

NICHE DIFFERENTIATION AMONG CYANOBACTERIAL POPULATIONS REVEALED VIA ECO-TRANSCRIPTOMIC SURVEYS OF LAKE ERIE

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While toxic cyanobacterial blooms in Lake Erie threaten drinking water supplies and are promoted by nutrient loading, the precise nutrient regime that selects specific cyanobacteria populations is poorly understood. Here, we assess shifts in cyanobacterial abundances and global gene expression patterns in response to natural and manipulated gradients in nitrogen (N) and phosphorus (P) in western Lake Erie to identify gene pathways that facilitate dominance by different genera. Gradients in orthophosphate concentrations played a key role in shaping cyanobacteria communities and had the largest effect on transcriptomic responses. Under high P conditions, *Anabaena* and *Planktothrix* were the dominant cyanobacterial populations and P promoted *nifH* expression in *Anabaena*. While additions of P elicited the upregulation of genes involved in phage infection defense, genomic rearrangement, and nitrogen acquisition in *Microcystis*, these conditions also led to lower *Microcystis* abundances. In the presence of low levels of P, however, *Microcystis* became the dominate cyanobacteria as it upregulated genes associated with P scavenging (*pstSCAB*, *phoX*) and storage (*ppk1*). Nitrogen did not alter *Microcystis* abundances but did increase the expression of protease inhibitors (*aer*, *mcn* gene sets) that may deter zooplankton grazing as well as microcystin synthetase genes (*mcy*) with urea enrichment yielding significant increases in microcystin concentrations. The expression of genes that facilitate the adaptation of *Anabaena* and *Planktothrix* to high P regions and *Microcystis* low P zones suggest that management schemes that reduce the delivery of P to western Lake Erie may alter the composition, but not the persistence of cyanobacterial blooms.