

Global analysis of growth phase-associated transcriptomes in the toxic dinoflagellate, *Karenia brevis*

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Molecular mechanisms regulating senescence and cell death in phytoplankton have received increased attention within the last decade due to their prospective roles in population structuring, species succession, biodiversity/selection, bloom termination, and biogeochemical cycling (Bidle and Falkowski, 2004; Franklin, 2006). To gain insight into gene expression indicative of aging and/or cell death in *Karenia brevis*, the toxic dinoflagellate responsible for the near annual harmful algal blooms in the Gulf of Mexico, oligonucleotide microarrays were employed to monitor transcriptomic changes over a complete growth curve. Mid-logarithmic phase (day 6) was used as the point of comparison to the transition into stationary phase (day 10), mid-stationary phase (day 14), and late-stationary (day 18). The data were subjected to three stringency filters to encompass a wide array of statistical and technical requirements to identify the full breadth of future research directions. Of the 10263 genes assessed using the most stringent filtering scheme, 29% (2959) of the features on the array were significantly changing, suggesting a drastic reorganization of the *K. brevis* transcriptome at the transition from logarithmic to stationary phase growth. Analysis of the distribution of genes with increased and decreased expression in stationary phase with respect to functional classes (Gene Ontology enrichment) for each stringency filter (GO Slim, Modified Fisher's Exact, FDR < 0.05) identified coordinated expression of transcripts involved in energy production, calcium ion homeostasis, regulation of gene expression, and response to stress at the transition from logarithmic to stationary phase growth. While further research is needed to discern the functions of the *K. brevis* transcripts responsive to the transition between growth and maintenance phases, this work may serve as a diagnostic for determining the growth status of field populations.

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