



Correction

Correction: Multilocus Sequence Analysis for *Leishmania braziliensis* Outbreak Investigation

The PLOS Neglected Tropical Diseases Staff

There is an error in Table 1. The primer sequence for Heat-shock protein 70 (hsp 70) should be:

Forward: GAC GGT GCC TGC CTA CTT CAA, Reverse: CCG CCC ATG CTC TGG TAC ATC.

Table 1. Amplicon size, analyzed sequence fragment length and primer sequence of the target regions for the six loci studied.

Locus	Amplicon size (bp)	Analyzed sequence length (bp)	Primer sequence (5'-3')
<i>6-phosphogluconate dehydrogenase (6pgd)</i>	836	666	CTCAAGGAACATGAGCACGA TTGCCTTGACTTGCTCACG
<i>Manose-6-phosphate isomerase (mpi)</i>	681	569	GGCAAGATGTATGCGGAGTT CTCCCAGGAACCATCTGTA
<i>Isocitrate dehydrogenase (icd)</i>	1022	755	GAATCGGGAAGGAGATCACA CATCATAGCCCCAGAGAGGA
<i>Heat-shock protein 70 (hsp70)</i>	1022	896	GACGGTGCCTGCCTACTTCAA CCGCCCATGCTCTGGTACATC
<i>Malate dehydrogenase mitochondrial (mdhmt)</i>	821	666	TGCCGACCTCTCCATATTC GAGTGAGGTGCGTCTTCACA
<i>Malate dehydrogenase nuclear (mdhnc)</i>	1010	803	TCACAACCGCAACTACGA CTA CTACGATAACGGCAGA

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Reference

- Marlow MA, Boité MC, Ferreira GEM, Steindel M, Cupolillo E (2014) Multilocus Sequence Analysis for *Leishmania braziliensis* Outbreak Investigation. PLoS Negl Trop Dis 8(2): e2695. doi:10.1371/journal.pntd.0002695

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