

Supplemental Material for: Plant-derived benzoxazinoids act as antibiotics and shape bacterial communities

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Tables

Table S1. Phylogenetic signal lambda

Class	Order	Family	lambda	p.value
All - All				
All	All	All	0.763	0.0004 * *
Gram Negative - Proteobacteria				
All	All	All	0.817	0.0017 * *
Alpha	All	All	0	0.9998
Alpha	Rhizobiales	All	0	1.0000
Alpha	Rhizobiales	Phyllobacteriaceae	0	1.0000
Alpha	Rhizobiales	Rhizobiaceae	0.275	0.8837
Beta	All	All	1.034	0.0036 * *
Beta	Burkholderiales	All	0.147	0.6171
Beta	Burkholderiales	Comamonadaceae	0	1.0000
Gamma	All	All	1	0.0000 * *
Gamma	Xanthomonadales	All	1	0.0001 * *
Gram Positive - Actinobacteria				
Actinomycetia	Actinomycetales	All	0	1.0000
Actinomycetia	Actinomycetales	Intrasporangiaceae	0.98	0.2730
Actinomycetia	Actinomycetales	Microbacteriaceae	1.054	0.3751
Actinomycetia	Actinomycetales	Nocardoidaceae	0	1.0000
Actinomycetia	All	All	0	1.0000
Gram Positive - All				
All	All	All	0.421	0.0325 *
Gram Positive - Firmicutes				
Bacilli	All	All	0	1.0000

Table S2. Syncom strains

Strain	Genus	Family	Order	Class	Phylum
Mixed					
Root70	Acidovorax	Comamonadaceae	Burkholderiales	Betaproteobacteria	Proteobacteria
Root236	Aeromicrobium	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root100	Aminobacter	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root239	Bacillus	Bacillaceae	Bacillales	Bacilli	Firmicutes
Root483D1	Bosea	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root342	Caulobacter	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria
Root137	Cellulomonas	Cellulomonadaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root1480D1	Duganella	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root231	Ensifer	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root420	Flavobacterium	Flavobacteriaceae	Flavobacteriales	Bacteroidia	Bacteroidetes
Root268	Hoeflea	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root209	Hydrogenophaga	Comamonadaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root107	Kitasatospora	Streptomycetaceae	Streptomycetales	Actinomycetia	Actinobacteria
Root96	Lysobacter	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root133	Massilia	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root172	Mesorhizobium	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root180	Microbacterium	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root1257	Nocardioides	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root444D2	Paenibacillus	Paenibacillaceae	Paenibacillales	Bacilli	Firmicutes
Root101	Phycococcus	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root1204	Rhizobium	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root214	Sphingopyxis	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	Proteobacteria
Tolerant					
Root217	Acidovorax	Comamonadaceae	Burkholderiales	Betaproteobacteria	Proteobacteria
Root1280	Acinetobacter	Moraxellaceae	Pseudomonadales	Gammaproteobacteria	Proteobacteria
Root495	Aeromicrobium	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root123D2	Afipia	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Soil762	Arthrobacter	Micrococcaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root239	Bacillus	Bacillaceae	Bacillales	Bacilli	Firmicutes
Root565	Bordetella	Alcaligenaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root381	Bosea	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1472	Caulobacter	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria
Root919	Cupriavidus	Burkholderiaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root685	Devosia	Hyphomicrobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1312	Ensifer	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1212	Hoeflea	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Soil729	Knoellia	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root112D2	Leifsonia	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root133	Massilia	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root102	Mesorhizobium	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1272	Methylibium	Burkholderiales	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root166	Microbacterium	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root135	Mycobacterium	Mycobacteriaceae	Mycobacteriales	Actinomycetia	Actinobacteria
Root157	Nitrateductor	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root79	Nocardioides	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root189	Noviherbaspirillum	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root918	Oerskovia	Cellulomonadaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root700	Phenylobacterium	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria

