

## Call for Abstracts: 2019 DELTAS AFRICA AGM and SCIENTIFIC CONFERENCE

<b>Abstract Title</b>	Diversity of brucellosis and multi-strain co-infection in a transboundary livestock production system between Tanzania and Kenya
<b>Submission by</b>	Mr. James Akoko
<b>Reference number</b>	ABS/19/200

### Abstract

<b>1. Abstract Title</b>	Diversity of brucellosis and multi-strain co-infection in a transboundary livestock production system between Tanzania and Kenya
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<b>2. Authors and Affiliations</b>
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### 3. Abstract

**Objective:** Brucellosis is a debilitating zoonotic disease affecting humans and animals with high prevalence in Kenya and Tanzania. This study was conducted to detect and identify the *Brucella* species circulating in various susceptible livestock hosts at the human, livestock and wildlife interfaces in Marsabit, Isiolo and Narok, Kenya as well as in Northern Tanzania. Data on *Brucella* species circulating in various susceptible hosts and the transmission dynamics is insufficient in Kenya and Tanzania, thus limiting diagnostic tool development and species or host-targeted control strategies.

**Method:** Mixed livestock herds (n=72), cattle (n=5), sheep (n=1), goats (n=1) and camels (n=15) with suspected cases of brucellosis were identified for blood, milk and abortion material sampling. Genomic DNA was extracted using Qiagen blood and tissue DNA extraction kit. Real-time PCR, with the genus-specific primers, was then used for screening, before performing a real-time multiplex PCR with *B. melitensis* and *B. abortus*-specific primers. A proportion of the real-time PCR positive samples were further subjected to conventional PCR with the genus-specific primer (B4/B5), and the PCR product sequenced.

**Results:** Most sampled herds had mixed livestock (80%). *Brucella spp.* was detected in 54 out of 72 samples that were sequenced. A total of 113 out of 800 samples tested positive on the genus-specific real-time PCR. We found *B. abortus* to be the most dominant species, accounting for up to 80% of all cases, *B. melitensis* 5% (3 camels, 1 goat and 2 sheep). On average, in 9% of samples both *B. melitensis* and *B. abortus* was detected while 6% were not classified as either *B. abortus* or *B. melitensis*.

**Conclusion:** The detection of zoonotic species of *Brucella* (*B. abortus* and *B. melitensis*) in all the major livestock species (cattle, sheep, goats and camels) present a serious public health risk. The co-infection detected could be as a result of close interaction between different animal species.

### 4. Non Technical or Lay Abstract

**Objective:** Brucellosis is a debilitating zoonotic disease affecting humans and animals with high prevalence in Kenya and Tanzania. This study was conducted to detect and identify the *Brucella* species circulating in various susceptible livestock hosts in Kenya and Tanzania

**Method:** Mixed livestock herds (n=72), cattle (n=5), sheep (n=1), goats (n=1) and camels (n=15) with suspected cases of brucellosis were identified for blood, milk and abortion material sampling. Genomic DNA was extracted using Qiagen blood and tissue DNA extraction kit. Real-time PCR, was used to detect and identify *Brucella* species.

**Results:** Most sampled herds had mixed livestock (80%). *Brucella spp.* was detected in 54 out of 72 samples that were sequenced. A total of 113 out of 800 samples tested positive on the genus-specific real-time PCR. We found *B. abortus* to be the most dominant species, accounting for up to 80% of all cases, *B. melitensis* 5%. On average, in 9% of samples both *B. melitensis* and *B. abortus* was detected while 6% were not classified as either *B. abortus* or *B. melitensis*.

**Conclusion:** The detection of zoonotic species of *Brucella* in all the major livestock present a serious public health risk. The co-infection detected could be as a result of close interaction between different animal species.

### 5. Abstract's Thematic Area

Neglected Tropical Diseases