

Science writer **Meriel Jones** takes a look at some recent papers in SGM journals which highlight new and exciting developments in microbiological research.

## The fight against blight – a potential viral solution

**Hacker, C.V., Brasier, C.M. & Buck, K. W. (2005).** A double-stranded RNA from a *Phytophthora* species is related to the plant endornaviruses and contains a putative UDP glucosyltransferase gene. *J Gen Virol* **86**, 1561–1570

Researchers think that they have found an RNA virus that may affect pathogenicity in one species of *Phytophthora*. All members of this genus are plant pathogens. The most famous caused potato blight in Ireland in the 1840s. Chemical control is not always effective, so researchers continue to look for new ways to control these pathogens. Some phytophthoras contain virus-like double-stranded RNA molecules that may have potential as biocontrol agents. Ken Buck and Caroline Hacker from Imperial College in London, UK, together with Clive Brasier from the Forest Research Agency, have studied one of these RNAs from a phytophthora infecting a Douglas fir tree. The viruses most closely related to this novel piece of RNA were in the genus *Endornavirus*, which affects plants such as rice and beans, although *Phytophthora* is not a plant. This is therefore the first non-plant member of the *Endornavirus* genus and has been given the name phytophthora endornavirus 1 (PEV1).

The RNA contained a single gene that appeared to encode several proteins joined together. All endornaviruses have a single gene that encodes one very large protein. From comparisons with other proteins, there were regions that should act as enzymes to synthesize the RNA

◀ Coloured scanning electron micrograph of the potato blight fungus *Phytophthora infestans*, emerging from a potato leaf. Andrew Syred / Science Photo Library

molecule. Researchers assume that a proteinase enzyme cuts it up into functional proteins.

The interesting new feature of PEV1 is that it contains a region that looks like a glycosyltransferase, an enzyme that attaches a glucose sugar molecule onto a lipid sterol. When the researchers went back and looked more closely at the sequence of the polyprotein from other endornaviruses, they spotted regions similar to this enzyme in two of them. This is the first time a glycosyltransferase gene has been seen in an RNA virus.

This enzyme exists in some DNA viruses, especially ones that infect insects. Researchers think that the gene must benefit the virus and have been acquired from the host organism at some point in the evolution of the virus. The glycosyltransferase in PEV1 was not particularly similar to the gene in *Phytophthora* protists. Indeed, it was as closely related to the gene in bacteria, fungi or plants, suggesting that it was acquired by an ancient endornavirus before the separation of bacteria, fungi and plants. That would explain why it appeared in a similar place in two other endornaviruses from rice that the researchers examined. The benefit of glycosyltransferase to, for example, baculovirus is that infected insects remain as caterpillars and increase the yield and spread of the virus. Although the researchers do not know what happens in *Phytophthora*, some fungal pathogens need a similar enzyme as part of their pathogenicity mechanism, and the endornavirus might therefore affect pathogenicity. The researchers are therefore quite excited that they may have discovered a new way to investigate, and maybe control, the potential for disease caused by this important group of pathogens.

## A novel soil bacterium and antibiotic-resistant TB

**Cook, A.E., le Roe, M. & Meyers, P.R. (2005).** *Actinomadura napiensis* sp. nov., isolated from soil in South Africa. *Int J Syst Evol Microbiol* **55**, 703–706

Tuberculosis (TB) is a serious health problem in South Africa, exacerbated by low success with treatments, an increase in the level of strains resistant to current medication and the high incidence of co-infection with HIV. Indeed, TB is the leading cause of death among people who are HIV-positive in the country. New treatments are needed to tackle the antibiotic-resistant strains of *Mycobacterium tuberculosis* (the bacterium that causes TB).

Ironically, many antibiotics originate from compounds secreted by bacteria. The group of bacteria called the actinomycetes is the leading producer of antimicrobial compounds of biological origin. Researchers keep on looking for new species of actinomycetes as sources of new antibacterial compounds that can be developed into treatments for TB and other bacterial diseases.

Researchers led by Paul Meyers at the University of Cape Town have therefore been searching for new actinomycetes and testing them for new antibacterial compounds. One strain isolated from soil was particularly interesting. The appearance of the bacterial cells and the cell wall composition, along with the sequence of a characteristic gene, identified it as an actinomycete from the genus *Actinomadura*. It was sufficiently different to be named as a new species, *Actinomadura napiensis*, indicating that it came from the town of Napier (in the Western Cape province of South Africa). It secreted an antibacterial compound which the researchers managed to partially purify. Bioassays showed that the compound killed several species of bacteria, although unfortunately not *M. tuberculosis*.