Root9	Pseudomonas	Pseudomonadaceae	Pseudomonadales	Gammaproteobacteria	Proteobacteria
Root1203	Rhizobium	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root561	Rhodanobacter	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root66D1	Streptomyces	Streptomycetaceae	Streptomycetales	Actinomycetia	Actinobacteria
Root85	Terrabacter	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Soil756	Tetrasphaera	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Sensitive					
Root70	Acidovorax	Comamonadaceae	Burkholderiales	Betaproteobacteria	Proteobacteria
Root236	Aeromicrobium	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root100	Aminobacter	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Soil531	Bacillus	Bacillaceae	Bacillales	Bacilli	Firmicutes
Root483D1	Bosea	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root137	Cellulomonas	Cellulomonadaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root142	Ensifer	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root935	Flavobacterium	Flavobacteriaceae	Flavobacteriales	Bacteroidia	Bacteroidetes
Root209	Hydrogenophaga	Comamonadaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root983	Lysobacter	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root172	Mesorhizobium	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root61	Microbacterium	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root240	Nocardioides	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Soil750	Paenibacillus	Paenibacillaceae	Paenibacillales	Bacilli	Firmicutes
Root1277	Phenylobacterium	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria
Root563	Phycococcus	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root274	Rhizobium	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root214	Sphingopyxis	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	Proteobacteria
Soil811	Terrabacter	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root434	Variovorax	Comamonadaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Random					
Root217	Acidovorax	Comamonadaceae	Burkholderiales	Betaproteobacteria	Proteobacteria
Root1280	Acinetobacter	Moraxellaceae	Pseudomonadales	Gammaproteobacteria	Proteobacteria
Root344	Aeromicrobium	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root123D2	Afipia	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1464	Agromyces	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Soil736	Arthrobacter	Micrococcaceae	Actinomycetales	Actinomycetia	Actinobacteria
Soil531	Bacillus	Bacillaceae	Bacillales	Bacilli	Firmicutes
Root565	Bordetella	Alcaligenaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root381	Bosea	Bradyrhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root342	Caulobacter	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria
Root137	Cellulomonas	Cellulomonadaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root919	Cupriavidus	Burkholderiaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root105	Devosia	Hyphomicrobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root1480D1	Duganella	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root1252	Ensifer	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root420	Flavobacterium	Flavobacteriaceae	Flavobacteriales	Bacteroidia	Bacteroidetes
Root268	Hoeflea	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Soil728	Janibacter	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root107	Kitasatospora	Streptomycetaceae	Streptomycetales	Actinomycetia	Actinobacteria
Soil729	Knoellia	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root1293	Leifsonia	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root604	Lysobacter	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root133	Massilia	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root1471	Mesorhizobium	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria

Root1272	Methylibium	Burkholderiales	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root322	Microbacterium	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria
Soil538	Mycobacterium	Mycobacteriaceae	Mycobacteriales	Actinomycetia	Actinobacteria
Root157	Nitratireductor	Phyllobacteriaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Root136	Nocardia	Nocardiaceae	Mycobacteriales	Actinomycetia	Actinobacteria
Root1257	Nocardioides	Nocardioidaceae	Propionibacteriales	Actinomycetia	Actinobacteria
Root189	Noviherbaspirillum	Oxalobacteraceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root22	Oerskovia	Cellulomonadaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root52	Paenibacillus	Paenibacillaceae	Paenibacillales	Bacilli	Firmicutes
Root700	Phenylobacterium	Caulobacteraceae	Caulobacterales	Alphaproteobacteria	Proteobacteria
Root563	Phycococcus	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root329	Pseudomonas	Pseudomonadaceae	Pseudomonadales	Gammaproteobacteria	Proteobacteria
Root65	Pseudoxanthomonas	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root29	Rhizobacter	Pseudomonadaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root708	Rhizobium	Rhizobiaceae	Rhizobiales	Alphaproteobacteria	Proteobacteria
Soil772	Rhodanobacter	Xanthomonadaceae	Xanthomonadales	Gammaproteobacteria	Proteobacteria
Root1294	Sphingomonas	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	Proteobacteria
Root214	Sphingopyxis	Sphingomonadaceae	Sphingomonadales	Alphaproteobacteria	Proteobacteria
Root1310	Streptomyces	Streptomycetaceae	Streptomycetales	Actinomycetia	Actinobacteria
Soil811	Terrabacter	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Soil756	Tetrasphaera	Intrasporangiaceae	Actinomycetales	Actinomycetia	Actinobacteria
Root411	Variovorax	Comamonadaceae	Burkholderiales	Gammaproteobacteria	Proteobacteria
Root332	Yonghaparkia	Microbacteriaceae	Actinomycetales	Actinomycetia	Actinobacteria

