GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Proteomic and bioinformatic analysis of outer membrane proteins of the protobacterium *Bartonella henselae* (Bartonellaceae)

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Genet. Mol. Res. 10 (3): 1789-1818 (2011)
Received November 26, 2010
Accepted February 10, 2011
Published August 26, 2011
DOI http://dx.doi.org/10.4238/vol10-3gmr1153

ABSTRACT. *Bartonella henselae*, an infectious agent causing cat-scratch disease and vasculoproliferative disorders in humans, is a fastidious facultative intracellular pathogen. The outer membrane proteins of *B. henselae* are key molecules that play a primary role in host-cell interactions. We isolated *B. henselae* outer membrane proteins, using the ionic detergent N-lauroyl sarcosine sodium salt and sodium carbonate, purification by two-dimensional (2-D) gel electrophoresis, and protein identification using mass spectrometry. Treatment with buffers containing ASB-14 and ZWITTERGENT 3-10 increased solubilization of *B. henselae* proteins, particularly proteins with basic p*I*. Three hundred and sixty-

eight spots were detected from the sarcosine-insoluble outer membrane fraction; 94 distinct protein species were identified from 176 spots. In the outer membrane fraction from carbonate incubation, 471 spots were calculated and 259 spots were identified, which included 139 protein entries. There were six outer membrane proteins in the sarcosine-insoluble outer membrane fraction compared with nine outer membrane proteins from samples subjected to carbonate incubation. We used bioinformatic analysis to identify 44 outer membrane proteins by prediction of their domains and tertiary structures and documented the potential virulence factors. We established the 2-D reference maps of the outer membrane subproteome of *B. henselae* using the two different extraction methods, which were partly complementary to each other. Sodium carbonate extraction isolated low-abundance and basic proteins better than the lauroyl sarcosine sodium salt extraction, which enriched high-abundance porins.

Key words: *Bartonella henselae*; Outer membrane protein; 2-D gel electrophoresis; MS; Bioinformatics

