CORRECTIONS

Cloning and Expression of Complementary DNAs for Multiple Members of the Human Cytochrome P450IIC Subfamily, by Marjorie Romkes, Michael B. Faletto, Joyce A. Blaisdell, Judy L. Raucy, and Joyce A. Goldstein*, Volume 30, Number 13, April 2, 1991, pages 3247–3255.

The sequence of clones 6b and 29c (two alleles of 2C18) differs from that originally reported by a TA → AT at positions 5–6 (coding for an Asp rather than Val at positon 2) and by the addition of a C at position 1413 and the deletion of a G at position 1433 (corrected sequence: ^{1408}ACCCCCATTGCCAATGCATTTGGTCGT^{1434}). The corrected amino acid sequence reads ^{472}IleAlaAsnAlaPheGlyArg^{478}. In the noncoding region of these clones, we found four A's instead of three at positions −50 to −53 in the 200-base 5′-leader of clone 29c and several sequencing errors in the 3′-region of 6b. The sequences of 2C18 (29c and 6b) have been corrected in Genbank (Accession Numbers M61856 and M61853, respectively).

There were four errors in the coding region of clone 11a (2C19) which have been corrected in Genbank (Accession Number M61854). The corrections are an A → G at position 782 (Gln^{261} → Arg), a G → A at position 857 (Ser^{286} → Asn), a GC → CA at positions 902–903 (Ser^{301} → Thr), and an AC → GA at positions 1250–1251 (Asp^{417} → Gly). In the 3′-noncoding region, a T should be added between two G's at position 1601; there is a change from five to six A's at positions 1620–1626 and from three to four C's at positions 1654–1657. Our two 2C9 clones (65 and 25) were resequenced in areas of known allelic variations. The silent difference reported between the clones at base 840 did not exist. Both clones contained a T at this position. The sequence of clone 65 (Accession Number M61857) has been corrected in Genbank.

In resequencing a partial cDNA clone, 254c, we found that we had erroneously classified it as a separate gene, 2C17 (Romkes et al., 1991). Several gels contained ambiguous sequences, and a new primer, 11a.270R, read through what appeared to be a junction between two clones at bp 169. Sequence comparisons indicated that the reverse sequence from 260 to 169 was identical to 2C19, but the sequence then continued from base pair 1291 through 1235 of 2C18. Therefore, it appeared likely that 254c was a composite clone containing two similar sequences with overlapping information. We therefore selected a *Dra*III site present at bp 490 in both 2C18 and 2C19 and subcloned two nonoverlapping fragments. The first was a 1.1-kb *Dra*III fragment presumably containing 2C18 from bp 490 to bp 1291 and continuing with 2C19 through bp 490. The remainder of the clone which was thought to contain a 1.1-kb 2C19 insert from bp 490 to the 3′-end of the clone was religated and sequenced. The 5′-end of the original clone was read with the Bluescript KS primer. Sequencing of these fragments confirmed that the 5′-end of 254c was part of a 2C18 cDNA, beginning at bp 361 and continuing through bp 1291. At bp 1291, the sequence switched to that of 2C19 beginning at bp 169 and continuing through bp 1632. Base pair 169 marks the beginning of exon 2 in rabbit 2C1, 2C2, 2C3, and 2C4, while base pair 1290–1293 represents the end of exon 8 in rabbit 2C3 and 2C5 [Chan, G., & Kemper, B. (1990) *Biochemistry 29*, 3743–3750]. Clone 254c may have originated as a transcript of a pseudogene, a hybrid gene, from erroneous splicing of a composite 2C18/2C19 pre-mRNA transcript or by intermolecular splicing between two separate transcripts (*trans*-splicing). There were two allelic differences between the 2C18 sequence and the previously published clones: at base pair 387 a G → A change, which resulted in a coding change of a Met^{129} → Ile^{129}, and a change in a G → A at bp 1004, which changed Arg^{335} → Gln^{335}. There was also one allelic difference between the 2C19 portion of 254c and the previously reported sequence of 2C19 at bp 991, A → G changing Ile^{331} → Val^{331}. The erroneous sequence was deleted from Genbank (previously Accession Number M61858) and the corrected sequence of the composite 254c cDNA given a new Accession Number (L07093).

Annexin I-Mediated Vesicular Aggregation: Mechanism and Role in Human Neutrophils, by Paul Meers,* Tanya Mealy, Nellie Pavlotsky, and Alfred I. Tauber, Volume 31, Number 28, July 21, 1992, pages 6372–6382.

Page 6379. In the first paragraph of the Discussion, Goldstein et al., 1984, should read Goldstein et al., 1974.

Page 6381. The following references should be included:

Gennaro, R., Pozzan, T., & Romeo, D. (1984) *Proc. Natl. Acad. Sci. U.S.A. 81*, 1416–1420.

Goldstein, I. M., Korn, J. K., Kaplan, H. B., & Weissman, G. (1974) *Biochem. Biophys. Res. Commun. 60*, 807–812.

Naccache, P. H., Volpi, H., Showell, H. J., Becker, E. L., & Sha'afi, R. I. (1979) *Science 203*, 461–463.