

AUTHOR CORRECTION

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Correction to: Comparison of the gut microbiota composition between wild and captive sika deer (*Cervus nippon hortulorum*) from feces by high-throughput sequencing

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Correction to: AMB Expr (2017) 7:212

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The authors regret the following errors occurred in the original publication of the article (Guan et al. 2017). The corrected texts have been presented with this erratum.

In Abstract section, the sentence should read, “Here, we characterized the gastrointestinal bacterial communities of wild (7 samples) and captive (12 samples) sika deer from feces, and compared their gut microbiota by analyzing the V4 region of 16S rRNA gene using high-throughput sequencing technology on the Illumina Hiseq platform”.

In the section titled, “16S rRNA gene PCR and sequencing”, the first paragraph should read, “16S rRNA gene was amplified using the 16S universal amplicon PCR primers: F515 (5'-CACGGTCGKCGGCCATT-3') and R806 (5'-GGACTACHVGGGTWTCTAAT-3'), and V4 region of 16S rRNA gene were our final target fragments for sequencing. A total final volume of 50 µl mixture for polymerase chain reaction: 6 µl of template fecal DNA, 25 µl of 2× Taq PCR Master Mix (0.1 U/µl), 2 µl of each primer (10 µM) and 15 µl ddH₂O to complement the reaction system. Then DNA was amplified using the

conditions below: 3 min at 94 °C for initial denaturation, then followed 28 cycles of 94 °C for 30 s, 53 °C for 40 s and 72 °C for 1 min. Finally, followed by an extension step of 72 °C for 5 min”.

These corrections do not alter any conclusions or results of our study.

The original article can be found online at <https://doi.org/10.1186/s13568-017-0517-8>.

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