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Probiotic Consortia Are Not Uniformly Effective Against Different Amphibian Chytrid Pathogen Isolates

Rachael E. Antwis¹,²*, Xavier A. Harrison³#

1. School of Environment and Life Sciences, University of Salford, Salford, UK
2. Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
3. Institute of Zoology, Zoological Society of London, Regent’s Park, London NW1 4RY

# Both authors contributed equally to this paper

Addresses for Correspondence:

Dr Rachael Antwis, University of Salford, Room 336, Peel Building, The Crescent, Salford, M5 4WT, UK, 01612954641, r.e.antwis@salford.ac.uk

Dr Xavier Harrison, Institute of Zoology, Regents Park, NW1 4RY, UK, xav.harrison@gmail.com

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Probiotic diversity alters Bd growth

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The authors declare no conflict of interest.
Symbiotic bacterial communities can protect their hosts from infection by pathogens. Treatment of wild individuals with protective bacteria (probiotics) isolated from hosts can combat the spread of emerging infectious diseases. However, it is unclear whether candidate probiotic bacteria can offer consistent protection across multiple isolates of globally-distributed pathogens. Here we use the lethal amphibian fungal pathogen *Batrachochytrium dendrobatidis* to investigate whether probiotic richness (number of bacteria) or genetic distance among consortia members influences broad-scale *in vitro* inhibitory capabilities of probiotics across multiple isolates of the pathogen. We show that inhibition of multiple pathogen isolates by individual bacteria is rare, with no systematic pattern among bacterial genera in ability to inhibit multiple *B. dendrobatidis* isolates. Bacterial consortia can offer stronger protection against *B. dendrobatidis* compared to single strains, and this tended to be more pronounced for consortia containing multiple genera compared with those consisting of bacteria from a single genus (i.e. with lower genetic distance), but critically this effect was not uniform across all *B. dendrobatidis* isolates. These novel insights have important implications for the effective design of bacterial probiotics to mitigate emerging infectious diseases.
INTRODUCTION

The last 50 years have seen the emergence of several virulent wildlife pathogens with broad host ranges (Tompkins et al 2015). These emerging infectious diseases have decimated wildlife populations globally and are major contributors to the current global loss of biodiversity (e.g. Skerratt et al 2007; McCallum 2012). Broad-scale treatments and/or prophylaxis for such pathogens are often lacking for wild animals (Sleeman 2013; Garner et al 2016). Developing such treatments is often complicated by broad variation in genetic and phenotypic traits such as virulence exhibited by these pathogens (e.g. de Jong & Hien 2006; Schock et al 2010; Farrer et al 2011). Successful mitigation of infectious diseases in the wild demands that preventative or curative therapies demonstrate broad activity over as many genetic variants of the pathogen as possible, and developing mitigation strategies that satisfy this criterion remains a major outstanding research goal.

*Batrachochytrium dendrobatidis* is a highly infectious fungal pathogen responsible for the global decline in amphibians and a major driver of the current “amphibian extinction crisis” (reviewed in Garner et al 2016). This pathogen comprises multiple deeply diverged lineages and is capable of rapid evolution through extensive genomic recombination (Farrer et al 2011; 2013). Endemic hypovirulent lineages of *B. dendrobatidis* have been identified including *BdCAPE* (South Africa), *BdCH* (Switzerland), *BdBrazil* (Brazil) and a lineage from Japan (Goka et al 2009; Farrer et al 2011; Schloegel et al 2012; Rodriguez et al 2013), although these may also be implicated in population declines in novel regions (e.g. *BdCAPE* in Mallorcan midwife toads, *Alytes muletensis*; Doddington et al 2013). However, it is the globally distributed hypervirulent global panzootic lineage (*BdGPL*) that is associated with phenomenal mass mortalities and rapid population declines of amphibians around the world (Fisher et al 2009; Farrer et al 2011; Olson et al 2012). Isolates within this lineage exhibit enormous and unpredictable variation in virulence, even within a single host species exposed under laboratory conditions (Farrer et al 2011; Farrer et al 2013). There is currently no cure for this disease in the wild (reviewed in Garner et al 2016). Given that amphibian communities may be host to multiple *B. dendrobatidis* variants (Morgan et al 2007; Rodriguez et al 2014) and that global movement of humans and wildlife continues to transport the pathogen (Garner et al 2016), any prophylactic or curative treatment needs to be effective against multiple *B. dendrobatidis* variants.
Bacterial probiotics represent a promising tool to combat emerging infectious diseases in the wild, including *B. dendrobatidis* (Bletz et al. 2013, Hoyt et al. 2015; Rebollar et al. 2016). Laboratory and field studies have shown host-associated bacterial communities protect amphibians from *B. dendrobatidis* infection and that it is possible to artificially augment the microbiota with probiotic bacteria to improve survivorship in response to the pathogen (Harris et al. 2009; Muletz et al. 2012; Bletz et al. 2013; Becker et al. 2015; Walke et al. 2015; Kueneman et al. 2017). However, inhibitory capabilities of individual bacteria are not uniform across the variation presented by *B. dendrobatidis* (Antwis et al. 2015; Muletz-Wolz et al. 2017; Bletz et al. 2017a). In addition, previous work has found either no (Becker et al. 2015) or weak evidence (Bletz et al. 2017a) of a phylogenetic signal in the ability of bacterial genera to inhibit a singular *B. dendrobatidis* isolate. However, a major gap in our understanding concerns whether some bacterial genera are more likely to show broad-spectrum inhibition across a range of *B. dendrobatidis* isolates, allowing a more focused search for effective amphibian probiotics. Furthermore, the importance of a complex and diverse microbiota for resilience to infection has been repeatedly demonstrated across a range of host taxa (e.g. Dillon et al. 2005; Matos et al. 2005; Van Elsas et al. 2012; Eisenhauer et el. 2013). An alternative strategy for probiotic development involves a ‘bacterial consortium’ approach, whereby multiple inhibitory bacterial strains are applied simultaneously. Multi-species consortia can increase inhibition of *B. dendrobatidis* growth through increased competition and the production of emergent metabolites (Loudon et al. 2014; Piova-Scott et al. 2017), and may offer greater inhibitory capabilities across a wider range of *B. dendrobatidis* isolates. However, the generality of this pattern across multiple pathogen variants remains untested. Addressing this shortfall in our understanding is critical for developing effective tools for the mitigation of emerging infectious diseases in the wild.

