promoter and an i^{100} early amber mutant gene. This prophage overproduces repressor some two hundred-fold which means sufficient of the i^{100} repressor protein can be obtained for its amino-acid sequence to be determined and its properties characterized. The tetrameric repressor specified by the i^{100} gene binds the inducer IPTG; it cross-reacts with antibody against wild type repressor albeit to a ten-fold lesser extent than the wild type protein, and it has a molecular weight of about 135,000 which is about 8 per cent less than the wild type repressor.

Analysis of the monomeric subunits of the i^{100} repressor indicates that the polypeptide chains have a molecular weight of about 34,000 and the amino-terminal sequence is Ala–Glx–Leu–Aspx–. This same sequence occurs at residues 43–46 of the wild type subunit and in the wild type subunit it is immediately preceded by a methionine residue at position 42. This is the first methionine residue in the wild type sequence. Methionine is, of course, in a formylated state the initiating amino-acid of bacterial proteins and it seems clear that the amber mutation in the i^{100} strain precedes position 42 and that after translation is terminated by the amber codon it reinitiates at the methionine codon at position 42, goes to completion and then the initiating formyl-methionine residue is cleaved to leave the wild type position 43 amino-acid as the amino-terminus of the i^{100} repressor subunit. Although the position 42 methionine codon can act as an initiation signal in these circumstances, at least 99 per cent of the repressor subunit chains specified by the wild type *i* gene are of full length with an internal methionine residue at position 42. What tells the translation machinery to read the position 42 codon as a start signal after premature termination is a fascinating and unsolved question.

Finally, although the i^{100} repressor protein binds IPTG and is a tetramer it does not *in vivo* repress the *lac* operon. Platt *et al.* therefore conclude that the first forty-two amino-acids of the repressor subunits are essential for repressor activity, either because they are directly involved in association with the operator or because they are required if the repressor is to have the conformation it needs to recognize the operator. And as Jobe, Riggs and Bourgeois (*J. Mol. Biol.*, **64**, 181; 1972) have stressed, allosteric mutants of *lac* repressor protein have strikingly different affinities for inducer and the *lac* operator. Indeed, as they comment, repressors from different inducible strains of *E. coli* which have hitherto been thought of as wild type and identical in fact differ considerably in their kinetics on binding to inducer and operator.

CELL BIOLOGY

Aspects of Ageing

from a Correspondent

Two principal approaches to the problem of cellular aspects of ageing emerged at a joint meeting of the British Society for Cell Biology and the European Cell Biology Organization Study Group on Ageing at the University of East Anglia on April 5–7. First, that ageing is a clonal phenomenon resulting from the accumulation of errors at the molecular level, and, second, that ageing is a final and deliberate result of cell differentiation and is essentially an intercellular process.

The Searle lecturer, Dr L. Orgel (Salk Institute, La Jolla), reviewed the molecular theories of ageing, but concluded that no single theory is likely to prove correct. Rather, cellular ageing is probably the result of an accumulation of errors of various kinds, leading to the interaction of levels of imperfection, the breakdown in any system being both caused by and the cause of breakdowns in other systems. In a critical review, Dr H. von Hahn (Neurologisches Universitätsklinik, Basle) pointed out that research on nucleic acids and ageing had been too heterogeneous, inconclusive, contradictory and non-reproducible to be of much value, and hoped that new ideas would emerge before the next ECBO meeting on the subject. Dr J. Gallant (University of Washington, Seattle) described a bacterial system in which errors in protein synthesis could be elicited, their frequency measured and their effect on survival assessed, and reported that present evidence suggested that bacterial cells can tolerate a great deal of aberrant protein. Dr I. Gibson (University of East Anglia) said that ciliate protozoans undergo a fission-dependent series of phenotypic changes demonstrable in terms of sexual immaturity, maturity and senescence, and controlled by the macronucleus.

Several speakers considered the implications of Hayflick's theory that normal somatic cells inevitably age and die after a finite number of replications. Dr R. Holliday (National Institute for Medical Research, Mill Hill) considered evidence for the accumulation of defective proteins and reported that a minor fraction of heat-labile G6PD and 6PGD appears as diploid cultured human fibroblasts become senescent, but that this fraction represents 20–30 per cent of the total activity just before death. Dr A. Maciera-Coelho (Villejuif) reported that chick fibroblasts given 100 rads at intervals show accelerated growth decline in proportion to the total irradiation received. Dr Y. Courtois (Institut St Pierre, Paris) considered that changes in chromatin in ageing chick fibroblasts might be associated with an imbalance in nucleoprotein synthesis. Mr P. Godsell and Dr M. Balls (University of East Anglia) doubted whether Hayflick's theory could be applied to amphibian cells, because a number of stable diploid and haploid lines from a number of species had been maintained *in vitro* for more than 200 cell generations. Drs A. Guillouzo, G. Gueguen and Y. Le Guilly (INSERM, Rennes) described morphological, ultrastructural and metabolic changes in ageing diploid human liver cell strains similar to the changes occurring in senescent animals.

Professor H. Woolhouse (University of Leeds) said that, if plant cells age at all (they seem to carry on indefinitely

Origin of X-ray Background Radiation

CAN the X-ray background radiation of the universe be explained in terms of the smoothed out radiation from a number of discrete sources? This question has yet to be resolved to the satisfaction of all astronomers, but in next Monday's *Nature Physical Science* (May 8), A. C. Fabian lays down the framework within which any satisfactory resolution of this problem must lie. Fabian concludes, on the basis of recent observations, that it is still not possible to rule out the idea that this radiation originates within clusters of galaxies; but it does seem clear that, as pointed out by Wolfe and Burbidge (*Nature*, **228**, 1170; 1970), an origin in sources equivalent to superclusters is not consistent with the observations.

Determination of the nature of the background remains, of course, largely a matter for statistics to resolve, and what Fabian has done is to provide the appropriate statistical techniques in a form immediately suitable for the problem. It will be interesting to see how future observations can be analysed in this way; at present, the data allow a model in which the X-ray background originates in clusters which have a Gaussian distribution and are characterized by a radial size less than 3.5 Mpc. The space density of cluster centres in such a model would be about 10^{-3} Mpc^{-3} to produce the observed flux.

According to Fabian, it is a relatively simple matter to allow cluster parameters (size, density and luminosity) to vary with redshift when determining the overall background produced in models of this kind. It seems, therefore, that as observations improve and more data are gathered the study of the X-ray background will provide an invaluable tool for the study of the structure of the universe.