**Supplementary Material**

*The potential effect of the oral bacterial community in Melanophryniscus admirabilis (admirable red-belly toads) conservation*

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**Table S1.** Percentage and average of identified phyla among the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phyla | TAO1 I | TA02 II | TA04 IV | TA05 | TA07 VII | TA10 X | TA11 XI | TA12 XII | AC421 | AC422 | AC423 | Average |
| Proteobacteria | 50% | 71% | 62% | 60% | 39% | 60% | 66% | 52% | 53% | 51% | 22% | 53% |
| Firmicutes | 10% | 16% | 20% | 17% | 14% | 18% | 10% | 16% | 15% | 18% | 48% | 18% |
| Bacteroidetes | 22% | 7% | 9% | 15% | 38% | 13% | 12% | 13% | 23% | 21% | 17% | 17% |
| Actinobacteria | 6% | 2% | 5% | 5% | 5% | 6% | 3% | 7% | 5% | 4% | 9% | 5% |
| Cyanobacteria | 3% | 0% | 0% | 0% | 0% | 0% | 2% | 8% | 0% | 1% | 2% | 2% |
| Fusobacteria | 2% | 1% | 0% | 1% | 4% | 1% | 1% | 2% | 2% | 4% | 2% | 2% |
| Acidobacteria | 1% | 0% | 2% | 0% | 0% | 1% | 2% | 1% | 0% | 0% | 0% | 1% |
| Verrucomicrobia | 1% | 0% | 2% | 0% | 0% | 0% | 1% | 0% | 0% | 0% | 1% | 0% |
| Armatimonadetes | 1% | 0% | 0% | 0% | 0% | 0% | 1% | 0% | 0% | 0% | 0% | 0% |
| Spirochaetes | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 1% | 0% | 0% | 0% |
| Tenericutes | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% |
| Planctomycetes | 0% | 0% | 0% | 0% | 0% | 1% | 0% | 0% | 0% | 0% | 0% | 0% |
| Chloroflexi | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% |
| Chlamydiae | 0% | 1% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% |
| Crenarchaeota | 0% | 1% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% |
| Nitrospirae | 0% | 0% | 0% | 1% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% |
| Others | 1% | 0% | 0% | 1% | 0% | 0% | 2% | 1% | 1% | 1% | 1% | 2% |
| Unknown | 1% | 0% | 0% | 0% | 0% | 0% | 1% | 1% | 0% | 0% | 0% | 0% |

**Table S2.**  Percentage and average of identified order among the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Order | TAO1 I | TA02 II | TA04 IV | TA05 | TA07 VII | TA10 X | TA11 XI | TA12 XII | AC421 | AC422 | AC423 | Average |
| Burkholderiales | 17% | 17% | 22% | 35% | 12% | 32% | 33% | 23% | 35% | 21% | 9% | 23% |
| Bacteroidales | 19% | 7% | 8% | 14% | 24% | 11% | 4% | 11% | 21% | 20% | 16% | 14% |
| Lactobacillales | 5% | 3% | 4% | 7% | 6% | 8% | 4% | 8% | 5% | 9% | 31% | 8% |
| Clostridiales | 4% | 10% | 12% | 10% | 7% | 7% | 2% | 4% | 7% | 7% | 15% | 8% |
| Enterobacteriales | 4% | 16% | 12% | 7% | 3% | 4% | 10% | 9% | 1% | 11% | 1% | 7% |
| Pseudomonadales | 5% | 22% | 5% | 1% | 8% | 4% | 3% | 2% | 0% | 1% | 1% | 5% |
| Actinomycetales | 5% | 2% | 5% | 4% | 4% | 6% | 3% | 6% | 5% | 3% | 8% | 5% |
| Sphingomonadales | 5% | 6% | 10% | 5% | 2% | 7% | 7% | 2% | 1% | 4% | 2% | 4% |
| Neisseriales | 4% | 2% | 3% | 4% | 5% | 1% | 1% | 4% | 4% | 5% | 3% | 3% |
| Pasteurellales | 6% | 3% | 1% | 2% | 4% | 1% | 1% | 1% | 5% | 5% | 4% | 3% |
| Rhizobiales | 3% | 3% | 4% | 4% | 2% | 8% | 4% | 3% | 1% | 1% | 0% | 3% |
| Bacillales | 1% | 3% | 3% | 0% | 0% | 3% | 3% | 2% | 2% | 1% | 1% | 2% |
| Fusobacteriales | 2% | 1% | 0% | 1% | 4% | 1% | 1% | 2% | 2% | 4% | 2% | 2% |
| Others | 18% | 5% | 10% | 5% | 16% | 6% | 19% | 20% | 7% | 5% | 6% | 11% |
| Unknown | 3% | 1% | 1% | 1% | 3% | 2% | 6% | 3% | 2% | 2% | 1% | 2% |

