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CORRECTION
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Corrigendum: Genome-Based Genetic Tool Development for *Bacillus methanolicus*: Theta- and Rolling Circle-Replicating Plasmids for Inducible Gene Expression and Application to Methanol-Based Cadaverine Production

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A Corrigendum on

Genome-Based Genetic Tool Development for *Bacillus methanolicus*: Theta- and Rolling Circle-Replicating Plasmids for Inducible Gene Expression and Application to Methanol-Based Cadaverine Production

by Irla, M., Heggeset, T. M. B., Nærdal, I., Paul, L., Haugen, T., Le, S. B., et al. (2016). Front. Microbiol. 7:1481. doi: 10.3389/fmicb.2016.01481

In the original article, there was a mistake in **Table 2** as published. The cadaverine concentrations reported were miscalculated and overestimated by 41.6%, because the HPLC standard solution consisted of "cadaverine dihydrochloride (175.1 g/mol)" and not "cadaverine (102.18 g/mol)." The corrected **Table 2** appears below.

Because of the error reported above, a correction has been made to the **Abstract**:

"*Bacillus methanolicus* is a thermophilic methylotroph able to overproduce amino acids from methanol, a substrate not used for human or animal nutrition. Based on our previous RNA-seq analysis a mannitol inducible promoter and a putative mannitol activator gene *mtlR* were identified. The mannitol inducible promoter was applied for controlled gene expression using fluorescent reporter proteins and a flow cytometry analysis, and improved by changing the −35 promoter region and by co-expression of the *mtlR* regulator gene. For independent complementary gene expression control, the heterologous xylose-inducible system from *B. megaterium* was employed

Table 2 | Fed-batch methanol fermentation production data of strains MGA3(pBV2mp-*cadA*) and MGA3 (pTH1mp-*cadA*).

Strain	CDW[a]	μ[b]	Asp[c]	Glu[c]	Ala[c]	Lys[c]	Cad[c]
	g/L	h^{-1}	g/L	g/L	g/L	g/L	g/L
MGA3(pBV2mp-*cadA*)	60.9	0.38	1.6	72.2	9.2	0.5	10.2
MGA3(pTH1mp-*cadA*)	65.5	0.45	1.5	71.8	10.2	0.0	6.5

Mean values of duplicate cultures for B. methanolicus MGA3(pBV2mp-cadA) are shown. Deviation did not exceed 10%. The MGA3(pTH1mp-cadA) data was imported from Nærdal et al. (2015). CDW, cell dry weight; μ, specific growth rate; Asp, L-aspartate; Glu, L-glutamate; Ala, L-alanine; Lys, L-lysine; Cad, cadaverine. [a]Biomass concentrations are maximum values from the stationary growth phase. [b]Specific growth rates are maximum values calculated from the exponential growth period. [c]Cadaverine and amino acid concentrations are maximum values and volume corrected.

and a two-plasmid gene expression system was developed. Four different replicons for expression vectors were compared with respect to their copy number and stability. As an application example, methanol-based production of cadaverine was shown to be improved from 6.5 to 10.2 g/L when a heterologous lysine decarboxylase gene *cadA* was expressed from a theta-replicating rather than a rolling-circle replicating vector. The current work on inducible promoter systems and compatible theta- or rolling circle-replicating vectors is an important extension of the poorly developed *B. methanolicus* genetic toolbox, valuable for genetic engineering and further exploration of this bacterium."

Additionally, a correction has been made to the **Results, Cadaverine Production From Methanol by Expression of a Heterologous Lysine Decarboxylase Gene From a Theta-Replicating Plasmid:**

"The plasmids pTH1mp and pBV2mp, containing the *mdh* promoter were used to study cadaverine production in *B. methanolicus* during fed-batch methanol fermentation. We have previously reported a methanol-based cadaverine production titer of 6.5 g/L by *B. methanolicus* MGA3 (pTH1mp-*cadA*), a strain overexpressing the lysine decarboxylase *cadA* gene from *E. coli* (corrigendum to Nærdal et al., 2015). We compared cadaverine production in the strain overexpressing *cadA* from a theta-replicating plasmid during high cell density fed-batch fermentation. The *B. methanolicus* strain MGA3 (pBV2mp-*cadA*) was tested in duplicates under comparable fermentation conditions. Samples for cadaverine and amino acid analysis, cell dry weight and OD_{600} were taken throughout the cultivation. As presented in **Table 2**, we obtained a cadaverine production titer of 10.2 g/L based on the alternative theta-replicating pBV2mp plasmid. A substantial 55% production increase compared to the previously reported (pTH1mp-*cadA*)-based strain was observed. While biomass and by-product levels were similar between the two strains, the specific growth rate of MGA3 (pBV2mp-*cadA*) was lower than that of MGA3 (pTH1mp-*cadA*) (**Table 2**)."

Lastly, in the original article, the reference for "(Nærdal et al., 2015)" was incorrectly written as "Nærdal, I., Pfeifenschneider, J., Brautaset, T., and Wendisch, V. F. (2015). Methanol-based cadaverine production by genetically engineered *Bacillus methanolicus* strains. *Microb. Biotechnol.* 8, 342–350. doi: 10.1111/1751-7915.12257".

It should be "Nærdal, I., Pfeifenschneider, J., Brautaset, T., and Wendisch, V. F. (2015). Methanol-based cadaverine production by genetically engineered *Bacillus methanolicus* strains. *Microb. Biotechnol.* 8, 342–350. doi: 10.1111/1751-7915.12257. *Microb. Biotechnol.* 2019, 12, 182-183".

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

REFERENCES

Nærdal, I., Pfeifenschneider, J., Brautaset, T., and Wendisch, V. F. (2015). Methanol-based cadaverine production by genetically engineered Bacillus methanolicus strains. *Microb. Biotechnol.* 8, 342–350. doi: 10.1111/1751-7915.12257. *Microb. Biotechnol.* 2019, 12, 182–183.