

Electronic Supplementary Material

Arthropod–bacteria interactions influence assembly of aquatic host microbiome and pathogen defense

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Summary: For bromeliad microecosystems containing tadpoles exposed to *Batrachochytrium dendrobatidis* (Bd), a water treatment (natural or pre-sterilized), and an arthropod treatment (present or absent) for 17 d: rarefaction curves for bacterial sequences, average relative abundance of the most common bacterial phyla, results of generalized linear models and permutation multivariate analyses of variance, and differentially abundant OTUs for each treatment.

Figure S1. Rarefaction curves for all samples. At a rarefaction level of 10,000 sequences per sample, the curves have plateaued, indicating comprehensive representation of the bacterial communities within each sample. At the same time, this level of rarefaction minimized exclusion of samples (with < 10,000 total sequences). All tadpole samples and 39/48 environmental samples were retained at this level of rarefaction.

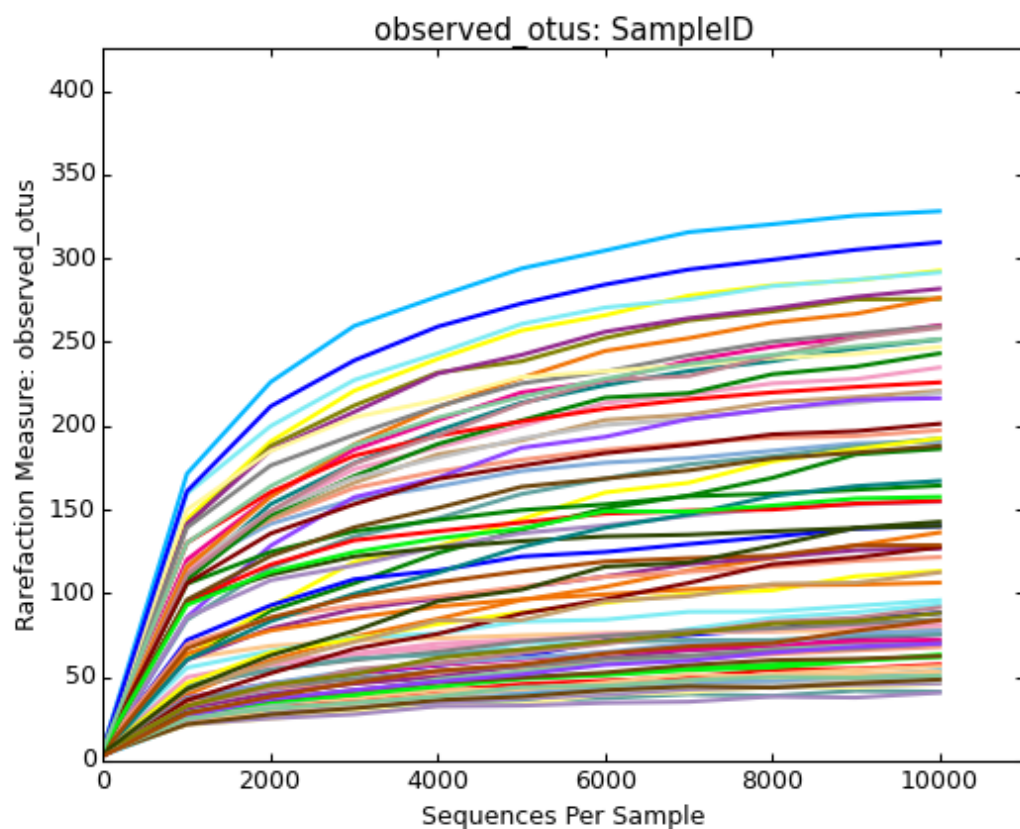


Figure S2. Average relative abundance of the most common bacterial phyla in environmental bacterial communities and tadpole microbiomes. All samples were rarefied to 10 000 reads.

