

TABLE
Results for the major hits obtained after BLAST analysis of the 234 bp-hsp70C polymerase chain reaction and sequencing

| Sample | Description | Max score | Total score | Query cover | E value | Max identity | Accession number |
|--------------------------------------|---------------------------------------------------------------------------------------------------------------------|-----------|-------------|-------------|-----------|--------------|-----------------------------|
| 2 - <i>Evandromyia saulensis</i> | <i>Leishmania braziliensis</i> MHOM/BR/75/M2904 putative heat-shock protein hsp70 (LBRM_28_2970) mRNA, partial cds | 261 | 261 | 78% | 2,00E-66 | 96% | gi 389601962 XM_001566273.2 |
| 6 - <i>Trichophoromyia auraensis</i> | <i>L. braziliensis</i> MHOM/BR/75/M2904 putative heat-shock protein hsp70 (LBRM_28_2970) mRNA, partial cds | 217 | 217 | 97% | 2,00E-53 | 97% | gi 389601962 XM_001566273.2 |
| 3 - <i>Pressatia</i> sp | <i>L. braziliensis</i> MHOM/BR/75/M2904 putative heat-shock protein hsp70 (LBRM_28_2970) mRNA, partial cds | 250 | 250 | 100% | 3,00E-63 | 95% | gi 389601962 XM_001566273.2 |
| 11 - <i>Th. auraensis</i> | <i>L. braziliensis</i> MHOM/BR/75/M2904 putative heat-shock protein hsp70 (LBRM_28_2970) mRNA, partial cds | 289 | 289 | 100% | 6,00E-75 | 100% | gi 389601962 XM_001566273.2 |
| 5 - <i>Th. auraensis</i> | <i>L. braziliensis</i> strain MHOM/BR/2002/NMT-LTCP 14440-P clone B heat shock protein 70 (hsp70) gene, partial cds | 379 | 379 | 100% | 5,00E-102 | 99% | gi 316891027 GU368187.1 |

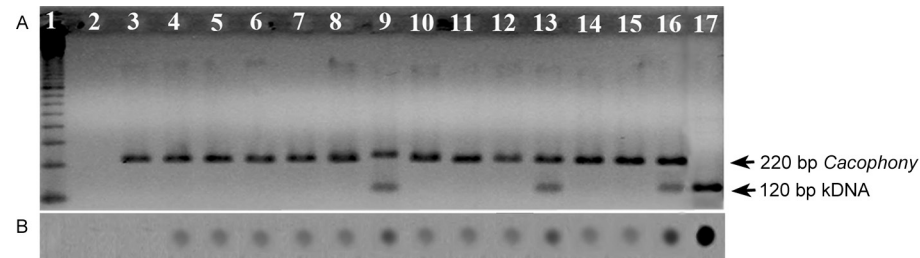


Fig. 1: natural infection by *Leishmania* spp in sandflies. (A) multiplex polymerase chain reaction (PCR) directed to the 220 bp fragment of the cacophony gene (sandflies) and the 120 bp of kDNA conserved minicircle sequence (*Leishmania* spp.) was performed individually in 173 sandfly DNA extracts. Amplified products were visualised on 2% agarose gel stained with ethidium bromide. 1: molecular weight 100 bp DNA ladder (Invitrogen); 2: negative control for PCR reaction (no DNA added); 3: negative control for DNA extraction (DNA extracted from male sandflies); 4-15: single female sandflies subjected to molecular diagnosis that revealed positivity in two samples (lines 9 and 13); 16: positive control (DNA extracted from laboratory-bred *Lutzomyia longipalpis* females); 17: positive control (DNA from cultivated *L. (V.) braziliensis*) [10 ng]. (B) dot blot hybridisation of PCR-amplified products with a specific byotinylated probe for *Leishmania* subgenus *Viannia*. 4-5: *Evandromyia saulensis* - Area of forest (area I); 6: *Pressatia* sp. - Area of forest (area II); 7-15: *Trichophoromyia auraensis* - Area of forest (area II); 16: positive control (DNA extracted from laboratory-bred *Lu. longipalpis* females); 17: positive control (DNA from cultivated *L. (V.) braziliensis*).

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>11_Trichophoromyia auraensis
GATGCGTCGAAGTACGAGCAGGCCGACAAGATGCAGCGCGAGCGCGTGGAGGCCGAAGAACGGCCTGGA
GAACTACGCGTACTCGATGAAGAACACGGTCTCCGACACGAACGTGTCCGGCAAGCTGGAGGA
>3_Pressatia sp
CAACCAGGAGGCGTCGAAGGAAGAGCAGGCCGACAAGATGCAGCGCGAGCGCGTGGAGGCCGAAGAACG
GCCTGGAGAACTACGCGTACTCGATGAAGAACACGGTCTCCGACACGAACGTGTCCGGCAAGCTGGAC
GAGATCGA
>6_Trichophoromyia auraensis
CGTCGAAGGAAGAGCAGGCCGACAAGATGCAGCGCGAGCGCGTGGAGGCCGAAGGACGGCCTGGAGAAC
TACGCGTACTCGATGAAGAACACGGTCTCCGACACGAACGTGTCCGGCAAGCTGGACGAGATCG
>5_Trichophoromyia auraensis
GATGCGTCGAAGTGCAGCAGGCCGACAAGATGCAGCGCGAGCGCGTGGAGGCCGAAGAACGGCCTGGA
GAACTACGCGTACTCGATGAAGAACACGGTCTCCGACACGAATGTGTCCGGCAAGCTGGAGGAGAGCG
ACAGGTCCGCGCTGAACTCGGCGATCGACACGGCGCTGGAGTGGCTGAAC
>2_Evandromyia saulensis
GATGCGTCGAAGGAAGAGCAGGCCGACAAGGTGCAGCGCGAGCGCGTGGAGGCCGAAGAACGGCCTGGA
GAACTACGCGTACTCGATGAAGAACACGGTCTCCGACACGAACGTGTCCGGCAAGCTGKACGAGACG
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Fig. 2: edited consensus sequences of the 234 bp-*hsp70C* polymerase chain reaction products.