Table S3. PERMANOVA

term	Df	SumsOfSqs	MeanSqs	F.Model	R2	p.value
Random						
Timepoint	3	1.1953	0.3984	14.7627	0.3100	0.001 * *
Treatment	2	1.5522	0.7761	28.7561	0.4026	0.001 * *
Timepoint:Treatment	6	0.1363	0.0227	0.8420	0.0354	0.594
Residuals	36	0.9716	0.0270	NA	0.2520	NA
Total	47	3.8555	NA	NA	1.0000	NA
Tolerant						
Timepoint	3	0.9527	0.3176	10.9268	0.3293	0.001 * *
Treatment	2	0.6252	0.3126	10.7561	0.2161	0.001 * *
Timepoint:Treatment	6	0.2687	0.0448	1.5410	0.0929	0.098
Residuals	36	1.0463	0.0291	NA	0.3617	NA
Total	47	2.8929	NA	NA	1.0000	NA
Mixed						
Timepoint	3	0.1909	0.0636	1.2030	0.0199	0.296
Treatment	2	7.2278	3.6139	68.3271	0.7544	0.001 * *
Timepoint:Treatment	6	0.2575	0.0429	0.8115	0.0269	0.621
Residuals	36	1.9041	0.0529	NA	0.1987	NA
Total	47	9.5803	NA	NA	1.0000	NA
Sensitive						
Timepoint	3	0.0395	0.0132	1.9094	0.0631	0.130
Treatment	2	0.2605	0.1303	18.9085	0.4166	0.001 * *
Timepoint:Treatment	6	0.0774	0.0129	1.8728	0.1238	0.081
Residuals	36	0.2480	0.0069	NA	0.3966	NA
Total	47	0.6254	NA	NA	1.0000	NA

Table S4. PERMANOVA comparing only two treatments

term	Df	SumsOfSqs	MeanSqs	F.Model	R2	p.value
Random - APO						
Treatment	1	1.0477	1.0477	18.1201	0.3766	0.001 * *
Residuals	30	1.7346	0.0578	NA	0.6234	NA
Total	31	2.7823	NA	NA	1.0000	NA
Random - BOA						
Treatment	1	0.0412	0.0412	0.8416	0.0273	0.435
Residuals	30	1.4680	0.0489	NA	0.9727	NA
Total	31	1.5092	NA	NA	1.0000	NA
Tolerant - APO						
Treatment	1	0.4742	0.4742	8.3739	0.2182	0.001 * *
Residuals	30	1.6988	0.0566	NA	0.7818	NA
Total	31	2.1730	NA	NA	1.0000	NA
Tolerant - BOA						
Treatment	1	0.0617	0.0617	1.5378	0.0488	0.197
Residuals	30	1.2028	0.0401	NA	0.9512	NA
Total	31	1.2645	NA	NA	1.0000	NA
Mixed - APO						
Treatment	1	5.1799	5.1799	70.8788	0.7026	0.001 * *
Residuals	30	2.1924	0.0731	NA	0.2974	NA
Total	31	7.3724	NA	NA	1.0000	NA
Mixed - BOA						
Treatment	1	0.0577	0.0577	4.6442	0.1341	0.020 *
Residuals	30	0.3726	0.0124	NA	0.8659	NA
Total	31	0.4303	NA	NA	1.0000	NA
Sensitive - APO						
Treatment	1	0.0229	0.0229	20.8918	0.4105	0.001 * *
Residuals	30	0.0329	0.0011	NA	0.5895	NA
Total	31	0.0559	NA	NA	1.0000	NA
Sensitive - BOA						
Treatment	1	0.1120	0.1120	10.3315	0.2562	0.003 * *
Residuals	30	0.3251	0.0108	NA	0.7438	NA
Total	31	0.4370	NA	NA	1.0000	NA

Table S5. ANOVA: Observed taxa

term	df	sumsq	meansq	statistic	p.value
Random					
Treatment	2	0.05101594	0.025507971	4.1016798	2.484563e-02 *
Timepoint	3	0.25046221	0.083487403	13.4247681	4.907087e-06 * *
Treatment:Timepoint	6	0.01463861	0.002439768	0.3923145	8.790628e-01
Residuals	36	0.22388070	0.006218908	NA	NA
Tolerant					
Treatment	2	0.21585880	0.107929398	13.1512316	5.156453e-05 * *
Timepoint	3	0.32902545	0.109675150	13.3639521	5.118265e-06 * *
Treatment:Timepoint	6	0.03393162	0.005655270	0.6890965	6.596909e-01
Residuals	36	0.29544444	0.008206790	NA	NA
Mixed					
Treatment	2	2.32954036	1.164770180	41.3453120	4.720082e-10 * *
Timepoint	3	0.35051038	0.116836792	4.1473019	1.268430e-02 *
Treatment:Timepoint	6	0.31516138	0.052526897	1.8645231	1.140745e-01
Residuals	36	1.01418334	0.028171759	NA	NA
Sensitive					
Treatment	2	0.46631836	0.233159182	30.3635644	1.877482e-08 * *
Timepoint	3	0.07701343	0.025671142	3.3430696	2.974336e-02 *
Treatment:Timepoint	6	0.09728286	0.016213809	2.1114718	7.590701e-02
Residuals	36	0.27644088	0.007678913	NA	NA

