Correction: Multilocus Sequence Analysis for \textit{Leishmania braziliensis} Outbreak Investigation

The \textit{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’)                      |
|------------------------------|--------------------|-------------------------------|---------------------------------------------|
| 6-phosphogluconate dehydrogenase (6pgd) | 836                | 666                           | CTCAAGGAACATGAGCAGA TTGCTCTTGACTTGCTACG     |
| Manose-6-phosphate isomerase (mpi)  | 681                | 569                           | GGCAGATGTATGGGAGTTC TCCCCAGGAACATCTGTA      |
| Isocitrate dehydrogenase (icd)   | 1022               | 755                           | GAATGGGAAGAGATCCACCA CATCATAGCCCCAGAGAGGA   |
| Heat-shock protein 70 (hsp70)    | 1022               | 896                           | GACGCTGCTGCTACTTCACCCGCCATGTCTCTGATGATCG    |
| Malate dehydrogenase mitochondrial (mdhmt) | 821                | 666                           | TGCGAATCTTCCATATC CAGTGAGGTGCTCTTCA         |
| Malate dehydrogenase nuclear (mdhnc) | 1010               | 803                           | TCACACCGGAACATACCA CTACTCAGGATAACGCAAGAGA   |

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Reference

1. Marlow MA, Boïté MC, Ferreira GEM, Steindel M, Copolillo E (2014) Multilocus Sequence Analysis for \textit{Leishmania braziliensis} Outbreak Investigation. \textit{PLoS Negl Trop Dis} 8(2): e2695. doi:10.1371/journal.pntd.0002695