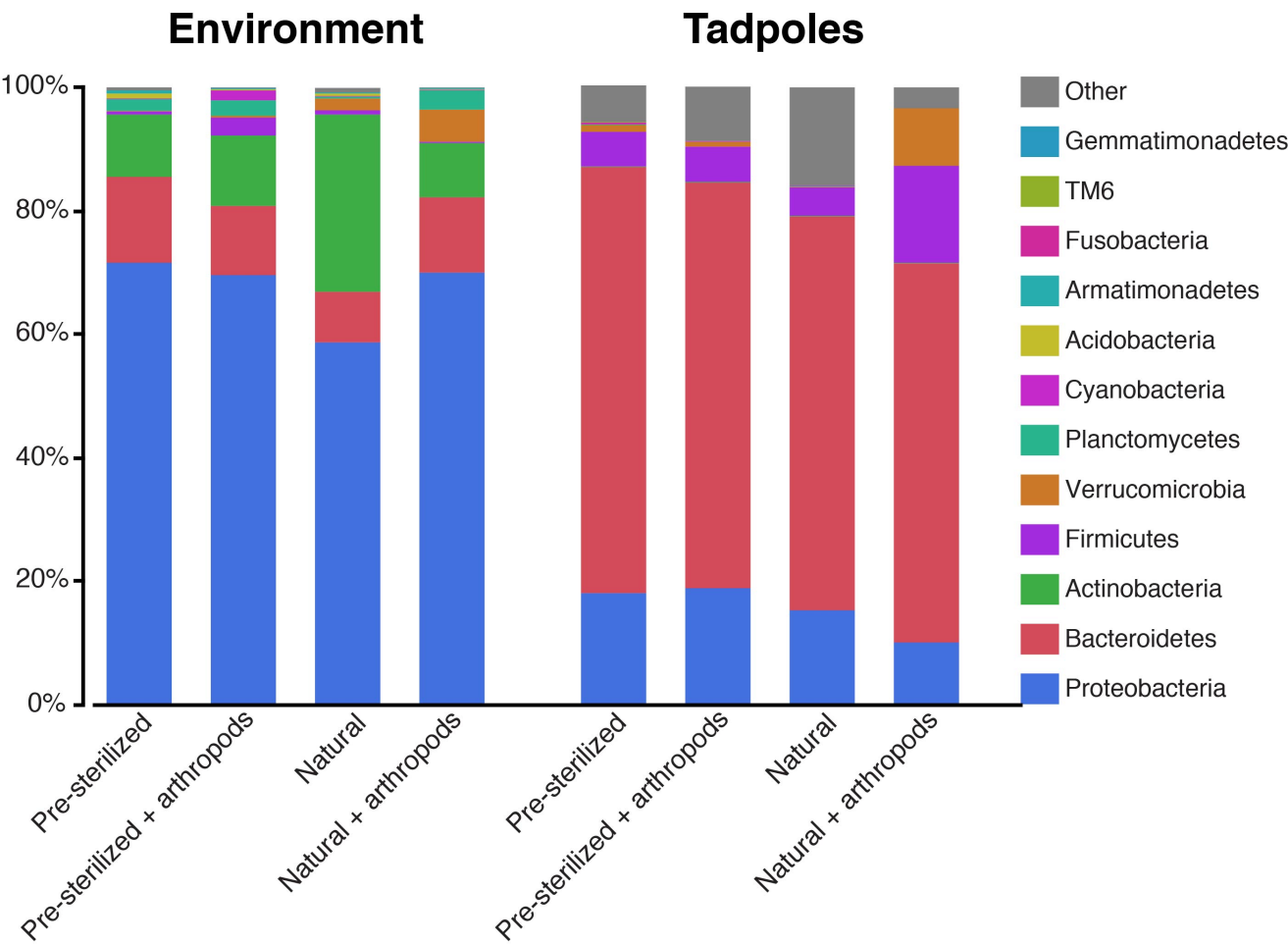


Table S1. Generalized linear models (GLM) and permutation analyses of variance (PERMANOVA) testing effects of water treatment, arthropod treatment, and their interactions on environmental bacterial community structure, host (tadpole) bacterial community (microbiome) structure, fungal pathogen abundance, tadpole body mass, and water quality.

Environment: phylogenetic bacterial diversity

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	10.968	0.745	14.72	<0.0001
Water (natural or pre-sterilized)	4.055	0.785	5.17	<0.0001
Arthropods (present or absent)	-0.190	0.785	-0.24	0.811
Water*Arthropods	-2.232	1.587	-1.41	0.170

Whole model: $F_{3,29} = 9.587$, $R^2 = 0.498$, $p = 0.0001$

Environment: OTU richness

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	155.925	14.533	10.73	<0.0001
Water (natural or pre-sterilized)	88.078	15.300	5.76	<0.0001
Arthropods (present or absent)	18.828	15.300	1.23	0.228
Water*Arthropods	-45.023	30.947	-1.45	0.157

