**Biochemistry.** In the article "Cloning and sequence analysis of the rat augmenter of liver regeneration (ALR) gene: Expression of biologically active recombinant ALR and demonstration of tissue distribution" by Michio Hagiya, Antonio Francavilla, Lorenzo Polimeno, Izumi Ihara, Harumi Sakai, Tatsuya Seki, Manabu Shimonishi, Kendrick A. Porter, and Thomas E. Starzl, which appeared in number 17, August 16, 1994, of *Proc. Natl. Acad. Sci. USA* (**91,** 8142–8146), the authors would like to correct the nucleotide sequence of rat ALR cDNA exhibited in Fig. 2. In supplementary experiments, an additional G has been found in position 266; A has been shifted to position 267 and subsequent nucleotides have been advanced by one. The revised sequence is as follows:

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CGCGCGCTGG CGGTGGCATG CGCGCTGCTC TGTCCCGTCT CCTGCACGCC CTCTTGGCCC    60

CGCTGCTCGT ACGCCAGCAA TATGGCGGCG CCCAGCGAAC CCGCAGGTTT CCCTCGCGGC   120

AGTCGCTTCT CCTTCCTGCC GGGCGGCGCG CACTCGGAGA TGACCGACGA CCTGGTGACT   180

GACGCGCGGG GCCGCGGCGC AAGGCATAGA AAAGACAACG CCCCTGCCGC GGCCCCGGCG   240

CCGAAAGGTT TGGAGCACGG GAAGCGACCG TGCCGGGCCT GCGTGGACTT CAAGTCGTGG   300

ATGCGGACCC AGCAGAAGCG GGACATCAAG TTTAGGGAGG ACTGTCCACA GGATCGGGAA   360
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FIG. 2 Nucleotide sequence of rat ALR cDNA and the deduced amino acid sequence. Amino acid residues are numbered below the sequence; nucleotide positions are numbered on the right. Chemically determined peptide sequences are underlined. The poly(A) additional signal is indicated with a double underline.

The underlined boldface G is the additional G; the ATG initiation sites are underlined. The added nucleotide does not change the results of the recombinant ALR protein of 125 amino acids that was originally characterized. However, the additional G generates two other in-frame ATG initiation sites, which are 5′ to the initiation site of the ALR protein previously reported, thus raising the possibility of other ALR variants ("long forms"). The correction has been made in the GenBank data base (accession no. D30735).

**Evolution.** In the article "DNA sequence support for a close phylogenetic relationship between some storks and New World vultures" by John C. Avise, William S. Nelson, and Charles G. Sibley, which appeared in number 11, May 24, 1994, of *Proc. Natl. Acad. Sci. USA* (**91,** 5173–5177), the authors request that the following error be noted. The mtDNA sequence from the sample denoted as "Jabiru Stork" is incorrect, the mistake apparently stemming from a sample mix-up, mislabel, or PCR error. Reexamination of bona fide Jabiru Stork mtDNA sequences by our laboratory (and independently confirmed elsewhere) now places this species closest phylogenetically to the Wood Stork and Marabou Stork (among the species assayed). We wish to alert readers to this change and to retract all conclusions regarding the Jabiru Stork from the original paper. This finding weakens but does not overturn the suggestion that the New World vultures are more closely related to the storks than to the Old World vultures. The corrected Jabiru Stork sequence has been deposited in GenBank (accession number U19611).

**Biochemistry.** In the article "Functional chicken gizzard heavy meromyosin expression in and purification from baculovirus-infected cells" by Hirofumi Onishi, Kayo Maéda, Yuichiro Maéda, Akihiro Inoue, and Keigi Fujiwara, which appeared in number 3, January 31, 1995, of *Proc. Natl. Acad. Sci. USA* (**92,** 704–708), the following note should be added.

While our paper was under review, a publication by Trybus (30) appeared that reported essentially the same results and used the same methods.

30. Trybus, K. M. (1994) *J. Biol. Chem.* **269,** 20819–20822.

**Biochemistry.** In the article "*crnA* encodes a nitrate transporter in *Aspergillus nidulans*" by S. E. Unkles, K. L. Hawker, C. Grieve, E. I. Campbell, P. Montague, and J. R. Kinghorn, which appeared in number 1, January 1, 1991, of *Proc. Natl. Acad. Sci. USA* (**88,** 204–208), the authors request that the following correction be noted. Due to a processing error, the 5′ end of the third intron was incorrectly determined, which resulted in a frameshift beyond intron 3 in the protein sequence in Fig. 3 (p. 206). The DNA sequence is correct, but the last 34 amino acid residues of the published deduced protein sequence are incorrect. The protein is 24 residues longer than previously reported—i.e., 507 amino acids long—and contains 12 putative membrane-spanning regions instead of 10 as shown in Figs. 5 and 6 (p. 207). The deduced protein sequence has been amended accordingly (now assigned GenBank accession no. M61125). The authors thank B. G. Forde (IACR–Rothamsted, Harpenden, U.K.) for pointing out this error.