

## Supplementary Material

# The oral bacterial community in *Melanophryniscus admirabilis* (admirable red-belly toads): Implications for conservation.

Michele Bertoni Mann<sup>1</sup>, Janira Prichula<sup>2</sup>, Ícaro Maia Santos de Castro<sup>2</sup>, Juliana Mello Severo<sup>2</sup>, Michelle Abadie<sup>3</sup>, Thayná Mendes De Freitas Lima<sup>4</sup>, Valentina Caorsi<sup>4,5</sup>, Márcio Borges-Martins<sup>4</sup>, Jeverson Frazzon<sup>6</sup>, Ana Paula Guedes Frazzon<sup>1</sup>

**Table S1.** Percentage and average of identified phyla (>1%) 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 2.** Percentage and average of identified order (>1%) 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%

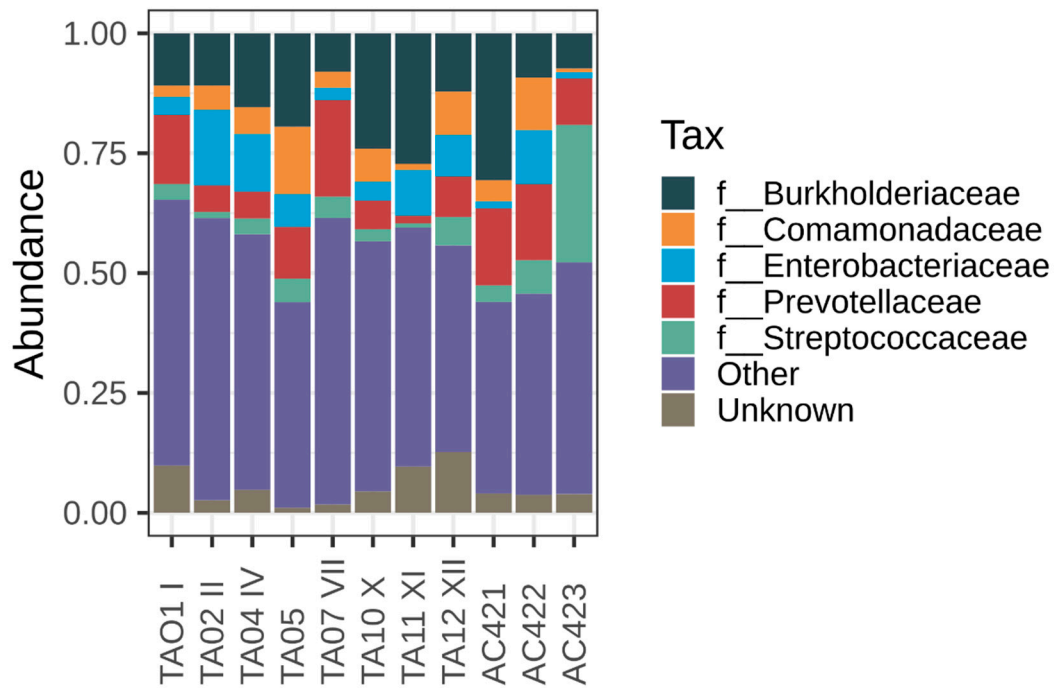
<b>Neisseriales</b>	4%	2%	3%	4%	5%	1%	1%	4%	4%	5%	3%	3%
<b>Pasteurellales</b>	6%	3%	1%	2%	4%	1%	1%	1%	5%	5%	4%	3%
<b>Rhizobiales</b>	3%	3%	4%	4%	2%	8%	4%	3%	1%	1%	0%	3%
<b>Bacillales</b>	1%	3%	3%	0%	0%	3%	3%	2%	2%	1%	1%	2%
<b>Fusobacteriales</b>	2%	1%	0%	1%	4%	1%	1%	2%	2%	4%	2%	2%
<b>Others</b>	18%	5%	10%	5%	16%	6%	19%	20%	7%	5%	6%	11%
<b>Unknown</b>	3%	1%	1%	1%	3%	2%	6%	3%	2%	2%	1%	2%

**Table 3.** Percentage and average of identified family (>1%) among the eleven oral samples of wild *Melanophryniscus admirabilis* (admirable red-belly toads).

