Mahidol University
Faculty of Science

SCBC Special Seminar

How synthetic genomes can tidy up evolution's mess

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Abstract

Unlike in bacteria, eukaryotes rarely organise sets of genes in their genomes according to function, instead having most genes spread randomly across different chromosomes and loci. However, with the advent of genome engineering, synthetic co-location of genes that together encode a cell function has now become possible, allowing us to explore the pros and cons of 'defragmenting' genomes, and how this can help towards future modular and minimal genomes for synthetic biology. Working in *Saccharomyces cerevisiae* we showcase the construction of Synthetic Genome Modules (SGMs) encoding functions of external sensing, amino acid metabolism and cell cycle control. In this talk I describe how the SGM approach allows us to fine-tune, evolve and minimise the sets of genes required by yeast for each function, and how a new synthetic transcription factor tool, called dCreSIR, can be used to switch on and off SGM expression and even silence entire synthetic chromosomes. Together, our work offers insights into genome organisation and establishes new principles and tools for the future design and construction of modular synthetic yeast genomes.