Evolutionary rescue and reintroduction of resistant frogs allows recovery in the presence of a lethal fungal disease

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Vast alteration of the biosphere by humans is causing a sixth mass extinction. Adaptation to modified environments often is the only means for species to persist, but the extent to which such "evolutionary rescue" can prevent or reverse biodiversity loss is largely unknown. Using results from genomic analyses, a 15-year reintroduction effort, and population modeling, we provide a compelling example of evolution reversing the declines of an imperiled amphibian and allowing the reestablishment of extirpated populations. The once-common mountain yellow-legged (MYL) frog is threatened with extinction by the human-facilitated emergence of a lethal fungal pathogen (*Batrachochytrium dendrobatidis*; "Bd"). Although most MYL frog populations are extirpated following disease outbreaks, some persist and eventually begin to recover. Using an exome capture approach, we show that MYL frogs have undergone substantial evolutionary change following disease outbreaks. Moreover, in naturally recovering populations observed changes in immune function loci are associated with increased resistance/tolerance to Bd infection. Large-scale reintroduction of frogs from rescued populations resulted in the establishment of reproducing populations despite ongoing disease. In addition, results from viability modeling suggest that established populations have a low probability of extinction over 50 years. Collectively, these results provide a rare example of how evolutionary rescue and the reintroduction of resistant/tolerant individuals can allow the landscape-scale recovery of disease-impacted species. This example has potentially broad implications for the many taxa worldwide that are threatened with extinction by anthropogenic stressors.

Human activities are intensifying threats to global biodiversity (1), with important implications for ecosystem resilience and human welfare (2). To persist, affected taxa will often need to adapt to their altered environment or face decline and possible extinction. The process whereby rapid evolutionary change increases the frequency of adaptive alleles and restores positive population growth is known as "evolutionary rescue" (3). In addition to preventing extinction of declining populations, individuals from rescued populations could also disperse, or be reintroduced, to empty habitats and promote larger-scale recovery. Although this overall scenario is potentially of critical importance for the conservation of an ever-growing number of imperiled taxa, descriptions of its occurrence and effectiveness in the wild are lacking.

One consequence of human alteration of the biosphere is an increase in emerging infectious diseases (4, 5). Such diseases pose a severe threat to wildlife populations (6), and have caused dramatic declines and extinctions in a wide range of taxa, including echinoderms, mammals, birds, and amphibians (7–10). Amid this global loss of biodiversity, some populations decimated by disease have subsequently recovered to varying extents (11–13). Although we know relatively little about the mechanisms underlying recovery (14, 15), host evolution is one possibility (3, 16). This process is known from a diversity of wildlife populations (17–20), and often results in increased host resistance and/or tolerance (see 21, for definitions). However, linking these evolutionary responses to population recoveries is difficult and few clear examples exist. In addition to promoting recovery of disease-impacted populations, the resistant/tolerant individuals in such populations could potentially be used to reestablish populations that were extirpated following disease emergence (14, 22). To date, the use of resistant/tolerant individuals for species recovery is rare (but see 23), and studies that evaluate its potential utility are critically needed.

The mountain yellow-legged (MYL) frog, composed of the sister species *Rana muscosa* and *Rana sierrae* (24), is emblematic of the unprecedented global declines of amphibians caused by the recently-emerged amphibian chytrid fungus (*Batrachochytrium dendrobatidis,* 9). Once the most common amphibian in the high elevation portion of California's Sierra Nevada mountains (USA, 25), during the past century this frog has disappeared from more than 90% of its historical range (24). Due to the severity of its decline and the increasing probability of extinction, both species are now listed as "endangered" under the U.S. Endangered Species Act. In the Sierra Nevada, this decline was initiated by the introduction of non-native trout into

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the extensive historically-fishless region (26, 27) starting in the late 1800s. The arrival of *B. dendrobatidis* (Bd) in the 1960s and its subsequent spread (28) caused additional large-scale population extirpations (29, 30). These Bd-caused declines are fundamentally different from the fish-caused declines because removal of fish populations is feasible and results in the rapid recovery of frogs (31, 32). In contrast, Bd appears to persist in habitats even in the absence of amphibian hosts (33), and therefore represents a long-term alteration of invaded ecosystems that amphibians will need to overcome to reestablish populations.

Despite the catastrophic impact of Bd on MYL frogs, wherein most Bd-naive populations are extirpated following Bd arrival (29), some populations have persisted after epizootics (34) and are now recovering (13). Frogs in these recovering populations show reduced susceptibility to Bd infection, consistent with selection for more resistant/tolerant genotypes (13). Furthermore, exploratory efforts to reintroduce frogs collected from recovering populations to sites from which frogs were previously extirpated indicate that population establishment is possible despite ongoing Bd infection (23).

In the current study, we combine results from genomic analyses, a 15-year landscape-scale frog reintroduction effort, and a detailed population model to provide an unprecedented example of how evolution in response to disease allows the successful reestablishment of extirpated MYL frog populations. Specifically, we used exome capture methods to show that MYL frogs have undergone substantial evolutionary change associated with Bd exposure, changes that might provide a genetic basis for the increased resistance/tolerance to Bd infection observed in naturally recovering populations (13). We then use the reintroduction of resistant/tolerant frogs to 24 sites and results from long-term capture-mark-recapture (CMR) surveys to describe the dynamics and drivers of population establishment. These data are also used to parameterize a population model that extends our inferences of population establishment well beyond the temporal extent of the CMR data. Collectively, these results provide one of the first examples of how evolutionary rescue and the reintroduction of resistant/tolerant animals can allow the large-scale recovery of disease-impacted species.

Results

Frog evolution in response to Bd. To determine whether MYL frog populations show an evolutionary response to Bd, we compared frog genomes between populations with contrasting histories of Bd exposure. Specifically, we compared frog genomes sampled in 4 populations that have not yet experienced a Bd-caused epizootic ("naive") (35) versus in 5 populations that experienced a Bd epizootic during the past several decades and have since recovered to varying degrees ("recovering"; Figure 1) (13, 29). These recovering populations exist in an enzootic state (34), characterized by high Bd prevalence and, in adults, moderate Bd infection intensity ("load") that is typically well below the level expected to cause mortality (29). (See SI Appendix for additional details regarding the study design.)

We conducted a principal component analysis (PCA) of the genomic data to describe the relationships between sampled populations, and then used two complementary approaches to identify regions of the genome under selection. First, we used a multivariate linear mixed model to evaluate associations between population type (i.e., naive versus recovering) and individual variants, including single nucleotide polymorphisms (SNPs) and insertions/deletions (INDELS). Second, we used a splined window analysis to identify larger genomic regions showing differences between population types in F_{ST} and nucleotide diversity ($\pi_{diff} = \pi_{naive}$ - $\pi_{recovering}$).

