

AUTHOR'S CORRECTION

Multi-Virulence-Locus Sequence Typing Identifies Single Nucleotide Polymorphisms Which Differentiate Epidemic Clones and Outbreak Strains of *Listeria monocytogenes*

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Volume 45, no. 3, p. 835–846, 2007. In this article, isolate BL0027 was identified as a nonoutbreak isolate, and the sequencing analysis also clustered this isolate into nonoutbreak clusters (Table 1 and Fig. 1). Recently obtained information revealed that BL0027 was an isolate associated with the pâté outbreak in the United Kingdom in 1989. A reexamination of the original sequences of BL0027 and a resequencing of *inlB* revealed that in the original article, an extra nucleotide was mistakenly inserted close to the end of the *inlB* loci, which caused a shift in the rest of the nucleotides. After correcting this error, we found that the sequence type of BL0027 is identical to that of the isolates from the pâté outbreak and therefore that BL0027 should be identified as part of epidemic clone IV. In addition, isolate BL3102 (Table 1) was isolated from one sporadic case in the United States in 1989 and thus is not part of an outbreak.