

Combining Phylogenetic and phylogenomic approaches for the discovery of a new *Seiridium* species

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Introduction - Cypress Canker Disease (CCD)

Cypress canker disease:

Seiridium: ascomycete (*Sordariomycetes*, *Xylariales*, *Sporocadaceae*)

7 species cause cankers on *Cupressaceae*

S. cardinale, *S. neocupressi*, *S. cuopressi*, *S. unicorne*, *S. cancrinum*, *S. pseudocardinale*, *S. kenianum*.



Infection: initial phase



Developing cankers



Dieback



Acervuli on bark



Conidia

Introduction - 10 years ago...

Disease Notes

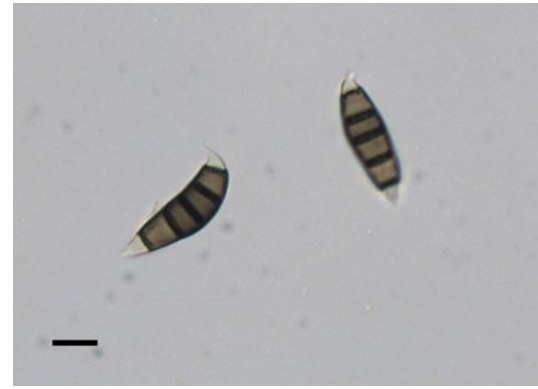


First Report of *Seiridium unicorne* Causing Bark Cankers on a Monterey Cypress in California

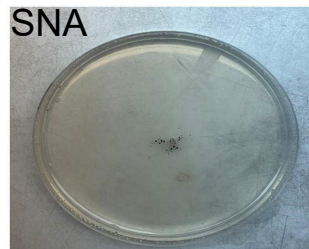
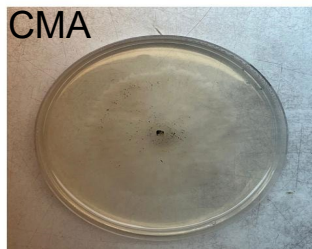
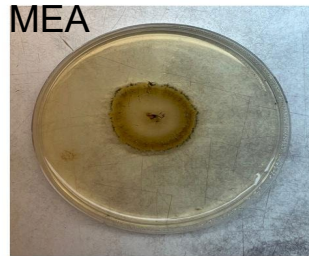
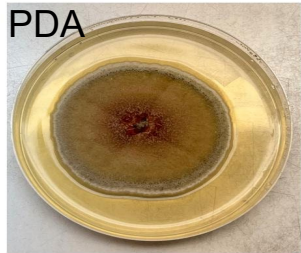
G. Della Rocca, R. Danti, and M. Garbelotto

- This isolate was tentatively identified as *S. unicorne* 500. Morphology did not match.
- The genome of this isolate has been sequenced.

Location: Glen Ellen (CA)



Introduction - After 10 years...



Isolate: CDFA-S1647
Record No. MVAP50003647-A
Date: 4/28/2022
Location: Santa Cruz Co.
Host: *Hesperocyparis sargentii*

**ISOLATE MVAP50003647-A
(Seiridium species??)**

QUESTION: Seiridium sp.?

Materials and Methods - Phylogenetic and Phylogenomics

Seiridium (*Sporocadaceae*): an important genus of plant pathogenic fungi

[G. Bonthond](#),¹ [M. Sandoval-Denis](#),^{1,2} [J.Z. Groenewald](#),¹ and [P.W. Crous](#)^{1,3,4}

4 genes phylogenetic approach: -ITS -RPB2 -TUB -TEF

- 1) MVAP50003647 and *S. unicornis* 500 were morphologically similar.
- 2) We therefore used a hybrid approach, phylogenetic and phylogenomic.
- 3) These 4 genes above were sequenced for isolate MVAP50003647.
- 4) Using a blast approach, we extracted in-silico the same 4 genes from the genome of *S. unicornis* 500.

