



Non-cyanobacterial diazotrophs dominate dinitrogen fixation in biological soil crusts at the early stage of crust formation.

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1 ABSTRACT

Biological soil crusts (BSC) cover a vast global area and are key components of ecosystem productivity in arid soils. In particular, BSC contribute significantly to the nitrogen (N) budget in arid ecosystems via N₂-fixation. N₂-fixation in mature crusts is largely attributed to heterocystous cyanobacteria, however, early successional crusts are dominated by non-heterocystous cyanobacteria and this suggests that microorganisms other than cyanobacteria mediate N₂-fixation during the early stages of BSC development. DNA stable isotope probing (DNA-SIP) with ¹⁵N₂ revealed that *Clostridiaceae* and *Proteobacteria* are the most common microorganisms to assimilate ¹⁵N in early successional 'light' crusts. Incorporation of ¹⁵N₂ by cyanobacteria was not observed through cyanobacteria were dominant in the crust sample. The maximum relative abundance of ¹⁵N₂-assimilating taxa in the BSC was 0.00225% and 0.00127% for taxa that belong to *Clostridiaceae* and *Proteobacteria*, respectively. Their low abundance in the BSC may explain why these heterotrophic diazotrophs have not previously been characterized in BSC. Diazotrophs play a critical role in BSC formation and characterization of these organisms represents a crucial step towards understanding how anthropogenic change will effect the formation and ecological function of BSC in arid ecosystems.

2 INTRODUCTION

Biological soil crusts (BSC) are specialized microbial mat communities that form at the soil surface in arid environments and fill a variety of important ecological functions in arid ecosystems. BSC occupy plant interspaces and cover a wide, global geographic range (Garcia-Pichel et al., 2003b). The ground cover of BSC on the Colorado Plateau has been measured as high as 80% by remote sensing (Karnieli et al., 2003). The global biomass of BSC *Cyanobacteria* alone is estimated at 54 x 10¹² g C (Garcia-Pichel et al., 2003b). BSC play important roles in arid ecosystem productivity and are responsible for significant nitrogen (N) flux (for review of BSC N-fixation see Belnap (2003)). For example, N-input via N-fixation versus atmospheric deposition was predominant in five times as many BSC samples from North America, Africa and Australia (Evans and Belnap, 1999). The presence of BSC is positively correlated with vascular plant survival due in part to BSC ecosystem N contributions (for review of BSC-vascular plant interactions see Belnap et al. (2003)). Climate change and disturbance alter BSC microbial community structure and membership and therefore can alter diazotroph diversity and the BSC N-budget.

BSC N-fixation rate studies (typically employing the acetylene reduction assay (ARA)) have explored BSC diazotroph activity across various ecological gradients. Reported BSC N-fixation rates vary significantly (Evans and Lange, 2001). The reasons for this variability are complex and likely include the spatial heterogeneity of BSC (Evans and Lange, 2001) and the impact of recent environmental conditions on N-fixation rates (see Belnap (2001) for discussion). Moreover, the ARA assay is subject to methodological artifacts that preclude cross-study and possibly intra-study but inter-environment type comparisons (see Belnap (2001) for review). Nonetheless, mature BSC N-fixation rate measurements have been higher than younger, developing BSC N-fixation rate measurements (Belnap, 2002; Yeager et al., 2004). This difference may be due to the proliferation of heterocystous *Cyanobacteria* in older mats and is consistent with the theory that heterocystous *Cyanobacteria* are the primary BSC diazotrophs. Alternatively, the N-fixation rate differences between young and old BSC might be attributable to methodological artifacts. For instance, Johnson et al. (2005) show that N-fixation rates peak at a lower depth in developing BSC as compared to mature BSC. When N-fixation is measured from intact cores of developing BSC the measurement may be artifactually low due to delayed acetylene/ethylene diffusion through the crust to and from the peak N-fixation rate depth in a typical ARA incubation timeframe. Diffusion would not be an issue when measuring N-fixation rates in mature crust as nitrogenase activity peaks near the surface. When total N-fixation rates were calculated by integrating rates over 1-3 mm depth slices along full BSC cores (thus mitigating ethene/acetylene flux limitations), N-fixation rate differences between developing and mature BSC were not statistically significant (Johnson et al., 2005).

Molecular studies of BSC microbial diversity include explorations of the BSC microbial community vertical profile (Garcia-Pichel et al., 2003a), BSC *nifH* gene content surveys (e.g. Yeager et al. (2004), Yeager et al. (2012), Yeager et al. (2006) and Steppe et al. (1996)), and next-generation-sequencing (NGS) enabled studies of BSC SSU rRNA gene content across wide geographic ranges (Garcia-Pichel et al., 2013; Steven et al., 2013). *nifH* surveys have been conducted across BSC development stages (Yeager et al., 2004), as well as across seasons, temperatures and precipitation gradients (Yeager et al., 2012). Mature, more fully developed BSC possess greater numbers of heterocystous *Cyanobacteria* (e.g. *Nostoc*, *Scytonema*) than developing BSC but both young and old BSC are dominated by non-heterocystous *Cyanobacteria* (*Microcoleus vaginatus* or *M. steenstrupii*) (Yeager et al., 2004; Garcia-Pichel et al., 2013). Young or recently disturbed BSC are often described as "light" in appearance relative to "dark" mature BSC (Belnap, 2002; Yeager et al., 2004). Heterocystous *Cyanobacteria* are the numerically dominant BSC diazotrophs in *nifH* clone libraries (Yeager et al., 2006, 2004, 2012) although an early survey of Colorado Plateau BSC *nifH* diversity recovered *nifH* genes related to *Gammaproteobacteria* as well as a clade that included *nifH* genes from the anaerobes *Clostridium pssteurianum*, *Desulfovibrio gigas* and *Chromatium buideri*. Specifically, Yeager et al. (2006)—in a study of overall BSC *nifH* diversity—categorized 89% of 693 *nifH* sequences derived from Colorado Plateau and New Mexico BSC samples as heterocystous cyanobacterial (non-cyanobacterial *nifH* sequences were largely attributed to alpha- and beta- *proteobacteria*). The heterocystous cyanobacterial BSC diazotrophs fall into three genera, *Scytonema*, *Spirirestis*, and *Nostoc* (Yeager et al., 2006, 2012).

The influence of microbial community membership and structure on BSC N-fixation is an ongoing research question (Belnap, 2013). While the presence/abundance of heterocystous *Cyanobacteria* has been proposed as the mechanism behind increased N-fixation in mature BSC, it is unclear if mature BSC actually fix more N (see Johnson et al. (2005)). More studies are necessary to elucidate the microbial membership influence on BSC N-fixation and to determine if heterocystous *Cyanobacteria* are the only keystone diazotrophs. The first step in defining structure function relationships with respect to N-fixation is a full accounting of BSC diazotrophs. Towards this end we conducted $^{15}\text{N}_2$ DNA stable isotope probing (DNA-SIP) experiments with light, developing Colorado Plateau BSC. DNA-SIP with $^{15}\text{N}_2$ has not been attempted with BSC. DNA-SIP would provides an accounting of *active* diazotrophs whereas *nifH* clone libraries account for microbes with the genomic potential for N-fixation. Further, we track the distribution of putative diazotrophs uncovered in this study through collections of NGS SSU rRNA libraries from BSC microbial diversity surveys over a range of spatial scales and soil types (Garcia-Pichel et al., 2013; Steven et al., 2013).

3 RESULTS

3.1 COMPARISON OF SEQUENCE COLLECTIONS AT "STUDY"-LEVEL

79 *3.1.1 Comparisons of OTU content:* There were 3,079 OTUs (209,354 total sequences after quality
 80 control) in the DNA-SIP data, 3,203 OTUs (129,033 total sequences after quality control) in the Garcia-
 81 Pichel et al. (2013) study, and 2,481 OTUs (129,358 total sequences after quality control) in the Steven
 82 et al. (2013) study. Of the 4,340 OTU centroids established for this study (including sequences from
 83 Steven et al. (2013) and Garcia-Pichel et al. (2013)) 445 have matches in the Living Tree Project (LTP)
 84 (a collection of 16S gene sequences for all sequenced type strains (Yarza et al., 2008)) at greater or equal
 85 than 97% (LTP version 115). That is, 445 of 4,340 are closely related to cultivars. The DNA-SIP data
 86 set shares 56% OTUs with the Steven et al. (2013) data and 46% of OTUs with the Garcia-Pichel et al.
 87 (2013) data (where total OTUs are from the combined data for each pairwise comparison). The Steven
 88 et al. (2013) and Garcia-Pichel et al. (2013) share 46% of OTUs.

89 *3.1.2 Comparisons of Taxonomic Content:* *Cyanobacteria* and *Proteobacteria* were the top two
 90 phylum-level sequence annotations for all three studies but only the DNA-SIP data had more
 91 *Proteobacteria* annotations than *Cyanobacteria*. *Proteobacteria* represented the 29.8% of sequence
 92 annotations in DNA-SIP data as opposed to 17.8% and 19.2% for the Garcia-Pichel et al. (2013) and
 93 Steven et al. (2013) data, respectively. There is a stark contrast in the total percentage of sequences
 94 annotated as *Firmicutes* between the raw environmental samples and the DNA-SIP data. *Firmicutes*
 95 represent only 0.21% and 0.23% of total phylum level sequence annotations in the Steven et al. (2013)
 96 and Garcia-Pichel et al. (2013) studies, respectively (Figure 1). In the DNA-SIP sequence collection
 97 *Firmicutes* make up 19% of phylum level sequence annotations. Also in sharp contrast for the DNA-
 98 SIP versus environmental data is the number of putative heterocystous *Cyanobacteria* sequences. Only
 99 0.29% of *Cyanobacteria* sequences in the DNA-SIP data are annotated as belonging to "Subsection IV"
 100 which is the heterocystous order of *Cyanobacteria* in the Silva taxonomic nomenclature (Pruesse et al.,
 101 2007). In the Steven et al. (2013) and Garcia-Pichel et al. (2013) studies 15% and 23%, respectively, of
 102 *Cyanobacteria* sequences are annotated as belonging to "Subsection IV".

3.2 ORDINATION OF CSCL GRADIENT FRACTION SSU RRNA LIBRARIES

103 Ordination of Bray-Curtis (Bray and Curtis, 1957) distances between CsCl gradient fraction sequence
 104 libraries with principal coordinates analysis shows the labeled gradient fraction libraries diverge from
 105 control at the "heavy" of the CsCl gradients (Figure 2). When the labeled and control CsCl gradient
 106 fraction 16S rRNA gene libraries are paired such that each pair contains a control fraction and labeled
 107 fraction from the same incubation day with a density difference below 0.003 g/mL, the Bray-Curtis
 108 distance between the fraction pair is positively correlated to the density of the labeled fraction (p-value:
 109 0.00052, r^2 : 0.3315) (inset Figure 2). Additionally, the label/control category for heavy fractions is
 110 statistically significant by the Adonis test (p-value: 0.001, r^2 : 0.136) (Anderson, 2001). The first principal
 111 axis appears to be correlated with fraction density (Figure 2) and the Adonis test p-value for density versus
 112 pairwise Bray-Curtis distances with all CsCl fraction libraries is 0.001 (r^2 0.117).