Table S6. Observed diversity means and pairwise comparisons

Treatment	estimate	95% CI	Group ¹
Random - 24h			
BOA	1.148	[1.068 - 1.228]	a
APO	1.216	[1.136 - 1.296]	a
Control	1.224	[1.144 - 1.304]	a
Random - 48h			
BOA	1.221	[1.141 - 1.301]	a
APO	1.282	[1.202 - 1.362]	a
Control	1.297	[1.217 - 1.377]	a
Random - 72h			
APO	1.329	[1.249 - 1.409]	a
BOA	1.349	[1.269 - 1.429]	a
Control	1.435	[1.355 - 1.515]	a
Random - 96h			
BOA	1.328	[1.248 - 1.408]	a
APO	1.351	[1.271 - 1.431]	a
Control	1.407	[1.327 - 1.487]	a
Tolerant - 24h			
BOA	0.964	[0.872 - 1.056]	a
Control	0.994	[0.902 - 1.086]	ab
APO	1.125	[1.033 - 1.217]	b
Tolerant - 48h			
Control	1.055	[0.963 - 1.147]	a
BOA	1.145	[1.053 - 1.237]	ab
APO	1.275	[1.183 - 1.367]	b
Tolerant - 72h			
Control	1.128	[1.036 - 1.22]	a
BOA	1.165	[1.073 - 1.257]	ab
APO	1.315	[1.223 - 1.407]	b
Tolerant - 96h			
Control	1.208	[1.117 - 1.3]	a
BOA	1.247	[1.155 - 1.339]	a
APO	1.295	[1.203 - 1.387]	a
Mixed - 24h			
BOA	0.539	[0.368 - 0.709]	a
Control	0.666	[0.496 - 0.836]	ab
APO	0.907	[0.737 - 1.078]	b
Mixed - 48h			
BOA	0.228	[0.057 - 0.398]	a
Control	0.344	[0.174 - 0.514]	a
APO	1.027	[0.856 - 1.197]	b
Mixed - 72h			
BOA	0.250	[0.08 - 0.42]	a

Control	0.423	[0.253 - 0.593]	a
APO	0.739	[0.569 - 0.909]	b
Mixed - 96h			
BOA	0.385	[0.215 - 0.555]	a
Control	0.532	[0.361 - 0.702]	ab
APO	0.814	[0.644 - 0.984]	b
Sensitive - 24h			
APO	0.041	[-0.048 - 0.13]	a
Control	0.210	[0.121 - 0.299]	b
BOA	0.220	[0.131 - 0.309]	b
Sensitive - 48h			
APO	0.044	[-0.045 - 0.133]	a
Control	0.144	[0.055 - 0.233]	a
BOA	0.377	[0.289 - 0.466]	b
Sensitive - 72h			
APO	0.024	[-0.065 - 0.113]	a
Control	0.057	[-0.032 - 0.146]	a
BOA	0.308	[0.22 - 0.397]	b
Sensitive - 96h			
APO	0.021	[-0.068 - 0.109]	a
Control	0.043	[-0.045 - 0.132]	ab
BOA	0.174	[0.085 - 0.262]	b

¹Different letters indicate significant differences within one Syncom / Timepoint combination (alpha = 0.05), Tukey adjusted

Table S7. ANOVA: Shannon Diversity

term	df	sumsq	meansq	statistic	p.value
Random					
Treatment	2	0.04965670	0.024828351	3.9818448	2.740000e-02 *
Timepoint	3	0.25834405	0.086114684	13.8106353	3.764333e-06 * *
Treatment:Timepoint	6	0.02053069	0.003421782	0.5487681	7.675710e-01
Residuals	36	0.22447400	0.006235389	NA	NA
Tolerant					
Treatment	2	0.20619734	0.103098670	11.8582100	1.106005e-04 * *
Timepoint	3	0.31193275	0.103977584	11.9593009	1.392757e-05 * *
Treatment:Timepoint	6	0.03231331	0.005385552	0.6194357	7.133662e-01
Residuals	36	0.31299430	0.008694286	NA	NA
Mixed					
Treatment	2	2.20186153	1.100930766	37.4317591	1.611570e-09 * *
Timepoint	3	0.31214721	0.104049071	3.5376791	2.413246e-02 *
Treatment:Timepoint	6	0.31328626	0.052214376	1.7752942	1.320402e-01
Residuals	36	1.05882033	0.029411676	NA	NA
Sensitive					
Treatment	2	0.64164868	0.320824339	33.1316491	6.894276e-09 * *
Timepoint	3	0.09113328	0.030377760	3.1371226	3.717840e-02 *
Treatment:Timepoint	6	0.12710073	0.021183455	2.1876233	6.692054e-02
Residuals	36	0.34859950	0.009683319	NA	NA