## The flexible *E. coli* genome

**Hejnova, J., Dobrindt, U., Nemcova, R., Rusniok, C., Bomba, A., Frangeul, L., Hacker, J.H., Glaser, P., Sebo, P. & Buchrieser, C. (2005).** Characterization of the flexible genome complement of the commensal *Escherichia coli* strain A0 34/86 (O83:K24:H31). *Microbiology* **151**, 385–398

Harmless commensal strains of *E. coli* frequently inhabit the human colon. However, other strains are distinctly pathogenic, causing serious enteric and diarrhoeal disease. Now that all the genes in several strains of *E. coli* have been sequenced, detailed comparisons may indicate how particular ones are linked to disease symptoms. Researchers have focused on pathogenic strains, learning about specific subsets of genes associated with virulence or the ability to thrive in a particular environment. These genes are frequently associated with others that permit them to move between bacterial cells. Researchers have therefore developed the idea that *E. coli* has a core set of genes found in all members of

the species and a flexible gene pool that allows a strain to live in a particular environment or have a particular type of pathogenicity.

However, the difference between strains is surprising. One comparison of the entire collection of genes in three strains showed that only 39.2% of them were the same. A multinational collaborative project has focused on identifying the features of one strain of *E. coli*, called A0 34/86 (serotype O83:K24:H31), that makes it positively beneficial. It is used routinely as a live oral vaccine in the Czech and Slovak Republics. The strain was originally isolated from pig faeces, but for over 30 years A0 34/86 has protected premature and newborn infants at risk of diarrhoeal infections. Colonization with A0 34/86 probably displaces pathogens and allows the normal gut flora to redevelop. In the longer term, A0 34/86 seems to make the children significantly less prone to repeated infections and developing allergies. Obviously, it would be good to know exactly what makes this strain so beneficial.

The collaborators used a number of techniques and came up with information that challenges the current view of what makes *E. coli* a pathogen. To their surprise, only about 5% of its genes were specific to A0 34/86, and many usually described as virulence factors were present. It even had genes for adhering to cells and synthesizing toxins characteristic of strains causing urinary tract infections. The researchers tested how well A0 34/86 colonized the gut of piglets to discover exactly why it was exceptionally good at colonizing a host. One group of genes, which included ones that helped other bacteria adhere to cells and cause infections, also seemed to be important for successful colonization of the piglets. It looks as if these genes are also the reason why A0 34/86 is so good at colonizing the gut and providing protection from infections. Researchers have clearly got more to learn about the relationship between pathogenic and commensal strains of *E. coli*.

▶ Cultured human small intestinal mucosa infected with enteropathogenic *E. coli*. Stuart Knutton, University of Birmingham



## Getting attached

**Rubinsztein-Dunlop, S., Guy, B., Lissolo, L. & Fischer, H. (2005).** Identification of two new *Helicobacter pylori* surface proteins involved in attachment to epithelial cell lines. *J Med Microbiol* **54**, 427–434

Hans Fischer and his colleagues at Lund University in Sweden and Aventis Pasteur in France have come up with a new way to identify bacterial proteins that can cling to human cells. Pathogenic bacteria have to be able to hang onto the cells of their host, whether the host is an unwilling human, animal or plant. Understanding how this happens could lead to new antibacterial treatments. However, it is not always easy to identify the features of bacterial and host cells that lead to a close attachment. The authors of this paper have invented a way to test whether any particular protein plays a role.

The bacterium *Helicobacter pylori* causes chronic gastritis and peptic ulcers. The infections can also lead to some types of cancer. However, since *H. pylori* inhabits the stomach of at least half the human population, researchers would like to know why it makes only a few people ill. One factor must be the interaction between the surfaces of the bacterial and human cells in the stomach. Researchers have already identified one protein that helps *H. pylori* adhere, but know that there must be more.

The DNA sequence containing all the genes in *H. pylori* has already been worked out. The researchers compared regions of unknown function with other bacterial genes to work out whether any had the characteristics for a protein on the cell surface. They picked out five genes, synthesized the corresponding proteins and attached them to microscopic beads to produce something that mimicked a bacterial cell.

The researchers mixed cultured human cells with the protein-coated beads to test whether there was the same attachment response as between human and real *H. pylori* cells. None of the human cells attached to the beads alone, but two out of the five unknown proteins allowed some types of human cells to cover the beads entirely within 24 hours. The strongest interaction was with cells that originally came from the lining of the stomach, although cells from the surfaces of the large intestine and kidney also attached to the pseudo-bacteria. Even cells derived from the bladder and small intestine surfaces showed a small amount of attachment. This small-scale trial has proved that the method can identify proteins that are important in attaching bacteria to surfaces, and in the process the researchers have provided a role for the products of uncharacterized genes. In addition, the human stomach cells remained alive and thrived on the beads, so this might be a useful way to study the carcinogenic effects of *H. pylori*.