

PathoSystem Resource Integration for *Rickettsia spp.* and *Coxiella burnetii*

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Virginia Bioinformatics Institute (VBI) and its partners have been awarded a 5-year, \$10.3 million contract from NIH-NIAID to establish a national Bioinformatics Resource Center (BRC) that consists of a multi-organism relational database to facilitate research on microbial pathogens (<http://patric.vbi.vt.edu/>). As part of this initiative, VBI is developing the PathoSystems Resource Integration Center (PATRIC), a multi-organism relational database to support infectious disease research, especially as it affects biodefense. We expect PATRIC to be used as a computational resource in gaining a better insight into the pathogenic mechanisms of microbes and the development of improved vaccines, diagnostics and therapeutics. The database will contain high quality curated data: sequence annotations from published whole and partial genomes; all relevant experimental data; metabolic pathway data; taxonomic data; relevant literature, and a suite of visualization and analysis tools. Research experts and members of the scientific community will be closely involved at each step of the curation/annotation process. VBI is curating information on eight different pathogen classes that include both bacteria and viruses. Two of these are (a) members of the genus *Rickettsia*, which cause various arthropod-borne infections in humans and (b) *Coxiella burnetii*, the etiologic agent of Q fever. Because of their possible use as bioterror weapons, the *Rickettsia spp.* and *C. burnetii* have been listed as NIAID/CDC category B bioterrorism agents. At present we have archived the annotations of the 6 rickettsial pathogens that have been completely sequenced (<http://patric.vbi.vt.edu/organisms/Rickettsia/>) and the whole genome annotation of *C. burnetii* (<http://patric.vbi.vt.edu/organisms/Coxiella/>). These sites represent the initial step in our efforts to curate data on *Rickettsia spp.* and *C. burnetii*. We welcome and expect the *Rickettsia/Coxiella* research community to actively participate in the development of PATRIC as a useful computational resource for infectious disease research.