



Figure 1 A comparison of the way in which flagellin proteins (represented by hands) incorporate themselves into the flagellar filament that propels bacteria, and into a three-dimensional crystal. a, The flagellar filament, understood at the relatively low resolution of about 10 Å, is a cylindrical structure, which can be thought of as a set of 11 protofilaments (centred on the blue circles) arranged in parallel and slightly tilted with respect to the filament's axis (dashed line). One protofilament is emphasized by a darker shade and a line indicating its direction. b, To obtain a three-dimensional crystal, Samatey *et al.*¹ used a version of flagellin that was truncated at both ends to inhibit filament formation. The subunits on one of the three crystal axes correspond closely to those in protofilaments, although now arranged in antiparallel fashion. The authors built this high-resolution (2 Å) structure into the lower-resolution filament structure. Only slight adjustments had to be made for the fact that the protofilaments in the filament are helices, gradually winding around the particle axis, whereas the protofilaments in the crystal are straight.

the protein's ability to form filaments was removed, yet its structure was largely retained. The authors then persuaded the truncated protein to form three-dimensional crystals. The crystals were exceedingly thin, being only a few micrometres wide. This presented technical difficulties that could be overcome only by using some of the most powerful beam lines available to generate X-rays for analysis, and by taking advantage of recent advances in low-temperature crystallography and data analysis. Samatey *et al.* thereby succeeded in obtaining data at atomic resolution (2.0 Å).

An interesting result emerged. The intersubunit distance on one of the three crystal axes was 51.8 ± 0.1 Å — more or less identical to the intersubunit distance of 51.9 Å within an R-state protofilament. This was unlikely to be a coincidence, and with only minor adjust-

ments, images of this high-resolution structure (Fig. 1b) could be built into images of the lower-resolution filament structure obtained by electron microscopy. In the natural filament, the protofilaments are parallel, whereas in the crystal they are antiparallel. So the lateral interactions between protofilaments in the filament are entirely different in the two cases. Yet the fact that the protofilaments look so similar means that lateral interactions, though undoubtedly important for stability, are not essential for the fundamental organization of a protofilament, which is therefore likely to be the cooperative unit for switching.

The flagellin that Samatey *et al.* crystallized had the information at its amino- and carboxy-termini deleted. Could this be resulting in a false picture? This seems unlikely because of how well the crystal structure fits into the lower-resolution structure of the filament, which is made from full-length flagellin. Also, other studies indicate that the termini lie towards the inside of the hollow filament, contributing to its strength and rigidity, but probably not to its switching capability.

For technical reasons, analysis of flagellar filaments is always restricted to mutant forms in which all 11 protofilaments are in the same state, either L or R. Oddly, Samatey *et al.* found that both L and R flagellins (that is, flagellins that form L and R protofilaments, respectively) crystallized into the R state. This would have been a disappointment if the authors wished (as surely they must have) to look directly at the molecular switch between states. In the hope of simulating the slightly longer L state, they used a computer to gradually stretch their R-type protofilament images, and slightly adjusted the structure obtained at each step so as to minimize its energy. For several steps, nothing happened but (for the most part) the gradual stretching of α -helices. But at one point, a local feature of the structure, at the intersubunit interface, changed abruptly, slightly distorting the protofilament. The authors suggest, quite plausibly, that this may be the key event in switching.

Samatey *et al.*'s work¹ represents a major jump forwards in our understanding of this sophisticated structure and the protein subunit from which it is built. Yet, for a full understanding of how the filament switches between states, one really needs high-resolution crystal structures of both states. Crystallization conditions that make this possible may eventually be found. ■

Robert M. Macnab is in the Department of Molecular Biophysics and Biochemistry, Yale University, 266 Whitney Avenue, PO Box 208114, New Haven, Connecticut 06520-8114, USA. e-mail: robert.macnab@yale.edu

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Daedalus

A near miss

In the last days of the year 2000, a meteor (later designated Y2000) passed within 480,000 miles of Earth, and so had a chance of a few parts per million of a direct hit. Daedalus is more interested in an event of 10 August 1972, when a meteor weighing maybe 4,000 tons skimmed through Earth's atmosphere, coming to within 58 kilometres over the United States and Canada. Daedalus reckons that such a close entry into the resistive atmosphere must have slowed the object to less than orbital velocity, so that its subsequent trajectory will have intercepted the Earth, possibly over land, but more likely in the sea. If it had hit the land it would surely have been noticed.

Two-thirds of meteors hit the sea anyway; and indeed sea impacts have been blamed for many important events, such as the extinction of the dinosaurs. Yet no sea impact has ever been observed and its remains studied. The chance should surely be taken. So Daedalus recommends that the trajectory of the 10 August 1972 meteor should be carefully analysed. The results will determine where in the ocean the incomer splashed down — somewhere on the great circle extension of the trajectory seen over North America. The area of greatest probability will be an ellipse, very likely over some area of ocean.

DREADCO oceanographers will then study that area, using submersible craft equipped with very sensitive cameras. Daedalus regrets the use of powerful lights by such craft, as they blind all the poor sea-creatures that have evolved sensitive retinas. The workers could also look for an altered magnetic signature of the ocean floor. Daedalus has no idea what his oceanographers will make of the results. In principle, a large hot object hitting the sea should make a giant boiling splash, killing all sea life within a large radius. The remains should then descend to the seabed, which might be deep ooze or teeming continental shelf. Because the impact was only 29 years ago, the main remnant should still be interpretable, even if it is only a magnetic anomaly.

It is possible, of course, that the bolide exceeded impact velocity even after its encounter with the atmosphere — in which case it may still be in low Earth orbit, waiting for a chance to deliver its deadly warning again. But then Daedalus would expect that Earthly radio detection or radar, which failed so signally to detect the near miss of 2000, would have picked it up by now, and would predict a good impact site.

David Jones