TABLE 1 The frequency of Cm^r reversion mutations

	pBR325, natural orientation		pBR523, *CAT* gene reversed	
	Plasmid	Reversion frequency	Plasmid	Reversion frequency
p1	pBR325p1	$44\times10^{-9}\pm 20\times10^{-9}$	pBR523p1	$2.0\times10^{9}\pm 0.9\times10^{-9}$
n1	pBR325n1	$3.7\times10^{-9}\pm 0.9\times10^{-9}$	pBR523n1	$2.7\times10^{-9}\pm 0.9\times10^{-9}$

To determine reversion frequencies, 25 ml of *E. coli* DH5 containing the plasmids were grown to a density of 5×10^{8} cells ml^{-1} in K medium containing 10 $\mu g\ ml^{-1}$ tetracycline from 1 ml of an overnight culture. Reversion frequencies are the number of Cm^r cells in the population, which is determined by plating a known number of cells on Luria plates containing tetracycline and chloramphenicol (25 $\mu g\ ml^{-1}$ each). Total viable cells were determined by plating on medium containing tetracycline. The frequency represents the average of 6–8 to individual experiments in which the variation between experiments was typically within a factor of two. Analysis of plasmid copy number showed no detectable difference for any of these plasmids. The structure of the revertants was determined by digestion with *Eco*RI and analysis of the 129-bp *Alu*I fragment, which contained the *Eco*RI site, to establish the size of the deletion to within about 2 bp. The DNA sequence of the region was determined for several revertants from each deletion insert. In >95% of the revertants examined for pBR325p1 (and n2 and p4 inserts) complete deletion of the insert and one copy of the direct repeat occurred. For the n1 plasmids and pBR523p1 the revertants consisted of complete deletions in addition to some revertants which have not completely deleted the insert. We examined 12–24 independent revertants for each plasmid.

frequency was about 10–20-fold lower, or $2\text{–}3.7\times10^{-9}$, consistent with the interpretation that misalignment stabilized by a hairpin has a higher reversion frequency than misalignment in which a loop is formed. Analysis of other inserts provides additional evidence in support of this interpretation (T.Q.T. and R.R.S., manuscript in preparation). Based on these results, if deletion between direct repeats occurred preferentially on the lagging strand, pBR325p1 should have a higher reversion frequency than pBR523p1. The results suggest that misalignment leading to deletion may occur preferentially in the lagging strand and its template.

Although our results are consistent with differential mutagenesis in the leading and lagging strands, we cannot exclude the possibility that differences in reversion frequencies are due to differences in the effects of orientation of these sequences on homologous or illegitimate recombination, or aberrant repair of spontaneous damage. As reversions frequencies were measured in *rec*A^- strains homologous recombination should be minimal and there seems no reason to expect different rates of recombination in the insert when the whole gene is reversed. In addition, if such differences did exist, they might be expected to be seen with all deletion inserts. The correlation of deletion frequencies with potential for the formation and stability of possible replication intermediates therefore strongly supports the hypothesis that the observed deletion events are the result of replication errors (T.Q.T and R.R.S., manuscript in preparation).

Eukaryotic cells repair DNA damage in active genes more efficiently than in inactive genes[10]. In addition, a preference for repair of the transcribed strand has been demonstrated in both *E. coli*[11] and eukaryotic cells[12]. As asymmetric DNA replication complexes are involved in eukaryotes[13] and prokaryotes[6] a difference in the rate of spontaneous mutagenesis in different strands might not be unexpected. An initial investigation did not reveal a large difference in the fidelity of misincorporation during DNA replication in an *in vitro* HeLa cells system[14]. Our results present the first evidence for differential mutagenesis in the leading or lagging strand of *E. coli*. □

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ERRATUM

Homozygous prion protein genotype predisposes to sporadic Creutzfeldt–Jakob disease

Mark S. Palmer, Aidan J. Dryden, J. Trevor Hughes & John Collinge

Nature **352,** 340–342 (1991)

IN this letter in the 25 July issue, the sentence beginning in line 1 on page 341 should read: "Of the 22 CJD cases, 16 were homozygous for Met 129, 5 homozygous for Val 129 and only one was a heterozygote, while of the suspected CJD cases, 13 were Met-129 homozygotes, 4 were heterozygotes and 6 were Val-129 homozygotes." The published version incorrectly referred to 11 Met-129 homozygotes.

CORRECTION

Novel myosin heavy chain encoded by murine *dilute* coat colour locus

John A. Mercer, Peter K. Seperack, Marjorie C. Strobel, Neal G. Copeland & Nancy A. Jenkins

Nature **349,** 709–713 (1991)

WE have discovered frameshift errors made in the assembly of our published cDNA sequence affecting only the region of nucleotides 1138–1180, corresponding to amino acid residues 367–379. The correct sequence is available on the EMBL database under accession number X57377, release 28. These errors do not affect the conclusions of the paper in any way. We thank D. Cheney, E. Espreafico, R. Larson, and M. Mooseker for sharing unpublished sequence data.