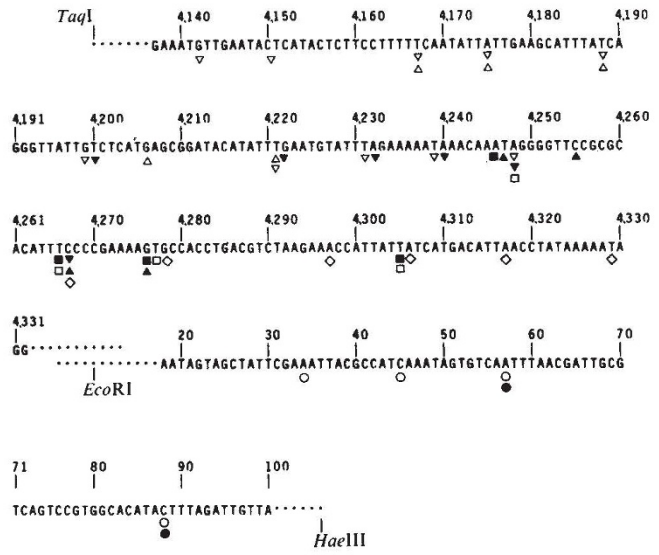

Fig. 2 Summary of ^{125}I-Hoechst 33258 binding/breakage sites on portions of the *Eco*RI–*Taq*I and *Eco*RI–*Hae*III fragments of pBR322. The numbers correspond to the base pair numbering of the 4,362 bp pBR322 sequence as described by Sutcliffe[16]. The symbols indicate the centres of hotspots on sequencing gel autoradiographs. Each symbol represents a different experiment. The regions examined in each experiment were: ○, ●, 28–100; ▽, 4,136–4,253; △, 4,160–4,225; ▼, 4,192–4,268; ▲, 4,242–4,290; □, ■, 4,242–4,310; ◇, 4,260–4,331.

have indirect information about the details of each probability distribution, and that[7] suggests that the majority of breaks occur within 3–4 bp on either side of the decaying atom. Thus, for each tetranucleotide binding site for ^{125}I-Hoechst 33258 we would expect two such distributions, each corresponding to one of the alternative polarities of ^{125}I-Hoechst 33258 binding and centred either side of the tetranucleotide binding site. The composite of these two distributions would be centred near (depending on the relative contributions of the binding configurations) the middle of the binding site. Apparently most DNA strands in the population of ^{125}I-Hoechst–DNA complexes sustain more than one break per ^{125}I decay in the vicinity of a binding site. However, only the shortest ^{32}P-labelled fragments are represented in the distribution detected as the hotspot, and hence the marked bias toward the ^{32}P-labelled side of the binding site. There are two immediate consequences of this interpretation. The first is that if the experiment were repeated using 5′ ^{32}P-labelled target fragments, a new collection of hotspots should be detected, corresponding to a displacement of about 5 bp from those in Fig. 2. Second, detailed examination of the actual distribution of the ^{32}P label in the population of fragments in a given hotspot should allow the generation of strand-break probability distributions by computer modelling. We are now investigating both of these avenues.

While the finding that each hotspot is associated with an (A/T) tetranucleotide is interesting *per se*, the most intriguing aspect of the results is that some potential sites of four consecutive A·T base pairs do not bind significant amounts of the labelled ligand. Zimmer *et al.*[19] have recently reported the use of netropsin, which binds to the minor groove of B-DNA but does not bind significantly to Z-DNA or A-DNA, as a specific probe for B-DNA. If I-Hoechst 33258 has as marked a preference for B-DNA as uniodinated Hoechst 33258[18], then it is tempting to speculate that the potential binding sites that show low affinity are in another than B-conformation. In any case, it is reasonable to suggest that the observed patterns of binding/damage are a result of both the affinity of the probe for a 'consensus' sequence, and regional perturbations in conformation along the DNA helix. Such structural features have been detected recently with a phenanthroline–copper (II) complex[20,21]. Note that although our experiments were performed at very low ligand:DNA ratios, the possibility that the I-Hoechst 33258 cooperatively induces conformational changes in the target DNA cannot be excluded. Such effects are likely to complicate the interpretation of the results from another recently reported method for investigating sequence selectivity of DNA ligands, based on patterns of inhibition of cleavage by methidium–EDTA·Fe(II)[22].

We suggest that ^{125}I-Hoechst and other similarly labelled DNA ligands may be useful as probes to investigate variations of conformation in relatively long DNA molecules which at present are beyond the reach of analysis by X-ray crystallography. Moreover, probes such as ^{125}I-Hoechst 33258 do not rely on an enzyme activity, and can be used in the relatively extreme conditions which are known to induce conformational changes in DNA. Finally, we should point out that our results also demonstrate an approach for investigating the sequence selectivity of any DNA ligand which can be labelled with ^{125}I.

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Errata

In the article 'Deuterium excess in an East Antarctic ice core suggests higher relative humidity at the oceanic surface during the last glacial maximum' by J. Jouzel, L. Merlivat and C. Lorius, *Nature* **299,** 688–691 (1982), the address given for J. Jouzel and L. Merlivat is incorrect. The address should read: Laboratoire de Géochimie Isotopique, DPC, Centre d'Études Nucléaires de Saclay, 91191 Gif-sur-Yvette Cedex, France.

In the letter 'Overlapping spreading centres: new accretion geometry on the East Pacific Rise' by K. C. Macdonald and P. J. Fox, *Nature* **302,** 55–58 (1983), on pages 56 and 57 the legends of Figures 2 and 3 were transposed.

Corrigenda

In the letter 'Evidence for ^{13}C/^{12}C fractionation between tree leaves and wood' by S. W. Leavitt and A. Long, *Nature* **298,** 742–744 (1982), on page 743 the monthly Tucson temperatures in the first line of the second column are incorrect. The correct temperatures are: 22.8, 24.4, 30.4, 30.3, 31.5 and 28.8 °C. The temperature and correlation coefficients were correct.

In the article 'Activation of a cellular oncogene by DNA rearrangement: possible involvement of an IS-like element' by G. Rechavi, D. Givol and E. Canaani, *Nature* **300,** 607–611 (1982), the acknowledgement on page 610 should have indicated support from the Edith C. Blum Foundation, not the Blum Foundation.