

# Isolation of *Brucella* in cattle milk in Uganda: Public Health Implications

## CONCLUSIONS AND RECOMMENDATION

- *Brucella* sero-positive cattle are more likely to shade the organisms in milk.
- Cattle rearing systems that limit mixing of herds should be encouraged to reduce the prevalence of the disease in cattle
- Boiling centres should be encouraged
- Further studies need to be done to establish the observed genetic linkage of the isolates with the vaccine strain RB 51

## BACKGROUND

Milk is a fundamental source of animal proteins in resource poor cattle keeping households world wide. However zoonotic infections compromise its safety both at household level and along the informal milk market linkages. In Uganda the majority of the milk which is produced by small holder farmers is consumed by children and the middle class in urban and peri-urban areas. However the safety of this milk especially at the animal level, the primary point of contamination is not well documented.

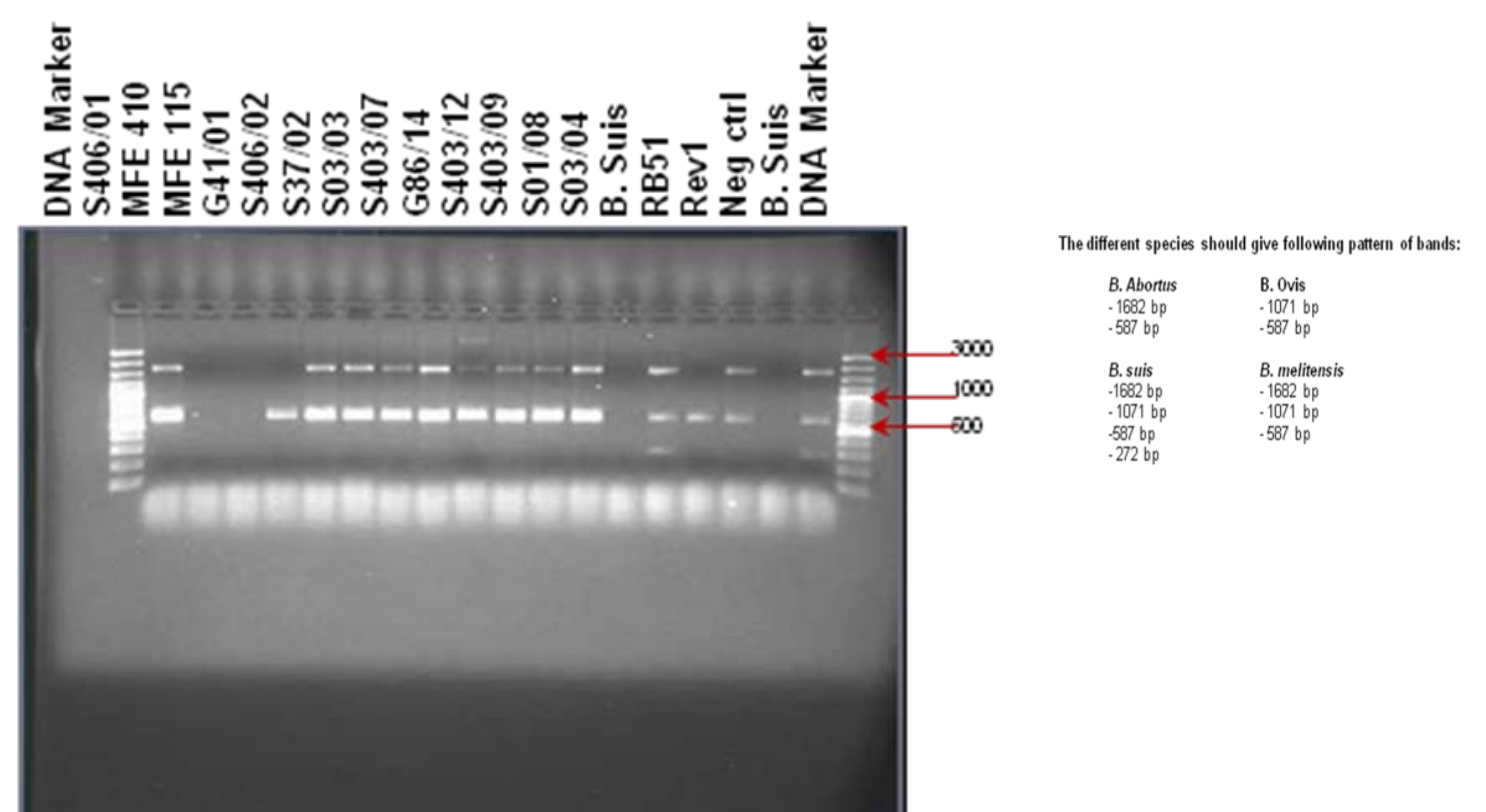
In the present study, we evaluated the contamination of individual cow milk in urban and peri-urban Gulu and Soroti with *Brucella*, a zoonotic causative agent of human brucellosis. Human brucellosis is a debilitating zoonotic disease caused by different biovars of *B. abortus*, *B. melitensis*, *B. suis* and *B. canis*. Brucellosis in humans is acquired by ingestion of *Brucella* contaminated animal products like un-pasteurised milk and milk products, occupational exposure through wounds and cuts in abattoir workers and veterinarians, and through aerosols in laboratory workers.

## Materials & Methods

Blood and milk samples were collected from lactating cattle in Gulu and Soroti towns of Uganda. Sera were analysed by i-ELISA and positive reactors confirmed with c-ELISA. The milk was cultured on both Farrel's and CITA selective media supplemented with calf serum. The resultant colonies were biotyped and the DNA extracted using the Norgen bacterial genomic DNA isolation kit. Isolates were confirmed as brucella using a real time multiplex fluorescent PCR assay. *Brucella* speciation by PCR was done using a multiplex PCR assay (bruce-ladder) kit (Ingenssa, Spain). Species and biovar confirmation and genotyping by PCR were performed using the multiple locus variable number tandem repeat analysis (MLVA), using the 16 primer pair assay. The MLVA PCR products were sequenced per loci to determine the number of tandem repeats. The MLVA sequences were compared with what is in the *Brucella* 2012 MLVA data base.

## RESULTS

- 5.3% (11/207) of the milk samples were *Brucella* culture positive.
- 64.7% (11/17) sero-positive cattle were culture positive
- All sero-negative cattle were culture negative
- 5.45% (6/110) of sero-positive lactating cattle were from Gulu
- 11.3% (11/97) of seropositive lactating cattle were from Soroti
- 81.8% (9/11) of seropositive lactating cattle in Soroti were culture positive
- 33.3% (2/6) of seropositive lactating cattle in Gulu were culture positive
- All the 11 *Brucella* isolates were *B. abortus*
- All the 11 *Brucella* isolates closely resembled *Brucella melitensis biovar abortus 2308 genotype*, which is a wild smooth strain of the vaccine strain RB 51.



Gel picture showing MLVA-16 assay; locus 1-6; extreme left, right and intermediate lanes = ladder, lane 2 (left) = *B. suis*

