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Author

Pratap, Abhishek

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Genome Sequence to Genome Function: Comprehensive Transcriptome Analysis in Chlamydomonas reinhardtii

Abhishek Pratap^{1*}, Chew Yee Ngan¹, James Han², Chia-Lin Wei¹

¹LBL/Department of Energy Joint Genome Institute, Walnut Creek, California, USA

²LLNL/Department of Energy Joint Genome Institute, Walnut Creek, California, USA

* To whom correspondence should be addressed. E-mail: apratap@lbl.gov

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From Genome Sequence to Genome Function: Comprehensive Transcriptome Analysis in Chlamydomonas reinhardtii

Authors: Abhishek Pratap^{1*}, Chew Yee Ngan¹, James Han², Chia-Lin Wei¹

¹LBNL/Department of Energy Joint Genome Institute, Walnut Creek, California, USA

²LLNL/Department of Energy Joint Genome Institute, Walnut Creek, California, USA

As part of institutional endeavor to disclose genome information from diverse bio-energy related model organisms, JGI is engaging on one of the unmet challenges to annotate genomes for their regulatory elements and identify all the transcription units. Thus, a comprehensive catalog and map of all the expressed genes (transcriptome) are the basis towards the elucidation of genome functions. Here, we applied a combination of sequencing techniques in transcriptome analysis, including ultra-deep strand specific amplification free RNA-Seq, 5'3' RNA-PET and non-coding RNA-seq to define comprehensive transcriptome maps in *C. reinhardtii*. From over 500 million sequences, we applied a hybrid Tophat/Cufflinks assembly approach and defined 14,704 gene structures and 24,679 expressed coding transcripts. We defined hundreds of new genes and improved transcription boundary demarcation; which resulted more than half of the *C. reinhardtii* genome was found to be transcribed. Furthermore, 1,285 putative non-coding RNAs were discovered with antisense and lincRNA characteristics. To validate the authenticity of these new genes, whole genome transcription start sites were determined by chromatin mark H3K4me3 ChIP-Seq and found highly correlated with these new transcription units. Such efforts will provide a solid foundation from which to build a full understanding of the transcript expression, processing and regulation. Furthermore, a complete catalog of transcript variants is the gateway to map molecular interaction network and provide a robust framework to enable system-wide genetic manipulation in algae biodiesel regulation.