

The supernova connection

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They are the most energetic events in the Universe, but the origin of γ -ray bursts has been hard to establish. Observations of a burst close to our Galaxy now show that supernovae are, as suspected, likely culprits.

The fog surrounding the identity of the progenitors of γ -ray bursts (GRBs) is beginning to lift, at least for the class of GRBs known as 'long' bursts. This is thanks to a series of observations of a burst that began on 29 March 2003, very close to our Galaxy. On pages 843, 844 and 847 of this issue, Uemura *et al.*¹, Price *et al.*² and Hjorth *et al.*³ reveal the evolution of this burst in unprecedented detail — and show that behind the GRB is the unmistakable signature of a supernova.

The GRB population divides neatly into long ones and short ones, depending on whether the burst of γ -rays lasts more or less than a few seconds⁴. About two-thirds of all observed bursts are long, and these are the only ones for which longer-lasting 'afterglows' at X-ray, optical and radio wavelengths have also been found. These afterglows may last up to several months, and from them the distance to the GRB and the identity of its host galaxy can be determined. There is good evidence that long bursts are largely associated with active, star-forming regions in small, blue galaxies. And, in at least three cases, there has been tantalizing evidence that GRBs are associated with a particular type of supernova⁴ — although that interpretation has so far been fraught with uncertainty.

A 'usual' supernova arises when the core of a massive star collapses, ejecting the stellar outer envelope. The majority of such supernovae result from parent stars that are less than about 30 times heavier than the Sun, and the core collapse produces a neutron star. These supernovae are normally detected weeks after the collapse, because the ejected envelope only brightens sufficiently to be detected at optical wavelengths some weeks later. The only signals of the collapse that are expected to reach the Earth promptly are a flux of tiny particles called neutrinos (which was picked up for the supernova SN1987a by the Japanese neutrino detector Kamio-kande) and gravitational waves (which have yet to be detected).

For heavier stars, however, the core is thought to collapse into a black hole, and the resulting brief episode of mass accretion has been proposed as the central engine driving GRBs⁵. This kind of collapse was initially referred to as a 'failed' supernova, as it was thought that the stellar envelope would not be ejected. A GRB would instead result from

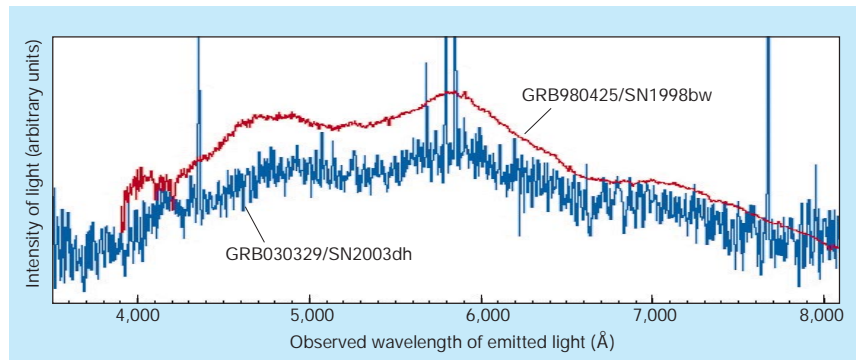


Figure 1 A good match. The spectra of the wavelengths of radiation from the γ -ray burst GRB030329, believed to be associated with the supernova SN2003dh, and from GRB980425/SN1998bw are remarkably similar in shape¹⁵, suggesting that in general the GRB and supernova phenomena are related. Detailed observations^{1–3} of GRB030329 offer the strongest proof yet that γ -ray bursts are indeed produced by supernovae that result when the core of a massive star collapses.

a relativistic jet of gas fed by the black hole; it would break through the stellar envelope, leading to radiative shocks in the rarefied environment outside the star.

