PLOS ONE

CORRECTION

Correction: Microbial diversity in two traditional bacterial douchi from Gansu province in northwest China using Illumina sequencing

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The figure legends for Fig 2, Fig 3, Fig 4 and Fig 5 are incorrect. Please see the corrected figures here.

Citation: Zhang W, Luo Q, Zhu Y, Ma J, Cao L, Yang M, et al. (2018) Correction: Microbial diversity in two traditional bacterial douchi from Gansu province in northwest China using Illumina sequencing. PLoS ONE 13(5): e0197527. https://doi.org/10.1371/journal.pone.0197527

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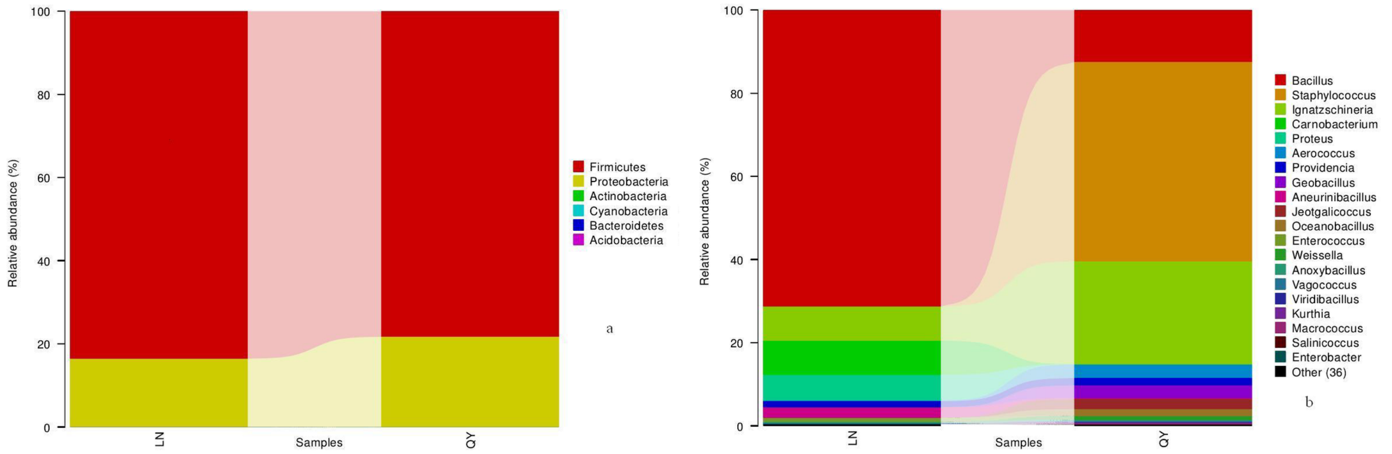

Fig 2. Relative abundance of bacterial phyla (a) and genera (b) in samples.

https://doi.org/10.1371/journal.pone.0197527.g001

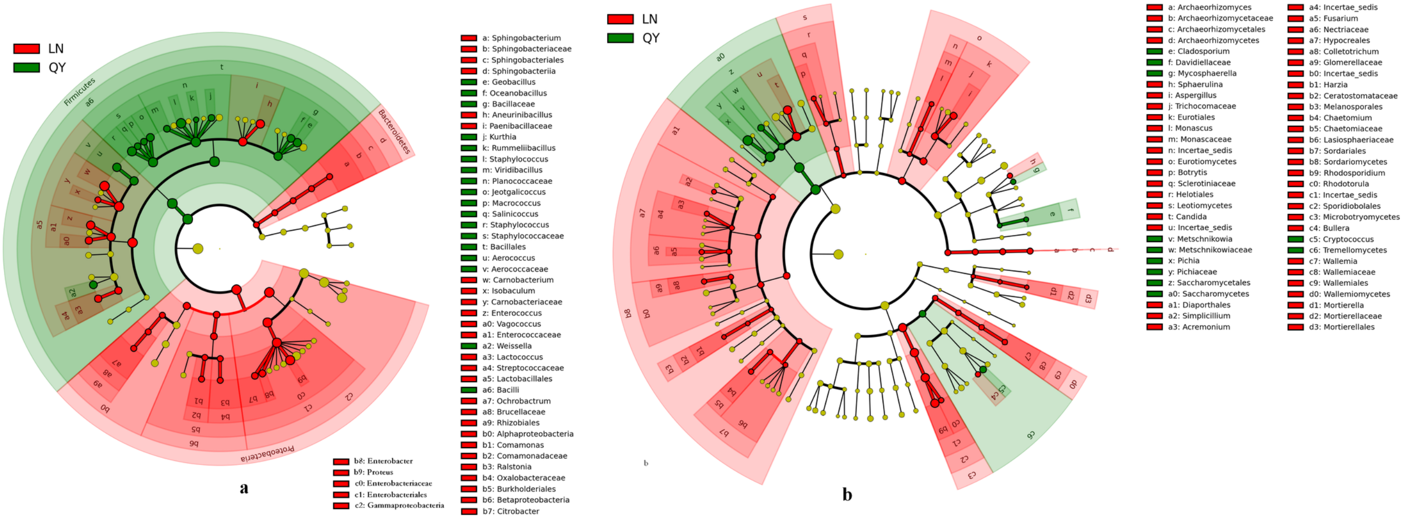

Fig 3. Linear discriminant analysis of microbial community compositions in douchi samples for bacteria (a) and fungi (b). The node size represents the difference in relative abundance. Green or red nodes indicate OTUs with significant differences of relative abundance, yellow nodes indicate OTUs with no significant differences in relative abundance.