3.3 IDENTITIES OF POSSIBLE ^{15}N INCORPORATORS

113 The OTUs that have enriched proportion means in labeled gradient heavy fractions versus control gradient
 114 heavy fractions are those that have incorporated the stable isotope tracer into their DNA. We found 38
 115 OTUs that appeared to incorporate ^{15}N into DNA (or "responders"). Of these 38, 26 are annotated as
 116 *Firmicutes*, 9 as *Proteobacteria*, 2 as *Acidobacteria* and 1 as *Actinobacteria* (The inset of Figure 3
 117 summarizes the Family level taxonomic profile of stable isotope responders). Figure 3 summarizes the
 118 ratio of proportion means for each OTU where means are calculated from proportions in heavy fractions
 119 within labeled or controlled gradients and the ratio is labeled over control (see methods). If the OTUs

are ranked by descending, moderated proportion mean labeled:control ratios, the top 10 ratios (i.e. the 10 OTUs that were most enriched in the labeled gradients considering only heavy fractions) are either *Firmicutes* (6 OTUs) or *Proteobacteria* (4 OTUs). Figure 4 shows the relative abundance values for the top 10 OTUs in heavy fractions of labeled and control gradients. Table 2 summarizes the results from BLAST searching the centroid sequences for these top 10 OTUs against the LTP database *Proteobacteria* OTU centroid sequences for the top 10 responders all share high identity (>98.48% identity, Table 2) with cultivars from genera known to possess diazotrophs including *Klebsiella*, *Shigella*, *Acinetobacter*, and *Ideonella*. None of the *Firmicutes* OTUs in the top 10 responders share greater than 97% sequence identity with sequences in the LTP database (release 115) (see Table 2).

3.4 DISTRIBUTION OF BSC DIAZOTROPHS IN ENVIRONMENTAL SAMPLES

3.4.1 *Clostridiaceae*: Five of the 6 *Firmicutes* in the top 10 responder OTUs (above) belong in the *Clostridiaceae*. We only observed one of these strongly responding *Clostridiaceae* in the data presented by Garcia-Pichel et al. (2013), "OTU.108" (closest BLAST hit in LTP Release 115 – *Caloramotor proteoclasticus*, BLAST %ID 96.94, Accession X90488). OTU.108 was found in two samples both characterized as "light" crust. One other *Clostridiaceae* OTU with a proportion mean ratio (labeled:control) p-value less than 0.10 but outside the top 10 responders was found in the Garcia-Pichel et al. (2013) data and also in a "light" crust sample. None of the strongly responding *Clostridiaceae* were found in the sequences provided by Steven et al. (2013).

Figure 5 depicts the phylogenetic breadth of *Clostridiaceae* ¹⁵N responder OTUs from this experiment. The phylogenetic tree was constructed from near full-length reference sequences, and edge width demonstrates the placements of short OTU centroid sequences in the backbone tree (see methods for description of placement algorithm and selection criteria for reference sequences). As shown, *Clostridiaceae* ¹⁵N-responder OTU centroid 16S sequences are generally more closely related to environmental than cultivar 16S gene sequences.

3.4.2 *Proteobacteria*: Only "OTU.342" (closest BLAST hit in LTP Release 115, BLAST %ID 100, Accession ZD3440, *Acinetobacter johnsonii*) of the *Proteobacteria* OTUs in the top 10 most strongly responding OTUs was found in the Garcia-Pichel et al. (2013) sequences. None of the strongly responding *Proteobacteria* OTUs were found in the Steven et al. (2013) sequences. There were 133 responder OTU-sample occurrences (responder OTU was found in a sample library) in the Steven et al. (2013) data. 83 were in "below crust" samples, 50 in BSC samples.

3.4.3 *Other taxa*: Two potentially diazotroph OTUs were found in an extensive number of environmental samples (61 of 65 samples from the combined data sets of Garcia-Pichel et al. (2013) and Steven et al. (2013)). Both OTUs were annotated as *Acidobacteria* but shared little sequence identity to any cultivar SSU rRNA gene sequences in the LTP (Release 115), with best LTP BLAST hits of 81.91 and 81.32% identity. Additionally, the evidence for ¹⁵N incorporation for each OTU was weak relative to other putative responders (adjusted p-values of 0.090 and 0.096). Of the remaining 36 stable isotope responder OTUs, only 14 were observed in the environmental data. Figure 6 summarizes the OTU-sample occurrences in both the Steven et al. (2013) and the Garcia-Pichel et al. (2013) data with occurrences distributed into the most relevant sample classes of each study.

3.5 RICHNESS ESTIMATES

Figure 9 (inset) summarizes the fraction of observed OTUs over total OTUs as estimated by CatchAll for each sample 16S library. Rarefaction curves for each sample are shown in Figure 9. Qualitatively, rarefaction curves show below crust samples to be more rich than BSC samples in the Steven et al. (2013) data.

4 DISCUSSION

4.1 STUDY-LEVEL DIFFERENCES

162 The DNA-SIP data has increased relative abundance of *Firmicutes* sequence annotations relative to
163 environmental data (Figure 1). The DNA-SIP data also has more *Proteobacteria* sequence annotations
164 than environmental datasets. (Figure 1). The increased *Firmicutes* and *Proteobacteria* annotations are
165 consistent with the phylum-level taxonomies of the most strongly ^{15}N responding OTUs (see results).
166 At the distal ends of a CsCl DNA-SIP gradient there is little DNA, but, since we are working with
167 compositional data and gradient fraction libraries are not weighted by absolute DNA content, OTUs
168 found at the ends of CsCl gradients are inflated in overall abundance relative to their abundance in the
169 non-fractionated DNA. DNA from OTUs that incorporate ^{15}N into their biomass moves towards the
170 heavy end of the CsCl gradient and therefore OTUs in “labeled” DNA are enriched in the full data pool
171 relative to bulk DNA.

4.2 ORDINATION OF CSCL GRADIENT FRACTION 16S LIBRARIES

172 The ordination of Bray-Curtis distances between CsCl gradient fraction 16S libraries show that control
173 fractions differ from labeled fractions in the “heavy” range of the CsCl gradients (Figure 2). If each
174 control fraction is paired to the labeled fraction from the same incubation day for which it is closest in
175 density, there is a positive and statistically significant correlation between Bray-Curtis distances within
176 fraction pairs and density of the pair (see inset Figure 2). Therefore, the “heavy” end of the control
177 and labeled gradients differ and the OTUs enriched in the labeled fractions (relative to control) would
178 have incorporated ^{15}N into their DNA during the incubation timeframe. If the incubation timeframe is
179 appropriate, the ^{15}N -incorporators would most likely have incorporated the ^{15}N from atmospheric $^{15}\text{N}_2$.

4.3 BSC DIAZOTROPHS IDENTIFIED IN THE STUDY

180 BSC N-fixation has long been attributed to heterocystous *Cyanobacteria* and molecular microbial ecology
181 surveys of BSC *nifH* gene content have been consistent with this hypothesis finding cyanobacterial
182 *nifH* types to be numerically dominant in *nifH* gene libraries (Yeager et al., 2006, 2004, 2012). It is
183 possible, however, that PCR-driven molecular surveys of *nifH* gene content have been biased against
184 non-heterocystous *Cyanobacteria*. In general the *nifH* PCR primers used by Yeager et al. (2006, 2004,
185 2012) (19F and *nifH*3) for the first round of nested PCR have broad specificity and display at least 86% *in*
186 *silico* coverage for *Proteobacteria*, *Cyanobacteria* and “Cluster III” *nifH* reference sequences (Gaby and
187 Buckley, 2012). In the second round of the nested PCR protocol (Yeager et al., 2006, 2004, 2012), primer
188 *nifH*11 is ‘slightly biased against “Cluster III” (50% coverage) but biased in favor of *Proteobacteria* (79%
189 *in silico* coverage against 67% for *Cyanobacteria*) and *nifH*22 matches *Proteobacteria*, *Cyanobacteria*
190 and “Cluster III” reference sequences poorly (16%, 23% and 21% *in silico* coverage, respectively) (Gaby
191 and Buckley, 2012). Unfortunately, it is difficult to assess or quantify this bias (in either direction) without
192 knowing the *nifH* gene content *de novo*. Another potential bias in favor of *Cyanobacteria* in BSC *nifH*
193 gene libraries is heterocysts (the specialized N-fixing cells along the trichome of filamentous heterocystous
194 *Cyanobacteria* such as *Nostoc* and *Scytonema*) may be overrepresented with respect to non-cyanobacterial
195 diazotrophs because heterocysts make up a fraction cells along a trichome and even non-heterocyst cells
196 in a trichome will possess the *nifH* gene. Moreover, it should also be noted that *nifH* gene content is not
197 directly extrapolable to the taxonomic relative abundances of nitrogenase proteins.

198 We did not observe evidence for N-fixation by heterocystous *Cyanobacteria* in the “light” crust samples
199 used in this study. One possible explanation for our results is that the “light”, still developing BSC samples
200 used in this study possessed too few heterocystous *Cyanobacteria* to statistically evaluate their ^{15}N -
201 incorporation. Indeed, only 0.29% of sequences from this study’s DNA-SIP 16S rRNA gene sequence
202 libraries were from heterocystous *Cyanobacteria* (see results) as opposed to 15% and 23% of total

sequences in the Steven et al. (2013) and Garcia-Pichel et al. (2013) data, respectively. It is difficult to compare relative abundance values from CsCl gradient fractions against environmental libraries, but, a three order of magnitude difference between the environmental libraries and the CsCl gradient fractions is stark. Nonetheless, we would still expect even low abundance diazotrophs to show evidence for ^{15}N -incorporation, provided sequence counts were not too sparse in heavy fractions. The OTUs defined by selected heterocystous *Cyanobacteria* sequences presented in Yeager et al. (2006), however, all fall below the sparsity threshold used in our analysis (see methods, Figure 10). Given the sparsity of heterocystous *Cyanobacteria* sequences in the DNA-SIP data set, it is not possible to assess whether heterocystous *Cyanobacteria* incorporated ^{15}N during the incubation.

The OTUs that did appear to incorporate ^{15}N during the incubation were predominantly *Proteobacteria* and *Firmicutes*. The *Proteobacteria* OTUs for which ^{15}N -incorporation signal was strongest all shared high sequence identity ($\geq 98.48\%$ sequence identity) with 16S sequences from cultivars in genera with known diazotrophs (Table 2). The *Firmicutes* that displayed signal for ^{15}N -incorporation (predominantly *Clostridiaceae*) were not closely related to any cultivars (Table 2, Figure 5). These BSC *Clostridiaceae* diazotrophs represent a gap in culture collections. As culture-based ecophysiological studies have proven useful towards explaining ecological phenomena in BSC 16S rRNA gene sequence libraries (Garcia-Pichel et al., 2013), it would seem that these putative *Clostridiaceae* diazotrophs would be prime candidates for targeted culturing efforts. Assessing the physiological response of these diazotrophic *Clostridiaceae* to temperature would be useful for predicting how climate change will affect the BSC nitrogen budget.

Although too undersampled in the environmental data sets to reach statistical conclusions, non-cyanobacterial diazotrophs were found more often in below crust samples (as opposed to BSC samples) in the Steven et al. (2013) data and in "light" BSC samples in the Garcia-Pichel et al. (2013) data (Figure 6). This result generates some hypotheses that are counter to prior discussions regarding BSC diazotroph temporal dynamics (keeping in mind this phenomenon has not been evaluated statistically). Specifically, the transition of BSC from a light colored, developing crust to a dark, mature crust may not mark the emergence of diazotrophs in BSC but rather the transition of the diazotroph community from heterotroph dominance to cyanobacterial. Additionally, the soil beneath BSC may contribute significantly to the N budget in arid ecosystems.

