

Robustness analysis on interspecies interaction network for iron and glucose competition between *Candida albicans* and zebrafish during infection

Che Lin 1, Chin-Nan Lin 2, Yu-Chao Wang 3, Fang-Yu Liu 2, Yu-Wen Chien 1, Yung-Jen Chuang 4, Chung-Yu Lan 5, Wen-Ping Hsieh 6, Bor-Sen Chen 2

1 Institute of Communication Engineering, National TsingHua University, Taiwan

2 Department of Electrical Engineering, National TsingHua University, Taiwan

3 Institute of Biomedical Informatics, National Yang-Ming University, Taiwan

4 Department of Medical Science and Institute of Bioinformatics and Structural Biology, National TsingHua University, Taiwan

5 Department of Life Science and Institute of Molecular and Cellular Biology, National TsingHua University, Taiwan

6 Institute of Statistics, National TsingHua University, Taiwan

Abstract

Candida albicans has emerged as an important model organism for the study of infectious disease. Using high-throughput simultaneously quantified time-course transcriptomics, this study constructed host-pathogen interspecies interaction networks between *C. albicans* and zebrafish during the adhesion, invasion, and damage stages. Given that iron and glucose have been identified as crucial resources required during the infection process between *C. albicans* and zebrafish, we focused on the construction of the interspecies networks associated with them. Furthermore, a randomization technique was proposed to identify differentially regulated proteins that are statistically eminent for the three infection stages. The behaviors of the highly connected or differentially regulated proteins identified from the resulting networks were further investigated.

“Robustness” is an important system property that measures the ability of the system tolerating the intrinsic perturbations in a dynamic network. This characteristic provides a systematic and quantitative view to elucidate the dynamics of iron and glucose competition in terms of the interspecies interaction networks. Here, we further estimated the robustness of our constructed interspecies interaction networks for the three infection stages.

The constructed networks and robustness analysis provided significant insight into dynamic interactions related to iron and glucose competition during infection and enabled us to quantify the system’s intrinsic perturbation tolerance ability during iron and glucose competition throughout the three infection stages. Moreover, the networks also assist in elucidating the offensive and defensive mechanisms of *C. albicans* and zebrafish during their competition for iron and glucose. Our proposed method can be easily extended to identify other such networks involved in the competition for essential resources during infection.