Individual frogs clustered into 3 separate groups in principal component space (Figure S1A), and clusters reflected the species split (i.e., *R. muscosa* versus *R. sierrae*) and the strong signature of isolation by distance that is characteristic of MYL frogs (36, 37). Importantly, each cluster contained at least one population from both the naive and recovering groups, allowing us to distinguish allelic associations of individuals sampled in the 2 population types versus allelic associations resulting from population structure and genetic drift.

Results from the individual variant and splined window analyses show that recovering populations have signatures of strong selection on multiple regions of the genome. The analysis of individual variants identified 11 "outlier" SNPs (i.e., showing significantly different allele frequencies between naive versus recovering populations) from 7 distinct genes across 4 contigs (Figure S1B, C; SI Appendix: Datasets S1, S2). One of the 7 identified genes (LOC108802036) did not have an associated annotation. For the outlier SNPs, frequency differences between the naive and recovering populations ranged from 41% to 86%. Most of these SNPs showed frequency differences in only a subset of the sampled populations (Figure 1A, B), but the SNP in the RIN3 gene showed consistent differences in frequencies across all populations (Figure 1C). This is suggestive of strong - and parallel - selection at this locus associated with exposure of frogs to Bd across multiple populations.

The splined window analysis identified 33 outlier regions for π_{diff} and 58 outlier regions for F_{ST} (Figure 2A, B). Of these, 9 regions were outliers for both metrics ("shared regions") and 2 of these shared regions also contained one or more of the outlier SNPs described above. A total of 33 annotated genes were found in the 9 shared regions (SI Appendix: Datasets S3, S4). Given this large number of genes, here we focus on those with the strongest signal of selection and/or immune-related functions. The largest π_{diff}, indicative of directional selection, occurred in a 163kb region on Contig19, 12.9Mb upstream of the RIN3 outlier SNP (Figure 2C). This region contains approximately 500 SNPs and one annotated gene called "interferon-induced very large GTPase 1-like" (GVINP1). Additionally, a shared outlier region on Contig1 contained two complement factor genes (C6 and C7). Interestingly, this region had a large negative π_{diff} value, consistent with balancing selection. Finally, one shared outlier region on Contig8 contained one outlier SNP (TCF19) and was within 360kb of another outlier SNP (VARS) (Figure 2D, Figure S2). This region (854kb from the beginning of the outlier window to the VARS SNP) contained a total of 8 annotated genes. In *Xenopus*, five of these genes occur in the extended major histocompatibility complex (MHC) Class I region (FLOT1, TUBB, MDC1, CCHCR1, TCF19) and three occur in the extended MHC Class III region (HSP70, LSM2, VARS) (38). Therefore, this

region under selection is part of the extended MHC Class I and III complex and shows synteny with other amphibian genomes.

Frog population recovery. To determine whether frogs from recovering populations could be used to reestablish extirpated populations, we conducted 24 reintroductions in Yosemite National Park (2006–2020). Each of the reintroductions involved collection of adult frogs from 1 of 3 recovering, Bd-positive "donor" populations and translocating them (39) to 1 of 12 nearby recipient sites (Figure S3). The donor populations included 2 of the 5 recovering populations in the frog evolution study described above (Figure 1A: population 1 and 4). Following translocation, adult survival and recruitment of new adults was estimated from CMR surveys and counts of tadpoles and juveniles were obtained from visual encounter surveys (VES).

Estimates of frog survival during the 1-year period following translocation indicate that survival was highly variable between recipient sites, but relatively constant within recipient sites (for the subset of sites that received multiple translocations; Figure 3). As such, the average survival of frogs in the first translocation to a site was an important predictor of survival of frogs in subsequent translocations to that site (Figure S4). This suggests an important effect of site characteristics and/or (site * frog) interactions on frog survival. In addition, 1-year survival was higher for frogs translocated later in the study period than earlier (Table S1), which we suggest resulted primarily from our improved ability to choose recipient sites with higher habitat quality for *R. sierrae*. Finally, Bd loads were fairly consistent before versus after translocation and loads were nearly always well below the level indicative of severe chytridiomycosis and associated frog mortality (Figure S5) (23, 29).

Of the 12 translocated populations, 9 (0.75) showed evidence of successful reproduction in subsequent years, as indicated by the presence of tadpoles and/or juveniles. For these 9 populations, one or both life stages were detected in nearly all survey-years following translocation (proportion of survey-years: median = 0.9, range = 0.29–1). These same populations were also those in which recruitment of new adults (i.e., progeny of translocated individuals) was detected. As with early life stages, recruits were detected in the majority of post-translocation survey-years (proportion of survey-years: median = 0.79, range = 0.12–1). In summary, survey results indicate that translocations resulted in the establishment of reproducing MYL frog populations at most recipient sites despite the ongoing presence of Bd.

To determine whether Bd load had a negative effect on adult survival, as would be expected if frogs were highly susceptible to Bd infection, we developed linear and multilevel models. The best model of 1-year frog survival identified several important predictors, but Bd load at the time of translocation was not among them (Figure S6). Important predictors included winter severity in the year following translocation, site elevation, and donor population (Figure 4). Males had somewhat higher survival than females, but this effect was only marginally important (Figure 4, Figure S6). Collectively, these results are consistent with frogs in recovering populations having evolved sufficient resistance/tolerance to minimize the adverse effects of Bd infection. In addition, the moderate Bd loads that characterized frogs following translocation (Figure S5) and relatively high survival of frogs in numerous translocated cohorts (Figure 3) suggests that frogs translocated from recovering populations can maintain the benefits of resistance/tolerance in non-natal habitats. Finally, in 3 locations where longer CMR time series allowed us to assess the survival of new adults recruited to the population, naturally recruited adults had equivalent or higher survival probabilities than the originally translocated adults (Figure S7). Therefore, frog resistance/tolerance in non-natal habitats is maintained across generations.

Long-term population viability. Results from frog translocations indicated that adult survival was often relatively high and that most populations showed evidence of successful reproduction and recruitment (described above). Although suggestive of population establishment, a decade or more of surveys may be necessary to confirm that populations are in fact self-sustaining (23). To extend our inferences of population establishment beyond those possible from the 2-16 years of site-specific CMR data, we developed a population viability model. Specifically, to test whether the observed yearly adult survival probabilities in translocated populations were sufficient to promote long-term viability, we built a stage-structured matrix model that captured known frog demography and included demographic and environmental stochasticity. We parameterized the model using CMR data from translocated populations and known life history values in this system (Table S2).