In 1998, observations of GRB980425 showed an anomalous brightening of its optical afterglow a few weeks after the burst, possibly linking it to a roughly contemporaneous supernova, known as SN1998bw, whose ejected envelope would have brightened at about that time. Suspicions grew that long GRBs might, after all, be associated with 'successful' supernovae. In fact, the few supernovae tentatively linked to GRBs appeared even more energetic than usual, and were dubbed 'hypernovae'⁶, or 'collapsars'⁷. There is also a more elaborate offshoot of the supernova idea — the 'supranova'⁸. Here, the core collapse is assumed to be a two-step affair: the first step produces a temporary neutron star and a supernova; in the second step, a few weeks or months later, the neutron star collapses into a black hole, producing a GRB.

The association of long GRBs with supernovae (or even supranovae) is based on the approximate coincidence in time of the GRB and the inferred instant of the supernova core-collapse. The latter is deduced from an extrapolation back from the peak brightness of emitted light — an extrapolation that is model-dependent and uncertain, not least because these objects are so far away and very faint. This situation changed dramatically with the observation of GRB030329 in March of this year. Its coordinates were

disseminated by the HETE-2 spacecraft within 90 minutes of its detection, enabling ground-based telescopes to make follow-up observations almost immediately. Although more than two billion light years away, GRB030329 may be the nearest cosmological GRB yet seen^{3,9}. (In terms of the conventional astronomical distance measure, its 'red-shift', z , is 0.169; previous GRBs have usually only been seen in the range 0.4–4.5; the exception is GRB980425, if its association with SN1998bw at $z=0.008$ is real.)

After a week, the pattern of light emitted by GRB030329 — its 'light curve' — started to show the beginnings of a slight bump. Ten days later, this bump was identified as being caused by an energetic supernova, labelled SN2003dh^{3,10}. Because this GRB is relatively close to us, the identification of the light-curve peak, and its wavelength spectrum, is significantly stronger than in previous cases. The extrapolation from the peak brightness indicates that the time off-set between the GRB and the collapse of the supernova is unlikely to be greater than about two days, and is compatible with the two events being simultaneous. Hjorth *et al.*³ interpret this as ruling out the supranova model: if the two-step collapse of a supranova were to happen within two days, it is unlikely that its γ -ray emission and afterglow would match the observations.

Another remarkable feature of GRB030329 is the spectrum of wavelengths it has emitted. There is a tantalizing match between the shape of the distribution for GRB030329/SN2003dh and that of

GRB980425/SN1998bw (Fig. 1) that signals a strong connection between the two phenomena. The light curve of GRB030329, as discussed by Price *et al.*², shows a steepening that they interpret as being caused by a broadening of the jet-like outflow from its progenitor. The light curve also contains a wealth of other, finely structured detail that has interesting implications for the identity of the central engine driving the GRB. Uemura *et al.*¹ have found numerous bumps in the optical light curve, whose relative duration remains approximately constant, and at each of which the normalization of the light curve moves up (Fig. 1 on page 843). Simple explanations — that a jet has encountered an inhomogeneous, blobby medium or is itself patchy — do not work. But there is a satisfactory explanation¹¹: as the leading edge of fast jet gas moves further away from the central engine of the burst, it starts to decelerate and is caught up by batches of slower-moving jet gas, creating a 'refreshed shock'¹². These slower batches of gas could have been ejected towards the end of the γ -ray-emitting period (which lasts tens of seconds); at each catch-up episode, more energy is added to the afterglow.

The detection of GRB030329 is a watershed event. It proves that some, if not all, long GRBs are definitely associated with core-collapse supernovae, and thus are a consequence of the evolution of massive stars. It also strengthens the interpretation that the variability of burst light curves over short timescales is caused (largely, if not exclusively) by variable input from the central engine, rather than by the γ -rays

encountering a variable external medium. These observations fill in important missing gaps in the phenomenology of GRBs.

