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Corrigendum

Corrigendum to “The effect of high concentrations of glycerol on the growth, metabolism and adaptation capacity of *Clostridium butyricum* DSP1”

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The authors regret an oversight on their part resulting in the omission of some important information from the work. They failed to state where the proteomic analysis whose results they included in the paper has been performed. They also omitted several facts regarding the methodology of the analysis. As the authors highly regard the analytical service provided by the laboratory to which they missed to give credit in the papers, they wish to rectify the situation by including the below to the Acknowledgments section:

The proteomic analysis was performed in cooperation with the Laboratory of Mass Spectrometry, Institute of Biochemistry and Biophysics, Polish Academy of Sciences.

Moreover, the authors would also like to introduce few additions in the Methods section, the Protein analyses subsection, as seen below:

Proteins were reduced (10 mM DTT, 30 min, 56°C) and alkylated with iodoacetamide in darkness (45 min, 20°C) and digested overnight with 10 ng/μL trypsin. The resulting peptide mixtures were applied to the RP-18 pre-column of a UPLC system (Waters) using water containing 0.1% FA as a mobile phase and then transferred to a nano-HPLC RP-18 column (internal diameter 75 μm, Waters) using ACN gradient (0–35% ACN in 160 min) in the presence of 0.1% FA at a flow rate of 250 μL/min. The column out-let was coupled directly to the ion source of an Orbitrap Velos mass spectrometer (Thermo). Each sample was measured in duplicate – once for protein sequencing (data-dependent MS to MS/MS switch) and once for quantitative information (MS only, sequencing disabled). The acquired MS/MS data were pre-processed with Mascot Distiller software (v. 2.3, MatrixScience) and a search was performed with the Mascot Search Engine MatrixScience, Mascot Server 2.4) against the set of *Clostridium* protein sequences derived from Uniprot, merged with its randomized version (16,294 sequences; 5,095,802 residues). The proteins that exactly matched the same set of peptides were combined into a single cluster. The mass calibration and

data filtering were carried out with MScan software, developed in-house (<http://proteom.ibb.waw.pl/mscan/>). The lists of peptides that matched the acceptance criteria from the LC–MS/MS runs were merged into one common list. This common list was overlaid onto 2-D heat maps generated from the LC–MS profile datasets by tagging the peptide-related isotopic envelopes with corresponding peptide sequence tags on the basis of the measured/theoretical mass difference, the deviation from the predicted elution time, and the match between the theoretical and observed isotopic envelopes. A more detailed description of the quantitative extraction procedure implemented by our in-house software is available in [1]. The abundance of each peptide was determined as the height of a 2-D fit to the monoisotopic peak of the tagged isotopic envelope. Quantitative values were normalized with LOWESS, proteins with more than 80% common peptides were clustered and the peptides unique for the cluster were used for statistical analysis. Statistical significance was assessed with an in-house software Diffprot [2]. Only proteins with q-value below 0.05 or those present in only one of two compared analytical groups were taken into consideration during further analysis. The protein concentration was measured by Bradford's method.

References

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