

# Researchers identify a worldwide-distributed clone of bacteria responsible for Legionnaire's disease

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A study published online today in *Genome Research* describes new insights into *Legionella pneumophila*, the bacteria responsible for most cases of Legionnaires' disease. This report investigates the genetic background of *L. pneumophila*, provides clues to the evolution and emergence of this pathogen, and describes the identification of a worldwide-distributed epidemic clone.

Legionnaire's disease is characterized by severe pneumonia, afflicting the elderly and individuals with weakened immune responses in particular. While *L. pneumophila*, a genetically diverse species and one of many *Legionella* species, is common in natural and drinking water supplies, the majority of Legionnaire's disease cases worldwide (approximately 84%) are caused by a single serogroup, *L. pneumophila* Sg1. Recent work has suggested that even though Sg1 is responsible for most clinical cases, this serogroup accounts for only about 30% of environmental *Legionella*.

As the prevalence of Sg1 in Legionnaire's disease cases does not appear to be a result of environmental predominance, the frequent occurrence of Sg1 in disease is likely due to higher virulence. In this study, researchers led by Dr. Carmen Buchrieser of the Institut Pasteur conducted a comparative genomics analysis to gain insight into the basis for the higher virulence of Sg1. To compare Sg1 and other *Legionella* isolates, the researchers constructed DNA-arrays containing genes

known to be variable in *L. pneumophila* strains, including a set of known and potential virulence genes. “We screened the gene content of 217 *L. pneumophila* strains and 32 other *Legionella* (non-*pneumophila*) strains that were isolated from humans and the environment,” describes Buchrieser. “We discovered core virulence- and eukaryotic-like genes are highly conserved, indicating strong selection pressures for their preservation.”

Importantly, a cluster of lipopolysaccharide (LPS) biosynthesis genes was found to be common in Sg1, even in different genetic backgrounds. This suggests that the gene cluster could be transferred horizontally between strains. “The LPS of Sg1 itself may confer to Sg1 strains the high prevalence in human disease,” explains Buchrieser. Variation in LPS, a component of the cell wall normally recognized by the innate immune system, could allow the bacteria to evade host immune responses.

Most significantly, this study identified a specific clone of Sg1 that is present in both sporadic cases and outbreaks worldwide. “The identification of this clone opens exciting possibilities of research to find out which genes contribute to improved interaction with the host, or to improved fitness in the environment, or to both,” describes Buchrieser.

Buchrieser cautions that there may be other genetic factors involved in the emergence of an epidemic strain. “Although the strains carrying this LPS cluster seem to be particularly adapted for causing human disease, additional genetic factors present in the genome may have allowed a particular clone of Sg1 to evolve within this highly diverse species.”

In addition to gaining insight into the genetic basis for *L. pneumophila* Sg1 virulence, Buchrieser suggests this work may lead to new methods of detection. “The findings of this comparative genomics approach will be invaluable for the development of novel tools to rapidly detect

*Legionella*-associated risk factors in water distribution systems of hospitals and other potential sites for *Legionella* infection.”

Citation: Cazalet, C., Jarraud, S., Ghavi-Helm, Y., Kunst, F., Glaser, P., Etienne, J., and Buchrieser, C. Multi-genome analysis identifies a worldwide distributed epidemic *Legionella pneumophila* clone that emerged within a highly diverse species. *Genome Res.*  
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