Here we extend previous work to quantify the ability of individual bacteria and co-cultured bacterial consortia to demonstrate broad-scale inhibition across a panel of *B. dendrobatidis* isolates. First, we test 54 bacterial strains from 10 genera for inhibition against a suite of 10 different BdGPL isolates to quantify; i) variation among bacterial genera in ability to demonstrate broad-spectrum BdGPL inhibition; and ii) variation among BdGPL isolates in susceptibility to inhibition. Second, we quantify the relative efficacy of using single bacterial strains or bacterial consortia to modify *B. dendrobatidis* growth rates in vitro. Specifically, we investigate; iii) whether consortia yield stronger inhibition than
single bacteria across three *B. dendrobatidis* isolates from two lineages (*Bd*GPL and *Bd*CAPE); and

iv) whether the genus-level diversity of a bacterial consortium affects inhibitory capabilities.

**METHODS**

*Taxonomic Classification*

*In vitro* challenges were conducted for 54 bacteria isolated from wild *Agalychnis* spp. frogs in Belize (Antwis et al 2015) to screen for inhibitory capabilities against 10 *Bd*GPL isolates (Table 1, Fig. 1).

*Batrachochytrium dendrobatidis* is present in the Maya Mountains from where these bacteria were collected, although declines in *Agalychnis* hosts were not seen in this area (Kaiser & Pollinger 2012; Antwis, pers. obvs.). Bacterial strains belonged to 10 genera with 3-11 bacteria per genus (Table S1).

Bacteria were identified using colony PCR to amplify the 16S rRNA gene (with primers 27F and 1492R) and sequenced at the University of Manchester (Antwis et al 2015). The forward and reverse sequences were aligned for each bacterium and blasted against the NCBI database (http://blast.ncbi.nlm.nih.gov/Blast.cgi). To calculate genetic distance among sequences, we aligned the sequences against the SILVA reference database (Quast et al 2013). We used the seqinr package (Charif & Lobry 2007) to import the aligned sequences and calculate the pairwise genetic distances among bacterial strains.

Inhibition challenges were conducted using an *in vitro* absorbance-based growth inhibition assay adapted from Bell et al. (2013), Woodhams et al (2014) and Becker et al (2015). Bacteria were grown by adding 50ul of frozen stock bacteria (stored in 30% glycerol, 70% tryptone solution at -80°C) to 15ml of 1% tryptone, and incubating at 18°C for 36 hours until turbid (three cultures per bacterial strain). Although cell density has been shown to influence metabolite production in culture (Yasumiba et al 2015), we decided not to count and adjust cell density prior to inhibition trials as subsequent addition of media may alter the metabolite profiles already produced by cultures. In addition, cultures were not grown in the presence of *B. dendrobatidis* as multiple *B. dendrobatidis* isolates were tested in this study.

Turbid cultures were filtered through a 0.22um sterile filter (Millipore, Ireland) to remove live cells, leaving only bacterial products (including metabolites) in the filtrate. These were then combined across the three cultures for a given bacterial strain and kept on ice until *B. dendrobatidis* challenges were
conducted. BdGPL (Table 1) isolates were grown in 1% tryptone broth until maximum zoospore production was observed (~3-4 days; ~1 × 10^6 zoospores ml^{-1}). As with bacteria, three flasks per *B. dendrobatidis* isolate were grown and then combined prior to challenges to minimise flask-effect. Zoospores were separated from sporangia by filtering through 20μm sterile filters (Millipore, Ireland).

