OPEN ACCESS Freely available online

ISSN: 2167-7956
Journal of Biomolecular Research & Therapeutics

Commentary

Metabolomics and its Applications in Systematic Metabolic Engineering

Jackson Mason*

Department of Biomolecules, University of Oxford, Oxford, UK

DESCRIPTION

The biological information offered by metabolomics is well-suited to the goals of metabolic engineering information on how the cell is currently using its biochemical resources is one of the greatest ways to inform strategies for designing a cell to create a target product. It is quite typical to use extracellular or intracellular amounts of the target substance (or a few closely similar compounds) to drive metabolic engineering [1]. However there is surprisingly little systematic use of metabolomics datasets for that purpose which simultaneously test hundreds of compounds rather than just a few. Commercial use of organisms in natural fermentation processes to create compounds such as ethanol and citric acid has a long history. Traditional bioprocess engineering comprises the design and optimization of the equipment and methods required to produce these and other biologically produced products efficiently.

The advancement of recombinant DNA technology allowed for the direct modification and enhancement of metabolic capabilities. As a result, metabolic engineering emerged as a distinct field from bioprocess engineering. Metabolic engineering is the (typically genetic) management of a live organism's metabolic functions in order to establish and maximize the production of desirable metabolites which are the class of tiny molecules that form the primary resources and intermediates of all cellular activity [2]. With a growing interest in ecologically sustainable industrial technologies, metabolic engineering is positioned to provide a cost-effective and efficient method of creating a variety of small molecule compounds from clean and renewable sources such as biofuels. Metabolic engineering aims to maximize the synthesis of certain metabolites in a cell whether these metabolites are produced naturally by the organism or by entire foreign pathways added by genetic engineering. The strategic small-scale observations and flux computations have been critical tools for metabolic engineering [3]. However the rise of systems-level analysis prompted by whole-genome sequencing and the rapid collection of data on RNA, protein and metabolite levels has opened up new avenues for better understanding the impacts of strain modifications. Outside of the targeted pathway, genetic modifications frequently have additional effects and a better understanding of the nature and extent of would lead to more effective strategies for redesigning strains as well as a better understanding of why a proposed design may fail to achieve its predicted performance. Metabolomics the most recent of the global analytic methodologies shares many similarities with its predecessor sciences of genomics, transcriptomics and proteomics.

Metabolomics analytical tools have now advanced to the point where metabolomics datasets can serve as a good complement to typical metabolic engineering methodologies. Metabolic engineering's ultimate goal is to produce desired metabolites and metabolomics provides a comprehensive and direct way of analyzing how well a strain fits those goals [4]. The most basic and direct application of metabolomics datasets is as an extension of previous small-scale metabolite investigations metabolomics allows for a more comprehensive assessment of a strain than a handful of selected measurements. Studies that take this method often compare strains and culture conditions or attempt to track the time-course evolution of multiple metabolite concentrations. These investigations make use of a mix of observed growth and production characteristics as well as direct assessment of metabolomics data [5]. Metabolomics is used far less frequently in metabolic engineering than other global analysis methodologies which may be due to the maturity of domains such as transcriptomics and proteomics compared to metabolomics. For metabolic engineering, proteomics, transcriptomics, and genomes have frequently been integrated with small-scale metabolite studies.

REFERENCES

1. Nissen P, Thirup S, Kjeldgaard M, Nyborg J. The crystal structure of Cys-tRNACys–EF-Tu–GDPNP reveals general and specific features in the ternary complex and in tRNA. Structure.1999; 7(2):143-56.
2. Hunter SE, Spremulli LL. Effects of mutagenesis of residue 221 on the properties of bacterial and mitochondrial elongation factor EF-Tu. Biochim Biophys Acta. 2004; 1699(1-2):173-82.

Correspondence to: Jackson Mason, Department of Biomolecules, University of Oxford, Oxford, UK, E-mail: mason@gmail.com

Received: 02-Jan-2023, Manuscript No. BOM-23-19821; **Editor assigned:** 05-Jan-2023, Pre QC No. BOM-23-19821(PQ); **Reviewed:** 20-Jan-2023, QC No. BOM-23-19821; **Revised:** 26-Jan-2023, Manuscript No. BOM-2 3-19821(R); **Published:** 03-Feb-2023, DOI: 10.35248/2167-7956.23.12.251.

Citation: Mason J (2023) Metabolomics and its Applications in Systematic Metabolic Engineering. J Biol Res Ther. 12:251.

3. Hunter SE, Spremulli LL. Mutagenesis of glutamine 290 in Escherichia coli and mitochondrial elongation factor Tu affects interactions with mitochondrial aminoacyl-tRNAs and GTPase activity. Biochemistry. 2004; 43(22):6917-27.
4. Hunter SE, Spremulli LL. Mutagenesis of Arg335 in bovine mitochondrial elongation factor Tu and the corresponding residue in the Escherichia coli factor affects interactions with mitochondrial aminoacyl-tRNAs. RNA Biol. 2004;1(2):95-102.
5. Kumazawa Y, Schwartzbach CJ, Liao HX, Mizumoto K, Kaziro Y, Miura KI, et al. Interactions of bovine mitochondrial phenylalanyl-tRNA with ribosomes and elongation factors from mitochondria and bacteria. Biochim Biophys Acta. 1991; 1090(2):167-72.