

intervals. This can be achieved either by high-resolution mapping or by accurate measurements of the pulsar's period. To an observer on Earth, the pulsar's period becomes shorter as we travel towards the pulsar or longer as we move away. By studying these changes in the period, the pulsar position can be estimated with very high precision. This method is referred to as 'pulsar timing'. Accurate measurements of the pulsar's position will allow us to work out the pulsar's age from the distance it has travelled since its birth. We expect such observations to be completed within the next few years. The finding that young pulsars are generally

older than was thought may explain why many apparently young pulsars are not associated with a supernova remnant. ■

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1. Gaensler, B. M. & Frail, D. A. *Nature* **406**, 158–160 (2000).
2. Lyne, A. G. & Graham-Smith, F. *Pulsar Astronomy* (Cambridge Univ. Press, 1998).
3. Manchester, R. N., Kaspi, V. M., Johnston, S., Lyne, A. G. & D'Amico, N. *Mon. Not. R. Astron. Soc.* **253**, 7P–10P (1991).
4. Lyne, A. G., Pritchard, R. S. & Smith, F. G. *Mon. Not. R. Astron. Soc.* **233**, 667–676 (1988).
5. Kaspi, V. M. et al. *Astrophys. J.* **422**, L83–L86 (1994).
6. Lyne, A. G. et al. *Mon. Not. R. Astron. Soc.* **381**, 497–498 (1996).

Plant pathology

## The bugs from Brazil

Michael Bevan

**A**gricultural crops are under constant threat from disease and the vagaries of climate, and in many areas of the world much human suffering stems from crop failure. Couple these factors with the demands of expected increases in human population, the continued encroachment on virgin and marginal land for agriculture, and decreasing water quality, and it is plain that food producers have a considerable challenge on their hands.

Genome sequencing is a potent new tool in the biologist's armoury, and it is being applied to a wide variety of organisms that directly or indirectly affect food supplies. A striking and welcome example of the approach comes on page 151 of this issue<sup>1</sup>, where a Brazilian sequencing consortium report the first public sequence of a free-living plant pathogen. The organism con-

cerned is the bacterium *Xylella fastidiosa* (Fig. 1), the cause of citrus variegated chlorosis, a serious disease of citrus fruit. Certain strains of *X. fastidiosa* also affect other commercially important produce such as coffee, nuts and other fruits<sup>2</sup>.

The *X. fastidiosa* genome sequence is one of 24 complete bacterial genomes now available<sup>3</sup>. Each reveals a gene complement and organization that reflects in marvellous detail the specific adaptations and lifestyles of the organism concerned.

The *X. fastidiosa* bacterium is highly specialized. It multiplies in the foregut of sharpshooter leafhoppers, which feed on sap in a plant's xylem, the main water-conducting tissue. The insect carrier delivers bacteria directly into the xylem system of host plants. There they multiply and cause symptoms of chlorosis — chlorophyll loss and yellowing

— and the premature production of fruit which are small, tough and therefore worthless. The disease is potentially devastating; the most effective control is to produce healthy bacteria-free material for plant propagation. Brazil produces around one-third of the world's orange fruit, and nearly half of the orange-juice concentrate. So the citrus and other fresh-fruit industries are of great national significance, and research into disease control has a high priority.

The gene complement of *X. fastidiosa* reflects its life in plant xylem in three main ways. First, the bacterium is adapted to use a variety of free sugars found in xylem sap, and to supplement these sugars with glucose derived from the breakdown of cellulose, the main component of plant cell walls. Adding to the picture of a honed-down metabolism, genes encoding the enzymes needed to make sugars from amino acids and other metabolites are missing; this shows that the organism has a strict requirement for carbohydrates as the sole energy provider and source of building blocks for all biosynthetic reactions.

Second, no fewer than 67 genes are devoted to the uptake of iron and other transition metals from xylem sap, and the authors suggest that depletion of these micronutrients contributes to symptoms of infection. Third, *X. fastidiosa* produces two distinct cell-adhesion systems. One comprises a matrix of extracellular polysaccharides, synthesized by the appropriately named *gum* genes, that embed the bacteria in a matrix in the xylem, eventually leading to blockage of xylem flow and host water-stress. The other system is for bacterial adhesion to the gut and mouthparts of the insect vector, and is specified by 26 genes encoding the so-called fimbrial proteins that are needed for bacterial adhesion and translocation across cell surfaces.