To conduct the absorbance-based growth inhibition assays, 50ul of bacterial filtrate and 50ul of *B. dendrobatidis* suspension were pipetted into 96-well plates. Each *B. dendrobatidis*-bacteria combination was run in triplicate. Positive controls were included using 50ul 1% tryptone instead of bacterial filtrate. Negative controls were included using 50ul sterile tryptone and 50ul of heat-treated *B. dendrobatidis* for each isolate. Plate readings were taken using a 492nm filter on initial construction of the challenge assays and every 24 hours for four subsequent days.

For each measurement, data were transformed using the equation Ln(OD/(1-OD)) and a regression analysis was used to gain the slope values for each sample over time. Slopes of triplicate replicates for each *B. dendrobatidis*-bacteria combination were averaged, and the slope of the negative controls subtracted. Total *B. dendrobatidis* inhibition was calculated using the formula: Inhibition (%) = [1-(slope of sample/slope of control)] x 100 to give an 'inhibition score'. A positive inhibition score represents inhibition of *B. dendrobatidis* growth and a negative score indicates enhanced growth of *B. dendrobatidis*. It should be noted that we did not use a nutrient depleted control in our experiments (Bell et al 2013), which means *B. dendrobatidis* inhibition relative to the controls may be slightly underestimated.

**Bacterial consortium challenges**

Three bacterial strains were then selected from each of five genera (*Chryseobacterium*, *Comamonas*, *Enterobacter*, *Staphylococcus* and *Stenotrophomonas*) based on their inhibition profiles; poor to medium inhibitors were selected to determine whether combining these bacteria would improve their inhibitory capabilities (mean percentage inhibition score of approximately 0 to +50; Fig. 1). Bacteria were grown individually until turbid and added to fresh tryptone either individually (strains A, B and C of each genus separately), or as a triple (strains A, B and C of each genus together to form five single-genus mixes, or a combination of strains across genera to form multi-genus consortia (20 multi-genus combinations tested)). For both individual and triple bacterial combinations, a total of 3ml of bacteria...
were added to 12ml of fresh 1% tryptone broth and left to grow together for 12 hours. The volume of each bacterium added depended on whether the consortium contained one or three bacteria, and the volume was split evenly between the number of bacteria added to each group. Following this, bacteria-*B. dendrobatidis* challenges were conducted using the same methods as described above against three *B. dendrobatidis* isolates (Table 1). Average inhibition percentages for each consortium-*B. dendrobatidis* combination were calculated as described above.

### Statistical Analysis

All statistical analyses were conducted in the software R v.3.3.2 (R Core Team 2016).

**Taxonomic Group Data:** To quantify differences among genera in proportion of *Bd*GPL isolates inhibited (i.e. for those where inhibition score > 0), we fitted a Binomial GLM with the proportion of the 10 *Bd*GPL isolates each bacterial strain inhibited as the response, and genus as a fixed effect. We used the quasibinomial error structure as the model was overdispersed (dispersion 6.4), and tested the model containing a genus term with the reduced intercept-only model using a likelihood ratio test.

To visualise the distribution of inhibition across bacterial strains and *B. dendrobatidis* variants, we constructed a heatmap using the *pheatmap* package in R (Kolde 2015). To quantify differences among genera in the degree of inhibition (size of inhibition score), we fitted a hierarchical model in the R package *MCMCglmm* (Hadfield 2010) with the individual inhibition scores of each bacterial strain (n=54) for each *Bd*GPL isolate (n=10; total n = 540) as a Gaussian response. We fitted both *Bd*GPL isolate and bacterial strain ID nested within bacterial genus as random effects. We also controlled for genetic distance among bacterial strains by passing the bacterial 16S gene tree to the model as a phylogenetic random effect. We use uninformative, parameter-expanded priors for the random effects as detailed in Hadfield (2010). We ran models for a total of 100,000 iterations following a burn-in of 10,000 iterations and using a thinning interval of 50. Inspection of model residuals from the frequentist analogue of this model fitted in *lme4* (Bates et al 2015) revealed normally-distributed residuals and no evidence of heteroscedasticity. Rerunning models with stronger priors has no effect on model results. Gelman-Rubin diagnostic of Markov chains indicated adequate convergence, with all potential scale reduction factors <1.01. We used Bayesian models here, rather than a frequentist analogue, due to
the ease of summarising uncertainty in point estimates of random effect conditional means using 95% credible intervals of Markov chain values. To calculate % variance in inhibition explained by BdGPL isolate, bacterial genus, and bacterial strain respectively, we extracted the variance components from the variance-covariance matrix of the model above. We expressed the variance of a component V as a percentage of the total variance calculated as \((V_{\text{BdGPL}} + V_{\text{genus}} + V_{\text{strain}} + V_{\text{residual}})\). We calculated both mean and 95% credible intervals using the posterior samples from the model. To construct Figures 1 and 2, we extracted the marginal means and 95% credible intervals for each bacterial strain and BdGPL isolate, respectively. That is, the bacterial strain modes are marginalised with respect to BdGPL, and vice versa, to quantify whether the average scores for each BdGPL isolate or bacterial strain are significantly different from zero.