Materials and Methods - bioinformatic analyses

PHYLOGENETIC

- Sanger sequencing
Single or small number of genes
- Phylogeny based on 4 loci: ITS, Beta-tubulin, Elongation factor, RNA polymerase II gene
- Assessing evolutionary relationship

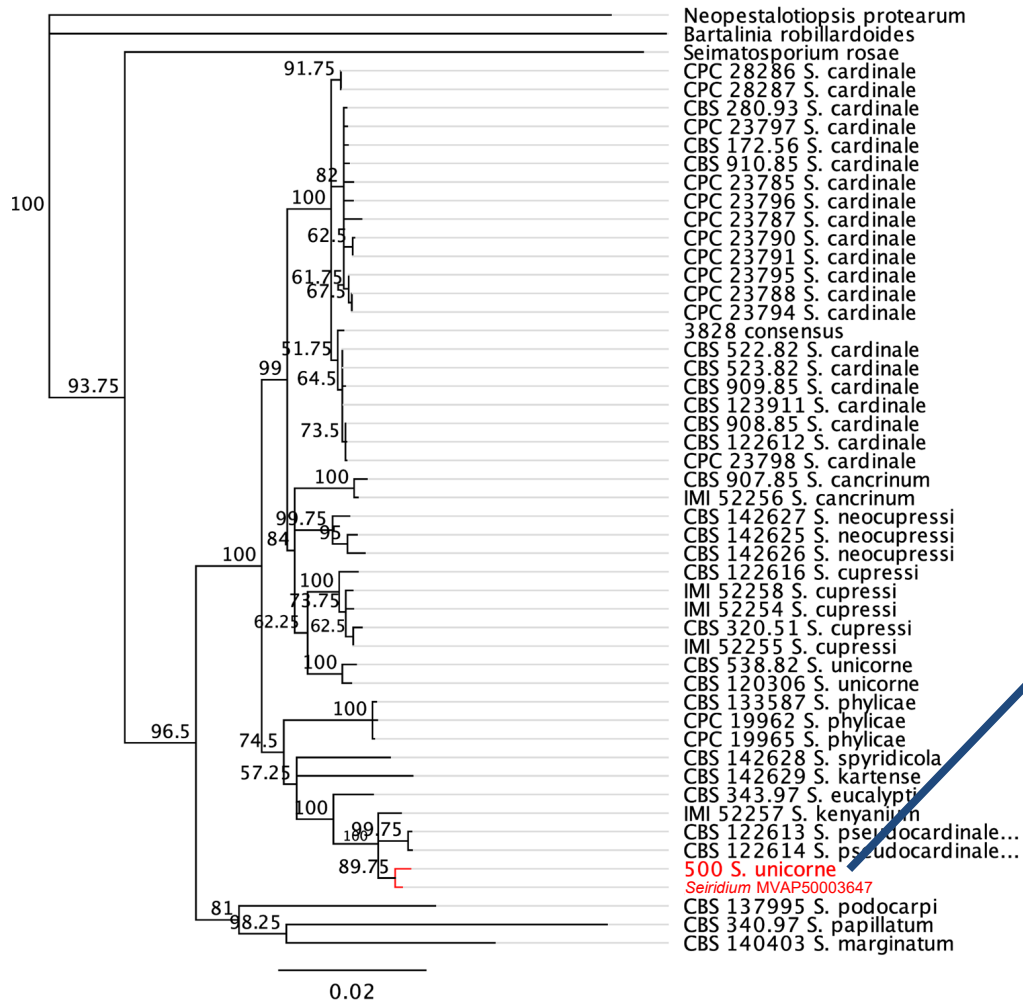
PHYLOGENOMICS

- Illumina sequencing
Entire or large portion of genomes
- Prediction of gene function
- Evolutionary relationship between *Seiridium spp.*
- Gene family evolution
- Gene flow prediction and tracing