**Table S3.** Percentage and average of identified family among the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Family | TAO1 I | TA02 II | TA04 IV | TA05 | TA07 VII | TA10 X | TA11 XI | TA12 XII | AC421 | AC422 | AC423 | Average |
| Burkholderiaceae | 11% | 11% | 15% | 19% | 8% | 24% | 27% | 12% | 31% | 9% | 7% | 16% |
| Prevotellaceae | 14% | 6% | 6% | 11% | 20% | 6% | 2% | 8% | 16% | 16% | 10% | 10% |
| Enterobacteriaceae | 4% | 16% | 12% | 7% | 3% | 4% | 10% | 9% | 1% | 11% | 1% | 7% |
| Streptococcaceae | 3% | 1% | 3% | 5% | 4% | 3% | 1% | 6% | 3% | 7% | 29% | 6% |
| Comamonadaceae | 2% | 5% | 6% | 14% | 3% | 7% | 1% | 9% | 4% | 11% | 1% | 6% |
| Veillonellaceae | 3% | 5% | 7% | 9% | 5% | 3% | 1% | 2% | 4% | 5% | 14% | 5% |
| Sphingomonadaceae | 5% | 6% | 10% | 5% | 2% | 7% | 6% | 2% | 1% | 4% | 2% | 4% |
| Moraxellaceae | 3% | 22% | 4% | 1% | 3% | 3% | 1% | 1% | 0% | 1% | 1% | 3% |
| Pasteurellaceae | 6% | 3% | 1% | 2% | 4% | 1% | 1% | 4% | 5% | 5% | 4% | 3% |
| Neisseriaceae | 4% | 2% | 3% | 4% | 5% | 1% | 1% | 4% | 4% | 5% | 3% | 3% |
| Bradyrhizobiaceae | 1% | 3% | 4% | 3% | 1% | 6% | 2% | 2% | 1% | 1% | 0% | 2% |
| Micrococcaceae | 2% | 1% | 1% | 2% | 3% | 1% | 0% | 2% | 2% | 2% | 4% | 2% |
| Paraprevotellaceae | 1% | 1% | 1% | 1% | 2% | 3% | 0% | 1% | 2% | 2% | 5% | 1% |
| Staphylococcaceae | 0% | 3% | 3% | 0% | 0% | 2% | 2% | 2% | 2% | 0% | 1% | 1% |
| Clostridiaceae | 1% | 4% | 3% | 1% | 1% | 2% | 1% | 0% | 2% | 1% | 0% | 1% |
| Pseudomonadaceae | 3% | 1% | 1% | 1% | 5% | 0% | 2% | 1% | 0% | 0% | 0% | 1% |
| Fusobacteriaceae | 2% | 1% | 0% | 1% | 2% | 1% | 0% | 1% | 2% | 2% | 1% | 1% |
| Porphyromonadaceae | 2% | 0% | 0% | 2% | 1% | 2% | 1% | 1% | 2% | 2% | 1% | 1% |
| Lactobacillaceae | 0% | 1% | 1% | 2% | 1% | 5% | 2% | 1% | 1% | 0% | 0% | 1% |
| Oxalobacteraceae | 3% | 0% | 0% | 1% | 1% | 1% | 5% | 1% | 0% | 0% | 0% | 1% |
| Chitinophagaceae | 2% | 0% | 1% | 0% | 1% | 1% | 3% | 1% | 2% | 0% | 0% | 1% |
| Sphingobacteriaceae | 1% | 0% | 0% | 0% | 4% | 0% | 4% | 0% | 0% | 0% | 0% | 1% |
| Caulobacteraceae | 1% | 1% | 4% | 0% | 0% | 0% | 0% | 0% | 1% | 0% | 0% | 1% |
| Corynebacteriaceae | 1% | 0% | 0% | 0% | 0% | 0% | 2% | 3% | 0% | 0% | 2% | 1% |
| Weeksellaceae | 0% | 0% | 0% | 0% | 6% | 1% | 0% | 0% | 0% | 0% | 0% | 1% |
| Carnobacteriaceae | 0% | 0% | 0% | 0% | 1% | 0% | 0% | 1% | 1% | 1% | 2% | 1% |
| Microbacteriaceae | 1% | 0% | 1% | 0% | 0% | 1% | 1% | 0% | 2% | 0% | 0% | 1% |
| Actinomycetaceae | 0% | 0% | 0% | 1% | 1% | 0% | 0% | 1% | 1% | 1% | 2% | 1% |
| Others | 15% | 15% | 9% | 7% | 10% | 9% | 16% | 12% | 6% | 8% | 5% | 10% |
| Unknown | 10% | 3% | 5% | 1% | 2% | 4% | 10% | 13% | 4% | 4% | 4% | 5% |

