

CORRECTION

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Correction to: Genome and transcriptome of the natural isopropanol producer *Clostridium beijerinckii* DSM6423

Hadrien Máté de Gérando^{1,2}, François Wasels², Angélique Bisson², Benjamin Clement², Frédérique Bidard², Etienne Jourdiere², Ana María López-Contreras¹ and Nicolas Lopes Ferreira^{2*}

Correction

Following the publication of this article [1], the authors noticed that Figs. 2, 3 and 4 were in the incorrect order and thus had incorrect captions. The images that were incorrectly published as Figs. 2, 3 and 4 should have been published as Figs. 3, 4 and 2 respectively.

The correct versions of Figs. 2, 3 and 4 with captions have been included in this Correction.

The original article has been corrected.

Author details

¹Wageningen Food and Biobased Research, Bornse Weiland 9, 6709WG Wageningen, The Netherlands. ²IFP Energies Nouvelles, 1 et 4 avenue de Bois-Préau, 92852 Rueil-Malmaison, France.

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1. de Gérando M, et al. *BMC Genomics*. 2018;19:242.

* Correspondence: nicolas.lopes-ferreira@ifpen.fr

²IFP Energies Nouvelles, 1 et 4 avenue de Bois-Préau, 92852 Rueil-Malmaison, France



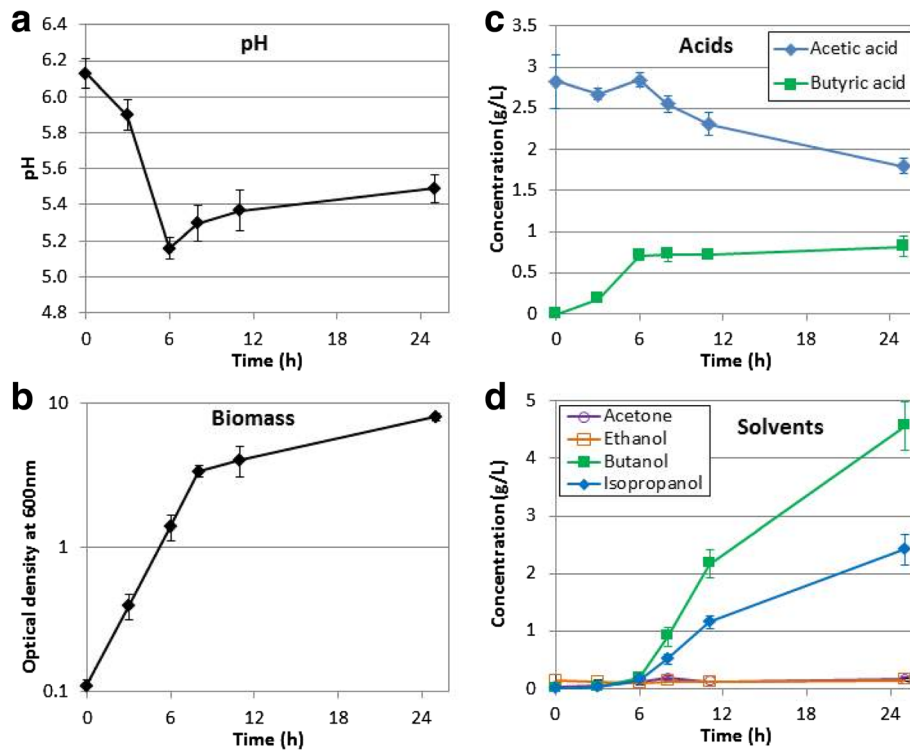


Fig. 2 Fermentation profile of *Clostridium beijerinckii* DSM 6423 on glucose. *C. beijerinckii* DSM 6423 was cultivated in bioreactors in GAPES medium. **a** pH, **b** biomass followed by OD₆₀₀, **c** acids and **d** solvents. Values are the mean and standard deviation of the 6 biological replicates. See Additional file 3 for details on the biological replicates

