

Department of Natural Resource Sciences

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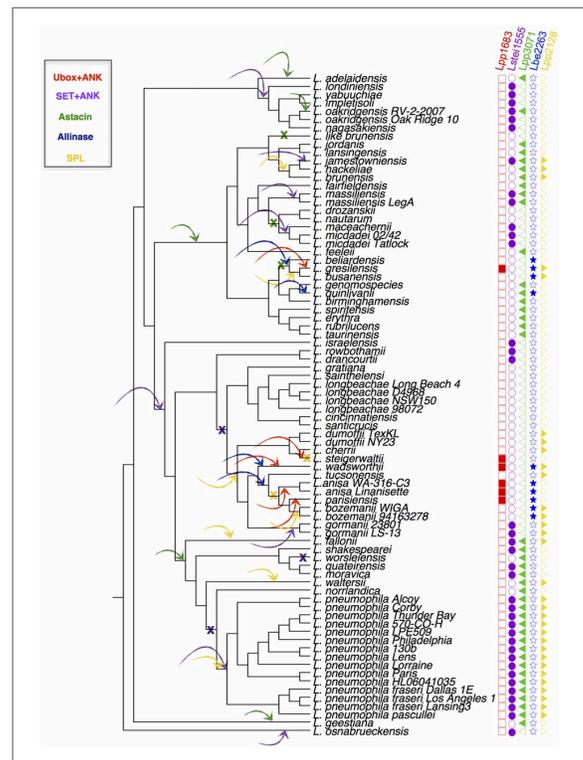
Macdonald-Stewart Building | R3-045

Intracellular parasitism, the driving force of evolution of *Legionella pneumophila* and the genus *Legionella*

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ABSTRACT: Bacteria of the genus *Legionella* are present in water environments where they replicate within protozoan hosts. However, when aerosolized bacteria are inhaled, they colonize the respiratory tract, invade alveolar macrophages and replicate therein causing a human disease called Legionnaires' disease. Our analyses revealed that the *Legionella* genomes encode a high number and great diversity of effector proteins used to subvert host cells function. They share structural and sequence similarity with eukaryotic proteins. To further understand the evolution of the effector proteins of these bacteria we have sequenced and analyzed 58 different *Legionella* species. Using comparative genomics and phylogenetic analyses, we identified an extraordinarily high diversity of eukaryotic domains, several never identified in a prokaryote before. We demonstrated that both lateral gene transfer from eukaryotic hosts and bacterial genes that became eukaryotic-like by convergent evolution contributed to the evolution of these proteins within the genus *Legionella*.



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BIO: Carmen Buchrieser is Professor at the Institut Pasteur, in Paris, France. She obtained her PhD from the University of Salzburg in Austria in 1986 for her work on antibiotic resistance of bacterial pathogens in developing countries. Her major interest is to understand how bacteria cause disease: what are the genetic factors conferring bacterial virulence, how do they evolve, how do they allow subverting host functions, how do human pathogens emerge. She has published 163 publications in international journals, 26 book chapters and is editor of two books. Her work has been recognized through a number of membership elections including the European Molecular Biology Organization (EMBO, 2013).