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Evolutionary genomics of *Salmonella*

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Summary

Genes acquired by *Salmonella enterica* during its evolution may have important roles in human infection

Significance and context

Salmonella species are Gram negative bacteria first discovered by the American veterinary scientist D.E. Salmon at the end of the 19th century, and are the cause of salmonellosis in humans. The salmonellae are taxonomically subdivided into *Salmonella enterica* and *Salmonella bongori*. To *S. enterica* belong over 2,000 serovars that are grouped into seven subspecies. It has recently been shown that a common ancestor acquired the mechanism of flagellar antigen shifting, which is considered to be an adaptation to life in warm-blooded hosts. Using DNA microarray technology, Porwollik *et al*. compared the genetic content of the entirely sequenced genome of the agent of mouse typhoid, *S. enterica* serovar *typhimurium* LT2, and that of several other salmonellae, revealing genes that may be responsible for LT2-related phenotypes in the salmonellae that infect humans.

Key results

A microarray of PCR-amplified whole open reading frames (ORFs) was constructed, consisting of more than 97% of the 4,596 coding sequences in the *S. enterica* sv. *typhimurium* LT2 genome. The genetic content of *S. enterica* sv. *typhimurium* LT2 was compared with that of other *S. enterica* strains and *S. bongori*. Porwollik *et al*. showed that 1,424 LT2 genes were absent or too divergent to be detected in at least one of the other *Salmonella* genomes tested. On comparison of the LT2 genomic content with that of other enteric bacteria, for example *Escherichia coli* K12 and O157:H7, *Klebsiella pneumoniae* MGH78578, and *Yersinia pestis* CO92, whose genomes have been sequenced, 935 LT2-specific genes were identified. Of those, 56 were present in all 22 *Salmonella* strains used in this study, and these included, for instance, genes encoding a DNA helicase, a tetrathionate reductase enzyme complex, anaerobic sulfide reductase, putative inner and outer membrane proteins, and other genes whose functions still need to be determined. Homologs of the five *Salmonella* pathogenesis islands (SPIs) vary among the different *Salmonella* strains. For example, most of the genes of SPI1 are present in all *Salmonella* strains tested but most of the genes of SPI2 are absent from *S. bongori*. Only *S. enterica* subspecies I has a full set of all SPIs present in *S. enterica* sv. *typhimurium* LT2. On the basis

of microarray analyses, a bifurcating taxonomic tree was constructed that suggests how *S. enterica* sv. *typhimurium* LT2 has evolved and which genes have been acquired during evolution. It was estimated that 513 genes were gained since the formation of the genus *Salmonella*. These include, for instance, genes encoding a second type-III secretion system, certain fimbrial genes, genes encoding a phosphoglycerate transport system, and the *rfb* cluster involved in the synthesis of lipopolysaccharides. Finally, when *S. enterica* sv. *typhimurium* LT2 evolved, it acquired another fimbrial operon, a number of prophages, and a large set of genes of unknown function.

Links

The *Salmonella typhimurium* LT2 complete genome sequence can be accessed at the National Center for Biotechnology Information, and information concerning proteome analysis is available.

Reporter's comments

Porwollik *et al*. compared the genetic content of *S. enterica* sv. *typhimurium* LT2, responsible for most *Salmonella* infections in humans, with that of a set of other *Salmonella* strains. They thereby determined a set of genes that are predicted to have been acquired during *Salmonella* evolution. Those genes may be important during infection of humans and/or survival in warm-blooded hosts. Future work should include a biochemical characterization of those genes accompanied by a study of their role during *Salmonella* infection. The fact that the function of a large number of those genes is currently unknown suggests that many steps in the mechanism of *Salmonella* infection of humans still need to be deciphered. This research should indicate candidate target proteins that will be useful in developing new therapeutic strategies.

Table of links

Proceedings of the National Academy of Sciences of the United States of America

Salmonella typhimurium LT2 complete genome

Proteome analysis at EBI

References

1. Porwollik S, Wong RM-Y, McClelland M: Evolutionary genomics of *Salmonella*: gene acquisitions revealed by microarray analysis. Proc Natl Acad Sci USA. 2002, 99: 8956-8961.