PERSPECTIVES

An Exploding Star in Motion

Roger A. Chevalier

Stars in other galaxies are normally far too small to be resolved at Earth, but as Marcaide et al. report on page 1475 of this issue, a sensitive array of radio telescopes in a worldwide network has now produced a time sequence of images of an exploding star (1). The supernova, designated SN 1993J, was discovered in the galaxy M81 by a Spanish amateur astronomer on 28 March 1993 (2). With an estimated distance from Earth of 12 million light years, it is relatively close for a supernova. Observations of the progenitor object imply that it is an extended star with a radius approximately equal to the Earth-sun distance. The explosion accelerated the outer stellar layers to a speed of more than 10,000 km s⁻¹ so that the star had expanded by a factor of more than 1000 at the time of the radio imaging. Despite the rapid expansion, the radio imaging could begin only 6 months after the initial explosion because of the great distance. The results directly show the expansion of a circular shell with some persistent structure.

Not all supernovae are strong radio emitters. The fact that the progenitor star was highly extended is a crucial aspect of the radio emission. Massive, extended stars in the late phases of evolution have slow, dense stellar winds; it is the collision of the supernova with this dense wind that gives conditions suitable for radio emission. The supernova sweeps up a shell of the wind gas (see figure), with a shock front at the leading edge. The shell tends to slow down with time, so that the cool, expanding supernova gas catches up with the shell and creates another shock front, the reverse shock. Shock fronts are sites of relativistic electron acceleration, and in the presence of the magnetic field in the swept-up shell, the high-energy electrons emit radio synchrotron radiation. This is the basis for the wind-interaction model of radio supernovae (3). Supernova SN 1987A was the first naked-eye supernova in nearly 400 years and was by a factor of 70 closer than SN 1993J, but it was a faint radio emitter. The reason is that its progenitor star was compact, by a factor of 10 smaller than that of SN 1993J, and it had a fast, lowdensity stellar wind. In that case, the observed radiative phenomena were powered by radioactivity and there was little evidence of the wind interaction.

The wind-interaction model predicted that the radio emission from SN 1993J would be in a fast shell, and the radio imaging has confirmed that this is the case. This would not be so for a central power source such as a pulsar. In more detail, the interaction model predicts that the inner boundary stant, as has already been attempted for SN 1979C (4). The problem is that imaging is difficult for distant supernovae and the radio observations can give only a crude size. The structure of the emitting shell is then important. The observations of Marcaide et al. (1) show a ratio of inner shell radius to outer of 0.7 and self-similar evolution; that is, the structure relative to the outer radius remains time invariant even though the outer radius is expanding. The interaction theory predicts self-similar evolution, but with a narrower emitting region. The ratio of inner to outer shock radius is about 0.8, and instabilities that can build up the magnetic field occur in only the inner half of the shell. The broader emitting region may



Shocking images. A sequence of SN 1993J radio images, produced by Marcaide *et al.*, reveals a year in the life of a supernova—and a symmetrical shock front development. [From (1)]

of the radio shell should be the reverse shock front. This shock front can initially heat the gas to a temperature of 10 million kelvin, hotter than the solar corona, and the gas radiates x-rays. If the density is sufficiently high, the radiation cools the gas to the point at which optical line radiation is emitted. Spectra of SN 1993J at optical and ultraviolet wavelengths show the broad-line emission expected from the cooling shock

wave, and the breadth of the lines gives the velocity of gas at the reverse shock front. Combining the velocity with the age yields the radius of the reverse shock front. The angular size measured from the radio image, combined with the distance to M81, also yields a physical size, which agrees within the errors with the first measurement.

For more distant supernovae with poorly determined distances, this technique has the promise of determining distances to galaxies and yielding a value of the Hubble conbe associated with clumping in the wind. Detailed calculations are necessary to investigate this association. Unfortunately, different supernovae may have different shell structures, which will introduce an uncertainty in Hubble constant estimates.

The radio images show the shell to be surprisingly circular, especially in view of detectable polarization at optical wavelengths (5). The wind and outer supernova



Detonation aftermath. The collision of the exploding star with the surrounding wind creates a shell of hot gas that is bounded by forward and reverse shock waves. The observed radio emission is likely to be associated with the hot shell.

