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Editorial

Escherichia coli Genome-scale metabolic models could guide construction of proof-of-principle strains

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Escherichia coli genome-scale metabolic models (GEMs) have been published with ability to predict metabolic engineering capabilities that could be consistent with experimental measurements. However, the GEMs have limited scope, and the models are of two types, metabolism models (M-model), and metabolism and gene expression (ME-model) that could guide the constructions of proof-of-principle strains of particularly *E. coli* bacterium that may find applications in metabolic engineering strategies, synthetic biology [1], and beyond.

GEMs have been clearly established to be capable of predicting metabolic engineering capabilities and could sometime lead to biological discoveries for missing reactions and/or missing gene functions [2–4]. In addition, systems metabolic engineering has proof useful with the use of GEMs where time consuming experimental trial and error was shortened by predicting engineering strategies using GEMs. Although sometimes prediction could fail to agree with experimental data, but in that circumstances missing knowledge can be uncovered and gaps in the reconstruction can therefore be bridged leading to novel biological discoveries [3,4].

The GEMs that is designated as M-model does not differentiate between isozymes as such its predictive capability is not as accurate as that of ME model, which integrates metabolism and gene expression data. The construction of the former model (M-model) is relatively much easier, as the full protocol has been previously published [5], while the ME model requires additional expertise, as it integrates both metabolism, and gene expression data [6]. These two models could serve as platforms for construction of proof-of-principle strains.

A number of proof-of-principle strains were constructed using *E. coli* GEMs for increasing succinic acid production [7–10] and/or other chemicals such as 1,-4 butanediol [11]. These strategies

used GEMs that are considered M-models, with limited scope and fairly accurate predictive power. What we hope to see in the future is the of extended version of M-model that could include gene expression data (ME-model) in predicting proof-of-concept studies that could be much more accurate predictive power that is greater than 80%.

In conclusion, the M-models of *E. coli* has been extensively used for the construction of proof-of-concept studies, particularly in increasing succinic acid production using a number of carbon sources, including glucose, and glycerol. Because of its limited scope and fair predictive accuracy, M-models are expected to be extended to ME-models for the construction of future proof-of-principle strains not limited to *E. coli* bacterium alone, but also for the forthcoming GEMs of microbial species with varieties of biotechnological applications in the field of medicine, agriculture, environment, industries and probably beyond.

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