

CORRECTION

Correction: A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enteroaggregative Hemorrhagic *Escherichia coli* O104:H4

The PLOS ONE Staff

The Acknowledgments section is incomplete. The correct Acknowledgments should appear as follows: We thank Aaron Darling and Hatch Stokes for their comments on an early draft of this manuscript.

The image for Fig 2 is incorrect. The publisher apologizes for the error. Please see the corrected Fig 2 here.



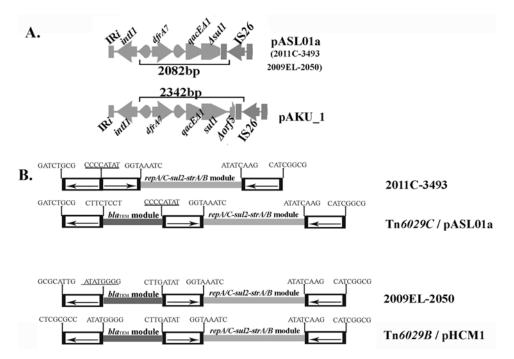
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**Fig 2. Molecular signatures created by the insertion of IS26.** A: The 3´-CS of class 1 integrons in pASL01a and pAKU\_1 has been structurally modified by different IS26-mediated deletion events such that PCR with L1 and JL-D2 primers is expected to generate 2082 and 2342 bp long amplicons respectively. B: Eight base pair signature sequences created by the insertion of IS26 found flanking the inverted repeats of IS26 elements clearly suggest that the CRL in strain 2011EC-3493 is a derivative of Tn6029C while 2009—2050 is a derivative of Tn6029B described previously in pHCM1. The eight base repeat on the left end of Tn6029B and that in 2009EL-2050 are different because in pHCM1 (Tn6029B) there is a deletion of the class 1 integron whereas in 2009EL-2050 the fragment adjacent to the left hand end of the insertion site is inverted by IS26-mediated events. These signatures are also consistent with the proposition that Tn6029C evolved from Tn6029B.

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## Reference

 Chowdhury PR, Charles IG, Djordjevic SP (2015) A Role for Tn6029 in the Evolution of the Complex Antibiotic Resistance Gene Loci in Genomic Island 3 in Enteroaggregative Hemorrhagic Escherichia coli O104:H4. PLoS ONE 10(2): e0115781. doi: 10.1371/journal.pone.0115781 PMID: 25675217