substrates. Significant TESO hydrolase activity, ~25% of the total recovered in the subcellular fractions, was observed in the mitochondrial fraction (Fig. 1), although the highest level was found in the cytosol. The subcellular distribution of epoxide hydrolase activity is very similar when *trans*-stilbene oxide (TSO) is used as substrate. Both TESO and TSO are negligibly hydrated by the microsomal epoxide hydrolase and the immunologically similar nuclear epoxide hydrolase. In contrast, the mitochondrial fraction poorly hydrates BPO, a substrate widely used to monitor epoxide hydrolase activity. Further, the low specific activity of BPO hydrolase in the mitochondrial fraction indicates minimal contamination of this fraction by nuclear and/or microsomal membranes as BPO hydrolase is a good marker enzyme for the microsomal and nuclear membranes[1,6]. Repeated washing of the mitochondrial fractions leads to a substantial decrease in BPO hydrolase specific activity and most of this activity is associated with the outer mitochondrial membrane. As styrene oxide and BPO hydrolase activity in the microsomes are immunologically identical[14], our data support the hypothesis of Oesch[1] that styrene oxide hydrolase activity in the mitochondrial fraction is probably due to microsomes adhering to the outer mitochondrial membrane. In contrast, the TESO hydrolase specific activity in the mitochondrial fractions increases following repeated washings.

Using lactate dehydrogenase, a widely accepted marker for the cytosol, we demonstrated that epoxide hydrolase activity in the mitochondrial and nuclear fractions does not result from cytosolic contamination (Fig. 1). Results using additional marker enzymes including cytochrome oxidase[15], NADPH cytochrome *c* reductase[16], cytochrome P_{450} (ref. 17), citrate synthase[18] and adenylate kinase[19] also support the relative purity of the subcellular fractions. Use of citrate synthase and adenylate kinase also showed that the cytosolic epoxide hydrolase activity does not arise from mitochondrial lysis during homogenization, as only 0.6 and 2% of the mitochondrial activity of these enzymes, respectively, was found in the cytosol.

Subsequent experiments using livers from mice treated with Triton WR-1339 (ref. 15) indicated that lysosomes and peroxisomes, monitored by acid phosphatase[19] and urate oxidase[20], respectively, have minimal TESO hydrolase activity. As such, epoxide hydrolase activity in the mitochondrial fraction does not arise from contamination by these organelles. When mitochondria are disrupted, a preponderance of the epoxide hydrolase activity is associated with the matrix and intermembrane space fraction with TESO as substrate and less activity is associated with the inner and outer mitochondrial membranes. Most of the activity associated with either of these membranes can be removed with a single wash, indicating contamination by the matrix and intermembrane space fraction. The mitochondrial fraction is able to hydrate a wide variety of epoxidized compounds including epoxidized fatty acids and glycidal ethers, with a spectrum of activity similar to that of the cytosolic epoxide hydrolase, but distinct from that of the microsomal enzyme.

As the nuclei and mitochondria are excluded from the activation/deactivation systems used in many short-term mutagenicity assays[21], these systems may not provide a valid picture of the ability of cells to degrade potentially mutagenic epoxides. However, this effect may be more quantitative than qualitative, because the mitochondrial epoxide hydrolase demonstrates a spectrum of activity similar to that of the cytosolic epoxide hydrolase.

The present study and published literature[1,6,7,22] illustrate the apparently ubiquitous nature of epoxide hydrolases in cellular components. Although the information needed to understand fully the biological role of epoxide hydrolases is lacking, their ability to metabolize some xenobiotics is clear. The association of epoxide hydrolases with the mitochondria and nuclei of the cell may serve to protect the structural integrity of these organelles as well as their nucleic acid content. It was recently shown[23,24] that mitochondrial DNA is more easily alkylated by polyaromatic hydrocarbons and their diol-epoxides than nuclear DNA. Such results are not altogether surprising because of the nature of mitochondrial DNA and the oxidases occurring in the mitochondria[25,26] which can activate the polyaromatic hydrocarbons to reactive electrophiles. Although the mitochondrial epoxide hydrolase activity reported here does not appreciably metabolize BPO, these epoxide hydrolases can potentially protect the mitochondria from those reactive epoxides which are substrates. Therefore, our study certainly illustrates the need for increased research on these important enzymes using a variety of potential substrates in all subcellular components.

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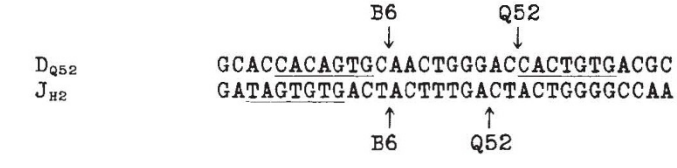
Errata

In the letter 'Human immunoglobulin variable region genes—DNA sequences of two V_κ genes and a pseudogene' by D. L. Bentley and T. H. Rabbitts, *Nature* **288,** 730–733 (1980), Fig. 3 shows the DNA sequence of a human V_κ pseudogene (not V_λ).

In the article 'Sequence and organization of the human mitochondrial genome' by S. Anderson *et al.*, *Nature* **290,** 457–465, line 56 on page 462 should read '... of the anticodon of mammalian mt RNAs is *not* known, it is ...'

In the article 'Identification of D segments of immunoglobulin heavy-chain genes and their rearrangement in T lymphocytes' by Y. Kurosawa *et al.*, *Nature* **290,** 565–570, the arrows indicating recombination sequences in the text figure on page 570 were positioned incorrectly. The correct version is shown below:



Corrigendum

In the letter 'A nonrandom component in cosmic rays of energy $\geq 10^{14}$ eV' by C. L. Bhat *et al.*, *Nature* **288,** 147–149 (1980), the RA values shown in Figs 2 and 3 have been found to be incorrect. The correct values are those obtained by subtracting the values given from 24 hours. This excludes the pulsar PSR 0525+21 as a possible origin. The results are consistent with a point-source origin in the RA range 20±3 hours.