Whole model: $F_{3,29} = 12.309$, $R^2 = 0.560$, $p < 0.0001$

Environment: proportion anti-Bd OTUs

Predictor	Estimate	Std. Error	χ^2	<i>p</i>
Intercept	-1.788	0.076	729.940	<0.0001
Water (natural or pre-sterilized)	-0.374	0.074	25.073	<0.0001
Arthropods (present or absent)	0.145	0.074	3.822	0.051
Water*Arthropods	0.078	0.152	0.260	0.610

Whole model: $\chi^2 = 30.381$, $df = 3$, $p < 0.0001$

Environment: bacterial community composition (unweighted UniFrac distance)

Term	D.f.	F	R^2	<i>p</i>
Water (natural or pre-sterilized)	1	4.630	0.123	0.001
Arthropods (present or absent)	1	2.639	0.070	0.001
Water*Arthropods	1	1.320	0.035	0.085
Residuals	29		0.772	

Environment: bacterial community composition (weighted UniFrac distance)

Term	D.f.	F	R^2	<i>p</i>
Water (natural or pre-sterilized)	1	1.193	0.034	0.279
Arthropods (present or absent)	1	4.090	0.116	0.002
Water*Arthropods	1	1.032	0.029	0.349
Residuals	29		0.821	

Environment: density of Bd zoospores

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	2.668	0.269	9.90	<0.0001
Water (natural or pre-sterilized)	-0.181	0.292	-0.62	0.541
Arthropods (present or absent)	-0.799	0.290	-2.76	0.011
Water*Arthropods	-0.069	0.585	-0.12	0.907

Whole model: $F_{3,26} = 2.657$, $R^2 = 0.235$, $p = 0.069$

Environment: water turbidity

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	4.544	0.946	4.80	< 0.0001
Water (natural or pre-sterilized)	1.096	0.980	1.12	0.274
Arthropods (present or absent)	-2.796	0.969	-2.89	0.008
Water*Arthropods	-1.412	1.980	-0.71	0.482

Whole model: $F_{3,26} = 3.430$, $R^2 = 0.284$, $p = 0.032$

Environment: water pH

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	5.320	0.169	31.52	< 0.0001
Water (natural or pre-sterilized)	0.268	0.181	1.48	0.151
Arthropods (present or absent)	0.124	0.180	0.69	0.498
Water*Arthropods	-0.324	0.364	-0.89	0.381

Whole model: $F_{3,27} = 1.166$, $R^2 = 0.115$, $p = 0.341$

Tadpoles: phylogenetic bacterial diversity

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	6.668	0.587	11.35	< 0.0001
Water (natural or pre-sterilized)	3.025	0.668	4.53	< 0.0001
Arthropods (present or absent)	-1.306	0.668	-1.96	0.058
Water*Arthropods	-2.770	1.337	-2.07	0.045

Whole model: $F_{3,38} = 9.792$, $R^2 = 0.436$, $p < 0.0001$

Tadpoles: bacterial dispersion

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	0.538	0.008	67.39	< 0.0001
Water (natural or pre-sterilized)	-0.016	0.009	-1.71	0.096
Arthropods (present or absent)	-0.031	0.009	-3.43	0.002
Water*Arthropods	-0.044	0.018	-2.39	0.022

Whole model: $F_{3,38} = 6.6126$, $R^2 = 0.343$, $p = 0.001$

Tadpoles: OTU richness

Predictor	Estimate	Std. Error	<i>t</i>	<i>p</i>
Intercept	73.126	8.479	8.62	< 0.0001
Water (natural or pre-sterilized)	40.344	9.642	4.18	0.0002
Arthropods (present or absent)	-18.744	9.642	-1.94	0.059
Water*Arthropods	-35.783	19.302	-1.85	0.072

Whole model: $F_{3,38} = 8.470$, $R^2 = 0.401$, $p = 0.0002$

Tadpoles: bacterial community composition (unweighted UniFrac distance)

Term	D.f.	F	R^2	<i>p</i>
Water (natural or pre-sterilized)	1	3.664	0.076	0.001
Arthropods (present or absent)	1	3.179	0.066	0.001
Water*Arthropods	1	3.140	0.065	0.001
Residuals	38		0.792	

Tadpoles: bacterial community composition (weighted UniFrac distance)

