

Common adaptive strategies in hydrothermal vent and pathogenic Epsilonproteobacteria revealed by comparative genomic and physiological analyses

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The reconstruction of the evolutionary history of key biochemical functions is critical to understand how microbial life co-evolved along with Earth's changing conditions. Closely related microorganisms, whose members inhabit "relic" environments that resemble the early Earth (e.g., high temperature hydrothermal vents), as well as more "recent" habitats (e.g., the gastrointestinal tract of animals), provide excellent models to reconstruct how metabolism evolved and adapted to different environmental conditions within the various lineages of the group. Epsilonproteobacteria are such a group of closely related bacteria, as they are abundant in marine geothermal environments but have also adapted to colonize mammalian hosts. Recent phylogenetic studies showed that Epsilonproteobacteria that colonize mammalian hosts, such as the rumen commensal *Wollinella*, and the human pathogens *Campylobacter* and *Helicobacter* spp., have evolved from anaerobic, thermophilic relatives currently represented by species that inhabit deep-sea hydrothermal vents (e.g., *Caminibacter*, *Nautilia*, *Cetia* spp.). We have integrated comparative genomics and physiological approaches to identify core adaptive strategies conserved in Epsilonproteobacteria that colonize different habitats. Among the adaptive strategies common to all Epsilonproteobacteria, we have specifically investigated cell-to-cell communication via quorum sensing, chemotaxis and proteolytic activity. We believe that these conserved functions may play a critical role in basic microbial processes, such as biofilm formation and host colonization.