

CORRIGENDUM

In the paper by R. MILKMAN and M. MCKANE BRIDGES (*GENETICS* **126**: 505–517; November, 1990) entitled “Molecular evolution of the *Escherichia coli* chromosome. III. Clonal frames,” the following corrections should be noted. Starting on page 506, column 1, the last paragraph should begin, “It appears that a clone may be able to spread worldwide in as few as 1.3×10^6 generations. We now estimate, as will be described, a recombination rate of 7×10^{-12} replacements per bp per generation, or about 3×10^{-5} per genome per generation (at about 4.7×10^6 bp/genome). In 0.33×10^6 generations, then, an individual genome will acquire an average of 10 replacements . . . The importance of the size of these replacements becomes clear after 3.3×10^6 generations . . . In the case of a clone whose origin was about 13×10^6 generations ago, an average replacement size of 10^5 bp would leave the average clonal frame composing about e^{-8} , or 0.03% of the genome. . . .”

On page 507, the scale in Figure 3 should read “ 3×10^5 bp” and the legend should begin, “A 3×10^5 -bp stretch of chromosome, assuming 7×10^{-12} replacements per bp per generation, 10^6 generations after the origin of a clone.” The scale in Figure 4 should read “ 3×10^4 bp” and the legend should read, “A shorter (3×10^4 bp) stretch after a longer period of time (10^7 generations), otherwise as in Figure 2.”

On page 514, Table 7, the four decimal entries in the second column headed “Estimated age (gen.)” should be reduced threefold to read 1.3, 1.5, 1.3 and

0.7. In the second column of text on page 514, the value “ 5×10^{-12} ” in lines 16 and 18–19 should read “ 7×10^{-12} .”

Starting on page 515, column 1, the last paragraph should read, “The cumulative recombination rate, r_c , is the product of the recombinational replacement rate per nucleotide per generation, r_r , and the number of generations, g , since divergence. For a pair of compared sequences, divergence time is calculated as

$$\begin{aligned} g &= (1/4k')\ln[X_e/(X_e - X_o)] \\ &= (1/4k')\ln[0.167/(0.167 - X_o)], \end{aligned}$$

where k' is the retained nucleotide substitution rate per generation for those nucleotides having neutral alternatives. The proportion of nucleotide differences expected at equilibrium in translated DNA is taken to be $1/3 \times 1/2 = 1/6$, or 0.167, assuming that an average 1/3 of all nucleotides have an average of one neutral alternative, so that half of these nucleotides will differ in any pairwise comparison at equilibrium (MILKMAN and STOLTZFUS 1988; note that $0.5/\text{codon} = 0.167/\text{nucleotide}$). X_e is the proportion of nucleotide differences expected at equilibrium and X_o is the proportion of nucleotide differences. For the K12 level II clone, whose members' average substitution frequency of 5×10^{-4} must be doubled to give pairwise divergence, the divergence time comes to 1.5×10^7 generations.”