**Table S4.** Relative abundance of amplicon sequence variants belonging to the persistent groups in relative KEGG Level 2 of xenobiotic/drug metabolism identified among the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Prediction of xenobiotic/drug metabolism | TAO1 I | TA02 II | TA04 IV | TA05 | TA07 VII | TA10 X | TA11 XI | TA12 XII | AC421 | AC422 | AC423 | Average |
| Aminobenzoate degradation | 26543 | 10601 | 8973 | 26842 | 23135 | 5909 | 13470 | 155851 | 5663 | 28225 | 25530 | 30067 |
| Atrazine degradation | 6248 | 1281 | 1407 | 4193 | 4974 | 1302 | 1833 | 28134 | 1349 | 5711 | 4908 | 5576 |
| Benzoate degradation | 46840 | 23216 | 16979 | 52638 | 45425 | 9234 | 22936 | 271823 | 10172 | 51881 | 48206 | 54486 |
| Bisphenol degradation | 4201 | 1449 | 1135 | 4777 | 3102 | 997 | 2455 | 27209 | 1233 | 4321 | 4594 | 5043 |
| Chloroalkane and chloroalkene degradation | 20729 | 9522 | 8404 | 26265 | 20413 | 5494 | 10887 | 122095 | 4809 | 22317 | 25829 | 25160 |
| Chlorocyclohexane and chlorobenzene degradation | 5751 | 2678 | 2078 | 7032 | 6080 | 866 | 2713 | 29006 | 1290 | 5908 | 8003 | 6491 |
| Dioxin degradation | 6884 | 2122 | 1581 | 4850 | 7302 | 1185 | 2664 | 35636 | 1286 | 5038 | 6767 | 6847 |
| Drug metabolism by cytochrome P450 | 19450 | 7983 | 5708 | 21104 | 20457 | 2723 | 6953 | 89812 | 4201 | 18265 | 22496 | 19923 |
| Ethylbenzene degradation | 7032 | 4031 | 3129 | 11442 | 10435 | 1173 | 3504 | 46942 | 1724 | 10134 | 7355 | 9718 |
| Fluorobenzoate degradation | 5822 | 2617 | 1864 | 5199 | 6489 | 818 | 2541 | 25821 | 1188 | 4651 | 7490 | 5864 |
| Metabolism of xenobiotics by cytochrome P450 | 19169 | 7941 | 5700 | 20973 | 20166 | 2679 | 6909 | 89420 | 4156 | 18137 | 22424 | 19789 |
| Naphthalene degradation | 14895 | 5927 | 4433 | 16761 | 18166 | 2920 | 6575 | 75681 | 3354 | 13992 | 20872 | 16689 |
| Nitrotoluene degradation | 11702 | 4368 | 5387 | 10417 | 10158 | 2000 | 4523 | 64578 | 3016 | 11073 | 11362 | 12598 |
| Polycyclic aromatic hydrocarbon degradation | 2991 | 549 | 223 | 1301 | 2102 | 415 | 1306 | 10820 | 687 | 1940 | 2851 | 2290 |
| Toluene degradation | 33755 | 18146 | 14374 | 37192 | 39358 | 6942 | 14039 | 167743 | 6884 | 35684 | 32328 | 36950 |
| Xylene degradation | 4036 | 948 | 484 | 1664 | 4612 | 649 | 1774 | 22998 | 723 | 2819 | 4018 | 4066 |

**Table S5.** Average of relative abundance of amplicon sequence variants and standard deviation ofxenobiotic functional prediction in oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads)

|  |  |  |
| --- | --- | --- |
| **Prediction of xenobiotic/drug metabolism** | **Average of ASV** | **Standard Deviation** |
| Benzoate degradation | 54486 | 70593 |
| Toluene degradation | 36950 | 42999 |
| Aminobenzoate degradation | 30067 | 40670 |
| Chloroalkane and chloroalkene degradation | 25160 | 31591 |
| Drug metabolism by cytochrome P450 | 19923 | 23261 |
| Metabolism of xenobiotics by cytochrome P450 | 19789 | 23163 |
| Naphthalene degradation | 16689 | 19647 |
| Nitrotoluene degradation | 12598 | 16805 |
| Ethylbenzene degradation | 9718 | 12260 |
| Dioxin degradation | 6847 | 9375 |
| Chlorocyclohexane and chlorobenzene degradation | 6491 | 7493 |
| Fluorobenzoate degradation | 5864 | 6661 |
| Atrazine degradation | 5576 | 7373 |
| Bisphenol degradation | 5043 | 7150 |
| Xylene degradation | 4066 | 6155 |
| Polycyclic aromatic hydrocarbon degradation | 2290 | 2845 |

Chart, bar chart

Description automatically generated

**Figure S1.** Oral bacterial microbiota composition at the family level in the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads). Taxonomic composition of the oral microbiota among the eleven samples was compared based on the relative abundance (reads of a taxon/total reads in a sample).

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**Figure S2.** Heatmap display of the relative abundance of predicted genes assigned to Kyoto Encyclopedia of Genes and Genomes – KEGG) categories for metabolism in each of the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads).