strains, but the improved performance in the present study may also be a result of the development of the Vitek 2 database. Identification of C. guilliermondii and Candida lusitaniae was problematic, both in the study by Graf et al. [8] and in the present study, whereas all C. glabrata isolates were identified without difficulty. This is in contrast to the study by Massonet et al. [9], in which most difficulties were encountered with C. glabrata. The reason for this discrepancy is unknown. As in the study by Graf et al. [8], the present database was unable to separate Candida inconspicua and Candida norvegensis.

Conventional identification methods are still considered to be the reference standard for the identification of yeast isolates, but are laborious and time-consuming, and are suited better to research than to clinical laboratories. The Vitek 2 system identifies most clinically important Candida spp. reliably within 15 h, and appears to be an excellent alternative identification method for clinical laboratories performing fungal diagnostics.

ACKNOWLEDGEMENTS

The technical assistance of S. Laitinen is gratefully acknowledged.

REFERENCES


RESEARCH NOTE

A new variant of Brucella melitensis

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ABSTRACT

Brucella melitensis is highly pathogenic and constitutes a serious risk to public health. In Argentina, biovar 1 has been isolated from infected animals, but the Rev.1 strain vaccine is not authorised for use. This report describes nine atypical B. melitensis isolates obtained from humans. These isolates grew slowly, produced small colonies and were susceptible to penicillin and dyes, similar to the B. melitensis Rev.1 vaccine strain, but were inhibited by streptomycin 2.5 mg/L. The isolation of such atypical B. melitensis variants has never been reported from animals in Argentina, and could indicate the emergence of a new mutant variant.

Keywords Brucella melitensis, identification, phenotypic characteristics, Rev.1 vaccine, variant

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Although the organisms constituting the genus Brucella are highly homogeneous, the genus is classified currently into six nomen species: Brucella abortus, Brucella suis, Brucella melitensis, Brucella canis, Brucella ovis and Brucella neotomae [1–3]. This taxonomic scheme correlates somewhat with the preferential natural host, although the first three species can also infect other animals [4]. Differences in virulence have been observed, and the apparent rank virulence order shown in guinea-pigs seems to be similar to that in humans: i.e., B. melitensis >> B. suis >> B. abortus [5]. Each species is subdivided into biovars on the basis of cultural, biochemical and serological differences, but the three biovars of B. melitensis are distinguished solely by their immunochemical reactions with monospecific anti-lipopolysaccharide (LPS) A and M-determinant sera [6]. Isolation of atypical B. melitensis variants in Israel, and of dye-sensitive strains in various countries, has been reported, indicating that differences are not limited to the agglutination pattern [7,8].

The Argentine National Human Brucellosis Network (NHBN) at the ANLIS Dr C.G. Malbrán (Buenos Aires, Argentina) studied 118 B. melitensis isolates from humans during the period 1994–2004. The isolates were obtained from clinical laboratories in Argentine provinces, and were sent to the NHBN headquarters for characterisation. The present study reports the isolation and typing of nine B. melitensis isolates with atypical phenotypic characteristics that could indicate the emergence of a new mutant variant. All nine atypical isolates were differentiated from other Gram-negative organisms on the basis of morphology, motility, lactose fermentation on MacConkey agar, acid production on agar containing glucose, haemolysis on blood agar, catalase, oxidase and urease (Christensen method) reactions, and nitrate and citrate reduction. Rough/smooth phase variation was observed using obliquely reflected light, suspending a colony in acriflavine, and by staining colonies with crystal violet [6].

