Supernova Maser Emission

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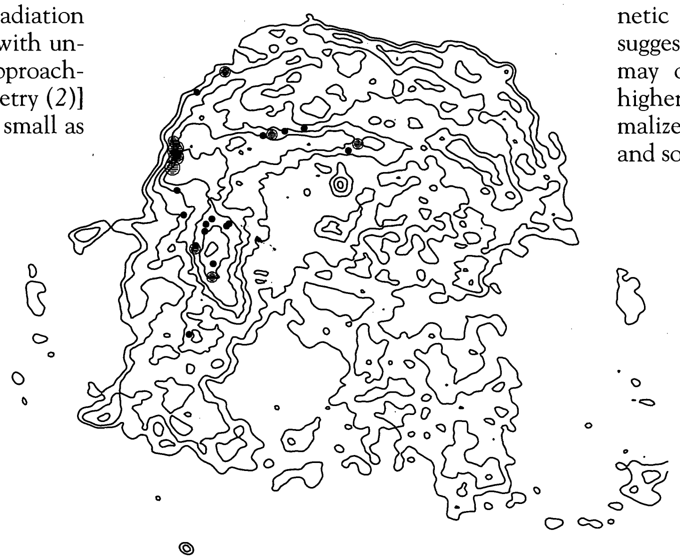
Maser emission (the microwave analog of laser light) from the energy levels of an inverted population of interstellar molecules was first discovered in 1965 (*1*). This finding had a strong impact on astronomy and related fields, including molecular physics. Cosmic maser emission has been extensively used to probe dynamics and physical conditions of the interstellar gas around galactic nuclei, protostars, and evolved stars. The extremely high brightness and narrow spectral width unique to maser radiation has allowed astronomers to detect with unprecedented angular resolution [approaching 10^{-3} arc sec by radio interferometry (*2*)] compact gas clouds whose size is as small as one astronomical unit.

At present, seven molecular species—H_2O, OH, CH_3OH, SiO, HCN, H_2CO, and NH_3—are known to emit strong maser lines. Elsewhere in this issue (*3*), Yusef-Zadeh and his colleagues report observational results obtained with the Very Large Array (VLA) in New Mexico showing that the 1720-MHz maser of OH delineates well the interaction of supernova shocks with surrounding molecular gas in the galactic center region. The OH 1720-MHz transition has somehow escaped intensive scrutiny so far, compared with the other three transitions of OH at frequencies from 1612 to 1667 MHz, observed toward regions of massive star formation or evolved stars. This work (*3*), along with another study of the same maser transition toward supernova remnant W28 (see figure) (*4*), strongly indicates that the OH 1720-MHz maser can be used to probe the shock-excited gas around supernova remnants at high angular resolution.

The evolutionary time scale of a star whose mass is greater than 10 solar masses is fairly short, about 10 million years, so such massive stars are likely to be found near their parent molecular clouds. They experience catastrophic explosions at the end of the stable, nuclear-burning phase of their stellar evolution, and these explosions produce nearly spherical shock waves with stellar remnants, such as neutron stars or black holes, at their center. Such shock waves propagate into interstellar space and dynamically interact with the ambient gas, forming a supernova remnant. Although one may expect to see various indications of shocks, it has been discouraging that observational studies have rarely found such interactions near supernova remnants.



Remnant masing. Radio-frequency map of W28, a supernova remnant that has in its vicinity several sources of OH maser emission. The OH maser spots are shown by dots. [Adapted from (*4*), courtesy of D. A. Frail]

The rotational transition of interstellar CO molecules at a wavelength of 2.6 mm is often used to observe interstellar molecular gas. A CO survey at coarse angular resolution has indicated several cases in which CO is anticorrelated with a supernova remnant in spatial distribution, but such evidence is circumstantial at best (*5*). Only in one case, for supernova remnant IC443, is very broad CO emission over 20 km s^{-1} found, unambiguously indicating shock-accelerated gas (*6*). The physical conditions of the shocked gas cannot be generally estimated from CO, because most of the CO emission comes from unshocked gas under regular physical conditions. The detection of shock-excited maser action near a supernova remnant, on the other hand, can be used to probe the conditions of shocked neutral gas directly.

The object observed by Yusef-Zadeh *et al.* is a well-defined circular supernova remnant located near the galactic center, which has a stellar density 10^4 times greater than that of the solar neighborhood. Their map shows that the locations of the unresolved OH maser spots coincide well with the shell-like distribution of this supernova remnant. In particular, the most intense OH maser spot shows remarkably good positional coincidence with the brightest knot of radio continuum emission, which indicates strong shock compression or acceleration of high-energy electrons and magnetic fields. This coincidence is strong enough to make plausible a physical connection between the OH maser spots and the supernova remnant.

According to a theoretical study of the OH maser (*7*), the 1720-MHz transition may be inverted because of collisions with particles in shock fronts at a rather narrow density range of 10^3 to 10^5 cm^{-3} and at a kinetic temperature between 25 and 200 K, suggesting that the OH 1720-MHz maser may occur under limited conditions. At higher densities, the transition will be thermalized, owing to collisional deexcitation, and so will emit normal radiation whose intensity is close to what is expected at a local kinetic temperature. Before the work of Yusef-Zadeh *et al.*, a study with the VLA of the region near W28 (*4*), another galactic supernova remnant outside the galactic center, showed that the OH 1720-MHz maser delineates well the spots of strong interaction of the supernova remnant with the associated gas (see figure). The results by Yusef-Zadeh *et al.* (*3*) reveal the second case in which the OH maser radiation is shock excited.

