

**Applicable *in vivo* metabolic flux analysis: Contribution of the amino acids of yeast extract to the cellular proteins**

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A novel method for metabolic pathway studies of central metabolism has been developed based on <sup>13</sup>C labeling experiments. This approach is well-established tool to provide more accurate flux distribution. However, due to the complicated calculation, this method is utilized only in the culture system with defined medium. This limitation is crucial imperfection for understanding unknown cellular physiology considering that most of the industrial microbial is cultivated in semi-defined or complex medium. Herein, we investigated how much the amino acids of yeast extract contributed to the isotopic mass distribution of proteinogenic amino acids in semi-defined culture system. As a result, we determined the contribution coefficients and constructed the analysis system to estimate in the semi-defined or complex culture system. [This work was supported by a grant from the MOST (Korean Systems Biology Research Grant) and by the Brain Korea 21 Project]