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Correction

Correction: Tanida et al. Comparative Assessment of In-House Real-Time PCRs Targeting Enteric Disease-Associated Microsporidia in Human Stool Samples. *Pathogens* 2021, *10*, 656

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In the original publication [1], there was a mistake in Table 2 as published. All oligonucleotides of PCR 1 in Table 2 had erroneously been printed in reverse-complement style. The corrected Table 2 appears below. The authors apologize for any inconvenience caused and state that the scientific conclusions are unaffected. The original publication has also been updated.

Table 2. Details of the real-time PCR assays 1–6, which were included in the test comparison without a reference standard with perfect accuracy for the diagnosis of microsporidia in stool samples. Positive control plasmid inserts are provided in Appendix A.

	PCR 1	PCR 2	PCR 3	PCR 4	PCR 5	PCR 6
Target specificity	Small subunit ribosomal RNA gene of *Enterocytozoon bieneusi*, *Encephalitozoon cuniculi*, *Encephalitozoon hellem*, and *Encephalitozoon intestinalis*	Small subunit ribosomal RNA gene of *Enterocytozoon bieneusi*, *Encephalitozoon cuniculi*, *Encephalitozoon hellem*, and *Encephalitozoon intestinalis*	Small subunit ribosomal RNA gene of *Enterocytozoon bieneusi*	Internal transcribed spacer (ITS) sequence of *Enterocytozoon bieneusi*	Small subunit ribosomal RNA gene of *Encephalitozoon cuniculi*, *Encephalitozoon hellem*, and *Encephalitozoon intestinalis*	Internal transcribed spacer (ITS) sequence of the non-target microorganism *Microsporidium* spp.
Amplicon length	394 base pairs	280 base pairs	202 base pairs	105 base pairs	227 base pairs	87 base pairs
Cycle number	50	40	40	50	40	45
Forward primer 1	5′-CACCAGG TTGATTC TGCCTGA-3′	5′-CAGGTT GATTCTGC CTGACG-3′	5′-CCAGGGT CAAGTCA TTCGTT-3′	5′-TGTGTAG GCGTGAGA GTGTATCTG-3′	5′-CACCAGG TTGATTC TGCCTGAC-3′	5′-TCTTGCG CGTTAAT GATCCTT-3′
Forward primer 2	5′-TCCGGAG AGGGAG CCTGAG-3′	n.a.	n.a.	n.a.	n.a.	n.a.
Reverse primer 1	5′-GCTTGCC CTCCAAT TGCTTC-3′	5′-CCATCTC TCAGGCT CCCTC-3′	5′-TATTGTA TTGCGC TTGCTGC-3′	5′-CATCCAA CCATCACG TACCAATC-3′	5′-CTAGTTA GGCCATTACCC TAACTACCA-3′	5′-AGGTTGC GGGCGGC-3′
Reverse primer 2	5′-GACTTGC CCTCCAA TCACATG-3′	n.a.	n.a.	n.a.	n.a.	n.a.
Reverse primer 3	5′-CCGACTT GCCCTCC AGTAAA-3′	n.a.	n.a.	n.a.	n.a.	n.a.
Reverse primer 4	5′-CTTGGCC TCCAATC AATCTCG-3′	n.a.	n.a.	n.a.	n.a.	n.a.
Hybridization probe *	5′-TGGCAGC AGGCGCG AAACTTGT-3′	n.a.	5′-GATGCCC TTAGATA TCCTGG-3′	5′-CACTGCA CCCACATCC CTCACCCTT-3′	5′-CTATCAC TGAG+C+C GT+CC-3′	5′-ACGGAAGA GCTTCGG GGGCCA-3′

n.a. = not applicable. * Bases with a plus (+) in front of them are locked nucleic acid (LNA) bases.

Reference

1. Tanida, K.; Hahn, A.; Eberhardt, K.A.; Tannich, E.; Landt, O.; Kann, S.; Feldt, T.; Sarfo, F.S.; Di Cristanziano, V.; Frickmann, H.; et al. Comparative Assessment of In-House Real-Time PCRs Targeting Enteric Disease-Associated Microsporidia in Human Stool Samples. *Pathogens* **2021**, *10*, 656. [CrossRef] [PubMed]