sources for microbial growth. As a result, it is likely that the fungus grew on air-borne nutrients absorbed by the particles, rather than by using the allotrope itself as a carbon source (it is also possible that, despite its stated purity, the sample of buckminsterfullerene used here contained organic contaminants).

These observations once again illustrate the marked ability of fungi to grow in the apparent absence of nutrients. They also suggest that buckminsterfullerene, even when not contaminated with other substrates, will become overgrown with moulds when stored under a moist condition – a possibility that should be borne in mind should buckminsterfullerene eventually be used in industry or medicine.

Buckminsterfullerene can have an interstellar origin and may have played a role in the origin of life. Fullerenes have been found in a crater near Sudbury, Ontario, Canada, formed some 1.5 billion years ago when a meteorite the size of Mount Everest fell to Earth (5). Buckminsterfullerene deposited by meteorites may therefore have provided the organic carbon needed to get life started. One theory of the origin of life, panspermia, suggests that life came to this planet from outer space. The fact that fungi, and presumably also bacteria, can grow on buckyballs in the absence of added nutrients suggests the possibility that life may have travelled to Earth on buckminsterfullerene or else it may have helped extraterrestrial micro-organisms to grow once they had arrived on the planet.

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Microbiology welcomes sequence papers

At the *Microbiology* Editorial Board Meeting in March this year it was pointed out that the article I wrote entitled 'Complete sequence figures are out' may have given the mistaken impression that *Microbiology* was becoming less enthusiastic about publishing papers based on large bodies of sequence data. On the contrary, the journal recognizes the vital importance of these sorts of data in the rapid advancement of microbiology and wishes to play its role in making the knowledge resulting from these projects available to the scientific community. The journal's close involvement with the *Bacillus subtilis* genome project is an example of this.

This involvement also illustrates admirably the changes that the Editors see as necessary to cope with the growing volume of sequence data that is becoming available through the use of automated sequencing facilities. Electronic databases are now so universally accessible that the journal must assume that anyone who wishes to use DNA sequences will not need to have the primary sequence data presented in full. The job of a published article is to present the results of the analysis of the determined sequence and the experiments that make sense out of the sequence. The purpose of the previous article was therefore to signal to authors that they must approach preparation of figures with the principle that sequences should not be shown unless they illustrate an important feature of function or organization. It should have been clear from the article that we were not making rigid rules and that the Editor or Member of the Editorial Board dealing with the paper would use their discretion about what sequence data should be shown.

To help avoid confusion, the Guidelines for Authors have been reworded (see this issue or view them on the journal's Web pages at <http://www.socgenmicrobiol.org.uk>). We have also added a request that authors include a hard copy of the complete sequence covered by their paper for the Editors and referees. The sequences are often not available from the databases at this stage and so the reviewers are unable to check them.

Christopher M. Thomas
Genetics Editor