The consortium<sup>1</sup> also identified genes encoding other molecules involved in cell adhesion that were previously associated only with human and animal pathogens. This is further evidence that disease-causing bacteria of humans and plants have common mechanisms of pathogenicity<sup>4</sup>.

One of the barriers to breeding and engineering plant resistance to *X. fastidiosa* is a comparative lack of knowledge of its interplay with its citrus hosts. Usually, host-pathogen specificity is conferred by interactions between avirulence factors encoded by the pathogen and host resistance factors. Surprisingly, however, *X. fastidiosa* lacks recognizable avirulence genes and the secretion system that injects them directly into host cells. The authors<sup>1</sup> suspect that the direct injection of bacteria into host cells by the insect carrier bypasses avirulence gene function, and that the host ranges of *X. fastidiosa* are defined by other molecules. Exploring this aspect of the bacterium's biology will provide new perspectives on host-pathogen interactions, with the ultimate

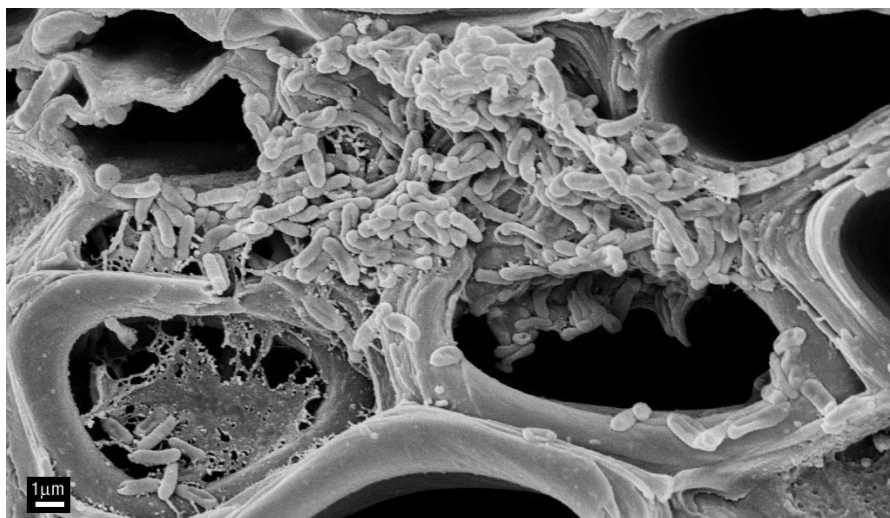


Figure 1 *Xylella fastidiosa*, a bacterium that causes severe damage to citrus trees and the citrus industry. Its genome sequence, now published<sup>1</sup>, shows it to be highly adapted to life in a plant's water-conducting system.

general goal of developing tolerance and resistance in crop plants.

The impending completion of several other bacterial and fungal plant-pathogen sequences, and the initiation of genome sequencing of *Rhizobium meliloti* (the nitrogen-fixing symbiont of legumes), adds further to the exciting possibilities in agricultural genomics. Moreover, the near-completion of the sequence of the favoured model plant *Arabidopsis* and the start of rice genome sequencing, along with farm-animal genome projects that draw strongly on mouse and human genome sequencing, are establishing a solid foundation for research. This is research with eminently practical ends: tackling current or imminent problems in food production, human nutrition and environmental degradation. For example, disease-resistant crops, and plants better adapted to grow in extreme conditions, are nearly ready for large-scale use.

Finally, to return to South America, this first implementation of large-scale sequencing in Brazil is only a harbinger of things to come. The same consortium is now sequencing another plant pathogen, *Xanthomonas citri*. This is the cause of citrus canker, a worldwide disease that can severely damage citrus crops unless strict quarantine zones are enforced. The citrus industry in Florida is currently under threat from *X. citri* spread by a tornado in 1996 (ref. 5). The successful sequencing of *X. fastidiosa* also shows that genome projects are a highly effective tool for science policy. Such projects provide a strong direction to and framework for biological

investigations; they direct disparate areas of biology towards common themes; and they result in the distribution of the latest technologies to many laboratories, allowing scientific talent to flourish more widely. ■

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#### Developmental biology

## Bringing two hearts together

Wolfgang Driever

Vertebrate development is a complicated business. Many structures, such as limbs, form as left–right pairs. Of other organs — such as those of the digestive system, which form by budding off the central gut tube — there is only one. And a few organs, most notably the heart, have a much more complicated genesis. The heart's origins can be traced back to the early embryo, specifically to two patches of tissue (primordia) located on either side of the vertical axis that marks the embryo's centre. During development, the heart primordia move towards this so-called dorsal midline and merge, forming the heart (Fig. 1, overleaf). How the primordia find each other has been one of life's mysteries. On page 192 of this issue<sup>1</sup>, Kupperman and colleagues shed first light on this process, by characterizing a gene — called *miles apart* — that is essential for guiding the migration of the primordia.

