Table S1

Bacterial species isolated from wild *Agalychnis callidryas* and *Agalychnis moreletii* and tested for anti-*Batrachochytrium dendrobatidis (Bd)* activity against *Bd*GPL isolates SFBC 014 and AUL 1.2 using in vitro challenges. Bacterial isolates used for quantitative assessment of inhibitory activity against three *Bd*GPL isolates (CORN 3.2, JEL 423, VA05) are indicated by an #.

Bacterial species	Host species	GenBank accession number	*Bd*GPL SFBC 014 inhibition	*Bd*GPL AUL 1.2 inhibition
Acinetobacter sp. 1 **(#)**	*Agalychnis moreletii*	KC853177		Yes
Acinetobacter sp. 2 **(#)**	*Agalychnis moreletii*	KC853194	Yes	Yes
Acinetobacter sp. 3	*Agalychnis moreletii*	KC853193		
Acinetobacter sp. 4	*Agalychnis callidryas*	KC853216		Yes
Agrobacterium sp. **(#)**	*Agalychnis callidryas*	KC853210	Yes	Yes
Arthrobacter sp. **(#)**	*Agalychnis callidryas*	KC853208		
Bacillus sp. 1	*Agalychnis callidryas*	KC853209		
Bacillus sp. 2	*Agalychnis callidryas*	KC853212		
Burkholderia sp.	*Agalychnis moreletii*	KC853184		
Buttiauxella sp.	*Agalychnis moreletii*	KC853180		
Chitinophaga sp.	*Agalychnis moreletii*	KC853191		
Chryseobacterium sp. 1 **(#)**	*Agalychnis moreletii*	KC853174		
Chryseobacterium sp. 2 **(#)**	*Agalychnis moreletii*	KC853182	Yes	Yes
Chryseobacterium sp. 3 **(#)**	*Agalychnis callidryas*	KC853202		Yes
Chryseobacterium sp. 4	*Agalychnis moreletii*	KC853179		
Chryseobacterium sp. 5	*Agalychnis callidryas*	KC853218		
Citrobacter sp.	*Agalychnis*	KC853213		

	callidryas		
Cupriavidus sp.	*Agalychnis callidryas*	KC853214	
Curtobacterium sp. 1	*Agalychnis moreletii*	KC853169	
Curtobacterium sp. 2	*Agalychnis moreletii*	KC853190	
Deinococcus sp.	*Agalychnis callidryas*	KC853204	
***Enterobacter sp. 1* (#)**	*Agalychnis moreletii*	KC853189	Yes
***Enterobacter sp. 2* (#)**	*Agalychnis moreletii*	KC853192	
Enterobacter sp. 3	*Agalychnis callidryas*	KC853197	
Enterobacter sp. 4	*Agalychnis callidryas*	KC853199	
Enterobacter sp. 5	*Agalychnis callidryas*	KC853205	
Enterobacter sp. 6	*Agalychnis callidryas*	KC853217	
Enterobacter sp. 7	*Agalychnis callidryas*	KC853221	
Enterobacter sp. 8	*Agalychnis callidryas*	KC853224	Yes
Erwinia sp.	*Agalychnis callidryas*	KC853200	
Gordonia sp.	*Agalychnis callidryas*	KC853207	
Kluyvera sp.	*Agalychnis moreletii*	KC853172	
***Lysobacter sp.* (#)**	*Agalychnis moreletii*	KC853178	Yes
Massilia sp.	*Agalychnis callidryas*	KC853215	
Microbacterium sp.	*Agalychnis moreletii*	KC853186	
Novosphingobium sp. 1	*Agalychnis callidryas*	KC853211	
Novosphingobium sp. 2	*Agalychnis callidryas*	KC853222	
Pseudomonas sp.	*Agalychnis callidryas*	KC853219	

