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#### Specialty section:

This article was submitted to Food Microbiology, a section of the journal Frontiers in Microbiology

**Received:** 17 April 2019 **Accepted:** 28 May 2019 **Published:** 12 June 2019

#### Citation:

Beno SM, Orsi RH, Cheng RA, Kent DJ, Kovac J, Duncan DR, Martin NH and Wiedmann M (2019) Corrigendum: Genes Associated With Psychrotolerant Bacillus cereus Group Isolates. Front. Microbiol. 10:1323. doi: 10.3389/fmicb.2019.01323

## REFERENCES

# **Corrigendum: Genes Associated With Psychrotolerant** *Bacillus cereus* **<b>Group Isolates**

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Keywords: Bacillus cereus, whole genome sequencing, psychrotolerant, spoilage, skim milk broth

#### A Corrigendum on

#### Genes Associated With Psychrotolerant Bacillus cereus Group Isolates

by Beno, S. M., Orsi, R. H., Cheng, R. A., Kent, D. J., Kovac, J., Duncan, D. R., et al. (2019). Front. Microbiol. 10:662. doi: 10.3389/fmicb.2019.00662

In the original article, there were two minor mistakes in **Figure 3** as published. The isolate FSL H8-0534 was mistakenly labeled as a clade VI isolate. We have updated the figure to demonstrate that this isolate is a clade I isolate. Additionally, isolate FSL M7-1219 had an additional "0" in the number sequence. The corrected **Figure 3** appears below.

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.

Kovac, J., Miller, R. A., Carroll, L. M., Kent, D. J., Jian, J., Beno, S. M., et al. (2016). Production of hemolysin BL by *Bacillus cereus* group isolates of dairy origin is associated with whole-genome phylogenetic clade. *BMC Genomics* 17:581. doi: 10.1186/s12864-016-2883-z Copyright © 2019 Beno, Orsi, Cheng, Kent, Kovac, Duncan, Martin and Wiedmann. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.



FIGURE 3 | Phylogenetic tree constructed from the core SNPs identified in the genomes of 23 *B. cereus* isolates. The maximum likelihood tree was constructed using a general time-reversible (GTR) model with gamma-distributed sites and 1,000 bootstrap repetitions. Roman numerals in parentheses represent the phylogenetic clade of the isolate, as defined previously (Kovac et al., 2016). QTC clusters representing isolates with similar growth patterns in BHI and SMB at 6°C (see Figure 1A) are mapped onto the phylogenetic tree. Isolates shown in red represent QTC cluster 1 isolates (non-psychrotolerant in BHI broth or SMB). Isolates shown in green represent QTC cluster 2 isolates (psychrotolerant in BHI broth but not SMB), and isolates shown in blue represent clade 3 isolates (psychrotolerant in both BHI broth and SMB). One isolate (FSL M7-0109) did not cluster with other isolates, and is therefore shown in black font. Numbers at branch points represent bootstrap values; only bootstrap values >70 are shown.