

a pesticide for over 40 years. Read *et al.*³ describe the genome sequence of a strain of *B. anthracis* that was isolated from a Texan cow and subsequently used as a standard laboratory strain around the world. The same group has previously shown that this strain is virtually identical to that used in the US postal attacks⁵ and is, therefore, still representative of a fully virulent strain. Read *et al.*³ also generated an incomplete sequence of a strain of *B. cereus* for comparative purposes, and manufactured a microarray to extend this comparison to further strains of *B. cereus*. Ivanova *et al.*⁴ have completed the sequence of a different strain of *B. cereus*, and compared it to the unfinished sequence of the postal bioterror strain generated by Read *et al.* in their earlier work.

To understand the biology of this group of organisms, one must first realize that bacteria often carry more than one form of genetic material. In addition to the chromosome that bears the bulk of the genes, bacteria often carry extra DNA molecules called plasmids — small, self-replicating and often mobile elements that carry genes for accessory functions. Plasmid functions are extremely diverse, ranging from the undetectable to the essential — the genes concerned often encode 'virulence factors'; proteins that confer resistance to antibiotics; and, crucially in this context, toxins.

It has been known for some time that plasmids confer distinct capabilities on the various members of the *B. cereus* group — which include *B. cereus* itself, *B. anthracis*, *B. thuringiensis* and related bacteria. For example, the plasmids of *B. anthracis*, pXO1 and pXO2, encode toxin and other proteins

essential for full virulence in animals, and a range of *B. thuringiensis* plasmids carry insect toxins that allow the bacterium to attack its favoured hosts. In addition, the size of the *B. cereus* genome is very variable between isolates, ranging from about 2.4 megabases to 6.4 megabases⁶. In contrast, *B. anthracis* isolates represent a group that is closely related genetically, probably indicating a recent evolutionary origin⁷. The unanswered questions around these certainties concern exactly how closely these organisms are related. Are they really separate species or, as has been suggested, the same species carrying different plasmids⁸?

The new work^{3,4} goes a long way towards answering these questions. It is clear from the results that the genomes sequenced are highly conserved, and that even many of the *B. anthracis* plasmid genes are present in other strains of the *B. cereus* group. The only significant and consistent differences between *B. anthracis* and *B. cereus* are the genes encoding toxin components, which are carried on an apparently recent insert (a pathogenicity island) within the *B. anthracis* pXO1 plasmid, and a loss by mutation in the *B. anthracis* genome of a regulator (PlcR) of the expression of a wide range of genes, many associated with virulence⁹. It is also clear from these analyses that factors involved in virulence are not restricted to the plasmid. Instead, the chromosome itself, which is often considered to be a relatively inert background for the virulence-determining plasmids, carries many genes that seem to be involved in virulence.

Read *et al.*³ and Ivanova *et al.*⁴ found that genes involved in pathogenicity for animal

and insect hosts were present on the chromosomes of both *B. cereus* and *B. anthracis*, and in many other representatives of the species. These include genes similar to those known to be involved in the pathogenicity of *Listeria* (a common food-poisoning organism in humans), and genes similar to those used by insect pathogens to attack the gut walls of their hosts. Far from being a repository of the staid metabolic genes, the chromosome is replete with its own arsenal of pathogenicity determinants. This suggests that the individual plasmids are not the only controls of virulence, but are instead more like accessory factors that can drive the overall virulence capabilities of the organism towards individual specific hosts.

This conclusion has led both groups^{3,4} to reassess the potential evolutionary niche of the ancestral organism of the *B. cereus* group. Using the genome to probe the potential metabolism of the organisms, they show that, unlike many of their relatives found in the wider environment, these bacteria seem to shun simple sugars and other carbohydrates of plant origin as a source of nutrients. Rather, they favour a more carnivorous diet of proteins, amino acids and the complex carbohydrates used by insects to build their bodies — a dietary foible taken to further extremes by a more distantly related insect pathogen, *B. sphaericus*, which is completely unable to metabolize any carbohydrates. All of this suggests that the immediate ancestor of the *B. cereus* group species was not simply a harmless soil-dwelling organism, but that it may have been saprophytic or even parasitic — that is, have preyed on the dead, or living, bodies of

Earth science

Subduction the hard way

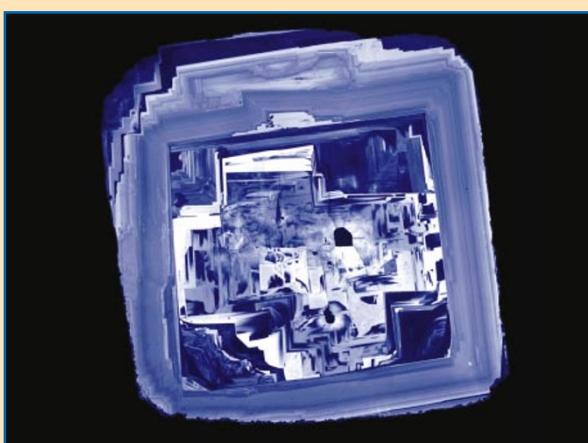
Diamonds are a geologist's best friend. Trapped inside the hardest natural substance is a relatively pristine record of the history of the continents — a record that can be exploited to investigate whether material that once formed the ocean floor of the early Earth was subducted into the mantle and preserved beneath the continental landmasses.

Earlier support for this view came from mantle rocks known as eclogite xenoliths. These are fragments of green, basalt-like material that were transported to the surface in volcanic magma. The ratio of the oxygen isotopes ¹⁸O and ¹⁶O in the eclogites suggested that they had originated as altered basalt on the ocean floor.

But the hot, turbulent past of the xenoliths means that there is no guarantee that this geological record is pure.

In this issue (*Nature* 423, 68–70; 2003), Daniel Schulze and colleagues report their analysis of diamonds mined in Guaniamo, Venezuela. This image, captured through cathodoluminescence, shows one of their samples, 2 mm across and known as 'Picasso's diamond' for its resemblance to the cubist masterpieces of the Spanish painter.

Trapped inside this diamond (and others like it) is coesite, a form of silicon dioxide. The oxygen-isotope ratio in the coesite matches that of altered ocean-floor



basalt — "compelling evidence", say Schulze *et al.*, in favour of subduction of oceanic plates

being instrumental in the formation of the early continents.

Alison Wright