

then absorbed out of the antiserum on a column of a covalently immobilized peptide fragment. This antibody fraction binds specifically to the given peptide fragment, as well as to the intact protein. The differences between the two kinds of antibodies manifest themselves in a number of ways, and the implication is that they are specific respectively for the native and disordered conformations of the antigenic fragment, in this case residues (99–149) of Staphylococcal nuclease. This is the C-terminal part of the chain, and is known from the X-ray structure to be highly α -helical in the native protein, but essentially a random coil in isolation. The native conformation of the nuclease is stabilized by the ligands, calcium and thymidine diphosphate; now whereas these species have only a small stimulatory effect on the precipitin curve of nuclease with native-state antibodies to the single segment, they induce strong inhibition of the interaction with random-state antibodies. Moreover, the former causes inhibition of nucleolytic activity of the enzyme, whereas the other has no such effect.

Contrariwise, interaction of native-state antibody with the free fragment was weak (the binding measurements being made by estimation of uncombined antibody in terms of its inhibitory effect on the activity of added native nuclease). An active enzyme can be made by recombination of N-terminal and C-terminal fragments, but Anfinsen and his colleagues have also found that fragment (6–43) will combine with (50–149) to give what seems to be a conformationally native molecule, with, however, no activity (for which some at least of the missing residues are essential). This, so to speak, emasculated enzyme will combine well with the native-state antibodies. If then one regards the separated fragments of the chain, which, as stated, are more or less random coils, as existing in a state of equilibrium between the random and the folded conformations, in which the former is overwhelmingly favoured, then introduction of the native-state antibody will trap the folded form, and so displace the equilibrium.

From a comparison of the antibody-antigen association constant with the antigen in the folded and unfolded forms (intact protein and free peptide respectively), the conformational equilibrium constant for the peptide fragment can in principle be easily enough determined. Many other well characterized situations involving coupled equilibrium of this kind are known. This approach offers what is probably the only rational basis at present available for some sort of experimental estimate of a conformational equilibrium constant, when the equilibrium favours one form to an immoderate degree.

HUBBLE CONSTANT

New Determination

from a Correspondent

SINCE 1939 when Rudolph Minkowski used the 100-inch telescope on Mount Wilson to obtain slit spectra of supernovae, their interpretation has been a major puzzle to astrophysicists. Minkowski himself described the spectra as being overlapping Doppler-broadened emission lines of unknown origin. Recently, however, the notion originally due to Pskovskii has been gathering support that many, if not all, the spectral features can be explained as very broad absorption lines superposed on a continuous spectrum.

This interpretation has now been applied to Type I supernovae by David Branch and Bruce Patchett of the Royal Greenwich Observatory in the *Monthly Notices of the Royal Astronomical Society* (161, 71; 1972). Hitherto the Type I spectra have been the most puzzling of supernovae spectra as they lack even the familiar landmark of the Balmer lines of hydrogen which are present in Type II supernovae. Branch and Patchett show that one can identify nearly all the intensity minima in the spectra of the two supernovae originally studied in the 1930s by Minkowski with lines of singly ionized iron with a blueshift of $10,000 \text{ km s}^{-1}$. Further, they construct synthetic spectra using lines of titanium, scandium, magnesium and silicon as well as iron. These show that, when the excitation state and abundance of each species are considered, the iron lines are indeed most prominent, that several remaining minima in the spectra are explained and that the overall agree-

ment of the observed and synthetic spectra is good.

Branch and Patchett then go on to use their line identifications and the outflow velocity derived therefrom to determine the distance to the supernovae by the first application of a method originally suggested by Leonard Searle of the Hale Observatories. Because by the Stephan-Boltzmann law the luminosity of the supernova is proportional to the product of the area of the star and the fourth power of the effective surface temperature, data on the light and colour variations of the supernova as the outburst proceeds give the fractional rate of increase of radius with time. Fixing the outflow velocity leads therefore to a value for the luminosity and hence distance of the supernovae. Although no light and colour curves exist for the supernovae studied by Minkowski, Type I supernovae are sufficiently homogenous to adopt mean curves for the class which are good enough to give an absolute magnitude $M_V \sim -20.8 \pm 0.8$.

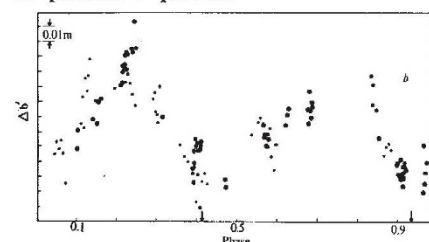
The real importance of this result is that the absolute magnitudes of such distant objects, in galaxies with appreciable cosmological recession velocities and beyond the effect of any local irregularities, provide a new method of determining the Hubble constant. This method is quite independent of the normal astronomical methods which rely on a step-by-step process of distance determination from nearby stars by way of a series of "standard candles" (variable stars, globular clusters, and so on) whereas the method used by Branch and Patchett is, if their model is correct, more directly related to the laws of

Optical Studies of Cyg X-1 (HDE 226868)

THE intriguing system Cyg X-1 is presently receiving attention from X-ray, optical and radio astronomers. The X-ray source was identified with the star HDE 226868 because of the coincidence of a radio outburst from that star with changes in the X-ray flux from Cyg X-1 (see *Nature*, 241, 246; 1972). The properties of that star have suggested to some astronomers that the X-ray emission must be coming from a black hole orbiting the BO supergiant; but the issue is still open.

In next Monday's *Nature Physical Science* (February 12), Lester, Nolt and Radostitz report photometric monitoring of HDE 226868 (see diagram). These observations do not show the same variability of hydrogen emission which others have reported (see, for example, Bolton, *Nature*, 235, 271; 1972) and in addition there is now some doubt about whether or not there is an eclipse of the associated X-ray source at all.

Lester *et al.* suggest that the evidence now favours one of two models. First, the companion may not be the source of X-ray emission, or the X-ray emitting region may not be eclipsed; second, the optical data at least are consistent with a tidally distorted binary with no optical eclipse (a possibility also considered by Bolton, *Nature Physical Science*, 240, 124; 1972). They do not come down on either side of the fence, and it looks as if Cyg X-1 will continue to present a puzzle.



Observations of HD 226868, b' filter measurements plotted against phase. Arrows indicate conjunction.