Correlation Between Genetic Distance and Inhibition: For each pair of bacterial strains, we calculated the correlation between the inhibition scores for the ten \(B. \text{dendrobatidis}\) isolates. If more closely related bacterial strains are more likely to have similar inhibition profiles, there should be a negative correlation overall between genetic distance and similarity of inhibition. To test this, we performed a Mantel test using the genetic distance and inhibition score similarity matrices in the R package ‘vegan’ (Oksanen et al 2015).

Consortium Data: To calculate the relative mean inhibition of single-genus vs multi-genus consortia, we fitted a mixed model in \texttt{MCMCglmm} with inhibition as a Gaussian response, consortium type as a 2-level factor, and a random effect of \(B. \text{dendrobatidis}\) isolate using uninformative priors. To calculate whether consortia exhibited stronger inhibition than the mean of their individual strains, we constructed a binary variable with an outcome of 1 if a consortium's inhibition was greater than the single strain mean, and 0 if equal to or lower. We fitted this as a response in a binary GLMM with consortium type as a fixed effect, \(B. \text{dendrobatidis}\) as a random effect and using uninformative priors. Neither model exhibited signs of autocorrelation and Geweke statistics for both models indicated convergence. We calculated mean genetic distance among members of consortia using the genetic distance measures outlined above. We fitted a Bayesian GLM where the percentage inhibition of a consortium was a function of the interaction between the genetic distance among consortium members and the \(B. \text{dendrobatidis}\) isolate identity. Genetic distance was standardised prior to model fitting to remove the correlation between main effects and interactions.
Consortium Randomisations: We used a randomisation approach to probe the relative effectiveness of single bacteria, single-genus consortia and multi-genus consortia (hereafter ‘probiotic types’) for modifying the growth rates of *B. dendrobatidis*. These randomisations used the ‘Taxonomic Group’ and ‘Consortium’ inhibition data from above to explore three different scenarios relevant to the application of probiotics to *B. dendrobatidis*. For each iteration of a randomisation we randomly selected a *B. dendrobatidis* isolate and then extracted the inhibition scores of a randomly chosen single bacterial strain, single-genus consortium, and multi-genus consortium. After 1000 iterations, we calculated i) the proportion of times a multi-genus consortium yielded higher inhibition than a single-genus consortium; ii) the proportion of times a multi-genus consortium yielded higher inhibition than a single bacterial strain; iii) the probability that a multi-genus, single-genus or single bacterial strain would yield at least 50% inhibition, which we classed as strong inhibition. This approach is more powerful than simply calculating differences in group means of each probiotic type, as group means can be skewed by large individual values, and therefore be misleading with respect to the efficacy of a particular strategy if the mean of that group is not reflective of the true variance in the data. However, we report group means alongside these statistics where appropriate for comparison. We derived 95% confidence intervals for each test statistic by performing 10,000 bootstrap samples with replacement from the test distributions. The three scenarios we tested were as follows:

**Scenario 1: Averaged over all *B. dendrobatidis* isolates:** For each iteration, we randomly selected a *B. dendrobatidis* isolate and then randomly selected both a single-genus and a multi-genus consortium. A single bacterial strain score was then selected randomly from one of the members of the multi-genus consortium.

**Scenario 2: *B. dendrobatidis* specific scores:** To investigate the potential for the effectiveness of consortia to differ depending on *B. dendrobatidis* isolate, we repeated the randomisation as in Scenario 1 but performed 1000 iterations for each *B. dendrobatidis* isolate.

**Scenario 3: Sequential *B. dendrobatidis* exposure:** Finally, we examined the ability of the three probiotic types to inhibit two *B. dendrobatidis* isolates encountered in series by randomly selecting two of the three *B. dendrobatidis* isolates. We assumed that the two isolates are not encountered simultaneously as co-occurrence of two *B. dendrobatidis* isolates may modify their growth rates and/or a bacterial strain’s ability to inhibit them. For each iteration, we selected a random multi-genus and single-genus consortium, followed by a randomly-selected single strain member from the multi-genus
consortium. Individual inhibition scores for these three groups were then extracted for both selected *B. dendrobatidis* isolates (i.e. probiotic ID was kept consistent over both pathogen isolates). We calculated the probability that the multi-genus consortium would yield superior inhibition to the single-genus consortium and single bacterial strain across both *B. dendrobatidis* isolates, and the probability that all three probiotic types would yield >50% inhibition.

