

## IN BRIEF

## UK sweetener review

The UK Food Additives and Contaminants Committee is to conduct a full review of the regulations controlling the use of artificial sweeteners in food. The committee, which falls under the aegis of four governmental departments, will thus extend its present studies of saccharin and of Aspartame; it has published two reports on cyclamates in the past.

## Waste now, power later

A three-member panel of the White House Council of Environmental Quality has, according to the *New York Times*, reported that an expansion of nuclear power in the United States should be made conditional upon a demonstrably safe method of containing nuclear waste. The verdict is seen less as a counter to President

Carter's energy plan than as an attempt to encourage work on waste disposal.

## IAEA reprocessing view

Though it was generally accepted that the number of nuclear fuel reprocessing plants should be kept to a minimum, to prohibit them would probably lead to a result opposite of that intended, according to Dr Sigvard Eklund, the Director General of the International Atomic Energy Agency (IAEA). He was speaking at the IAEA General Conference's 21st Regular Session in Vienna last week. Dr Eklund, who was appointed to his fifth consecutive term as director general, was also critical of those who wanted to eliminate the nuclear option.

## Accelerator approval

Approval has come for the construction of Brookhaven National Laboratory's 200 GeV superconducting

intersecting storage ring accelerator Isabelle. A joint US House-Senate committee last week authorised expenditures totalling nearly \$200 million. The device will enable protons to be fired at each other with centre of mass energies well in excess of those available elsewhere, providing detail on how and if the weak and electromagnetic interactions are unified.

## HSC report

A broad-ranging 51-page report from the UK Health and Safety Commission, published this week, details the work of the Commission and its Executive between their establishment in October 1974 and January 1975 respectively and March last year. The Commission emphasises that legislation can play only a part in achieving the objectives of the Health and Safety at Work Act, and indicates in its discussion of future strategy what more can be done.

The field of molecular evolution deals largely with comparisons of the sequences of 'informational macromolecules'—DNA, RNA and proteins. The first sequences that were available were of proteins: cytochromes *c* and haemoglobins, from different animals. The story is now familiar: the number and location of differences in corresponding amino acids were roughly proportional to the taxonomic separation of two species. For example, human and rhesus monkey haemoglobins differ in 12 locations; human and horse haemoglobins in 42; rhesus monkey and horse in 43. The differences between human and horse are not all in the same places, or of the same kind, as the differences between monkey and horse, thus showing that the three species have followed separate evolutionary pathways. These findings expanded and accumulated for various families of proteins, and were extended into comparisons between insects, green plants, yeasts and moulds. Various authors constructed large 'phylogenetic trees' based on such findings. It became evident that a 'molecular evolutionary clock', ticking away through the aeons, left its imprint in terms of divergence between sequences. The clock did not always run at the same rate, but, in the main, the divergences roughly corresponded to the passage of time as judged by other criteria, such as the fossil record.

But wait! The differences between proteins were merely the expression of changes in the base sequences of

'codes'. Quite often, two to four DNA molecules as reflected by the genetic code. And the genetic code, or amino acid code, is ambiguous in certain respects, because 18 of the 20 amino acids have from two to six

## Molecular evolution



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codes for the same amino acid differ only in the third base of the nucleic acid codon that specifies the amino acid. So a change of one amino acid, as measured in a protein, could reflect more than one change in a gene. Various 'educated guesses' were proposed to calculate the actual numbers of such unknown changes.

The discovery of procedures for

rapidly determining the sequences of long segments of DNA molecules is going to revise all this. One such method came from Sanger's group at Cambridge, and, more recently, the field has been galvanised by a chemical procedure devised by Maxam and Gilbert at Harvard. Such sequences can be matched against a protein sequence, even a partial one, and the exact code for each amino acid can be 'read off'. Furthermore, comparisons of DNA sequences obtained from homologous regions in related organisms tell precisely which nucleotides have undergone change during the period of evolutionary separation. There are preliminary indications that the synonymous 'third bases' of codons may undergo such changes more frequently than the first two bases, which specify amino acids.

New techniques, such as automated Edman degradation, are improving the accuracy of measuring amino acid sequences in proteins. A sequence between the 23rd and 30th residues in cytochrome *c* of *Neurospora crassa*, previously listed as -Gly-Glu-Gly-Gly-Asn-Leu-Thr-Gln- was found to be -Thr-Leu-Glu-Glu-Gly-Gly-Gly-Asn-. This was a bit of a shocker, and it called for some revision of evolutionary comparisons, but it is probably an extreme case. Other re-evaluations, and an expansion of ideas on evolution, will stem from forthcoming studies of DNA molecules. These studies should shed new light on the question of 'neutral' or 'near-neutral' evolutionary changes that occur in genes.