Correlation of antigenic expression with progress in antibiotic therapy of acute human brucellosis

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Human brucellosis is a zoonotic disease which is endemic in Saudi Arabia. The aim of this study was to investigate the humoral immune responses and identify the target antigens that persist at different stages in human brucellosis during antibiotic therapy. To do this, an acute case of accidental nosocomial infection was studied experimentally. Blood was collected from the patient at the time of diagnosis, and at weekly intervals during therapy until remission. IgG and IgM immunoblotting was used to characterize specific antigenic determinants, and ELISA antibody titration was performed to quantify the circulating antibodies. Results indicated that protein bands of 12–13.5 kDa bound IgG in the patient’s sera but did not bind IgM on immunoblots and are probably not specific for, or important in, early stage infections. However, an 18 kDa band persisted during infection through remission. The pivotal and most important findings were that the number of protein bands seen on immunoblots, the magnitude of ELISA antibody titres and the concomitant changes in the intensity of the polypeptide bands of 42–43 kDa were positively correlated with the stage of infection. High numbers of anti-IgG and -IgM immunoblot bands coupled with high ELISA antibody titres and a concomitant increase in intensity of the 42–43 kDa bands were positively correlated with acute and severe infection. Conversely, a reduction in the number of polypeptide bands as well as a decrease in the intensity, until the complete disappearance of the 42–43 kDa bands, coupled with low (baseline) ELISA antibody titration values indicated successful treatment and remission. The routine use of the methods described here to ascertain the stage of the disease, assess the progress of antimicrobial therapy and monitor cases of relapse in human brucellosis is suggested.

INTRODUCTION

Brucellosis is an important zoonotic disease. Four main Brucella species are capable of causing disease in humans but most human infections are caused by Brucella melitensis (Young, 1995). The disease is generally transmitted to humans by ingestion of contaminated dairy and meat products or by direct contact with infected animals. Occupational disease is common in animal herders, abattoir workers and veterinarians but a few cases of Brucella infections are acquired through accidental inhalation of contaminated aerosols during travel or in the laboratory (Young, 1995). If not detected and treated, human brucellosis can have deleterious and at times fatal sequelae.

The fact that the wealth of knowledge of Brucella pathogenicity was gained from studying animal models means that very little is known or documented for the aetio-immunology of acute human brucellosis. Brucella species consist of pathotypes or biovars and it is important to find out the specific aggressins that play key roles in the infections caused by them. It is also useful to identify candidate proteins that are important in cellular immunity or serve as protective antigens during infection. Such antigens can be further investigated for use as diagnostic markers and probes, or for developing vaccine(s) for immunotherapy. Additionally and most importantly, our ability to identify Brucella antigens that are expressed at particular stages during human infections will contribute immensely to our knowledge of the pathogenesis of brucellosis (Oliveira et al., 2002). Due to several reasons, including ethical constraints, it is difficult or impossible to experimentally follow and ascertain the stage of human Brucella infections from the onset through therapy until remission.

The aim of this study was to investigate the humoral immune responses and identify the target antigens that persist at different stages during antimicrobial therapy of acute human brucellosis.
brucellosis. Results of antibody titration, ELISA and IgG and IgM immunoblotting from the time of diagnosis through antibiotic therapy to complete remission are presented and some clinical correlates are discussed.

METHODS

Case history. A healthy male research worker complained of feeling feverish but without pyrexia during late afternoon for 10 days. All vital signs were normal and there were no complaints of night sweats, headaches, arthralgia, anorexia, myalgia or back pain. General physical examination was unremarkable and there was no splenomegaly or hepatomegaly. The only positive finding in the patient’s history before his symptoms appeared was that he had handled several biological samples, including human and animal sera, and had prepared protein antigens and isolated DNA from two Brucella cultures some 20–30 days before the onset of his symptoms.

Laboratory investigations and treatment regimen. Laboratory investigations, which were carried out with patient consent, included a liver function test, renal profile, blood culture and serology. Initially, blood was incubated at 37 °C in the automated Bact/Alert system using both aerobic and anaerobic culture media. Blood and serum samples were also taken at regular intervals for various tests until 21 days after antibiotic treatment ended. For serological tests, the tube agglutination and 2-mercaptoethanol (2-ME) agglutination assays were used to determine the presence of anti-Brucella antibodies.

For the identification of Brucella species the following biochemical tests were used: oxidase, urea, motility, nitrate, growth on blood agar and 2-ME agglutination tests. Antibiotic sensitivity testing was done on different isolates from the patient. Antibiotic sensitivity testing that was performed using the discontinuous method of Laemmli (1970), and immunoblotting experiments were performed with cytosolic Brucella antigen as previously reported (Parsons et al., 1986; Towbin et al., 1979).

RESULTS AND DISCUSSION

Cultures were positive after 4 days and Gram-negative cocacobacilli were isolated and identified as *B. melitensis*. The isolate was given the reference number KFSHRC.03-077-02372 and added to the King Faisal Specialist Hospital and Research Centre collection for further studies. Even though detailed biotype determination was not carried out, the isolate was positive in an agglutination test with *Brucella* antiserum, meaning that it belonged to either *B. melitensis* biovar 1 or 3. This information is in agreement with a previous report about biovars that occur in Saudi Arabia (Corbel, 1991).

Results of the first set of titres of *Brucella* tube agglutination and 2-ME titre indicated the presence of infection. These titres rose from relatively high initial values of 1 : 10 242 and 1 : 640 to even higher titres of 1 : 20 480 and 1 : 1280, respectively, within the first 14 days of diagnosis of the disease and the initiation of antibiotic therapy. Physical examination and detailed haematological findings indicated that the patient did not have any complications of brucellosis. The antibiotic sensitivity testing that was carried out on different isolates from the patient gave the same ‘antibiogram’ with the following MIC values: trimethoprim/sulfamethoxazole 0·125 μg ml⁻¹; rifampicin 1·5 μg ml⁻¹; streptomycin 0·5 μg ml⁻¹; tetracycline 0·094 μg ml⁻¹; imipenem 0·75 μg ml⁻¹; and ciprofloxacin 0·25 μg ml⁻¹. This indicated that the isolate was resistant to rifampicin.
It is known that there is a strong positive association of a high antibody titre with a positive blood culture, and together these are also predictive of a serious Brucella infection (Benjamin & Annobil, 1992). Consistent with this notion, the patient’s blood culture was positive and this was associated with high antibody titres.

In this study, crude cytoplasmic proteins prepared from sonicated whole killed cells from the B. melitensis isolate that caused the infection were used. The decision to use sonicated whole cytoplasmic proteins was based on the results of pilot studies in which proteins from bacterial surface washes, outer-membrane vesicles and whole cell sonicates were compared. SDS-PAGE of these three antigen preparations (results not shown) indicated that bacterial extracts prepared by sonication contained a complete mixture of all the protein bands and some contaminating LPS when compared to surface washes and outer-membrane preparations. The use of such a preparation in the serodiagnosis of human systemic disease as has been demonstrated here has been reported to have the added advantage that it can also be used for the serodiagnosis of human neurobrucellosis, which is an otherwise difficult condition to diagnose (Baldi et al., 1999).

Since the main aim of this study was to find out which antigens are important in human Brucella infections so as to be able to assess the stage of the disease and follow the success of antimicrobial therapy, immunoblotting was used to identify these antigens. Apart from the initial surge in antigenic expression, it was clear during antibiotic treatment that the patient’s Brucella tube agglutination, 2-ME and antibody titration by ELISA started reducing, and so did the number and intensities of various immunoreactive protein bands. This correlation was true for both IgM and IgG immunoblot spectra. An IgG immunostaining band of 12–13.5 kDa was present in all serum samples, including the pooled human serum, but was absent in the patient’s pre-infection serum. The slight presence of this band in pooled normal human serum from the local population probably means
that the band indicates exposure to but not necessarily infection with Brucella. Chirhart-Gilleland et al. (1998) studied a Brucella protein of similar molecular mass (14 kDa) from Brucella abortus for its reactivity in naturally infected animals and its T-cell reactivity but were unable to establish its protective capability. It is noteworthy that this 12–13.5 kDa band did not have an equivalent band on the IgM blots, indicating that it is probably not always pathognomonic.

In a study of 144 patients and 62 healthy humans, Leiva et al. (1990) identified 21 protein bands that were heterogeneous between different patients. In the present study, 24 protein bands were identified in one patient’s serum at the peak of infection (day 14) and in comparison most of these bands were similar to those reported by other investigators (Zygmunt et al., 1992; Stabel et al., 1990; Matar et al., 1996), including several of the 21 bands reported by Leiva et al. (1990). Leiva et al. (1990) reported that nine of these bands were the ‘most significant’ based on the frequency at which they occurred in different patients. Out of the nine protein bands that they identified, only two bands of 41 and 38 kDa were similar to those identified in the present study of a single patient. The complexity of comparing sera

**Fig. 2.** (a) Antigen spectra in human brucellosis. SDS-PAGE of Coomassie brilliant blue stained molecular mass markers (i) and Brucella polypeptides (ii, iii). Arrows in the left margin are Pharmacia low molecular mass markers: phosphorylase b (94 kDa), albumin (67 kDa), ovalbumin (43 kDa), carbonic anhydrase (30 kDa), trypsin inhibitor (20.1 kDa) and lactalbumin (14.4 kDa). Immunoblots of SDS-PAGE separated Brucella proteins were transferred onto nitrocellulose membranes. Strips were individually reacted with predetermined dilutions of each of the different sera. IgM (ii) and IgG (iii) immunoreactive bands are shown. Lanes: 1, pooled normal human serum; 2, patient’s pre-infection serum; 3–11 sera taken from the patient for 9 weeks from the day that the infection was diagnosed. Note that three of the most recurring common bands have been labelled x, y and z in the right margin. z is absent on the IgM blots. (b) Histogram showing the number of bands counted per strip in (a).
from heterogeneous sources was evident in their observations, hence emphasizing the need to study single cases of infection as well as large samples.

In the results presented here, a band of 18 kDa was persistent irrespective of the stage of infection and even after remission. A band of similar size has been identified and investigated over several years for its suitability as diagnostic antigen. Goldbaum et al. (1999) characterized and described an 18 kDa protein (lumazine) to be of diagnostic value in brucellosis. This protein has been investigated and confirmed to be highly immunogenic and potentially useful for the development of a vaccine for human and animal brucellosis (Goldbaum et al., 1991, 1993, 1999).

Several antigen bands were seen at the initial stages of the infection. This observation is consistent with a well-known microbial pathogenicity phenomenon: once microbial invaders gain entry into the host, the host begins to respond to eliminate the invaders (Smith, 1999). Successful intracellular pathogenic bacteria like Neisseria and Brucella lodge an ‘armoury’ to minimize the effectiveness of host defences (Smith, 1999). This is usually accomplished by producing bacterial products, which have been variously referred to as impedins (Glynn, 1972), auxiliary pathogenic factors or aggressins (Smith, 1999), and they enable the survival of these successful pathogens within their hosts (Smith, 1999). It appears that in this instance the armoury of the bacterium was minimized, probably due the host’s efficient immune responses, and the expression of these factors started diminishing as antibiotic therapy progressed.

The fact that the 42–43 kDa protein is probably the most important marker for the determination of the presence or absence of infection is exemplified by several references made to this protein by other investigators. Denoel et al. (1997) studied proteins in Brucellergene, a commercial delayed-type hypersensitivity allergen from the B. melitensis strain B1115, for their ability to induce T-cell proliferation and IFNγ production in peripheral blood. Interestingly, four out of the five proteins that are considered to be the most pathogemonic in the present study (namely the 18, 20, 36–38 and 42–43 kDa proteins) also belong to this group of T-cell active proteins. Furthermore, due to the specificity of the 43 kDa polypeptide, a commercially available PCR kit has been developed for routine diagnosis of brucellosis, based on the amplification of a 635 bp fragment of the gene coding for the 43 kDa outer-membrane protein from B. abortus strain 19 (Fekete et al., 1990).

These facts clearly demonstrate that this 42–43 kDa protein has already proved useful for its diagnostic value (Denoel et al., 1997; Fekete et al., 1990; Queipo-Ortuno et al., 1997). The present findings not only confirm these published facts, but emphasize in addition that the protein is a useful marker for staging Brucella infections as demonstrated in immunoblots here.

Many investigations have been carried out using different techniques and associating an array of proteins with Brucella infections (Oliveira et al., 2002; Wanke et al., 2002; Estein et al., 2002; Fekete et al., 1990; Queipo-Ortuno et al., 1997; Ebani et al., 2000, 2003), but most of these studies have been conducted either on animals or in a variety of infected humans. For human studies the heterogeneity of the selection of patients often makes it difficult to accurately define the temporal relationships between the different proteins produced and the stage of infection.

The present report, although a study of only one patient, is a very important addition to our knowledge of human brucellosis because the infection was diagnosed early and carefully followed until remission, making it possible to accurately trace the course of infection. In agreement with other studies, the relevance of the proteins of 36–38 kDa to acute infections was also clearly demonstrated. About 24 different protein bands were seen on immunoblots during the acute phase (day 14) of infection and most of these bands were similar to several bands that have been described by other investigators (Oliveira et al., 2002; Wanke et al., 2002; Estein et al., 2002; Fekete et al., 1990; Queipo-Ortuno et al., 1997; Ebani et al., 2000, 2003; Debbah et al. 1995; Cloeckaert et al., 1995). The most immunodominant antigens reported in the present study were mainly polypeptides of apparent molecular masses of 12–13.5, 18, 25–29, 30–34, 36–38 and 42–43 kDa.

It can be concluded that the presence of higher numbers of IgG and IgM immunoblot protein bands coupled with high ELISA antibody titres and a concomitant increase in intensity of the 42–43 kDa bands, were positively correlated with the severity of disease. Conversely, a reduction in the number of these bands as well as a progressive decrease in the intensity, until the complete disappearance of the 42–43 kDa bands coupled with low (baseline) ELISA antibody titration values indicate the success of therapy up to complete remission of the infection. In addition to the existing standard methods, the routine use of the methods described in this report in following disease aetiology, to determine the effectiveness of antimicrobial therapy and to define total remission of human brucellosis is indicated.

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