**RESULTS**

*Bd*GPL Inhibition Within and Among Bacterial Genera

We assayed the ability of 54 bacterial strains from 10 genera to modify the growth rates of 10 *Bd*GPL isolates. Mean inhibition scores ranged from 100 (complete inhibition of growth) to -225 (strong facilitation of growth). There were no significant differences among genera in mean proportion of *Bd*GPL isolates inhibited (Binomial GLMM; $\chi^2 = 8.12, p=0.52$; Fig. 1; Table 2). Six strains from six genera showed at least weak inhibition across all 10 *B. dendrobatidis* isolates (Supplementary Table S1). We did not find a significant correlation between genetic distance and similarity of inhibition profiles (Mantel test $r = -0.027, p = 0.77$).

We detected considerably more variation in inhibition scores among bacterial strains within genera than among genera (Fig. 1). Variation among bacterial strains within genera explained 87.9% [95% credible interval (CRI) 80.25-94.47%] of the variation in *Bd*GPL inhibition scores compared to just 0.6% [0.007-3.8%] for bacterial genus. *Bd*GPL isolate explained 3.9% [0.1-8.7%] of the variation in inhibition scores. Heatmap hierarchical clustering of inhibition scores revealed two isolates that demonstrated predominantly enhanced growth in the presence of bacterial filtrates (JEL423 and AUL2; Fig. 2). In some cases, *B. dendrobatidis* isolates from similar locations (e.g. CORN isolates from Cornwall) showed similar clustering of inhibitions scores, whereas others (e.g. AUL isolates from the Pyrenees) showed markedly different inhibition fingerprints (Fig. 2).

Multi-Strain Consortia as Tools for Pathogen Mitigation
Consortia containing strains from multiple genera exhibited significantly higher mean inhibition scores compared to single-genus consortia when marginalising with respect to *B. dendrobatidis* isolate (multi-genus consortia mean inhibition: 36.88%; single-genus consortia mean: 16.9%; 95% CRI of difference 4.12 – 36.52%, \( p_{\text{MCMC}} = 0.02 \); Fig. 3). Multi-genus consortia had a 61% probability of demonstrating stronger inhibition than the mean of their single composite bacterial strains, which was significantly higher than the corresponding probability for single-genus consortia (26.6%, mean difference 39.4% [95% Credible Interval 11.2-65.1%], \( p_{\text{MCMC}} = 0.01 \)). Mean genetic distance among members of multi-genus consortia was significantly higher than among members of single-genus consortia (multi-genus mean distance = 0.45, single-genus mean =0.11, \( t = -15.5 \), \( p<0.001 \)). Consortia with higher mean genetic distance elicited significantly higher inhibition scores for *B. dendrobatidis* isolates *Bd*CAPE TF5a1 and *Bd*GPL MODS28.1 (\( p_{\text{MCMC}} = 0.009 \), but not for *Bd*GPL SFBC019, which had a significantly different slope to the other two *B. dendrobatidis* isolates (Fig. 4, \( p_{\text{MCMC}}=0.01 \)).

**Probiotic Consortium Randomisations**

**Scenario 1:** Our randomisation tests revealed that multi-genus consortia gave higher inhibition than single-genus consortia in 69.4% of cases when averaging over all *B. dendrobatidis* isolates (null expectation 50%, \( p_{\text{RAND}}<0.001 \)). Multi-genus consortia were more likely to produce inhibition greater than 50% (strong inhibition) (38.1% of iterations) compared to single-genus consortia (13.9% of iterations, \( p<0.001 \)), and outperformed a randomly chosen single bacterial strain in 61% of cases (null expectation 50%, \( p_{\text{RAND}}<0.001 \)). Mean inhibition for all multi-genus consortia across all *B. dendrobatidis* isolates was 36.7%, compared to 16.47% for single-genus consortia.

**Scenario 2:** When considering *B. dendrobatidis* isolates individually, multi-genus consortia outperformed single-genus consortia and single bacterial strains for only two of the three isolates (*Bd*GPL MODS28 and *Bd*CAPE TF5a1, but not for *Bd*GPL SFBC019; Fig. 5A). This pattern was also evident when determining the probability of yielding >50% inhibition by consortia (Fig. 5B).

