direction of the right hand lower corner. A crater 15 km in diameter, called Langrenus C, lies to the north of Langrenus. It has a small, flat floor on which domes or hills may be seen. It has a depth of about 1·7 km, or a depth/diameter ratio of about 0·1. This is not inconsistent with its being an impact crater and there appears to be some blanketing—presumably by ejecta from the crater—of topography around Langrenus C. Therefore it is plausible that the crater C formed later than Langrenus itself.

Relative dating in this fashion, by stratigraphy, is one example of how techniques that are standard in geology can be applied to the Moon. With the success of future soft landing missions, isotopic dating and analysis of lunar rocks will at last provide an anchor for lunar theories and assist in untangling not only the history of the Moon but also the history of the whole solar system.

MOLECULAR BIOLOGY

How the Code Began

WHAT were the origins of the genetic code ? The latest issue of the *Journal of Molecular Biology* offers two papers on the subject, from F. H. C. Crick (**38**, 367; 1968) and L. E. Orgel (**38**, 381; 1968). Although primarily concerned with the genetic apparatus, the papers necessarily come to terms with the origin of life itself, and they demonstrate how fully the successes of molecular biology have transformed our approach to the problem of life's origin.

The two papers complement each other nicely. Crick outlines a possible genealogy for the code largely by back extrapolation from its contemporary properties, while Orgel is more concerned with forward extrapolation from the primeval broth. Crick's analysis, first presented two years ago at a meeting of the British Biophysical Society, hinges on two properties of today's genetic code: its universality and the evident non-randomness of its structure. Crick distinguishes two theories which account for the universality. First, the relationships between triplet and amino-acid may be invariant, because they are determined in some way by the chemical structures involved. There have been several attempts to demonstrate some specific fit between amino-acid and either codon or anticodon, but none so far have been convincing, and Crick now says that he has more faith in a second theory, that the structure of the code is a frozen accident. This theory assumes the common ancestry of all organisms and it holds that the code is universal because, once established, any change in it would be lethal.

The second feature of the code provides for Crick a clue to its origins. Very early on in the evolution of life, there was probably a stage when nucleic acids managed to replicate themselves without the agency of protein. The high content of non-informational nucleic acid in today's machinery for protein synthesis may be a relic of this time, and, in a neat aphorism for the laboratory, Crick suggests that *t*RNA looks like nature's attempt to make RNA do the job of a protein.

But as amino-acids became available, presumably by abiogenic means, their chemical versatility may have led to their rapid incorporation into the primitive nucleic acid systems. As a coding system for amino-acids began to emerge—probably triplet from the first—the first few amino-acids probably spread over all the triplets. More amino-acids would be pressed into service, and they would tend to associate with triplets previously coding for similar amino-acids, a tendency which would minimize the disturbance created by their arrival. This process would have the outcome that similar amino-acids related to similar codons, as is the case in the present code.

Orgel considers the prospects for life without nucleic acids and life without proteins. Amino-acids appear from mixtures of simple gases more easily than do the nucleotide bases, but the tendencies to complementary replication inherent in the bases themselves make nucleic acid systems much the more hopeful as precursors of living organisms.

There remain formidable problems in explaining the origins of the contemporary genetic apparatus, but Orgel is hopeful that experiment may provide useful evidence. Clues may come from geological finds, meteorites, the space programme (two genetic codes would be easier to explain than one), further study of contemporary organisms and perhaps the discovery of "living fossils". There is a growth on the walls of Harlech Castle which thrives in 10 N ammonia and apparently resembles certain Pre-Cambrian fossils more closely than any surviving organism. Studies of its biochemistry and genetics are awaited with some interest.

RNA PHAGE

Strange Ends

from our Cell Biology Correspondent

A LITTLE more than a year ago, groups working on the RNA bacteriophages were surprised to learn that the very last base, an adenosine residue, at the 3′ end of the single-stranded RNA molecules, which act as genome and *m*RNA of these phages, is added after the rest of the molecule has been replicated by Watson Crick base pairing. It is still far from clear why this is an essential step in the replication or what the last base does, but the discovery showed that the replication of these phage RNA molecules is a far subtler process than once thought. Now, on page 233 of this issue of *Nature*, De Wachter and Fiers report an even more surprising feature of the replication of Qβ phage RNA.

They decided to analyse the sequence of the 5′ end of Qβ RNA to see to what extent the 5′ and 3′ ends have complementary sequences and could base pair to give the molecule secondary structure. To their surprise they found that for any given population of RNA molecules, from phage grown from a single parental phage particle, there are two types of 5′ sequence. Roughly half the molecules have the sequence GGGGAAC whereas the other half have GGGGGAAC. These two sequences, one beginning with five G residues the other with four, were found in four separate phage preparations in the same proportions so they are not likely to be the result of a chance mutation in one experiment or some other artefact.