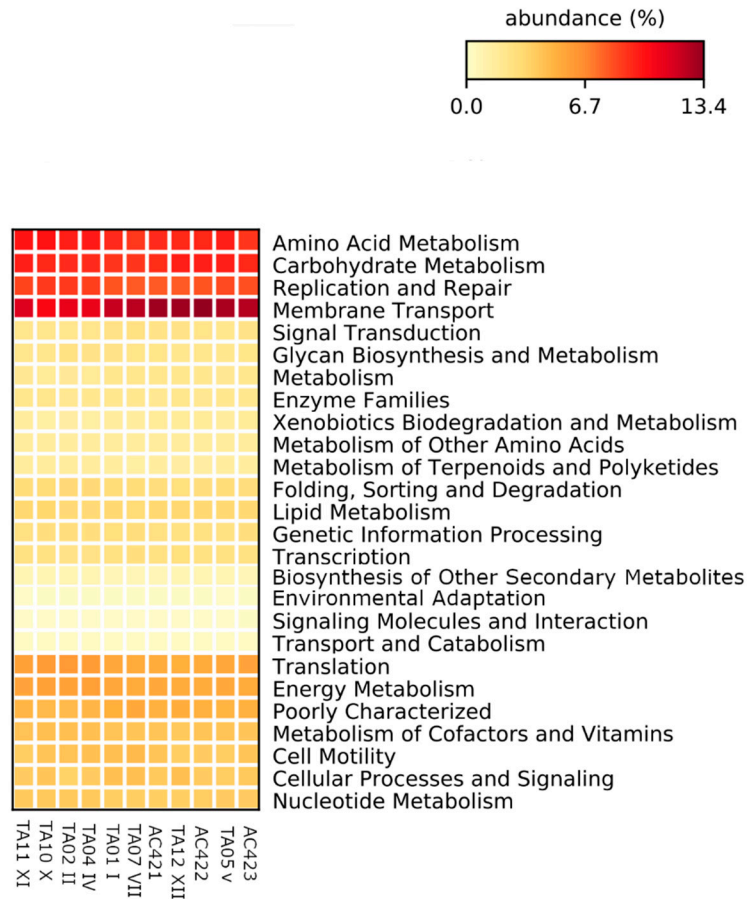
<b>Family</b>	<b>TAO1</b>	<b>ITA02</b>	<b>II TA04</b>	<b>IV TA05</b>	<b>TA07</b>	<b>VII TA10</b>	<b>X TA11</b>	<b>XI TA12</b>	<b>XII AC421</b>	<b>AC422</b>	<b>AC423</b>	<b>Average</b>
<b>Burkholderiaceae</b>	11%	11%	15%	19%	8%	24%	27%	12%	31%	9%	7%	16%
<b>Prevotellaceae</b>	14%	6%	6%	11%	20%	6%	2%	8%	16%	16%	10%	10%
<b>Enterobacteriaceae</b>	4%	16%	12%	7%	3%	4%	10%	9%	1%	11%	1%	7%
<b>Streptococcaceae</b>	3%	1%	3%	5%	4%	3%	1%	6%	3%	7%	29%	6%
<b>Comamonadaceae</b>	2%	5%	6%	14%	3%	7%	1%	9%	4%	11%	1%	6%
<b>Veillonellaceae</b>	3%	5%	7%	9%	5%	3%	1%	2%	4%	5%	14%	5%
<b>Sphingomonadaceae</b>	5%	6%	10%	5%	2%	7%	6%	2%	1%	4%	2%	4%
<b>Moraxellaceae</b>	3%	22%	4%	1%	3%	3%	1%	1%	0%	1%	1%	3%
<b>Pasteurellaceae</b>	6%	3%	1%	2%	4%	1%	1%	4%	5%	5%	4%	3%
<b>Neisseriaceae</b>	4%	2%	3%	4%	5%	1%	1%	4%	4%	5%	3%	3%
<b>Bradyrhizobiaceae</b>	1%	3%	4%	3%	1%	6%	2%	2%	1%	1%	0%	2%
<b>Micrococcaceae</b>	2%	1%	1%	2%	3%	1%	0%	2%	2%	2%	4%	2%
<b>Paraprevotellaceae</b>	1%	1%	1%	1%	2%	3%	0%	1%	2%	2%	5%	1%
<b>Staphylococcaceae</b>	0%	3%	3%	0%	0%	2%	2%	2%	2%	0%	1%	1%
<b>Clostridiaceae</b>	1%	4%	3%	1%	1%	2%	1%	0%	2%	1%	0%	1%
<b>Pseudomonadaceae</b>	3%	1%	1%	1%	5%	0%	2%	1%	0%	0%	0%	1%
<b>Fusobacteriaceae</b>	2%	1%	0%	1%	2%	1%	0%	1%	2%	2%	1%	1%
<b>Porphyromonadaceae</b>	2%	0%	0%	2%	1%	2%	1%	1%	2%	2%	1%	1%
<b>Lactobacillaceae</b>	0%	1%	1%	2%	1%	5%	2%	1%	1%	0%	0%	1%
<b>Oxalobacteraceae</b>	3%	0%	0%	1%	1%	1%	5%	1%	0%	0%	0%	1%
<b>Chitinophagaceae</b>	2%	0%	1%	0%	1%	1%	3%	1%	2%	0%	0%	1%
<b>Sphingobacteriaceae</b>	1%	0%	0%	0%	4%	0%	4%	0%	0%	0%	0%	1%
<b>Caulobacteraceae</b>	1%	1%	4%	0%	0%	0%	0%	0%	1%	0%	0%	1%
<b>Corynebacteriaceae</b>	1%	0%	0%	0%	0%	0%	2%	3%	0%	0%	2%	1%
<b>Weeksellaceae</b>	0%	0%	0%	0%	6%	1%	0%	0%	0%	0%	0%	1%
<b>Carnobacteriaceae</b>	0%	0%	0%	0%	1%	0%	0%	1%	1%	1%	2%	1%
<b>Microbacteriaceae</b>	1%	0%	1%	0%	0%	1%	1%	0%	2%	0%	0%	1%
<b>Actinomycetaceae</b>	0%	0%	0%	1%	1%	0%	0%	1%	1%	1%	2%	1%
<b>Others</b>	15%	15%	9%	7%	10%	9%	16%	12%	6%	8%	5%	10%
<b>Unknown</b>	10%	3%	5%	1%	2%	4%	10%	13%	4%	4%	4%	5%

