

Table 1: Model summaries for the phylogenetic mixed models of cooperative traits

Model	Structure	Effect	Posterior mean	CI95%
Siderophores				
	Fixed effect	Intercept	-10.572	-16.11
		Mean relatedness	1.558	0.418
		Log(genome size)	1.322	0.699
	(Co)variance	Phylogenetic	0.488	0.207
		Residual (non-phylogenetic)	0.011	0.000
Biofilm				
	Fixed effect	Intercept	-9.275	-14.03
		Mean relatedness	1.059	0.055
		Log(genome size)	1.245	0.700
	(Co)variance	Phylogenetic	0.290	0.111
		Residual (non-phylogenetic)	0.012	0.000
Antibiotic degradation				
	Fixed effect	Intercept	-9.267	-14.41
		Mean relatedness	0.861	-0.251
		Log(genome size)	1.201	0.597
	(Co)variance	Phylogenetic	0.267	0.066
		Residual (non-phylogenetic)	0.009	0.000
Secretome				
	Fixed effect	Intercept	-7.681	-10.27
		Mean relatedness	0.593	0.075
		Log(genome size)	1.289	0.978
		Gram positive	0.602	0.372
	(Co)variance	Phylogenetic	0.134	0.051
		Residual (non-phylogenetic)	0.008	0.000
Secretion systems				
	Fixed effect	Intercept	-10.213	-25.41
		Mean relatedness	0.479	-2.273
		Log(genome size)	1.156	-0.461
	(Co)variance	Phylogenetic	2.702	0.000
		Residual (non-phylogenetic)	0.378	0.000
Quorum sensing				
	Fixed effect	Intercept	-0.967	-10.93
		Mean relatedness	0.393	-1.341
		Log(genome size)	0.056	-1.121
	(Co)variance	Phylogenetic	1.188	0.445
		Residual (non-phylogenetic)	0.023	0.000

CI95%: 95% credible interval of the posterior distribution
pMCMC: taken as twice the posterior probability that the estimate is negative