**Scenario 3:** We also tested the ability of both multi-genus and single-genus consortia to inhibit the growth of two different *B. dendrobatidis* isolates in series, as individuals in a single location may be exposed to multiple variants of a pathogen (Goka et al 2009; Schloegel et al 2012; Rodriguez et al 2014; Jenkinson et al 2016), or strong spatial structure of the pathogen and high host dispersal...
may expose individuals to multiple pathogen variants consecutively. Applying the same multi-genus consortium to two different randomly-chosen *B. dendrobatidis* isolates in series achieved stronger inhibition than single-genus consortia in 49.4% of cases (null expectation 25%, $p_{\text{RAND}} < 0.001$). This compared to only 7.9% of cases where single-genus consortia exhibited superior inhibition for both *B. dendrobatidis* isolates. Multi-genus consortia exhibited strong inhibition (>50%) for both isolates in 14.7% of cases, compared to zero cases where single-genus isolates did so. Applying a single bacterial strain instead of a single-genus or multi-genus consortium resulted in strong inhibition for both *B. dendrobatidis* isolates in only 4% of cases (Fig. 5C). The full results of these randomisations, including confidence intervals for tests, can be found in Supplementary Table S2.

**DISCUSSION**

The principal objectives of this study were two-fold: i) to determine whether certain genera of bacteria are better able to inhibit a broad range of *BdGPL* isolates; and ii) to examine the relative effectiveness of single bacteria and bacterial consortia to inhibit multiple isolates of *B. dendrobatidis*. We found no evidence of variation among bacterial genera in their ability to exhibit broad-range inhibition across multiple *BdGPL* isolates. There was considerable within-genus variation in inhibitory capabilities of bacteria compared to between-genus variation, meaning genus is not a reliable indicator of anti-*B. dendrobatidis* capabilities across multiple isolates of this pathogen. Furthermore, our data suggested consortia can provide superior *B. dendrobatidis* inhibition compared to individual bacteria, and that this is contingent on consortium taxonomic diversity, but critically this pattern is not uniform across pathogen isolates. Our results have important implications for developing effective strategies for designing probiotic therapies to mitigate lethal infectious disease.

**BdGPL Inhibition Within and Among Bacterial Genera**

We found no evidence of systematic variation among bacterial genera in their ability to inhibit multiple *BdGPL* isolates. In our data, the principal source of variance in inhibition was among bacterial strains, with the number of strains demonstrating broad-spectrum facilitation of *BdGPL* being roughly equal to the number exhibiting broad-scale inhibition of the pathogen. These data support previous work...
suggesting *B. dendrobatidis* inhibition capability is distributed widely across bacterial genera (Antwis et
al 2015; Becker et al 2015; Bletz et al 2017a); several strains demonstrated at least weak inhibition for
all 10 *Bd*GPLs but were spread across multiple genera with no clear pattern. That there is clear
functional redundancy among genera in this host-protective trait suggests it is not prudent to focus on
any one genus in the search for beneficial probiotics (Becker et al 2015), as highly divergent microbial
communities can still possess similar functional traits (e.g. Bletz et al 2016; 2017b).

We identified one *Bd*GPL isolate that was significantly prone to inhibition (08MG04) and a further two
isolates that demonstrated strong resistance to inhibition (i.e. facilitated growth; AUL2 and JEL423).
The phenomenon of *Bd*GPL growth facilitation has been described previously for single pathogen
isolates (Bell et al 2013; Becker et al 2015), but crucially our results suggest that a bacterial strain’s
ability to facilitate the growth of *B. dendrobatidis* extends across a broad suite of pathogen isolates.
Thus, facilitation of *B. dendrobatidis* growth is not simply a rare phenomenon arising from specific
*Bd*GPL/bacterial combinations, and different *Bd*GPL isolates may differ systematically in their growth
rates when exposed to bacterial filtrates (see also Muletz-Wolz et al 2017). It is unclear why some
bacterial strains facilitate *B. dendrobatidis* growth, but one likely explanation is that certain bacterial
metabolites can act as growth substrates or facilitators for fungi (Garbaye 1994; Hardoim et al 2015).
In addition, different bacterial metabolites may alter the abiotic environment (e.g. pH) to confer
different growth rates (Romanowski et al 2011) or hormesis may occur whereby the growth of *B.*
*dendrobatidis* is facilitated at low or intermediate concentrations of particular bacterial products (Bell et
al 2013).

Further research is required to determine whether a *Bd*GPL isolates’ susceptibility to inhibition or
facilitation correlates with virulence, and how genotypic traits associated with the pathogen map on to
inhibition profiles and taxonomic traits of bacteria. It would also be valuable to further explore the
effects of co-culturing bacteria with *B. dendrobatidis* prior to inhibition challenges, which may influence
anti-*B. dendrobatidis* capabilities (Becker et al 2015). In particular, *B. dendrobatidis* isolates that elicit
particularly strong metabolites from bacteria (i.e. *B. dendrobatidis* isolates that are readily inhibited)
could be used to prime probiotic bacteria to make these more effective at inhibiting other more
resistant *B. dendrobatidis* isolates, such as AUL2 and JEL423 in this study.
Consortium-Based Approaches to Combatting Fungal Pathogens

Our results revealed that the relationship between taxonomic diversity of a probiotic consortium and its ability to inhibit *B. dendrobatidis* growth was not consistent across *B. dendrobatidis* isolates. Multi-genus consortia outperformed both single-genus consortia and single bacterial strains in *B. dendrobatidis* inhibition, and were far more likely to produce strong inhibition of 50% or greater, but this is true for only two of the three pathogen variants. Previous work has demonstrated a link between consortium species richness and *B. dendrobatidis* inhibition but only for a single pathogen isolate (Loudon et al 2014; Piova-Scott et al 2016). Our data suggest that this pattern may not be general, with marked variation among pathogen isolates in their susceptibility to multi-genus consortia.

