Correction

MICROBIOLOGY. For the article "*Yersinia pestis*, the cause of plague, is a recently emerged clone of *Yersinia pseudotuberculosis*" by Mark Achtman, Kerstin Zurth, Giovanna Morelli, Gabriela Torrea, Annie Guiyoule, and Elisabeth Carniel, which appeared in number 24, November 23, 1999, of *Proc. Natl. Acad. Sci. USA* (**96,** 14043–14048), the authors note the following correction. In describing the homologies among sequences of housekeeping gene fragments from *Yersinia pestis*, *Yersinia pseudotuberculosis*, and *Yersinia enterocolitica*, the *thrA*, *trpE*, and *manB7* sequences reported from *Y. enterocolitica* were incorrect and are from residual *Escherichia coli* DNA contaminating the *Taq* polymerase used for PCR amplification. The *thrA* and *trpE* alleles now have been sequenced by using a combination strategy of inverse PCR and subcloning, and the correct sequences have been deposited in the GenBank database under the accession nos. AJ250241, AJ270409, and AJ288275-AJ288285. We have been unable to sequence the *manB* allele from strains formerly reported as possessing *manB7* and have removed the GenBank entry AJ270447. As a result of these new data, several statements in the publication need correcting.

Seven different alleles of *thrA* and five alleles of *trpE* were found among the 13 strains of *Y. enterocolitica* that were tested (Table 1). Formerly, we concluded that *thrA* and *trpE* were homogeneous in *Y. enterocolitica*. Instead, the mean genetic distances between these alleles within *Y. enterocolitica* and between *Y. pestis* and *Y. enterocolitica* are comparable or slightly higher than those described previously (1) for *glnA*, *tmk*, or *dmsA* (Table 2). The data from these five genes allow estimating the date of separation between *Y. pestis* and *Y. enterocolitica* to be 42–187 million years. We have confirmed that the other sequences described previously are correct. None is related to *E. coli* sequences or to those of other bacteria with which we have worked. We also resequenced all six genes from 23 representative strains of *Y. pestis* and *Y. pseudotuberculosis* and did not find any differences from those reported previously. Thus, the conclusions regarding the relationships between *Y. pestis* and *Y. pseudotuberculosis* remain unchanged, as are the proposals for their evolutionary history.

Table 1. Alleles of three gene fragments in *Y. enterocolitica*

IP number	*thr A*	*trpE*	*manB*
383	6	4	10
21349	9	4	10
21650	6	5	10
864	8	4	
21699	8	4	
134	8	4	
885	8	4	
24636	8	4	
25963	12	9	9
21708	10	6	
21506	11	6	9
Ye8081	7	8	8
WA	7	7	8

IP number, Institut Pasteur strain designation. Empty cells indicate the lack of data.

Table 2. Mean percent pairwise differences at synonymous (% D_S) and nonsynonymous (% D_N) sites of three gene fragments

Gene (size)	Distance	*enterocolitica* (13)*	pe→ent
thrA (393 bp)	% D_S	12.2 (0–40)	154 (144–176)
	% D_N	0.3 (0–1)	1.5 (1.0–2.2)
trpE (351 bp)	% D_S	3.7 (0–8.4)	146 (136–177)
	% D_N	<0.06	3.0 (2.9–3.1)
manB (442 bp)	% D_S	154 (0–289)	>100
	% D_N	14 (0–24)	16 (13–20)

pe, *Y. pestis*; ent, *Y. enterocolitica*.

*The number of strains is indicated in parentheses after the species designation.

1. Achtman, M., Zurth, K., Morelli, G., Torrea, G., Guiyoule, A. & Carniel, E. (1999) *Proc. Natl. Acad. Sci. USA* **96,** 14043–14048.