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## Targeted metabolomics: A tool to identify bottlenecks in microbial biosynthetic pathways

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Recently, there has been a push in the biosciences to understand the functions associated with gene products due to many genes not being under transcriptional control and the incomplete prediction of the proteome from the transcriptome. Consequently, phenotypic information from the metabolome has been highly sought after, as it reflects more closely metabolic activities within a cell. At present, complete global metabolite profiles (comprehensive metabolomics) are not yet feasible due to the chemical complexity of the metabolome and the inability of current analytical techniques to simultaneously measure all metabolites. Thus, a targeted strategy involving the quantification of localized metabolism (targeted metabolomics) is currently the favored approach. Targeted metabolomics highlights aspects of metabolomics data that are truly meaningful and can be used to reveal bottlenecks in biosynthetic pathways by monitoring pathway intermediates and cofactors. Moreover, when combined with knowledge of microbial physiology, metabolism that is closely related to engineered biosynthetic pathways can be accurately determined. This information can then be used to assess the impact of an engineered pathway on microbial metabolism and physiology. Herein, the effectiveness of this strategy will be demonstrated via the identification of bottlenecks in the heterologously expressed mevalonate pathway in *Escherichia coli*. This approach can be directed towards engineering robust microbial cell factories for producing valuable renewable bioproducts.

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