FEBS openbio

FEBS PRESS
science publishing by scientists

FEBS openbio

Volume 8 Supplement 1 July 2018

POSTERS

Table of Contents

Abstracts submitted to the 43rd FEBS Congress, taking place in Prague, Czech Republic from 7th to 12th July 2018, and accepted by the Congress Organizing Committee are published in this Supplement of *FEBS Open Bio*. Late-breaking abstracts are not included in this issue.

About these abstracts

Abstracts submitted to the Congress are **not peer-reviewed**. In addition, abstracts are published as submitted and are **not copyedited** prior to publication.

We are unable to make **corrections of any kind** to the abstracts once they are published.

Indexing

Abstracts published in *FEBS Open Bio* Supplement for the 43rd FEBS Congress will be included individually in the Conference Proceedings Citation Index published by Web of Science.

How to cite these abstracts

AuthorOne, A., AuthorTwo, B. (2018). Abstract title. FEBS Open Bio, 8: Abstract number*. doi:10.1002/2211-5463.12453

strain produced up to 11.4 g/L of 3HP under fed-batch condition from cellobiose with a yield of 13% (g-3HP/g-sugar).

P.07-047-Tue
Metabolic design of *Escherichia coli* for muconic acid production

R. Fujiwara[1], S. Noda[2], T. Tanaka[1], A. Kondo[1,2]
[1]*Kobe University, Kobe, Japan,* [2]*RIKEN, Yokohama, Japan*

Adipic acid(AA) is a versatile bulk chemical to be used for raw materials such as nylon 6.6. Currently, AA biosynthesis from bio-resources has received a lot of attention in recent years as environment-friendly and renewable AA production process. Muconic acid(MA), also known as 2,4-hexadienoic acid, is expected as a biosynthesis precursor of AA. There are Several studies on MA biosynthesis using *Escherichia coli* introduced foreign genes. In those studies, MA is synthesized from intermediate products of the shikimate pathway. In this work, the MA synthesis pathway was introduced into the strain whose shikimate pathway was enhanced, and optimized for that strain. In our previous studies, we designed the metabolic pathway of *E. coli* to enhance the shikimate pathway and to produce chorismate derivatives in high yields. Firstly, we selected the MA synthesis pathway from three candidates. Secondly, the selected pathways were enhanced by overexpressing *aroC* encoding chorismate synthase, or *aroD* encoding 3-dehydroquinate dehydratase. Finally, an effect of overexpressing fusion proteins by gene-level fusion method was investigated which containing chorismate synthase and isochorismate synthase, or 3-dehydroquinate dehydratase and 3-dehydroshikimate dehydratase.

P.07-048-Wed
Metabolomics and proteomic analysis of serpentinite-associated bacterium *Rhodococcus* sp. S10

I. V. Khilyas[1], A. V. Sorokina[1], L. T. Shafigullina[1], T. Timm[2], G. Lochnit[2], L. M. Bogomolnaya[1,3], M. R. Sharipova[1]
[1]*Kazan Federal University, Institute of Fundamental Medicine and Biology, Kazan, Russia,* [2]*Protein Analytics, Institute of Biochemistry, Faculty of Medicine, Giessen, Germany,* [3]*Texas A&M University Health Science Center, Texas, Bryan, United States of America*

Iron is an essential trace element in regulation of vital metabolic processes in living organisms. It is well known that iron can considerably modulate the structure of microbial communities in different environments. Microorganisms adapted to geochemically extreme conditions through synthesis and secretion of specific molecules that can chelate iron from the environment and make it available for bacteria. These secreted secondary metabolites and proteins are highly interesting for functional studies because of their direct contact with a mineral surface. Here we report the results of metabolomics and proteomic studies of *Rhodococcus* sp. S10 isolated from serpentinite minerals. We showed that *Rhodococcus* sp. S10 can produce siderophores in CAS agar assay. To study the metabolomic profile of *Rhodococcus* sp. S10 the HPLC analysis was performed. It was demonstrated that *Rhodococcus* sp. S10 grown in a minimal medium under iron-depleted condition produced several types of siderophores. Growth of *Rhodococcus* sp. S10 in the presence of 100 mM ferric chloride inhibited the siderophores synthesis. Proteomic analysis of the extracellular proteins secreted in the minimal medium simultaneously with accumulation of siderophores by *Rhodococcus* sp. S10 showed approximately 600 protein spots on the 2D gels and their localization predominantly in the range of pH 3 to 6. Thus, comprehensive analysis of metabolites and proteins excreted by *Rhodococcus* sp. S10 under iron-limited conditions will reveal the mechanisms of adaptation to geochemically extreme conditions and their potential role in the serpentinite biomineralization. This work was performed within the Program of Competitive Growth of Kazan Federal University and supported by RFBR (grant no. 16-34-60200) and the scholarship of the President of the Russian Federation for young scientists and graduate students.

P.07-049-Mon
Sugarcane molasses as an alternative cheap carbon source for polyhydroxybutyrate production by *Halomonas elongata* 2FF under non-sterile conditions

A. Cristea[1], N. Leopold[2], C. G. Floare[3], P. A. Bulzu[1], H. L. Banciu[1]
[1]*Department of Molecular Biology and Biotechnology, Faculty of Biology and Geology, Babes-Bolyai University, Cluj-Napoca, Romania,* [2]*Department of Biomolecular Physics, Faculty of Physics, Babes-Bolyai University, Cluj-Napoca, Romania,* [3]*Department of Molecular and Biomolecular Physics, National Institute for Research and Development of Isotopic and Molecular Technologies, Cluj-Napoca, Romania*

Polyhydroxyalkanoates (PHAs) are natural biodegradable lipid biopolymers synthesized as intracellular carbon storage material by numerous *Bacteria* and a few *Archaea* representatives. The accumulation of PHAs in microorganisms is favored by growth under nutrient imbalance (*i.e.*, excess of C source and limitation of P and N). The requirement for excess of (relatively expensive) C source alongside maintenance of sterile conditions may raise the costs of PHA production. Here we evaluate the ability of *H. elongata* to produce polyhydroxybutyrate (PHB) using sugarcane molasses (SM) as cheap C source under non-sterile (NS) and saline conditions. The 16S rRNA gene-based identification indicated that the 2FF strain isolated from a hypersaline lake pertained to *Halomonas elongata*. After 48 h of growth in mineral M1 medium containing 1 and 2% (SM), at 5% NaCl, and under NS conditions, *H. elongata* 2FF accumulated lipid granules as evidenced by fluorescence microscopy using Nile Red dye staining. Furthermore, no contamination of culture was observed during 6-days incubation at 37°C. The quantification of extracted PHA was evaluated by crotonic acid assay and the chemical structure was revealed by FTIR, Raman, and ^{1}H-NMR spectroscopy. The FTIR and Raman spectra of extracted polymer were similar to that of standard PHB. The ^{1}H-NMR analyses showed same H chemical shifts for the extracted PHA and the standard PHB. Moreover, partial *phaC* gene coding for Class I PHA synthase in *H. elongata* 2FF strain was successfully cloned and sequenced. Overall, we concluded that *H. elongata* 2FF produced PHB using SM as alternative C source under saline and NS conditions. In perspective, optimization of culture conditions alongside testing of various cheap C sources and subsequent assessment of PHA productivity will be considered to achieve a cost-effective PHB production by *H. elongata* 2FF. We acknowledge the grant from CNCS–UEFISCDI, project PN-III-P4-ID-PCE-2016-0303.

FEBS Open Bio **8** (Suppl. S1) (2018) 107–496 DOI: 10.1002/2211-5463.12453