

# Scientists reveal evolutionary intricacies of *Rickettsia* pathogens

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Scientists from the Virginia Bioinformatics Institute (VBI) at Virginia Tech and the University of Maryland School of Medicine have unveiled some of the evolutionary intricacies of rickettsial pathogens by analyzing over a decade's worth of genomic data. Some species of *Rickettsia* are known to cause harmful diseases in humans, such as epidemic typhus (*R. prowazekii*) and Rocky Mountain spotted fever (*R. rickettsii*), while others have been identified as emerging pathogens and organisms that might possibly be used for the development of biological weapons.

The new data, which are publicly available via the PATRIC project web site ([patric.vbi.vt.edu](http://patric.vbi.vt.edu)), open up exciting new possibilities for future research. The paper is featured in the April 16, 2008 edition of the online publication PLoS ONE.

Dr. Joseph Gillespie, a bioinformatician at the Virginia Bioinformatics Institute and leader of the study, remarked: "Over the past ten years, an average of one genome per year has been sequenced for the *Rickettsia*, which represents a considerable genomic treasure trove for evolutionary studies. We have systematically probed the genomic data available for *Rickettsia* to reveal how rickettsial genomes have given rise to the great diversity of organisms that we know today. This approach sheds light on the evolutionary intricacies of *Rickettsia* and suggests how some members of the group have developed into potent pathogens responsible for significant diseases in humans."

In the study, the researchers defined a core *Rickettsia* genome by

looking at a large number of genes that could potentially encode for proteins in the ten genomes under investigation. This information was used to generate over 700 groups of orthologous proteins that theoretically could have originated from a common ancestor. A similar exercise yielded over 1,300 orthologous groups of proteins that define the accessory genome. Digging further into the accessory genome yielded signature proteins that define the four major rickettsial groups, as well as species infecting common arthropod hosts and species harboring plasmids. Surprisingly, and contrary to previous dogma regarding rickettsial genome evolution, the accessory genome contained many likely elements of the bacterial mobile gene pool.

VBI Director and PATRIC Principal Investigator Bruno Sobral remarked: “Virulent species of *Rickettsia* are of great interest both as emerging agents of infectious disease and potential bioterror agents. We believe the current work provides a robust evolutionary framework that allows for the interpretation of the genomic characteristics of the four main lineages of *Rickettsia*. As such it provides an ideal resource for research directed at developing vaccines, diagnostics and therapeutics for the diverse group of pathogens that constitute the *Rickettsia*.”

Dr. Gillespie concluded: “The results obtained in this study are consistent with the recent explosion in the number of identified plasmids in *Rickettsia*. By making these data available we hope to enable future research into these intriguing organisms.”

Source: Virginia Tech

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