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matter appear to be symmetric, and any asymmetry is more centrally located. Despite the symmetric shape, there are brightness variations around the shell that persist with time (1). One possible reason for this behavior is that the efficiency of particle acceleration at the outer shock front depends on the magnetic-field orientation. The magnetic field in a stellar wind should have a spiral pattern aligned about the stellar rotation axis. The magnetic field is too weak to affect the shock-wave dynamics, but it

could imprint a pattern on the radio synchrotron emission.

The observations thus confirm the basic wind-interaction model but raise issues that will require more detailed modeling and computer simulation. The combination of high densities and high velocities creates extreme conditions that are comparable with those in quasars, but here we have a clear picture of the physical situation. When the radio observations are combined with observations at optical, ultraviolet,

Molecular Mimicry in Protein Synthesis?

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 ${f T}$ his week's issue of Science includes the first report by the Aarhus group of the crystal structure of elongation factor Tu (EF-Tu) complexed with aminoacylated phenylalanyl transfer RNA (tRNA) and guanosine triphosphate (GTP)-the EF-Tu ternary complex (1). EF-Tu and its eukaryotic homolog EF-1 α deliver aminoacyl tRNAs to the ribosome during the elongation phase of protein synthesis (see figure). In addition to providing insights into the way aminoacyl tRNAs get to the ribosome, this structure addresses a long-standing, mechanistic question: Why does EF-Tu deliver only aminoacylated elongator tRNAs to the ribosome, never uncharged tRNAs or initiator tRNAs? Both because of the biological importance of protein synthesis and because of the long scientific history of this complex, the publication of its structure is a landmark.

The article by the Aarhus group does more than present an important structure, however. Nissen and co-workers have discovered that the overall shape of the ternary complex resembles that of the guanosine diphosphate (GDP) form of elongation factor G (EF-G; EF-2 in eukaryotes), the protein that catalyzes the translocation step of elongation (see figure). During translocation, the ribosome moves down its messenger RNA (mRNA) by three bases, and the tRNAs bound to it are rearranged so that the ternary complex called for by the next codon can be accepted.

That EF-G and EF-Tu are structurally related was already known. Their amino-terminal domains bind guanine nucleotides and are conformationally similar, as are their second domains (2-5). The new observation is that three domains at the carboxyl-terminal end of EF-G, which have no homologs in EF-Tu, together resemble tRNA and, relative to EF-G's nucleotide binding site, are positioned the same way as tRNA in the ternary complex. It seems that we have just been given a huge-albeit Delphic-hint about the mechanism of protein synthesis.

and x-ray wavelengths, we have a chance to follow and understand the initial expansion phases of the most extreme explosive events in nearby galaxies—supernovae.

References and Notes

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It was also known that EF-G and EF-Tu are functionally related (6, 7). EF-G and EF-Tu compete for a single factor binding site on the ribosome. Both bind to the ribosome when complexed with GTP and have guanosine triphosphatase (GTPase) activities that are activated by binding. Furthermore, both adopt conformations that have a low affinity for ribosomes after GTP hydrolysis. Nevertheless, the discovery that EF-G resembles the ternary complex suggests that the mechanism of EF-G-catalyzed translocation resembles the mechanism of EF-Tu-catalyzed tRNA binding at a far deeper level.

EF-G's function is easier to understand than EF-Tu's (6, 7). Translocation results when an elongating ribosome switches from its pretranslocational state to its posttranslocational state. EF-G-GTP binding



Elongation cycle of protein synthesis. The cycle starts with the binding of ternary complex to the ribosome (upper left), which results in the discharge of deacylated tRNA from the E site, placement of a new aminoacyl tRNA in the A site, and conversion of the ribosome from the post- to the pretranslocational state. Peptide transfer follows (right, middle). The binding of EF-G-GTP to the ribosome (lower right) restores the ribosome to the posttranslocational state, the mRNA advances by one codon, and its tRNAs are rearranged so that another cycle of elongation can ensue (8). Ribosomes are shown as rectangles; the upper third is the large subunit and the lower third is the small subunit. When the subunits are aligned, the ribosome is in its posttranslocational state. When they are misaligned, ribosomes are in the pretranslocational state. Transfer RNAs appear as colored bars, and their amino acids as small circles of the same color. Square, EF-Tu; large circle, EF-G. Messenger RNA is shown as a horizontal line that crosses the small subunit. Its colored segments represent specific codons, whose colors match those of the corresponding amino acids.

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