in only one peptide, and between the nine mutants the changed peptide was one of two. In both cases a lysine was replaced; one of the two lysines gave place variously to arginine, asparagine or threonine, the other always to arginine. The substitution is, moreover, characteristic of the allele type, regardless of the strain. From the sequence data so far available, it appears that the two susceptible lysines occur at positions 42 and 87 in the chain, which agrees nicely with the conclusions of genetic mapping experiments. The substitutions in all cases correspond to simple-base mutations. In a streptomycin-dependent mutant, the substitution is again at position 42 where a glutamine residue now appears. The allele types differ in the degree of translational fidelity of which the ribosome is capable and it thus seems that this function depends profoundly on the residue in this position.

The isolation in Wittmann's laboratory of the set of proteins from both the large and small subunits has opened the way to a variety of other approaches to the assignment of specific roles. An example is to be found in the identification by Gray *et al.* (*Eur. J. Biochem.*, **28**, 412; 1972) of the proteins implicated in anchoring the 5S RNA, which is an integral part of the large subunit. Gray and Monier had reported earlier that in the presence of a fraction of the group of proteins that are extracted at defined salt concentrations from the ribosome (the so-called "split proteins"), 5S RNA would associate with 23S to form a complex, retained by membrane filters. Two-dimensional gel electrophoresis now allows an identification of the proteins in the relevant fraction, and by examining the ability of separated proteins of the large subunits, singly and in combination, to cause the retention of a 1:1 complex of 5S and 23S RNA by a membrane filter, the identity of the binding proteins could be established. The upshot is that one protein (L18) is indispensable, but not in itself sufficient for complex formation. When either of two other proteins (L6 and L25) was added, binding ensued. Another protein (L2) also stimulates the retention of the RNA by the filters, but this result has no counterpart in sucrose gradient sedimentation, which suggests that L2 may merely exert some effect on the RNA so as to increase the interaction of the complex with the filter. Of the three essential proteins only one has a primary binding site on the 23S RNA, whereas the other two will bind to 5S RNA. All three proteins are released from the ribosome, together with the 5S RNA, at high salt concentrations. The same proteins appear contrariwise to be necessary for the reincorporation of 5S RNA into the unfolded large subunit, and it therefore seems not at all unlikely that they are part of the attachment site in the native particle.

Gray and Monier have also shown that part of the 23S RNA can be removed without disturbing the 5S binding site, and they have now made some progress towards the hallowed end of identifying a (presumably multiple) protein binding site on the 5S RNA (*FEBS Lett.*, **24**, 156; 1972). When a complex, containing unlabelled 23S RNA, labelled 5S RNA and protein, is exposed to ribonuclease a considerably smaller proportion of labelled nucleotides is released than from the uncomplexed 5S RNA. The residual hot RNA, when extracted and subjected to nucleotide mapping, then reveals which parts of the chain are protected in the complex. The largest piece to be found extends from residue 69 to the 3′ end (residue 120), and contains also the 5′ terminal sequence from residues 1 to 11, which is complementary to, and presumably base-paired with, the tract at the 3′ end, to form a kind of stem. In most of the fragments, however, this stem is missing, because of a break at residue 110. The rest of the molecule contains a sizable internally complementary tract, with breaks at three bonds, at the presumed turn. It seems likely then that the important protein binding sites occur in the sequence 69–110, though parts of the chain are still accessible to the nuclease.

A completely different approach to the assignment of functions to particular proteins in the ribosome involves the use of covalent affinity labels. Czernilofsky and Kuechler (*Biochim. Biophys. Acta*, **272**, 667; 1972) have bound phenylalanyl-tRNA, modified at the amino-acid with a reactive and radioactively labelled p-nitrophenylcarbamyl group. In the presence of poly U, and only then, this binds to the 50S subunit, leaving a strong label in two ribosomal proteins, after digestion with ribonuclease. A definitive identification of the two proteins, which can be presumed to lie in or near the ribosomal A-site, has not yet been achieved. Pellegrini, Oen and Cantor (*Proc. US Nat. Acad. Sci.*, **69**, 837; 1972), using the same strategy, labelled only one protein. Whether this was a consequence of the different specificity of their reactive derivative (bromoacetylphenylalanyl-tRNA) or, as Czernilofsky and Kuechler suggest, the low levels of radioactivity incorporated, is not clear.

Pulsations in White Dwarf Stars

THE application of modern statistical techniques, such as power spectrum analysis, to astronomy has resulted in an explosion of information about variable objects of all kinds. These techniques have been applied by various groups to the study of objects as diverse as the Sun and quasars; now, however, a continuing flow of data is coming from a systematic study of rapidly varying stars being made by one group. In next Monday's *Nature Physical Science* (September 4), B. Warner and E. Robinson report that studies at the McDonald Observatory, Texas, have resulted in the discovery of five "new" periodicities in the cataclysmic variable systems. These short period binaries show a variety of variations in their light curves, including considerable random contributions to the flickering caused by mass transfer. So this discovery of five periodic white dwarfs could only have been possible using a combination of sophisticated statistics and the best optical systems available.

Some idea of the importance of this combination is provided by the figures Warner and Robinson quote for the level at which visual inspection of light curves can detect periodicities (1 per cent of intensity) compared with the capability of power spectrum analysis to pick out periodic variations of only 0.001 mag in an 18 mag object (provided long data runs are available). The objects in which periodic variations have now been detected are Z Cam, CN Ori, UX Uma, AH Her and AM CVn (HZ29); the latter object is discussed in some detail, by the same authors, in the current issue of the *Monthly Notices of the Royal Astronomical Society*.

These results are important because they lend weight to the theory that the white dwarf component in these binary systems is likely to be oscillating in a non-radial mode, as suggested by Chanmugam (*Nature*, **236**, 83; 1972). Indeed, Warner and Robinson believe that they have identified discrete modes of oscillation, and that their observations show transitions between these modes. It seems likely that such detailed information about the behaviour of white dwarfs in close binary systems will not only reveal details of the structure of white dwarfs themselves but will also provide an insight into the processes causing the outbursts of these cataclysmic variables, which are at present far from completely understood. The classic example of such a system is WZ Sge; it is gratifying that the development of a theory about the evolution of the archetype (see, for example, Faulkner, *Astrophys. J. Lett.*, **170**, L99; 1971) and improved observations of other members of the same family seem to be leading towards the same coherent picture of cataclysmic variables.