

PhotobiontDiversity

Genetic diversity of lichen photobionts
and related organisms

Green Algal Photobionts: Trebouxia

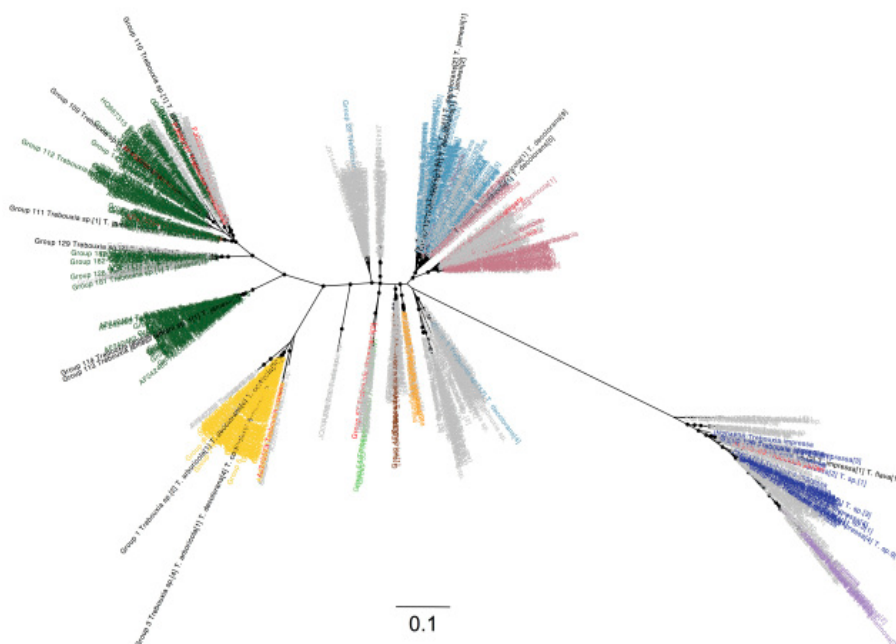
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Having beaten the phylogeny of symbiotic cyanobacteria into submission in my [previous post](#), I am now tackling the green algae. My plan was to start with a big-picture analysis of 18S ribosomal RNA sequences, but my initial blast search returned over 10,000 454 reads from metagenomic projects which was a lot more “environmental isolate XXX” than I felt like dealing with. Besides, I don’t know that I could add much to [this](#) recent overview. Therefore, I am going to focus on the most important lineage of lichenized algae: *Trebouxia*. There have been a large number of studies that have obtained photobiont ITS sequences from a variety of *Trebouxia* associated lichens, so these are the data that I looked at.

The methods are the same as the ones that I described in detail [previously](#) for *Nostoc* ITS sequences. Briefly, I used two ITS sequences (*T. impressa* JN204819 and *T. arboricola* JQ993781) as queries to identify all homologous (E-value $\leq 1e-100$) sequences in the nt database. Sequences were aligned with MAFFT, duplicate sequences were removed with MetaPIGA, alignment positions corresponding to gaps in the references sequence (*T. arboricola* JQ993758) were removed with trimal, and phylogenetic relationships were inferred with PhyML.

This procedure produced a tree with 794 taxa representing 1840 *Trebouxia* ITS sequences. The actual number of *Trebouxia* associated lichens that have been sequenced is much higher than this because many authors only deposit representative sequences of each haplotype that they obtained. At some point I will dig into the papers where this has been done to extract the real numbers, but I have not done so yet.

For now, I am going to focus on the taxonomy of the algae. I will leave a discussion of the host-association patterns for a future post. Here is the *Trebouxia* ITS phylogeny color-coded by species (tree file can be found [here](#)):



Trebouxia ITS phylogeny color-coded by species (dark green: *T. jamesii*, yellow: *T. corticola*, light green: *T. incrustata*, brown: *T. asymmetrica*, orange: *T. gigantea*, purple: *T. gelatinosa*, dark blue: *T. impressa*, light red: *T. arboricola*, light blue: *T. decolorans*, dark red: other, grey: *T. sp.*). Sequences recovered from multiple named species are in black. Black circles indicate aLRT support > 0.9

With a few exceptions, sequences from named algae tend to cluster very well. *T. gelatinosa* (purple) is nested within *T. impressa* (dark blue), though given the long branch separating these two species from all of the others, I don't entirely trust the rooting of this clade. *T. jamesii* (dark green) is a very heterogeneous group as has been recognised [previously](#). A number of photobionts that group with *T. decolorans* (light blue) have been identified as *T. arboricola* (light red). Three major lineages have no named members (except for some presumably misidentified *T. decolorans* sequences).

In addition to the differentially coloured species, there are several additional species names that are represented by a small number of sequences, all of which are colored dark red in the tree. *T. australis*, *T. brindabellae*, *T. showmanii* and *T. usneae* are each found in distinct clusters and are likely to represent additional good species. *T. australis* and *T. brindabellae* are both in clusters near the base of one of the *T. jamesii* clades (dark green). Two *T. showmanii* sequences form the sister group to *T. incrustata* (light green). *T. usneae* forms a distinct lineage with a misidentified *T. corticola* sequence sister to the *T. corticola* lineage (yellow). All other rare species are deeply nested within other common species and appear not to be distinct. These include *T. potteri* which is nested within *T. impressa* (dark blue), *T. aggregata* and *T. crenulata* which are nested within *T. arboricola* (light red) and *T. simplex*, which includes six sequences that are identical to *T. jamesii* (black) and two other sequences that are nested within one of the *T. jamesii* clades (dark green). *T. flava* is identical to a *T. impressa* sequence and is coloured black in the tree.

In conclusion, >1840 *Trebouxia* ITS sequences that have been obtained from lichens cluster into about 24 distinct species, 13 of which appear to have suitable named representatives in the database. Two of the *T. jamesii* clusters have been given the provisional names *T. "vulpineae"* and *T. "letharii"* but it looks like at least three additional names are needed for this group.

That's it for now. In my next post I will map host information onto this tree.

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