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Transcriptome analysis of Emiliania huxleyi cells grown under different conditions using high-throughput sequencing data

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Coccolithophores are ideal for studying genes responsible for biomineralization processes due to relatively small genome sizes, ability to grow in culture, and as a natural model system for measuring expression of calcification-related genes in two life stages. As the Emiliania huxleyi has several annotated calcification-related proteins, we have concentrated on analyzing its genes and promoter areas. Many recent studies have focused primarily on transcriptome analysis of E. huxleyi using nutrient-limited conditions to get more information about up-regulated genes involved in biomineralization and calcification processes. Although there are more than 100,000 EST sequences for E. huxleyi available from these projects in public databases, that data is often insufficient to identify the exact position of transcription start site (TSS) to perform precise analysis (nucleotide content, motif search) of core promoters and regulatory mechanisms in immediate flanking areas. ESTs are not ideal for these kinds of analyses because the standard technologies of producing 5' EST libraries do not guarantee that the exact 5' end of the transcript will be captured. To determine the extent and accurate positions of 5' ends of transcripts and therefore the positions of core promoters, Cap analysis of gene expression (CAGE) sequencing method was used for sequencing RNA of E. huxleyi in both stages, calcifying and non-calcifying. As an additional info, gene expression levels of RNA for 21 samples were retrieved with whole transcriptome shotgun sequencing (RNA-Seq). The collections of reads these methods produced were used to map and annotate genes on several samples and measure the RNA expression levels in different conditions. Although there are not much data available for close organisms, it is possible to compare these results with other species to find conserved regulatory mechanisms between genes related to calcification. Visualization tools allowing browsing of annotated genes, genome sequence, mapped reads and other information will be demonstrated.