GENOMICS

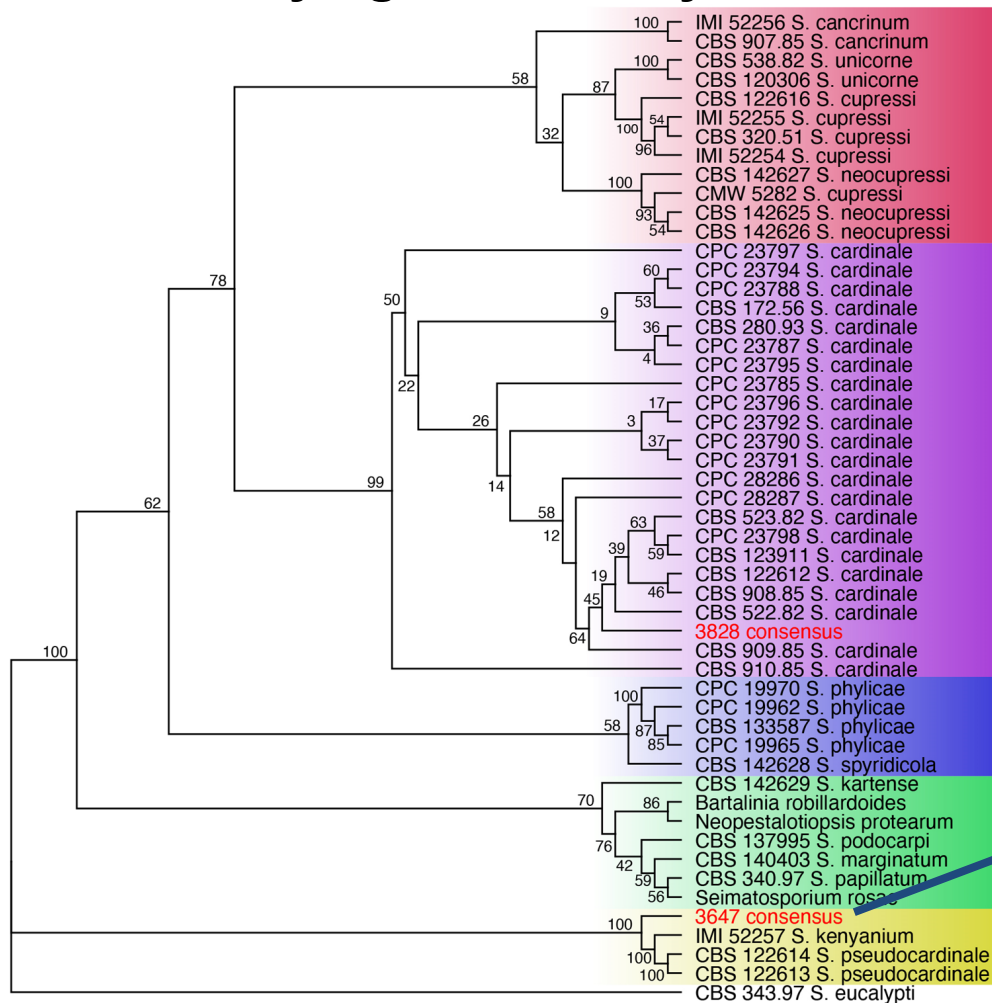
- Genome assembly: **SPAdes**
- QC: **Busco**
- Gene prediction: **AUGUSTUS, Genemark-ES**
- Annotation: **MAKER3, Blast, Interproscan**