It is unclear why BSC *nifH* gene surveys have overwhelmingly recovered heterocystous, cyanobacterial *nifH* genes, which would be in contrast to our results. Even poorly developed BSC samples have yielded predominantly cyanobacterial *nifH* genes (Yeager et al., 2004). And, "sub-biocrust" samples have yielded entirely heterocystous cyanobacterial *nifH* genes (Yeager et al., 2012). One explanation might be that the samples from this study are simply different in diazotrophic community structure than those surveyed in Yeager et al. (2006), Yeager et al. (2004) and Yeager et al. (2012). Indeed, it appears that the "light" crusts used here had a paucity of heterocystous *Cyanobacteria* from the beginning (see above). It should be noted that "light" and in particular "sub-biocrust" samples possess much less heterocystous *Cyanobacteria* in general (Figure 8) so the samples used in this study are not necessarily unrepresentative of typical poorly developed BSC simply because they are lacking heterocystous *Cyanobacteria*. Additionally, cyanobacterial *nifH* genes would be found in every heterocystous cyanobacterial cell, not just the heterocysts. Therefore, the relative abundance of heterocystous *Cyanobacteria nifH* in *nifH* gene libraries could easily overwhelm the numbers of *nifH* genes from non-cyanobacterial diazotrophs. Polyploidy could further exacerbate this bias, as many *Cyanobacteria* are estimated to have multiple genome copies per cell (Griese et al., 2011). In any case, the DNA-SIP discovered diazotrophs for the "light", poorly developed BSC used in the study were not cyanobacterial. It is unknown, however, if non-cyanobacterial diazotrophs would be identified by $^{15}\text{N}_2$ DNA-SIP using mature BSC samples. Regardless, our results suggest that BSC N-fixation may include a significant non-cyanobacterial component that requires further assessment across a more comprehensive sampling of BSC types.

4.4 SEQUENCING DEPTH

While it is somewhat alarming how few of the putative diazotrophs found in this study were also found by Garcia-Pichel et al. (2013) and Steven et al. (2013), it is important to point out that even next-generation sequencing efforts of BSC 16S rRNA genes have only shallowly sampled the full diversity of BSC microbes. Rarefaction curves of all samples from Steven et al. (2013) and Garcia-Pichel et al. (2013) are still sharply increasing especially for "below crust" samples (Figure 9). Parametric richness estimates of BSC diversity indicate the Steven et al. (2013) and Garcia-Pichel et al. (2013) sequencing efforts recovered on average 40.5% (sd. 9.99%) and 45.5% (sd. 11.6%) of existing 16S OTUs from samples (inset Figure 9), respectively. Further, the Steven et al. (2013) and Garcia-Pichel et al. (2013) sequence collections only share 57.6% of total OTUs found in at least one of the studies. In fact, this study shares more OTUs with Steven et al. (2013), 62.4% of OTUs in the combined data, than the Steven et al. (2013) study shares with Garcia-Pichel et al. (2013).

4.5 ANALYSIS OF NEXT-GENERATION-SEQUENCING DNA-SIP DATA

Although DNA-SIP is a powerful technique, analysis of DNA-SIP data is not without ambiguities. One limitation is the discrete, selected boundary in the form of a adjusted p-value threshold (or false discovery rate) that marks which OTUs we consider to be enriched in the heavy fractions of labeled CsCl gradients (and thus have likely incorporated ^{15}N into their DNA during the incubation). In reality the metric we use to quantify the magnitude of an OTU's response to a stable isotope is continuous, and there is only an artificial boundary between which OTUs appear to have "responded" and which OTUs have unknown response. For this reason, we have presented all the OTUs that satisfy our "response" criteria but focused on the most strongly responding OTUs. As with any hypothesis-based statistical test, care should be taken when interpreting the significance of results where p-values are near the selected threshold for rejecting the null hypothesis.

4.6 CONCLUSION

It is unlikely, given their ubiquity and abundance, that heterocystous *Cyanobacteria* are not key contributors to the BSC N-budget. But, the putative diazotrophs elucidated in this study and in Steppe et al. (1996) in addition to the N-fixation rate data presented by (Johnson et al., 2005) suggest there may be significant non-cyanobacterial BSC diazotrophs specifically within the *Clostrideaceae* and *Proteobacteria*. It seems clear that heterocystous *Cyanobacteria* increase in abundance with BSC age (Yeager et al., 2004). It is less clear if this transition marks the emergence of diazotrophy versus a re-structuring of the BSC diazotroph community from one dominated by *Firmicutes* and *Proteobacteria* to one predominantly heterocystous *Cyanobacteria*. DNA-SIP is a valuable tool in the molecular microbial ecologist's toolbox for identifying members of microbial community functional guilds (Neufeld et al., 2007). PCR-based surveys of diagnostic marker genes and DNA-SIP are both used to connect microbial phylogenetic types to microbial activities, but they occupy a non-overlapping set of strengths and weaknesses. Combined these tools can powerfully reveal connections between ecosystem membership/structure and function. Here we supplement previous surveys of BSC *nifH* diversity, a diagnostic marker PCR-driven approach, with $^{15}\text{N}_2$ DNA-SIP, and, while we do not confirm previous results, we expand knowledge of BSC diazotroph diversity. Predicting BSC N-fixation with respect to climate change, altered precipitation regimes and physical disturbance requires a careful accounting of diazotrophs including non-cyanobacterial types.

5 MATERIALS AND METHODS

5.1 FIELD SITE AND SAMPLE DESCRIPTION

289 Samples were taken from Green Butte, Arizona as previously described (site CP3, Beraldi-Campesi et al.
290 (2009)). All samples were from light crusts as described by Johnson et al. (2005).

5.2 SOIL CRUST INCUBATION

291 Light crust samples (37.5 cm², average mass 35 g) were incubated in sealed chambers under controlled
292 atmosphere and in the light for 4 days. Crusts were dry prior to time zero and were wetted at initiation of
293 experiment. Treatments included control air (unenriched headspace) and enriched air (>98% atom ¹⁵N₂)
294 headspace. Samples were taken at 2 days and 4 days incubation. Acetylene reduction rates were measured
295 daily. DNA was extracted from 1 g of crust.

5.3 DNA EXTRACTION

296 DNA from each sample was extracted using a MoBio PowerSoil DNA Isolation Kit (following
297 manufacturers protocol, but substituting a 2 minute bead beating for the vortexing step), and then gel
298 purified. Extracts were quantified using PicoGreen nucleic acid quantification dyes (Molecular Probes).

5.4 DNA-SIP

299 Gradient density centrifugation of DNA was undertaken in 6 mL polyallomer centrifuge tubes in a
300 TLA-110 fixed angle rotor (both Beckman Coulter) in CsCl gradients with an average density of 1.725
301 g/mL. Average density for all prepared gradients was checked with an AR200 refractometer before runs.
302 Between 2.5-5 µg of DNA extract was added to the CsCl solution, and gradients were run under conditions
303 of 20C for 67 hours at 55,000 rpm (Lueders et al., 2004). Centrifuged gradients were fractionated from
304 bottom to top in 36 equal fractions of 100 µL, using a displacement technique similar to Manefield et
305 al. (2002). The density of each fraction was determined using a refractometer. DNA in each fraction was
306 desalted through four washes with 300 µL TE per fraction.

5.5 PCR, LIBRARY NORMALIZATION AND DNA SEQUENCING

307 Barcoded PCR of bacterial and archaeal 16S rRNA genes, in preparation for 454 Pyrosequencing, was
308 carried out using primer set 515F/806R (Walters et al., 2011). The primer 806R contained an 8 bp barcode
309 sequence, a "TC" linker, and a Roche 454 B sequencing adaptor, while the primer 515F contained the
310 Roche 454 A sequencing adapter. Each 25 µL reaction contained 1x PCR Gold Buffer (Roche), 2.5 mM
311 MgCl₂, 200 µM of each of the four dNTPs (Promega), 0.5 mg/mL BSA (New England Biolabs), 0.3 µM
312 of each primers, 1.25 U of Amplitaq Gold (Roche), and 8 µL of template. Template for each sample was
313 added at normalized amounts in an attempt to prevent chimera formation, and each sample was amplified
314 in triplicate. Thermal cycling occurred with an initial denaturation step of 5 minutes at 95C, followed
315 by 40 cycles of amplification (20s at 95C, 20s at 53C, 30s at 72C), and a final extension step of 5 min
316 at 72C. Triplicate amplicons were pooled and purified using Agencourt AMPure PCR purification beads,
317 following manufacturers protocol. Once cleaned, amplicons were quantified using PicoGreen nucleic acid
318 quantification dyes (Molecular Probes) and pooled together in equimolar amounts. Samples were sent to
319 the Environmental Genomics Core Facility at the University of South Carolina (now Selah Genomics) to
320 be run on a Roche FLX 454 pyrosequencing machine.

Table 1. Chosen 16S sequences for strains in Yeager et al. (2006) included as OTU centroids

| Accession of representative 16S rRNA sequence | Species Name |
|-----------------------------------------------|---------------------------------------|
| DQ531701.1 | <i>Scytonema hyalinum</i> DC-A |
| DQ531697.1 | <i>Scytonema hyalinum</i> FGP-7A |
| DQ531696.1 | <i>Spirirestis rafaelsensis</i> LQ-10 |
| DQ531703.1 | <i>Nostoc commune</i> MCT-1 |
| DQ531699.1 | <i>Nostoc commune</i> MFG-1 |
| DQ531700.1 | <i>Calothrix</i> MCC-3A |

5.6 DATA ANALYSIS

5.6.1 *Sequence quality control* Sequences were initially screened by maximum expected errors at a specific read length threshold (Edgar, 2013) which has been shown to be as effective as denoising reads with respect to removing pyrosequencing errors. Specifically, reads were first truncated to 230 nucleotides (nt) (all reads shorter than 230 nt were discarded) and any read that exceeded a maximum expected error threshold of 1.0 was removed. After truncation and max expected error trimming, 91% of original reads remained. The first 30 nt representing the forward primer and barcode on high quality, truncated reads were trimmed. Remaining reads were taxonomically annotated using the "UClust" taxonomic annotation framework in the QIIME software package (Caporaso et al., 2010; Edgar, 2010) with cluster seeds from Silva SSU rRNA database (Pruess et al., 2007) 97% sequence identity OTUs as reference (release 111Ref). Reads annotated as "Chloroplast", "Eukaryota", "Archaea", "Unassigned" or "mitochondria" were culled from the dataset. Finally, reads were aligned to the Silva reference alignment provided by the Mothur software package (Schloss et al., 2009) using the Mothur NAST aligner (DeSantis et al., 2006). All reads that did not appear to align to the expected amplicon region of the SSU rRNA gene were discarded. Quality control parameters removed 34716 of 258763 raw reads.

5.6.2 *Sequence clustering* Sequences were distributed into OTUs using the UParse methodology (Edgar, 2013). Specifically, cluster seeds were identified using USearch with a collection of non-redundant reads sorted by count as input. The sequence identity threshold for establishing a new OTU centroid was 97%. After initial cluster centroid selection, select 16S rRNA sequences trimmed to the same 16S position as the other centroids from Yeager et al. (2006) were added to the centroid collection. Specifically, Yeager et al. (2006) Colorado Plateau or Moab, Utah sequences were added which included the 16S sequences for *Calothrix* MCC-3A, *Nostoc commune* MCT-1, *Nostoc commune* MFG-1, *Scytonema hyalinum* DC-A, *Scytonema hyalinum* FGP-7A, *Spirirestis rafaelsensis* LQ-10. Centroid sequences that matched selected Yeager et al. (2006) sequences with greater than to 97% sequence identity were subsequently removed from the centroid collection. With USearch/UParse, potential chimeras are identified during OTU centroid selection and are not allowed to become cluster centroids effectively removing chimeras from the read pool. All quality controlled reads were then mapped to cluster centroids at an identity threshold of 97% again using USearch. 95.6% of quality controlled reads could be mapped to centroids. Unmapped reads do not count towards sample counts and are essentially removed from downstream analyses. The USearch software version for cluster generation was 7.0.1090.

