

# 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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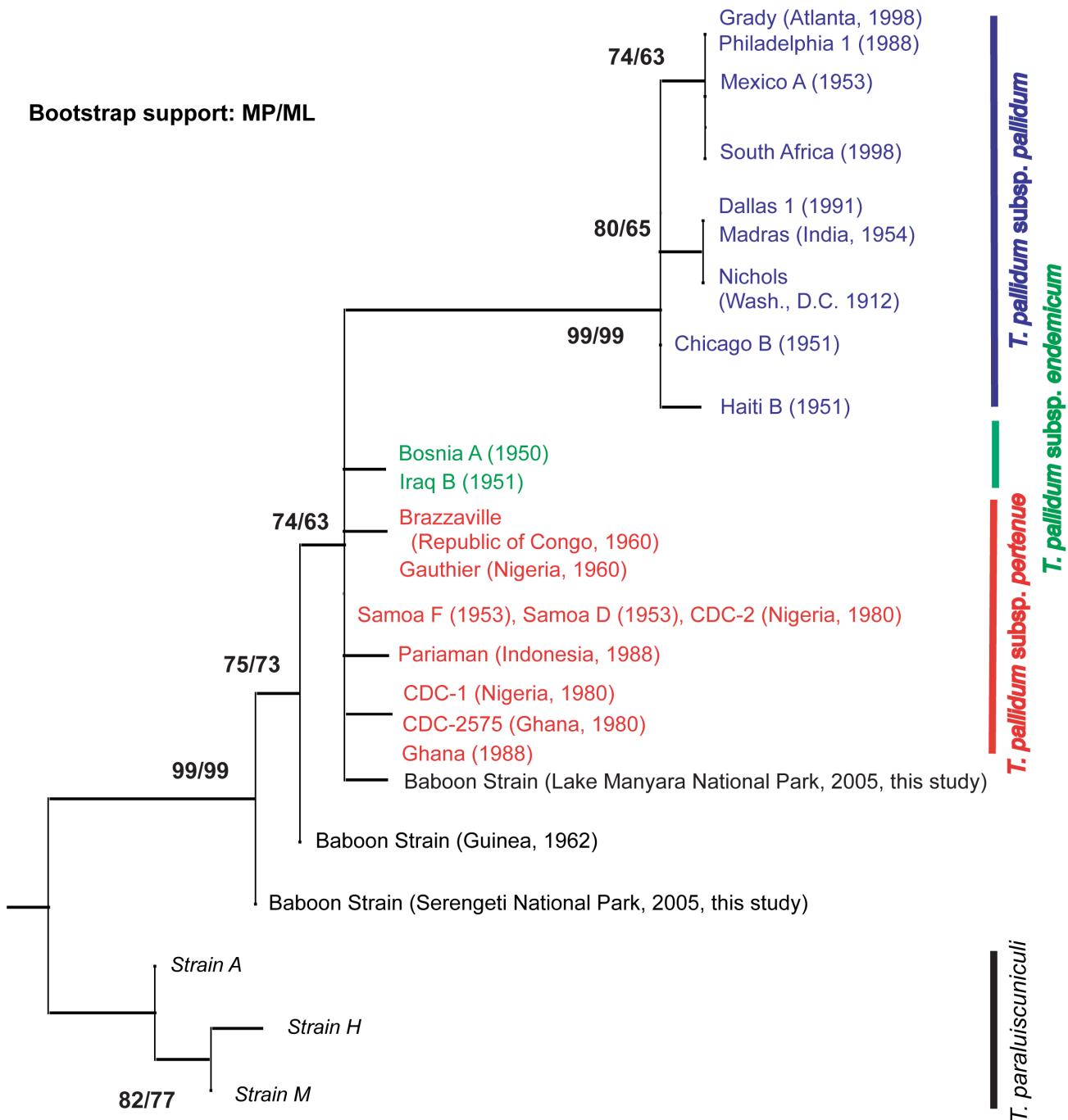
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**Table 2.** Table of polymorphisms included in phylogenetic analysis.

<i>T. pallidum</i> subspecies	Strain <sup>a</sup>	deoD	spd	tp92	tp92	tpF-1
endemicum	Bosnia	T	T	G	C	G
Iraq		T	T	A	G	C
pertenuis	Brazzaville	T	T	A	G	C
CDC1		T	T	A	G	C
CDC2		T	T	A	G	C
CDC2575		T	T	A	G	C
Gauthier		T	T	A	G	C
Ghana		T	T	A	G	C
Parhamian		T	T	A	G	C
Samoa D		T	T	A	G	C
Samoa F		T	T	A	G	C
Chicago B		T	C	A	A	C
Dallas		T	C	A	A	C
Grady		T	C	A	A	C
Haiti B		T	C	A	A	C
Madras		T	C	A	A	C
Mexico A		T	C	A	A	C
Nichols		T	C	A	A	C
Philadelphia 1		T	C	A	A	C
South Africa		T	C	A	A	C
N/A	TPC A	C	T	G	G	C
N/A	TPC H	C	T	G	G	C
N/A	TPC M	C	T	G	G	C
N/A	Baboon: SNP	C	T	A	G	C
N/A	Baboon: LMNP	T	T	A	G	C
N/A	Baboon: Guinea	T	T	A	G	C
Synonymous or Nonsynonymous Substitution	S	S	S	N	N	N
Nucleotide Residue	744	759	459	579	1592	1964
					1966	1967
					2101	2101
					2209	2326
					2388	2382-2399
					2405	2408
					2421	137
					143	151
					121	303
					117	122

TPC = *Treponema paraluisicuniculi* (agent that causes rabbit syphilis); SNP = Serengeti National Park; LMNP = Lake Manyara National Park

<sup>b</sup> Deletion from nucleotide residues 2384-2391 per centagen. [doi:10.1371/journal.pone.0050882.t002](https://doi.org/10.1371/journal.pone.0050882.t002)



**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

- 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