

Avian haemosporidian infections in rufous-collared sparrows in an Andean dry forest: diversity and factors related to prevalence and parasitaemia – CORRIGENDUM

Corrigendum

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The following error in [Table 1](#) has come to the authors' attention:

Current information: BAEBIC02 (GenBank: KF537291)

Correct information: BAEBIC02 (GenBank: KF537287)

The corrected version of the Table is shown below, with the corrected information in bold:

Table 1. Association of molecular lineage (amplified by PCR) and morphospecies (identified by microscopy) found in *Z. capensis* sampled in Bosque Protector Jerusalem Quito-Ecuador. The first morphospecies denotes the morphospecies responsible for the main infection, whereas the other represents a coinfection

Molecular lineage	d/s ¹	Morphospecies by microscopy	d/s ²
ZC1(GenBank KC480265)	86/177	<i>Haemoproteus</i> (<i>Parahaemoproteus</i>) sp. 1.	64/74
		<i>Haemoproteus</i> (<i>P.</i>) sp. 1., <i>H. (P.) coatneyi</i>	6/74
		<i>P. (Haemamoeba) cathemerium</i> , <i>Haemoproteus</i> (<i>P.</i>) sp. 1	1/74
		<i>Haemoproteus</i> (<i>P.</i>) sp. 1., <i>H. (P.) erythrogravidus</i>	3/74
BAEBIC02 (GenBank KF537287)	34/177	<i>P. (Novyella) homopolare</i>	20/25
		<i>P. (N.) homopolare</i> , <i>H. (P.) coatneyi</i>	1/25
		<i>P. (N.) nucleophilum</i> , <i>P. (N.) homopolare</i>	3/25
		<i>Haemoproteus</i> (<i>P.</i>) sp1., <i>P. (H.) cathemerium</i>	1/25
ZOCAP15 (GenBank MK077679)	4/177	<i>P. (H.) cathemerium</i> , <i>H. (P.) erythrogravidus</i>	1/1
Coinfection BAEBIC02/ZC1	3/177	<i>P. (N.) homopolare</i>	2/2
Coinfection ZOCAP15/ZC1	2/177	<i>Haemoproteus</i> (<i>P.</i>) sp. 1	1/1
Coinfection undetermined	4/177	<i>Haemoproteus</i> (<i>P.</i>) sp. 1	3/3
Lineage undetermined	2/177	Not screened	
Total*	135/177		106/106

*Totals are different because not all samples diagnosed by PCR were diagnosed by morphology. Out of the 135 samples that were positive by PCR, four were undetermined coinfections and two were not identified to lineage. (d/s¹) number of samples detected positive for molecular lineage /number of samples screened by PCR-sequencing (d/s²) number of samples detected positive for morphospecies /number of samples screened by microscopy once molecular lineage was determined

