specify are under parallel but not co-ordinate control ; *arg*E and *arg*CBH are repressed by the same conditions but differ in the extent of their response. Another indication is that nonsense mutants which inactivate the *arg*E enzyme do not affect the others ; but such mutations in *arg*C may inhibit the expression of both *arg*B and *arg*H just as mutants in *arg*B may inhibit expression of *arg*H. This implies that *arg*E is expressed by the transcription and translation of one messenger RNA and *arg*CBH by the synthesis and expression of another, reading the genes in the order *arg*C *arg*B *arg*H.

Because deletions in the middle of the gene cluster may apparently change the expression of *arg*H, it has previously been thought that *arg*E is controlled from its left end, so that deletion of the second control elements between *arg*E and *arg*C places *arg*H under the control which usually acts only on *arg*E. By selecting cells for their ability to synthesize the enzyme coded by *arg*C in conditions in which they can only do so by losing their usual response to the regulator gene, that is by gaining operator mutations, Jacoby has identified the operator locus which governs the *arg*CBH cluster. But these cells also have a changed control of *arg*E. The operator locus maps between *arg*E and *arg*C, and has the usual *cis*-dominant control of expression of the structural genes.

An attractive explanation of these results is to suppose that the gene cluster has one operator—which controls both *arg*E and *arg*CBH—but two promoters, one for each unit. This would explain how both units respond to the same repression, but are expressed to different extents—their promoters must have different affinities for RNA polymerase. Ideas of this sort are borne out by the results of Elseviers *et al.*, whose analysis of deletion strains, taken together with recent demonstrations that the arginine genes are indeed controlled at the level of transcription (Cunin and Glansdorff, *FEBS Lett.*, **18**, 135 ; 1971 ; Krzyzek and Rogers, *J. Bact.*, **110**, 945 ; 1972), suggests that there is but one operator-promoter complex, located between the two genetic units.

A deletion which covers *arg*C and *arg*B but does not appear to extend into *arg*E seems to reduce greatly the extent of synthesis of enzyme from *arg*E ; this suggests that the elements which control expression of *arg*E are located at the right end of the gene, before *arg*C which starts the next cluster. In strains with such deletions, *arg*E expression can be restored by a mutation which may be located in this region. This supports the idea that *arg*E and *arg*CBH may be transcribed from opposite strands of DNA in opposing directions, *arg*E to the left of a central control site and *arg*CBH to the right. The sequence of sites in the cluster suggested by both articles is *arg*E, promoter$_{CBA}$, operator $_{E/CBA}$, promoter$_{E}$, *arg*CBH. By binding to the single operator, the represser protein could prevent synthesis of RNA from both promoters. This model presents problems of organization during expression, of course, for RNA polymerase may be forced to transcribe both strands in the central region and there may presumably be stereochemical interference between them. More precise mapping of control sites will be needed to determine whether this model is correct, of course, but it may not be unique, for Guha *et al.* (*J. Mol. Biol.*, **56**, 53 ; 1971) have discovered a similar case of divergent transcription from a central site in the biotin locus of *E. coli*.

When I wrote recently (*Nature*, **239**, 69 ; 1972) of the advantages of internal promoters for working out the mechanisms of gene expression, only two such elements, located in the histidine operon of *Salmonella typhimurium* and the tryptophan operon of *E. coli*, were commonly known. Deletions in the centre of the *arg*ECBH locus which delete the control sites seem, however, to allow independent expression of *arg*H. This complicates analysis of the locus, but seems to result from the presence of an internal promoter, located either in *arg*B or between *arg*B and *arg*H. This suggests that occurrence of these structures may be common rather than rare.

ASTRONOMY

Cen X-3 a White Dwarf?

by our Cosmology Correspondent

PROPONENTS of the pulsating white dwarf model of pulsars have been hard to find during the past couple of years in which rotating neutron star models have swept the board. But with the advent of the new age of X-ray astronomy, ushered in by Uhuru, has come evidence to suggest that, even if pulsars are not white dwarfs, other high energy sources may well be represented by these models, updated and with the dust blown off. The best candidate for a pulsating white dwarf now seems to be Cen X-3, which has a period of 4.8 s which can be explained, according to G. Vauclair of Meudon Observatory, in terms of the first harmonic radial pulsation of a 0.6 $M_{\odot}$ white dwarf (*Astrophys. Lett.*, **12**, 17 ; 1972).

As soon as reports of the 4.8 s periodicity came in last year, several groups were quick to point out that the period found corresponded well with the radial vibration periods of the white dwarf models developed in the early days of pulsar hunting (*Nature Physical Science*, **233**, 18 ; 1971 ; and *Astrophys. J.*, **173**, 213 ; 1972). In that earlier work, however, it was suggested that Cen X-3 might contain a white dwarf of mass roughly 1.1 $M_{\odot}$ vibrating in its fundamental radial pulsation. According to Vauclair, the first harmonic is always more unstable than the fundamental (see also *Astrophys. Lett.*, **9**, 161 ; 1971), and to explain the 4.8 s periodicity of Cen X-3 in this way would require that the mass of the vibrating star be 0.6 $M_{\odot}$; if Vauclair is correct, the most likely periodic vibration to be excited in a 1.1 $M_{\odot}$ model would be the first overtone 1.6 s oscillation.

An upper limit on the mass of the X-ray variable in the system has recently been derived by van den Heuvel and Heise (*Nature Physical Science*, **239**, 67; 1972; see also *Nature*, **239**, 256 ; 1972). Using the parameters of the binary orbit they deduce that the mass

Fracture of Polymers

THE standard methods of metallurgical testing can be usefully applied to organic polymer materials to obtain information about their physical properties. Interpretation of the results is, however, more difficult because the more complex structure of a polymer allows energy changes and distributions to be more varied. Studies on polymethyl methacrylate by Johnson and Radon, to be published in *Nature Physical Science* next Monday (October 9), have been concerned with accurate determinations of the fracture toughness by Charpy impact testing.

By monitoring the effects of temperature on the fracture toughness they have shown the effects of changes within the molecular structure of the polymer. The well known β-relaxation point attributed to the ester side groups was prominent, and a novel effect observed was attributed to a transition in the γ-methyl group. Johnson and Radon calculated activation energies for both these changes.

A reasonable correlation between data derived from electrical techniques, n.m.r. and tensile testing was evident, and the fracture toughness was found to be dependent on the dissipation of relaxation energy.

The results suggest that the fracture toughness of a glassy polymer is independent of strain rate—with the important proviso that the test method should not affect the structure, thermally or mechanically. During fast crack propagation, for example, adiabatic heating was observed. If such effects can be eliminated it seems likely that accurate studies of fracture toughness will allow the detection of changes in the molecular configurations of polymeric materials.