GENE REGULATION IN *KARENIA BREVIS*: INSIGHTS FROM MICROARRAYS AND SEQUENCE ANALYSIS

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Karenia brevis is a dinoflagellate whose expressed genome is of significant interest because of its role in producing harmful algal blooms. The longevity of a *K. brevis* bloom is dependant on the cell's ability to adapt to the coastal environment. Transcription of general stress response genes is known to be a key regulatory step in the development of a broad stress resistance. To gain a better understanding of gene regulation in *K. brevis*, we developed a DNA microarray containing 10,265 unigenes. To identify if a general stress response program exists in *K. brevis*, the microarray was used to measure transcriptional changes in response to acute heat, peroxide, lead, paraquat, or sodium nitrite. Consistent with a general stress response that includes a transient shut-off of general mRNA transcription, genes involved in ATP driven processes were downregulated following each of the treatments. However, transcription of stereotypical heat shock proteins and other stress related genes, known to be induced at the protein level in *K. brevis*, were not seen, implicating post-transcriptional regulation of these mRNAs.

The lack of transcriptional regulation found following acute environmental stress along with the distinctive nuclear organization in dinoflagellates suggests that *K. brevis* may have evolved alternative regulatory mechanisms for regulating gene expression. There are several similarities between the gene organization of dinoflagellates and their sister group, the trypanosomes, including polycistronic transcription and the lack of identifiable transcriptional regulators suggesting that dinoflagellate RNA transcription may be similar to trypanosomes. In trypanosomes, long stretches of chromosome are constitutively transcribed into polycistronic units with concurrent splice leader *trans*-splicing and polyadenylation of the nascent chains. The presence of this regulatory mechanism in a closely related genus prompted us to investigate trypanosome-like *trans*-splicing in *K. brevis*. Following sequence analysis of our *K. brevis* unigene set, we identified several mRNA sequences that contain a consensus 22-bp leader sequence. Furthermore, we isolated a gene from genomic DNA encoding a potential SL RNA. This gene shares several key features to the previously characterized SL RNAs. This study provides evidence for the occurrence of SL *trans*-splicing in a dinoflagellate and lends tremendous insight into regulation of gene expression in these early branching eukaryotes.

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