That said, the general relationship (for two of the three pathogen variants) between inhibition and consortium diversity was in the expected direction; low community relatedness (i.e. high community dissimilarity) and high species richness both increase the resistance of a bacterial community to pathogenic ‘invaders’ (e.g. Jousset et al 2011; Eisenhauer et al 2012, 2013). That multi-genus consortia can provide superior inhibition for some pathogen variants is suggestive of synergistic effects, whereby the combined pool of metabolites from multiple bacteria inhibits *B. dendrobatidis* more strongly than the individual strains (Loudon et al. 2014). Superior inhibition from consortia, rather than single strains, may arise as a by-product of the interference competition over resources created by co-culture (Scheuring & Yu 2012). Bacteria that are weak inhibitors when used individually (as in this study) could increase the overall inhibitory power of a consortium by creating a competitive environment that favours greater production of anti-fungal compounds.

We found that one of the three *B. dendrobatidis* isolates (*BdGPL SFBC019*) was not susceptible to inhibition from more diverse consortia as exhibited the other two pathogen variants (*BdCAPE TF5a1* and *BdGPL MODS 28.1*). That *B. dendrobatidis* isolate can alter the strength of the relationship between consortium diversity and inhibition is a highly novel finding. *BdGPL SFBC019* appears largely resistant to inhibition irrespective of whether individual bacteria or consortia are used, with individual bacterial inhibition scores that were often negative (Fig. 3). This suggests resistance to inhibition from single strains may not necessarily be overcome by the putative synergistic effects from co-culturing bacteria, in the same way that total microbial communities (along with other anti-*B. dendrobatidis* factors associated with the skin) of amphibians may not always be resistant to particular variants of the pathogen (Antwis et al 2017). The underlying cause for this variation is unclear as our data
suggests this variation in consortia-based inhibition does not appear to correlate with *B. dendrobatidis* lineage. In addition, the results of the single strain challenges with 10 BdGPL isolates showed all four isolates from one locality in the UK (“CORN” isolates; Table 1; Fig. 2) showed similar levels of inhibition across all bacterial strains, whereas the two isolates from the same locality in France (“AUL” isolates; Table 1; Fig. 2) exhibited markedly different inhibition profiles. This suggests even pathogen isolates collected from the same host species and locality have the potential to exhibit markedly different responses to bacterial probiotics. More work is required to determine the relative inhibition profiles of multiple *B. dendrobatidis* isolates challenged with single- and multi-bacteria probiotics across a spectrum of diversity, and to determine the mechanisms driving the responses of *B. dendrobatidis* variants to these.

In the study presented here, some metabolites (and other bacterial products) will have been carried over from bacterial strains whilst constructing single and multi-species consortia, and it is also possible that after 12 hours of co-culture, the proportions of bacteria in the multi-species consortia were not equal. Thus, it would be beneficial to determine how inhibition profiles of mixed-species consortia alter over time and whether this can be optimised for the mitigation of wildlife disease. Similarly, understanding the response of the host microbiome to inoculation by probiotics, and concurrent factors that determine the longevity of probiotics on the skin of amphibians, would provide significant steps forward in developing effective treatments.

