ASTROPHYSICS

Brightness Changes in Quasars

THE way in which the dimensions of quasars are estimated is questioned in a letter to the *Astrophysical Journal* (**152**, L139; 1968) from Morrison and Sartori of the Massachusetts Institute of Technology, who suggest that quasars may be much larger than hitherto suspected. New estimates of the sizes of quasars based on the report by Morrison and Sartori also have implications for the vexed question of quasar distances. So far, knowledge of the sizes of quasars has been largely based on changes in their observed brightness. The argument goes that the region giving rise to the brightness variations cannot be larger than a dimension given by the product of the time scale of the brightness variation and the velocity of light. Morrison and Sartori say that this upper limit is not necessarily valid. What may be happening during the brightness fluctuations, they say, is that an outburst from a small nucleus is transmitted to the surrounding matter by a disturbance which may be in the form of electromagnetic radiation, particle flux or a shock wave, and that the surrounding matter is then excited to emit the radiation detected by telescopes. Morrison and Sartori agree that the size of the nucleus triggering the emission must be limited by the time scale of its outburst, but hold that the dimension of the region emitting the observed radiation is not restricted in the same way.

Several implications follow. There is evidence that the quasar 3*C* 287 has shown a brightening over about a year, covering an angular extent of 2″. From the original argument, this would mean that the size of the emitting region is 1 light yr at a distance of only 10^5 light yr. Morrison and Sartori say that, in fact, 3*C* 287 may have a radius of about 10^3 light yr, placing it at a distance of the order of 10^8 light yr. This still excludes a cosmological interpretation for this quasar, but, as Morrison and Sartori point out, one is at least not forced to accept an extreme local model.

This fresh view of the implications of the brightness variations of quasars can also be extended to point sources. Here, by assuming quasars are at cosmological distances and adding the condition that the emitting region does not become large enough to allow the angular diameter to be distinguished, diameters approaching 10^6 light yr are conceivable for quasars showing brightness variations with a time scale of a year. Dimensions as large as this are not likely, however, as a quasar experiencing such an outburst in the past would have eventually reached a measurable size.

When the new concept of brightness variations is extended to radio observations of angularly unresolved components of quasars, such as 3*C* 273*B*, emitting regions having dimensions of 10^3 light yr are possible taking the objects to be at cosmological distances. The outcome is that yet more uncertainty is added to the quasar problem.

NUCLEIC ACIDS

Sticky Ends

from our Cell Biology Correspondent

DNA molecules from λ-phage have what are known as sticky ends. In other words, the two antiparallel strands of the DNA molecule are staggered so that they are base paired for their entire length except for a few nucleotides at the 5′ ends of both chains, which protrude as single chains from each end of the double stranded molecule. Because the base sequences of the protruding 5′-ends are complementary, the linear molecule can be converted into a circular molecule simply by rolling it on itself. The two 5′-ends then come into lateral register, the bases are held together with hydrogen bonds between their complementary sequences and the result is a circular double stranded molecule with a single break in the phosphodiester bond backbone of each strand. These breaks can be sealed by the enzyme DNA ligase to form circular molecules which are completely covalently bonded. Sticky ends obviously also provide a mechanism for joining DNA molecules end to end in a linear catenate. DNA molecules with sticky ends are not restricted to phage λ—many other temperate phages have them, so they may well provide a general mechanism for joining DNA molecules.

In the current issue of the *Journal of Molecular Biology* (**35**, 523; 1968), Wu and Kaiser report a partial determination of the sequence of the sticky ends of λ phage, which they have made in rather a novel way. They have exploited the properties of the Kornberg DNA polymerase from *E. coli* which, under defined conditions, will use as template the single strand ends but not the double stranded part of the λ DNA and which will add complementary bases to the 3′-end of the complementary chain. The number and sequence of the bases added by the polymerase reveal the length and the sequence of the sticky ends which are acting as template, and Wu and Kaiser have found that the polymerase primed with λ DNA added just forty bases to each DNA molecule. Because there are two sticky ends to each molecule, the most likely explanation is that each end is twenty bases long. Purified DNA polymerase, however, has a 3′-exonucleolytic activity (exonuclease II) and can remove nucleotides one by one from the 3′-end of a DNA chain in a reversal of synthesis. In theory, this property might confuse the interpretation of the number of bases added by the enzyme to λ DNA, but control experiments ruled out this formal possibility. Controls also established that the 5′-ends of DNA molecules are stable, so that no bases are being added to the 5′-termini. In other words, all the bases added in the polymerase reaction are added to the complement of the sticky ends.

The forty added bases comprised 13 dGMP, 13 dCMP, 7 dAMP and 7 dTMP residues. The equivalence of the G and C, and A and T, residues immediately suggests either that the sequences of the sticky ends of the two chains are complementary or, in theory at least, that each sticky end is self complementary. Studies of the incorporation one by one of nucleotides have ruled out the second alternative and at the same time have revealed the partial sequence of the ends. One end, starting from the 5′-terminal base, is $GGGG_{\wedge}$ $CGCG_{\wedge}$ $C_{\wedge}$ with another G at one or other of the three caret marks. That accounts for ten bases. The next nine bases must be some combination of six A or T residues and three G or C residues, and the twentieth base in from the 5′-end is T. The other sticky end has a complementary sequence.

The sequence has two striking features; first, it is rich in G and C residues and, second, the G and C