

Salinity Tolerance in Cyanobacteria: evaluating assumptions in ancestral state reconstructions

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Introduction: The irreversible oxygenation of Earth's atmosphere occurred at the Great Oxidation Event (GOE) approximately 2.3 billion years ago. However geochemical evidence for localized oxic conditions exists in the geologic record dating back to 3.0 billion years ago. Cyanobacteria are believed to have been the driving force behind the oxygenation of Earth's atmosphere, and there are two basic hypotheses about how they effected this major geobiological transition.

One hypothesis posits that upon the evolution of oxygenic photosynthesis in ancestral cyanobacteria, cyanobacterial productivity dominated the global ecosystem and drove a geologically instantaneous increase in atmospheric oxygen at the GOE (Shih et. al. 2017). As a counterpart to this 'origination' hypothesis, a second, 'ecological' hypothesis posits that ancestral cyanobacteria were physiologically restrained to freshwater benthic habitats until they evolved the ability to thrive in marine environments, thereby reconciling early evidence for localized oxidation with the delayed oxygenation of Earth's atmosphere (Lalonde et. al. 2015, Sánchez-Baracaldo et. al. 2017).

One key aspect of the 'ecological' hypothesis is that reconstructions of the ancestral habitats of early cyanobacteria imply a strong intolerance to seawater salinity levels (≈ 35 ppt; Sánchez-Baracaldo et. al. 2017). These ancestral reconstructions of salinity tolerance in Cyanobacteria have been based on the habitats of isolation of modern cyanobacteria and a consideration of salinity tolerance as a binary discrete cyanobacterial trait (Sánchez-Baracaldo et. al. 2017).

Ancestral state reconstructions of this kind rely on three assumptions. The first, and least controversial, is that the trait characters and distributions in the extant Cyanobacteria are derived from ancestral characters and distributions. Next, they assume that the distribution of physiological responses in modern Cyanobacteria reflects the potential limits of adaptive responses in ancestral cyanobacteria. And finally, they assume that cyanobacterial traits, once evolved, remain constant over geologic time (Knoll 2004).

Here we provide a meta-analysis of literature data on cyanobacterial salinity tolerance, supplemented by experimental data on key cyanobacterial strains, to evaluate whether salinity tolerance in Cyanobacteria can be accurately modeled as a discrete binary trait.

Results: Our analysis indicates that salinity tolerance cannot be broken down into two discrete categories: freshwater and marine (Figure 1). Additionally, while habitat of isolation sometimes corresponds to the ultimate expression of salinity tolerance (especially for strains isolated from freshwater environments), more often than not, it is a poor predictor of whether a given cyanobacterial strain can survive over a range of salinities. Our experimental data support these results, and in addition show that some cyanobacterial strains retain a phenotypic plasticity that enables them to acclimate to significant changes in salinity, from freshwater to marine and vice versa, on the timescale of weeks.

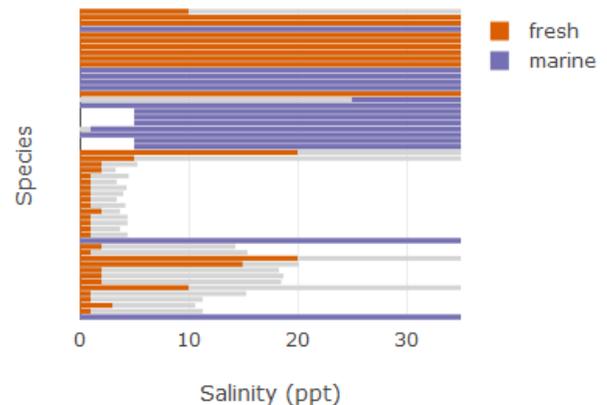


Figure 1: Discrete growth of cyanobacteria across a range of salinities compiled from the literature. Tested ranges are indicated in grey.

Implications: Salinity tolerance is a continuous cyanobacterial trait and should not be treated as a binary discrete one. Recently developed phylogenetic methods allow for a quantitative consideration of the evolution of continuous traits, which when combined with the results reported here, may enable an improved understanding of the original habitats of ancestral cyanobacteria.

References:

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