Preface

*Corynebacterium glutamicum* was discovered in 1956 by Shukuo Kinoshita, Shigezo Udaka, and Masakazu Shimono of Kyowa Hakko Kogyo Company as a natural glutamate producer from an avian-feces-contaminated soil sample collected from Ueno Zoo in Tokyo, Japan. It has since become apparent that *C. glutamicum* exhibits numerous ideal intrinsic attributes as a microbial factory upon which one after another efficient production process for not just amino acids for the food and feed industry but also nucleotides and vitamins has been developed. The post-genomic era provides a new technological platform upon which further optimization of *C. glutamicum* as a biocatalyst can be done to dramatically expand its product portfolio to include a variety of commodity chemicals. At present, *C. glutamicum* is on the verge of recruitment as an industrial microbial workhorse to produce chemicals such as lactate and succinate, poly-3-hydroxybutyrate, 1,2-propanediol for the materials (plastics) industry and fuels such as ethanol or isobutanol for the transportation industry. The microorganism has revealed strong inherent potential to produce recombinant proteins, owing to its industrial robustness and efficient protein secretion pathways. As a biotechnology workhorse of the emerging biorefinery industry, the fundamental advantages of *C. glutamicum* are threefold. First, the ability of the cells to retain robust catalytic functionality under growth-suppressed conditions permits high-cell-density bulk preparations in dedicated centralized factories well in advance of their actual use. The preparations can be stored and transported on demand to points of use, thereby not only saving on transportation costs of bulky raw materials but also optimizing reactor sizes to achieve capital expense reductions. Second, the growth-independent nature of the catalysis limits the impact of inevitable lignocellulose-derived inhibitors such as furans and phenols, retaining high productivities with many substrates derived from renewable resources. Third, the native ability of *C. glutamicum* to catabolize different sugars in parallel has been harnessed to build efficient pentose catabolic and transport pathways into the microorganism to further enhance its conversion efficiency of renewable resources in effort to eschew competition between biorefinery and food or feed supply.

The purpose of this monograph is on the one hand to explore the plasticity of *C. glutamicum* physiology, as well as recent advances in the molecular biology techniques available to engineer the microorganism. On the other hand, the
monograph sets out to illustrate how the information made available by complete genome sequencing enables the rational engineering of the entire cellular metabolism, including how systems biology can improve *C. glutamicum*’s attributes as an industrial biocatalyst. The monograph interrogates the latest molecular biological techniques available for *C. glutamicum*, including promoters, plasmid vectors, and genome engineering, as well as the most recent global analyses such as transcriptome, proteome, metabolome, and bioinformatic regulatory networks. Moreover, topics regarding gene regulation of sugar uptake, glycolysis, pentose phosphate pathway, TCA cycle, glyoxylate shunt, respiratory chain, and energy metabolism, besides mechanisms for amino acid export, protein secretion, and cell division, are covered. The monograph also describes amino acid production utilizing the most important intrinsic attributes of the microorganism and more recent and highly regarded biorefinery applications. We sincerely hope that readers of the monograph will enjoy and use it as a reference for their studies in this field.

We greatly appreciate the excellent contributions of all the authors of the monograph. We thank Springer for publishing the monograph and especially Jutta Lindenborn for her valuable suggestions and support.

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