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Brucella strain-specific proteomes

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Summary

Experimental analysis of the proteomes of virulent and non-virulent strains of *Brucella melitensis* reveals differences in the proteins involved in iron metabolism

Significance and context

Brucella melitensis, an aerobic, non-motile, Gram-negative bacterium, causes brucellosis, an infectious disease that can affect most species of domestic animal, with sheep and goats being most susceptible. In humans, the disease is known as Malta fever. Animal infection most often occurs by inhalation or through abraded skin. Humans usually get infected by ingestion of contaminated milk or food. *B. melitensis* is prevalent in Mediterranean and Middle Eastern countries, through Central Asia to China. Regions of Africa, India, Central and South America are also affected. Symptoms include fever, depression, arthritis and nervous signs. An attenuated strain, Rev 1, of *B. melitensis* is nowadays most often used in live vaccines. Eschenbrenner *et al.* have compared the proteomes of *B. melitensis* Rev 1 and the virulent strain *B. melitensis* 16M using two-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization mass spectrometry.

Key results

Analysis of the proteomes of *B. melitensis* strains 16M and Rev 1 demonstrated the presence of 513 and 522 protein spots, respectively, in a pH range from 4.0 to 7.0. Proteins could be subdivided into those that were uniquely present in either strain 16M or Rev 1, and those that were under- or over-expressed in strain Rev 1 compared to strain 16M. Proteins that were expressed only by strain 16M include peptidyl-prolyl *cis-trans* isomerase and aconitate hydratase, and those unique to Rev 1 include a sugar-binding protein, nitrate reductase and two chromosome-partitioning proteins. Proteins underexpressed by strain Rev 1 compared to 16M include an arylesterase precursor (pH range 4.0-5.0), a D-galactose-binding periplasmic protein precursor, a D-ribose-binding periplasmic protein precursor, isovaleryl-CoA dehydrogenase and 4-hydroxybutyrate dehydrogenase (pH range 4.5-5.5), and proteins involved in DNA protection during starvation, hydroxypyruvate isomerase and acetylglutamate kinase (pH range 5.0-6.0). Proteins overexpressed by Rev 1 compared to 16M include an acyl-CoA dehydrogenase, a peptidoglycan-associated lipoprotein and an alcohol dehydrogenase (pH range 4.0-7.0), an iron(III)-binding periplasmic protein precursor (pH range 4.0-5.0), an isovaleryl-CoA

dehydrogenase (pH range 4.5-5.5), and a transaldolase (pH range 5.0-6.0). A striking difference between strain Rev 1 and 16M is the greater expression by strain Rev 1 of a set of proteins involved in iron metabolism, suggesting that strain Rev 1 may have an increased ability to assimilate iron.

Links

The entire genome sequence of *B. melitensis* 16M is accessible at [The Institute of Genomic Research: *Brucella melitensis* 16M](#) and [Access to the *Brucella melitensis* 16M Genome Data](#), and updates of proteome analyses based on the genome sequence can be found at the [Proteome analysis: *Brucella melitensis*](#) page at the European Bioinformatics Institute.

Reporter's comments

Eschenbrenner *et al.* have demonstrated a variety of metabolic differences between the proteomes of the vaccine strain *B. melitensis* Rev 1 and the virulent strain 16M. Future work should include the construction of mutants affected in the expression of the identified differentially produced proteins. Analysis of the infective behavior of such mutants, together with an expression analysis of the relevant genes, should illustrate their importance for the development of disease. Study of the proteomes could also show up proteins that might be candidate targets for drug development.

Table of links

[Journal of Bacteriology](#)

[The Institute of Genomic Research: *Brucella melitensis* 16M](#)

[Access to the *Brucella melitensis* 16M Genome Data](#)

[Proteome analysis: *Brucella melitensis*](#)

References

1. Eschenbrenner M, Wagner MA, Horn TA, Kraycer JA, Mujer CV, Hagijs S, Elzer P, DelVecchio VG: Comparative proteome analysis of *Brucella melitensis* vaccine strain Rev1 and a virulent strain, 16M. J Bacteriol. 2002, 184: 4962-4970.