

Correction

# Correction: Ruiz-Rodríguez et al. Gut Microbiota of Great Spotted Cuckoo Nestlings Is a Mixture of Those of Their Foster Magpie Siblings and of Cuckoo Adults. *Genes* 2018, 9, 381

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The authors wish to make the following changes in their paper [1]. The hypervariable DNA region we sequenced was the V6-V8 rather than the V4 as we erroneously wrote in the printed version. For the corrected version, we have added information on the universal primer used, as well as the performed modifications to include the Illumina Nextera adapters and barcodes. Moreover, we have also modified Table 1 where SE and *t*-values were erroneously preceded by a negative sign and are now shown between parentheses.

The following information is about the primer used, in Section 2.3. and now reads:

“B969F (5′-AATGATACGGCGACCACCGAGATCTACAC-NNNNNNNN-TCGTCGGCA GCGTCAGATGTGTATAAGAGACAG**ACGCGHNRAACCTTACC**-3′) and BA1406R (5′-CAAGCA GAAGACGGCATAAGAGAT-NNNNNNNN-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG **ACGGGCRGTGWGTRCAA**-3′), where the Nextera adapters (L and R arm) are in normal font (to either side of the barcodes), the barcodes are represented by NNNNNNNN, and the specific primer regions are bold + underlined.”

The following table is the correct one:

**Table 1.** Comparisons of gut microbiome of magpie and great spotted cuckoo nestlings and of great spotted cuckoo adults in terms of bacterial richness,  $\alpha$ -diversity, composition (weighed and unweighed unifracs  $\beta$ -diversity) and abundance and prevalence of bacterial families.

VARIABLE CONSIDERED	TYPE OF SAMPLE			COMPARISONS				
	(A) Adult cuckoos ( <i>N</i> = 6)	(B) Nestling cuckoos ( <i>N</i> = 12)	(C) Nestling magpies ( <i>N</i> = 7)	ANOVA  <i>F</i> <sub>2,22</sub> (SE)	<i>p</i> (SE)	POST-HOC (Tukey tests)		
	Mean (SE)	Mean (SE)	Mean (SE)			<i>p</i>	<i>p</i>	<i>p</i>
Bacterial Richness	73.8 (12.1)	123 (8.5)	52.3 (11.2)	14.42 (0.19)	<b>0.0001</b> <b>(0.000008)</b>	<b>0.008</b>	<b>0.405</b>	<b>0.0003</b>
$\alpha$ -diversity (Shannon index)	3.92 (0.43)	4.45 (0.31)	2.66 (0.4)	6.50 (0.03)	<b>0.006</b> <b>(0.00001)</b>	0.585	0.106	<b>0.005</b>
				PERMANOVA		POST-HOC (Pair-wise <i>t</i> -tests)		
Microbiome composition				Pseudo-F (SE)	<i>p</i> (SE)	<i>p</i> ( <i>t</i> -value)	<i>p</i> ( <i>t</i> -value)	<i>p</i> ( <i>t</i> -value)
Weighted unifracs $\beta$ -diversity				4.35 (0.01)	<b>0.00022</b> <b>(0.00004)</b>	0.559 (0.85)	<b>0.0002</b> <b>(2.87)</b>	<b>0.0001 (2.63)</b>
Unweighted unifracs $\beta$ -diversity				5.37 (0.07)	<b>0.0001</b> <b>(0.0001)</b>	<b>0.0002</b> <b>(1.72)</b>	<b>0.0007</b> <b>(2.47)</b>	<b>0.0001</b> <b>(2.61)</b>
Abundance of Families (Bray–Curtis distance matrices)				5.33 (0.03)	<b>0.00013</b> <b>(0.00002)</b>	0.58 (0.9)	<b>0.0008</b> <b>(3.00)</b>	<b>0.002 (2.94)</b>
Prevalence of Families (Jaccard distance matrices)				6.43 (0.12)	<b>0.0001</b> <b>(0.00001)</b>	<b>0.0034</b> <b>(1.62)</b>	<b>0.0006</b> <b>(2.55)</b>	<b>0.0001 (2.86)</b>

Bold fonts highlight statistically significant results ( $p < 0.05$ ).

The changes do not affect the scientific results. The manuscript will be updated and the original will remain online on the article webpage, with a reference to this Correction.

## Reference

1. Ruiz-Rodríguez, M.; Martín-Vivaldi, M.; Martínez-Bueno, M.; Soler, J.J. Gut Microbiota of Great Spotted Cuckoo Nestlings is a Mixture of Those of Their Foster Magpie Siblings and of Cuckoo Adults. *Genes* **2018**, *9*, 381. [[CrossRef](#)] [[PubMed](#)]



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