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OCCURRENCE OF *BRUCELLA* VIRULENCE-ASSOCIATED GENES ISOLATED FROM CATTLE, SHEEP, AND GOATS IN SELECTED MUNICIPALITIES IN THE EASTERN CAPE, SOUTH AFRICA

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B*rucella*, the causative of brucellosis, has some potential virulence factors involved in *Brucella* replication and its strategies to circumvent the immune response. The *Brucella* species generally considered pathogenic for humans, in decreasing order of virulence, are *Brucella melitensis*, *Brucella suis*, and *Brucella abortus*. The objective of this study was to determine the occurrence of *Brucella* virulence-associated genes isolated from cattle, sheep, and goats in 4 municipalities in the Eastern Cape, South Africa. A total of 130 isolates confirmed as *B. abortus* (62.3%) and *B. melitensis* (37.7%) in 4 municipalities were screened for the presence of the *ManA*, *ManB*, *Omp25*, *Omp31* and *ZnuA* virulence-associated genes. Gene detection showed *ManA* (100%), *Omp25* (100%) and *Omp31* (34.6-76.9%) to be the highest genes detected while *ManB* (11.5-38.5%) and *ZnuA* (10.3-19.2%) were the lowest from all isolates in the 4 municipalities. The results of the present study showed that most *Brucella* isolates from this region have virulence factor genes (*ManA*, *ManB*, *Omp25*, *Omp31* and *ZnuA*) in their genome that have been hypothesized to play a role in the pathogenesis of disease and this may be a cause of concern for human health. There is a need for implementing control measures and raising public awareness on the zoonotic transmission of brucellosis.

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