impossible to resample or retest them on the basis of the information provided by Shorter *et al.* in their paper. Soil classification facilitates their study, use and understanding by giving soil types specific names. This represents a shorthand for numerous characteristic properties. Researched soil bodies should be properly identified and classified, in a similar fashion to vegetation, biomes, minerals or rocks, to facilitate recognition and data transfer.

Each of the biomes listed in Table 2 of the paper by Shorter *et al.* includes many different soil types, not necessarily possessing the same properties and reactivity as those tested. The degradation process is, after all, a function of the soil environment; hence, an appropriate soil identification is desirable, not only when sampling the soils, but also when extrapolating such data to other soil landscapes and regions.

Soil scientists recognize several hundred main soil types, and commonly use two or three worldwide soil classification schemes, mostly the Soil Map of the World scheme from the Food and Agriculture Organization (FAO), or the US Soil Taxonomy. I have recently updated soil classifications (*Catena* **24**, 233–241; 1995), listing and reviewing the newest publications. The areal extent of the major global soil groups has been published in various places and can be obtained from computerized databases. The most recent figures on the areal soil distribution for regional or global extrapolation of the major mapped soil units can be obtained from the Land and Water Development Division of FAO, Rome, with references for the FAO soil classification scheme, and from the Division of Soil Survey, Natural Resources Conservation Service, US Department of Agriculture, Washington DC, for the soil taxonomy scheme.

Leading soil-science journals require that soils reported in publications be classified according to one of the two or three internationally recognized and used soil-taxonomy schemes. My appeal is thus that those submitting data on soils to *Nature* and similar multidisciplinary journals follow this sound rule to enhance international communication.

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A covalently crosslinked histone

SIR — Post-translational modification of core histones is essential to processes requiring chromatin remodelling. We report here a novel histone modification, involving crosslinking between a glutamine residue of histone H2B (ref. 1) and a lysine residue of histone H4 (ref. 2), in sperm of the starfish, *Asterina pectinifera*.

A unique nuclear protein, designated p28, was isolated from a histone fraction prepared from starfish testes. Amino-acid analysis of the acid-hydrolysed p28 revealed that the amino-acid profile was nearly the same as the sum of the amino acids in testicular histones H2B and H4 (data not shown). Furthermore, electrospray ionization mass spectra showed the relative molecular mass of p28 to be 24,654, which is 17 mass units less than the sum of the observed relative molecular masses of histones H2B (13,362) and H4 (11,309).

The structure of p28 was investigated by digestion with *Achromobacter lyticus* protease I or *Staphylococcus aureus* V8 protease. Analysis of the proteolytic fragments after separation by high-performance liquid chromatography suggested that they might be identical to the amino-acid sequences of both H2B and H4, except for the amino-terminal portion (solid box in *a* in the figure): K8, derived from *A. lyticus* protease I digestion. Amino-acid analysis of K8 using constant boiling HCl indicated a composition of Ser:Glu:Gly:Lys:Arg of 1:1:5:3:1, which corresponds to Gly 8–Lys 10 of H2B and Ser 1–Lys 8 of H4. Sequence analysis of K8 yielded Gly-X-Lys, where X denotes a missing residue. Sequence analysis after treatment with trifluoroacetic acid[3] gave the sequence Ser-Gly-Arg-Gly-X-Gly-Gly-Lys, corresponding to the N-terminal sequence of H4, in addition to Gly-X-Lys of H2B.

The positive-ion fast-atom bombardment tandem mass spectrum of K8 not only gave the product ions arising from the loss of the constituent amino-acid residues, but also those involved in the crosslink, ε-(γ-glutamyl)lysine (see figure). Finally, K8 was digested sequentially with subtilisin, leucine aminopeptidase and carboxypeptidase Y. Amino-acid analysis of the digest revealed the presence of one molecule of ε-(γ-glutamyl)lysine.

From these data, the structure of p28 was unambiguously shown to be a heterodimer composed of histones H2B and H4, probably formed through an acyl transfer reaction catalysed by transglutaminase[4] between the Gln 9 of H2B and the Lys 5 of H4. We believe this to be the first demonstration of a covalently crosslinked histone heterodimer in eukaryotes.

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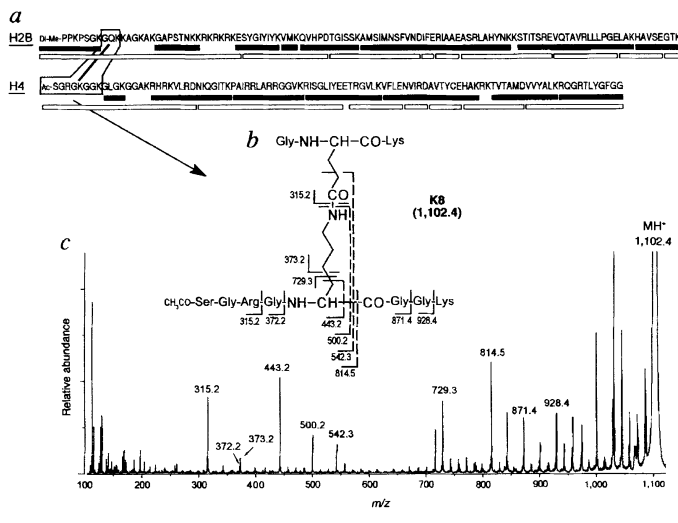

a, Closed and open bars below the sequence (single-letter code) of histones H2B and H4 indicate the proteolytic fragments produced by digestion of p28 with *A. lyticus* protease I (closed bars) or *S. aureus* V8 protease (open bars). Fragments were identified by gas-phase automated sequence analysis, amino-acid analysis and positive-ion fast-atom bombardment tandem mass spectrometry[5], following separation by HPLC using a reverse-phase C_{18} column. *b*, Deduced structure of fragment K8. *c*, Positive-ion fast-atom bombardment tandem mass spectrum of K8.

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