Term	D.f.	F	R^2	p
Water (natural or pre-sterilized)	1	2.980	0.056	0.022
Arthropods (present or absent)	1	2.696	0.051	0.032
Water*Arthropods	1	9.224	0.174	0.001
Residuals	38		0.718	

Tadpoles: Bd burden

Predictor	Estimate	Std. Error	t	p
Intercept	1.658	0.122	13.58	<0.0001
Water (natural or pre-sterilized)	0.437	0.139	3.15	0.003
Arthropods (present or absent)	-0.173	0.139	-1.25	0.220
Water*Arthropods	-0.222	0.278	-0.80	0.429

Whole model: $F_{3,38} = 4.152$, $R^2 = 0.247$, $p = 0.012$

Tadpoles: body mass

Predictor	Estimate	Std. Error	t	p
Intercept	0.025	0.002	11.15	<0.0001
Water (natural or pre-sterilized)	-0.007	0.003	-2.94	0.006
Arthropods (present or absent)	0.000	0.003	-0.02	0.982
Water*Arthropods	0.002	0.005	0.005	0.669

Whole model: $F_{3,38} = 2.938$, $R^2 = 0.188$, $p = 0.046$

Environment: chlorophyll a

Predictor	Estimate	Std. Error	t	p
Intercept	129.755	66.664	1.95	0.063
Water (natural or pre-sterilized)	173.380	69.030	2.51	0.019
Arthropods (present or absent)	-57.608	68.242	-0.84	0.406
Water*Arthropods	-145.763	139.519	-1.04	0.306

Whole model: $F_{3,26} = 2.730$, $R^2 = 0.240$, $p = 0.064$

Table S2. Differentially abundant OTUs for each treatment identified with LEfSe analysis. OTUs from the environment and from the microbiomes of tadpoles are grouped separately. For bacterial taxonomy, p = phylum, c = class, o = order, f = family, and g = genus.

Taxonomy	LDA score	<i>p</i>
Environment: natural water + arthropods		
p_Armatimonadetes.c__Fimbriimonadia.o__Fimbriimonadales.f__Fimbriimonadaceae.g_Fimbriimonas	3.19053118	0.01194387
p_Bacteroidetes.c__Saprospirae.o__Saprospirales.f_unnamed	3.05859852	0.011074
p_Bacteroidetes.c__Saprospirae.o__Saprospirales.f.g_unnamed	3.06768584	0.011074
p_Bacteroidetes.c_Cytophagia.o_Cytophagales.f_Cytophagaceae.g_Flectobacillus	3.80449305	0.00949955
p_Bacteroidetes.c_Flavobacteriia.o_Flavobacteriales.f__Weeksellaceae.g_Cloacibacterium	3.54919003	0.0001642
p_Bacteroidetes.c_Sphingobacteriia.o_Sphingobacteriales.f_unnamed	3.65212942	0.00141499
p_Bacteroidetes.c_Sphingobacteriia.o_Sphingobacteriales.f.g_unnamed	3.65212939	0.00141499
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales	3.73662381	0.01666761
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales.f_Caulobacteraceae	3.73662381	0.01666761
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales.f_Caulobacteraceae.g_unnamed	3.34758519	0.01588659
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales.f_Caulobacteraceae.g_Arthrospira	3.10761471	0.02408124
p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales	3.63962778	6.03E-05
p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae	3.55699584	5.88E-05
p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae.g_Rhodobacter	3.56070163	5.91E-05

p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomorphales.f_Sphingomonadaceae.g_Sphingobium	3.54639448	0.0053172
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae	5.10131538	0.00947027
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Delftia	3.64004632	0.0395675
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Hydrogenophaga	4.90240548	3.66E-05
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Pseudomonadales.f_Moraxellaceae.g_Perlucidibaca	3.58953886	0.00028523
p_Verrucomicrobia	4.42346988	0.000428
p_Verrucomicrobia.c_Opitutae	3.21265416	0.01228411
p_Verrucomicrobia.c_Opitutae.o_Opitutales	3.21323961	0.01228411
p_Verrucomicrobia.c_Opitutae.o_Opitutales.f_Opitutaceae	3.2145075	0.01228411
p_Verrucomicrobia.c_Opitutae.o_Opitutales.f_Opitutaceae.g_Opitutus	3.22819872	0.00105068
p_Verrucomicrobia.c_Verrucomicrobiae	4.40183634	6.26E-05
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales	4.40182808	6.26E-05
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae	4.40183815	6.26E-05
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae.g_Prostheco bacter	4.19980831	0.00021302
Environment: pre-sterilized water + arthropods		
p_Bacteroidetes.c_Cytophagia.o_Cytophagales.f_Cytophagaceae.g_Emticicia	3.43597458	0.00095989
p_Firmicutes	4.07215678	0.01648919

