

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

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ArticleInfo		
ArticleID	:	4312
ArticleDOI	:	10.1186/gb-2002-3-12-reports0063
ArticleCitationID	:	reports0063
ArticleSequenceNumber	:	35
ArticleCategory	:	Paper report
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2002-11-19 Received : 2002-11-19 OnlineDate : 2002-12-6
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	

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Summary

The genome sequence of *Brucella suis* suggests that this animal pathogen may have evolved from a soil/plant-associated ancestor

Significance and context

Brucellosis, a disease that infects domestic animals and wildlife worldwide, is caused by species of the bacterium *Brucella*, including *B. abortis* and *B. suis*. These are facultative intracellular pathogens that survive in macrophages by inhibiting phagosome-lysosome fusion. Hoofed animals become infected by ingesting *Brucella* and symptoms of infection include abortion, retained placenta, reduced milk production and difficulty in becoming pregnant. Humans can become infected, resulting in Malta fever, after direct contact with infected animals or their reproductive tissues, or after drinking unpasteurized milk from an infected herd. Symptoms of brucellosis in humans include weakness, anorexia, aches, sweating and inattentiveness. Treatment is difficult, no vaccines are currently available, and *B. suis* is considered a candidate microorganism for bioterrorism. Paulsen *et al.* have now determined the entire genome sequence of *B. suis*.

Key results

The genome of *B. suis* 1330 consists of chromosomes (chr) I and II. Chr I contains 2,107,792 base-pairs (bp), has a G+C content of 57.2%, and contains 2,185 protein-coding genes with an average length of 842 bp. Chr II contains 1,207,381 bp, has a G+C content of 57.3%, and contains 1,203 protein-coding genes with an average length of 897 bp. In contrast to Chr I, Chr II contains a set of replication genes that are similar to those found on, for instance, the *Agrobacterium* Ti plasmids. Chr I carries mainly genes that are involved in transcription, translation and protein synthesis, whereas Chr II mainly carries genes required for energy metabolism, membrane transport, regulatory functions and plasmid functions. A comparison of the *B. suis* genome with that of *B. melitensis* revealed that more than 90% of the genes were 98-100% identical between these two organisms. The less similar genes mainly encode hypothetical proteins that are supposed to be responsible for the difference in pathogenicity and host preference between these species. Other proteins that are unique to *B. suis* or *B. melitensis* include, for example, transposases, an outer membrane protein, ATP-binding cassette (ABC) transporters, cell-surface protein, and propionyl-CoA carboxylase beta chain. The genome sequence of *B. suis* has a total

of 1,902 open reading frames (ORFs) with significant similarity to ORFs in the plant symbiotic bacteria *Mesorhizobium loti* and *Sinorhizobium meliloti*, and the plant pathogen *Agrobacterium tumefaciens*, which are members of the same bacterial order (the Rhizobiales) as *Brucella*. In addition, analysis of the genome sequence suggests that *B. suis* has the capacity to use plant-derived compounds, and that 29 insertion sequences are present. Finally, the genome sequence reveals the presence of genes encoding proteins involved in adhesion (for example, adhesin with autotransporter domain, putative surface-exposed proteins, putative outer membrane proteins), in invasion and trafficking (for example, invasins, hemolysins), and in detoxification (for example, ureases, Fe-Mn superoxide dismutase, alkyl hydroperoxide reductase).

Links

The entire genome sequence of *B. suis* 1330 can be accessed at The%20Institute%20for%20Genomic%20Research:%20Brucella%20suis%201330.

Reporter's comments

The analysis of the genome sequence of the animal pathogenic bacterium *B. suis* by Paulsen *et al.* reveals a striking similarity between an animal pathogen and plant symbiotic/pathogenic bacteria. It would be tempting to determine the molecular requirements to change a plant symbiotic bacterium into a plant pathogenic bacterium and subsequently into an animal pathogen. When supported by expression and mutant analysis, and biochemical investigation, this study will enhance our understanding of which molecules are required for pathogenesis.

Table of links

Proceedings%20of%20the%20National%20Academy%20of%20Sciences%20of%20the%20United%20States%20of%20America

The%20Institute%20for%20Genomic%20Research:%20Brucella%20suis%201330

References

1. Paulsen IT, Seshadri R, Nelson KE, Eisen JA, Heidelberg JF, Read TD, Dodson RJ, Umayam L, Brinkac LM, Beanan MJ, et al: The *Brucella suis* genome reveals fundamental similarities between an animal pathogen and plant pathogens and symbionts. Proc Natl Acad Sci USA. 2002, 99: 13148-13153.