**S3 Table. Characteristics of the sequences and the structure of each primer and PCR reaction conditions.**

| MLST | Target | Primer | Primer Sequence | Product size | Characteristics | PCR concentrations | PCR cycling conditions | Reference |
|---|---|---|---|---|---|---|---|---|
| Clasical MLST | *arf* (ADP-ribosylation factor) | arf1 | AGAATATGGGGCAAAAAGGA | 470 | The sequence is composed by the exon 2 covering the region from 1 to 98 bp and exon 3 from 290 to 478 bp, these are separated by an intron region. | Buffer / 1X<br>MgCl2 / 1,5 mM<br>DNTPs / 0,2 mM<br>Forward Primer / 0,2 mM<br>Reverse Primer / 0,2 mM<br>DNA Taq / 1 U<br>DNA / 2 µl<br>Reaction volume / 50 µl | 94ºC / 3 min<br>94ºC / 15 seg<br>54,8ºC / 30 seg<br>72ºC / 1 min<br>72ºC / 5 min<br>12°C / ∞ | Kasuga, Taylor, and White 1999 |
| | | arf2 | CGCAATTCATCTTCGTTGAG | | | | | |
| | *H-anti* (H antigen precursor gene) | H-anti3 | CGCAGTCACCTCCATACTATC | 412 | The sequence is composed by 3 CDS covering the regions from 1 to 112 bp, 233 to 330 bp and 387 to 413 bp, separated by two intron regions. | | | Kasuga, Taylor, and White 2000 |
| | | H-anti4 | GCGCCGACATTAACCC | | | | | |
| | *ole* (Delta-9 fatty acid desaturase) | ole3 | TTTAAACGAAGCCCCCACGG | 425 | The sequence is composed by 2 CDS covering the regions from 1 to 273 bp and 368 to 428 bp and the intron region from 254 to 367 bp. | | | Kasuga, Taylor, and White 2001 |
| | | ole4 | CACCACCTCCAACAGCAGCA | | | | | |
| | *tub1* | tub1 | GGTGGCCAAATCGCAAACTC | 278 | The sequence is | | | Kasuga, |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | (Alpha-tubulin) | tub2 | GGCAGCTTTCCGTTCCTCAGT | | composed by 2 CDS which cover the regions from 1 to 10 bp and 119 to 145 bp and 2 intron regions from 11 to 118 bp and 146 to 263 bp. | | | Taylor, and White 2002 |
| | ITS (Internal transcribed spacers 1 rRNA genes) | ITS4 | TCCTCCGCTTATTGATATGC | 656 | This region contains the partial sequence of 18S ribosomal RNA gene; the complete sequence of the internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2; and the partial sequence of 28S ribosomal RNA gene. | | | Kasuga, Taylor, and White 2003 |
| | | ITS5 | GGAAGTAAAAGTCGTAACAAGG | | | | | |
| **Diagnostic PCR** | *Hcp100* (Protein 100 KDa Human - like) | HcI | GCGTTCCGAGCCTTCCACCTCAAC | 319 | The sequence is a partial CDS region. In the sequences, the CDS cover all region. | Buffer / 1X MgCl2 / 2 mM DNTPs / 0,2 mM Forward Primer / 0,2 mM Reverse Primer | 94ºC / 5 min 94ºC / 30 seg 66ºC / 30 seg 72ºC / 1 | Bialek et al. 2002 |
| | | HcII | ATGTCCCATCGGGCGCCGTGTAGT | | | | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | / 0,2 mM DNA Taq / 1 U DNA / 2 µl Reaction volume / 50 µl | min 72ºC / 5 min 12°C / ∞ | |
| | SCAR 220 | 1281-1283-220-F | CATTGTTGGAGGAACCTGCT | 220 | Both sequences were selected as characteristic inside *H. capsulatum* genome. But SCAR 230 is a partial CDS region from the alpha-amylase A. | Buffer / 1X MgCl2 / 2,5 mM DNTPs / 0,2 mM Forward Primer / 0,2 mM Reverse Primer / 0,2 mM DNA Taq / 1 U DNA / 2 µl Reaction volume / 50 µl | 94ºC / 5 min 94ºC / 30 seg 52ºC / 30 seg 72ºC / 1 min 72ºC / 5 min 12°C / ∞ | Frías De León et al. 2012 |
| | | 1281-1283-220-R | GAGCTGCAGGATGTTTGTTG | | | | | |
| | SCAR 230 | 1281-1283-230-F | GGAGCCATGACGTTAAATGG | 230 | | | | Frías De León et al. 2013 |
| | | 1281-1283-230-R | TATTGCCAATGGGTTTGTCA | | | | | |
| | *M antigen* (M antigen gene) | Msp1F | ACAAGAGACGACGGTAGCTTCACG | 318 | The sequence is a partial CDS from the region codifying the *H. capsulatum* Catalase B. In the sequences, the CDS cover all region. | Buffer / 1X MgCl2 / 1,5 mM DNTPs / 0,2 mM Forward Primer / 0,2 mM Reverse Primer / 0,2 mM DNA Taq / 1 U | 95ºC / 5 min 94ºC / 1 min 60ºC / 1 min 72ºC / 1 min 72ºC / 5 min | Ohno et al. 2013 |
| | | Msp2R | ACCAGCGGCCATAAGGACGTC | | | | | |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | DNA / 2 µl<br>Reaction<br>volume / 50 µl | 12°C / ∞ | |

Reagents were as follow the Deoxynucleoside triphosphates from Thomas Scientific, Swedesboro, NJ., the synthesis of the primers by Integrated DNA Technologies (IDT, Coralville, IA, USA), and the Taq polymerase form Thomas Scientific, Swedesboro, NJ.