Given observed yearly adult survival probabilities (from analysis of CMR data) and a baseline yearly recruitment probability ω of 0.3 (i.e., the probability that, following survival, juveniles successfully recruit to the adult class), our stage-structured model predicted that six of twelve translocated populations should experience a long-run growth rate λ greater than 1 in the presence of Bd (Figure 5A; median predicted λ ranges from 1.15-1.36 for these six populations). These six populations all had observed yearly adult survival greater than 0.5. When we reduced the probability of successful recruitment ω to 0.1 (a highly conservative estimate), long-run growth rate of five of these six populations was still greater than 1 (Figure 5A).

Even when incorporating (i) demographic stochasticity and (ii) environmental stochasticity in the probability of juvenile recruitment to the adult class ω (the transition that we expect to be the most subject to environmental variability in the presence of Bd), populations with high adult survival are likely to persist over a 50 year time horizon. Our model predicted that, following a single introduction of 40 adult individuals into a population and using the baseline value for ω of 0.3, the six populations with the highest adult survival probabilities ($\sigma_{A_R} > 0.5$) had 50-year extinction probabilities of 0 to 0.32 (Figure 5B). This indicates strong potential for long-term persistence in the presence of Bd and environmental variability in recruitment. When we decreased ω from 0.3 to a conservative estimate of 0.15, 50-year extinction probability remained less than 0.5 for three populations and was 0.79 to 0.94 for three additional populations (Figure 5B). In contrast, for the six populations where yearly adult survival probability $\sigma_{A_R} < 0.5$, extinction probability over 50 years was always predicted to be 1. To test the validity of our model predictions, we demonstrated that our stochastic model could describe the general recovery trajectory of our translocated population with the longest survey history (Figure 5C; population 70550, surveyed for 16 years).

In summary, our model demonstrates that given observed yearly adult survival probabilities of translocated frogs, 50% of our translocated populations have a high probability of population growth and long-term viability in the presence of Bd. This is likely a conservative estimate because there is evidence that naturally-recruited adults have higher survival probability than translocated adults (Figure S7), but we considered these probabilities to be equal in all but three of our populations where we had sufficient data to distinguish these different probabilities. In addition, 5 of the 7 populations translocated after 2013 were predicted to have long-term viability, compared to only 1 of 5 populations translocated prior to 2013 (Table S1). Thus, there is some trend suggesting that our ability to select high quality habitats that promote long-term viability of translocated populations improved over time.

Discussion

Disease-induced population declines are decimating global biodiversity (6), but strategies to recover affected species are generally lacking. Here, we tested the possibility that populations of resistant/tolerant individuals could be used to reestablish extirpated populations. Although previously proposed (22, 40), this strategy has rarely been used in the wild (see 23, for a small-scale example). In particular, although numerous studies have documented signatures of selection in hosts following disease-induced declines (e.g., 18, 19), we are unaware of any that used individuals bearing the resulting adaptive alleles to reestablish extirpated populations. The results of our study provide evidence that (1) MYL frogs have experienced strong selection following exposure to a recently-emerged lethal fungal disease and that some of the genomic regions under selection contain genes related to disease resistance/tolerance, and (2) reintroduction of individuals from these resistant/tolerant populations allows the successful reestablishment of viable frog populations despite ongoing disease.

Previous field studies in MYL frogs show that frog-Bd dynamics and frog survival in the presence of Bd are fundamentally different between naive and recovering populations. Following the arrival and establishment of Bd in previously-naive populations, adult frogs develop high Bd loads that lead to mass die-offs (29). In contrast, in recovering populations adult frogs typically have low-to-moderate and relatively constant Bd loads and mass die-offs are not observed (34, 41, see also Figure S5). The differences in Bd load of frogs from naive and recovering populations are also observed in controlled laboratory studies (see Figure 4 in 13). The observed reduced susceptibility of frogs from recovering populations could in theory be due to several factors, including natural selection for more resistant/tolerant genotypes and/or acquired immunity, but until now evidence to evaluate the role of evolution was lacking.

Results from our genomic analyses strongly suggest that natural selection for adaptive alleles and resulting increased resistance/tolerance is at least partially responsible for the reduced susceptibility of frogs in recovering populations. We identified specific alleles and genomic regions showing signatures of selection between adjacent Bd-naive and recovering MYL frog populations, consistent with strong selection following Bd exposure. Importantly, some regions under selection are associated with cellular and immunological mechanisms known to contribute to disease resistance, including in amphibians (42). For example, the MHC plays an important role in immunity. In our study, we identified a region that shows evidence of selection in recovering populations and contains eight genes associated with either the MHC Class I or Class III regions. These results corroborate numerous previous studies linking MHC genes to amphibian resistance/tolerance against Bd (e.g., 43, 44). Similarly, the region with the strongest indication of directional selection (as measured by π_{diff}) contains the interferon-related gene GVINP1. Several previous studies have found this gene to be differentially expressed during Bd infection (e.g., 45, 46) and in populations differing in Bd susceptibility (45). This gene is also strongly linked to disease in salmon, explaining a notable 20% of the resistance phenotype (47, 48). We also identified a region, characterized by high F_{ST} and low π_{diff}, that contained the complement genes C6 and C7. The complement system plays an important role in innate immunity (49), and our results could indicate that balancing selection is acting in this region of the genome to favor a diverse set of alleles, as is known for C6 in humans (50). Finally, based on the analysis of individual outlier variants, the RIN3 gene showed a consistent pattern of allele frequency differences across all nine of the frog populations sampled in this study, indicating consistent selection in populations distributed across a wide geographic area. This gene is associated with inflammation response and in *Xenopus* is highly expressed in wound stumps following amputation of tadpole tails (51). Also in this analysis, the outlier variant with the lowest p-value (uncharacterized gene LOC108802036) is located adjacent to a type I interferon gene (Np-IFNi2) in another frog genome (52), and together with GVINP1 further suggests the importance of interferon-related genes in this system.

Reintroduction of resistant/tolerant MYL frogs was remarkably successful in reestablishing viable populations in the presence of Bd. Of the 12 translocated populations, approximately 80% showed evidence of both successful reproduction and recruitment of new adults. Bd loads measured before and after translocation were similar and generally remained well below the level at which frog mortality occurs. Annual survival for 12 of the 24 translocated cohorts exceeded 50%, and > 70% of translocated cohorts had survival above this 50% level when the earliest translocations are excluded (i.e., translocations conducted when methods were still being refined). The fact that the relatively low Bd loads and correspondingly high frog survival in the presence of Bd was maintained between the natal/donor sites and the recipient sites indicates that these characteristics of naturally-recovering populations were not solely an effect of the natal/donor site or site * frog interactions, but instead were due at least in part to resistance/tolerance inherent in the frogs. In addition, the relatively high survival of translocated frogs was maintained in their progeny, as expected if resistance/tolerance has a genetic basis. Results from the population viability model were also encouraging. In particular, translocated populations with > 50% survival in the first year post-translocation were predicted to have a low probability of extinction over 50 years (probability of extinction = 0 - 0.32). In light of the generally low success rate of amphibian reintroduction efforts (53), our success in reestablishing MYL frog populations via translocation of resistant/tolerant individuals is striking, and even more so given that this success occurred despite ongoing

infection of frogs with Bd.

