

## ABSTRACT

Serum samples were obtained from 350 animals comprising of 302 sheep and 48 goats with signs of brucellosis from different localities in West Bank, Palestine. None of the animals were vaccinated against *Brucella*. These samples were subjected to serological examination for the detection of specific *brucella* antibodies. The percentage of the positive brucellosis sera was found to be as follows: 31% in sheep sera and 52% in goats sera by Rose Bengal test (RBT), giving overall seroprevalence of 34%. The overall seropositivity using Complement Fixation Test (CFT) was 31%; 29% in sheep sera and 44% in goats sera. Eighty milk samples collected from seropositive animals were subjected to bacteriological examination. *Brucella* organisms were detected in 38 (47.5%) of the samples. Testing the milk samples by polymerase chain reaction (PCR), all the 38 positive samples detected by bacterial examination were also detected by PCR. Furthermore, with the PCR, we were able to additionally detect 24 (30%) infected milk samples that were negative by the bacterial isolation method. *B. melitensis* was identified from 42 out of 80 milk samples. The hemagglutinin gene sequence of two of the *B. melitensis* genes was PCR-amplified using the primers ORF and IS711, sequenced and subsequently aligned with other GenBank-accessible gene sequences of *B. melitensis* and other *Brucellae* spp. using version 2.0 of BLAST. These sequences were identical to that of the recent sequence of type strain of *B. melitensis* (ATCC 23456). Nucleotide comparison and restriction enzyme analysis of hemagglutinin revealed that the two current isolates were different from vaccine (Rev.1). The results of phylogenetic analysis revealed that they

were genetically close to the isolates from different Mediterranean countries, particularly those from France, Spain and Israel.