Table S8. Shannon diversity means and pairwise comparisons

Treatment	estimate	95% CI	Group ¹
Random - 24h			
BOA	1.130	[1.05 - 1.21]	a
Control	1.224	[1.144 - 1.305]	a
APO	1.225	[1.145 - 1.305]	a
Random - 48h			
BOA	1.235	[1.155 - 1.315]	a
APO	1.282	[1.202 - 1.362]	a
Control	1.296	[1.216 - 1.376]	a
Random - 72h			
APO	1.329	[1.249 - 1.409]	a
BOA	1.354	[1.274 - 1.435]	a
Control	1.437	[1.357 - 1.517]	a
Random - 96h			
BOA	1.330	[1.25 - 1.41]	a
APO	1.349	[1.269 - 1.429]	a
Control	1.406	[1.326 - 1.486]	a
Tolerant - 24h			
BOA	0.995	[0.9 - 1.09]	a
Control	1.023	[0.928 - 1.117]	a
APO	1.142	[1.047 - 1.236]	a
Tolerant - 48h			
Control	1.071	[0.976 - 1.166]	a
BOA	1.162	[1.067 - 1.256]	ab
APO	1.290	[1.195 - 1.384]	b
Tolerant - 72h			
Control	1.148	[1.053 - 1.242]	a
BOA	1.182	[1.087 - 1.276]	ab
APO	1.333	[1.239 - 1.428]	b
Tolerant - 96h			
Control	1.231	[1.137 - 1.326]	a
BOA	1.263	[1.169 - 1.358]	a
APO	1.317	[1.223 - 1.412]	a
Mixed - 24h			
BOA	0.517	[0.343 - 0.691]	a
Control	0.651	[0.477 - 0.825]	ab
APO	0.917	[0.743 - 1.091]	b
Mixed - 48h			
BOA	0.233	[0.059 - 0.407]	a
Control	0.353	[0.179 - 0.527]	a
APO	1.021	[0.847 - 1.195]	b
Mixed - 72h			
BOA	0.258	[0.084 - 0.432]	a

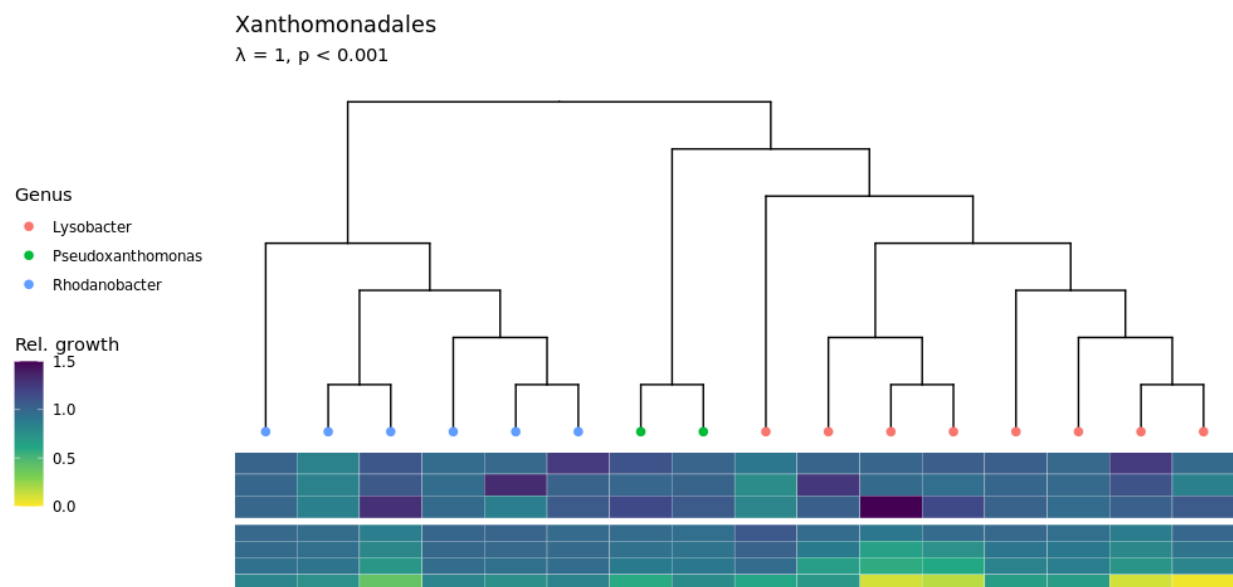
Control	0.443	[0.269 - 0.617]	ab
APO	0.723	[0.549 - 0.897]	b
Mixed - 96h			
BOA	0.402	[0.228 - 0.576]	a
Control	0.555	[0.381 - 0.729]	ab
APO	0.789	[0.615 - 0.962]	b
Sensitive - 24h			
APO	0.043	[-0.057 - 0.143]	a
Control	0.234	[0.134 - 0.334]	b
BOA	0.247	[0.147 - 0.347]	b
Sensitive - 48h			
APO	0.051	[-0.049 - 0.151]	a
Control	0.172	[0.072 - 0.272]	a
BOA	0.439	[0.339 - 0.539]	b
Sensitive - 72h			
APO	0.032	[-0.068 - 0.131]	a
Control	0.073	[-0.027 - 0.173]	a
BOA	0.368	[0.268 - 0.467]	b
Sensitive - 96h			
APO	0.027	[-0.073 - 0.127]	a
Control	0.056	[-0.044 - 0.156]	ab
BOA	0.214	[0.114 - 0.314]	b

