that alternative routes could arise to meet specific metabolic needs of different organisms.

How could such metabolic pathways evolve? Dr E. C. C. Lin (Harvard University) showed how *Aerobacter* "borrowed" a permease from one pathway and a dehydrogenase from another when "learning" to grow on xylitol. Subsequent gene-doubling events would allow selection for greater specificity while preserving the parent pathway. One should expect to find families of enzymes with common mechanisms but different specificities. Dr N. O. Kaplan (University of California, San Diego) gave reason to believe that some dehydrogenases may form such a family, and Dr K. Muench (University of Miami) hinted that amino acyl tRNA synthetases may be another.

Dr B. S. Hartley (University of Cambridge) reminded the participants that the pancreatic serine proteinases are a family with identical conformations of the polypeptide chain, though the surface of these enzymes varies considerably. Yet a single amino-acid change is sufficient to explain the difference in specificity of trypsin and chymotrypsin. Bovine thrombin is similarly homologous with the pancreatic enzymes, but a bacterial proteinase, subtilisin, differs in both primary and tertiary structure. Nevertheless convergent evolution has produced a similar arrangement of catalytic residues in its active site. Dr D. R. Whitaker (University of Ottawa) also told of other serine proteinases from a bacterium and a mould which resemble chymotrypsin rather than subtilisin. Wald's "analogies" and "homologies" appeared as three dimensional molecular models in this symposium.

NUCLEIC ACIDS

Circles not Rolling

from our Cell Biology Correspondent

THE rolling circle model of bacterial and bacteriophage chromosome replication as proposed by Gilbert and Dressler was one of the chief talking points at the 1968 Cold Spring Harbor Symposium on DNA replication (see *Nature*, **219**, 17; 1968). But since then evidence on balance seems to have been running against the rolling circle model as a unitary explanation of the mechanism of chromosome replication in all phages and bacteria.

The model was originally proposed to explain the replication of the single stranded circular chromosome of øX174, and for this phage, and perhaps all phages with similar chromosomes, it still seems valid. Kiger and Sinsheimer (*J. Mol. Biol.*, **40**, 467; 1969) as well as Gilbert and Dressler have detected recently DNA strands longer than complete øX174 chromosomes in infected *E. coli*—the occurrence of such DNA strands is one of the chief predictions of the rolling circle model. On the other hand, attempts to extend the model to the replication of the double stranded circular chromosomes of bacteria, phages and viruses, such as polyoma, have not been convincing. The burden of existing and new experimental evidence, accumulated since 1968, has supported Cairns's model of replication of these chromosomes, which envisages a replicating point moving round a circular DNA unwinding and replicating the complementary strands as it progresses. This model, of course, predicts that the replicating point will be a Y shaped fork and DNA molecules longer than one genome's length should not occur.

Cairns originally proposed this model to explain his autoradiographs of replicating *E. coli* chromosomes and lately electron micrographs of structures presumed to be replicating λ phage and polyoma chromosomes have been obtained, which are, in essentials, identical to Cairns's autoradiographs. Electron micrographs are, of course, always open to familiar criticisms, but recently Bourgaux, Bourgaux-Ramoisy and Dulbecco (*Proc. US Nat. Acad. Sci.*, **64**, 701; 1969) have reported a centrifugation analysis of replicating polyoma virus chromosomes which is completely consistent with the Cairns model. They have identified a replicative intermediate which is ring shaped, forms a heterogeneous population containing strands of variable length, has nicked DNA, and is larger than the relaxed circular DNA that can be obtained from virions. Moreover, label chases from this intermediate into the superhelical DNA of the virions. All the properties of this replicative intermediate fulfil the requirements of Cairns's model of replication; on the other hand, Bourgaux *et al.* found no evidence of single DNA strands longer than those found in the virus, which should, of course, be present if the polyoma chromosome replicated as a rolling circle.

Some of the conflicting ideas about the replication of λ phage chromosomes have also been resolved recently by Carter, Shaw and Smith (*Biochim. Biophys. Acta*, **195**, 494; 1969). In the past there has been argument as to whether λ DNA replication involves circular molecules or linear concatemers, and the answer seems to be that both forms occur at different stages in the replicative cycle. During the first phase, completed within the first 15 minutes, circular λ chromosomes are replicated, apparently by the Cairns mechanism, to yield covalently closed twisted circular progeny DNA, but these molecules according to Carter *et al.* are never packaged into progeny phage. Indeed, their role is a complete mystery. By 15 minutes after infection linear concatemers up to eight times as long as the λ genome appear and this DNA is fragmented and packaged into progeny phage. Unfortunately the experiments tell nothing about the origin of the concatemers; what data there are are equally consistent with the rolling circle or Cairns model of replication. This means, of course, that the rolling circle model cannot yet be dismissed as irrelevant to replication of λ chromosomes, and the electron micrographs of Cairns type structures isolated from λ infected *E. coli* may be irrelevant to the replication of DNA destined to be packaged into progeny phage. They may simply be pictures of molecules in the first, and apparently abortive, phase of replication.

ICHTHYOLOGY

Another Goby in British Waters

THE discovery that a fish presumed to be absent from British waters has actually been lurking in the shallows of south-west Ireland for at least thirty years is a blow to the complacency of those who like to think that the British fish fauna is thoroughly well known. Gobies are familiar members of the British sea shore fauna and commonly caught by holidaymakers with shrimping nets. But nobody knew that *Gobius cruentatus* came so far north until Dr A. Wheeler of the British Museum (Natural History) found a neglected specimen in the National Museum of Ireland. It had been