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1. Simpson, A. *et al.* *Nature* **406**, 151–157 (2000).
2. Machado, M. A. <http://www.dcc.unicamp.br/genoma/xylella.html> (1997).
3. Genomes OnLine Database <http://wit.integratedgenomics.com/GOLD/>
4. Rahme, L. G. *et al.* *Science* **268**, 1899–1902 (1995).
5. Gabriel, D. W. <http://www.biotech.ufl.edu/~pcfcl> (2000).

The hearts of higher vertebrates have left and right chambers, but this does not mean that the heart is initially organized bilaterally. After the heart primordia merge, a single tube forms (Fig. 1c), which then undergoes a complex looping process to generate the chambers<sup>2</sup>. Because of this, the dual origin of the heart was not always clear. The first evidence came from observations of developmental defects that cause two heart tubes to form, a condition called cardia bifida. Found in a variety of organisms, from fish to humans, this disorder generally leads to death of the embryo because proper blood circulation cannot be established.

Zebrafish (*Danio rerio*) have proved a particularly useful genetic model for studying cardia bifida: their embryos are transparent, so the two heart tubes can be easily observed long before the embryos die of circulatory defects<sup>3</sup>. Systematic mutation of zebrafish genes and screening of the mutant animals has resulted in the identification of eight genes that, when mutated, cause cardia bifida<sup>3</sup>. One of these genes is *miles apart*.

In zebrafish with mutations in *miles apart*<sup>3</sup>, mesodermal tissue (from which muscle, blood and various other tissues form) forms the heart primordia in the normal way, but the primordia do not converge at the midline. Heart differentiation does not depend on this convergence — two beating heart tubes form, one on the left and one on the right of the embryo. Kupperman *et al.*<sup>1</sup> now show that *miles apart* encodes a receptor that binds lysosphingolipids. Members of one family of lysosphingolipid receptors transmit signals into the cells on which they are found via guanine-nucleotide-binding proteins, and the Miles apart protein belongs to this family.

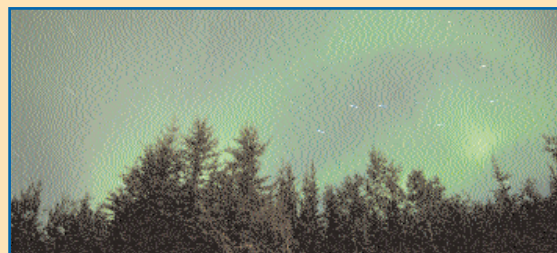
Kupperman *et al.* also show that the sphingolipid sphingosine-1-phosphate is probably the ligand that binds to the Miles apart protein to guide migration of the heart primordia. This lipid can be generated by cells from scratch or from sphingomyelin, a lipid that is stored in cell membranes<sup>4</sup>. Interestingly, the authors find that the Miles apart protein does not need to be expressed on the migrating heart precursor cells themselves:

#### Atmospheric physics

## Polar lights in the Caribbean

Auroras are spectacular displays of multicoloured light (right), rarely seen at low latitudes. But users of the world's largest radio telescope in Arecibo, Puerto Rico, can now create their own light shows. As L. M. Kagan *et al.* describe in *Physical Review Letters* (**85**, 218–221; 2000), shining powerful radio waves into the night sky produces a green fluorescent glow. This provides us with the first ever pictures of clouds of metal ions in the lower ionosphere — a phenomenon that strongly disrupts radio and satellite communications.

The ionosphere is an ion-rich region of the Earth's atmosphere that reflects radio waves over long distances. The



density of ions increases with altitude in response to the ionizing effects of the Sun's radiation. A faint airglow — caused by emission of green and red light from ionized oxygen and nitrogen — can be seen at higher altitudes by sensitive detectors. But the lower ionosphere, such as the E layer, doesn't glow.

Metal ions in the E layer, torn from passing meteorites,

can build up into patches of stronger ionization that interfere with satellite signals. Intense radio waves from Arecibo were used to excite these metal ions, which in turn heat up free electrons. These energetic electrons collide with oxygen ions making them glow, as in a natural aurora. Who needs northern lights when you can have aurora equatoralis? Sarah Tomlin