p_Firmicutes.c_Clostridia	3.87175024	0.00464821
p_Firmicutes.c_Clostridia.o_Clostridiales	3.87193785	0.00396938
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae	3.32979454	0.01561476
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Veillonellaceae.g_unnamed	3.36394916	0.01762377
p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_unnamed	3.25527636	0.03806228
p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_.g_unnamed	3.27337376	0.03806228
p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae.g_unnamed	3.33428575	0.03083813
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Alcaligenaceae	3.12415702	0.0206123
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Alcaligenaceae.g_Achromobacter	3.12632869	0.03349825
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Comamonas	3.4325653	0.00643601
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Leptothrix	3.45596316	0.01712047
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamonadaceae.g_Limnohabitans	3.52415887	0.00574854
p_Proteobacteria.c_Betaproteobacteria.o_Neisseriales.f_Neisseriaceae.g_Chromobacterium	4.53153709	0.03958335
p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.g_Zoogloea	3.8046315	0.00262014
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales	3.43441497	0.02623449
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales.f_Aeromonadaceae	3.43444236	0.02623449
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales.f_Aeromonadaceae.g_unnamed	3.43431929	0.02623449

p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Citrobacter	3.50914288	0.00104064
Environment: natural water		
p_Acidobacteria.c_Acidobacteriia	3.15621963	0.04543871
p_Acidobacteria.c_Acidobacteriia.o_Acidobacteriales	3.15669819	0.04543871
p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Cellulomondaceae	4.9385145	0.03026916
p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Cellulomonadaceae.g_Cellulomonas	4.9385145	0.03026916
p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Mycobacteriaceae	3.20887636	0.0087242
p_Actinobacteria.c_Actinobacteria.o_Actinomycetales.f_Mycobacteriaceae.g_Mycobacterium	3.20887636	0.0087242
p_Bacteroidetes.c_Bacteroidia	3.53277714	0.02853167
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales	3.53277714	0.02853167
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae	3.50054754	0.03899318
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Paludibacter	3.46854243	0.00706794
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Hyphomicrobiaceae.g_Devosia	3.19612105	0.03963216
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae.g_Rhodoblastus	3.77776678	0.00402317
p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Acetobacteraceae.g_Rhodovarius	3.69724162	0.00132237
p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.g_Propionivibrio	3.15897575	0.02539737
p_Proteobacteria.c_Gammaproteobacteria.o_Xanthomonadales.f_Sinobacteraceae.g_Nevskia	4.05661357	0.02122905

p_Verrucomicrobia.c__Spartobacteria	3.20106244	0.0129086
p_Verrucomicrobia.c__Spartobacteria_o__Chthoniobacterales_	3.19892386	0.0129086
p_Verrucomicrobia.c__Spartobacteria_o__Chthoniobacterales.f__Chthoniobacteraceae_	3.20263006	0.0129086
p_Verrucomicrobia.c__Spartobacteria_o__Chthoniobacterales.f__Chthoniobacteraceae.g_	2.96968967	0.00206045
p_Verrucomicrobia.c__Spartobacteria_o__Chthoniobacterales.f__Chthoniobacteraceae.g_heteroC45_4W	3.16715561	0.00533662
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae.g_Luteolibacter	3.24672827	0.00013744
Environment: pre-sterilized water		
p_Bacteroidetes.c_Flavobacteriia	4.45309118	0.03557445
p_Bacteroidetes.c_Flavobacteriia.o_Flavobacteriales	4.45309118	0.03557445
p_Bacteroidetes.c_Flavobacteriia.o_Flavobacteriales.f__Weeksellaceae_	4.48192293	0.00509839
p_Bacteroidetes.c_Flavobacteriia.o_Flavobacteriales.f__Weeksellaceae.g_Chryseobacterium	4.48147758	0.03066667
p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae	3.35671321	0.02703064
p_Firmicutes.c_Bacilli.o_Bacillales.f_Bacillaceae.g_Bacillus	3.3462405	0.02703064
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales	4.86931178	0.01136306
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae	4.35057184	0.00901134
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae.g_Pleomorphomo0s	3.98520666	0.0006478
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Xanthobacteraceae	4.53251388	0.01530137

