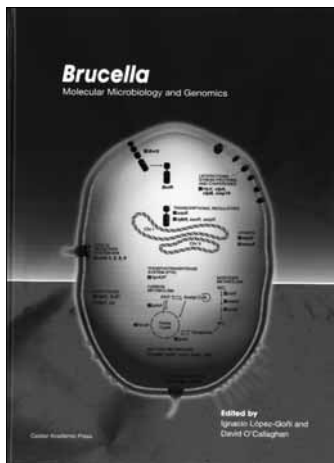


BOOK REVIEWS

INTERNATIONAL MICROBIOLOGY (2011) 14: 235-236
ISSN: 1139-6709 www.im.microbios.org



***Brucella.* Molecular microbiology and genomics**

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2012. Caister Academic Press
261 pp, 18 × 25 cm
Price: £159
ISBN 978-1-904455-93-6

Brucellosis is a zoonotic infection transmitted from animals to humans by the ingestion of infected food products, direct contact with an infected animal, or the inhalation of aerosols. Among these, inhalation is remarkably efficient given the relatively low concentration of organisms (10–100 bacteria) needed to establish infection in humans. *Brucella* is a facultative intracellular pathogen that survives and multiplies in phagocytes, and it has evolved to avoid the host's immune system. Brucellosis is usually characterized by the long-term persistence of the bacteria in the body. The diagnosis can be challenging since the disease can involve any body organ or system, and its symptoms may overlap with those of a wide spectrum of infectious, as well as non-infectious conditions. The clinical presentations of brucellosis are not only undulant fever but also joint manifestations, such as spondylitis, and neurological complications, often associated with personality changes (anxiety, amnesia, delusions, hallucinations, delirium, phobias and irritability), in addition to prolonged frontal or occipital headaches. Additional symptoms are anorexia and abdominal pain.

"*Micrococcus melitensis*" was first isolated in 1887 by David Bruce (1855–1931), who detected the bacterium in the spleen of humans who had died from undulant fever in Malta. It is believed that Florence Nightingale (1820–1910, the famous nurse driving implement of hygiene in hospitals) endured over 25 years of the illness, including personality changes (neurobrucellosis) and spondylitis, which left her bedridden for six years. The severity of this disease and the lack of vaccines suitable for use in humans have led to the

investigation of *Brucella* as bioterrorism agents. Indeed, the American military weaponized *Brucella suis* in 1954; however, changing global politics resulted in the abandonment of these studies following the Biological and Toxic Weapons Convention of 1972.

The book *Brucella. Molecular microbiology and genomics* introduces the reader to what is known thus far and to the current challenges in the taxonomy, genomics and proteomics, diagnosis and epidemiology, vaccine development, virulence mechanisms, and life cycle posed by these enigmatic bacteria. The authors of the 13 chapters are experts in the field and they are the book's editors, Ignacio López-Goñi (University of Navarra, Spain) and David O'Callaghan (INSERM, Nimes, France).

The genus *Brucella* belongs to the alphaproteobacteria. In addition to the type genus *Brucella*, six further genera, *Crabtreeella*, *Daeguia*, *Mycoplana*, *Ochrobactrum*, *Paenochrobactrum*, and *Pseudochrobactrum*, are currently recognized within the family Brucellaceae. The closest phylogenetic neighbor of *Brucella* is *Ochrobactrum*. Initially, two species were described for *Brucella*, *B. melitensis* (melitensis in Latin refers to the Malta island) and *B. abortus* (named after the discovery that the organism is responsible for spontaneous abortion in cattle, Chapter 1). Currently, the genus *Brucella* consists of ten species with validly published names. Of these, the six so-called classical species show a preferential host range and other distinguishing phenotypic features: *B. melitensis* (infects mainly sheep and goats), *B. abortus* (cattle and other bovidae), *B. suis* (swine), *B. ovis* (sheep), *B. neotomae* (desert woodrats) and *B. canis* (dogs). The remaining four species comprise two from marine mammals, *B. ceti* and *B. pinnipedialis*, and the novel *B. microti* (common voles) and *B. inopinata* (recently isolated from a breast-implant infection in an elderly woman).

In 2002, two *Brucella* genomes were sequenced and analyzed. At present, 40 *Brucella* genomes have been sequenced (Chapter 2). The *Brucella* genome is composed of two chromosomes. Expression analysis in *Brucella* grown in vitro has confirmed a higher rate of synthesis of proteins encoded in chromosome I than in chromosome II (Chapter 5). The presence of two chromosomes could be consistent with the ability of *Brucella* to adapt and live in at least two very different environments, as free-living bacteria and intracellularly. In the latter, the bacterium must metabolically adapt to the intracellular environment and then manipulate its host cell's biology to create conditions for its survival and multiplication.

Thus, the identification of protein shifts and interactions is necessary to understand the *Brucella* life cycle (Chapter 6).

A major aspect of the pathogenicity of *Brucella* is its survival and replication within host macrophages. However, the *Brucella* genome does not seem to encode the classical virulence factors found in other bacterial pathogens; rather, its main virulence factors are a lipopolysaccharide (LPS) of low endotoxicity (Chapter 7), the BvrR/BvrS system, which controls the expression of a set genes involved in a broad range of species-specific functions (Chapter 10), and the type IV secretion system (Chapter 11). An interesting aspect of *Brucella*, albeit one thus far incompletely studied, is its gene clusters acquired by horizontal transfer, including genomic islands, whose acquisition and deletion may be related to the host preference manifested by the corresponding *Brucella* species (Chapter 3). The genomic islands contained in *Brucella* are made up of functional classes of genes that have been divided into two groups: one comprising virulence factors and the other, genes of metabolic or unknown function. Moreover, virulence may also depend on metal acquisition (Chapter 9).

Traditionally, brucellosis is diagnosed using cultural and serological approaches. The potential of molecular assays for *Brucella* identification based on 16S rRNA, the cell surface protein bcp31, IS711, etc., is a subject of current investigations (Chapter 4). However, such assays will need to be validated in clinical samples before they can be adapted for routine laboratory testing.

Brucellosis is an important bacterial zoonosis worldwide. In endemic areas (Mediterranean Europe, Middle East, Latin America), the incidence of the disease in humans may be more than 200 per 100,000 habitants. The classical treatment of brucellosis consists of a course of antibiotics (doxycycline and rifampicin) for six weeks. New antibacterials that are specifically active at the intracellular phase of *Brucella* are being developed. Such drugs would also have the potential to limit the selection pressure favoring the growth of resistant mutants, thereby reducing the secondary effects of antibiotic treatment on the human microbiota (Chapter 12). Other strategies aimed at the control of *Brucella* include a vaccine (Chapter 13).

Brucella. Molecular microbiology and genomics can be recommended to microbiologists, immunologists, veterinarians, and clinicians with an interest in microbial pathogenesis, host-bacterium interactions, and microbial diagnosis.

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