

Harnessing synthetic biology for the production of high-value chemicals

Eriko Takano

Manchester Centre for Synthetic Biology of Fine and Speciality Chemicals (SYNBIOCHEM),
Manchester Institute of Biotechnology, Faculty of Life Sciences, University of Manchester,
UK

Our ability to readily sequence complete genomes and to manipulate/re-design them on a large scale enables the design and construction of organisms with new functionalities of unprecedented scope ("synthetic biology"). We explore these possibilities in the context of high-value chemical production. Many microorganisms already have the machinery to produce diverse bioactive molecules that can be used in health, agriculture and food (Cimermancic et al., 2014). As a first step towards re-engineering these high-value chemical biosynthesis pathways for enhanced productivity and diversity, we aim to understand the interchangeability of biosynthetic parts (Diez et al., 2015) and to create orthogonal transcription mechanisms (based on signalling molecule circuits (Biarnes-Carrera et al., 2015)). In addition, we are expanding our collection of computational tools for the detection and analysis of secondary metabolite biosynthesis gene clusters, to enrich our library of parts and building blocks for pathway engineering (Weber et al., 2015). We combine this analysis with high-resolution mass spectrometry analysis, which we also employ for the debugging of the engineered systems (Jankevics et al., 2012). Furthermore, we are using computational modelling (constraint-based descriptions of bacterial metabolism) to identify suitable overproduction hosts and pinpoint biosynthetic bottlenecks to target for further cellular engineering in a synthetic biology strategy (Breitling et al., 2013).

References:

Biarnes-Carrera M, Breitling R, **Takano E**. Butyrolactone signalling circuits for synthetic biology. *Curr. Opin. Chem. Biol.* (2015) in press.

Breitling R, Achcar F, **Takano E** Modeling challenges in the synthetic biology of secondary metabolism. *ACS Synth. Biol.* (2013) 19:373-378.

Diez V, Loznik M, ..., **Takano E**. Functional exchangeability of oxidase and dehydrogenase reactions in the biosynthesis of hydroxyphenylglycine, a non-ribosomal peptide building block. *ACS Synth Biol* (2015) 4:796–807

Cimermancic P, Medema MH, Claesen J, Kurita K, Wieland Brown LC, Mavrommatis K, Pati A, Godfrey PA, Koehrsen M, Clardy J, Birren BW, **Takano E**, Sali A, Lington RG, Fischbach MA. Insights into secondary metabolism from a global analysis of bacterial biosynthetic gene clusters. *Cell* (2014) 158:412-21. **highlighted in Nature Chemical Biology, 10 798-800 (2014)**

Jankevics A, Merlo ME, de Vries M, Vonk RJ, **Takano E**, and Breitling R. Separating the wheat from the chaff: a prioritisation pipeline for the analysis of metabolomics datasets. *Metabolomics* (2012) 8:29-36.

Weber T, Blin K, ..., **Takano E**, Medema MH. antiSMASH 3.0-a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucl. Acids Res.* (2015) PMID:25948579