**Supplementary materials**

**hanges in the gut microbiota diversity of brown frogs (*Rana dybowskii*) after local** **antimicrobial therapy**

Qing Tonga,b,c, Li-Yong Cuib, Jia Bie a, Zong-Fu Hua Hong-Bin Wanga, Jian-Tao Zhanga\*

aCollege of Veterinary Medicine, Northeast Agricultural University, Harbin, 150030, China

bJiamusi Branch of Heilongjiang Academy of Forestry Sciences, Jiamusi, 154002, China

cCollege of Life Science, Jiamusi University, Jiamusi, 154007, China

**\*Corresponding author**

College of Veterinary Medicine, Northeast Agricultural University, Harbin, 150030, People's Republic of China

E-mail: zhangjiantao@neau.edu.cn; Tel.: +86-451-55190470

**Table S1**. Core OTUs among all samples

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phylum | Genus | OTU | C-Mean | C-Sd | G-Mean | G-Sd | R-Mean | R-Sd |
| Bacteroidetes | *Bacteroides* | OTU417 | 3.23% | 3.99% | 3.18% | 3.92% | 3.92% | 3.65% |
| Bacteroidetes | *Bacteroides* | OTU364 | 0.73% | 1.36% | 0.99% | 1.32% | 0.73% | 0.49% |
| Bacteroidetes | *Bacteroides* | OTU38 | 3.37% | 2.99% | 2.04% | 1.21% | 1.72% | 1.12% |
| Bacteroidetes | *Bacteroides* | OTU402 | 0.12% | 0.15% | 0.09% | 0.06% | 0.09% | 0.06% |
| Bacteroidetes | *Bacteroides* | OTU14 | 0.40% | 0.27% | 0.30% | 0.15% | 0.31% | 0.12% |
| Bacteroidetes | *Bacteroides* | OTU728 | 0.10% | 0.09% | 0.09% | 0.08% | 0.07% | 0.03% |
| Bacteroidetes | *Bacteroides* | OTU466 | 0.37% | 0.71% | 0.48% | 0.70% | 0.64% | 0.65% |
| Bacteroidetes | *Alistipes* | OTU416 | 1.04% | 1.94% | 1.42% | 1.87% | 1.07% | 0.68% |
| Firmicutes | *Faecalitalea* | OTU333 | 3.54% | 6.35% | 4.85% | 6.07% | 6.33% | 5.37% |
| Firmicutes | *Vagococcus* | OTU198 | 8.68% | 15.59% | 11.61% | 15.10% | 13.89% | 14.34% |
| Actinobacteria | *Rhodococcus* | OTU448 | 0.10% | 0.11% | 0.12% | 0.10% | 0.14% | 0.09% |
| Actinobacteria | *Microbacterium* | OTU165 | 0.16% | 0.22% | 0.21% | 0.20% | 0.20% | 0.16% |
| Actinobacteria | *Arthrobacter* | OTU753 | 2.35% | 3.48% | 3.08% | 3.26% | 3.44% | 3.07% |
| Proteobacteria | *Citrobacter* | OTU179 | 7.39% | 5.72% | 6.66% | 5.28% | 5.81% | 4.60% |
| Proteobacteria | *Acinetobacter* | OTU41 | 1.04% | 2.22% | 1.45% | 2.18% | 1.04% | 0.88% |
| Proteobacteria | *Morganella* | OTU470 | 1.10% | 1.00% | 1.18% | 0.92% | 1.14% | 0.67% |



**Fig. S1** Rarefaction curves.

(**A**) Sob curves and Shannon curves (**B**) of all samples. The Sob curves are plots of the number of OTUs as a function of the number of sequences. The Shannon curves reflect the micro-diversity of the samples.

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**Fig. S2** The Venn diagrams show the shared communities among the control (C), gentamicin (G), and recovery (R) groups at OTU levels.

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**Fig. S3** (A) Core OTUs and (B) shared OTUs.

The curve shows the core OTUs for all samples. The curve shows the core OTUs for control (C), gentamicin (G), and recovery (R) groups. The Venn diagrams show the shared communities among the control (C), gentamicin (G), and recovery (R) groups at OTU levels.

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**Fig. S4** Community bar plot of bacteria at the phylum level.



**Fig. S5** The microbial genes with a significant difference between the control, gentamicin, and recovery groups by Kruskal–Wallis H test*.*

A: *Morganella*,B: *Weissella*,C: *unclassified\_f\_\_Veillonellaceae*, D: *Crenobacter*, andE: *unclassified\_f\_\_Eggerthella*ceae. X-axis: the relative abundance of bacterial genera in each group. Difference between proportions (%) is displayed within the set confidence interval. \*: 0.01 < *P* ≤ 0.05; \*\*: 0.001 < *P* ≤ 0.01.

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**Fig. S6** Heatmap of the top 35 dominant bacteria at the genus level with respect to abundance. Cluster analysis was performed using Bray-Curtis distances and the average-linkage method. Each bar or column corresponds to a specimen. The data are calculated in terms of relative abundance, and the colours represent lg values.



**Fig. S7** The relative abundance of potentially pathogenic genera changes after antibiotic baths (Kruskal-Wallis H test; 0.01 < *P* ≤0.05 marked as \*, *P* ≤0.01 marked as \*\*).

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**Fig. S8** The relative abundance of predicted genes in the metagenome related to level-1 and level-2 KEGG pathways.

The left list represents KEGG pathways at level 1, the middle list represents KEGG pathways at level 2, and the heatmap represents the abundance of each functional pathway for each sample. Asterisks indicate significant differences among the groups (*P* < 0.05).