

**Correction.** In the article "Polymorphism and evolution of *Alu* sequences in the human low density lipoprotein receptor gene" by Helen H. Hobbs, Mark A. Lehrman, Tokuo Yamamoto, and David W. Russell, which appeared in number 22, November 1985, of *Proc. Natl. Acad. Sci. USA* (82, 7651-7655), the following correction should be noted. On p. 7654, in the nucleotide sequences in the right-hand column, the vertical lines to indicate nucleotide identities were absent from the published version. The correct sequences and the related text are reproduced here.

The occurrence of homology in the non-*Alu* sequences of the human and bovine 3' untranslated mRNAs allowed us to examine further the genetic events giving rise to the *Alu* cluster in exon 18 (Fig. 6). The first *Alu* sequence in this cluster is flanked by imperfect direct repeats of 15 nucleotides (7). At position 1143 of the bovine sequence a stretch of 15 nucleotides begins; 11 of these 15 nucleotides are identical with the direct repeats flanking *Alu* 1 (Fig. 6). The sequences of the left direct repeat and its cognate in the bovine sequence are as follows, with identities indicated by vertical lines:

```
Human (3686-3700) AAAACATGCACGGTG
                   ||| ||| ||| ||| ||| ||| ||| ||| |||
Bovine (1143-1157) GAAACATGCATGGCA.
```

The human *Alu* 1 and *Alu* 2 sequences are separated by a 23-nucleotide spacer (7). Between positions 1169 and 1190 of the bovine sequence, 13 of the 23 nucleotides match with this spacer region (Fig. 6). The sequences and their identities are as follows:

```
Human (4026-4048) CATCAGCAGCCCATGGCCTCTGG
                   | | | | | | | | | | | | | | |
Bovine (1169-1190) TAAGATGTGCTC-TGGGCTCGGG.
```

Finally, immediately distal to the *Alu* 3 sequence in the human exon 18 cluster are 15 nucleotides, of which 12 match with those occurring between positions 1193 and 1206 of the bovine sequence (Fig. 6). The two sequences are as follows:

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Human (4513-4527) TTTGACGGGACTTCA
                   ||| ||| ||| ||| ||| ||| ||| ||| |||
Bovine (1193-1206) TTTCATGGGA-TTCA.
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These homologies, in a contiguous stretch of 64 nucleotides in the cow, suggest that the events which led to the *Alu* sequences in the 3' untranslated region of the human mRNA may have occurred in two discrete steps (see *Discussion*).

**Correction.** In the article "Association of 16S and 23S ribosomal RNAs to form a bimolecular complex" by D. P. Burma, B. Nag, and D. S. Tewari, which appeared in number 16, August 1983, of *Proc. Natl. Acad. Sci. USA* (80, 4875-4878), the authors request that the following correction be noted. In the Introduction, the following paragraph should be inserted after paragraph 1.

Moller and Boedtger (25) have obtained evidence for complex formation between 16S and 23S RNAs and similar observations have been made by others (26-28).

The following references should be added.

25. Moller, W. & Boedtger, H. (1962) *Acides ribonucleiques et polyphosphates* (Centre National de la Recherche Scientifique, Paris), pp. 99-121.
26. Marcot-Queiroz, J. & Monier, R. (1965) *J. Mol. Biol.* **14**, 490-505.
27. Hayes, D. H., Hayes, F. & Guerin, M. F. (1966) *J. Mol. Biol.* **18**, 499-515.
28. Moore, P. B. & Asano, K. (1966) *J. Mol. Biol.* **89**, 21-37.