of her lab to confess that she and Bob are using quantum teleportation to transport the quantum state of the swing, and she generously offers to explain how teleportation works. For each experiment, she and Bob use a pair of swings, one at her lab and one at his, which are prepared in advance in the sort of entangled quantum state introduced by Einstein, Podolsky, and Rosen (EPR) in their classic 1935 paper (*7*). In the EPR state, both swings have completely uncertain positions and momenta, but their positions and momenta are correlated in a specific way. If Alice measures the position of her swing, she can predict with certainty that Bob's swing has the same position; likewise, if she measures momentum, she can predict that Bob's swing has the opposite momentum.

Alice uses entanglement in one other way. When she brings your swing into the lab, she makes two entangled measurements involving your swing and her swing from the EPR pair. She measures the difference between the two swings' positions and the sum of their momenta—measurements permitted by quantum mechanics. The position and momentum of Alice's swing being completely uncertain, these measurements have unpredictable results, which by themselves provide no information about the position or momentum of your swing. Yet because of the entanglement, Alice knows that Bob's swing from the EPR pair has the position and momentum of your swing, offset by the random results of her measurements. She communicates the measurement results to Bob, who applies suitable forces to his member of the EPR pair to remove the offsets, thus reconstructing in his swing the quantum state that your swing had initially.

The Caltech experiment teleported the coherent-state oscillations of the electromagnetic fields in a light beam, the big difference from the tale being that the two cities were in the same room at Caltech. An optical parametric oscillator (OPO) generated the entangled light beams, one of which was sent to Alice and one to Bob. Although the perfect correlations of an EPR state are an unattainable limit, the "squeezed states" generated by the OPO had sufficient entanglement to do the job. Alice made her two entangled measurements by first combining, at a 50/50 beam splitter, her output from the OPO with the coherent state to be teleported and then making homodyne measurements on the two outputs of the beam splitter. Bob corrected the state of his output from the OPO by using Alice's measurement results to modulate the amplitude and phase of a strong laser beam, which he combined with his output from the OPO at a highly asymmetric beam splitter. Certification of successful teleportation came from demonstrating that the teleported state matched the input coherent state better than the uncertainty principle would allow if Alice measured the coherent-state input and sent the results to Bob.

The uncertainty-principle limits on measuring and duplicating a quantum state are a special case of the more general restriction that quantum mechanics does not allow one to distinguish and identify nonorthogonal quantum states. This quantum-mechanical limitation, long thought to prohibit teleportation, turns out to be an essential feature of the entanglement-based teleportation procedure. The information Alice transmits to Bob provides no information about the teleported state.

This two-faced character of quantum mechanics seems to be a common theme in the emerging field of quantum information science. Although the huge amount of information stored in the state of a quantum system is inaccessible, it can be used in quantum cryptography and quantum computation. The apparently restrictive features of quantum mechanics turn out on closer examination to allow quantum systems to perform information-processing tasks that would be impossible in a classical world. Quantum teleportation of two-state systems or harmonic oscillators is a first step in developing an array of techniques for processing and thus taking advantage of the power of quantum information.

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PERSPECTIVES: GENOME SEQUENCING

Chlamydia: Old Ideas Crushed, New Mysteries Bared

Thomas Hatch

The report by Stephens and colleagues on page 754 of this week's issue summarizes the major findings of the *Chlamydia trachomatis* genome sequencing project, funded by the National Institutes of Health (*1*). Unlike other bacteria whose genome sequences have been published, chlamydia have an obligatory intracellular life-style, growing only within the cells of eukaryotic organisms. Its genome sequence reveals how chlamydiae have adapted to this nutrient-rich yet potentially hostile environment. As an additional benefit, the sequence provides a powerful tool for chlamydial research, which has been hampered by the difficulty of propagating large numbers of organisms and by the lack of a functional system for genetic transformation.

Chlamydia trachomatis is the agent of trachoma (still a major cause of blindness in Asia and Africa) and is the most common bacterial sexually transmitted disease in the United States. *Chlamydia pneumoniae*, which is also being sequenced as part of the ongoing Chlamydia Genome Project, is a common cause of a usually mild, community-acquired pneumonia. This organism, however, can spread from the respiratory tract into other parts of the body and has been detected in up to 70% of atheromatous lesions in blood vessels (*2*). Although exactly how *C. pneumoniae* contributes to the pathogenesis of atherosclerosis remains unknown, prophylactic antibiotic trials are planned for individuals at high-risk for coronary disease (*3*).

The roughly 1 million–base pair sequence has revealed surprises, as much by what was found as what was not found. For years chlamydiae were thought to lack key enzymes and cellular machinery for generating ATP, instead sequestering host nucleoside triphosphates by translocation mechanisms (*4*). The new sequence does reveal two potential ATP/ADP translocases, but it also identifies genes that may allow chlamydiae to generate at least minimal amounts of ATP on its own.

A long-standing paradox has been the inhibition of chlamydial cell division by penicillin in the apparent absence of the principal penicillin target, peptidoglycan (*5*). The peptidoglycan deficiency is thought to be compensated by a unique disulfide–cross-linked, supramolecular protein complex in the cell wall, which provides the structural stability normally afforded by peptidoglycan (*6*). The se-

The author is in the Department of Microbiology and Immunology, University of Tennessee, Memphis, TN 38163, USA. E-mail: thatch@utmem1.utmem.edu

quence has revealed the surprising result that chlamydiae actually have a full complement of peptidoglycan synthesis genes. But how much peptidoglycan is in fact made and for what purpose?

