

## AUTHOR'S CORRECTION

### *Escherichia coli* O157:H7 Shiga Toxin-Encoding Bacteriophages: Integrations, Excisions, Truncations, and Evolutionary Implications

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Volume 185, no. 12, p. 3596–3605. Page 3597: Table 1 erroneously designated *wrbA* as being occupied by a bacteriophage in the sorbitol-fermenting strains CB2755 and 493/89, whereas it is, in fact, intact (as demonstrated in Fig. 1). Therefore, the *stx*<sub>2</sub> bacteriophage integrated into a site or sites other than *wrbA* in these isolates. Thus, our assumptions that these sorbitol-fermenting organisms diverged from other members of the STEC1 lineage after the *stx*<sub>2</sub> bacteriophage integrated into *wrbA* and that integration of the *stx*<sub>2</sub> bacteriophage into *wrbA* is an ancestral event are not supported by the data. The corrected data, which suggest that the *stx*<sub>2</sub> bacteriophage inserted into *wrbA* at a later point in the evolution of the STEC1 clade after a truncated bacteriophage was acquired by *Escherichia coli* O157:H7, lead to a simpler evolutionary scenario which obviates the need to invoke lineages A, B, and C (see the revised Fig. 4 shown below).

Page 3600: The *stx*<sub>1A</sub> and *stx*<sub>1B</sub> labels in Fig. 2 were reversed.

Page 3603: Figure 4 and its legend should appear as shown below.

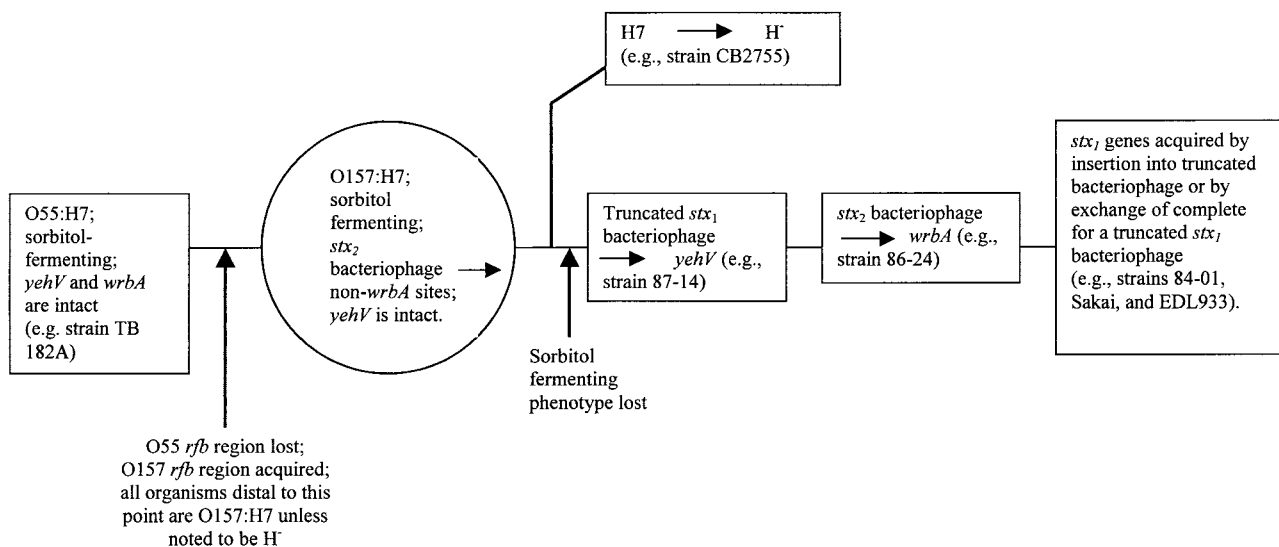


FIG. 4. Proposed evolutionary scenario for the STEC1 clade. Boxes represent organisms known to exist today. The circle represents a proposed intermediate organism between *E. coli* O55:H7 and *E. coli* O157:H7.