Meeting report
Microbial genome jambalaya
Timothy D Read

Address: The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850, USA. E-mail: tread@tigr.org

---

A report on the third American Society of Microbiology (ASM) and The Institute for Genomic Research (TIGR) Microbial Genomes Conference, New Orleans, USA, 29 January to 1 February 2003.

In January this year, the horde that descended on New Orleans' French Quarter spoke a language quite different from the local patois, with words such as "glycome" and "pathogenomic". The third ASM/TIGR conference was an opportunity to assess progress in microbial genomics. Perhaps the most striking theme to emerge at the conference was the prevalence of comparative genomic analysis: with whole-genome sequencing becoming accessible to an increasing number of institutions, many bacterial species now have multiple complete sequences. The adaptations of pathogenic microorganisms and how hosts respond to them was another key theme.

Comparative genomics

Julian Parkhill (Sanger Centre, Hinxton, UK) gave a description of the comparison of three closely related, completely sequenced genomes: *Bordetella bronchiseptica* (5.34 megabases, Mb), which causes respiratory disease in a range of animals, and *B. pertussis* (4.03 Mb) and *B. parapertussis* (4.73 Mb), both of which cause whooping cough. The more virulent strains show symptoms of recent genome change, especially an increased proportion of pseudogenes and insertion sequences; for example, there are more than 230 almost identical copies of the insertion element IS481 in the *B. pertussis* genome. Many changes involve loss of genes encoding cell-surface proteins, which may explain the reduced host range of *B. pertussis* and *B. parapertussis* compared with *B. bronchiseptica*.

Joseph Heitman (Duke University, Durham, USA) presented an initial look at the basidiomycete fungus *Cryptococcus neoformans*, three distinct serotypes of which are currently being sequenced at different genome centers. Among the features emerging from comparative genomic analysis mentioned by Heitman was the role of extended mating-type loci in virulence: pathogenesis of *C. neoformans* is associated with the α mating type, which is controlled by a key gene, *Sxi1α*. Several posters included analyses of three or more closely-related bacterial genome sequences, including *Xanthomonas* (D. Park, National Institute of Agricultural Biotechnology, Suwon, Republic of Korea), *Bacillus cereus* (Gary Xie, Los Alamos National Laboratory, USA), *Rickettsia* (Gregory Dasch, Centers for Disease Control and Prevention, Atlanta, USA) and *Campylobacter* (Derrick Fouts, TIGR, Rockville, USA). Fouts showed that strains of *Campylobacter jejuni* and *C. coli* that infect chickens contained phages and megaplasmids not seen in the strains that infect humans.

Mark Achtman (Max Planck Institute for Infection Biology, Berlin, Germany) detailed genome-based studies of the populations of two highly variable human pathogens, *Neisseria meningitidis* and *Helicobacter pylori*. Analysis of variation in conserved genes of diverse populations of *H. pylori* has led to reconstructions of the recent spread of the pathogen from foci in China and North Africa. Another highly diverse human pathogen is *Streptococcus pneumoniae*, and Susan Hollingshead (University of Alabama, Birmingham, USA) presented the results of extensive genome sequencing and comparative genomic hybridization of this organism. In one study, genomic DNA from D39, a strain originally isolated in 1916, and its descendants was used to probe a microarray made using the genome sequence of a modern strain. Many of the strains showed significant variation in their gene content from the modern strain, underlining the fact that bacteria cultured in the laboratory for even a short time (relative to the history of the organism) can acquire significant changes.

Pathogenic and parasitic microorganisms

The first annual Noel T. Keen Memorial Lecture was given by Clarence Kado (University of California, Davis, USA), who

presented a genomic analysis of genes that are potentially involved in the virulence of the bacterium that causes crown gall, *Agrobacterium tumefaciens*. The protein product of one of the genes he found, *ros*, is implicated in processing the fragment of bacterial DNA that is transported into the plant cell during infection, and its 'best match' was to a protein in the genome of the pufferfish, *Fugu rubripes*. Could a rare cross-kingdom gene-transfer event be responsible for this unusual finding? Following up on this possibility, Kado showed that bacteria isolated from sea squirts, marine organisms in the phylum Urochordata, also have homologs of *ros*.

Scott O'Neill (University of Queensland, St Lucia, Australia) described how the intracellular Gram-negative bacterium *Wolbachia*, which is transferred vertically between insect reproductive cells, manipulates its host to aid its own survival. Known effects of *Wolbachia* include feminization of male insects and cytoplasmic incompatibility between infected and uninfected sperm and eggs. Interestingly, sequencing of the *Wolbachia* genome has revealed phages, insertion sequences and possibly even laterally transferred genes, all signs that these intracellular bacteria may exchange DNA.

Brendan Wren (London School of Hygiene and Tropical Medicine, UK) described *Campylobacter jejuni*, the leading global cause of bacterial gastroenteritis, as a "boring genome". The 1.68 Mb NCTC11168 strain lacks prophages, insertion elements and most well-known bacterial virulence determinants. But the bacterium does have a remarkable ability to alter the composition of its exterior: many of its genes encode structural proteins whose expression is phase-variable - protein production is controlled by reversible changes in the DNA sequence of the gene. Furthermore, the *C. jejuni* genome sequence has led to the discovery of a novel polysaccharide capsule and a novel *N*-linked glycosylation pathway giving researchers a better picture of the external surface of pathogenic *C. jejuni*.

Alan Collmer (Cornell University, Ithaca, USA) described the sequencing of *Pseudomonas syringae* tomato DC3000, a 'stealth parasite' of plants, and his search within its genome for Harpin proteins (secreted elicitors of the plant hypersensitive response) and of the type III effector proteins secreted by the type III secretion system. These molecules, which according to Collmer are "produced in prokaryotes to do interesting things to eukaryotic cells", cause a variety of intriguing phenotypes in the host, including suppression of cell death. Collmer's approach for finding novel secreted proteins involved searching the genome for genes upstream of the previously characterized HrpL promoter, which is known to occur upstream of genes encoding secreted proteins. Vish Nene (TIGR) provided an example of another intriguing phenotype produced by a parasite: the ability of *Theileria parva*, a protozoan parasite of livestock in sub-Saharan Africa, to cause leukemia.

The response to pathogens
Robert Hancock (University of British Columbia, Vancouver, Canada) gave a presentation on the use of microarrays for profiling the innate response to different pathogens. Hancock suggested a novel approach to treatment of infectious diseases that involves boosting innate immunity rather than using antibiotics. Cationic peptides were suggested to be the agents that would work best in this kind of treatment. This approach both provides data on how the host deals with diverse invading microbes and additionally may be a method for improved disease diagnosis.

At the end of the meeting many delegates stayed on for the National Science Foundation/United States Department of Agriculture Microbial Sequencing Awardee Workshop. There was much excitement about the next ASM/TIGR conference, which is moving from the French Quarter of New Orleans to Paris, France, in April 2004.