Editorial

Microbial metabolism and the power of the small

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Metabolic networks in microbial organisms are highly diverse. Unravelling this metabolic flexibility not only reveals fundamental metabolic insights but also can yield benefits for society at large

icrobial organisms – such as yeast, bacteria or cyanobacteria – are adapted to survive and thrive in diverse environments, including extreme temperature, salinity or scarcity of nutrients. This adaptability is endowed by remarkably diverse metabolic networks, which enable microorganisms to use a variety of carbon or nitrogen sources, including some that would be considered unusual for metazoans. As a consequence, microorganisms can generate metabolic by-products that do not occur naturally in animals, many of which are of biotechnological or industrial interest.

Researchers have made great efforts to tweak microbial biochemical networks and take advantage of their metabolic versatility to produce desirable metabolites. However, this often proves more complicated than one would imagine, as changes in endogenous intracellular metabolic fluxes can have unexpected effects on cell growth, viability or production of the metabolite of interest. Therefore, refined metabolic design and engineering are needed to take full advantage of the microbial metabolic machinery and re-route the biochemical fluxes as desired. In our mission to feature exciting advances in all areas of metabolic biology, we have been following the developments in the field of metabolic engineering with interest. In our current issue, we feature not one but two intriguing studies on this topic.

The study from Lu et al. provides unique mechanistic insight into how cyanobacteria rapidly switch between carbon fixation and oxidative phosphorylation when subjected to highly dynamic changes in the amount of light they receive, as a result of exposure to fast currents in large bodies of water. This study also has fundamental implications for our understanding of how cyanobacteria contribute to global carbon balance and provides clues regarding how to enhance the production of sucrose from atmospheric CO_2 .

In the second study, Zhan et al. reconfigure bacterial metabolism to overcome metabolic blockage of propionate metabolism for increased production of polyketides, which are of medical and agricultural interest.

The two papers in our current issue continue a series of articles related to metabolic engineering published in our pages in recent months. For example, Gao et al. optimized the use of methanol as sole feedstock to substantially increase the production of fatty acids in yeast by manipulating metabolic fluxes to reduce methanol-derived toxicity. Similarly, Yu et al. presented an elegant strategy to redesign cytosolic metabolism in yeast, which enabled growth and survival and significantly boosted the generation of reduced compounds, such as fatty acids, that can be further used as biofuels. Chou et al., on the other hand, tweaked metabolism in bacteria to increase biosynthesis of one-carbon-derived products.

These intriguing studies share several common features. First, all went beyond manipulation of key enzymes to push metabolic flux in a specific direction and involved a deliberate reconfiguration of metabolic routes; they thus also offer insights into how microbial metabolic networks operate. Second, the findings are relevant to broader societal challenges related to sustainability and development. For example, they involve the use of cost-efficient and environmentally friendly precursors and the sustainable generation of biofuels or other products of general industrial interest, while minimizing waste and reducing the overall carbon footprint, or they shed light on how microbial metabolic networks contribute to the global carbon balance. And last, but not least, they lay out a path for a substantial increase in yield and efficiency in the production of biotechnologically relevant compounds.

Publishing exciting advances in microbial metabolic engineering is in line with the commitment of Springer Nature to support research towards addressing the sustainable development goals. We hope, therefore, to feature more such research in our pages in the future to support the community of metabolic researchers in working towards these important objectives.

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