¹Different letters indicate significant differences within one Syncom / Timepoint combination (alpha = 0.05), Tukey adjusted

Table S9. Correlation between change in relative abundance and change in growth

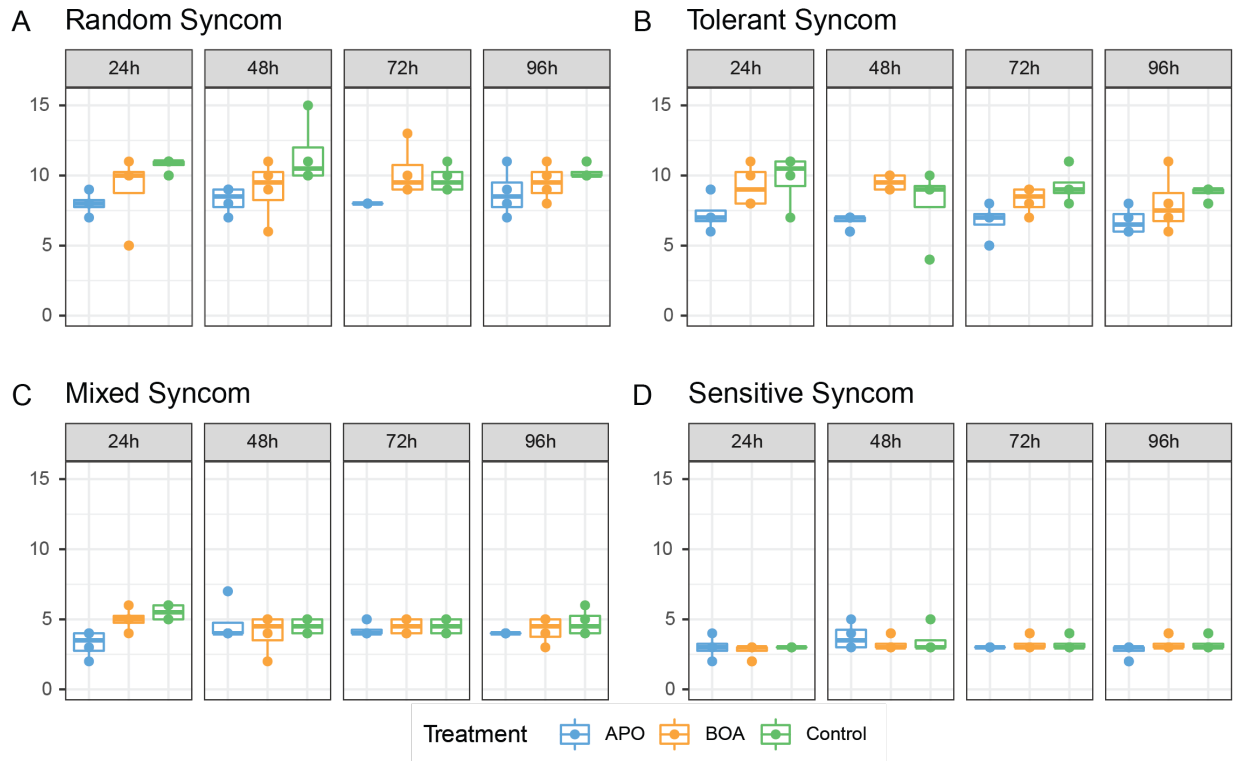
	r2	Treatment
log2FC vs absolute AUC		
	0.01983379	APO
	-0.01052433	BOA
log2FC vs relative AUC		
	0.01071874	APO
	0.01237386	BOA