Despite the resistance/tolerance of adult MYL frogs in recovering populations, individual and population-level impacts of Bd are still evident. In an earlier study of 2 of our 12 translocated populations (23), Bd infection and load had detectable effects on the survival of adults and may have influenced population establishment (sites referred to as "Alpine" and "Subalpine" in (23) are identified as "70550" and "70505" in the current study). Applying similar analyses to all 12 of our translocated populations would likely provide a broader perspective of the ongoing effect of Bd. In addition to these important but relatively subtle effects of Bd on adults, the impacts on younger life stages are more apparent. MYL frogs immediately following metamorphosis ("metamorphs") are highly susceptible to Bd infection (54) and as a result experience high mortality. This high susceptibility of metamorphs is documented in numerous species of anurans, and may result from the poorly developed immune system characteristic of this life stage (55). In naturally recovering and translocated MYL frog populations, we suggest that the high mortality of metamorphs is an important limitation on subsequent recruitment of new adults. Therefore, although adult MYL frogs appear relatively resistant/tolerant, Bd infection continues to have important limiting effects on recovering populations (see also 56).

The recent emergence of Bd worldwide has contributed to the decline of hundreds of amphibian species, some of which are now extinct in the wild (9). This unprecedented impact on global amphibian biodiversity is compounded by the lack of any effective and broadly applicable strategies to reverse these impacts (57, 58). Importantly, in addition to the natural recovery documented for MYL frogs (13), other species are also showing evidence of post-epizootic recovery in the presence of Bd (11, 12) and suggest the possibility of also using animals from these recovering populations to reestablish extirpated populations. As with MYL frogs, the feasibility and long-term success of such efforts will depend on the availability of robust donor populations containing individuals that have acquired via evolution the adaptive alleles necessary to allow frog survival and population growth in the presence of Bd. Despite the hopeful example of successful reestablishment of MYL frogs via evolutionary rescue and reintroductions, the challenge of recovering hundreds of Bd-impacted amphibian species worldwide is a daunting prospect. Although we now have a proven strategy to reestablish extirpated MYL frog populations, recovery across their large historical range will require substantial resources over many decades. The results of this study provide a hopeful starting point for that endeavor and other future efforts worldwide.

Evolutionary rescue may be increasingly critical for the survival of wildlife populations in a rapidly changing world. The importance of evolutionary rescue is known for a wide variety of taxa (e.g., 3, 59, 60), including in the specific context of disease-impacted systems (16). However, obtaining evidence in wild animal populations for all the causal links in this process (i.e., selection for adaptive alleles → increase in host fitness in the presence of the stressor → positive population growth and recovery) is difficult in most systems. Nonetheless, we provide a compelling example from the wild not only that evolutionary rescue can produce individuals that harbor adaptive alleles and allow population recovery, but importantly that these individuals can be used in translocations to reestablish extirpated populations. We expect that such evolutionary rescue-based translocations will be an essential tool in wildlife conservation in an era of accelerating global change.

Materials and Methods

Frog evolution in response to Bd

Sampling and Sequencing. We collected DNA samples via buccal swabbing (61) from 53 *Rana muscosa/Rana sierrae* individuals: 24 from 4 naive populations, and 29 from 5 recovering populations. These populations are located in the southern Sierra Nevada, from northern Yosemite National Park to northern Sequoia National Park (Figure 1). Samples were collected from 5-6 frogs per population. To minimize potential confounding effects caused by variation in frog genotypes across latitude (e.g., 36), we selected sampling sites such that both population types were represented across similar latitudinal ranges. DNA was extracted following Qiagen DNEasy manufacturer's protocols. We sequenced the samples using an exome capture assay as described in Byrne et al. (in review). Briefly, genomic libraries were prepared and captured using a custom Nimblegen capture pool. Capture baits were designed based on the coding regions of the *R. muscosa* transcriptome (GenBank accession GKCT00000000). Captured libraries were then pooled and sequenced on a NovaSeq 6000 150PE Flow Cell S1 at the Vincent J. Coates Genomics Sequencing Lab at UC Berkeley. Raw sequencing reads are available from NCBI SRA (PRJNA870451).

Data Pre-processing and Cleaning. Raw reads were filtered for adapters and contaminants using fastp (62) and aligned to the *Rana muscosa* genome (NCBI SRA: SRS6533475 (63)), with repetitive elements masked using bwa ("mem" mode) (64). Exact PCR duplicates were marked using Picard. Variants were then called following GATK best practices (v.4.2.0.0 (65)). Briefly, raw variants were called for each sample using HaplotypeCaller and combined using CombineGVCFs. Next, genotypes were jointly called using GenotypeGVCFs. Variants were then hard filtered using gatk VariantFiltration using the following parameters to remove low-quality sites: QD < 2.0, FS > 40.0, SOR > 3.0, MQ < 50.0, MQRankSum > 3.0, MQRankSum $<$ -3.0, ReadPosRankSum > 3.0, ReadPosRankSum $<$ -3.0. This initial filter resulted in 1,595,206 variant sites across 53 individuals.

We then further filtered our dataset at the individual and variant level. First, we trimmed our variants to only include those with minor allele frequency > 0.03, a maximum depth of 250 and minimum depth of 5, a minimum genotype quality of 20, and a maximum missing proportion of 0.5. This filter resulted in 427,038 sites, of which 353,172 were SNPs and 73,866 were INDELS. Finally, we trimmed samples with an average depth across filtered sites $<$ 7x. Our final dataset included 50 samples, 23 from naive and 27 from recovering populations, with an average depth of 16.7x (range = 7.4x – 26.1x).