**Table 4.** 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).

<b>Prediction of Xenobiotic/Drug Metabolism</b>	<b>TAO1 I</b>	<b>TAO2 II</b>	<b>TA04 IV</b>	<b>TA05</b>	<b>TA07 VII</b>	<b>TA10 X</b>	<b>TA11 XI</b>	<b>TA12 XII</b>	<b>AC421</b>	<b>AC422</b>	<b>AC423</b>	<b>Average</b>	<b>Standard Deviation</b>
<b>Aminobenzoate degradation</b>	26,543	10,601	8,973	26,842	23,135	5,909	13,470	15,5851	5,663	28,225	25,530	30,067	40,670
<b>Atrazine degradation</b>	6,248	1,281	1,407	4,193	4,974	1,302	1,833	28,134	1,349	5,711	4,908	5,576	7,373
<b>Benzoate degradation</b>	46,840	23,216	16,979	52,638	45,425	9,234	22,936	271,823	10,172	51,881	48,206	54,486	70,593
<b>Bisphenol degradation</b>	4,201	1,449	1,135	4,777	3,102	997	2,455	27,209	1,233	4,321	4,594	5,043	7,150
<b>Chloroalkane and chloroalkene degradation</b>	20,729	9,522	8,404	26,265	20,413	5,494	10,887	122,095	4,809	22,317	25,829	25,160	31,591
<b>Chlorocyclohexane and chlorobenzene degradation</b>	5,751	2,678	2,078	7,032	6,080	866	2,713	29,006	1,290	5,908	8,003	6,491	7,493
<b>Dioxin degradation</b>	6,884	2,122	1,581	4,850	7,302	1,185	2,664	35,636	1,286	5,038	6,767	6,847	9,375
<b>Drug metabolism by cytochrome P450</b>	19,450	7,983	5,708	21,104	20,457	2,723	6,953	89,812	4,201	18,265	22,496	19,923	23,261
<b>Ethylbenzene degradation</b>	7,032	4,031	3,129	11,442	10,435	1,173	3,504	46,942	1,724	10,134	7,355	9,718	12,260
<b>Fluorobenzoate degradation</b>	5,822	2,617	1,864	5,199	6,489	818	2,541	25,821	1,188	4,651	7,490	5,864	6,661
<b>Metabolism of xenobiotics by cytochrome P450</b>	19,169	7,941	5,700	20,973	20,166	2,679	6,909	89,420	4,156	18,137	22,424	19,789	23,163
<b>Naphthalene degradation</b>	14,895	5,927	4,433	16,761	18,166	2,920	6,575	75,681	3,354	13,992	20,872	16,689	19,647
<b>Nitrotoluene degradation</b>	11,702	4,368	5,387	10,417	10,158	2,000	4,523	64,578	3,016	11,073	11,362	12,598	16,805
<b>Polycyclic aromatic hydrocarbon degradation</b>	2,991	549	223	1,301	2,102	415	1,306	10,820	687	1,940	2,851	2,290	2,845
<b>Toluene degradation</b>	33,755	18,146	14,374	37,192	39,358	6,942	14,039	167,743	6,884	35,684	32,328	36,950	42,999
<b>Xylene degradation</b>	4,036	948	484	1,664	4,612	649	1,774	22,998	723	2,819	4,018	4,066	6,155



**Figure 1.** Five most abundant families presented 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 threlative abundance (reads of a taxon/total reads in a sample).



**Figure 2.** Heatmap of the significant predicted KEGG pathways from the oral bacterial community of the eleven wild *Melanophryniscus admirabilis* (admirable red-belly toads).