

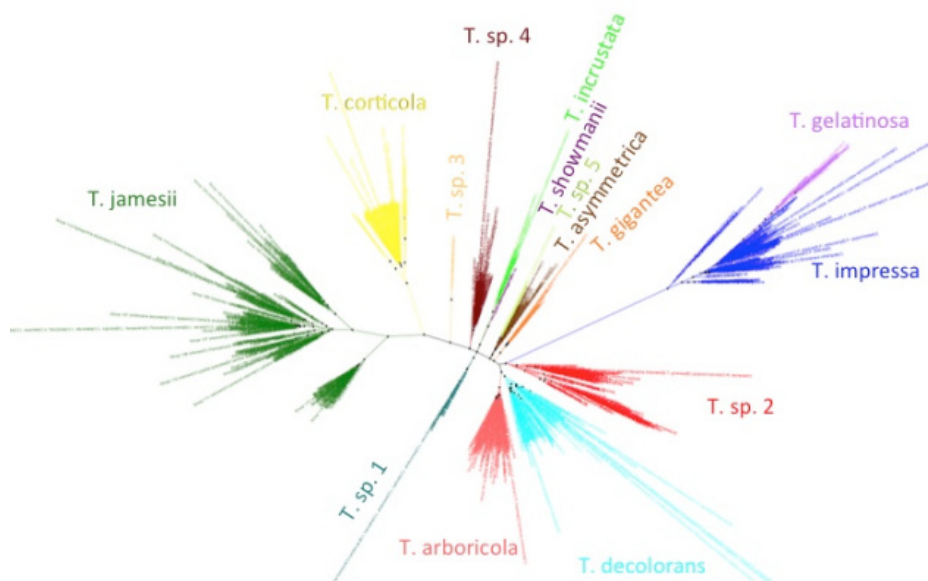
## PhotobiontDiversity

Genetic diversity of lichen photobionts  
and related organisms

### A preliminary look at host association patterns in *Trebouxia*

Posted on [June 5, 2013](#)

Having gone through the steps to build a phylogeny of the most common lichen photobiont, *Trebouxia* in my [last post](#), I will now go on to discussing the host association patterns that it reveals. Here is the *Trebouxia* ITS tree generated previously:



*Trebouxia* ITS phylogeny. Major clades are differentilly coloured and named according to authentic strains

I've coloured all of the taxa within clades according to the colours of the named strains and I've assigned unique colours to each clade that does not contain named strains. I have not attempted to break up *T. jamesii* or *T. impressa* into sub-clades, though doing so would probably be justified. This will be a topic for a future post. I should also point out that *T. jamesii* is referred to as *T. simplex* in [some papers](#).

In contrast to *Nostoc* photobionts where the fasta headers were consistently labeled with the host information, these sequences are ...not. I used a bioperl wrapper to NCBI's Eutils interface to download genbank format sequences and parsed them to extract host association information from the "host", "note" and "isolation source" annotations. I also extracted information about the author of each sequence and where it was published while I was at it:

```
../Scripts/GetGB.pl Trebouxia_ITS_acc.txt heath.obrien-at-gmail-dot-com > Trebouxia_ITS.gbk
```

```
../Scripts/ParseHost.pl Trebouxia_ITS.gbk > host_info.txt
```

```
../Scripts/GetRef.py Trebouxia_ITS.gbk > ref_info.txt
```

This information was added to *Trebouxia\_ITS\_metadata.txt* in Excel and missing values were filled in manually where possible. I also added culture collection numbers where available and started to fill in locality information, but I haven't gotten very far with the latter.

Next, I added information about which clade each sequence fell into to the *Trebouxia* metadata file. The [ETE](#) python toolkit was invaluable for this step and was my main proximate motivation for switching from perl to python for my scripting, but I was also really, REALLY tired of having to keep my '@'s and '%{'s straight:

```
../Script/GetClades.py -t Trebouxia_ITS.nwk -m Trebouxia_ITS_metadata.txt >temp
```

```
mv temp Trebouxia_ITS_metadata.txt
```

In this case, the information was added to the metadata file automatically.

Lastly, I wrote a script to count the number of times that *Trebouxia* from each clade was associated with each lichen genus that has been sampled:

```
../Scripts/CountAssociations.py -m Trebouxia_ITS_metadata.txt > AssociationCounts.txt
```

After some fiddling with conditional formatting in Excel, these analyses produced this:

