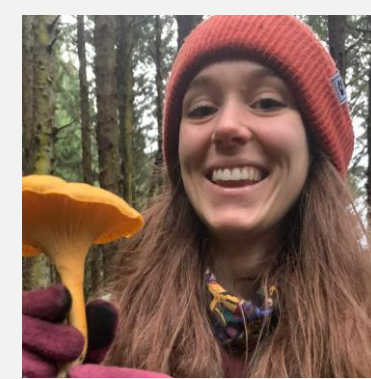


PRESENTER:

Kimberly Syring



Phylogenetics of *Ganoderma oregonense* and related species in the Pacific Northwest

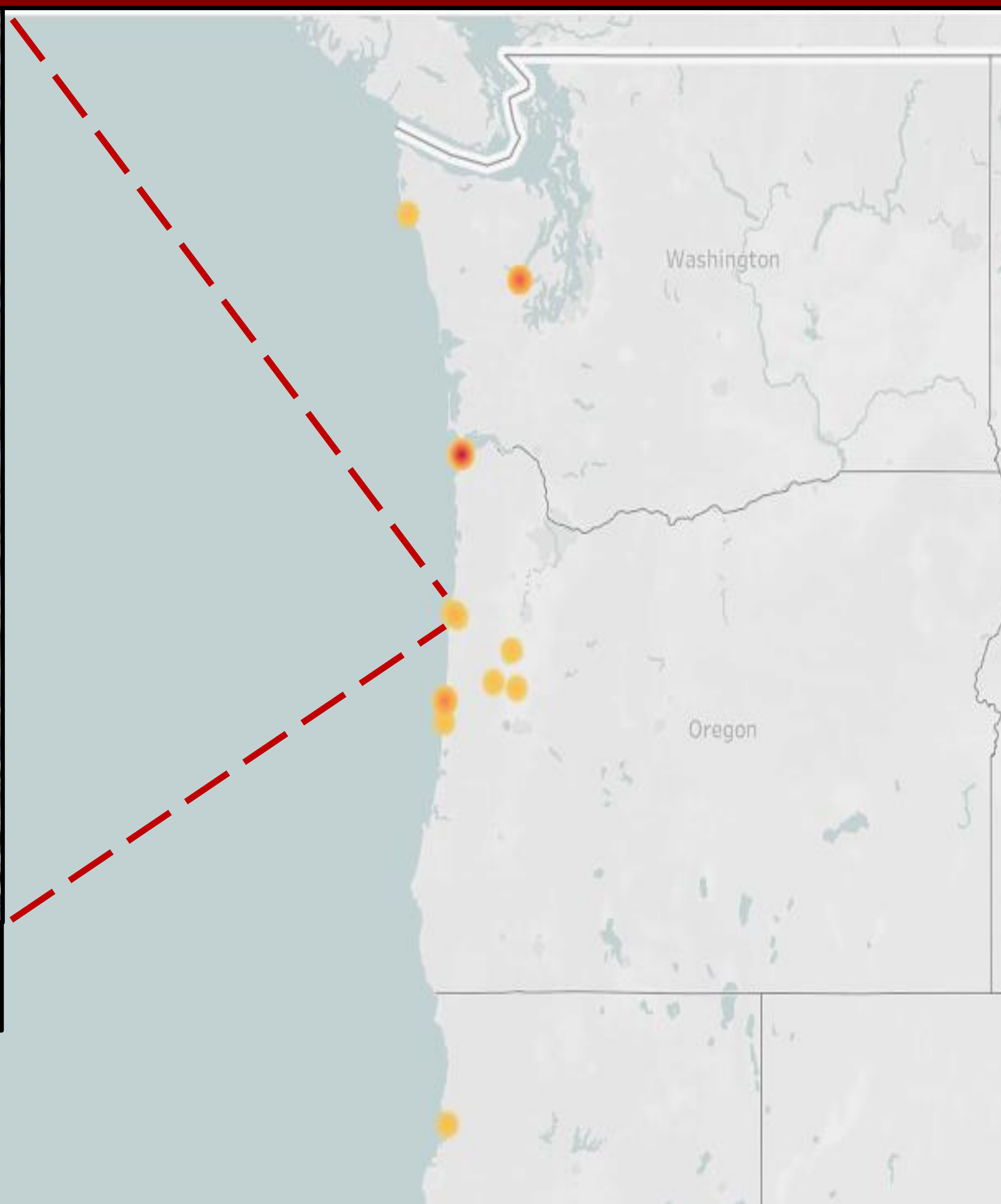
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BACKGROUND:

