been clearly identified in nuclear matter, forming the field of study of hypernuclear spectroscopy. How soon before we see charming nuclear spectroscopy? Thus there exists some knowledge of the level at which the effects appear. Similarly, excited nucleons (with strangeness zero), the so-called N*'s, have been considered in nuclear matter in the same way as they are considered in hadron–nucleon collisions, that is, as resonances, but now broadened by Doppler motion. But my question should really be reformulated: when N*'s, hyperons and so on are produced on nuclei is a nucleus then seen as a collection of quasifree nucleons, or can the effects of the nucleon binding, of the collective of particles forming the nucleus, and of the presence of pions during those exchanges that are responsible for the nuclear forces be discerned? Formulated in this way, it is evident that we ask questions which must be answered by the selection of rare situations or by very high precision. So far, the general feeling is that we have not succeeded in finding the answers. There has been a puzzling result, however.

Collisions between fast nucleons take times T_R of the order of R/c, with R being the nucleon radius in question and c the velocity of light, whereas experiments with fast projectiles take times T_L of the order L/c, where L is the length of our apparatus; the ratio of these time-scales is $T_R/T_L \simeq R/L \simeq 10^{-14}$ to 10^{-17}. Thus what is seen is something that has been fully developed in the apparatus, but may have very different aspects over periods of time that are but a few times T_R. Here the nuclei may be used as detectors enabling observations over nuclear distances R_N in the range $R \leqslant R_N \leqslant 6 \cdot R$ to be made. Developments in ordinary material extending over metre distances can be called 'macroscopic' and developments over nuclear dimensions and with nuclear densities 'microscopic'. The three main results may be summarised as follows (see for example Cronin *et al. 1976 Tbilisi Conference on High Energy Physics*).

Macroscopically, cascades of particles produced near the forward direction are found, that is the incoming hadron produces fast particles, which in turn produce fast particles and so on: microscopically, no such cascading results.

If the final state is a 3π or a 5π state, that is three pions produced or five pions produced, then macroscopically the chance of collision (the cross section) is respectively three times and five times that of a single pion; microscopically, the cross section is very closely equal to that for one pion in both cases.

When very large momenta are carried over in the collision (that is, when the struck particle gains a large amount of energy), a relatively rare event has occurred. Naively, it would be expected that the chance of such events occurring in nuclear matter would grow with nuclear mass number as the nuclear cross section, that is roughly proportional to $A^{2/3}$. Experimentally, the result is proportional to $A^{4/3}$.

These three main results need explanation and further study both experimentally and theoretically. It is not known whether they are nuclear or hadronic effects.

All this does not answer the central question: how many degrees of freedom should we consider in nuclear matter? And when are we to talk about a finite number of constituents and when about continuum? These problems are also linked to the next major point.

Are shock waves observed in nuclear matter?

Certain authors maintain that they have seen such waves but for me the interpretation is not clear. First, I have

Variable DNA repeat lengths

from Rosalind Cotter

AFTER the revelation of the chromatin beaded structure there followed much tangled discussion about the amount, if any, of string between the beads, which was based chiefly on the different unit sizes generated by micrococcal nuclease in Oregon and Cambridge. The argument has now moved from the level of technical disagreements involving digestion termination conditions or faulty calibration to a careful comparison of DNA repeat size in different types of chromatin. A correlation with genetic activity is beginning to emerge.

Chambon and coworkers have examined the DNA repeat length of subunits in chromatin from higher eukaryotes (*Proc. natn. Acad. Sci. U.S.A.* **73,** 4382; 1976). Cells of mature tissues have nucleosomes containing 196 base pairs of DNA, genetically dormant cells rather more, and cells from actively dividing tissues rather less. It has been suggested that smaller DNA repeat lengths are found in primitive eukaryotes, the value for yeast being about 165 base pairs (Thomas & Furber *FEBS Lett.* **66,** 274; 1976), for *Aspergillus nidulans* 154 base pairs (Morris *Cell* **8,** 357; 1976), while 170 base pairs are found in nucleosomes of *Neurospora crassa* (Noll *Cell* **8,** 349; 1976).

These and more recent studies (Lohr *et al. Proc. natn. Acad. Sci. U.S.A.* **74,** 79; 1977) have shown that, at early times of digestion with micrococcal nuclease, the most resistant portion of the repeating unit always has 140 base pairs. These core particles, formerly known as monomers, do not vary among species or from tissue to tissue (Morris *Cell* **9,** 627; 1976) with respect to size, histone content (two each of H2A, H2B, H3 and H4), and internal cleavage pattern by DNase I. The variations in repeat lengths are therefore attributable to the more nuclease-sensitive DNA spacer between core particles.

Lohr *et al.* observe a distribution of repeat sizes for yeast and HeLa chromatin, ranging from 140 (that is, no spacer) to 165 base pairs in yeast, to 190 base pairs in HeLa. Chicken erythrocyte oligomers however quickly reach constant sizes during digestion which are compatible with a regular array of core particles and 60 base-pair linkers. The authors speculate on a possible correlation between spacing mode and gene activity, which would be expected to be more complex along chromatin from active cells with sizeable transcribed and non-transcribed regions, and more regular in inactive chromatin in order to meet packaging requirements more efficiently.

The Cambridge group suggest that variations in spacer length may be brought about by histone H1. H1 is highly basic and is thought to interact with phosphates of DNA in the spacer regions. H1 from *Aspergillus* has fewer basic residues than *Neurospora* H1, and can therefore presumably protect only a shorter piece of inter-bead DNA. Morris notes a subunit repeat for chicken erythrocyte chromatin which is longer than that of chicken liver chromatin, and might be attributable to the partial substitution in the former of H1 by the more basic H5. He discusses the interesting possibility that specific recognition sites such as promoters might have altered accessibilities depending on whether they are incorporated into nucleosome cores or spacers; if then nucleosomes are phased with respect to recognition signals, this phasing could be altered by different H1-like proteins inducing changes in linker length. H1 is known to vary during development and cell differentiation and may therefore influence the accessibility of recognition sites in active chromatin.