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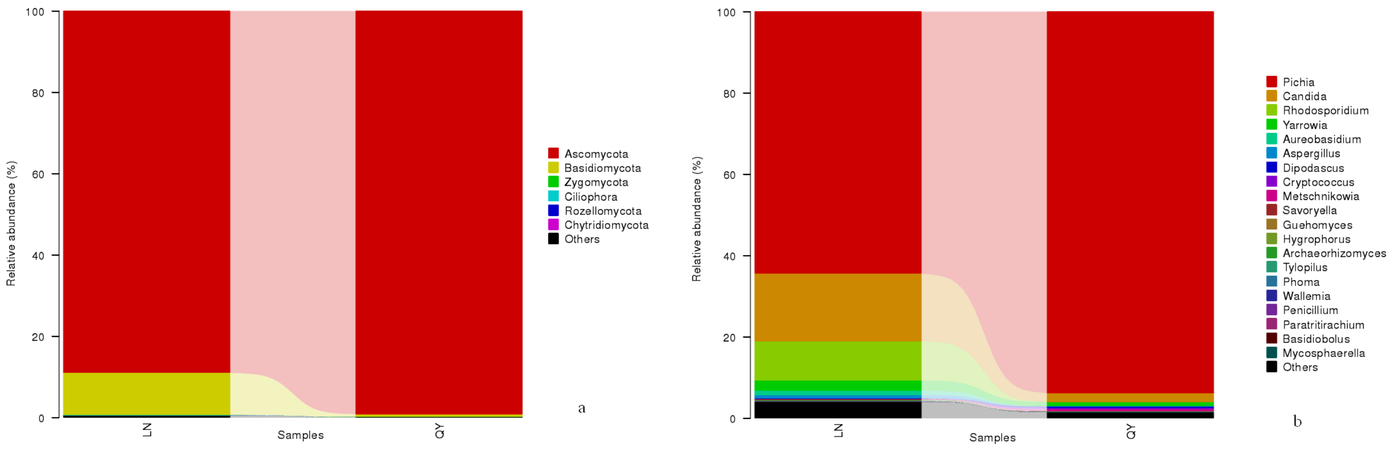

Fig 4. Relative abundance of fungal phyla (a) and genera (b) in the samples.

https://doi.org/10.1371/journal.pone.0197527.g003

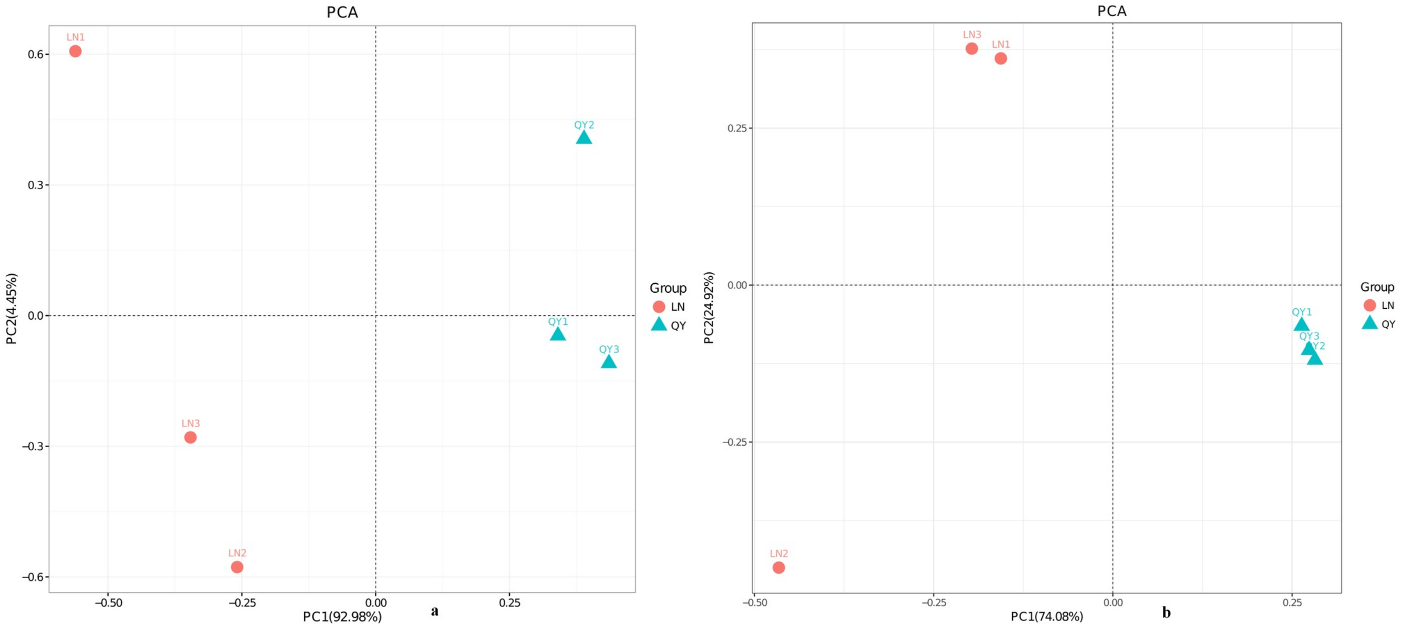

Fig 5. Principal components analysis for bacteria (a) and fungi (b).

https://doi.org/10.1371/journal.pone.0197527.g004

Reference

1. Zhang W, Luo Q, Zhu Y, Ma J, Cao L, Yang M, et al. (2018) Microbial diversity in two traditional bacterial douchi from Gansu province in northwest China using Illumina sequencing. PLoS ONE 13(3): e0194876. https://doi.org/10.1371/journal.pone.0194876 PMID: 29570735