Supplemental Figure S1



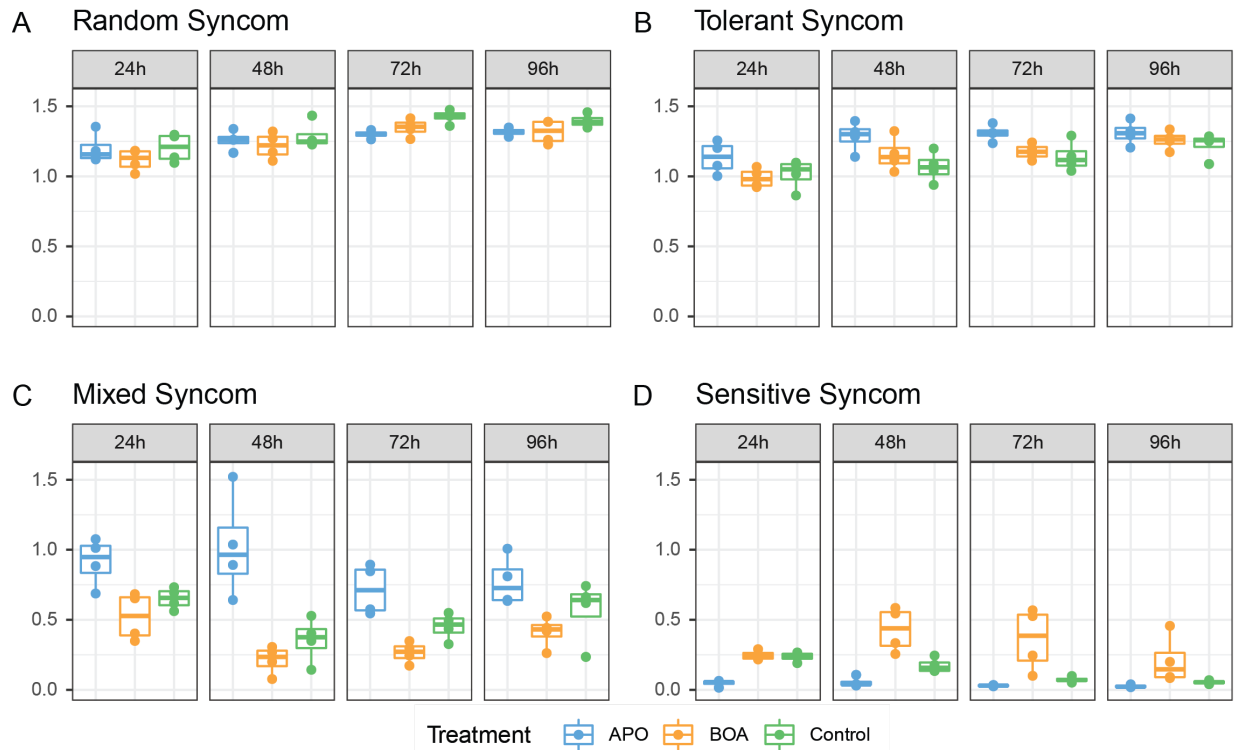
Supplemental Figure S1. Bx sensitivity of Xanthomonadales. Genera belonging to the Order Xanthomonadales are plotted. The tree was constructed from concatenated sequences (see methods). The upper 3 rows of the heatmap display relative growth in 10µM, 50µM and 100µM BOA (top to bottom), the lower four rows of the heatmap relative growth in medium supplemented with 1µM, 5µM, 10µM and 50µM APO.