5.6.3 *Merging data from this study, Garcia-Pichel et al. (2013), and Steven et al. (2013)* As only sequences without corresponding quality scores were publicly available from Garcia-Pichel et al. (2013) and Steven et al. (2013), these data sets were only quality screened by determining if they covered the expected region of the 16S gene (described above). All data (this study, Garcia-Pichel et al. (2013) and Steven et al. (2013)) were included as input to USearch for OTU centroid selection and subsequent mapping to OTU centroids.

5.6.4 *Phylogenetic tree* The alignment for the "*Clostridiaceae*" phylogeny was created using SSU-Align which is based on Infernal (Nawrocki and Eddy, 2013; Nawrocki et al., 2009). Columns in the alignment that were not included in the SSU-Align covariance models or were aligned with poor confidence (less than 95% of characters in a position had posterior probability alignment scores of at least 95%) were masked for phylogenetic reconstruction. Additionally, the alignment was trimmed to coordinates such that all sequences in the alignment began and ended at the same positions. The "*Clostridiaceae*" tree included all top BLAST hits (parameters below) for ^{15}N *Clostridiaceae* responders in the Living Tree Project database (Yarza et al., 2008) in addition to BLAST hits within a sequence identity threshold of 97% to ^{15}N responders from the Silva SSURef_NR SSU rRNA database (Pruesse et al., 2007). Only one SSURef_NR115 hit per study per OTU ("study" was determined by "title" field) was selected for the tree. FastTree (Price et al., 2010) was used to build the tree and support values are SH-like scores reported by FastTree.

Placement of short sequences into backbone phylogeny Short sequences were mapped to the reference backbone using pplacer (Matsen et al., 2010) (default parameters). pplacer finds the edge placements that maximize phylogenetic likelihood. Prior to being mapped to the reference tree, short sequences were aligned to the reference alignment using Infernal (Nawrocki et al., 2009) against the same SSU-Align covariance model used to align reference sequences.

5.6.5 *BLAST searches* BLAST searches were done with the "blastn" program from BLAST+ toolkit (Camacho et al., 2009) version 2.2.29+. Default parameters were always employed and the BioPython (Cock et al., 2009) BLAST+ wrapper was used to invoke the blastn program. Pandas (McKinney, 2012) and dplyr (Wickham and Francois, 2014) were used to parse and munge BLAST output tables.

5.6.6 *Identifying OTUs that incorporated ^{15}N into their DNA* SIP is a culture-independent approach towards defining identity-function connections in microbial communities (Buckley, 2011; Neufeld et al., 2007). Microbes incubated in the presence of ^{13}C or ^{15}N labeled substrates can incorporate the stable heavy isotope into biomass if they participate in the substrate's transformation. Stable isotope labeled nucleic acids can then be separated from unlabeled by buoyant density in a CsCl gradient. As the buoyant density of a macromolecule is dependent on many factors in addition to stable isotope incorporation (e.g. GC-content in nucleic acids (Youngblut and Buckley, 2014)), labeled nucleic acids from one microbial population may have the same buoyant density of unlabeled nucleic acids from another (i.e. each population's nucleic acids would be found at the same point along a density gradient although only one population's nucleic acids are labeled). Therefore it is imperative to compare density gradients with nucleic acids from heavy stable isotope incubations to gradients from "control" incubations where everything mimics the experimental conditions except that unlabeled substrates are used (and all DNA would be unlabeled). By contrasting "heavy" density gradient fractions in experimental density gradients (hereafter referred to as "labeled" gradients) against heavy fractions in control gradients, the identities of microbes with labeled nucleic acids can be determined

We used an RNA-Seq differential expression statistical framework (Love et al., 2014) to find OTUs enriched in heavy fractions of labeled gradients relative to corresponding density fractions in control gradients (for review of RNA-Seq differential expression statistics applied to microbiome OTU count data see McMurdie and Holmes (2014)). We use the term differential abundance (coined by McMurdie and Holmes (2014)) to denote OTUs that have different proportion means across sample classes (in this case the only sample class is labeled/control). CsCl gradient fractions were categorized as "heavy" or "light". The heavy category denotes fractions with density values above 1.725 g/mL. Since we are only interested in enriched OTUs (labeled versus control), we used a one-sided z-test for differential abundance (the null hypothesis is the labeled:control proportion mean ratio for an OTU is less than a selected threshold). P-values were corrected with the Benjamini and Hochberg method (Benjamini and Hochberg, 1995). We selected a \log_2 fold change null threshold of 0.25 (or a labeled:control proportion mean ratio of 1.19). DESeq2 was used to calculate the moderated \log_2 fold change of labeled:control proportion mean ratios

and corresponding standard errors. Mean ratio moderation allows for reliable ratio ranking such that high variance and likely statistically insignificant mean ratios are appropriately shrunk and subsequently ranked lower than they would be as raw ratios. To summarize, OTUs with high moderated labeled:control proportion mean ratios have higher proportion means in heavy fractions of labeled gradients relative to heavy fractions of control gradients, and therefore have likely incorporated ^{15}N into their DNA during the incubation.

5.6.7 Ordination Principal coordinate ordinations depict the relationship between samples at each time point (day 2 and 4). Bray-Curtis distances were used as the sample distance metric for ordination. The Phyloseq (McMurdie and Holmes, 2014) wrapper for Vegan (Oksanen et al., 2013) (both R packages) was used to compute sample values along principal coordinate axes. GGplot2 (Wickham, 2009) was used to display sample points along the first and second principal axes.

5.6.8 Differential abundance in environmental samples Significance of OTU proportion mean differences with mean annual temperature (for Garcia-Pichel et al. (2013) data) and sample type (“BSC” or “below crust” Steven et al. (2013) data) was determined using the DESeq2 framework (McMurdie and Holmes, 2014; Love et al., 2014). A sparsity threshold of 0.40 was set to screen out sparse OTUs. No p-value correction was done for differential abundance in environmental samples as only six OTUs were considered for any test.

5.7 RICHNESS ANALYSES

Rarefaction curves were created using bioinformatics modules in the PyCogent Python package (Knight et al., 2007). Parametric richness estimates were made with CatchAll using only the best model for total OTU estimates (Bunge, 2010).

REFERENCES

- Marti J. Anderson. A new method for non-parametric multivariate analysis of variance. *Austral Ecology*, 26(1):32–46, Feb 2001. doi: 10.1111/j.1442-9993.2001.01070.pp.x. URL <http://dx.doi.org/10.1111/j.1442-9993.2001.01070.pp.x>.
- J. Belnap. Factors Influencing Nitrogen Fixation and Nitrogen Release in Biological Soil Crusts. In *Biological Soil Crusts: Structure Function, and Management*, pages 241–261. Springer Science + Business Media, 2001. doi: 10.1007/978-3-642-56475-8_19. URL http://dx.doi.org/10.1007/978-3-642-56475-8_19.
- J. Belnap. Factors Influencing Nitrogen Fixation and Nitrogen Release in Biological Soil Crusts. In Jayne Belnap and OttoL. Lange, editors, *Biological Soil Crusts: Structure, Function, and Management*, volume 150 of *Ecological Studies*, pages 241–261. Springer Berlin Heidelberg, 2003. ISBN 978-3-540-43757-4. doi: 10.1007/978-3-642-56475-8_19. URL http://dx.doi.org/10.1007/978-3-642-56475-8_19.
- J. Belnap, R. Prasse, and K.T. Harper. Influence of Biological Soil Crusts on Soil Environments and Vascular Plants. In Jayne Belnap and OttoL. Lange, editors, *Biological Soil Crusts: Structure, Function, and Management*, volume 150 of *Ecological Studies*, pages 281–300. Springer Berlin Heidelberg, 2003. ISBN 978-3-540-43757-4. doi: 10.1007/978-3-642-56475-8_21. URL http://dx.doi.org/10.1007/978-3-642-56475-8_21.
- Jayne Belnap. Nitrogen fixation in biological soil crusts from southeast Utah USA. *Biology and Fertility of Soils*, 35(2):128–135, Apr 2002. doi: 10.1007/s00374-002-0452-x. URL <http://dx.doi.org/10.1007/s00374-002-0452-x>.
- Jayne Belnap. Some Like It Hot, Some Not. *Science*, 340(6140):1533–1534, 2013. doi: 10.1126/science.1240318. URL <http://www.sciencemag.org/content/340/6140/1533.short>.

