Understanding gene transfer between endosymbiotic organisms

Wenfa Ng

Unaffiliated researcher, Singapore, Email: ngwenfa771@hotmail.com

Abstract

Endosymbiosis occur when a prokaryotic cell was engulfed by a eukaryotic cell and the two organisms progressively evolved to become dependent on each other. Specifically, the fully functional prokaryotic cell may progressively lose genes encoding metabolic enzymes that result in the cell requiring the import of metabolites from the cytoplasm of the eukaryotic cell to survive. In a similar vein, the eukaryotic cell may acquire new functionalities from the embedded prokaryotic cell and progressively become accustomed to the influx of metabolites from the prokaryotic cell that the eukaryotic host previously has to expend significant amount of energy to manufacture. This would similarly result in loss of genes from the eukaryotic host. Recent work has created a neo-endosymbiosis cell where an auxotrophic Escherichia coli was engulfed by a larger eukaryotic Saccharomyces cerevisiae. Given that transfer of genes from an ancient endosymbiosis event occurred between mitochondria and chloroplast to the host nuclear genome, it would be interesting to observe if similar transfer of genes happened between endosymbiotic E. coli and S. cerevisiae, and more importantly, the genetic machinery responsible for such gene transfer. Specifically, a central question that needs to be answered is whether the machinery guiding gene transfer is still present in modern E. coli and S. cerevisiae. But, what is more important is deciphering the rationale for the specific transfer of particular genes from the prokaryotic cell to the eukaryotic genome. For example, is it due to selection of one gene variant that yield enzyme with higher activity and stability, and if yes, what guides the selection process? Specifically, how are the selection criteria encoded at the molecular mechanistic level? If the gene transfer is random, it would also be interesting to understand the machinery responsible for excising the target genes from the prokaryotic genome and transferring it to the eukaryotic genome and vice versa. Finally, the metabolic, biochemical and cell biological rationales underpinning the selective retention of specific genes in the prokaryotic genome should be elucidated. Collectively, endosymbiosis is the bedrock event in modern eukaryotic cell biogenesis, but many questions remain concerning the processes that potentiate gene transfer between prokaryotic endosymbiont and eukaryotic host. Primarily, we still lack understanding of the mechanisms selecting particular genes for transfer, as well as the molecular machinery mediating the gene transfer. Overall, research in this direction should reveal interesting insights on how sensing the metabolic activities of cells led to activation of molecular machinery for optimising cellular genetic repertoire.

Keywords: endosymbiosis, gene transfer, metabolites, genetic repertoire, prokaryotic cell, eukaryotic cell, *Escherichia coli*, *Saccharomyces cerevisiae*, mitochondria, chloroplast,

Subject areas: biochemistry, cell biology, microbiology, genetics, genomics,

Peer Preprints

Conflicts of interest

The author declares no conflicts of interest.

Funding

No funding was used in this work.