



Epidemiology of *Brucella* species in small holder dairy cattle in selected regions of Tanzania

Isaac Joseph Mengele, Nelson Mandela African Institute of Science and Technology (NM-AIST), Tanzania Veterinary Laboratory Agency (TVLA), International Livestock Research Institute (ILRI), Centre for Tropical Livestock Genetics and Health (CTLGH)

James Miser Akoko (ILRI), Gabriel Mkilema Shirima (NM-AIST), Shedrack Festo Bwatota (NM-AIST, ILRI, CTLGH), Shabani Kiyabo Motto (NM-AIST, TVLA, ILRI, CTLGH), Luis E. Hernandez-Castro (University of Edinburgh, CTLGH), Daniel Mushumbusi Komwihangilo (TALIRI), Eliamoni Lyatuu (ILRI), Barend Mark de Clare Bronsvort (University of Edinburgh, CTLGH), Elizabeth Anne Jessie Cook (ILRI, CTLGH)

Key messages

- Dairy cattle were predominantly infected with *B. melitensis*
- Vaccination of cattle and small ruminants recommended
- Future research needed to develop a bivalent vaccine (*B. abortus* + *B. melitensis*)
- Training required for livestock keepers regarding risky practices & biosecurity measures
- Further research studies needed on epidemiology of *Brucella* species circulating in cattle

Context

- Brucellosis is a zoonotic bacterial disease
- Considered one of the most widespread zoonotic diseases globally
- Caused by bacterium of the Genus *Brucella*
- Common species affecting domestic animals are *B. abortus* in cattle, *B. melitensis* in goats, *B. ovis* in sheep, *B. suis* in pigs, and *B. canis* in dogs
- Brucella* spp. are somewhat host specific, however, recent studies highlighted the importance of cross-species infection
- Brucellosis in cattle can also be caused by *B. melitensis* or *B. suis*

Our approach

- Aim: to identify *Brucella* spp. circulating in dairy cattle, molecular prevalence & risk factors
- Cross-section study in 6 regions of Tanzania - 2048 dairy cattle from 1371 farms (Figure 1)
- Samples collected – blood (EDTA) and vaginal swabs
- DNA extraction from blood and swab
- qPCR targeting the IS711 gene
- Positives retested for the alkB marker for *B. abortus* and BMEI1172 marker for *B. melitensis*
- Multivariable logistic regression analysis done to establish risk factors

Outcomes

- There were 35/2046 blood and 37/1893 swab samples *Brucella* genus-positive
- Majority of blood samples 19/35 (54.3%) and vaginal swabs 29/37 (78.4%) were PCR-positive for *B. melitensis* only
- B. abortus* was detected in 2/35 (5.7%) blood samples.
- A further 10/35 (28.6%) blood samples and 7/37 (18.9%) swabs were PCR-positive for both (*B. melitensis* and *B. abortus*)
- There were 4 blood and 1 swab samples where no species was identified
- Overall molecular (PCR) prevalence was 3.5% (95% CI: 2.8-4.4)
- Njombe region had the highest molecular (PCR) prevalence of 8.1%, followed by Arusha 4.7%, Mbeya 3.8%, and Kilimanjaro region 3.7% (Figure 2)
- Risk factors included new animals on the farm and absence of dogs (Table 1)

Variable	Level	OR	95% Confid. Interval		P_value
			Lower	Upper	
Dogs	have dog	-	-	-	-
	no dog	2.64	1.12	5.90	0.02
New animal	no	-	-	-	-
	yes	2.49	1.06	5.84	0.03
Bull	no	-	-	-	-
	yes	0.25	0.06	1.08	0.06

