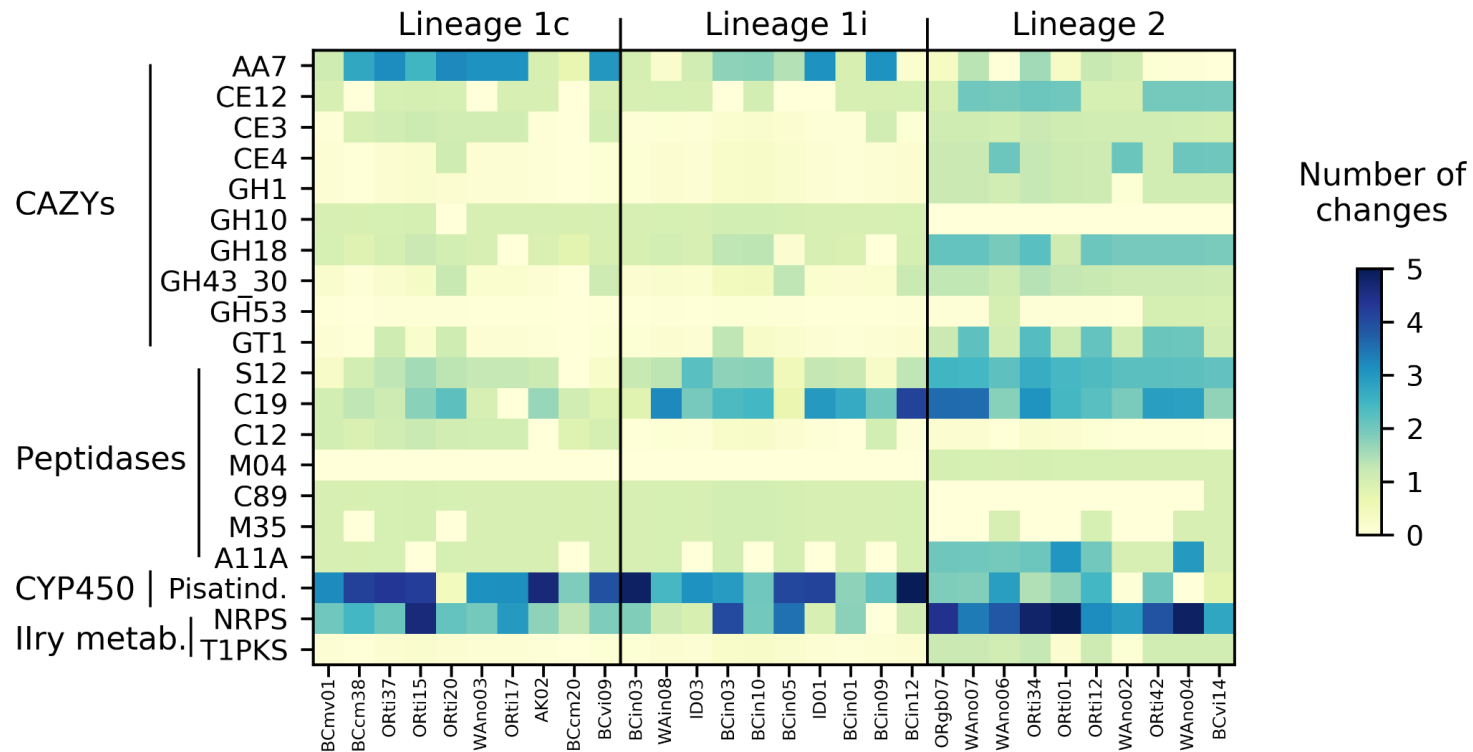
Comparative genomics in L1c, L2 and L1i

Ciaran Woods, PFC



Stone et al. 2008

Focus on Plant cell wall degrading enzymes :



Acknowledgments



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Don Wiggins (GWAS)

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Joey Tanney, PFC
Isabel Leal, PFC
Jun-Jun Liu, PFC
Cosmin Filipescu, PFC/CWFI
Pauline Hessenauer, U. Laval

Looking for a Master student - Fall 2025
(Transcriptomics/metabolomics SNC x Douglas-fir)

Looking for a postdoc April 2025-26. (not on SNC
project, but still a cool project)

Richard Hamelin, UBC
Juergen Elthing U. Victoria