- 446 Yoav Benjamini and Yosef Hochberg. Controlling the False Discovery Rate: A Practical and Powerful
447 Approach to Multiple Testing. *Journal of the Royal Statistical Society. Series B (Methodological)*, 57
448 (1):289–300, 1995. ISSN 00359246. doi: 10.2307/2346101. URL [http://dx.doi.org/10.](http://dx.doi.org/10.2307/2346101)
449 [2307/2346101](http://dx.doi.org/10.2307/2346101).
- 450 H. Beraldi-Campesi, H. E. Hartnett, A. Anbar, G. W. Gordon, and F. Garcia-Pichel. Effect of biological
451 soil crusts on soil elemental concentrations: implications for biogeochemistry and as traceable
452 biosignatures of ancient life on land. *Geobiology*, 7(3):348–359, jun 2009. doi: 10.1111/j.1472-4669.
453 2009.00204.x. URL <http://dx.doi.org/10.1111/j.1472-4669.2009.00204.x>.
- 454 J. Roger Bray and J. T. Curtis. An Ordination of the Upland Forest Communities of Southern Wisconsin.
455 *Ecological Monographs*, 27(4):325, Oct 1957. doi: 10.2307/1942268. URL [http://dx.doi.org/](http://dx.doi.org/10.2307/1942268)
456 [10.2307/1942268](http://dx.doi.org/10.2307/1942268).
- 457 Daniel H. Buckley. Stable Isotope Probing Techniques Using ¹⁵N. In *Stable Isotope Probing and*
458 *Related Technologies*, pages 129–147. American Society of Microbiology, jan 2011. doi: 10.1128/
459 9781555816896.ch7. URL <http://dx.doi.org/10.1128/9781555816896.ch7>.
- 460 John Bunge. Estimating the Number of Species with Catchall. In *Biocomputing 2011*, pages 121–130.
461 WORLD SCIENTIFIC, nov 2010. doi: 10.1142/9789814335058_0014. URL [http://dx.doi.](http://dx.doi.org/10.1142/9789814335058_0014)
462 [org/10.1142/9789814335058_0014](http://dx.doi.org/10.1142/9789814335058_0014).
- 463 C Camacho, G Coulouris, V Avagyan, N Ma, J Papadopoulos, K Bealer, and TL Madden. BLAST+:
464 architecture and applications. 10:421, Dec 2009.
- 465 JG Caporaso, J Kuczynski, J Stombaugh, K Bittinger, FD Bushman, EK Costello, N Fierer, AG Pea,
466 JK Goodrich, JJ Gordon, GA Huttley, ST Kelley, D Knights, JE Koenig, RE Ley, CA Lozupone,
467 D McDonald, BD Muegge, M Pirrung, J Reeder, JR Sevinsky, PJ Turnbaugh, WA Walters, J Widmann,
468 T Yatsunenko, J Zaneveld, and R Knight. QIIME allows analysis of high-throughput community
469 sequencing data. 7:335–6, 2010.
- 470 PJ Cock, T Antao, JT Chang, BA Chapman, CJ Cox, A Dalke, I Friedberg, T Hamelryck, F Kauff,
471 B Wilczynski, and Hoon MJ de. Biopython: freely available Python tools for computational molecular
472 biology and bioinformatics. 25:1422–3, 2009.
- 473 TZ Jr DeSantis, P Hugenholtz, K Keller, EL Brodie, N Larsen, YM Piceno, R Phan, and GL Andersen.
474 NAST: a multiple sequence alignment server for comparative analysis of 16S rRNA genes. 34:W394–9,
475 2006.
- 476 RC Edgar. Search and clustering orders of magnitude faster than BLAST. 26:2460–1, 2010.
- 477 RC Edgar. UPARSE: highly accurate OTU sequences from microbial amplicon reads. 10:996–8, 2013.
- 478 R. D. Evans and J. Belnap. Long-Term Consequences of Disturbance on Nitrogen Dynamics in an Arid
479 Ecosystem. *Ecology*, 80(1):150–160, Jan 1999. doi: 10.1890/0012-9658(1999)080[0150:ltcodo]2.
480 0.co;2. URL [http://dx.doi.org/10.1890/0012-9658\(1999\)080\[0150:LTCODO\]2.](http://dx.doi.org/10.1890/0012-9658(1999)080[0150:LTCODO]2.0.CO;2)
481 [0.CO;2](http://dx.doi.org/10.1890/0012-9658(1999)080[0150:LTCODO]2.0.CO;2).
- 482 R. D. Evans and O. L. Lange. Biological Soil Crusts and Ecosystem Nitrogen and Carbon Dynamics.
483 In *Biological Soil Crusts: Structure Function, and Management*, pages 263–279. Springer Science +
484 Business Media, 2001. doi: 10.1007/978-3-642-56475-8_20. URL [http://dx.doi.org/10.](http://dx.doi.org/10.1007/978-3-642-56475-8_20)
485 [1007/978-3-642-56475-8_20](http://dx.doi.org/10.1007/978-3-642-56475-8_20).
- 486 John Christian Gaby and Daniel H. Buckley. A Comprehensive Evaluation of {PCR} Primers to Amplify
487 the {nifH} Gene of Nitrogenase. {PLOS} {ONE}, 7(7):e42149, jul 2012. doi: 10.1371/journal.pone.
488 0042149. URL <http://dx.doi.org/10.1371/journal.pone.0042149>.
- 489 F. Garcia-Pichel, S. L. Johnson, D. Youngkin, and J. Belnap. Small-Scale Vertical Distribution of Bacterial
490 Biomass and Diversity in Biological Soil Crusts from Arid Lands in the Colorado Plateau. *Microbial*
491 *Ecology*, 46(3):312–321, Nov 2003a. doi: 10.1007/s00248-003-1004-0. URL [http://dx.doi.](http://dx.doi.org/10.1007/s00248-003-1004-0)
492 [org/10.1007/s00248-003-1004-0](http://dx.doi.org/10.1007/s00248-003-1004-0).
- 493 F. Garcia-Pichel, V. Loza, Y. Marusenko, P. Mateo, and R. M. Potrafka. Temperature Drives the
494 Continental-Scale Distribution of Key Microbes in Topsoil Communities. *Science*, 340(6140):
495 1574–1577, Jun 2013. doi: 10.1126/science.1236404. URL [http://dx.doi.org/10.1126/](http://dx.doi.org/10.1126/science.1236404)
496 [science.1236404](http://dx.doi.org/10.1126/science.1236404).
- 497 Ferran Garcia-Pichel, Jayne Belnap, Susanne Neuer, and Ferdinand Schanz. Estimates of global
498 cyanobacterial biomass and its distribution. *Algological Studies*, 109(1):213–227, 2003b.

- 499 Marco Griesse, Christian Lange, and Jrg Soppa. Ploidy in cyanobacteria. *FEMS Microbiology Letters*, 323
500 (2):124–131, sep 2011. doi: 10.1111/j.1574-6968.2011.02368.x. URL <http://dx.doi.org/10.1111/j.1574-6968.2011.02368.x>.
- 502 SL Johnson, CR Budinoff, J Belnap, and F Garcia-Pichel. Relevance of ammonium oxidation within
503 biological soil crust communities. 7:1–12, 2005.
- 504 A. Karnieli, R.F. Kokaly, N.E. West, and R.N. Clark. Remote Sensing of Biological Soil Crusts. In
505 Jayne Belnap and Otto L. Lange, editors, *Biological Soil Crusts: Structure, Function, and Management*,
506 volume 150 of *Ecological Studies*, pages 431–455. Springer Berlin Heidelberg, 2003. ISBN 978-
507 3-540-43757-4. doi: 10.1007/978-3-642-56475-8_31. URL [http://dx.doi.org/10.1007/](http://dx.doi.org/10.1007/978-3-642-56475-8_31)
508 [978-3-642-56475-8_31](http://dx.doi.org/10.1007/978-3-642-56475-8_31).
- 509 Rob Knight, Peter Maxwell, Amanda Birmingham, Jason Carnes, J Gregory Caporaso, Brett C Easton,
510 Michael Eaton, Micah Hamady, Helen Lindsay, Zongzhi Liu, Catherine Lozupone, Daniel McDonald,
511 Michael Robeson, Raymond Sammut, Sandra Smit, Matthew J Wakefield, Jeremy Widmann, Shandy
512 Wikman, Stephanie Wilson, Hua Ying, and Gavin A Huttley. {PyCogent}: a toolkit for making sense
513 from sequence. *Genome Biol*, 8(8):R171, 2007. doi: 10.1186/gb-2007-8-8-r171. URL <http://dx.doi.org/10.1186/gb-2007-8-8-r171>.
- 515 M. I. Love, W. Huber, and S. Anders. Moderated estimation of fold change and dispersion for {RNA}-
516 Seq data with {DESeq}2. Technical report, feb 2014. URL [http://dx.doi.org/10.1101/](http://dx.doi.org/10.1101/002832)
517 [002832](http://dx.doi.org/10.1101/002832).
- 518 Frederick A Matsen, Robin B Kodner, and E Virginia Armbrust. pplacer: linear time maximum-likelihood
519 and Bayesian phylogenetic placement of sequences onto a fixed reference tree. *BMC Bioinformatics*,
520 11(1):538, 2010. doi: 10.1186/1471-2105-11-538. URL [http://dx.doi.org/10.1186/](http://dx.doi.org/10.1186/1471-2105-11-538)
521 [1471-2105-11-538](http://dx.doi.org/10.1186/1471-2105-11-538).
- 522 Wes McKinney. pandas: Python Data Analysis Library. Online, 2012. URL <http://pandas.pydata.org/>.
- 524 PJ McMurdie and S Holmes. Waste not, want not: why rarefying microbiome data is inadmissible. 10:
525 e1003531, 2014.
- 526 EP Nawrocki and SR Eddy. Infernal 1.1: 100-fold faster RNA homology searches. 29:2933–5, Nov 2013.
- 527 EP Nawrocki, DL Kolbe, and SR Eddy. Infernal 1.0: inference of RNA alignments. 25:1335–7, May
528 2009.
- 529 JD Neufeld, J Vohra, MG Dumont, T Lueders, M Manefield, MW Friedrich, and JC Murrell. DNA
530 stable-isotope probing. 2:860–6, 2007.
- 531 Jari Oksanen, F. Guillaume Blanchet, Roeland Kindt, Pierre Legendre, Peter R. Minchin, R. B. O’Hara,
532 Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, and Helene Wagner. *vegan: Community*
533 *Ecology Package*, 2013. URL <http://CRAN.R-project.org/package=vegan>. R package
534 version 2.0-10.
- 535 MN Price, PS Dehal, and AP Arkin. FastTree 2—approximately maximum-likelihood trees for large
536 alignments. 5:e9490, Mar 2010.
- 537 E Pruesse, C Quast, K Knittel, BM Fuchs, W Ludwig, J Peplies, and FO Glckner. SILVA: a comprehensive
538 online resource for quality checked and aligned ribosomal RNA sequence data compatible with ARB.
539 35:7188–96, 2007.
- 540 PD Schloss, SL Westcott, T Ryabin, JR Hall, M Hartmann, EB Hollister, RA Lesniewski, BB Oakley,
541 DH Parks, CJ Robinson, JW Sahl, B Stres, GG Thallinger, Horn DJ Van, and CF Weber. Introducing
542 mothur: open-source, platform-independent, community-supported software for describing
543 and comparing microbial communities. 75:7537–41, 2009.
- 544 T.F. Steppe, J.B. Olson, H.W. Paerl, R.W. Litaker, and J. Belnap. Consortial N₂ fixation: a strategy
545 for meeting nitrogen requirements of marine and terrestrial cyanobacterial mats. *FEMS Microbiology*
546 *Ecology*, 21(3):149–156, Nov 1996. doi: 10.1111/j.1574-6941.1996.tb00342.x. URL <http://dx.doi.org/10.1111/j.1574-6941.1996.tb00342.x>.
- 548 Blaire Steven, La Verne Gallegos-Graves, Jayne Belnap, and Cheryl R. Kuske. Dryland soil microbial
549 communities display spatial biogeographic patterns associated with soil depth and soil parent material.
550 *FEMS Microbiol Ecol*, 86(1):101–113, May 2013. doi: 10.1111/1574-6941.12143. URL <http://dx.doi.org/10.1111/1574-6941.12143>.

- 552 WA Walters, JG Caporaso, CL Lauber, D Berg-Lyons, N Fierer, and R Knight. PrimerProspector: de novo
 553 design and taxonomic analysis of barcoded polymerase chain reaction primers. 27:1159–61, Apr 2011.
- 554 Hadley Wickham. *ggplot2: elegant graphics for data analysis*. Springer New York, 2009. ISBN 978-0-
 555 387-98140-6. URL <http://had.co.nz/ggplot2/book>.
- 556 Hadley Wickham and Romain Francois. *dplyr: dplyr: a grammar of data manipulation*, 2014. URL
 557 <http://CRAN.R-project.org/package=dplyr>. R package version 0.2.
- 558 Pablo Yarza, Michael Richter, Jörg Peplies, Jean Euzéby, Rudolf Amann, Karl-Heinz Schleifer, Wolfgang
 559 Ludwig, Frank Oliver Glöckner, and Ramon Rosselló-Móra. The All-Species Living Tree project: A
 560 16S rRNA-based phylogenetic tree of all sequenced type strains. *Systematic and Applied Microbiology*,
 561 31(4):241–250, Sep 2008. doi: 10.1016/j.syapm.2008.07.001. URL [http://dx.doi.org/10.](http://dx.doi.org/10.1016/j.syapm.2008.07.001)
 562 [1016/j.syapm.2008.07.001](http://dx.doi.org/10.1016/j.syapm.2008.07.001).
- 563 Chris M. Yeager, Jennifer L. Kornosky, Rachael E. Morgan, Elizabeth C. Cain, Ferran Garcia-Pichel,
 564 David C. Housman, Jayne Belnap, and Cheryl R. Kuske. Three distinct clades of cultured heterocystous
 565 cyanobacteria constitute the dominant N₂-fixing members of biological soil crusts of the Colorado
 566 Plateau USA. *FEMS Microbiology Ecology*, 60(1):85–97, 2006. doi: 10.1111/j.1574-6941.2006.00265.
 567 x. URL <http://dx.doi.org/10.1111/j.1574-6941.2006.00265.x>.
- 568 Chris M. Yeager, Cheryl R. Kuske, Travis D. Carney, Shannon L. Johnson, Lawrence O. Ticknor, and
 569 Jayne Belnap. Response of Biological Soil Crust Diazotrophs to Season Altered Summer Precipitation,
 570 and Year-Round Increased Temperature in an Arid Grassland of the Colorado Plateau, USA. *Front.*
 571 *Microbio.*, 3, 2012. doi: 10.3389/fmicb.2012.00358. URL [http://dx.doi.org/10.3389/](http://dx.doi.org/10.3389/fmicb.2012.00358)
 572 [fmicb.2012.00358](http://dx.doi.org/10.3389/fmicb.2012.00358).
- 573 CM Yeager, JL Kornosky, DC Housman, EE Grote, J Belnap, and CR Kuske. Diazotrophic community
 574 structure and function in two successional stages of biological soil crusts from the Colorado Plateau
 575 and Chihuahuan Desert. 70:973–83, 2004.
- 576 ND Youngblut and DH Buckley. Intra-genomic variation in G+C content and its implications for DNA
 577 stable isotope probing (DNA-SIP). Aug 2014.

