Additions and Corrections


Identification of a peroxisome proliferator-responsive element upstream of the human peroxisomal fatty acyl coenzyme A oxidase gene.

Usha Varanasi, Ruoyin Chu, Qin Huang, Raquel Castellon, Anjana V. Yeldandi, and Janardan K. Reddy

We have recently become aware of the possibility that the peroxisome proliferator-responsive element (PPRE) sequence of human peroxisomal fatty acyl-CoA oxidase (ACOX) gene we reported (AGGTCA C TGGTCA), which is a direct repeat of hexamer half-sites interspersed by a single nucleotide (DR1 motif), may be a mutant version. This raised questions about possible polymorphism in the PPRE, and more importantly regarding the validity or applicability of the results we obtained with a possible mutant sample, to extrapolate species sensitivity and responsiveness to peroxisome proliferators. To clarify this, we resequenced the promoter region (−2015 to −1725) shown in Fig. 8 (on page 2153) using the original P1 clone 177 that we obtained from the human foreskin fibroblast P1 bacteriophage library (Genome Systems, St. Louis), which we used to isolate the human peroxisomal fatty acyl-CoA oxidase gene (1994 Proc. Natl. Acad. Sci. U. S. A. 91, 3107–3111). We also resequenced the plasmid containing this promoter region, which was used to generate promoter-reporter constructs used in our work: pHACOXLUC1 (luciferase reporter), pβHACOX (β-galactosidase reporter), and pHACOXUOX (rat urate oxidase reporter). We then obtained a new sample of human P1 bacteriophage clone 177 from the Genome Systems and sequenced the promoter region. Finally, we amplified this ACOX promoter region from three independent human genomic DNA samples. All the samples (P1 clone, ACOX promoter used for reporter constructs, and three human genomic DNA samples) showed an identical PPRE consisting of AGGTCA G CTGTCA. The PPRE sequence we published, AGGTCA C TGGTCA, is a typographical transposition of three nucleotides (CTG instead of GCT) and does not reflect a mutation or polymorphism in PPRE. We thank Dr. Ruth A. Roberts (Zeneca Central Toxicology Laboratory, Alderley Park, Macclesfield, UK) for calling our attention to a possible polymorphism.


Human inter-a-trypsin inhibitor heavy chain H3 gene. Genomic organization, promoter analysis, and gene linkage.

Maryam Diarra-Mehrpour, Nasrin Sarafan, Jeannette Bourguignon, Florence Bonnet, Frédéric Bost, and Jean-Pierre Martin

Page 26818, Fig. 10: An incorrect version of this figure was printed. The correct version is shown below:

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