Legionella kin found, linked to pneumonia

Packed inside a tiny amoeba with hundreds of its ilk, this minuscule bacterium soon bursts the amoebic bubble to seek out a less crowded home. This quest bodes illness if it occurs in the lungs of an unwary human host.

The unnamed bacterium is one of a group called *Legionella*-like amoebic pathogens, or LLAPs. These pathogens are close cousins of *Legionella pneumophila*—the microbe thought to cause Legionnaires' disease—report Barry Fields of the Centers for Disease Control and Prevention in Atlanta and his colleagues in the July–September EMERGING INFECTIOUS DISEASES, a CDC online journal.

The LLAPs—so named because, like *Legionella*, they flourish in amoeba—are genetically similar to *Legionella* as well. A strand-to-strand comparison of their ribosomal DNA turned up a mere 2 percent difference. This analysis prompted the investigators to propose that the 12 LLAPs they studied represent at least "five new species of *Legionella*," although they have not been formally named.

Overall, epidemiologists had calculated that up to 15,000 of the 250,000 pneumonia cases of known origin that occur in the United States each year are caused by *Legionella*. The new study suggests that LLAPs may cause some of these 15,000 cases, as well as some of the 250,000 pneumonia cases of unknown origin that crop up in the United States annually.

"This indicates that there's a lot of Legionnaires' disease we don't know about," says Fields.

Indeed, the 12 examples of the newly described species were found using experimental methods after standard tests had failed to detect them. They were spotted either in people with Legionnaires' disease or in the sources of Legionnaires' disease outbreaks, including a whirlpool bath and a hospital shower.

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Sarcobium lyticum, *found in 1954, is now considered a relative of* Legionella.

The first LLAP recognized by scientists turned up more than 40 years ago in soil. This early finding and recent unpublished work by biologists at Middle Tennessee State University in Murfreesboro, who found the microbes in amoeba collected from moist soil under an air conditioner, indicate that LLAP bacteria may be abundant in nature.

"In all likelihood, these bacteria are widespread in the environment," concludes microbiologist Anthony Newsome of Middle Tennessee State.

"They're out there, everywhere," Fields agrees.

The study by Fields and his colleagues may explain, in part, why Legionnaires' disease is difficult to diagnose. Standard tests, which rely on antibodies to the 39 previously recognized *Legionella* strains, fail to detect many cases. In addition, the finicky bacteria are notoriously difficult to grow in the laboratory, says Paul H. Edelstein of the University of Pennsylvania in Philadelphia.

In some instances, the new study suggests, researchers may have been looking for the wrong species. — *S. Sternberg*

Genome sequenced for skin disease virus

By creating millions of people with weakened immune systems, HIV has thrown a spotlight on many lesser-known infectious agents that have come to plague AIDS patients. Among them is the virus that causes molluscum contagiosum, a skin disease marked by the formation of papules, small dome-shaped bumps.

In an advance that could lead to a treatment for the condition, investigators have now deciphered the entire genetic blueprint of the molluscum contagiosum virus (MCV). That feat, reported in the Aug. 9 SCIENCE, is especially significant because MCV has been difficult to study by other means.

Investigators haven't yet grown MCV in the laboratory, nor have they found a laboratory animal that they can infect with the virus. Considering those obstacles, "the best way to get information about the virus was to sequence its genes," says Bernard Moss of the National Institute of Allergy and Infectious Diseases in Bethesda, Md.

Moss and his colleagues spent more than a year determining the identity and order of the nearly 200,000 pairs of nucleotides, or chemical subunits of DNA, that make up MCV's genome.

Once researchers had the genetic sequence in hand, they compared it to the genomes of the related smallpox and cowpox viruses. The MCV genome contains at least 163 genes, 104 of which resemble genes belonging to the two better-known pox viruses. Most of the shared genes play a role in controlling the activity of viral genes or in allowing the viruses to reproduce, says Moss.

Reflecting the dissimilarity of the illnesses produced by MCV and the deadly smallpox virus, the two genomes differ significantly in the viral genes employed during interactions between the virus and an infected host. For example, more than 20 smallpox genes that encode proteins known to manipulate the host immune response are missing from MCV, notes Moss.

On the other hand, the MCV genome contains at least 59 genes whose functions remain unknown, though some data suggest that several interfere with host immunity. One MCV gene encodes a protein similar to a molecule used by cells to alert the immune system to infectious agents. The viral version of the protein may disrupt that defense system, suggests Moss.

Another MCV gene appears to encode an inactive form of a chemokine, a molecule used to attract immune cells to a site of infection. By producing this misshapen chemokine, viruses may prevent the normal version from helping the body to mount an immune response, says Moss.

The researchers are still looking for the genes that play a role in stimulating skin cells to form papules. Infection with MCV usually produces papules only in certain populations, such as young children, with their inexperienced immune systems, and adults who contract the virus through sexual contact. The impact of MCV can be more dramatic in HIV-infected people. The skin of late-stage AIDS patients with the affliction is often covered with hundreds of papules, many of which may join together to form large lesions.

"This infection is becoming more troublesome among immunodeficient individuals. While the infection is not life-threatening, for many people it is disfiguring and really hurts the quality of life," says Moss.

Researchers plan to use the newly identified MCV proteins as targets for potential antiviral drugs. At present, the only therapy for molluscum contagiosum is the removal of visible papules, a procedure that does not eliminate the underlying infection.

"Sequencing [MCV's] genome will have tremendous clinical ramifications," predicts Patricia L. Myskowski of Memorial Sloan Kettering Cancer Center in New York. — *J. Travis*