- *Ganoderma* species have a large geographic range including Asia, Europe, and North America (Lloyd et al. 2018).
- Species in this genus show antitumor, antioxidant, and antibacterial properties, specifically *G.tsugae* and *G.lucidum* (Cheng et al 2013, Hseu et al. 2019).
- *G.oregonense*, a PNW localized species, is closely related to *G.tsugae* and *G.lucidum* (Lloyd et al. 2018).
- Population diversity and genomic information of *Ganoderma oregonense* in the PNW lacks molecular data and a reference genome.
- Gathering improved location and molecular data will aid in creating a more accurate phylogeny of this genus.



Fig. 1 | *Ganoderma oregonense* growing near the Oregon coast.



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Fig. 2 | Map of specimens collected in this study of *Ganoderma* found in Oregon, Washington, and California (Fall 2021). Darker red areas indicate a greater concentration of specimens, while lighter yellow areas indicate fewer. Specimens are also noted in grey on Fig.4.

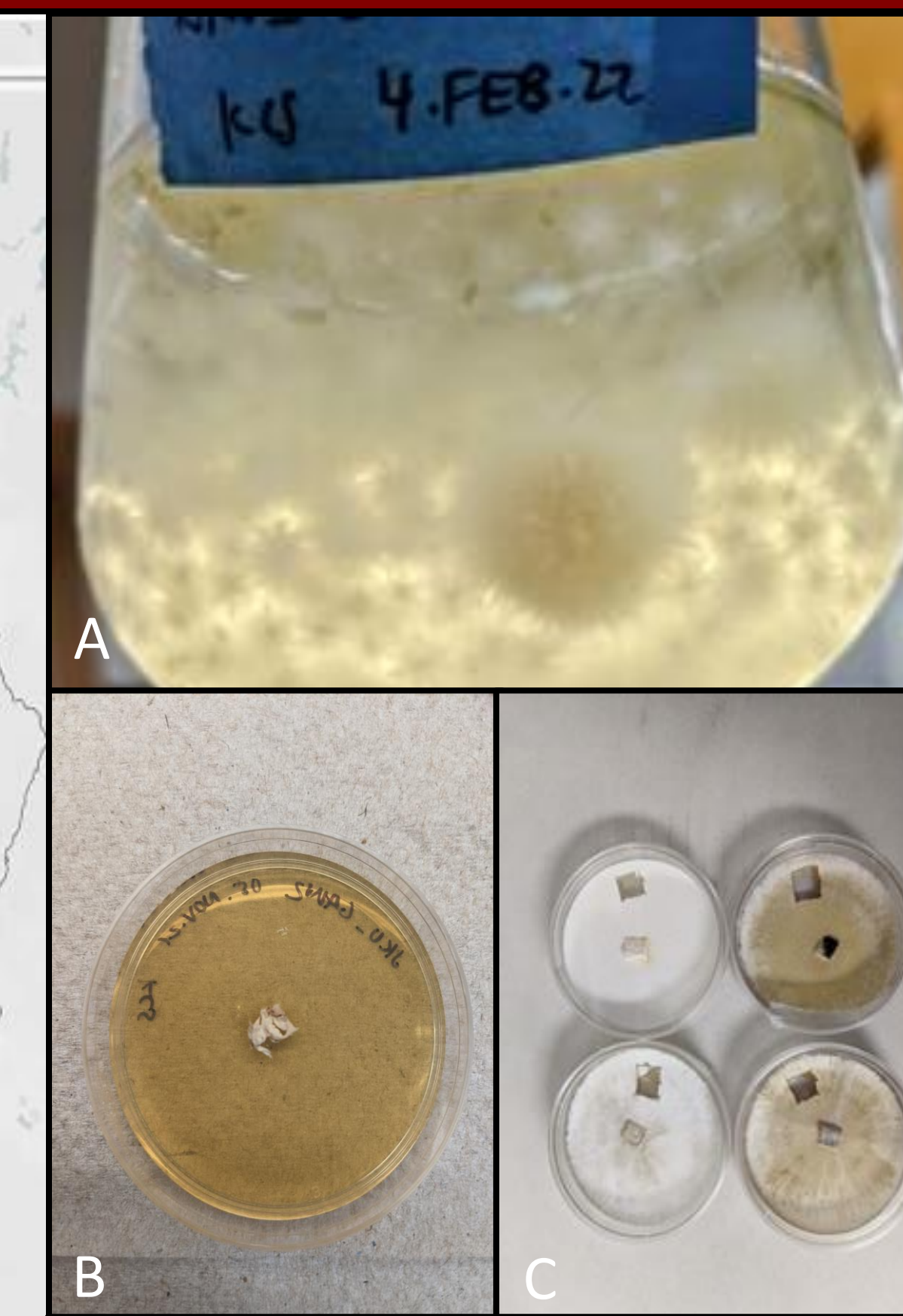


Fig. 3 | Cultures of *G.oregonense*. A: Liquid culture (MEB). B, C: Initial hyphae from fruiting body (B) prior to full colonization of the plate (C).

METHODS:

- 20 specimens with detailed GPS location data and photos were collected from Oregon, Washington, and California in the Fall of 2021.
- Ten specimens were successfully cultured onto malt extract agar (MEA) and additionally placed into malt extract broth (MEB) to ensure pure cultures for genomic sequencing.
- Three samples representing OR, WA, and CA were sent for Illumina genomic sequencing.