Data Analysis. To visualize the genomic relationships of our populations we conducted a PCA using the glPCA function in the adegenet R package (66). To detect regions of the genome under selection between naive and recovering populations, we used two approaches: (1) a multivariate linear mixed model to evaluate individual variants (SNPs and INDELs), and (2) a splined window analysis to evaluate larger genomic regions. For the variant analysis, we first used a stringent data filter to include only variants with $< 5\%$ missing data (missing for

no more than 2 individuals), and then calculated the likelihood ratio statistic for the resulting set of 148,307 high quality variants across 127 contigs using GEMMA (67). GEMMA calculates and incorporates a relatedness matrix for input samples, allowing us to account for relatedness and population structure when calculating likelihood ratio statistics. We identified variants showing different allele frequencies between naive versus recovering populations ("outliers") using a Bonferroni-corrected significance level of 0.01. We visualized the results using a Manhattan plot and qqplot. We developed a more liberal set of outlier variants using a Bonferroni-corrected significance level of 0.05 and used this set solely for the gene ontology (GO) analysis (see below and SI Appendix: Dataset S1, S2).

In the analysis of individual variants, for each outlier variant we determined whether the variant was synonymous (protein sequence the same for each variant) or non-synonymous (protein sequence differs between variants), and where in the gene it was located. To do this, we first extracted the reference genome sequence surrounding the variant using the bedtools "getfasta" function (68). Next, we re-annotated each sequence using BLAST to get the predicted gene location based on the closest annotated reference (69). We then translated each variant to amino acids and aligned this translation to that of the gene annotation to ensure proper frame of reference using Geneious (70). After ensuring proper translation, we characterized variants as within or outside the coding sequence of the gene and as either synonymous or non-synonymous.

In the splined window analysis, we identified outlier regions using F_{ST} and differences in nucleotide diversity (π_{diff}) between naive and recovering populations. First, we calculated per-site F_{ST} between the naive and recovering individuals for all bi-allelic SNPs in the 30 largest contigs (98% of all SNPs) using VCFtools (71). Next, we calculated per-site nucleotide diversity π separately for individuals from the naive and recovering populations using VCFtools, then calculated π_{diff} for each population ($\pi_{diff} = \pi_{naive} - \pi_{recovering}$). We concatenated the values for F_{ST} and π_{diff} in order of size-sorted chromosome number and adjusted the SNP position based on the relative position in the genome. We then used the GenWin R package (72) to conduct a splined discrete window analysis for F_{ST} and π_{diff}. This method calculates where non-overlapping window boundaries should occur by identifying inflection points in the fitted spline, therefore balancing false positive and false negative results that occur using other window-based methods (72). This method also calculates a W-statistic allowing for outlier identification. We identified outliers as those with a W-statistic greater than 4 standard deviations above the mean for F_{ST} or above/below the mean for π_{diff}. Shared outliers were then identified as those that were outliers in both analyses, meaning that they showed (1) high differentiation between naive and recovering populations, and (2) differential patterns of nucleotide diversity in the same region. Finally, we extracted gene transcripts mapped within each region and retrieved annotation for that region using BLAST (SI Appendix: Datasets S3, S4).

Using the liberal set of outlier variants, we performed a statistical overrepresentation test (Fisher's exact test) using Blast2GO (73). First, we retrieved the BLAST hits and mapped GO terms for each gene in our targeted transcriptome. Next, we compared the 30 unique outlier genes from the liberal set of outlier variants to the complete set of genes in our target transcriptome to determine if any GO biological functions, molecular functions, or cellular processes were overrepresented. We then repeated this process for the set of 33 genes located in the overlapping F_{ST} and π_{diff} splined windows. Code used for genomic analyses and to create figures is available from the following GitHub repository: https://github.com/allie128/mylf-selection.

Frog population recovery

Field methods. For the 24 translocations we conducted, we identified donor populations from which adult frogs ($\geq$ 40 mm snout-vent length) could be collected using several years of visual encounter surveys (VES) and skin swab collections (13), and results from population genetic analyses (37). The populations that we selected contained several hundred *R. sierrae* adults and hundreds or thousands of tadpoles. These relatively high abundances were the result of recent increases following previous Bd-caused declines (13). As is typical for recovering MYL frog populations, Bd prevalence in the donor populations was high (0.69–0.96) and Bd load (median $\log_{10}$(load) = 3.06–3.78 ITS copies) was two or more orders of magnitude below the level at which frog mortality is expected ($\log_{10}$(load) $\approx$ 5.78 copies)(23, 29). Recipient sites to which frogs were translocated were chosen based on previous *R. sierrae* presence (determined from VES and/or museum records) or characteristics that suggested high quality habitat for this species (74).

We conducted 1–4 translocations per site (Figure S3, Figure 3) and each translocated cohort included 18 to 99 frogs (median = 30). In preparation for each translocation, adult frogs were collected from the donor population and measured, weighed, swabbed, and PIT tagged. Frogs were transported to the recipient site either on foot or via helicopter. Following release, translocated populations were visited approximately once per month during the summer active season (median number of visits per summer = 2; range = 1–10) and assessed using diurnal CMR surveys and VES. CMR surveys allowed estimation of adult survival, adult population size, and recruitment of new adults, and VES provided estimates of tadpole and juvenile abundance. During 2006-2012, CMR surveys were conducted on a single day (primary period) per site visit, during which all habitats were searched repeatedly for adult frogs. Frogs were captured using handheld nets, identified via their PIT tag (or tagged if they were untagged), measured, weighed, swabbed, and released at the capture location. During 2013-2022, we generally used a robust design in which all habitats were searched during several consecutive days (median number of secondary periods per primary period = 3; range = 3–7), and frogs were processed as described above. However, when the number of frogs detected on the first survey day was zero or near zero, we typically conducted only a single-day CMR survey. When using a robust design, within a primary period, frogs that were captured during more than one secondary period were measured, weighed, and swabbed during the first capture, and during subsequent captures were only identified and released.

During each site visit, we conducted VES either immediately before CMR surveys or during the first day of CMR surveys. VES was conducted by walking the entire water body perimeter, first 100 m of each inlet and outlet stream, and any fringing ponds and wetlands, and counting all *R. sierrae* tadpoles and juveniles. These *R. sierrae* life stages have high detectability, and counts are highly repeatable and provide estimates of relative abundance (27).

Frog counts and reproductive success. For each of the translocated populations, we used the presence of tadpoles and/or juveniles from VES and counts of new recruits (i.e, untagged adults) in CMR surveys to provide two measures of successful reproduction. To calculate the proportion of years in which tadpoles/juveniles were present at a site, we excluded surveys conducted in the year of the initial translocation to that site. This exclusion accounted for the fact that all translocations were conducted after the breeding period and reproduction would therefore not have occurred until the following year. Similarly, to calculcate the proportion of years in which new recruits were present at a site, we excluded surveys conducted during the 3 years following the initial translocation. This accounted for the multi-year tadpole and juvenile stages in MYL frogs (Table S2).