Rhizobium sp.	*Agalychnis moreletii*	KC853173		
Sanguibacter sp. 1	*Agalychnis moreletii*	KC853168		
Sanguibacter sp. 2	*Agalychnis moreletii*	KC853187		
Sanguibacter sp. 3	*Agalychnis moreletii*	KC853188		
Serratia sp. 1 **(#)**	*Agalychnis moreletii*	KC853175	Yes	
Serratia sp. 2 **(#)**	*Agalychnis moreletii*	KC853176		Yes
Serratia sp. 3 **(#)**	*Agalychnis moreletii*	KC853181		
Serratia sp. 4 **(#)**	*Agalychnis callidryas*	KC853196	Yes	
Staphylococcus sp. 1	*Agalychnis moreletii*	KC853170		
Staphylococcus sp. 2	*Agalychnis callidryas*	KC853206		
Staphylococcus sp. 3	*Agalychnis callidryas*	KC853223		
Stentrophomonas sp. 1 **(#)**	*Agalychnis callidryas*	KC853203		Yes
Stentrophomonas sp. 2	*Agalychnis moreletii*	KC853183		
Stentrophomonas sp. 3	*Agalychnis moreletii*	KF444793		
Stentrophomonas sp. 4	*Agalychnis callidryas*	KC853198		
Stentrophomonas sp. 5	*Agalychnis callidryas*	KC853201		
Stentrophomonas sp. 6	*Agalychnis callidryas*	KC853220		Yes
Stentrophomonas sp. 7	*Agalychnis moreletii*	KC853171	Yes	

Table S2

Parameter estimates from the best supported model investigating the effects of bacterial genus and *Bd* isolate on inhibition score. The best supported model contained both *Bd* isolate and bacterial genus as main effects. The intercept is the reference category of *Bd* isolate = CORN 3.2 and Bacterial Genus = *Acinetobacter*. Both the Bacterial Genus *Enterobacter* and the *Bd* isolate VA05 were associated with significantly lower inhibition scores (credible intervals for both effects do not cross zero). In addition, we provide the cut-point estimates to allow back-transformation of scoring probabilities for the four bacterial genera and three *Bd*GPL genotypes.

	Posterior Mean	**lower95% CI**	**upper95% CI**
Genus/Bacteria	0.2100	0.0003	0.9800
	Posterior Mean	**lower95% CI**	**upper95% CI**
(Intercept)	0.37	-0.69	1.32
BdJEL423	0.33	-0.56	1.12
BdVA05	**-1.42**	**-2.46**	**-0.43**
GenusChryseobacterium	-0.16	-1.42	0.98
GenusEnterobacter	**-2.03**	**-3.53**	**-0.57**
GenusSerratia	-0.36	-1.44	0.61
	Cutpoints:		
	Posterior Mean	**lower95% CI**	**upper95% CI**
cutpoint.traitinhib.1	0.27	0.09	0.50
cutpoint.traitinhib.2	0.76	0.45	1.13
cutpoint.traitinhib.3	1.46	1.02	1.95
cutpoint.traitinhib.4	1.93	1.33	2.45
cutpoint.traitinhib.5	2.23	1.57	2.88
cutpoint.traitinhib.6	2.63	1.79	3.43
cutpoint.traitinhib.7	2.98	1.98	3.87

Table S3

Model selection results from five ordinal models fitted using the package ‘MCMCglmm’ (Hadfield, 2010) to investigate the effects of bacterial genus and *Bd* isolate on inhibition score. All five competing models contained the same random effects structure controlling for phylogenetic structure of bacterial relatedness. (~Genus/Bacteria). The most complex model contained *Bd*GPL, Bacterial genus, and their interaction as fixed effects. We also fitted all 4 nested models: BdGPL and Bacterial isolate as main effects without their interaction, *Bd* isolate only, Bacterial genus only, and an intercept only model. We compared all five models using the Deviance Information Criterion (DIC). All models were run for 100,000 iterations following a burnin of 20,000 iterations, with a thinning interval of 100. We used uninformative priors for the random effects (G) structure specifying V = 1 and nu = 0.002. As the residual variance is not identifiable for ordinal models, it was fixed at 1.

Model	**df**	**DIC**	**ΔDIC**
Bd + Genus	8	242.87	0
Bd	5	251.81	8.94
Bd * genus	14	257.72	14.85
Intercept Only	3	262.61	19.74
Genus	6	265.93	23.05
All models contained Bacterial Isolate nested within Genus as random effects			

Hadfield JD (2010) MCMC Methods for Multi-Response Generalized Linear Mixed Models: The MCMCglmm R Package. J Stats Softw **33**: 1-22.