

Biological invasions alter environmental microbiomes: a meta-analysis

Antonino Malacrinò, Victoria A. Sadowski, Tvisha K. Martin, Nathalia Cavichioli de Oliveira, Ian J. Brackett, James D. Feller, Kristian J. Harris, Orlando Combata Heredia, Rosa Vescio, Alison E. Bennett

S4 Table. Results from two different the linear mixed-effects model testing the abundance of each bacterial family against *sample type* (invaded or control), *organism* (plant, mammal, mussel), and their interactions. In Model 1 we included *studyID* as random factor, while in Model 2 we included both *studyID* and *environment* (soil or water) as random factors.

	Model 1*		Model 2 [§]	
Family	χ^2	P	χ^2	P
Burkholderiaceae	0.22	0.63	0.18	0.67
Sporichthyaceae	0.02	0.86	0.03	0.86
Chthoniobacteraceae	17.28	<0.001	17.28	<0.001
Chitinophagaceae	27.77	<0.001	27.78	<0.001
Gemmataceae	15.04	<0.001	17.42	<0.001
Solibacteraceae (Subgroup 3)	30.75	<0.001	30.68	<0.001
Gemmatimonadaceae	86.45	<0.001	86.46	<0.001
Xanthobacteraceae	1.23	0.26	1.22	0.27
Ord. Tepidisphaerales	3.80	0.05	3.76	0.05
Sphingomonadaceae	14.20	<0.001	14.21	<0.001
Pyrinomonadaceae	0.47	0.49	0.47	0.49
Pedosphaeraceae	12.09	<0.001	12.10	<0.001
Solirubrobacteraceae	10.36	<0.01	10.27	<0.001
Acetobacteraceae	33.30	<0.001	33.30	<0.001
Ord. Solirubrobacterales	2.74	0.09	2.71	0.10
Blastocatellaceae	32.42	<0.001	32.43	<0.001
Pirellulaceae	41.78	<0.001	41.10	<0.001
Beijerinckiaceae	4.01	0.05	4.01	0.05
Haliangiaceae	2.32	0.12	2.29	0.13
Micromonosporaceae	6.17	0.01	6.12	0.01
Nitrosomonadaceae	5.67	0.02	5.69	0.02

*lmer(Abundance ~ Sample_type * (1|Study_ID) * (1|Invasive_species))

§lmer(Abundance ~ Sample_type * (1|Study_ID) * (1|Environment) * (1|Invasive_species))