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Fundamental principles governing sporulation efficiency: A network theory approach

Camellia Sarkar¹, Saumya Gupta², Himanshu Sinha³ and Sarika Jalan^{1,4}

¹Centre for Biosciences and Biomedical Engineering, Indian Institute of Technology Indore, Khandwa Road, Simrol, Indore 453552, INDIA

²Department of Cancer Biology, Dana-Farber Cancer Institute, Department of Genetics, Harvard Medical School, Boston, MA 02215, USA

³Department of Biotechnology, Indian Institute of Technology Madras, Chennai 600036, INDIA

⁴Complex Systems Lab, Discipline of Physics, Indian Institute of Technology Indore, Khandwa Road, Simrol, Indore 453552, INDIA

Presenting author: camelliasarkar09@gmail.com

Abstract

Integrating network theory approaches over time-resolved genome-wide gene expression data, we proposed a network-based framework, which considered intricate dynamic regulatory relationships of transcription factors and target genes, for assessing the molecular underpinnings underlying extreme phenotypic differences between two strains of the yeast, *Saccharomyces cerevisiae*. Using network attributes which have demonstrated tremendous success in understanding and predicting behaviors in a wide range of complex biological and social systems, we identified factors and candidate genes that acted as crucial regulators of sporulation in the highly sporulating SK1 strain. We then carried out independent network-based investigations of S288c gene expression profiles and identified the molecular events that occur in SK1 strain but fail to occur in S288c strain, which eventually lead to low sporulation efficiency of S288c. Results suggested that late appearance of known early sporulation regulators and a delay in crosstalk between functional modules can be construed as the prime reasons behind low sporulation efficiency of the S288c. Revelation of meiosis-associated genes for SK1 and mitotic genes for S288c through weak ties analysis and late appearance of hierarchical modularity were further indications of delay in regulatory activities essential to initiate sporulation in S288c. Our results demonstrate the potential of this framework in identifying candidate nodes contributing to phenotypic diversity of developmental processes in natural populations.

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