p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Burkholderiaceae	4.18968901	0.00660002
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Burkholderiaceae.g_Pandoraea	4.14888715	0.0088624
p_Proteobacteria.c_Betaproteobacteria.o_Neisseriales	4.54429768	0.02942242
p_Proteobacteria.c_Betaproteobacteria.o_Neisseriales.f_Neisseriaceae	4.54429768	0.02942242
p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales	3.21877082	0.01262798
p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae	3.21877082	0.01262798
p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Desulfovibrio	3.21877082	0.01262798
Tadpoles: natural water + arthropods		
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae	5.15091442	0.03080508
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Dysgonomonas	4.08693868	0.0010301
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Rikenella	3.52994675	0.00012998
p_Firmicutes	4.75578221	0.00100699
p_Firmicutes.c_Clostridia	4.55641545	0.00368446
p_Firmicutes.c_Clostridia.o_Clostridiales	4.55652375	0.00368446
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Mogibacteriaceae	3.46653508	0.00141015
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Christensenellaceae	3.15553415	0.00092484
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Christensenellaceae.g_Christensenella	3.16986484	5.38E-05

p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae	3.15965032	5.46E-05
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Pseudoramibacter_Eubacterium	3.16050386	5.46E-05
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Robinsoniella	2.983951	0.00025076
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptostreptococcaceae.g_Clostridium	3.07645127	0.00168545
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae	4.28137718	0.00327146
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Clostridium	2.92899203	0.00555772
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Oscillospira	4.227966	0.00427501
p_Firmicutes.c_Erysipelotrichi	4.47723231	9.01E-05
p_Firmicutes.c_Erysipelotrichi.o_Erysipelotrichales	4.47723231	9.01E-05
p_Firmicutes.c_Erysipelotrichi.o_Erysipelotrichales.f_Erysipelotrichaceae	4.47723231	9.01E-05
p_Firmicutes.c_Erysipelotrichi.o_Erysipelotrichales.f_Erysipelotrichaceae.g__Eubacterium	4.4073819	0.0002831
p_Verrucomicrobia.c_Verrucomicrobiae	4.61240976	0.01565903
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales	4.61241479	0.01565903
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae	4.61242128	0.01565903
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae.g_Akkermansia	4.61378404	0.00044604
Tadpoles: Pre-sterilized water + arthropods		
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae	5.23062233	0.0007421

p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides	5.23062233	0.0007421
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae	3.51779618	0.00237783
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiaceae.g_Clostridium	3.54056947	0.0016225
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Peptostreptococcaceae.g__Clostridium	2.82165367	0.00643789
p_Proteobacteria	4.61910198	0.02812315
p_Proteobacteria.c_Gammaproteobacteria	4.82599483	0.00020861
p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales	4.76269263	0.00035978
p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae	4.76269263	0.00035978
p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Citrobacter	4.48610072	0.00965035
Tadpoles: natural water		
p_Acidobacteria	2.680587	0.00203741
p_Acidobacteria.c_Acidobacteriia	3.09972892	0.01308196
p_Acidobacteria.c_Acidobacteriia.o_Acidobacteriales	3.11425952	0.01308196
p_Acidobacteria.c_Acidobacteriia.o_Acidobacteriales.f_Koribacteraceae	3.2915923	0.04866697
p_Acidobacteria.c_Acidobacteriia.o_Acidobacteriales.f_Koribacteraceae.g_CandidatusKoribacter	3.37502932	0.04866697
p_Acidobacteria.c_Holophagae	2.77699663	0.00986874
p_Acidobacteria.c_Holophagae.o_Holophagales	2.77843765	0.00986874

