may act as stepping stones to foster evolution of new pathogens capable of attacking people with healthy immune systems[7]. With the possibility of using grafts from non-human species to replace tissues in humans, we also need to be aware of the potential for activation and genetic recombination of otherwise dormant retroviruses in the human genome or in the graft.

Antia *et al.* do not, however, emphasize cultural factors in disease emergence. Instead, they provide a way of identifying which agents are most worthy of attention — those closest to the epidemic threshold. An example suggested by Antia *et al.* is the threat of monkeypox in a world with little resistance to its relative smallpox, because of a lack of either vaccination or exposure. Furthermore, the result draws attention to the neglected topic of parasite dynamics in the pre-epidemic stages. This was brought into focus earlier this year when it was realized that the initial spread of severe acute respiratory syndrome (SARS; Fig. 1) depended heavily on the social connectivity of the first (index) case in a community. Such results and realizations give us a better understanding of how to contain infectious diseases, through early prevention rather than cure. Ultimately, we should learn where and when to apply our efforts to block transmission and so prevent an epidemic.

Currently, the resources and public attention devoted to an infectious disease depend on a combination of social, biological, economic and political factors specific to that disease. Disease virulence, transmissibility and incidence are included in such considerations. The complacency of the pre-HIV and pre-bioterrorism eras has yielded to a growing acceptance of the need to monitor pathogens and even pre-pathogens in our environment. It is not beyond imagination that, even with existing technology, methods could be developed for monitoring emerging pathogens, potentially distinguishing between strains with differing $R_0$ values. The means, provided by Antia *et al.*[1], of identifying these epidemics-in-waiting could become a critical tool in a global defence strategy against emerging pathogens. ■

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Quantum optics

# Light at a standstill

Marlan O. Scully

Nothing travels faster than light, but how slow can light go? Pulses of light have already been slowed to speeds of just a few metres per second, but now they have been brought to a complete halt.

Frozen light is a reality. As they report on page 638 of this issue, Bajcsy and colleagues[1] have trapped, and held, a pulse of light for a few hundredths of a millisecond, which is a long time in optical terms. To those unfamiliar with the realm of quantum optics, the notion of stationary light may seem rather strange. But ultraslow light — travelling at just a few, instead of 300 million, metres per second — is easily available in many labs these days. So bringing a light pulse to a full stop was the next logical step.

And it is of interest for many reasons. This is the latest development in a continuing paradigm shift in optics, occasioned by the marriage of quantum coherence in atoms and molecules with coherent light[2–5]. The ability to trap and hold light also holds promise for application to such diverse areas as quantum informatics, nonlinear optics and even the foundations of quantum mechanics. Perhaps most important of all, it is simply fascinating science.

To put the achievement of Bajcsy *et al.*[1] into perspective, let me briefly mention some of the key steps and issues that have led to the creation of frozen light pulses. The landmark slow-light experiment[6] — down to a speed of just 17 metres per second — was carried out in an ultracold gas. The advantage of such low temperatures is that they eliminate the spread in atomic frequencies that is caused by atomic motion: this optical Doppler effect could otherwise obscure, even spoil, the measurements of slow light. It is not necessary, however, to use trapped ultracold atoms and get rid of the Doppler effect to slow light down: this has been proved by the slowing of light to less than 100 metres per second in a hot gas of rubidium atoms[7].

It could be argued that the know-how to make slow light has been around since the late nineteenth century. The velocity of the peak of an optical pulse is called the group velocity because it takes a 'group' of two or more frequencies of light to make a pulse. Atoms and molecules tend to interact with light more strongly at certain frequencies, and this is manifest in a variation of the material's index of refraction, which causes different waves to move with different velocities. Of course, this affects the group velocity of the pulse — and is the reason that light is dispersed by a prism or water droplets to make a rainbow.

