

algorithm was formulated to locate protein coding sequences in prokaryotic DNA. This algorithm was applied to prokaryotic DNA sequences available in European Molecular Biology Laboratory (EMBL) nucleic acid sequence data base. Our results have shown that the method developed has an overall accuracy of 90%. Further, we can extend the approach to suggest whether particular DNA sequence would code with high expressivity or low expressivity. We have also analysed distribution of near neighbour codon pairs and shown that constituent codons in a pair interact strongly in large number of cases. These interactions are mainly due to the need that two tRNA molecules should be present on the ribosome to give rise to constraints in the choice of synonymous codons.

Zoology

Changes in conformation and expression in the genome of the rat during its life span by M. S. Kanungo, *Department of Zoology, Banaras Hindu University, Varanasi 221 005, India.*

Specific timings of birth, maturity and cessation of reproductive ability in mammals, more or less fixed life spans of individuals of a species, sequential changes in the isoenzymes, and the ability of genes to alter their expression under the influence of hormones, show that various components of the genome governing these

functions are not static. An analysis of the chromatin housing the genes, by digestion with endonuclease DNase I, that cuts the DNA at 10 base pair intervals, shows that it undergoes increasing condensation with age. Digestion of chromatin by DNase I and EcoRI, followed by nick-translation to quantitate incorporation of dTMP into DNA, for the measurement of DNA synthesis shows that the incorporation is 50% less in the old. Digestion by the isoschizomers MspI/HpaII which quantitate methylation in CCGG sequences, followed by nick-translation shows that the incorporation after Hpa II digestion is 50% less in the old. This indicates increasing methylation with progressive age. Since increasing methylation is correlated with compaction, the inference drawn from these studies is that chromatin becomes more compact with increasing age. This may account for the lower level of several enzymes that may lead to old age.

If this is so, one should see decreasing transcription/expression of genes, and correspondingly less messenger RNAs. Indeed, normal transcription of mRNA which is carried out by RNA polymerase II is lower in the old. Even when exogenous eukaryotic RNA polymerase II is added to old nuclei, the transcription is not raised to the level of that of the young. This shows that either the genes are inaccessible to RNA polymerase II or that they are no longer in active conformation that is required for transcription. Use of probes for specific genes gives similar results.

Thus the genes undergo continuous and sequential changes in activity during the life span of an organism.

ANNOUNCEMENT

KALINGA PRIZE

Sir Peter Medawar, British Biologist and a Nobel Prize winner for medicine has been awarded the Kalinga Prize for popularisation of science. The

Kalinga Prize was instituted by UNESCO on the initiative of Kalinga Foundation in India in 1951.