- 43 sequences were obtained from GenBank of the internal transcribed spacer region (ITS) of *Ganoderma sp.* to create a preliminary phylogeny.
- MEGA v.11.0.11 was used to align the sequences and create a maximum likelihood (ML) tree using a general time reversal (GTR) model and 100 bootstrap replicates. iTOL (Interactive Tree of Life) was used to visualize and annotate the tree.

Expanded collection, culturing, and sequencing of new specimens of *G. oregonense* in the Pacific Northwest offers a targeted approach to better define its residence within the genus and will help inform studies aiming to understand the diversity and functional genomics of closely related species.

DISCUSSION:

Ganoderma oregonense is closely related to both *G.lucidum* and *G.tsugae*, with considerable overlap between *G.tsugae* and *G.oregonense*. Considering the promising medicinal research surrounding these two species, *G.oregonense* may be another good candidate for similar studies. ITS sequencing can only provide us with a snapshot of how these species are related, which is why it is important to assemble and annotate the novel genome of *G.oregonense*. A genomic scale phylogeny to the species *G.lucidum* and *G.tsugae* will provide an updated and more accurate understanding of how these organisms are related. Studying secondary metabolites and functional genomics of *G.oregonense* to *G.tsugae* and *G.lucidum* will allow us to better determine the medicinal potential of *G.oregonense*, in addition to better describing this genus.

RESULTS:

