

Accepted Manuscript

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PII: S0168-1605(16)30220-3
DOI: doi: [10.1016/j.ijfoodmicro.2016.05.011](https://doi.org/10.1016/j.ijfoodmicro.2016.05.011)
Reference: FOOD 7227

To appear in: *International Journal of Food Microbiology*

Received date: 10 September 2015
Revised date: 24 February 2016
Accepted date: 8 May 2016



Please cite this article as: Schmid, Daniela, Rademacher, Corinna, Kanitz, Elisabeth Eva, Frenzel, Elrike, Simons, Erica, Allerberger, Franz, Ehling-Schulz, Monika, Elucidation of enterotoxigenic *Bacillus cereus* outbreaks in Austria by complementary epidemiological and microbiological investigations, 2013, *International Journal of Food Microbiology* (2016), doi: [10.1016/j.ijfoodmicro.2016.05.011](https://doi.org/10.1016/j.ijfoodmicro.2016.05.011)

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Elucidation of enterotoxigenic *Bacillus cereus* outbreaks in Austria by complementary epidemiological and microbiological investigations, 2013

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Abstract

Identifying *Bacillus cereus* as the causative agent of a foodborne outbreak still poses a challenge. We report on the epidemiological and microbiological investigation of three outbreaks of food poisoning (A, B, and C) in Austria in 2013. A total of 44% among 32 hotel guests (A), 22% among 63 employees (B) and 29% among 362 residents of a rehab clinic (C) fell sick immediately after meal consumption. *B. cereus* isolated from left overs or retained samples from related foods were characterized by toxin gene profiling, and molecular typing using *panC* sequencing and M13-PCR typing (in outbreak A and C). We identified two *B. cereus* strains in outbreak A, and six *B. cereus* strains, each in outbreak B and C; we also found *Staphylococcus aureus* and staphylococcal enterotoxins in outbreak A. The *panC* sequence based phylogenetic affiliation of the *B. cereus* strains, together with findings of the retrospective cohort analyses, helped determining their etiological role. Consumption of a mashed potatoes dish in outbreak A (RR: ∞), a pancake strips soup in outbreak B (RR 13.0; 95%CI 1.8-93.0) and of a fruit salad (RR 1.5; 95% CI 1.09-2.00) and deer ragout (RR: 1.99; 95%CI 1.23-3.22) were associated with increased risk of falling sick.

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