6 FIGURES AND LONG TABLES

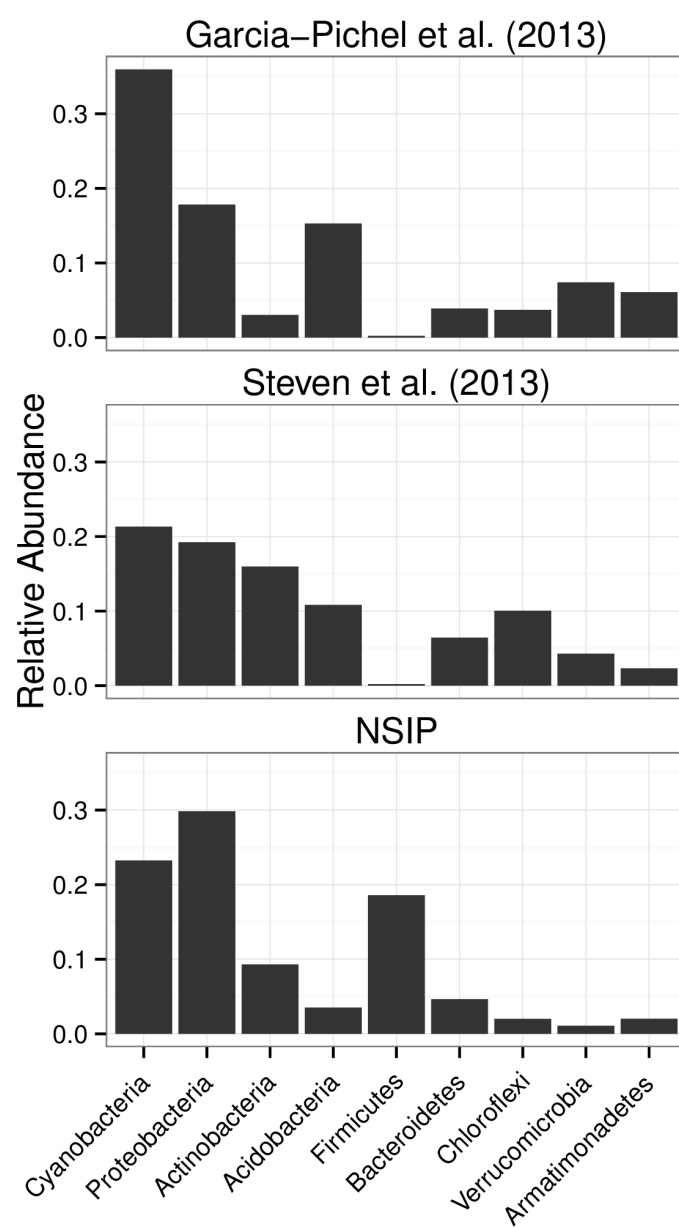


Figure 1. Distribution of sequences into top 9 phyla (phyla ranked by sum of all sequence annotations).

Table 2. ^{15}N responders BLAST against Living Tree Project

| OTU ID | Species Name | BLAST percent identity | accession |
|----------|------------------------------------------------------|------------------------|-----------|
| OTU.108 | <i>Caloramator proteoclasticus</i> | 96.94 | X90488 |
| OTU.14 | <i>Pantoea rwandensis</i> | 99.49 | JF295055 |
| | <i>Pantoea rodasii</i> | 99.49 | JF295053 |
| | <i>Kluyvera intermedia</i> | 99.49 | AF310217 |
| | <i>Kluyvera cryocrescens</i> | 99.49 | AF310218 |
| | <i>Klebsiella variicola</i> | 99.49 | AJ783916 |
| | <i>Klebsiella pneumoniae subsp. rhinoscleromatis</i> | 99.49 | Y17657 |
| | <i>Klebsiella pneumoniae subsp. pneumoniae</i> | 99.49 | X87276 |
| | <i>Erwinia aphidicola</i> | 99.49 | FN547376 |
| | <i>Enterobacter soli</i> | 99.49 | GU814270 |
| | <i>Enterobacter ludwigii</i> | 99.49 | AJ853891 |
| | <i>Enterobacter kobei</i> | 99.49 | AJ508301 |
| | <i>Enterobacter hormaechei</i> | 99.49 | AJ508302 |
| | <i>Enterobacter cloacae subsp. dissolvens</i> | 99.49 | Z96079 |
| | <i>Enterobacter cancerogenus</i> | 99.49 | Z96078 |
| | <i>Enterobacter asburiae</i> | 99.49 | AB004744 |
| | <i>Enterobacter amnigenus</i> | 99.49 | AB004749 |
| | <i>Enterobacter aerogenes</i> | 99.49 | AB004750 |
| | <i>Buttiauxella warmboldiae</i> | 99.49 | AJ233406 |
| | <i>Buttiauxella noackiae</i> | 99.49 | AJ233405 |
| | <i>Buttiauxella izardii</i> | 99.49 | AJ233404 |
| | <i>Buttiauxella agrestis</i> | 99.49 | AJ233400 |
| OTU.1673 | <i>Clostridium drakei</i> | 95.9 | Y18813 |
| | <i>Clostridium carboxidivorans</i> | 95.9 | FR733710 |
| OTU.327 | <i>Clostridium hydrogeniformans</i> | 94.92 | DQ196623 |
| | <i>Clostridium amylolyticum</i> | 94.92 | EU037903 |
| OTU.330 | <i>Clostridium lundense</i> | 96.94 | AY858804 |
| OTU.342 | <i>Acinetobacter johnsonii</i> | 100.0 | Z93440 |
| OTU.4037 | <i>Fonticella tunisiensis</i> | 93.85 | HE604099 |
| OTU.54 | <i>Shigella sonnei</i> | 100.0 | FR870445 |
| | <i>Shigella flexneri</i> | 100.0 | X96963 |
| | <i>Escherichia fergusonii</i> | 100.0 | AF530475 |
| | <i>Escherichia coli</i> | 100.0 | X80725 |
| OTU.57 | <i>Fonticella tunisiensis</i> | 93.88 | HE604099 |
| | <i>Caloramator proteoclasticus</i> | 93.88 | X90488 |
| OTU.586 | <i>Vitreoscilla filiformis</i> | 98.48 | HM037993 |
| | <i>Ottowia pentelensis</i> | 98.48 | EU518930 |
| | <i>Ideonella dechloratans</i> | 98.48 | X72724 |
| | <i>Diaphorobacter nitroreducens</i> | 98.48 | AB064317 |
| | <i>Comamonas terrigena</i> | 98.48 | AF078772 |

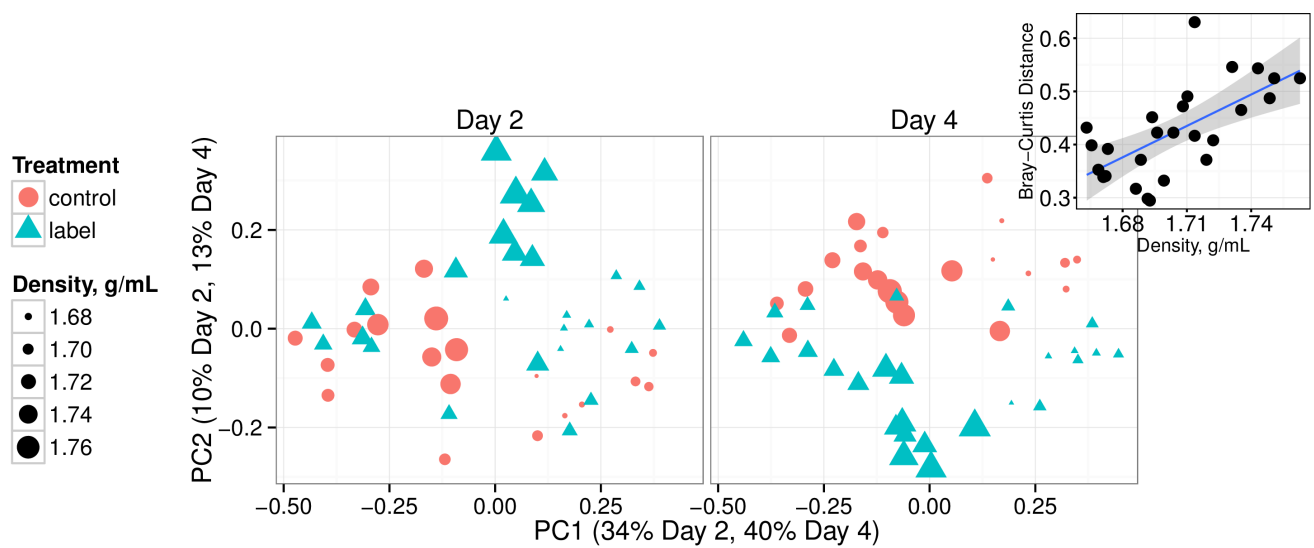


Figure 2. Ordination of Bray-Curtis sample pairwise distances for each incubation time. Point area is proportional to the density of the CsCl gradient fraction for each sequence library, and color/shape reflects control (red triangles) or labeled (blue circles) treatment. Inset shows Bray-Curtis distances for paired control versus labeled CsCl gradient fractions (i.e. fractions from the same incubation day and same density) against the density of the pair (p-value: $4.526e^{-5}$, r^2 : 0.434).