p_Acidobacteria.c_Holophagae.o_Holophagales.f_Holophagaceae	2.80302423	0.00986874
p_Acidobacteria.c_Holophagae.o_Holophagales.f_Holophagaceae.g_unnamed	2.8061342	0.00986874
p_Acidobacteria.c_Solibacteres	3.33221588	0.01308196
p_Acidobacteria.c_Solibacteres.o_Solibacterales	3.37161651	0.01308196
p_Acidobacteria.c_Solibacteres.o_Solibacterales.f_unnamed	3.34478244	0.04866697
p_Acidobacteria.c_Solibacteres.o_Solibacterales.f.g_unnamed	3.35490348	0.04866697
p_Armatimonadetes	2.42948243	0.01312251
p_Armatimonadetes.c__Fimbriimonadia__	2.58847666	0.01312251
p_Armatimonadetes.c__Fimbriimonadia_.o__Fimbriimonadales__	2.6303724	0.01312251
p_Armatimonadetes.c__Fimbriimonadia_.o__Fimbriimonadales_.f__Fimbriimonadaceae	2.59656453	0.01312251
p_Armatimonadetes.c__Fimbriimonadia_.o__Fimbriimonadales_.f__Fimbriimonadaceae.g_unnamed	2.86869632	0.04866697
p_Armatimonadetes.c__Fimbriimonadia_.o__Fimbriimonadales_.f__Fimbriimonadaceae.g_Fimbriimonas	3.18469156	0.01304148
p_Bacteroidetes.c__Saprospirae__	2.77841739	0.00084589
p_Bacteroidetes.c__Saprospirae_.o__Saprospirales	2.78354792	0.00084589
p_Bacteroidetes.c__Saprospirae_.o__Saprospirales.f_unnamed	3.52670916	0.01292048
p_Bacteroidetes.c__Saprospirae_.o__Saprospirales.f_unnamed.g_unnamed	3.31848671	0.01292048
p_Bacteroidetes.c__Saprospirae_.o__Saprospirales.f_Chitinophagaceae	2.76880091	0.00084527

p_Bacteroidetes.c__Saprospirae.o__Saprospirales.f_Chitinophagaceae.g_unnamed	2.68395297	0.00300348
p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Paludibacter	2.87216971	0.00202291
p_Bacteroidetes.c_Sphingobacteriia.o_Sphingobacteriales.f_unnamed	3.05415402	0.00118135
p_Bacteroidetes.c_Sphingobacteriia.o_Sphingobacteriales.f_.g_unnamed	3.05608066	0.00118135
p_Chlamydiae	2.5894883	0.01070885
p_Chlamydiae.c_Chlamydiia	2.58762965	0.01070885
p_Chlamydiae.c_Chlamydiia.o_Chlamydiales	2.59137559	0.01070885
p_Firmicutes.c_Clostridia.o_Clostridiales.f_unnamed	2.76983152	0.04845753
p_Firmicutes.c_Clostridia.o_Clostridiales.f__Mogibacteriaceae_.g_Anaerovorax	3.41967106	0.00292731
p_Firmicutes.c_Clostridia.o_Clostridiales.f_.g_unnamed	2.77230453	0.04845753
p_Firmicutes.c_Clostridia.o_Clostridiales.f_Christensenellaceae.g_unnamed	2.76637057	0.00319859
p_Lentisphaerae	2.76153073	0.00072154
p_Lentisphaerae.c__Lentisphaeria	2.76168786	0.00072154
p_Lentisphaerae.c__Lentisphaeria_.o_Victivallales	2.76155639	0.00072154
p_Lentisphaerae.c__Lentisphaeria_.o_Victivallales.f_Victivallaceae	2.76171567	0.00072154
p_Lentisphaerae.c__Lentisphaeria_.o_Victivallales.f_Victivallaceae.g_Victivallis	2.81814709	0.00072154
p_Planctomycetes.c_Planctomycetia.o_Gemmatales.f_Gemmataceae	2.83845999	0.03946682

p_Planctomycetes.c_Planctomycetia.o_Gemmatales.f_Gemmataceae.g_Gemmata	2.85890208	0.0428893
p_Planctomycetes.c_Planctomycetia.o_Planctomycetales	3.10947014	0.01221899
p_Planctomycetes.c_Planctomycetia.o_Planctomycetales.f_Planctomycetaceae	3.11568079	0.01221899
p_Planctomycetes.c_Planctomycetia.o_Planctomycetales.f_Planctomycetaceae.g_Planctomyces	3.09231089	0.01221899
p_Proteobacteria.c_Alphaproteobacteria	3.35325477	0.0079725
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales	2.84091367	0.03103242
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales.f_Caulobacteraceae	2.80487757	0.03103242
p_Proteobacteria.c_Alphaproteobacteria.o_Caulobacterales.f_Caulobacteraceae.g_unnamed	2.57211401	0.0032145
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales	3.266465	0.00356453
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae	3.11051586	0.00179007
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae.g_unnamed	2.90361283	0.00158797
p_Proteobacteria.c_Alphaproteobacteria.o_Rhizobiales.f_Methylocystaceae.g_Rhodoblastus	2.96183796	0.00583233
p_Proteobacteria.c_Alphaproteobacteria.o_Rhodospirillales.f_Acetobacteraceae	2.95090983	0.03514347
p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomorphales.f_Sphingomorphaceae.g_Novosphingobium	2.84855139	0.00233623
p_Proteobacteria.c_Betaproteobacteria	4.09084642	0.00227011
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_unnamed	3.12760482	0.01308196
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_unnamed.g_unnamed	3.12698095	0.01308196