After the isolates were identified as members of the genus Brucella, their species identification and biovar were established according to the recommendations of the International Committee on Bacterial Nomenclature (ICBN), Subcommittee on Taxonomy of the Genus Brucella [2]. Serum and CO2 requirements, H2S production, and growth in the presence of thionin (20 mg/L), basic fuchsin (20 mg/L), safranin O (100 mg/L), erithrytol (1 g/L), penicillin (5000 IU/mL) and streptomycin (2.5 mg/L) added to Brucella Agar (BBL Microbiology Systems, Cockeysville, MD, USA) were determined. Growth patterns on thionin blue and malachite green (2 mg/L) were investigated, both with and without the presence of CO2 5% v/v. Urease tests (Bauer’s method) and agglutination with polyclonal monospecific anti-A, -M and -R antiserum were performed [6]. Susceptibility to Brucella phages was determined using Tb, R/C, Wb and Iz phages at 1 and 104 routine test dilution (RTD) [9]. Reference strains B. abortus 544-2, B. suis 1330, B. melitensis biovar 1 16 M, biovar 2 63/9 and biovar 3 Ether, and B. melitensis Rev.1, were included in each test as controls. Finally, PCR-RFLP (restriction fragment length polymorphism) analysis was performed by digesting the amplified omp25 gene with EcoRV, and the amplified rpsL gene with NciI [10,11].

Brucellosis is not a sustainable disease in humans, and the source of infection always resides in domestic or wild animals, or their derived products. However, new Brucella strains and species may emerge as those existing already adapt to social and agricultural changes [12–14]. In Argentina, the sheep population (c. 15 million) is concentrated mainly in the south and north-east of the country, while goats (c. 4 million) are located mostly in the north-west. Surveys revealed a 0.5–0.8% prevalence of caprine brucellosis in the north-western provinces, with the isolation of B. melitensis biovar 1 from infected goats, although the use of the B. melitensis Rev.1 vaccine has not been authorised. Ovine brucellosis caused by B. ovis was found in regions where sheep are located, but B. melitensis has only been isolated from a few sheep [15].

Of the 118 B. melitensis isolates from humans, 107 (90.67%) belonged to biovar 1, two (1.69%) belonged to biovar 3, and nine (7.6%) were atypical. Isolate 874 was characterised in 1986 at the Pan American Zoonosis Center (PAHO/WHO) as atypical B. melitensis biovar 1 (Table 1). To check its stability, a suspension containing 108 CFU/mL was injected into two guinea-pigs and...
was recovered after 6 weeks from their spleens. The isolates had the same phenotypical characteristics as the original strain, indicating that the isolate could be considered stable following animal passage.

All nine atypical isolates were smooth, grew slowly, produced small colonies and were susceptible to penicillin and dyes, similar to the Rev.1 vaccine strain, but were inhibited by streptomycin 2.5 mg/L (Table 2). A slight increase in the growth pattern on basic fuchsin was observed when CO₂ 5% v/v was present during incubation, and also when sterile equine serum 5% v/v was added to the basal medium. However, growth was inhibited by thionin blue and mala-chite green, even in the presence of CO₂. Of the nine atypical B. melitensis isolates, eight were identified as biovar 1 and one as biovar 2, based on a difference in the quantitative distribution of the A and M antigens.

In Argentina, only B. melitensis biovar 1 has been isolated from animals, while two cases of infection with biovar 3 have been reported in humans [16] (IX Congreso de Argentino de Microbiología, Buenos Aires, 2001, abstract 220), probably because infected animals are diagnosed mainly by serological tests. The nine patients in the present study (Table 1) were hospitalised with fever and weight loss as the main symptoms. A girl (aged 7 years, isolate 290) relapsed 6 months after completing treatment and the same strain was isolated.

PCR-RFLP of the omp25 gene with EcoRV showed that all nine isolates were true B. melitensi-
sis. Susceptibility of *B. melitensis* to dyes and penicillin has been reported previously, as well as the finding that polymorphism of the *omp2* porin gene correlates with dye sensitivity [7,17,18].

This virulent atypical *B. melitensis* variant could not have originated from the vaccine Rev.1 strain (as determined by PCR-RFLP of the *rpsl* gene with NciI), although some of its phenotypic characteristics resembled the vaccine strain. The variant could have been introduced into the country via an infected animal, since brucellosis can exist in a latent form for several years [19], or it could be a new adaptation variant of *B. melitensis*.

ACKNOWLEDGEMENTS

We are very grateful to D. B. Hasan for helpful assistance with the typing of the isolates, and to K. Nielsen for critically reading the manuscript.

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