

Bovine tuberculosis shows genetic diversity throughout Africa

January 18 2018



Mozambique cattle. Credit: Margarida Correia-Neves, 2017

Bovine tuberculosis (BTB) is an infectious disease caused by *Mycobacterium bovis* that affects cattle as well as other animals and humans. Now, by combining genotyping *M. bovis* samples from cows

across African countries, researchers have been able to study the diversity and evolution of the disease. The new results are published this week in *PLOS Neglected Tropical Diseases*.

BTB is of global concern for multiple reasons—the [economic impact](#) on animal production, the potential spread to wildlife, and the risk of transmission to humans. While BTB is known to be widespread in Africa, limited data exists combining its prevalence and distribution across borders. Efforts to determine to what extent human tuberculosis is due to *M. bovis* are ongoing.

In the new work, Margarida Correia-Neves of the University of Minho, Portugal, and colleagues obtained 228 *M. bovis* samples from both small-scale and large commercial herds of cattle in 10 districts of Mozambique. They then genotyped each sample to determine how the strains were related, and used previous datasets to compare this data and integrate the results in a new phylogenetic tree with other *M. bovis* found throughout Africa.

The data revealed a deeply geographically structured diversity of *M. bovis*, with isolates from Mozambique falling into one of a handful of clades; some had a signature seen in the British Isles and former UK colonies, others represented sub-branches of the South African clade, and a third cluster suggested a local Mozambique clade. Overall, the results throughout Africa suggested that the diversity of *M. bovis* is unlikely to be shaped by the recent importation of cattle, but is maintained within regions through the constant reinfection of animals.

"It is of vital importance to continue the efforts made in Mozambique in order to completely characterize and understand the extent of BTB," the researchers say. "The information concerning *M. bovis* presented here represents a foundation stone in that process."

More information: Machado A, Rito T, Ghebremichael S, Muhate N, Maxhuza G, Macuamule C, et al. (2018) Genetic diversity and potential routes of transmission of *Mycobacterium bovis* in Mozambique. *PLoS Negl Trop Dis* 12(1): e0006147. doi.org/10.1371/journal.pntd.0006147

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Citation: Bovine tuberculosis shows genetic diversity throughout Africa (2018, January 18)
retrieved 23 April 2024 from
<https://medicalxpress.com/news/2018-01-bovine-tuberculosis-genetic-diversity-africa.html>

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