

# Correction: *Treponema pallidum* Infection in the Wild Baboons of East Africa: Distribution and Genetic Characterization of the Strains Responsible

## The PLOS ONE Staff

In Table 2, the sequence information for the Nichols and Mexico A strains at nucleotide position 2,388 of the tp92 gene was inadvertently switched. The correct sequence at this position is as follows: a deletion in Mexico A and an A in Nichols. Please see the corrected Table 2 here.

The incorrect information in Table 2 was used to create the phylogenetic tree in Figure 2. Please see the corrected Figure 2 here.

The authors' explanation of the changes can be viewed on the Comments tab of the article page.

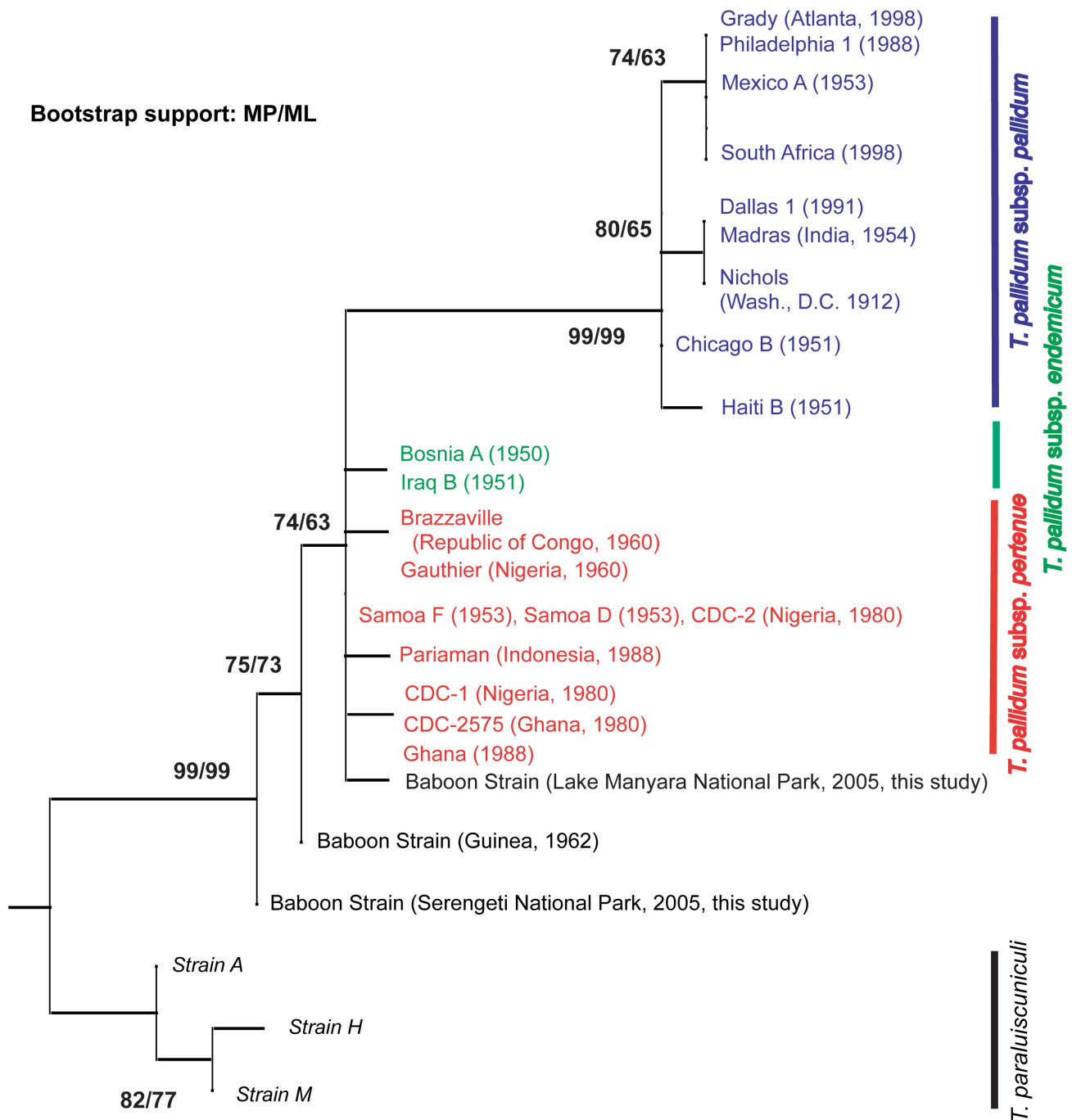
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**Citation:** The PLOS ONE Staff (2014) Correction: *Treponema pallidum* Infection in the Wild Baboons of East Africa: Distribution and Genetic Characterization of the Strains Responsible. PLoS ONE 9(3): e92489. doi:10.1371/journal.pone.0092489

**Published** March 20, 2014

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**Figure 2. A phylogeny demonstrates that *T. pallidum* strains infecting baboons in Serengeti National Park and Lake Manyara National Park are genetically distinct from one another.** Phylogenies were constructed using both Maximum Parsimony and Maximum Likelihood methods to analyze 25 polymorphisms in six concatenated regions of the *Treponema* genome. The phylogenies were congruent and a Maximum Parsimony tree was chosen for display, with bootstrap support displayed at all nodes that received greater than 50% using both methods. doi:10.1371/journal.pone.0050882.g002

## Reference

1. Harper KN, Fyumagwa RD, Hoare R, Wambura PN, Coppenhaver DH, et al. (2012) *Treponema pallidum* Infection in the Wild Baboons of East Africa: Distribution and Genetic Characterization of the Strains Responsible. PLoS ONE 7(12): e50882. doi:10.1371/journal.pone.0050882