Estimation of frog survival and abundance. We estimated survival of translocated frogs, recruitment of new frogs into the adult population, and adult population size using a Bayesian open-population Jolly-Seber mark-recapture model with known additions to the population (i.e., translocated cohorts), as implemented by the mrmr package (75) and using R Statistical Software (v4.4.4, 76). The model tracks the states of M individuals that comprise a superpopulation made up of real and pseudo-individuals (see 23, for details). The possible states of individuals include "not recruited", "alive", and "dead". The possible observations of individuals include "detected" and "not detected". We assume that individuals that are in the "not recruited" or "dead" states are never detected (i.e., there are no mistakes in the individual

$$\begin{bmatrix} L_1 \\ L_2 \\ L_3 \\ J_1 \\ J_2 \\ A_R \\ A_T \end{bmatrix} (t+1) = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & \sigma_{A_R} p_F F & \sigma_{A_T} p_F F \\ \sigma_{L1} p_{L1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_{L2} p_{L2} & 0 & 0 & 0 & 0 & 0 \\ \sigma_{L1}(1-p_{L1}) & \sigma_{L2}(1-p_{L2}) & \sigma_{L3} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma_{J1} p_{J1} & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma_{J1}(1-p_{J1})\omega & \sigma_{J2}\omega & \sigma_{A_R} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{A_T} \end{bmatrix} \begin{bmatrix} L_1 \\ L_2 \\ L_3 \\ J_1 \\ J_2 \\ A_R \\ A_T \end{bmatrix} (t) \qquad [1]$$

PIT tag records). For all models, we used mrmr defaults for priors, number of chains (4), and warmup and post-warmup iterations (2000 for each). We evaluated convergence of the Markov chain Monte Carlo (MCMC) algorithm using trace plots and Gelman-Rubin statistics (Rhat).

Predictors of post-translocation frog survival. To identify important predictors of frog survival following translocation, we developed linear and multilevel models in a Bayesian framework. We performed all analyses with the rstanarm package (77) and R Statistical Software (v4.4.4, 76), and used default, weakly informative priors. Starting models included all relevant population-level effects and, when data contained possible hierarchical structure, we included group-level effects in the full model. We evaluated model fit using leave-one-out ("LOO") cross-validation (78–80), as implemented by the loo package (81).

We conducted two analyses. In the first, we addressed the more general question of whether survival of frogs in the first translocation to a site predicted the survival of frogs in subsequent translocations. Group-level effects included site_id or translocation_id. The second analysis focused specifically on identifying predictors of post-translocation frog survival using a wide range of variables describing characteristics of frogs, sites, and translocations (predictor variables: Bd load, sex, frog size, site elevation, winter severity in the year of translocation, winter severity in the year following translocation, donor population, day of year on which a translocation was conducted, and translocation order). In both analyses we used 1-year survival as a single metric of survival that was available for all translocated populations regardless of how many years of post-translocation data were available (range = 3–16). Group-level effects included site_id, translocation_id, or translocation_id nested within site_id. In both analyses, the response variable, probability of 1-year frog survival, was rounded to integer values to produce a binomial outcome, and all models used a bernoulli family. For all models, we used default priors, four chains, and 5000 iterations each for warmup and post-warmup. We checked convergence of the MCMC algorithm using trace plots and Rhat.

Changes in Bd load following translocation. We analyzed skin swabs using standard Bd DNA extraction and qPCR methods (82, see SI Appendix for details). To assess the magnitude of changes in Bd load on frogs following translocation, we compared Bd loads measured before versus after translocation. Before-translocation loads were quantified using skin swabs collected from all to-be-translocated frogs at the donor site on the day before or the day of the translocation. After-translocation Bd loads were based on all swabs collected from translocated frogs at the recipient site in the year of and the year following translocation. Individual frogs and their associated Bd loads were included in the dataset only if frogs were captured at the recipient site at least once during the year 0-1 period. We used an analysis workflow similar to that described above. Briefly, the response variable was before-translocation load and the predictor variable was after-translocation load. We compared models with and without group-level effects, and group-level effects included pit_tag_id, pit_tag_id nested within site_id, or pit_tag_id nested within translocation_id. All models used a negative binomial family. Priors, chains, iterations, and checks were as described above.

Code to replicate all of the analyses described above is available from the following GitHub repositories: https://github.com/SNARL1/translocation; https://github.com/SNARL1/cmr-analysis.

Population viability modeling

Model description. To determine the implications of observed 1-year adult survival on the long-term viability of populations established via translocation, we developed a population model for MYL frogs. Our central question was: How does the magnitude and variation in observed adult survival probability across translocated populations affect the long-term persistence probability of populations? We developed a model that tracked seven state variables of a frog population: density of translocated adults (A_T), density of adults naturally recruited into the population (A_R), density of first-year tadpoles (L_1), density of second-year tadpoles (L_2), density of third-year tadpoles (L_3), density of first-year juveniles (J_1), and density of second-year juveniles (J_2). We divided adults into two classes A_T and A_R because there is evidence that the survival probability of translocated adults and naturally recruited adults differs (Figure S7).

We modeled the dynamics of these seven state variables using a discrete-time, stage-structured model where a time step is one year. The dynamics are given by equation 1.

The parameters in this model are yearly survival probability $\sigma_{\cdot}$ (the subscript "$\cdot$" indicates a particular state variable), probability that a female frog reproduces in a given year p_F, number of eggs produced by a female frog in a year that successfully hatch F, probability of a first-year tadpole remaining as a tadpole p_{L1}, probability of a second-year tadpole remaining as a tadpole p_{L2}, and probability of a first-year juvenile remaining as a juvenile p_{J1}, and the probability of a juvenile successfully recruiting to an adult ω.

In this model we ignore density-dependent recruitment because we were interested in the growth of the population from an initial reintroduction and whether this growth was sufficient to prevent extinction over 50 years following the introduction. We also did not directly consider the dynamics of Bd in this model. We made this decision because (i) translocated populations are infected with Bd at high prevalence (23), and (ii) host density does not seem to play a significant role in multi-year Bd infection dynamics in this system (83). Thus, ignoring Bd infection dynamics and instead assuming all host vital rates are in the presence of high Bd prevalence significantly simplifies the model without much loss of realism. Additional details are provided in the SI Appendix.

Model analysis. After parameterizing our model with CMR-estimated adult frog survival probabilities and other known vital rates (Table S2), we performed four analyses. First, we compute the long-run growth rate λ for each of our 12 translocated populations to determine if the populations were deterministically predicted to grow or decline in the long-run. Second, we compute the elasticity of λ to model parameters, to quantify how much changes in adult survival, for example, affected the long-run growth rate. Third, we included demographic and environmental stochasticity in our model and simulated the 50-year viability (i.e., 1 - extinction probability) of populations given an introduction of 40 adult individuals into an unoccupied habitat. Finally, we fit our model to our longest translocation trajectory to confirm that our model could reasonably reproduce the observed recovery trajectories of MYL frogs following reintroductions. Additional details are provided in the SI Appendix. Code to replicate the analyses can be found at https://github.com/SNARL1/translocation.