Results - Phylogenetic analysis



***S. unicorne* 500 and
Isolate MVAP50003647
cluster together and are
the same species!**

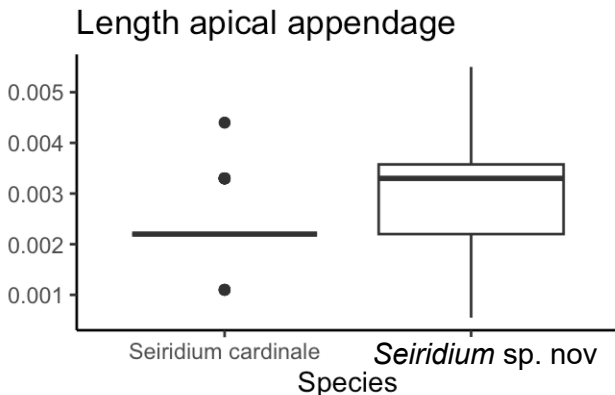
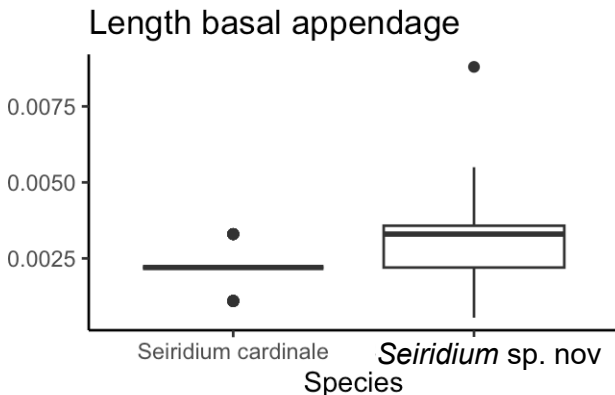
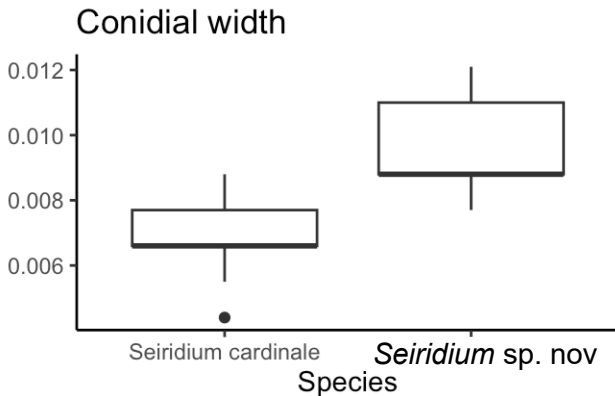
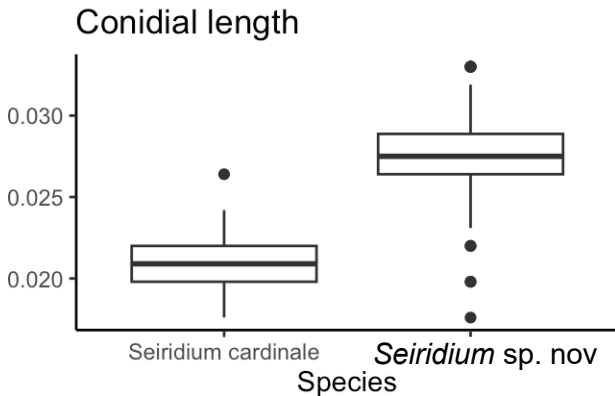
Results - Phylogenetic analysis



