



Correction

Correction: Mongruel et al. Expanding the Universe of Hemoplasmas: Multi-Locus Sequencing Reveals Putative Novel Hemoplasmas in Lowland Tapirs (*Tapirus terrestris*), the Largest Land Mammals in Brazil. *Microorganisms* 2022, 10, 614

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Citation: Mongruel, A.C.B.; Medici, E.P.; Canena, A.d.C.; Calchi, A.C.; Machado, R.Z.; André, M.R. Correction: Mongruel et al. Expanding the Universe of Hemoplasmas: Multi-Locus Sequencing Reveals Putative Novel Hemoplasmas in Lowland Tapirs (*Tapirus terrestris*), the Largest Land Mammals in Brazil. *Microorganisms* 2022, 10, 614. *Microorganisms* 2024, 12, 1326. <https://doi.org/10.3390/microorganisms12071326>

Received: 11 June 2024
Accepted: 17 June 2024
Published: 28 June 2024



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In the original publication [1], there was a mistake in Tables 1 and 7 as published. The corrected tables appear below.

In Table 1 for the 16S rRNA partial amplification, a different combination of the cited primers was used. Regarding the *dnaK* primer sequences, a formatting oversight resulted in identical representations for forward and reverse primers.

In Table 7 the statistical analysis was calculated based on the total sampled animals. However, DNA samples from three animals failed to amplify both of the tested house-keeping genes and were consequently excluded from hemoplasma molecular screening, as explained in the Materials and Methods and Results sections. Although the significance of the tested variables did not change, the statistical analysis was corrected. The corrected table appears below.

The authors state that the scientific conclusions are unaffected. This correction was approved by the Academic Editor. The original publication has also been updated.

Table 1. Target genes, primers, thermal conditions, and reagent protocol used in the PCR assays for hemoplasmas based on the 16S rRNA, 23S rRNA, *RNAse P*, and *dnaK* genes.

Target Gene	Primer Sequences	Thermal Conditions	Reagent Volumes and Concentrations	Fragment Size	Primers Reference
16S rRNA	1st round: 5'-AGAGTTTGATCCTGGCTCAG-3' 5'-TACCTTGTACGACTTAACT-3' 2nd round: 5'-ATATTCCTACGGGAAGCAGC-3' 5'-TACCTTGTACGACTTAACT-3'	95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 57 °C for 30 s, extension at 72 °C for 1 min, and final extension at 72 °C for 10 min for both rounds.	1st reaction: 2.5 µL from 10X Buffer, 0.75 µL from 50 mM MgCl ₂ , 2 µL from 10 mM dNTP mix, 1 µL from each primer at 10 mM, 0.25 µL from 5 U/µL Taq polymerase, 12.5 µL from ultrapurified water and 5 µL from template DNA. 2nd reaction: Ultrapurified water (16.5 µL) and template DNA (1 µL) quantity changes.	~1107 bp	Harasawa et al., 2014; Di Cataldo et al., 2020
23S rRNA	5'-TGAGGGAAAGAGCCAGAC-3' 5'-GGACAGAATTTACCTGACAAGG-3'	94 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 54 °C for 30 s, extension at 72 °C for 1 min, and final extension at 72 °C for 10 min.	2.5 µL from 10X Buffer, 0.75 µL from 50 mM MgCl ₂ , 2 µL from 10 mM dNTP mix, 1 µL from each primer at 10 mM, 0.25 µL from 5 U/µL Taq polymerase, 12.5 µL from ultrapurified water and 5 µL from template DNA.	~800 bp	Mongruel et al., 2020
<i>RNAseP</i>	5'-GATKGTGYGAGYATATAA AAAATAAARCTCRAC-3' 5'-GMGGRGTTTACCGCTTTCAC-3'	95 °C for 2 min, followed by 50 cycles of denaturation at 94 °C for 30 s, annealing at 59 °C for 30 s, extension at 72 °C for 30 s and final extension at 72 °C for 1 min.	2.5 µL from 10X Buffer, 1.0 µL from 50 mM MgCl ₂ , 2 µL from 10 mM dNTP mix, 1 µL from each primer at 10 mM, 0.25 µL from 5 U/µL Taq polymerase, 12.25 µL from ultrapurified water and 5 µL from template DNA.	~164 bp	Maggi et al., 2013
<i>dnaK</i>	5'-GGGTGGAGATGATTGAGACCA-3' 5'-AGCCACCCCTCCTAGAGTTT-3'	95 °C for 5 min, followed by 45 cycles of denaturation at 95 °C for 20 s, annealing at 55.5 °C for 30 s, extension at 72 °C for 45 s and final extension at 72 °C for 7 min.	2.25 µL from 10X Buffer, 1.0 µL from 50 mM MgCl ₂ , 2 µL from 10 mM dNTP mix, 1 µL from each primer at 10 mM, 0.15 µL from 5 U/µL Taq polymerase, 12.6 µL from ultrapurified water and 5 µL from template DNA.	~544 bp	Descloux et al., 2020

Table 7. Statistical analysis comparing the occurrence of hemotropic *Mycoplasma* sp. in sampled tapirs and outcomes (gender, sampling location, and age).

Variable		16S rRNA <i>Mycoplasma</i> spp. PCR				<i>p</i> -Value
		+/n	(%)	OR	95% CI	
Gender	Male	21/50	42	1.641	0.71–3.75	0.1198
	Female	15/49	30.61			
	Total	36/99				
Location	Pantanal	30/61	49.18	5.161	1.887–14.11	0.0003915
	Cerrado	6/38	15.79			
	Total	36/99				
Age	Sub-adult	20/46	43.48	1.779	0.77–4.06	0.08528
	Adult	16/53	30.19			
	Total	36/99				

+, Number of positive animals; n, number of samples; 95% CI, 95% confidence interval; OR, odds ratio. *p*-values < 0.05 were considered statically significant and are highlighted in bold.

Reference

- Mongruel, A.C.B.; Medici, E.P.; Canena, A.d.C.; Calchi, A.C.; Machado, R.Z.; André, M.R. Expanding the Universe of Hemoplasmas: Multi-Locus Sequencing Reveals Putative Novel Hemoplasmas in Lowland Tapirs (*Tapirus terrestris*), the Largest Land Mammals in Brazil. *Microorganisms* **2022**, *10*, 614. [[CrossRef](#)] [[PubMed](#)]

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