p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamo0daceae.g_Limnohabitans	3.45285745	0.02699834
p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Comamo0daceae.g_Rhodoferax	3.01306561	0.04873686
p_Proteobacteria.c_Betaproteobacteria.o_Procabbacteriales	2.83580976	0.00310052
p_Proteobacteria.c_Betaproteobacteria.o_Procabbacteriales.f_Procabbacteriaceae	2.83366375	0.00310052
p_Proteobacteria.c_Betaproteobacteria.o_Procabbacteriales.f_Procabbacteriaceae.g_unnamed	2.79694699	0.00817138
p_Proteobacteria.c_Betaproteobacteria.o_Procabbacteriales.f_Procabbacteriaceae.g_Leeia	2.85171128	0.01110209
p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.g_Azospira	3.26818294	0.01304148
p_Proteobacteria.c_Betaproteobacteria.o_Rhodocyclales.f_Rhodocyclaceae.g_Propionivibrio	2.7432491	0.00321981
p_Proteobacteria.c_Deltaproteobacteria.o_Myxococcales	2.79971286	0.01151971
p_Proteobacteria.c_Deltaproteobacteria.o_Myxococcales.f_unnamed	2.70014152	0.00214654
p_Proteobacteria.c_Deltaproteobacteria.o_Myxococcales.f_g_unnamed	2.69175373	0.00214654
p_Verrucomicrobia.c__Pedosphaerae	2.80300218	0.00014718
p_Verrucomicrobia.c__Pedosphaerae.o__Pedosphaerales	2.8029989	0.00014718
p_Verrucomicrobia.c__Pedosphaerae.o__Pedosphaerales.f_auto67_4W	3.25981366	0.0007102
p_Verrucomicrobia.c__Pedosphaerae.o__Pedosphaerales.f_auto67_4W.g_unnamed	3.28167764	0.0007102
p_Verrucomicrobia.c__Pedosphaerae.o__Pedosphaerales.f_Ellin515	3.49812478	0.04845753
p_Verrucomicrobia.c__Pedosphaerae.o__Pedosphaerales.f_Ellin515.g_unnamed	3.46241324	0.04845753

p_Verrucomicrobia.c__Spartobacteria	2.87702549	0.00051761
p_Verrucomicrobia.c__Spartobacteria.o__Chthoniobacterales	2.88873682	0.00051761
p_Verrucomicrobia.c__Spartobacteria.o__Chthoniobacterales.f__Chthoniobacteraceae	2.88780017	0.00051761
p_Verrucomicrobia.c__Spartobacteria.o__Chthoniobacterales.f__Chthoniobacteraceae.g_unnamed	3.10836817	0.01310222
p_Verrucomicrobia.c__Spartobacteria.o__Chthoniobacterales.f__Chthoniobacteraceae.g_heteroC45_4W	2.44775521	0.00014801
p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae.g_unnamed	3.62361245	0.01304148
Tadpoles: pre-sterilized water		
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales	4.13709923	0.02349047
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales.f_Aeromonadaceae	4.13709923	0.02349047
p_Proteobacteria.c_Gammaproteobacteria.o_Aeromonadales.f_Aeromonadaceae.g_unnamed	4.13614069	0.02349047
p_TM6	2.66181968	0.00134607
p_TM6.c_SJA_4	2.66639088	0.00134607
p_TM6.c_SJA_4.o_unnamed	2.6866994	0.00134607
p_TM6.c_SJA_4.o.f_unnamed	2.64678622	0.00134607
p_TM6.c_SJA_4.o.f.g_unnamed	2.6757648	0.00134607