Table 1. Results of multivariable logistic regression analysis

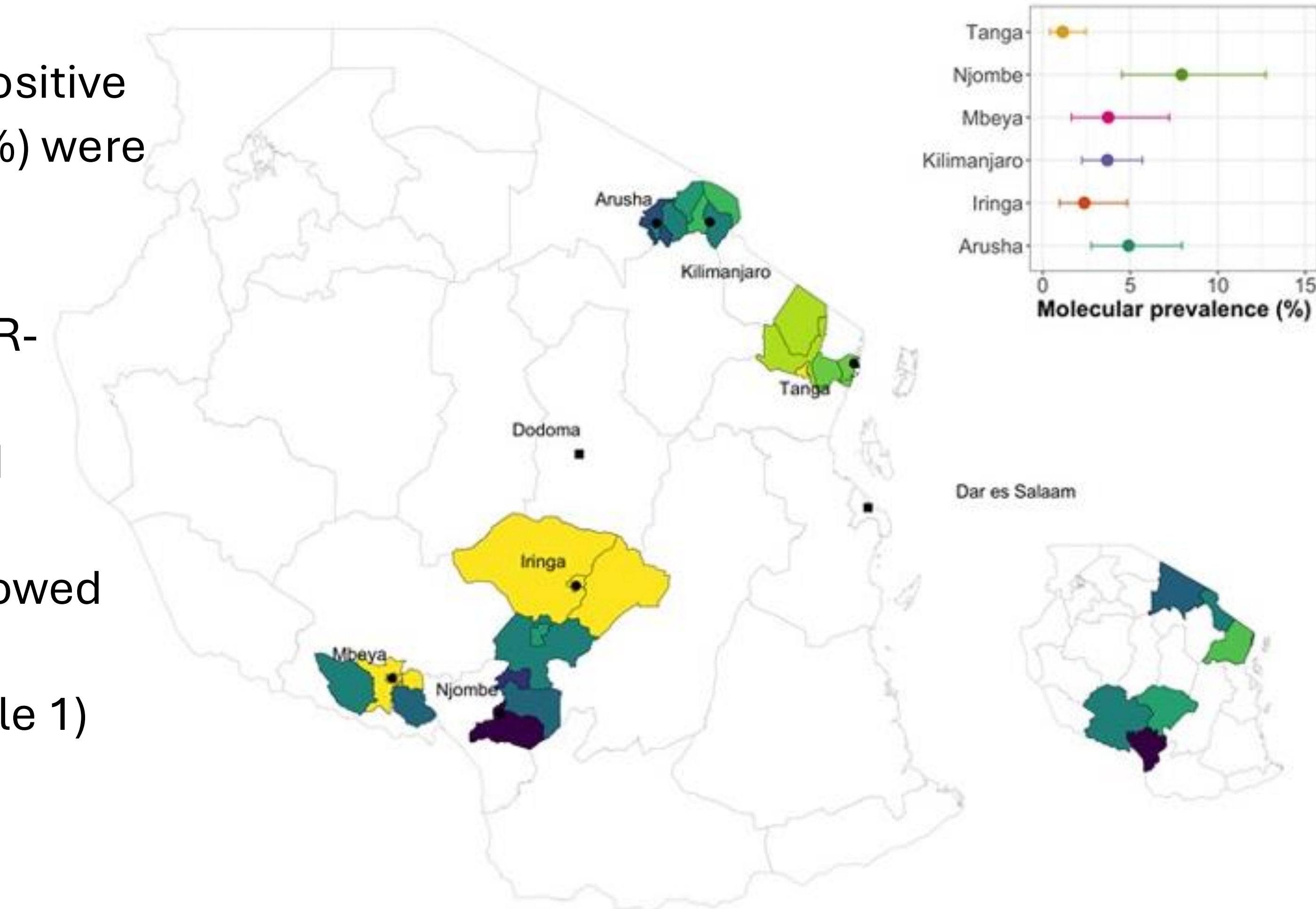


Figure 2. Choropleth map showing the regional prevalence (insets) and the prevalence by local authority in each region.

Conclusions

- Dairy cattle are predominantly infected with *B. melitensis* but also *B. abortus* and other unknown species
- New animals are a risk for *Brucella* transmission and should be screened before entering a herd
- Dairy cattle are a potential source of *B. melitensis* infections in humans

Contact
Isaac Mengele

isaac.Mengele@tvla.go.tz
mengele13@yahoo.com