Table 1: Model summaries for the phylogenetic mixed models of cooperative traits when including sporulation scores and relative abundance as predictors

Model	Structure	Effect	Posterior mean	CI95%
Siderophores				
	Fixed effect	Intercept	-10.725	-16.2...
		Mean relatedness	1.432	0.243...
		Mean relative abundance	0.415	-3.378...
		Sporulation score	-1.600	-4.333...
		Log(genome size)	1.401	0.780...
	(Co)variance	Phylogenetic	0.456	0.158...
		Residual (non-phylogenetic)	0.011	0.000...
Biofilm				
	Fixed effect	Intercept	-9.619	-14.4...
		Mean relatedness	1.015	-0.000...
		Mean relative abundance	2.227	-1.020...
		Sporulation score	-0.306	-2.589...
		Log(genome size)	1.289	0.745...
	(Co)variance	Phylogenetic	0.265	0.084...
		Residual (non-phylogenetic)	0.012	0.000...
Antibiotic degradation				
	Fixed effect	Intercept	-9.332	-14.0...
		Mean relatedness	0.612	-0.465...
		Mean relative abundance	3.209	-0.008...
		Sporulation score	-1.795	-3.839...
		Log(genome size)	1.267	0.715...
	(Co)variance	Phylogenetic	0.158	0.000...
		Residual (non-phylogenetic)	0.010	0.000...
Secretome				
	Fixed effect	Intercept	-7.586	-10.2...
		Mean relatedness	0.599	0.087...
		Mean relative abundance	-0.333	-2.038...
		Sporulation score	0.007	-1.330...
		Log(genome size)	1.280	0.954...
		Gram positive	0.597	0.348...
	(Co)variance	Phylogenetic	0.144	0.059...
		Residual (non-phylogenetic)	0.008	0.000...
Secretion systems				
	Fixed effect	Intercept	-11.008	-26.8...
		Mean relatedness	0.278	-2.437...
		Mean relative abundance	2.715	-8.050...
		Sporulation score	-1.370	-8.529...
		Log(genome size)	1.297	-0.516...
	(Co)variance	Phylogenetic	3.130	0.001...
		Residual (non-phylogenetic)	0.344	0.000...
Quorum sensing				
	Fixed effect	Intercept	-1.800	-10.6...
		Mean relatedness	0.644	-1.048...
		Mean relative abundance	7.386	1.229...
		Sporulation score	4.422	0.498...
		Log(genome size)	-0.048	-1.114...
	(Co)variance	Phylogenetic	0.764	0.149...
		Residual (non-phylogenetic)	0.028	0.000...

CI95%: 95% credible interval of the posterior distribution

pMCMC: taken as twice the posterior probability that the estimate is negativ...