PECULIAR STARS

Astronomical glasnost

Bruce Margon

BULGARIA is not often viewed by Western astronomers as central to mainstream research. But on page 637 of this issue[1], Tomov *et al.* report fascinating new observations of the odd star MWC560, an object first listed in the Mount Wilson Catalogue nearly 50 years ago[2], although it was never studied in detail. Their discovery stands as a reminder that even bright stars may still hide truly odd behaviour, merely awaiting a spectroscopist sufficiently interested to obtain a single modern observation. Despite the arsenal of complex electronic solid-state detectors in use at most telescopes, these new observations were made with the most classical of techniques, the photographic plate.

The spectra described by Tomov *et al.* indicate the presence of a red giant star, plus an additional source of excitation which causes intense emission lines to be superposed on the spectrum. The integrated light output of the star is also erratically variable on timescales extending from days to years. All of these characteristics are shared by a class of binary system known as the symbiotic stars, of which more than a hundred are known. These systems are thought to consist of a red giant plus a highly evolved white dwarf, which is too faint to be seen directly, but causes the emission lines by inducing mass transfer through an accretion disk.

The unique aspect of MWC560 now pointed out is that the hydrogen emission lines are accompanied by prominent, violet-shifted absorption lines. The Doppler shifts of the absorptions indicate that the gas velocities vary from night to night, and can grow as large as 6,000 km s^{-1}. The profiles of the absorption lines are complex, and also vary erratically. Similar spectral and photometric observations were reported several years ago at a meeting[3], but failed to draw anyone's attention, perhaps as they were never published in a journal. The Bulgarian report will not suffer a similar fate. Already extensive satellite observations of the ultraviolet spectrum of the star have been submitted for publication[4], again indicating erratic, very high velocity ejection of matter.

It is too early to form a coherent model of this odd behaviour, but all of the observers[1,3,4] suggest that there is mass transferred from the giant onto a compact companion, followed by ejection of this matter from the system, thus explaining the high-velocity spectral absorption features. However, the peak velocities observed are far higher than those seen in symbiotic stars, or even in the far more spectacular nova phenomenon. Why MWC560 is uniquely different is the prize question — perhaps the nature of the secondary star will bear on the answer.

The story of MWC560 carries some poignancy owing to the recent death of Nicholas Sanduleak, formerly of Case Western Reserve University in Ohio. Sanduleak spent a lifetime of work patiently surveying and cataloguing peculiar stars; the bizarre relativistic object SS433 and the progenitor of the 1987 supernova in the Large Magellanic Cloud, Sk −69° 202, both bear his name as the initial cataloguer. Just three weeks before his untimely death, Sanduleak, who was also responsible for one of the earliest spectral comments[5] on MWC560, submitted a circular to the International Astronomical Union[6] discussing observations obtained a few weeks before, and motivated by an early announcement of the work by Tomov *et al.*. It was Sanduleak's final contribution to the literature. Although he was not the very first to call attention to MWC560, this object will most certainly prove to be his kind of star. □

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3. Bond, H.E., Pier, J., Pilachowski, C., Slovak, M. & Szkody, P. *Bull. Am. astr. Soc.* **16**, 516 (1984).
4. Michalitsianos, A.G. *et al. Astrophys. J.* (submitted).
5. Sanduleak, N. & Stephenson, C.B. *Astrophys. J.* **185**, 899–913 (1973).
6. Sanduleak, N. *IAU Circ. No. 4997* (1990).

GENOME MAPPING

Clone maps made simple

Peter Little

IF the human genome project is to reach its ultimate goal of establishing the DNA sequence of the entire 3×10^9 base pairs of human DNA, it will need to use cloned DNA 'maps' to break the genome up into manageable chunks. These maps are collections of recombinant DNAs that are aligned in an overlapping fashion, such that the whole genome is represented in the clone arrays and that any individual DNA base is contained in one or more clones (*a* in the figure). Hans Lehrach and colleagues now report[1] the first practical results of a method that Lehrach has been developing for the past seven years which may be powerful enough to generate large maps of whole genomes in a relatively non-labour-intensive fashion.

What is the method? Consider a random, short DNA sequence of N bases. One would expect this to occur once in 4^N bases (assuming all four bases occur with equal probability). As the sequence gets longer the frequency of occurrence must decrease and in principle it is possible to select a length and sequence of DNA, generally of around 10 bases that should be found every 40,000 base pairs or so, such that there is about a 50 per cent probability of any 40,000-base-pair fragment containing the sequence. Now consider two different DNA fragments cloned in cosmid vectors — these contain 40,000 base pairs of passenger DNA. The probability that a given sequence occurs at random in both of these cosmids is about 25 per cent but the probability of two unrelated DNAs having 10 or 20 sequences in common is tiny. We can build up a signature of presence or absence of sequences in each cosmid that could be presented as a binary string — 1 for present, 0 for absent.

Now consider the case if our two chosen cosmids overlap in the DNA they contain. Clearly, they will contain a similar pattern of sequences (*b* in the figure). Cosmids 1 and 2 overlap in region A and cosmids 2 and 3 overlap in B and therefore will have identical sequences in these regions. As long as there are sufficient test sequences, the overlap will be above statistical noise (that is, the probability of random similarity of occurrence patterns will be negligible) and we can generate the map of the three cosmids shown.

This scheme can be practically applied by using short DNA oligonucleotides as hybridization probes to cosmid clones: this is what Craig *et al.*[1] have done, using the 153-kilobase herpes simplex virus (HSV) genome as a model system. They used 22 12-base probe sequences from known positions in the completely sequenced HSV DNA and hybridized these to arrays of 384 cosmids. Although the probes were in defined positions in the genome, the analysis does not use this information. Instead, the 'binary' signature of each cosmid is analysed by computer programs that try to work out an optimum order for the probes by consideration of potential overlapping clone signatures, based on both presence and absence of sequences in clones. Thus the final solution to the analysis is both a map of cosmid clones and also a map of probe locations. The method seems to work well, and noise levels, which comprise cross-hybridization to related sequences, actual repeats of sequences, and spurious artefacts, seem to be well within the error limits.

What are the prospects for larger application of the technique? Lehrach has presented random-number simulations[2]