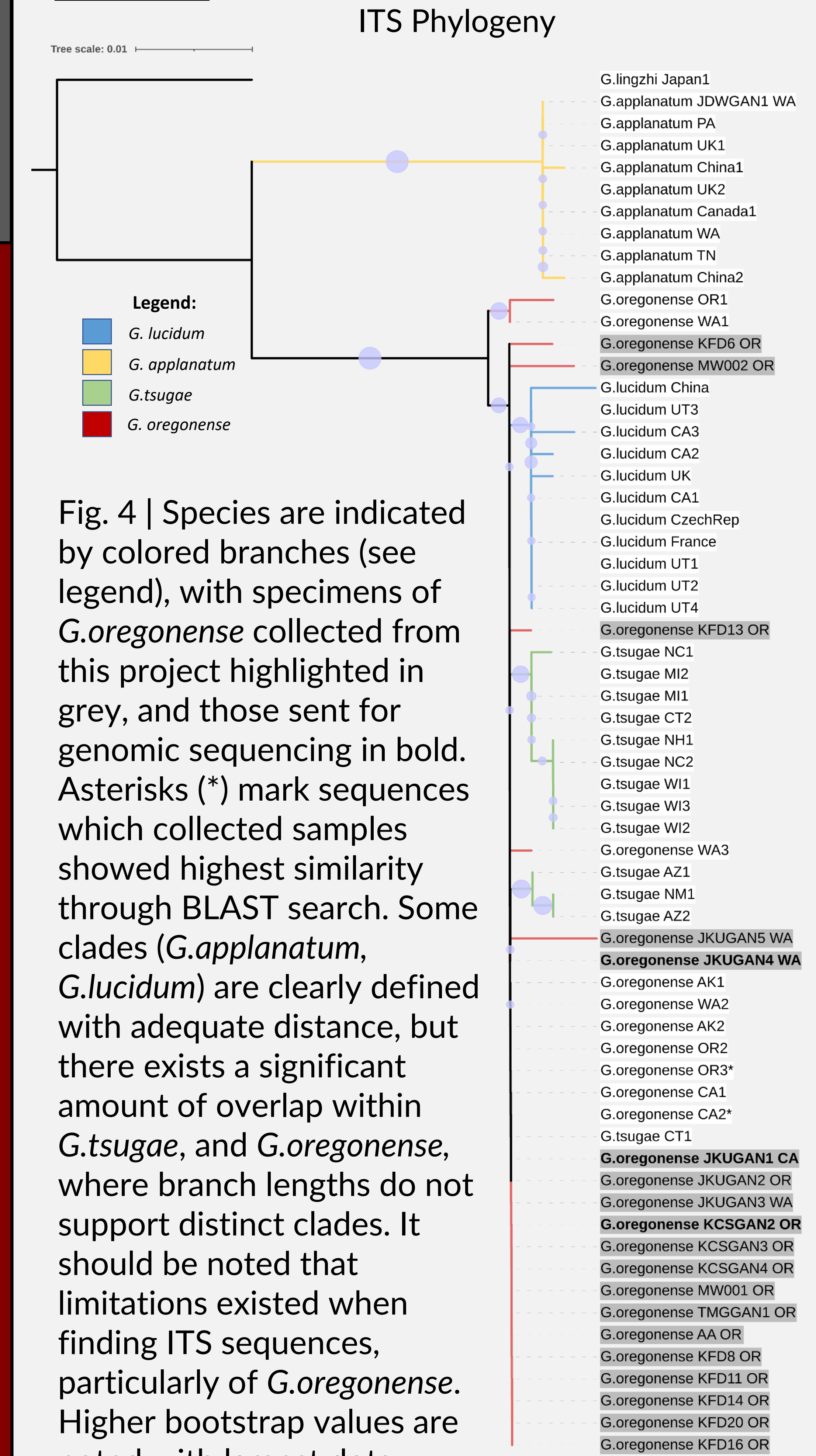


Fig. 4 | Species are indicated by colored branches (see legend), with specimens of *G.oregonense* collected from this project highlighted in grey, and those sent for genomic sequencing in bold. Asterisks (*) mark sequences which collected samples showed highest similarity through BLAST search. Some clades (*G.applanatum*, *G.lucidum*) are clearly defined with adequate distance, but there exists a significant amount of overlap within *G.tsugae*, and *G.oregonense*, where branch lengths do not support distinct clades. It should be noted that limitations existed when finding ITS sequences, particularly of *G.oregonense*. Higher bootstrap values are noted with largest dots.

FUTURE RESEARCH:

Next steps include the novel assembly and annotation of the *G.oregonense* genome. Comparative media studies using existing cultures to explore metabolomic and transcriptomic nuances could expand on this research. Comparing functional genomics to *G.tsugae* and *G.lucidum* will frame future research goals.

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