Genus	Family	T. arboricola	T. asymmetrica	T. corticola	T. decolorans	T. gelatinosa	T. gigantea	T. impressa	T. incrustata	T. jamesii	T. showmanii	T. sp 1	T. sp 2	T. sp 3	T. sp 4	T. sp 5
Acarospora	Acarosporaceae															
Polysporina	Acarosporaceae															
Sarcogyne	Acarosporaceae															
Rimularia	Agaricaceae															
Arandinea	Caliciaceae															
Buellia	Caliciaceae															
Dimeraria	Caliciaceae															
Candelaria	Candelariaceae															
Austroblea	Catillariaceae															
Chaenotheca	Coniosporaceae															
Diplotelium	Graphidaceae															
Thamnia	Imbricariaceae															
Lecidea	Lecanoraceae															
Carbonia	Lecanoraceae															
Lecanora	Lecanoraceae															
Lecidea	Lecanoraceae															
Rhizoglyph	Lecanoraceae															
Agapicilia	Megastromataceae															
Everniastrum	Parmeliaceae															
Tuckermanniopsis	Parmeliaceae															
Ulexia	Parmeliaceae															
Imbricaria	Parmeliaceae															
Pseudovernia	Parmeliaceae															
Hypogynia	Parmeliaceae															
Flavocetraria	Parmeliaceae															
Evernia	Parmeliaceae															
Cetraria	Parmeliaceae															
Letharia	Parmeliaceae															
Flavoparmelia	Parmeliaceae															
Melanella	Parmeliaceae															
Parmelia	Parmeliaceae															
Parmelia	Parmeliaceae															
Parmotrema	Parmeliaceae															
Pleurosticta	Parmeliaceae															
Punctelia	Parmeliaceae															
Xanthoparmelia	Parmeliaceae															
Anaptychia	Physciaceae															
Phaeophyscia	Physciaceae															
Physcia	Physciaceae															
Physconia	Physciaceae															
Ricodina	Physciaceae															
Rinodina	Physciaceae															
Boreopora	Ramaliaceae															
Ramalina	Ramaliaceae															
Torinia	Ramaliaceae															
Lepraria	Streptocaulaceae															
Schaeria	Teloschistaceae															
Caloplaca	Teloschistaceae															
Fulgensia	Teloschistaceae															
Huea	Teloschistaceae															
Sclerophora	Teloschistaceae															
Teloschistes	Teloschistaceae															
Xanthomendoza	Teloschistaceae															
Xanthoria	Teloschistaceae															
Tephromela	Tephromelaceae															
Lasalia	Umbilicariaceae															
Umbilicaria	Umbilicariaceae															

Counts of associations between Trebouxia clades and lichen genera. Colour coding matches the phylogeny

Before discussing the patterns, I should point out that these counts are of how many sequence records have been deposited in genbank, not the number of specimens that have been sampled as many authors deposit representative haplotype sequences rather than all of their data. Incorporating this information will change the counts dramatically in some cases.

The most extensively sampled genus is *Letharia*, which is exclusively associated with *Trebouxia jamesii*. In fact, there [appears](#) to be strong reciprocal specificity acting between species of *Letharia* and subclades within *T. jamesii*, a topic I would like to explore further in the future.

Eight other genera in the Parmeliaceae are also exclusively associated with *T. jamesii* photobionts, including *Cetraria* (76 sequences), *Evernia* (19 sequences), *Flavocetraria* (17 sequences), *Hypogymnia* (12 sequences) and *Pseudevernia* (10 sequences). However, *Parmelia* (10 sequences), *Flavoparmelia* (6 sequences), and 4 other genera associate with photobionts in the *T. impressa*/*T. gelatinosa* clade (among others) and *Parmotrema* is highly specific for *T. corticola* photobionts, with 135 *P. tinctorum* photobionts grouping with *T. corticola* (the *Trebouxia* sp. 3 photobiont is from a different *Parmotrema* species). The *P. tinctorum* / *T. corticola* association is another case of reciprocal specificity as 135 of 141 *T. corticola* sequences are from *P. tinctorum* photobionts.

All photobionts from *Lasallia* (28 sequences) and most from *Umbilicaria* (105 of 131 sequences) also grouped with *T. jamesii*, with most of the exceptions being specimens collected in the [Antarctic](#) (see also [this](#) paper). *T. jamesii* was also the predominant photobiont of *Thamnolia* (22 out of 28 sequences) and *Chaenotheca* (7 of 8 sequences). *T. jamesii* was also a common photobiont of *Lecanora* and *Lecidea*, but photobiont diversity in both of these genera, and the Lecanoraceae in general, is extremely high, with *Lecanora* photobionts falling into 11 different species and *Lecidea* photobionts falling into 8. Indeed, 6 species of photobiont [have been recovered from \*L. rupicola\* alone](#). Lichens in the Lecanoraceae are the hosts for the vast majority of *T. asymmetrica*, *T. incrustata*, *T. showmanii* and *T. sp. 1* photobionts that have been sampled.

Similar to the Parmeliaceae, most of the genera in the Physciaceae are specific for the same *Trebouxia* lineage, while other genera do not associate with it at all. *Physconia* (40 sequences) and *Phaeophyscia* (7 sequences) are exclusively associated with *T. impressa*, as are 29 out of 36 *Physcia* sequences while only 2 of 5 *Rinodina* photobionts and none from *Anaptychia* (8 sequences) group with *T. impressa*.

All but 9 of 133 *Xanthoria* photobionts belong to *T. decolorans* or *T. arboricola*, which are sister species. These photobionts also predominate in most of the other genera in the Teloschistaceae, including 53 of 65 *Caloplaca* photobionts, 4 of 4 *Huea* photobionts, and 34 of 68 *Tephromela* photobionts, a genus that is also frequently associated with *Trebouxia* sp. 2 photobionts.

Specificity is also high for *Ramalina*, with 139 of 150 photobiont sequences restricted to two *Trebouxia* clades. *Boreoplaca* is associated with one of the same photobionts (*Trebouxia* sp. 2), but not with the most common *Ramalina* photobiont (*T. decolorans*; 116 of 150 sequences).

Thus, there is a wide range of association patterns, from extreme reciprocal specificity (135 of 141 *T. corticola* sequences associated with *Parmotrema* and all *P. tinctorum* specimens associated with *T. corticola*) to generalism (*Lecanora rupicola* associating with 6 different *Trebouxia* species). There is some evidence of phylogenetic inertia, as lichen genera from the same family are more likely to share similar photobiont association patterns than unrelated lichens, but there is also a lot of plasticity. There are a lot of ideas out there about the ecological and life history factors that could be causing these differences, but given the complexity of the patterns and our lack of knowledge of things like lichen demography and dispersal mechanisms, it will probably be some time before definitive explanations can be provided.

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