Supplementary Information

Table S2.1: Kruskal-Wallis multiple comparison using the post-hoc Dunn method (1964) for differences in nucleotide diversity between different cyanobacteria morphologies. P values adjusted with the Holm method [(Holm, 1979)](https://www.zotero.org/google-docs/?l1gP60). Anova with non-normal distribution assumption - Kruskal-Wallis chi-squared = 902.06, df = 3, p-value < 2.2e-16

|  |  |  |  |
| --- | --- | --- | --- |
| Comparison | Z | p\_unadjusted | p\_adjusted |
| Colonial - Filamentous | 29.64 | 4.45e-193 | 2.67e-192 |
| Filamentous - Solitary | -16.36 | 3.68e-60 | 1.47e-59 |
| Stalked - Colonial | -3.27 | 1.07e-03 | 1.07e-03 |
| Stalked - Solitary | 4.72 | 2.41e-06 | 4.82e-06 |
| Colonial - Solitary | 19.26 | 1.06e-82 | 5.28e-82 |
| Stalked - Filamentous | 10.58 | 3.60e-26 | 1.08e-25 |

Table S2.2: Interannual nucleotide diversity (π) linear regression output for the cyano-mOTUs that passed the minimum presence threshold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| mOTU | t | p | Slope | Sig | trend | Lm trend | Clade |
| PSEUDA\_13 | 2.06 | 0.069 | 1.7E-05 | fail | pos | No-sig change | Pseudanabaena |
| PSEUDA\_70 | -1.27 | 0.29 | -9.6E-04 | fail | neg | No-sig change | Pseudanabaena |
| NODOS\_105 | 1.78 | 0.12 | 1.8E-04 | fail | pos | No-sig change | Nodosilinea |
| APHAN\_134 | -0.54 | 0.59 | -1.6E-05 | fail | neg | No-sig change | Filamentous-1 |
| CYANO\_106 | -3.87 | 0.061 | -2E-04 | fail | neg | No-sig change | Filamentous-1 |
| DOLIS\_187 | -0.031 | 0.98 | -4.1E-06 | fail | neg | No-sig change | Filamentous-1 |
| CYANO\_45 | 1.46 | 0.19 | 3.1E-05 | fail | pos | No-sig change | Filamentous-1 |
| MCYST\_2 | 1.44 | 0.17 | 1.3E-04 | fail | pos | No-sig change | Microcystis |
| MCYST\_31 | 1.94 | 0.071 | 2.1E-04 | fail | pos | No-sig change | Microcystis |
| MCYST\_62 | 0.98 | 0.34 | 1.1E-04 | fail | pos | No-sig change | Microcystis |
| MCYST\_56 | 0.24 | 0.81 | 2.3E-05 | fail | pos | No-sig change | Snowella |
| CYBIM\_101 | -1.26 | 0.24 | -3.2E-04 | fail | neg | No-sig change | Cyanobium |
| CYBIM\_104 | -0.07 | 0.95 | -1.3E-05 | fail | neg | No-sig change | Cyanobium |
| CYBIM\_157 | -4.58 | 0.0059 | -6.6E-04 | pass | neg | Negative, Sig | Cyanobium |
| CYBIM\_190 | 0.88 | 0.41 | 2.1E-04 | fail | pos | No-sig change | Cyanobium |
| CYBIM\_63 | -2.35 | 0.043 | -5.5E-04 | pass | neg | Negative, Sig | Cyanobium |
| CYBIM\_73\_1 | -1.02 | 0.35 | -2.4E-04 | fail | neg | No-sig change | Cyanobium |
| CYBIM\_89 | -0.78 | 0.49 | -3.9E-04 | fail | neg | No-sig change | Cyanobium |
| CYBIM\_90 | -0.42 | 0.68 | -4.6E-05 | fail | neg | No-sig change | Cyanobium |
| CYBIM\_119 | -2.87 | 0.011 | -1.1E-04 | pass | neg | Negative, Sig | Solitary-1 |
| CYBIM\_119\_1 | 2.70 | 0.035 | 8E-05 | pass | pos | Positive, Sig | Solitary-1 |
| CYBIM\_200 | 3.63 | 0.17 | 0.0027 | fail | pos | No-sig change | Solitary-1 |
| CYBIM\_31 | -0.74 | 0.54 | -5.4E-04 | fail | neg | No-sig change | Solitary-1 |
| CYBIM\_73 | -0.56 | 0.58 | -3.8E-05 | fail | neg | No-sig change | Solitary-1 |
| VULCA\_20 | 0.71 | 0.49 | 1.9E-05 | fail | pos | No-sig change | Vulcanococcus |
| VULCA\_28 | 2.71 | 0.016 | 3.5E-05 | pass | pos | Positive, Sig | Vulcanococcus |
| VULCA\_96 | -2.45 | 0.05 | -3.3E-04 | pass | neg | Negative, Sig | Vulcanococcus |

A graph of different colored lines

AI-generated content may be incorrect.

Figure S2.1: Individual time series of nucleotide diversity (π) across TYMEFLIES metagenomes. The 27 cyano-mOTUs shown were detected in a minimum of 20 metagenomes with at least 10x mean read depth and 80% breadth (percent of its genome with 10x coverage). Plots are titled by the mOTUs abbreviated name and taxon information is available in Table 2.1. Individual plots are colored by their respective defined clades (light green - *Pseudanabaena*, green - *Nodosilinea*, dark green - Filamentous-1,  pink - *Snowella*, orange - *Microcystis*, light blue - *Cyanobium*,  blue - Solitary-1, purple - *Vulcanococcus*). 

A graph of different colored lines

AI-generated content may be incorrect.

Figure S2.2: Subpopulation structure, represented as different haplotypes, calculated by the bioinformatic pipeline STRONG [(Quince et al., 2021)](https://www.zotero.org/google-docs/?em5Ps2) for the (C) MCYST\_2 (*Microcystis panniformis*) and (D) APHAN\_134 (*Aphanizomenon flos-aquae*) defined populations. A single metagenome-mOTU pair from each year with the highest recorded mean coverage was selected for this analysis. Normalized coverage with point size controlled by the mean nucleotide diversity (π) for each metagenome selected for (A) MCYST\_2 and (B) APHAN\_134.

A screenshot of a graph

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Figure S2.3: Linkage disequilibrium metrics, D’ and r2, between SNP pairs that are 5 - 250 bps apart for the 18 cyano-mOTUs that had high quality paired read data for at least 20 metagenome samples. Both normalized (subsampled SNP pairs to 20x read depth) and raw D’ and r2 are shown. Point size is controlled by the total number of SNP pairs that went into the mean metric at the respective distance.