

Comprehensive Analysis of Intracellular Metabolites by Capillary Electrophoresis Mass Spectrometry

Tomoyoshi Soga
Inst. Adv. Biosci. Keio Univ.
Tsuruoka, Yamagata, 997-0017
Japan
soga@sfc.keio.ac.jp

Takaaki Nishioka
Grad. Sch. Agric. Sci. Kyoto Univ.
Sakyo-ku, Kyoto, 606-8502
Inst. Adv. Biosci. Keio Univ.
Tsuruoka, Yamagata, 997-0017
Japan
nishioka@scl.kyoto-u.ac.jp

Masaru Tomita
Inst. Adv. Biosci. Keio Univ.
Tsuruoka, Yamagata, 997-0017
Japan
mt@sfc.keio.ac.jp

ABSTRACT

In the post genome era, elucidation of gene function is a main focus. Multi-parallel analysis of mRNA and proteins are central to today's functional genomics initiatives. However, these results do not provide direct interpretation of biological meanings on cellular and tissue events. Quantitative comprehensive analysis of metabolites compared with data obtained from mRNA and proteins analysis is crucial to elucidate a change in biological function. However, the comprehensive analysis of intracellular metabolites is still in the early stage, therefore only few studies have been reported¹⁻³.

We describes here are novel methods for the quantitative comprehensive analysis of metabolites using capillary electrophoresis coupled to mass spectrometry (CE-MS). More than 30 positively charged metabolites including amino acids and amines were roughly separated by CE and selectively detected by MS. On the other hand many kinds of negatively charged metabolites such as organic acids were simultaneously analyzed with the other condition. The detection limits for those metabolites were in the range from sub μ M to μ M⁴. The proposed method is simple, rapid, and selective and then could be readily applied to the real samples.

Bacillus subtilis 168 cells were grown in glucose or malate rich culture. The intracellular metabolites were extracted with ice-cold methanol and then analyzed by CE-MS system. A large number of intracellular metabolites were quantitatively determined. Metabolic pathway networks and microbial metabolic functionality will be discussed from these chemical data.

ADDITIONAL AUTHORS

Yuki Ueno, Hisako Naraoka (Inst. Adv. Biosci. Keio Univ.),

Keiko Matsuda (Grad. Sch. Agric. Sci. Kyoto Univ.) and Yasutaro Fujita (Dept. Engineering Fukuyama Univ.)

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