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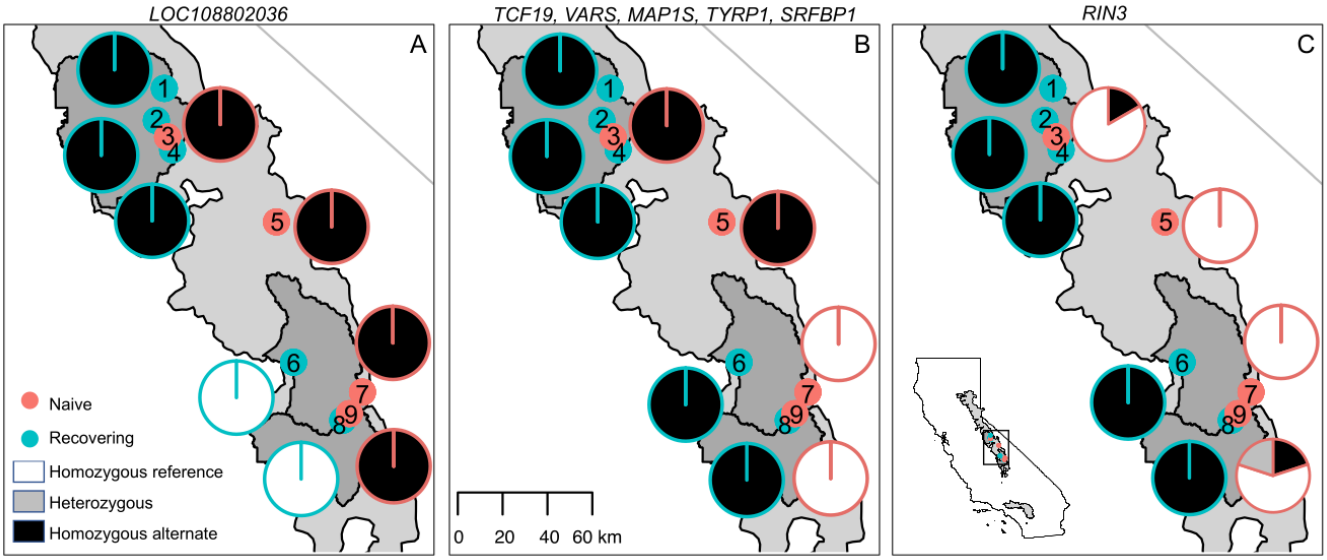

Fig. 1. Evidence for selection on individual variants in recovering MYL frog populations at the landscape scale. For each of the 9 naive and recovering MYL frog populations (indicated by numbered points), adjacent pie charts show allele frequencies for the 11 outlier SNPs from 7 distinct genes: (A) LOC108802036, (B) TCF19, VARS, MAP1S, TYRP1, and SRFBP1, and (C) RIN3. Charts are superimposed on a map of the Sierra Nevada study area, with Yosemite, Kings Canyon, and Sequoia National Parks (from north to south) shown in dark gray, and the range boundary for MYL frogs shown in light gray. The inset map locates the study area and range boundary in California.

