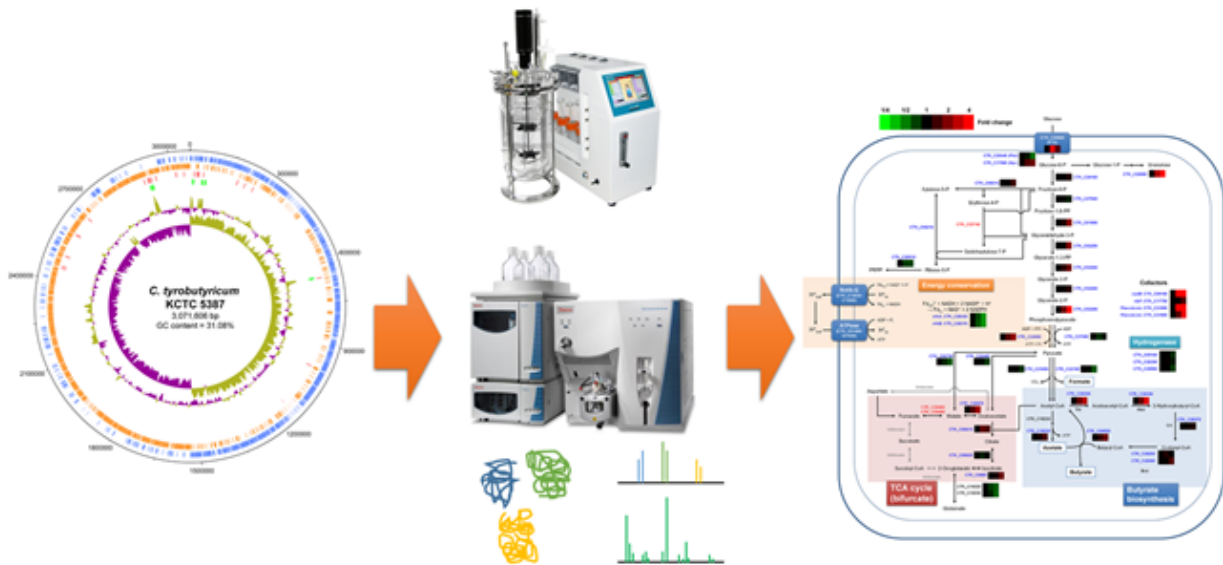


# Unveiling the distinctive features of a promising industrial microorganism

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The complete genome sequence, global protein expression profiles, and the genome-based metabolic characteristics during batch fermentation of *C. tyrobutyricum*. Credit: KAIST

*Clostridium tyrobutyricum*, a Gram-positive, anaerobic spore-forming bacterium, is considered a promising industrial host strain for the production of various chemicals including butyric acid which has many applications in different industries such as a precursor to biofuels. Despite such potential, *C. tyrobutyricum* has received little attention, mainly due to a limited understanding of its genotypic and metabolic

characteristics at the genome level.

A Korean research team headed by Distinguished Professor Sang Yup Lee of the Chemical and Biomolecular Engineering Department at the Korea Advanced Institute of Science and Technology (KAIST) deciphered the genome sequence of *C. tyrobutyricum* and its proteome profiles during the course of batch fermentation. As a result, the research team learned that the bacterium is not only capable of producing a large amount of butyric acid but also can tolerate toxic compounds such as 1-butanol. The research results were published in mBio on June 14, 2016.

The team adopted a genoproteomic approach, combining genomics and proteomics, to investigate the metabolic features of *C. tyrobutyricum*. Unlike *Clostridium acetobutylicum*, the most widely used organism for 1-butanol production, *C. tyrobutyricum* has a novel butyrate-producing pathway and various mechanisms for energy conservation under anaerobic conditions. The expression of various metabolic genes, including those involved in butyrate formation, was analyzed using the "shotgun" proteome approach.

To date, the bio-based production of 1-butanol, a next-generation biofuel, has relied on several clostridial hosts including *C. acetobutylicum* and *C. beijerinckii*. However, these organisms have a low tolerance against 1-butanol even though they are naturally capable of producing it. *C. tyrobutyricum* cannot produce 1-butanol itself, but has a higher 1-butanol-tolerance and rapid uptake of monosaccharides, compared to those two species.

The team identified most of the genes involved in the central metabolism of *C. tyrobutyricum* from the whole-genome and shotgun proteome data, and this study will accelerate the bacterium's engineering to produce useful chemicals including butyric acid and 1-butanol, replacing

traditional bacterial hosts.

Professor Lee said: "The unique metabolic features and energy conservation mechanisms of *C. tyrobutyricum* can be employed in the various microbial hosts we have previously developed to further improve their productivity and yield. Moreover, findings on *C. tyrobutyricum* revealed by this study will be the first step to directly engineer this bacterium."

Director Jin-Woo Kim at the Platform Technology Division of the Ministry of Science, ICT and Future Planning of Korea, who oversees the Technology Development Program to Solve Climate Change, said "Over the years, Professor Lee's team has researched the development of a bio-refinery system to produce natural and non-natural chemicals with the systems metabolic engineering of microorganisms. They were able to design strategies for the development of diverse industrial microbial strains to produce useful chemicals from inedible biomass-based carbon dioxide fixation. We believe the efficient production of [butyric acid](#) using a metabolic engineering approach will play an important role in the establishment of a bioprocess for chemical production."

**More information:** Joungmin Lee et al, Deciphering Metabolism Based on the Whole-Genome Sequence and Proteome Analyses, *mBio* (2016). [DOI: 10.1128/mBio.00743-16](https://doi.org/10.1128/mBio.00743-16)

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