

Category	: International Rice Research Conference
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	: Annotation
Genome biology Structure Function and Comparison Keyword 2	:
Genome biology Structure Function and Comparison Keyword 3	:
Title of Entry	: Genome-wide In silico Analysis of Biologically Significant Rice Cis-regulatory Elements (CREs)
Presenting author	: Chai-LIng HO
Presenting author email	: clho@upm.edu.my
Co author 1	: Matt Geisler
Co author 2	:
Affiliation presenting author	: Universiti Putra Malaysia
Affiliation 1	: Southern Illinois University Carbondale
Affiliation 2	:
Select only one type of presentation	: 15 minute oral presentation

Abstract : Genome-wide In silico Analysis of Biologically Significant Rice Cis-regulatory Elements (CREs)
 Chai-Ling Ho¹ and Matt Geisler²
¹Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400 UPM-Serdang, Selangor, Malaysia (clho@upm.edu.my)
²Department of Plant Biology, Southern Illinois University Carbondale, 1125 Lincoln Ave., Life Science II, Carbondale, Illinois 62901-6509, United States of America (mgeisler@plant.siu.edu)

The availability of rice genome and transcriptome resources allows gene function discovery and gene regulatory network reconstruction by large scale meta-analysis and systems biology approaches. Many in silico analyses of cis-regulatory elements (CREs) suffer from a common weakness whereby the biological significance of the CREs was not examined. In this study, CREs (herein defined as non-coding segments of the genomic sequence that are positively correlated with a pattern of gene expression), were identified from rice gene sequences covering the 1 kb and 3 kb upstream sequences from the transcription start sites (where known or start codon), 5' untranslated regions, introns and 1 kb downstream sequences from the translational stop codons of co-expressed genes identified from 231 rice cDNA microarray data series. The biologically significant role of each CRE was determined by correlating their absence and presence in each gene with the expression profile of that gene. Using this approach, novel CREs corresponding to drought, salt,

biotic stress, anaerobic conditions, specific tissues and developmental stages were identified from rice. The effectiveness of some, but not all CREs was found to be affected by copy number, position and orientation. The corresponding transcription factors that were most likely correlated with each CRE were also identified. This information contributes to the prioritization of candidate rice CREs and transcription factors for genetic and biochemical analyses. The transcription factor-CRE predictions will also provide links for reconstructing CRE-anchored gene regulatory networks in rice. Keywords: Biologically significance, cis-regulatory elements; genome-wide; in silico; rice; transcription factors

[Read Less»](#)

Uploaded Files »

No files found.