not angled, and so there would be a strong likelihood that part of the vagina would be perforated, because the uterus usually tilts forward at the top of the vagina. The result of this would have been peritonitis, which was probably a common consequence of ancient abortions (and is still a danger with back street operations). In this respect a Romano–British uterine probe, found at Hockwold in Norfolk, on the edge of the fens, is superior. This instrument is angled, and Dr Wells has found that it has exactly the same proportions as a modern version made about two thousand years later. A further danger in the use of rather blunt dilators, such as those found in Peru, is that sudden death may follow uterine cervical shock or embolism. Abortion was clearly a hazardous business in ancient Peru.

## MOLECULAR BIOLOGY

# A Termination Enzyme?

from our Cell Biology Correspondent

LAST year Cuzin and his colleagues (Cuzin, Kretchmer, Greenberg, Hurwitz and Chappeville, *Proc. US Nat. Acad. Sci.*, **58**, 2079; 1967) reported the isolation of an enzyme from *E. coli* which hydrolyses N-acyl-amino-acyl-*t*RNAs to yield N-acyl-amino-acids and free *t*RNAs. Cuzin *et al.* were, of course, searching for an enzyme involved in chain termination, specifically in the release of the completed polypeptide chain from the *t*RNA. The enzyme they isolated possesses this property; it releases N-acetyl-amino-acids, N-substituted oligopeptides and diphenylalanine from the linkage with *t*RNA. The enzyme, however, has different charge properties to the protein factor, isolated by Cappechi, which is required for chain termination directed by an amber codon. Kössel and RajBhandary (*J. Mol. Biol.*, **35**, 539; 1968) have now further characterized this enzyme from *E. coli* and have detected a similar activity in baker's yeast, but the combined data of the two groups are still insufficient to draw definite conclusions about its role *in vivo*.

The enzyme has no effect on amino-acyl-*t*RNAs but it hydrolyses N-acetyl-amino-acyl-*t*RNAs; this means that it can distinguish between a free and an acylated amino group. It is specific for L amino-acids and N-formyl-methionyl-$t\mathrm{RNA_F}$ and N-acetyl-methionyl-$t\mathrm{RNA_F}$ are not cleaved to any considerable extent. In other words, the enzyme does not hydrolyse the specific chain initiating amino-acid attached to the initiator *t*RNA. On the other hand, it does hydrolyse N-acetyl-methionyl-$t\mathrm{RNA_M}$. The size of the RNA moiety of the substrate affects the hydrolysis; when N-acetyl-amino-acyl-*t*RNAs are digested with ribonuclease $T_1$ so that the *t*RNA is reduced to a short oligonucleotide attached to the acylated amino-acid, the enzyme fails to hydrolyse the ester bond. This suggests that *in vivo* the true substrate of the enzyme contains polynucleotide, most probably a *t*RNA molecule, rather than an oligonucleotide. With regard to the acyl-amino-acid moiety of the substrate, by similar argument Kössel and RajBhandary conclude that *in vivo* the substrate may well be an oligo or polypeptidyl-*t*RNA rather than a simple N-acyl-amino-acyl-*t*RNA.

From these data it is impossible to decide whether the enzyme functions in chain termination or chain initiation. As the enzyme differs from the factor which catalyses the release of polypeptide from the polypeptidyl-*t*RNA-*m*RNA-ribosome complex under the influence of an amber (UAG) codon, it may not be involved in termination. Because it is involved in the metabolism of N-acyl-amino-acyl-*t*RNAs the enzyme might ensure correct initiation by destroying oligopeptidyl-*t*RNAs which can replace N-formyl-methionyl-$t\mathrm{RNA_F}$ in chain initiation. In this context the fact that the enzyme is without effect on N-formyl-methionyl-$t\mathrm{RNA_F}$ is probably significant.

## EVOLUTION

# Where Cuckoos Come From

NEW light on the evolution of the parasitic habit of the glossy cuckoo has been provided by Dr Herbert Friedmann, director of the Los Angeles County Museum, in a recent issue of the *US National Museum Bulletin* (No. 265, 1968). For the twelve species of glossy cuckoo, *Chrysococcyx*, now widely distributed in New Zealand, Australia, the East Indies and the islands of the south-west Pacific, south-eastern Asia, and all of Africa south of the Sahara, Dr Friedmann suggests a common origin in the Australo–Malaysian area possibly in Pliocene times, from the stock represented today by *Cacomantis* and *Cuculus*, or at least from the common stock that gave rise to them.

The genus *Chrysococcyx* is one of several genera of cuckoos that are brood parasites. The species are all small and, because of their glossy metallic plumage, they form a natural assemblage, closely related to, but distinct from, *Cacomantis* and *Cuculus*. (*Cuculus canorus* is the common European cuckoo.) In an earlier paper on *Clamator* (*Smithsonian Misc. Collections*, 146; 1968), Dr Friedmann pointed out how the various genera of parasitic cuckoos reveal divergent paths of development in their specialization as parasites. *Chrysococcyx*, for example, has the same evicting habit as *Cuculus* in the early nestling stage, a phenomenon not present in *Clamator*. As in *Cuculus* and *Clamator*, the adult cuckoos have the habit of removing the host eggs from parasitized nests. In this latest paper Dr Friedmann has brought together and compared for the first time information on the phylogeny, differentiation, dispersal and behaviour of all the glossy cuckoos. All twelve species have between them a very wide range of host–parasite situations, although none has as many adaptive specializations as *Cuculus canorus*. Some species of *Chrysococcyx* have only a very small number of regular hosts, while others, for example, *basalis* and *caprius*, have many dozens of different hosts apiece.

## MEDICINE

# Old Diseases—New Ideas

ARE there hereditary factors in the pathogenesis of leprosy? Persons exposed to lepers for prolonged periods do not always contract leprosy. It is also known that consanguinity increases the chances of contracting it and that environmental factors cannot change typical lepromatous forms (lesions contain abundant *Mycobacterium leprae* bacilli) into tuberculoid ones (lesions contain few bacilli), or vice versa. It is hardly surprising therefore that several research workers are searching for associations between *Mycobacterium leprae* infections and certain genetic markers. This is the subject