Single-Embryo Metabolomics and Systematic Prediction of Developmental Stage in Zebrafish

Shunsuke Hayashi\textsuperscript{a}, Mako Yoshida\textsuperscript{a}, Toshinobu Fujiwara\textsuperscript{b,c}, Shingo Maegawa\textsuperscript{d}, and Eiichiro Fukusaki\textsuperscript{a,*}

\textsuperscript{a} Department of Biotechnology, Graduate School of Engineering, Osaka University, Yamadaoka, Suita 565-0871, Japan. Fax: +81-(0)6-6879-7424. E-mail: fukusaki@bio.eng.osaka-u.ac.jp
\textsuperscript{b} Department of Chemical Science and Engineering, Kobe University, 1-1 Rokkodaicho, Nadaku, Kobe 657-8501, Japan
\textsuperscript{c} Precursory Research for Embryonic Science and Technology, Japan Science and Technology Agency, 4-1-8 Honcho, Kawaguchi, Saitama 332-0012, Japan
\textsuperscript{d} Department of Intelligence Science and Technology, Graduate School of Informatics, Kyoto University, Yoshida-Honmachi, Sakyō, Kyoto 606-8501, Japan

* Author for correspondence and reprint requests

Z. Naturforsch. 66c, 191 – 198 (2011); received August 20, 2010/January 6, 2011

Metabolites, the end products of gene expression in living organisms, are tightly correlated with an organism’s development and growth. Thus, metabolic profiling is a potentially important tool for understanding the events that have occurred in cells, tissues, and individual organisms. Here, we present a method for predicting the developmental stage of zebrafish embryos using novel metabolomic non-target fingerprints of “single-embryos”. With this method, we observed the rate of development at different temperatures. Our results suggest that this method allows us to analyse the condition, or distinguish the genotype, of single-embryos before expression of their ultimate phenotype.

Key words: Single-Embryo, Embryogenesis, Metabolomics