But other questions have not been addressed, such as what the magnetic content of the jets¹³ is, or whether all long bursts are associated with supernovae. Also, what is the connection between GRBs and the related, but fainter and softer phenomenon of X-ray flashes? The identity of the progenitors of the short GRBs is also an open question (a candidate might be mergers of double neutron stars), but it may be addressed by the Swift mission¹⁴, to be launched this December. From the present observations^{1–3} and their interpretation, however, it is clear that a new plateau has been reached in our understanding of the GRB phenomenon. ■

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Genome biology

Tales of the Y chromosome

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Determining the sequence of the human Y chromosome presented a daunting challenge to genome researchers. But the task is now done, and the secrets revealed justify the effort.

Ancient maps showed the known world in colourful detail, beyond the edges of which lay vast expanses of *terra incognita*. Much creative thought went into portraying this unexplored territory, often featuring nasty-looking serpents and dragons. Only when Magellan managed to circumnavigate the globe did it become apparent that the unknown was in fact navigable, and that the serpents and dragons, if not illusory, could at least be tamed. The human genome has its *terra incognita* too, some of it known, much of it subject to alternating angst and fascination by genome biologists, and all of it to be avoided if possible — until now. On pages 825 and 873 of this issue^{1,2}, a group of modern-day Magellans describe how they sailed headlong

into the frothy seas of duplicated, inverted and otherwise troublesome sequences on the human Y chromosome. They have emerged safely on the other side, with tales to tell.

Because of its distinctive role in sex determination, the Y chromosome has long attracted special attention from geneticists, evolutionary biologists and even the lay public. It is known to consist of regions of DNA that show quite distinctive genetic behaviour and genomic characteristics. The two human sex chromosomes, X and Y (Fig. 1), originated a few hundred million years ago from the same ancestral autosome — a non-sex chromosome — during the evolution of sex determination³. They then diverged in sequence over the succeeding

aeons. Nowadays, there are relatively short regions at either end of the Y chromosome that are still identical to the corresponding regions of the X chromosome, reflecting the frequent exchange of DNA between these regions ('recombination') that occurs during sperm production⁴. But more than 95% of the modern-day Y chromosome is male-specific, consisting of some 23 million base pairs (Mb) of euchromatin — the part of our genome containing most of the genes — and a variable amount of heterochromatin, consisting of highly repetitive DNA and often dismissed as non-functional. Now, in an accomplishment that can only be described as heroic, Skaletsky *et al.*¹ report the complete sequence of the 23-Mb euchromatic segment, which they designate the MSY, for 'male-specific region of the Y'.

Prioritization in the Human Genome Project had led to the heterochromatic regions of the Y and other chromosomes being set aside to be dealt with later, if ever. But there was reason to hope that the euchromatin of the Y chromosome would present no more difficult a sequencing challenge than that found elsewhere in the genome. That supposition could not have been more wrong. As Skaletsky *et al.* report, the MSY is a mosaic of complex and inter-related sequences that made this one of the most problematic regions of the human genome thus far to be successfully sequenced and assembled.

For instance, about 10–15% of the MSY consists of stretches of sequence that moved there from the X chromosome within only the past few million years. These stretches are still 99% identical to their X-chromosome counterparts and are dominated by a high proportion of interspersed repetitive sequences, with only two genes. A further 20% of the MSY consists of a class of sequences ('X-degenerate' sequences¹) that are more distantly related to the X chromosome, reflecting their more ancient common origin. And the remainder comprises a web of Y-specific repetitive sequences that make up a series of palindromes — sequences that read the same on both strands of the DNA double helix, with two 'arms' stretching out from a central point of mirrored symmetry. These palindromes come in a range of sizes, up to almost 3 Mb in length, with more than 99.9% identity between the two arms of each palindrome.

The repetitive sequences, particularly the palindromes, caused some difficulties for sequence assemblers. Genome-sequencing projects involve fragmenting the genome in question into small, overlapping pieces, sequencing them, and then using computer algorithms to put the pieces together in the correct order. There are various ways of doing this; assembling the MSY's palindromes (and discriminating between their arms) required an iterative mapping and