The good news is that strong dispersion is easy to achieve: the light frequency should be tuned close to the resonant frequency of the atoms, and then the group velocity may be slowed by a factor of a thousand or more. The bad news is that minimum pulse velocity also means maximum absorption of the light by the material: the pulses move very slowly, but they are so strongly absorbed that they penetrate only a few wavelengths' distance through the material.

But the last decade of the twentieth century saw revolutionary changes in optical science. We now have 'phase-coherent' materials, which give the huge dispersion associated with resonance but do not absorb light. These materials are truly a new state of matter, aptly called 'phaseonium', and their electromagnetically induced transparency[8] has proved useful in slowing light down to just a few metres per second. It has been shown[9,10] that the quantum state of a light beam can be stored in phaseonium vapour and then retrieved by a later pulse of light. This works because in slow-light propagation, part of the light beam is converted into atomic excitation (that is, it is mapped onto atomic spins). This transfer of the information contained in the light's quantum state onto the atoms (writing), together with its subsequent retrieval (reading), is a vital tool in the emerging field of quantum information, including cryptography and computing. However, although the concept of storing light by 'drawing' its quantum blueprint in the atomic medium is interesting, this is not the same as freezing light.

In fact, there are several possible routes to frozen light. For example, my own group is investigating the passage of slow-light pulses through a moving phase-coherent medium, such that the pulse would appear stationary to a fixed camera in the laboratory[11]. The route chosen by Bajcsy *et al.*[1], following the theoretical outline of ref. 12, does not involve a moving medium. Instead, a light pulse is trapped inside a gaseous, phase-coherent medium by changing the optical properties of the medium. There are two steps to the process: first, two laser pulses, the 'control' and 'signal' fields, are injected into a medium in which all the atoms are in the lowest-energy, ground state; then, with both control and signal fields in the medium, the control pulse is turned off. This results in the atoms' absorbing the signal field and storing the quantum state of the signal. Following the example of previous work, the next step

would be to regenerate the signal field (or its time-reversed partner) using a forward-propagating (or backward-propagating) 'read' field in the same direction as the first coupling laser.

But in their experiment, Bajcsy *et al.*[1] put in forwards and backwards read fields simultaneously to regenerate the signal. Now the plot thickens. The forwards and backwards fields interfere, producing a spatially periodic variation of light intensity, which in turn results in spatially varying atomic absorption. This acts like a stack of mirrors, which reflect and contain the regenerated field. The two laser pulses play a dual role: they convert the stored state into a signal pulse, and modulate the atomic absorption to localize or freeze the regenerated field.

Frozen light naturally suggests several interesting applications. First, as there is little or no loss, there will be little or no noise. This augurs well for applying such techniques to quantum informatics, where the suppression of noise is vital to avoid decoherence. Furthermore, the nonlinear coefficients associated with phase-coherent matter are very large: in a stationary pulse, even tiny amounts of light will cause large nonlinear effects, which have long been sought in both classical and quantum signal processing. One thing is clear — frozen, stationary pulses of light mark a new chapter in quantum optics. ■

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Chemistry

# Cellulose stacks up

Mike Jarvis

The long chains of cellulose pack laterally into microfibrils of two crystalline forms. Comparison of the structures of these two forms reveals unexpected patterns of bonding that tie the chains together.

There is more cellulose on Earth than any other organic substance. It is the main constituent of plant cell walls — and so of the paper on which the printed version of this article appears. For nearly a century the details of its structure have been elusive. But two crystallographic structures, published in *Journal of the American Chemical Society*[1,2], now show how cellulose fibres are put together.

There is nothing complicated about a single cellulose molecule; it is an unbranched chain of glucose units linked head to tail. The unsolved question has been how these cellulose chains pack side by side to form microfibrils, linear crystals that in most plants are some 3 nm thick, but which reach widths of more than 20 nm in certain algae and in tunicates or sea squirts, the only animals that make cellulose.

