Corrigenda

Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

by Burton D. Clark, Kathleen L. Collins, Melinda S. Gandy, Andrew C. Webb and Philip E. Auron

Nucleic Acids Research, 14, 7897–7914 (1986)

The legend to Figure 7 should be corrected as follows:

Figure 7. Southern blot analysis of Hind III restriction fragments of human genomic DNA derived from different cell sources which hybridize to radio-labeled proIL-1β cDNA. DNA samples in each lane are: (1) bacteriophage clone BDC-454, (2) placenta, (3) HeLa, (4) U937, (5) THP-1, (6) monocyte, (7) leukocyte, (8) Colo 16. The BDC-454 clone was digested with both Hind III and Sal I to remove the genomic insert from the λ vector sequence. The sizes of fragments are indicated in kilobase pairs.

These corrections do not alter the conclusions of the paper.

In each of the following papers there was an error in paragraph 1. The corrected versions are reprinted below:

Sequence of the rbcL gene for the large subunit of ribulose bisphosphate carboxylase-oxygenase from petunia

by Jane Aldrich, Barry Cherney, Ellis Merlin and Jeff Palmer

Nucleic Acids Research, 14, 9534 (1986)

The sequence of the chloroplast-encoded rbcL gene from Petunia hybrida cv. Mitchell is shown compared to tobacco (1). Petunia and tobacco share 97.3% nucleotide sequence homology in the coding region as well as in the 5' flanking region. The 3' flanking region is identical to tobacco except for a 21 bp insertion in tobacco. Of the amino acid changes, (13/477; 97.3% homology) 46% are non-conservative. The second ATG (+1) in the open reading frame is the probable translation start site (2, 3).

Sequence of the rbcL gene for the large subunit of ribulose bisphosphate carboxylase-oxygenase from alfalfa

by Jane Aldrich, Barry Cherney, Ellis Merlin and Jeff Palmer

Nucleic Acids Research, 14, 9535 (1986)

The sequence of the chloroplast-genome encoded rbcL gene from Medicago sativa cv. Regen S is shown compared to pea (1). Alfalfa shares 94.1% nucleotide sequence homology with pea for 1721 bases spanning the gene beginning 213 bases upstream of the coding sequences through 88 bases into the 3' flanking region ending at position 1888. Pea sequences are highly divergent from alfalfa after this point. The deduced amino acid sequence is 94.3% homologous to that of pea, with 50% (15/27) of the substitutions non-conservative. The second ATG codon (+1) in the open reading frame is the probable translation start site (2, 3).