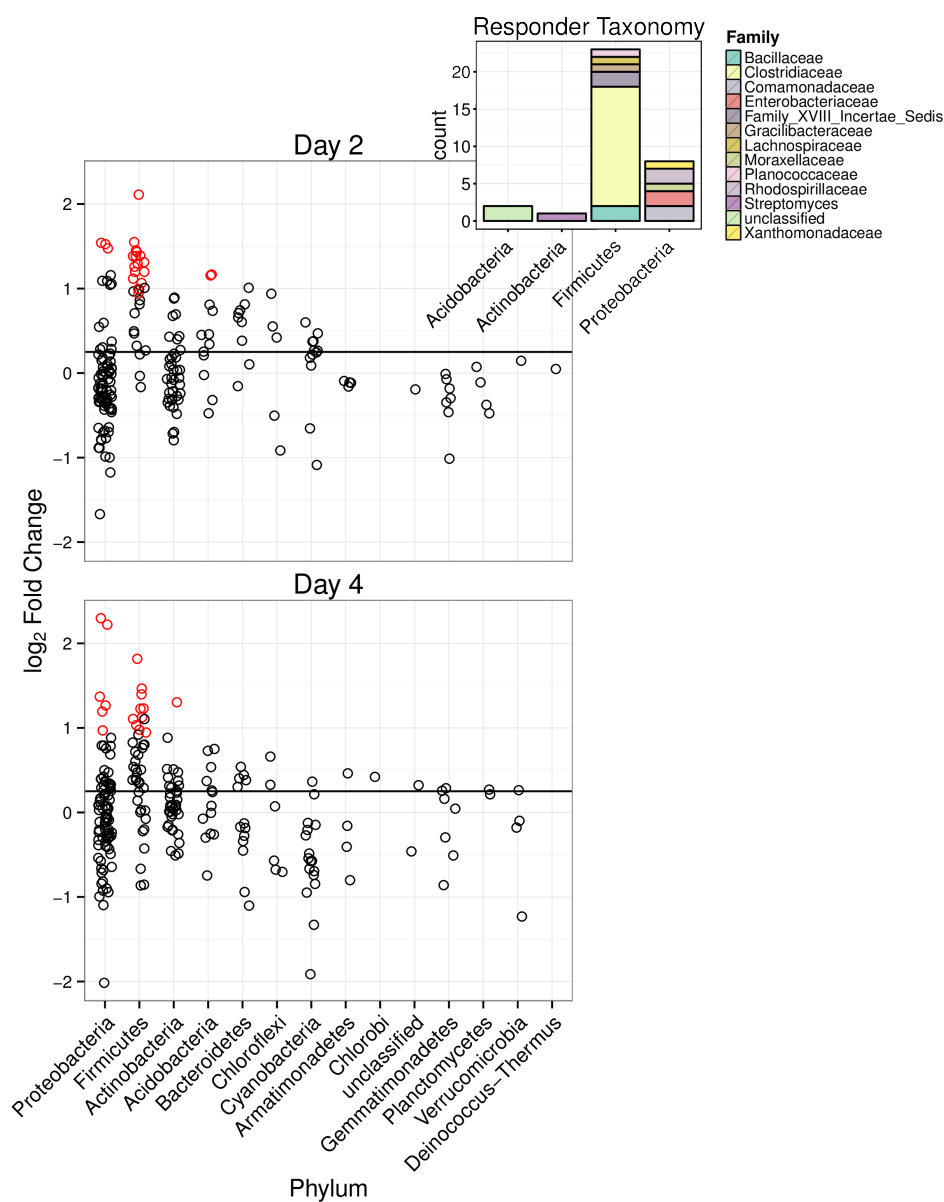


Figure 3. Moderated \log_2 of proportion mean ratios for labeled versus control gradients (heavy fractions only, densities ≥ 1.725 g/mL). All OTUs found in at least 62.5% of heavy fractions at a specific incubation day are shown. Red color denotes a proportion mean ratio that has a corresponding adjusted p-value below a false discovery rate of 10% (the null model is that the proportion mean is ratio is below 0.25). The horizontal line is the proportion mean threshold for the null model, 0.25. The inset figure summarizes the taxonomy of OTUs that with proportion mean ratio p-values under 0.10 for at least one time point.

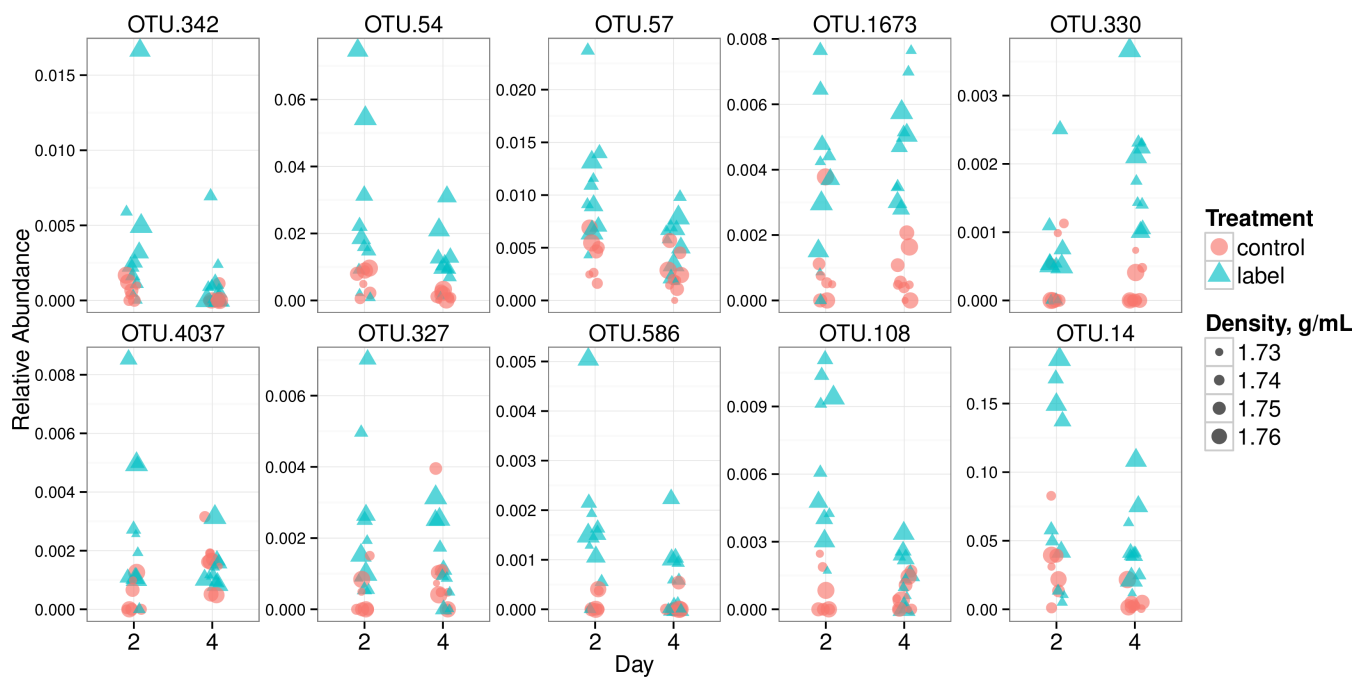


Figure 4. Relative abundance values in heavy fractions (density greater or equal to 1.725 g/mL) for the top 10 ^{15}N "responders" (putative diazotrophs, see results for selection criteria of top 10) at each incubation day. See Table 2 for BLAST results of top 10 responders against the LTP database (release 115). Point area is proportional to CsCl gradient fraction density, and color signifies control (red) or labeled (blue) treatment.



Figure 5. See methods for selection criteria for sequences in backbone tree. Edge width is proportional to number of short putative *Clostridiaceae* diazotroph sequences placed at that position. Placement of short sequences can be spread across multiple edges Matsen et al. (2010). Reference sequences from cultivars have boxes at tips and full species names. Tips with only accession annotations are from environmental reference sequences.

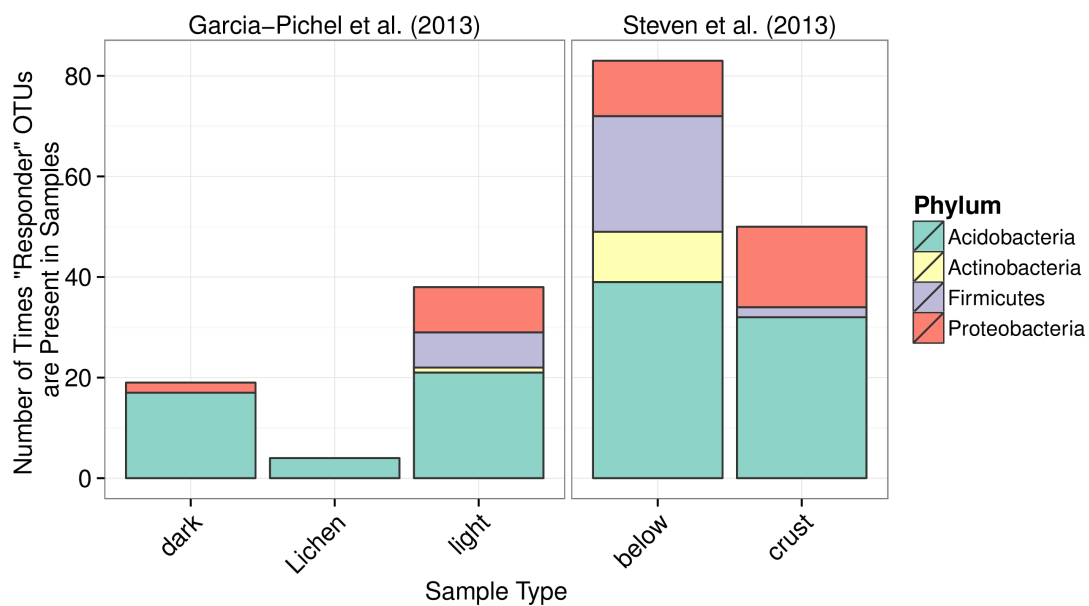


Figure 6. Counts of "responder" OTU occurrences in samples from Steven et al. (2013) and Garcia-Pichel et al. (2013). Steven et al. (2013) collected BSC samples (25 samples total) and samples from soil beneath BSC (17 samples total, "below" column in figure). Garcia-Pichel et al. (2013) collected samples from "dark" (9 samples total) and "light" (12 samples total) crusts in addition to "lichen" (2 samples total) dominated crusts.

