

Corrigendum: Differences in Bioenergetic Metabolism of Obligately Alkaliphilic *Bacillaceae* Under High pH Depend on the Aeration Conditions

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Differences in Bioenergetic Metabolism of Obligately Alkaliphilic *Bacillaceae* Under High pH Depend on the Aeration Conditions

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In the original article, there was a mistake in the legend for **Figure 2** as published. It described that "The acid residue-abundant segment of Glu^{25} -Lys⁴⁶ (Glu^{6} -Lys²⁷ in the processed protein base) in *S. cohnii* DSM 6307^T is indicated by green box" at L2 –L3. The correct legend appears below.

Figure 2. Amino acid sequence alignment of membrane bound cytochrome *c*-550 from *Evansella clarkii* and other alkaliphilic and neutralophilic *Bacillaceae*. Asn (N)-rich segment, Asn (N)²¹-Asn (N)⁴³ [Asn (N)⁴-Asn (N)²⁶ in the processed protein base] in the *E. clarkii* cytochromes *c* is indicated by red box. The acid residue-abundant segment of Glu²⁵-Lys⁴⁶ (Glu⁶-Lys²⁷ in the processed protein base) in *S. cohnii* DSM 6307^T is indicated by red box. N-terminal amino acid residue in processed cytochrome *c*, [Cys (C)] is indicated by blue marker. The blue boxed sequences are heme sequences representing heme-binding site and axical ligands (H and M). Acidic and basic residues are indicated by blue and red letters. Although *A. pseudofirmus* OF4 is a facultative alkaliphile, the species *A. pseudofirmus* and the presented cytochrome *c* sequence are classified in obligate alkaliphile. Although *Sporosarcina pasteurii* is an obligate alkaliphile, its cytochrome *c* sequence is similar to those in the facultative alkaliphilic strains.

In the original article, there was a mistake in **Table 2** as published. The unit for respiratory rate was incorrect. The corrected **Table 2** appears below.

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

	Growth rate (μ _{max}) ¹	Cytochrome <i>c</i> content (nmol · mg ⁻¹) ¹	ΔΨ (mV) ^{1,2}	Respiratory rate (μmol · O₂ min ⁻¹ mg ⁻¹)²	H+/0 ¹	Maximum ATP synthesis rate ² (nmol · min ⁻¹ · mg ⁻¹) ²
<i>E. clarkii</i> DSM8720 ^T Low aeration	0.36	0.89 ± 0.07	-135 ± 8	ND	0.6 ± 0.1 (6)§	ND
<i>E. clarkii</i> DSM 8720 ^T High aeration	0.42	0.36 ± 0.01	-192 ± 3	0.19 ± 0.04	2.2 ± 0.2 (6)	26.2 ± 1.7
<i>S. cohnii</i> YN-2000 High aeration	0.38	0.62 ± 0.01	-173 ± 5	0.20 ± 0.03	2.6 ± 0.3 (6)	9.6 ± 0.9
<i>B. subtilis</i> IAM 1026 Low aeration	0.26	0.18 ± 0.06	-133 ± 13	ND	2.8 ± 0.8 (6)	ND
<i>B. subtilis</i> IAM 1026 High aeration	0.55	0.21 ± 0.02	-121 ± 7	0.50 ± 0.06	4.9 ± 0.1 (6)	2.0 ± 0.6

TABLE 2 Summary for high aeration and low aeration in obligate alkaliphilic Evansella clarkii, facultative alkaliphilic Sutcliffiella cohnii, and neutralophilic Bacillus subtilis*.

*These data cited from ¹Goto (2006) and ²Goto et al. (2016).

[§]The numbers in parentheses are based on the theoretically extruded H⁺ in 1/2O₂ consumption by the respiratory chain.

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