Phylogenetic analysis based on 4 concatenated loci
-ITS -RBP -TEF -TUB

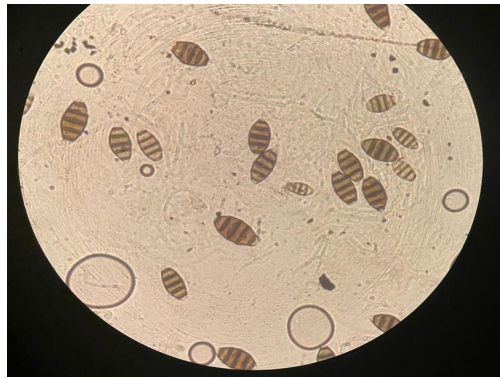
Isolate MVAP50003647-A

Results - Spores analyses



All p-val < 0.05

S. cardinale

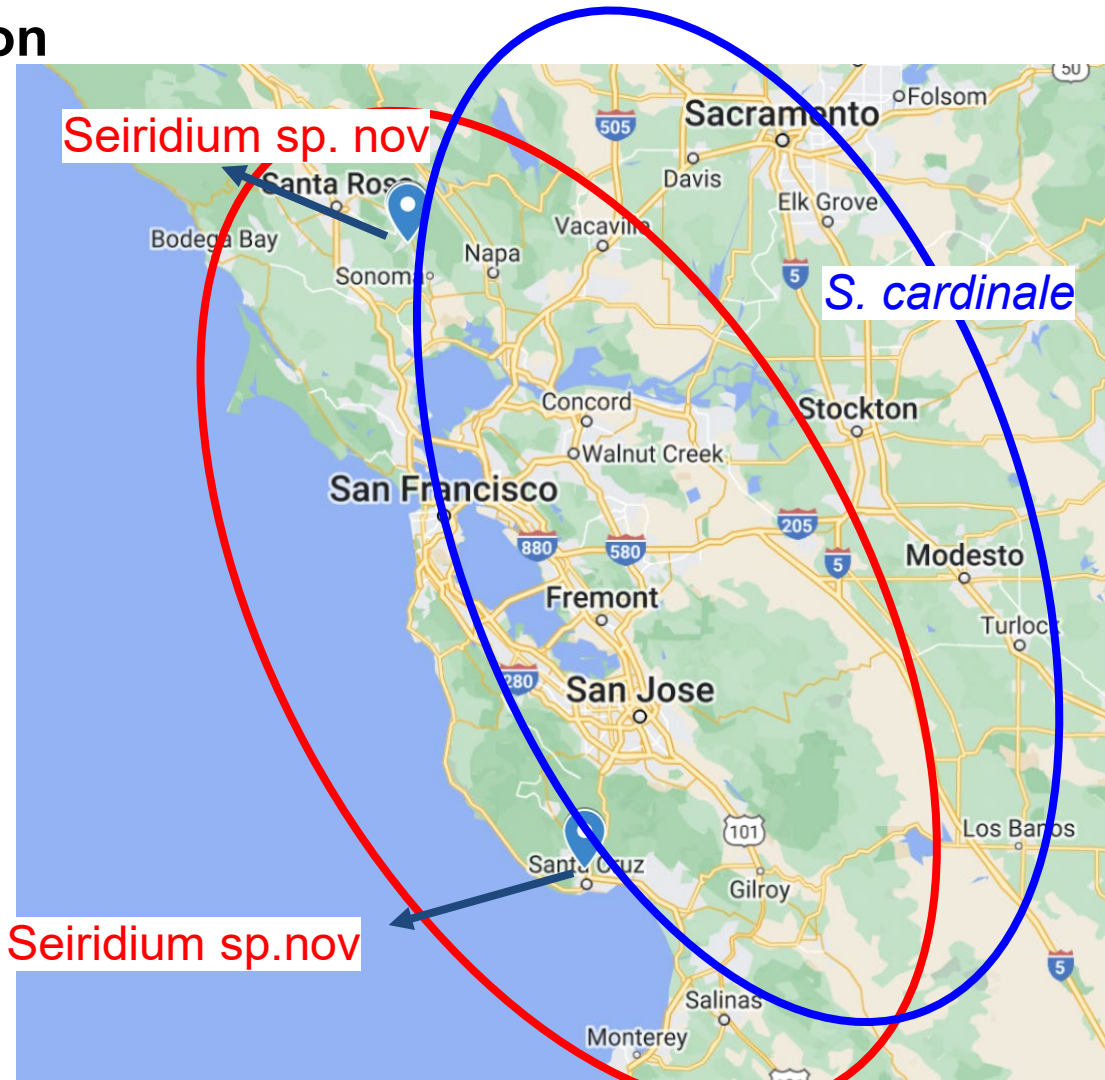


Seiridium sp. nov.



Results - geographic distribution

- This scenario opens further investigation hypotheses
- Is there an overlap between this new *Seiridium* spp. and Monterey cypress range?
- Could it cause CCD in zones that are too cold for *S. cardinale*?



Discussion -Main findings and further experiments

- Isolates MVAP50003647-A and *Seiridium* isolate 500 confirmed to be a new *Seiridium* species.
- Description of predicted genes for isolate MVAP50003647.
- Description of this new species.
- Evaluation of *Seiridium spp.* Californian distribution.
- Further investigation of *Seiridium spp.* evolution.

Thank you for
your time!



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Genome sequence and assembly of the causal agent of
Cypress Canker Disease *Seiridium cupressi*, isolates BM-
138-000234 and BM-138-000515

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