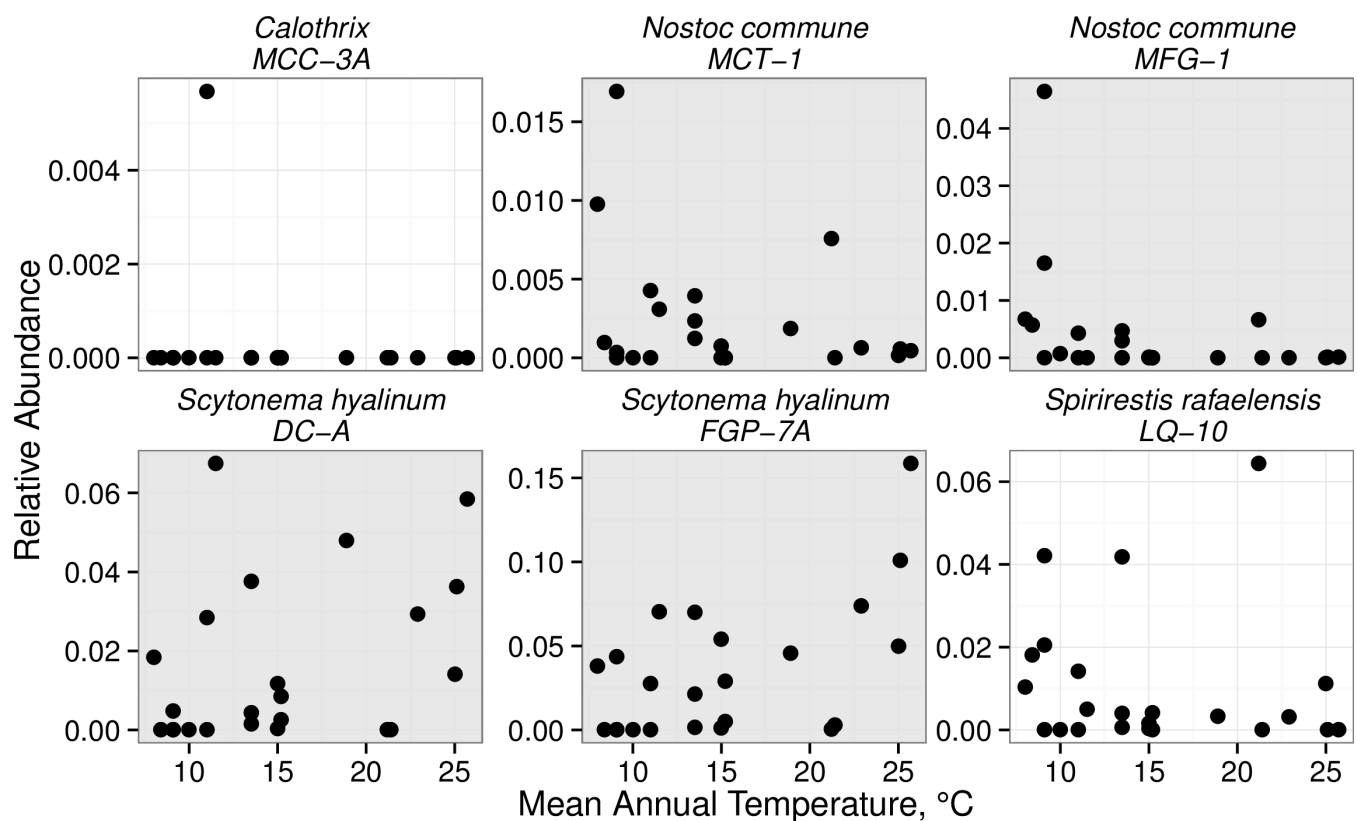


Figure 7. Relative abundance of selected heterocystous cyanobacterial OTUs with centroids from sequences described in Yeager et al. (2006) (see methods for selection criteria) in Steven et al. (2013) data set.

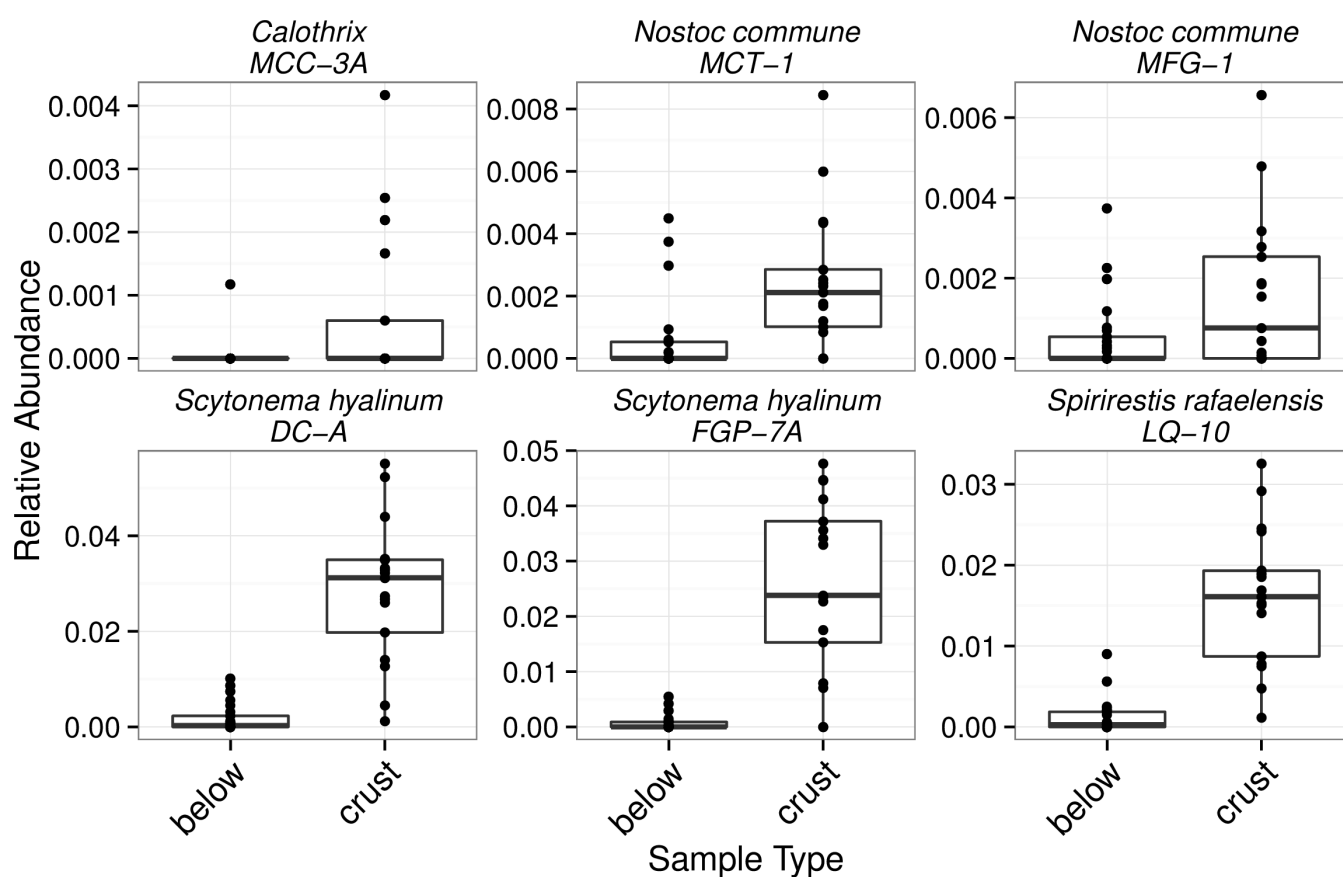


Figure 8. Relative abundance of selected heterocystous cyanobacterial OTUs with centroids from sequences described in Yeager et al. (2006) (see methods for selection criteria) in Steven et al. (2013) data set.

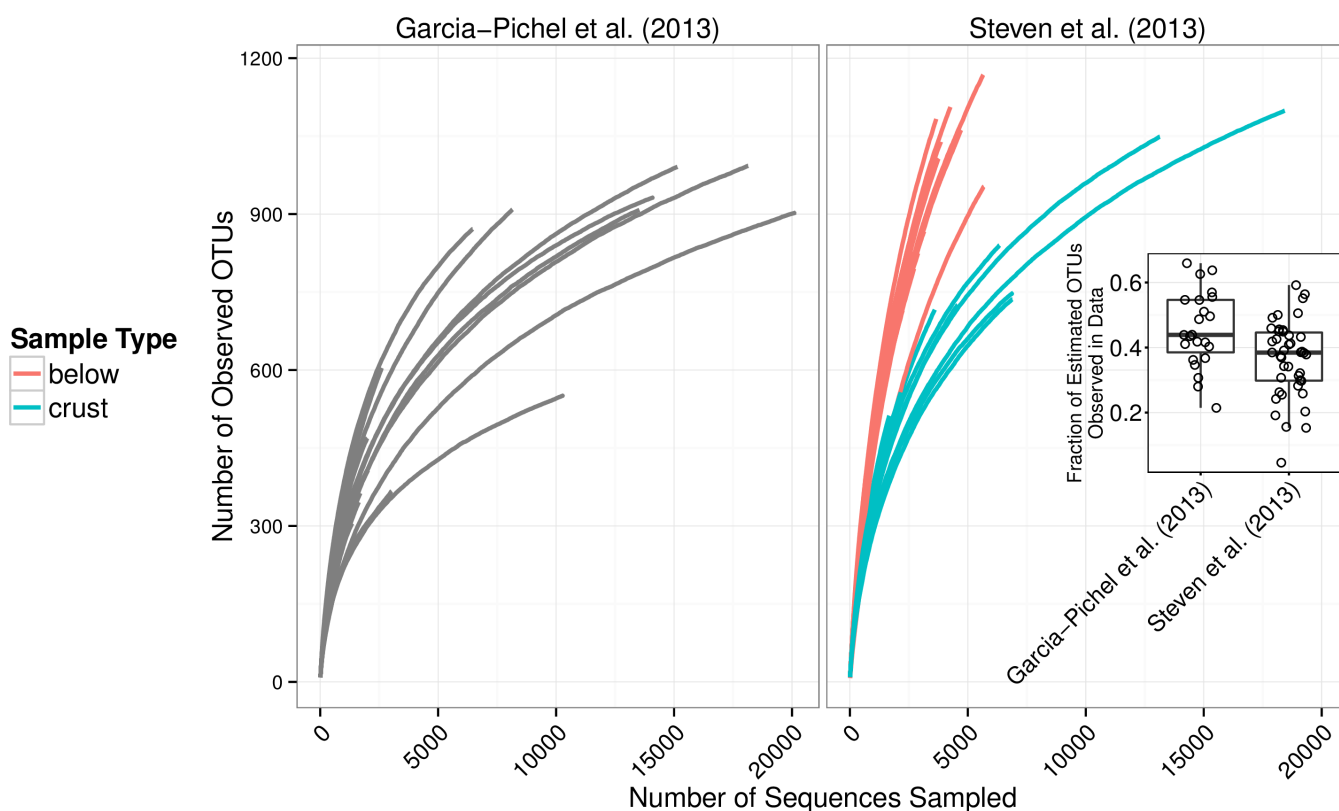


Figure 9. Rarefaction curves for all samples presented by Garcia-Pichel et al. (2013) and Steven et al. (2013). Inset is boxplot of estimated sampling effort for all samples in Garcia-Pichel et al. (2013) and Steven et al. (2013) (number of observed OTUs divided by number of CatchAll Bunge (2010) estimated total OTUs)

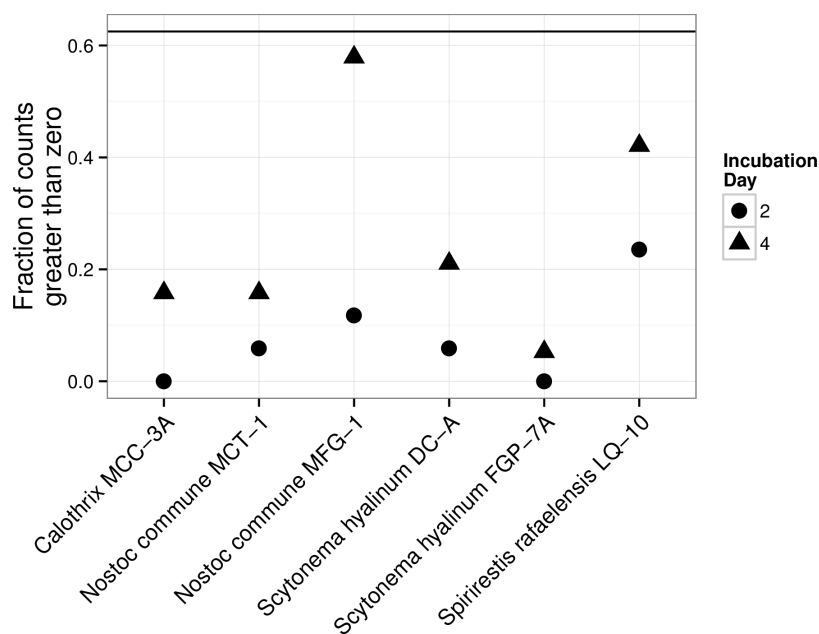


Figure 10. Relative abundance of selected heterocystous cyanobacterial OTUs with centroids from sequences described in Yeager et al. (2006) (see methods for selection criteria) in Steven et al. (2013) data set. Horizontal line is the sparsity threshold for independent OTU filtering prior to adjusting p-values when identifying OTUS enriched in labeled gradients (heavy fractions).