problem of lecture room space, and the meeting was as crowded as any at the old site.

By one reckoning Professor Davies's announcement brings the number of known pulsars to 43, and he commented that there are a further one or two possible pulsars being investigated at Jodrell Bank. The discovery is a result of repairs and improvements to the Mark 1 radio telescope which has now reached a stage where the telescope has to be pointed at the zenith for most of the time. No azimuth movement will be possible for about two months. During this period of forced inactivity all the time on the telescope is being devoted to a pulsar search, using a new technique developed by Professor Davies to look for individual dispersed pulses rather than period phenomena. The search is carried out at two frequencies separated by a few MHz near 480 MHz, and the advantage of the new method is that it is sensitive to the many pulsars which do not show continuous trains of pulses. Thus it is hardly surprising that the two new pulsars are more sporadic than the first pulsars to be found. Otherwise there is nothing remarkable about the periods or the positions of the two new pulsars which both lie close to the plane of the Milky Way. Professor Davies said that their positions will be measured more accurately during the coming weeks, and that the values of the periodicities can be improved. The final two sevens in the period of *JP* 2113 are doubtful, and the period is not corrected to the barycentre.

The lecture by Professor Schwarzschild, who is one of the society's gold medallists this year, reviewed the field of stellar evolution with particular relevance to globular clusters. He listed some of the outstanding problems which have to be solved for the further understanding of stellar evolution, a study which he has done so much to promote. For one thing it is not yet known how to handle the important question of convection in stars in the abnormal conditions of core flash. For example, at the time of the helium flash there must be a steep temperature gradient extending from the core which causes a convection layer. Convection cells eventually reach the hydrogen-burning layer and "lick" a little hydrogen back to the core. This could be the origin of the hydrogen in the hot core which was always thought to have been necessary for the s-process of build up of heavy elements. But it is still not known how the heavy elements are brought to the surface of the star and ejected into the interstellar medium to take part in future processes.

BACTERIOPHAGE

Almost All Present and Correct

from our Cell Biology Correspondent

It was of course the single stranded DNA genome of the coliphage ΦX174 which Kornberg, Goulian and Sinsheimer used as a substrate for the Kornberg DNA polymerase in their famous *tour de force*, the synthesis *in vitro* of complete and infectious phage DNA genomes. Even if the rumours are correct that the Kornberg DNA polymerase is not the enzyme which replicates the *E. coli* chromosome *in vivo* but perhaps a DNA repair enzyme, coliphage ΦX174 has a secure place in history. With a genome that contains enough information to specify only seven or eight proteins, ΦX174 DNA lends itself to the grand scale *in vitro* experiment. Hayashi and his colleagues, for example, are at present using the double stranded replicative form of ΦX174 DNA in an *E. coli* cell-free system in which they hope to couple the transcription of the ΦX174 DNA into messenger RNA with the translation of the messenger into phage protein.

So far they have shown that the system will incorporate UTP into RNA and also incorporate amino-acids into polypeptides (Bryan, Sugiura and Hayashi, *Proc. US Nat. Acad. Sci.*, **62**, 483; 1969). And hybridization analysis of the RNA being made shows that it is transcribed off the complete ΦX174 genome. The next step, characterization of the protein made in the system, which hopefully will prove to be ΦX174 protein, depends on an assay for the phage proteins, and polyacrylamide gel electrophoresis seems to fit the bill. In the latest issue of the *Journal of Molecular Biology*, Burgess and Denhardt (**44**, 377; 1969) and Gelfand and Hayashi (*ibid.*, 501) simultaneously report more or less identical electrophoretic characterizations of ΦX174 proteins synthesized in *E. coli* cells irradiated with ultraviolet light, so as to reduce the background host protein synthesis, and then infected with phage. Both groups have used the time honoured technique of comparing the proteins made in cells infected with wild type and amber mutant phage, and the proteins in the phage particles themselves, to prove which gene specifies which protein.

Burgess and Denhardt have resolved five proteins in extracts of phage-infected cells and a sixth protein, which, although not detectable in cell extracts, is present in phage particles themselves. Four of the six proteins are components of the phage coat (three can be detected in both infected cell and phage particle extracts). One of the other two proteins is involved in the lysis of the host cells during normal infection and the other is required for the synthesis of single stranded progeny ΦX174 genomes from the double stranded replicative form molecule. This accounts for six of the seven phage genes that have been identified by genetic complementation tests and may well comprise the entire genome. The seventh gene is known from the complementation work to specify a protein involved in the replication of replicative form; failure to detect it on the polyacrylamide gels may mean that it has the same electrophoretic mobility as one of the other proteins, possibly that involved in synthesis of single stranded progeny DNA, and is not therefore resolved.

Gelfand and Hayashi, using virtually identical techniques, have identified four ΦX174 proteins made in infected *E. coli* cells, but they failed to identify the fifth protein seen by Burgess and Denhardt, the lysis enzyme. But whatever the reason for this discrepancy the stage is now set for the characterization of the ΦX174 proteins made *in vitro* by coupled transcription and translation systems programmed with ΦX174 DNA.

RNA POLYMERASE

Multiple Forms

from our Cell Biology Correspondent

The discovery of sigma factor in *E. coli* (Burgess *et al.*, *Nature*, **221**, 43; 1969), which controls the template specificity of the bacterial DNA dependent RNA polymerase, has started a new chapter in the story of gene regulation in bacteria and bacteriophages. Already