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Adaptive response of yeast cells to triggered toxicity of phosphoribulokinase

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Abstract

Adjustment of plasmid copy number resulting from the balance between positive and negative impacts of borne synthetic genes, plays a critical role in the global efficiency of multistep metabolic engineering. Differential expression of co-expressed engineered genes is frequently observed depending on growth phases, metabolic status and triggered adjustments of plasmid copy numbers, constituting a dynamic process contributing to minimize global engineering burden. A yeast model involving plasmid based expression of phosphoribulokinase (PRKp), a key enzyme for the reconstruction of synthetic Calvin cycle, was designed to gain further insights into such a mechanism. A conditional PRK expression cassette was cloned either onto a low (ARS-CEN based) or a high (2-micron origin based) copy number plasmid using complementation of a trp1 genomic mutation as constant positive selection. Evolution of plasmid copy numbers, PRKp expressions, and cell growth rates were dynamically monitored following gene de-repression through external doxycycline concentration shifts. In the absence of RubisCO encoding gene permitting metabolic recycling, PRKp expression that led to depletion of ribulose phosphate, a critical metabolite for aromatic amino-acids biosynthesis, and accumulation of the dead-end diphosphate product contribute to toxicity. Triggered copy number adjustment was found to be a dynamic process depending both on plasmid types and levels of PRK induction. With the ARS-CEN plasmid, cell growth was abruptly affected only when level PRKp expression exceeded a threshold value. In contrast, a proportional relationship was observed with the 2-micron plasmid consistent with large copy number adjustments. Micro-compartment partitioning of bulk cultures by embedding individual cells into inverse culture medium/oil droplets, revealed the presence of slow and fast growing subpopulations that differ in relative proportions for low and high copy number plasmids.

Keywords: plasmid burden, cell toxicity response, population heterogeneity, metabolic engineering

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