Supplemental Figure S2



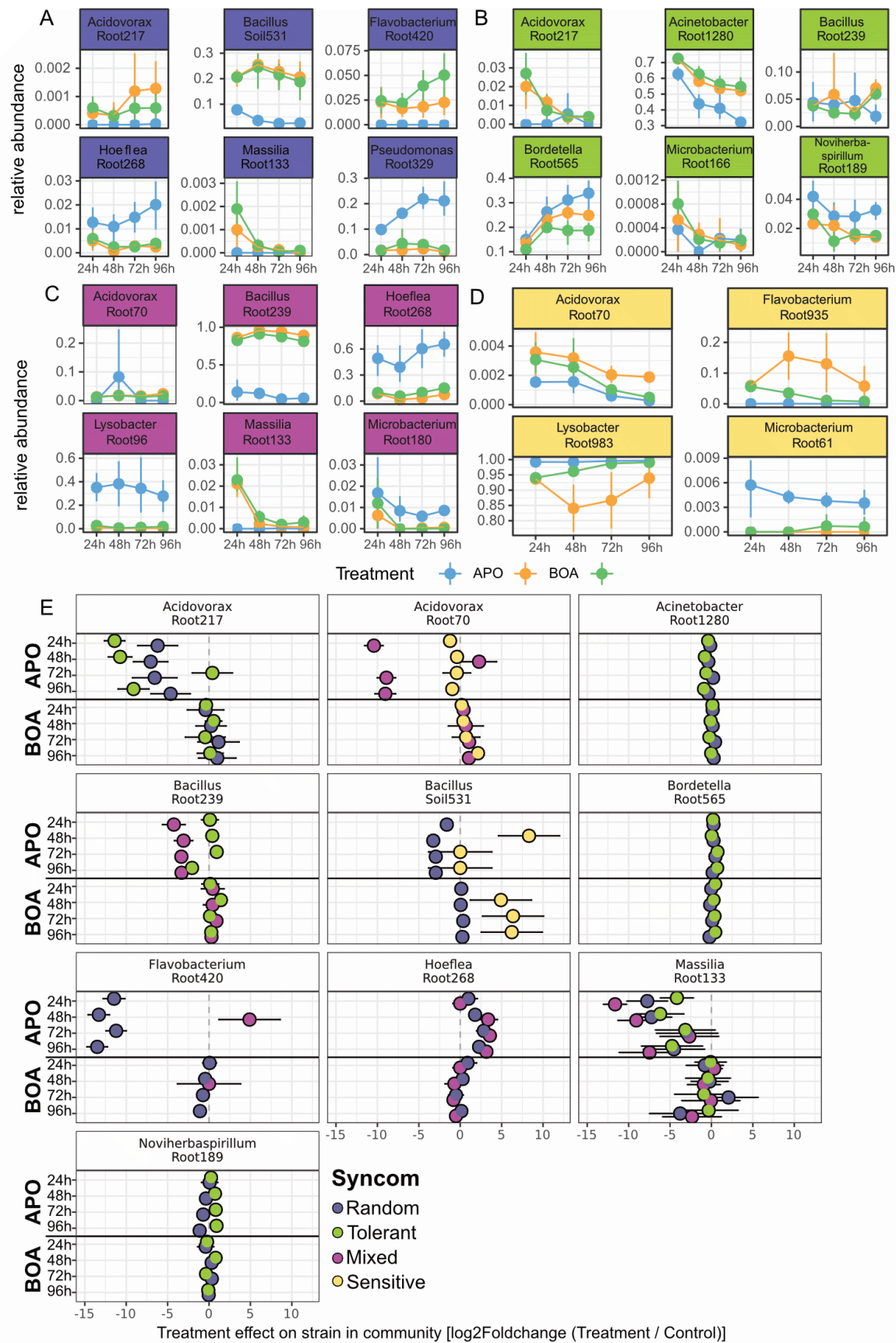
Supplemental Figure S2. Observed alpha diversity. The number of observed bacterial genera of the samples belonging to the four different syncoms (**A-D**) is shown for each time point (facet) and treatment (color). Each sample is plotted as a dot, and box-and-whisker plots show the summary statistics for each treatment / time point combination.

Supplemental Figure S3



Supplemental Figure S3. Shannon diversity indices of the synthetic communities. The Shannon indices of the samples belonging to the four different syncoms (A-D) are shown for each time point (facet) and treatment (color). Each sample is plotted as a dot, and box-and-whisker plots show the summary statistics for each treatment / time point combination.

Supplemental Figure S4



Supplemental Figure S4. Changes in relative abundance by community. A-D The relative abundance over time for different isolates that showed significant differences in relative abundance at at least one timepoint (compared to control). Relative abundance is shown per treatment and timepoint, errorbars indicate 95% CI. **E** Changes in relative abundance per treatment and timepoint for isolates that were found in more than one community. Errorbars indicate s.e. of the log2Foldchange.