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Corrigendum

Corrigendum to "The pathology and pathogenicity of a novel *Haemoproteus* spp. infection in wild Little Penguins (*Eudyptula minor*)" [Vet. Parasitol. 197 (1–2) (2013) 74–84]

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The authors regret that in the above reference, the incorrect primers were listed for the second nested PCR. Below is the corrected version of paragraph 2.3 in the Materials and Methods.

2.3. Molecular screening for haemosporidians and sequence analysis

DNA was extracted and purified from the liver of each bird using a Qiagen DNeasy Blood and Tissue Kit. Using polymerase chain reaction (PCR) a fragment of approximately 480 bp of the mitochondrial cytochrome-*b* (cyt-*b*) gene was targeted for *Plasmodium* and *Haemoproteus* using a nested PCR strategy. For each bird, at least three independent PCR amplifications were performed before being declared negative. Avian blood samples known to be positive for either *Haemoproteus* or *Plasmodium* were used as positive controls for the PCR. Samples were first amplified using the primers HaemNF (5′-CATATATTAAGAGAATTATGGAG-3′) and HaemNR2 (5′-AGAGGTGTAGCATATCTATCTAC-3′) described in Waldenstrom et al. (2004). A second nested PCR was performed using the inner primer pair HaemF (5′-ATGGTGCTTTCGATATATGCATG-3′) and HaemR2 (5′-GCATTATCTGGATGTGATAATGGT-3′) (Hellgren et al., 2004). PCR were set up as 15 μl reactions containing 50 ng template DNA, 0.75 units of AmpliTaq Gold (Applied Biosystems, Carlsbad, California), 1.5 μl of MgCl, 0.2 mM of each dNTP, and 0.5 mM of each primer. The PCRs were run using a programme of 94 °C for 8 min followed by 35 cycles of 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 45 s, and a final extension at 72 °C for 10 min. The conditions for HaemF and HaemR2 are identical except for an annealing temperature at 52 °C. An additional positive control to assess DNA quality was performed using avian-specific cyt-*b* primers as described in Cicero and Johnson (2001).

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