

The landscape of Transcription factor- DNA bindings reveals the metabolism communication in *E. coli* strain

Contact Ye Gao: yeg002@ucsd.edu

Introduction

Transcription factors are major regulators in organisms. Transcription factor - DNA interactions in bacteria control a variety of cellular processes, thereby playing a major role in maintaining cellular homeostasis. As we know, metabolism pathways consist of complex communication networks in cells, which are directly or indirectly regulated by these proteins. So far there are more than 185 transcription factors with verified experiments, but our knowledge of the profiles of uncharacterized transcription factors lags behind our understanding of metabolic pathways. In a previous study, we developed a workflow combining computational prediction with high-throughput experimental approaches in order to uncover the uncharacterized transcription factors. Here, we apply this workflow to verify many more transcription factor candidates and fully characterize the landscape of transcription factor-DNA bindings at the genome scale.

Specific aims

- Identify the functional bindings and biological roles using knock-out strains.
- Reconstruct the landscape of Transcription factor-DNA bindings to uncover the gap of regulation networks in the cell.

Experiments and expected results

1. To use the universal antibody to pull down the target protein-DNA complex and add the myc-tagging to the transcription factor candidates.
2. Using the robust immunoprecipitation method (ChIPexo) for protein-DNA interaction, identify the potential bindings of candidates at the genome.
3. To evaluate the functional relevance of a number of newly identified bindings, it is necessary to knock out the candidates.
4. Using RNAseq method, analyze and compare the differences between wild type and knock-out strains.

The data enables identification of new regulation network in the cells, and reveal the novel communication for metabolism pathways on the genome-scale.

This project is a good option for any undergraduate or MS students taking research credits or pursuing excellent lab experience/publications.