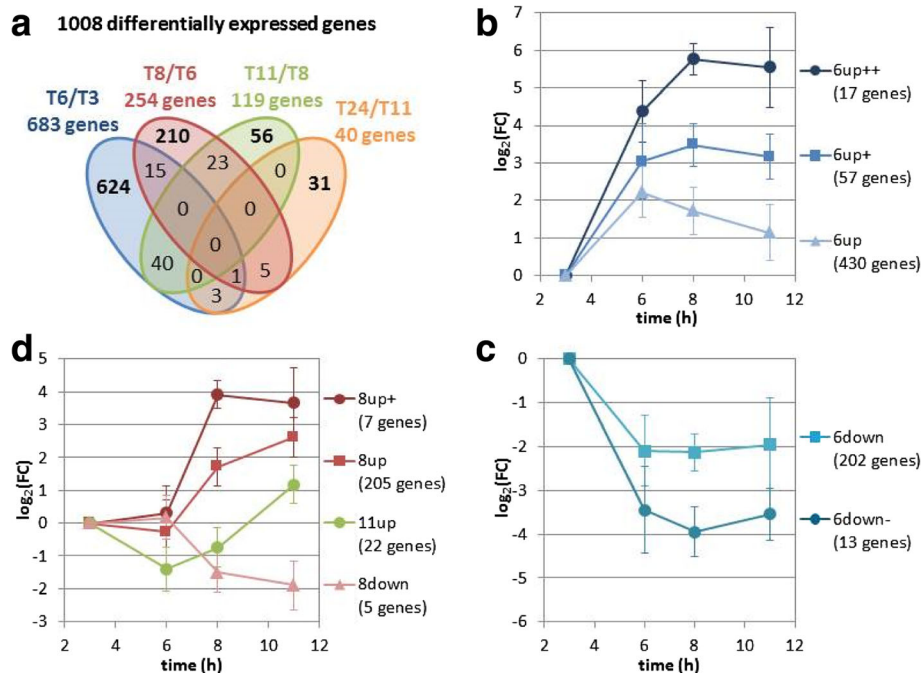


Fig. 3 Global transcriptomic analysis of *C. beijerinckii* DSM6423 fermentation on glucose. **a** Venn Diagram showing the number of genes regulated in various physiological time points. **b** to **d**: kinetic expression profiles of various clusters of genes: genes up-regulated at 6 h **b**, genes down-regulated at 6 h **c**, and genes regulated at 8 h or 11 h **d**

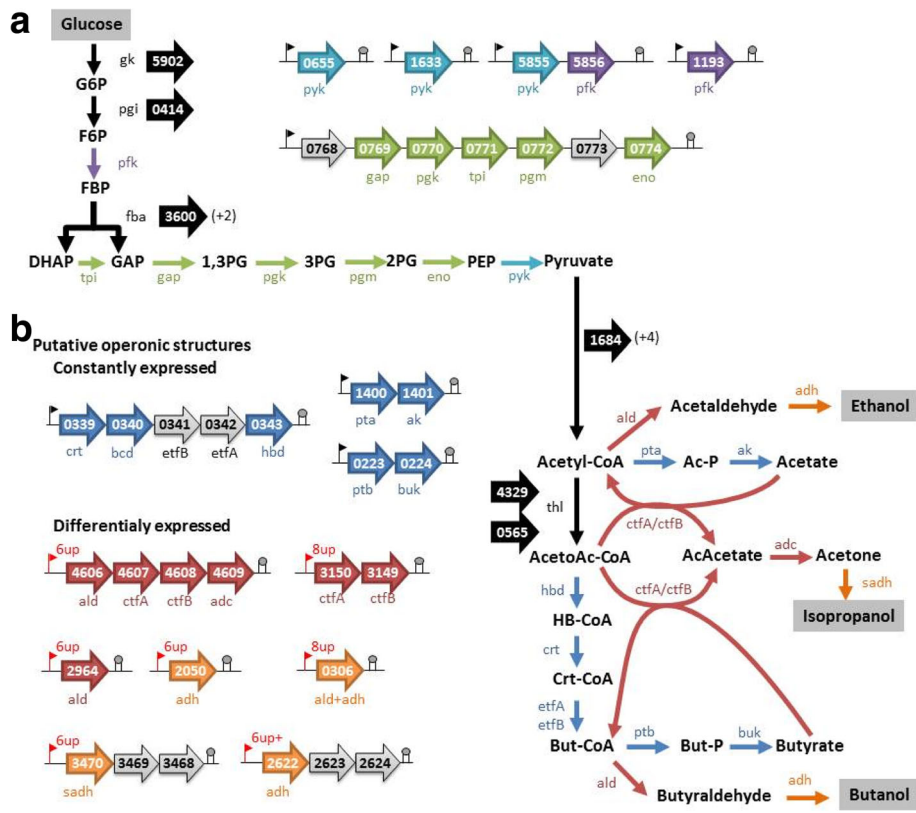


Fig. 4 Main genes and predicted operonic structures involved in the central metabolism of in *C. beijerinckii* DSM6423. **a** glycolysis; **b** acids and solvents production). Number of isozymes, predicted by Microscope tool (Genoscope, Evry, France) are indicated in brackets