**Conclusion**

Our work has highlighted that different isolates of a lethal wildlife pathogen can vary in their susceptibility to probiotic bacteria, meaning we cannot expect probiotic effectiveness to be uniform across the genetic or phenotypic landscape of the pathogen. That said, higher diversity (richness and taxonomic) of probiotic consortia may provide greater protective capabilities against pathogens than individual bacteria, although some *B. dendrobatidis* isolates may be largely resistant to the majority of bacterial probiotics, and using bacterial consortia may not overcome this. These patterns are informative with respect to potential strategies for the application of bacterial probiotics to mitigate *B. dendrobatidis* and other wildlife pathogens. Conservationists might not always know which particular *B. dendrobatidis* variant is infecting a local population, preventing targeted application of known strong
inhibitors for that variant (Muletz-Wolz et al 2017), and both time and expense may prevent the
establishment of such a database de novo if a probiotic intervention is required rapidly. Therefore, we
must employ strategies that maximise the chance of successful inhibition in the absence of perfect
knowledge of the pathogen. Although multi-genus consortia did not always outperform single-genus
consortia or single bacteria strains, our data did reveal that these consortia have the highest
probability of ‘strong’ inhibition of >50% if applied ‘naively’ without knowledge of the pathogen variant.
This finding is important; human-mediated spread of B. dendrobatidis through the amphibian trade
(Fisher & Garner 2007) means we cannot assume that local populations will be exposed to only one
pathogenic variant. Future work will expand this study to test multi-genus consortia against a broader
range of pathogen isolates to determine the generality of this pattern. It would be particularly
interesting to combine whole-genome sequencing of the pathogen with inhibition data from single
bacterial strains and consortia to assess whether closely related pathogen isolates are more likely to
show similar responses, or lack thereof, to bacterial consortia. Despite the potential merits of multi-
genus consortia for mitigating single and multiple B. dendrobatidis variants, it remains to be
determined how readily these consortia will be able to colonise the host skin in vivo. This is crucial for
quantifying how applicable inhibition measures derived in vitro are to real-world scenarios.
Additionally, though we tend to treat bacterial inhibition scores as fixed traits, this ignores the ability of
genetic recombination among B. dendrobatidis lineages to modify the relationship between bacterial
metabolites and pathogen growth rates. Even the application of probiotics themselves may represent
a strong selective pressure favouring genetic variants of B. dendrobatidis that lack susceptibility to
those probiotics. Although several trials have demonstrated the potential for probiotic prophylaxis
against B. dendrobatidis, we still lack the requisite data to measure selection caused by those trials on
the pathogen. In vitro experimental evolution assays between pathogen and bacteria may prove the
most powerful means for detecting such patterns.

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**DATA ACCESSIBILITY**

All code and data to reproduce the results in this paper will be uploaded to FigShare upon publication at DOI 10.6084/m9.figshare.5633821

**AUTHOR CONTRIBUTIONS**

RA and XH conceived the study, RA collected the data, XH analysed the data, RA and XH wrote the paper. Both authors contributed equally to this paper.

**REFERENCES**


TABLE LEGENDS

Table 1. *Batrachochytrium dendrobatidis* isolates used in the study.

Table 2. Mean Proportion of 10 *BdGPL* isolates for which at least weak inhibitory capability was observed, averaged over all bacterial strains in a genus. 95% CI: 95% confidence intervals from an overdispersion-corrected Binomial GLM.

FIGURE LEGENDS

Figure 1. Inhibition scores of 54 bacterial strains from 10 genera when tested against 10 *BdGPL* isolates. A positive value represents inhibition of *B. dendrobatidis* growth and a negative value indicates enhanced growth of *B. dendrobatidis*. Estimates are derived from a Bayesian mixed effects model with bacterial strain nested within genus, and *BdGPL* isolate fitted as random effects. Points are conditional modes of the individual bacterial strain random effects, marginalised with respect to *BdGPL* isolate. Error bars are 95% credible intervals. Bacterial strains from the same genus are denoted by the same colour.

Figure 2. Heat map of inhibition across all 54 bacterial strains and all 10 *B. dendrobatidis* isolates. Bacterial strains have been clustered according to phylogeny and *B. dendrobatidis* isolates have been clustered according to their similarity in inhibition profiles (dendrograms in left and top margins, respectively). Inhibition scores have been z-transformed across *B. dendrobatidis* isolates (rows) for each particular bacterial strain. Bacterial row names include both genus and strain ID. Blue indicates low inhibition, through to red, which indicates high inhibition.
Figure 3. Inhibition scores for Single-Genus (SG) and Multi-Genus (MG) Consortia across three *B. dendrobatidis* isolates (*BdGPL MODS28.1, BdGPL SFBC019 and BdCAPE TF5a1*). A positive value represents inhibition of *B. dendrobatidis* growth and a negative value indicates enhanced growth of *B. dendrobatidis*. Points have been jittered for display purposes.

Figure 4. Relationship between mean genetic distance among consortium members and *B. dendrobatidis* inhibition score. We detected a significant positive relationship between genetic distance and inhibition percentage for BdCAPE TF5a1 and BdGPL MODS28.1 but not BdGPL SFBC019. Fitted lines and shaded areas are mean and 95% confidence intervals from a linear model fit.

Figure 5. Randomisation results examining the relative efficacy of different probiotic strategies. (A) the probability of Multi-Genus Consortia (MGC) yielding higher inhibition compared to Single-Genus Consortia (SGC) or a single bacterial strain (Single); (B) the probability of MGC, SGC or single bacteria yielding inhibition > 50% when applied to each of three *B. dendrobatidis* isolates; (C) The probability of an individual consortium type yielding >50% inhibition when applied to two randomly chosen *B. dendrobatidis* isolates in series.
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<tr>
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