A unique family of four large surface-exposed outer membrane proteins (POMPs) were recently identified in *C. psittaci* (*7*). It was therefore not surprising to find orthologs in *C. trachomatis*. What was surprising was to find 9 POMP genes in *C. trachomatis* and 18 in the unfinished *C. pneumoniae* genome (*8*). Why so many paralogs in bacteria with small genomes?

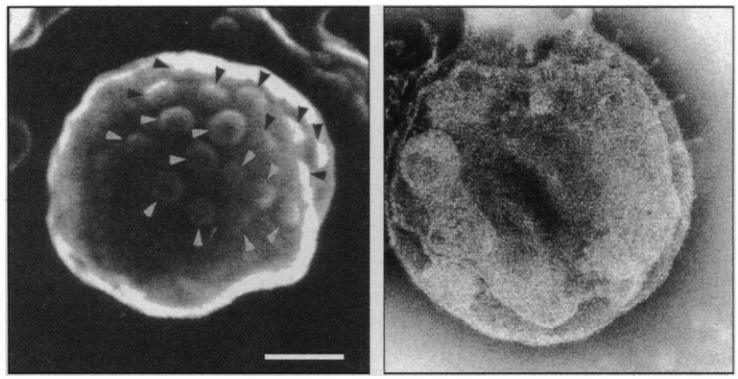
The genes encoding another potential surface structure, a type III secretion apparatus, were also found, extending an earlier study (*9*). Type III secretory systems not only permit export of proteins out of Gram-negative bacteria but also facilitate entry of the exported proteins into host cells with which the bacteria make contact. Type III secretion is common to many Gram-negative pathogens of plants and animals, and allows the bacteria to invade host cells or to subvert host defense mechanisms. The structural genes and those for assembly of the apparatus are conserved, but the substrates, which are secreted directly into host eukaryotic cells, tend to be unique to the species. Over 20 years ago, Matsumoto noted dome-shaped structures on the surface of chlamydiae, through which filamentous projections extend (see the figure). The projections were later found to penetrate through the vacuolar (inclusion) membrane within which chlamydiae reside throughout their intracellular sojourn (*10*). For years these structures, not seen in other bacteria, were speculated to play a role in nutrient acquisition. The discovery of the type III secretion genes in chlamydiae, together with recent electron microscopic evidence associating similar filaments with one of the type III systems of *Salmonella typhimurium* (*11*), suggests that transportation between the sequestered parasite and the host cell is not simply a one-way affair (*12*) and that the filaments serve as conduits for regulatory signals from parasite to host cell.

Several genes thought to be present in all bacteria were not found. The absence of some, such as those for *S*-adenosylmethionine and phosphoribosylpyrophosphate synthetases, may be explained by the metabolite-rich ecological niche occupied by chlamydiae. The absence of others, such as the highly conserved FtsZ gene that is found in Archaea and all Bacteria so far examined, defies simple explanation. FtsZ, a guanosine triphosphatase required for septum formation, was previously thought to be absolutely required for cell division of prokaryotes.

Perhaps the most intriguing finding for evolutionary microbiologists is that chlamydiae appear to have acquired an unusual number of eukaryotic genes, 20 or more, as compared to 3 or 4 in other bacteria whose genomes have been sequenced. Many of these genes more closely resemble those of plants than those of animals. Chlamydia-like intracellular bacteria have been found in the protozoan *Acanthamoeba*, and Stephens *et al.* (*1*) suggest the possibility that the ancestors of present-day chlamydiae may have first established an intracellular life-style in a plantlike single-cell organism, before the evolution of metazoans.

The authors have inferred a remarkable amount of information from the genome sequence. In the end, however, these results from the Chlamydia Genome Project raise more questions than they answer—perhaps the greatest contribution of this effort will be to stimulate further research in the field. What is secreted into the host by the type III apparatus? A factor that inhibits host cell apoptosis (*13*)? Factors that direct host vesicular membrane traffic to the inclusion containing the bacteria (*14*)? Chlamydia-synthesized proteins that have been identified in the inclusion membrane (*15*)? How do chlamydiae divide? Is there a connection between the absence of structural quantities of peptidoglycan in the cell envelope and the absence of key Fts proteins? What is the function of the POMPs? Escape from host immune defenses? Adaptation to different host-cell types?

The findings of this genome project extend earlier observations that suggested that chlamydial growth likely is restricted to an intracellular environment in nature because of unusual nutritional requirements found only in the cytoplasm of living cells. It is not clear, however, from the genome sequence what nutritional cocktail will permit host-free growth in the laboratory. Moreover, the inclusion membrane may be indispensably linked to nutrient acquisition, making attempts to achieve host-free growth an impractical if not futile effort. Finally, the number of potential peptides identified in the sequence that have no known relatives in other organisms is 236, or 27% of the total, not much different on a percentage basis from that of other sequenced bacteria. Nevertheless, some of the chlamydial proteins that have aroused the most biological interest in the past—the major outer membrane protein, the newly discovered POMPs, the major proteins involved in the disulfide-linked envelope protein complex, and the inclusion membrane proteins—are unique to chlamydiae. It would not be surprising, then, if the many mysteries still enshrouding these intracellular parasitic bacteria remain unsolved until the functions of these proteins are known.



Chlamydiae revealed. (Left) Scanning electron micrograph showing regularly spaced, dome-shaped bulges (arrowheads) on one hemisphere of chlamydiae. **(Right)** Transmission electron micrograph of envelope complexes revealing projections (upper right) that extend from the center of the domes, through the chlamydial inclusion membrane. The structures, long a mystery, may be part of a secretion apparatus that allows chlamydiae to alter host functions, thereby permitting its intracellular survival and growth.

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