These very large microfibrils are preferred for crystallography, but homogeneity matters as much as size. Native cellulose from almost every source is a mixture of two crystalline forms, $I_\alpha$ and $I_\beta$, in statistically variable proportions[3]. The two forms can occur alongside each other within one of the large algal microfibrils[4], whereas cellulose from higher plants also contains large numbers of ordered and disordered crystal-surface chains[5]. These problems were bad news for those trying to determine the crystal structure, for they have had to wait until organisms were found that made almost pure cellulose $I_\alpha$ or cellulose $I_\beta$.

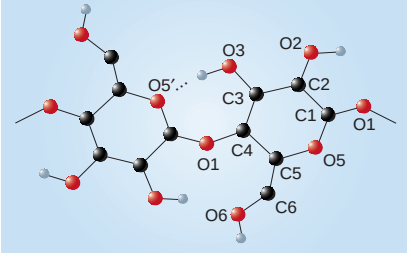


Figure 1 **Numbering system for carbon and oxygen atoms in two consecutive glucosyl units of cellulose. The O3–H···O5′ hydrogen bond shown is present in all crystalline forms of cellulose, but the pattern of hydrogen bonding from O2 and O6 varies. Hydrogen atoms are shown in grey.**

Nishiyama *et al.*[1] have now published the crystal structure of the $I_\alpha$ form isolated from the freshwater alga *Glaucocystis*. It can be compared with the structure of cellulose $I_\beta$ from the tunicate *Halocynthia*, published last year by three of the same authors[2]. Both structures harbour some surprises, and are instructive about the nature of hydrogen bonding.

Many features are common to both crystal forms. Each cellulose chain approximates to a flat ribbon, with alternate glucose units facing in opposite directions. They are locked in this position by a hydrogen bond between a hydroxyl group (O3–H; Fig. 1) of one glucose unit and the ring oxygen (O5′) of the next. All the cellulose chains lie parallel, hydrogen-bonded edge to edge. The sheets of chains so formed are stacked on top of one another with a stagger, along the microfibril, that differs between the $I_\alpha$ and $I_\beta$ forms.

Most of these features were already known or guessed, but there was a mystery about the forces that held sheets of chains together in a stack. Hydrophobic bonding had been suggested because, with the polar hydroxyl groups ranged along the edges of each ribbon-like chain, its upper and lower faces are relatively nonpolar. But Nishiyama *et al.*[1] point out that the chains are also correctly configured to provide an ordered multiplicity of weak C–H···O hydrogen bonds from one sheet to the next (Fig. 2, overleaf). C–H···O hydrogen bonding has been reported in other biopolymers[6], but it is remarkable to find it playing such a prominent part in the cohesion of an everyday material such as cellulose.

The $I_\alpha$ and $I_\beta$ forms were first distinguished by studies using nuclear magnetic resonance[3]. This work showed that each form contained two distinct kinds of glucose unit, more distinct in $I_\beta$ than in $I_\alpha$. This is confirmed in the crystal structures[1,2] and relates elegantly to their lattice symmetry (Fig. 2). In cellulose $I_\alpha$, alternating glucose units in each chain differ slightly in conformation but all chains are the same. Cellulose $I_\beta$ has chains of two kinds arranged in alternating sheets. These are termed 'origin' and 'centre' chains from their position in the unit cell. Within each chain, all glucose units are identical, although they face in alternate directions (Fig. 1).

An unexpected feature of both cellulose $I_\alpha$ and cellulose $I_\beta$ is disorder in the lateral hydrogen bonding that links adjacent chains within a sheet, revealed by analysis of neutron diffraction data with and without substitution of deuterium for the hydroxyl protons[1,2]. Each crystalline form has two alternative hydrogen-bond networks that differ only in the positions of the hydroxyl protons on O2 and O6. Their occupancy is not in an exact ratio.

In cellulose $I_\alpha$, adjacent chains are linked by a zig-zag, repeating O–H···O–H··· motif[1]. In one of the two networks, these stringed hydrogen bonds run continuously along the microfibril towards one end, whereas in the other network they are discontinuous and