Somewhat puzzling among the properties of the OH emission is the low and uniform velocity of the maser components. The apparent radial velocity of the OH is at about 5 km s^{-1}, much smaller than the typical velocity of the CO emission toward the supernova remnant, which is around 100 km s^{-1}. This gives an impression that the masing components are unusually quiescent for this region of rather violent gas motion. It may be that only molecular gas at such low velocity has conditions that satisfy the density range required for the OH maser, a somewhat ad hoc explanation; a few other more complex ways to explain this peculiar feature are presented by Yusef-Zadeh *et al.* (*3*). The finding may indicate another peculiarity unique to the galactic center region, for which we are still far from a convincing unified physical view.

These detections of shock-excited masers in supernova remnants should allow us to better understand the physical conditions of shocked gas. Detailed modeling of molecular processes in shocked gas and further searches for OH 1720-MHz masers will be highly valuable. In fact, a recent survey

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confirmed that at least 8 more supernova remnants emit the OH maser, among 66 observed (8).

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The Molecular Biology of Rice

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Rice: A valuable model system. [Photograph by Ronald R. Johnson/The Image Bank]

Rice provides the main source of food for 50% of the world's population and so may be the most important plant on Earth. It is also becoming an increasingly attractive plant for study by biologists. Rice has 24 chromosomes, and its genome is 4.3 megabases, one-tenth the size of the human genome and only three times that of *Arabidopsis thaliana*, a favorite plant of molecular biologists. A monocotyledonous plant, rice (*Oryza sativa* L.) belongs to the grass family (Poacea), which includes maize, sorghum, wheat, barley, and oats. A better understanding of the genetics and the biology of rice can therefore also help to improve these other food crops. New developments in two areas of rice molecular biology—genome analysis and transformation—will greatly influence future improvement of this important crop.

Researchers at the Rice Genome Research Program in Tsukuba, Japan, have recently constructed a genetic map of rice that contains 1383 markers, of which 883 are derived from expressed genes (*1*). The average interval between markers is 300 kb. Approximately 20,000 complementary DNAs (cDNAs) derived from a variety of tissues and cells cultured under different conditions were partially sequenced. This is the largest body of information on expressed plant cDNAs currently available and so will facilitate gene identification in other plants. One important finding to emerge from the analysis of cereal genomes is that, for much of the genome, the order of genes is well conserved among major cereals (*2*). This synteny extends to even the nucleotide level of the chromosome (*3*), suggesting that once genes with products of interest to agriculture are isolated from rice, counterparts in wheat, maize, and other cereals can be easily identified. Because the genome size of wheat is 34 times larger, and that of maize is 6 times larger, than the genome size of rice, information from rice may be crucial in finding genes in other cereals. A recent study in *Science* indicates that this synteny extends to quantitative trait loci that determine variation in complex phenotypes such as seed size, seed dispersal, and flowering time in the cereal genomes (*4*). These findings reinforce the notion that grasses can be considered a single genetic system (*5*).

The first successful positional cloning of cereal genes is reported by Song *et al.* in this issue of *Science* (*6*). The gene cloned is *Xa21*, which confers resistance to leaf blight, one of the major bacterial diseases of rice. The gene has novel features compared with other recently identified disease resistance genes in plants: *Xa21* has leucine-rich repeats, which are important for protein-protein interaction, and a serine-threonine kinase domain, which transmits a signal to quickly activate the plant's defense mechanisms against pathogen attack. The authors of this report are also isolating genes that determine resistance to rice blast, a fungal disease, and flowering time.

An actively transcribed retrotransposon has recently been described in rice. Tos17 is a member of the rice retrotransposon family and is actively transcribed in tissue culture (*7*). Many copies of this gene are inserted in numerous different sites in the chromosomes during tissue culture. Therefore, if a large number of plants are generated from cultured rice cells, some plants may have Tos17 in some of their genes. Indeed, insertion of this element in three different genes has recently been demonstrated (*7*). This finding implies that once a large pool of plants derived from cultured cells are prepared, mutants can be identified that have insertions in genes whose sequences are already known. This reverse genetic approach should become extremely powerful in defining the functions of genes with sequence information already in the database.

Functional analysis of isolated genes and crop improvement by molecular biological approaches require a simple and reliable method to transform plant cells. Rice is the first cereal in which fertile transgenic plants were obtained and is by far the easiest cereal to transform at present (*8*). Two methods are used for rice transformation: protoplast (cells without a cell wall) transformation, either by electroporation or polyethylene glycol (*9*), and particle bombardment of embryos (*10*). In both, transformed cells must be selected and plants regenerated from them. With these methods, rice with improved resistance to viral and fungal pathogens and insect pests has been generated (*11*). Transgenic rice has also provided information on promoter elements of monocot genes that confer tissue-specific and inducible expression (*12*).

Although these two methods are routinely used in laboratories worldwide, they are still laborious and time consuming. A simpler method is desirable. Monocots, including rice, are thought to be a poor host for *Agrobacterium* infection. Thus, *Agrobacterium* transformation, which is the most widely used method for plant transformation, has not been effectively used for rice and other monocots. But callus tissues from the scutellum of the mature embryo are highly competent for *Agrobacterium* infection in the presence of acetosyringone, an inducer of gene transfer from the bacterium to plant cells. By this means transgenic plants can be produced with high frequencies (*13*). This finding is important in three ways. First, cell culture and selection steps are much simpler than the two other methods. Second, the same transformation vector system can now be used for dicots such as *Arabidopsis* and tobacco and for rice, a monocot. Lastly, this method does not require any special equipment. This is particularly important for the progress of rice biotechnology in many rice-growing countries. This transformation method will likely open up a new era for the genetic engineering of rice.

Development of a saturated molecular map

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