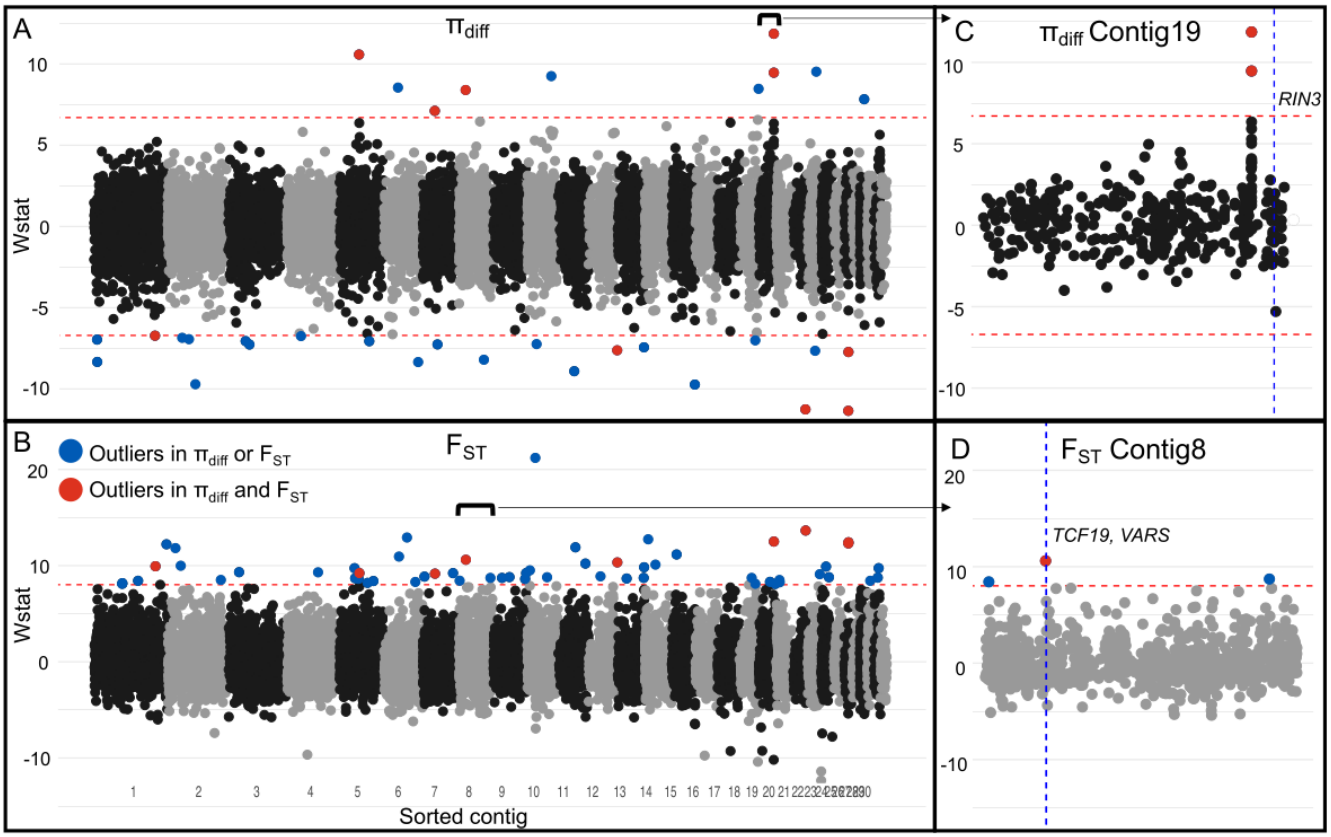

Fig. 2. Evidence for selection on genomic regions in recovering MYL frog populations. Manhattan plot of the results from the splined window analysis showing outlier regions for the difference in (A) nucleotide diversity π_{diff} and (B) F_{ST}. In (A), outlier regions are shown above the upper red dashed line and below the lower red dashed line. In (B), outlier regions are shown above the single dashed red line. Outlier regions for either π_{diff} or F_{ST} are shown in blue and outlier regions for both π_{diff} and F_{ST} are shown in red. (C) Magnified Contig19 from (A) showing two adjacent outlier regions for π_{diff} 12.9Mb upstream of the RIN3 outlier SNP (indicated with a dashed vertical blue line). (D) Magnified Contig8 from from (B) showing the F_{ST} outlier region that includes the outlier SNPs TCF19 and VARS. This region of the genome contains 8 annotated genes known to occur in the extended MHC Class I and III regions.

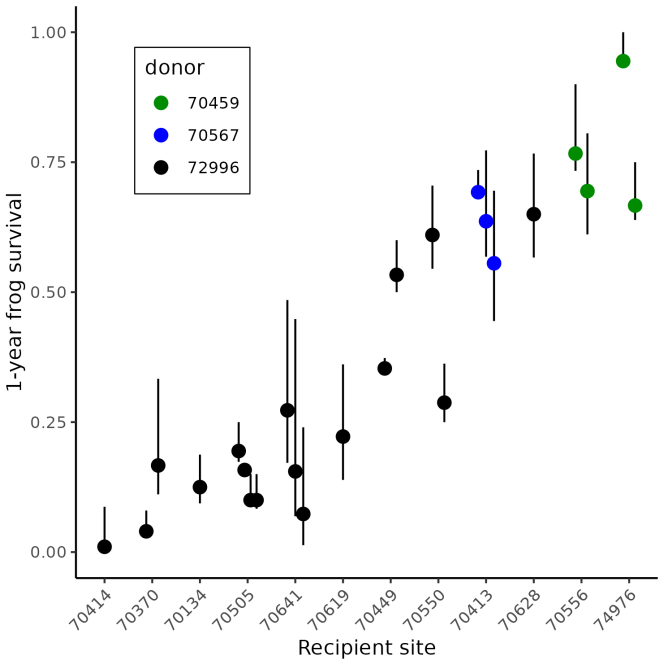

Fig. 3. Evidence for frog survival at the recipient sites following translocation. Median 1-year survival for each cohort of translocated frogs at the 12 recipient sites. Error bars show the 95% uncertainty intervals. Sites are arranged along the x-axis using the average of the median 1-year survival per translocation at each site. Dot colors indicate the donor population from which frogs in each translocated cohort were collected. When multiple translocations were conducted to a site, points and error bars are slightly offset to avoid overlap.

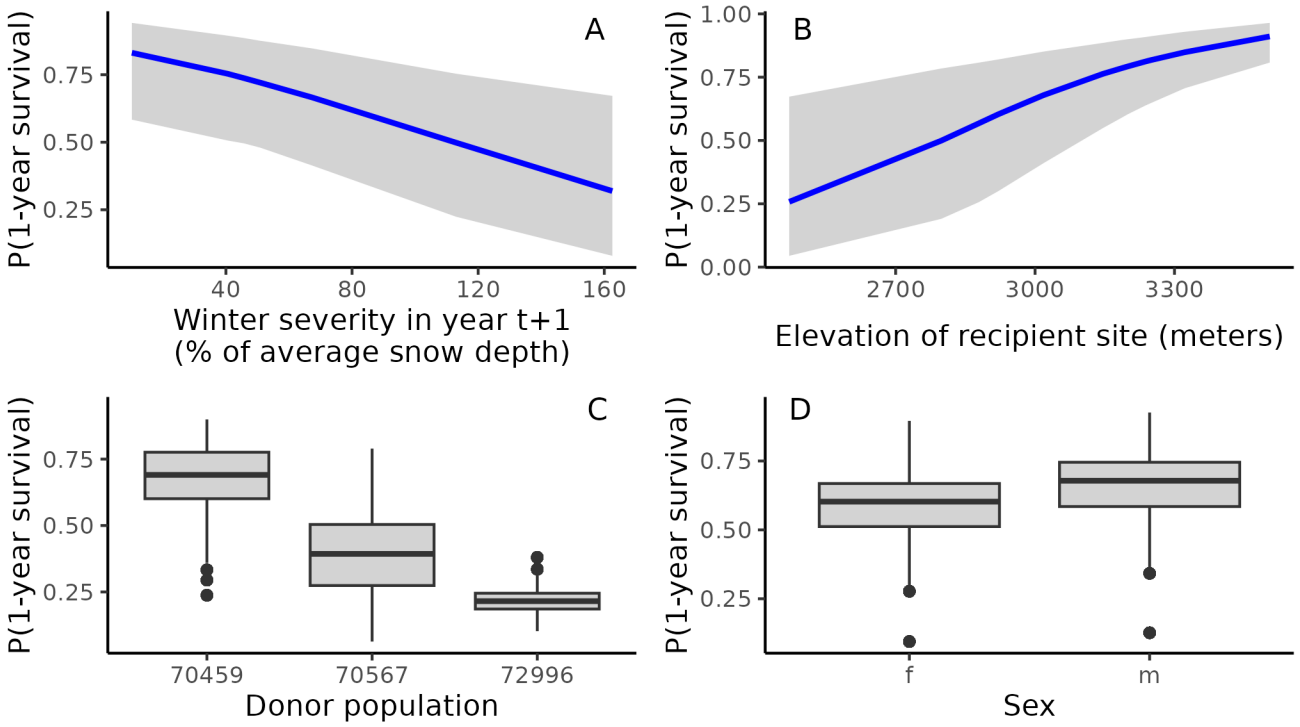

Fig. 4. Evidence for reduced impacts of Bd on MYL frogs as indicated by the lack of an effect of Bd load on survival. Results show conditional effects of the important predictors of 1-year frog survival (survival is expressed as a probability). (A) winter severity in the year following translocation, (B) elevation of recipient site, (C) donor population, and (D) sex. In (A) and (B), blue lines are medians and gray ribbons are 95% uncertainty intervals. In (C) and (D), box plots show medians, first and third quartiles, largest and smallest values within 1.5x interquartile range, and values outside the 1.5x interquartile range.

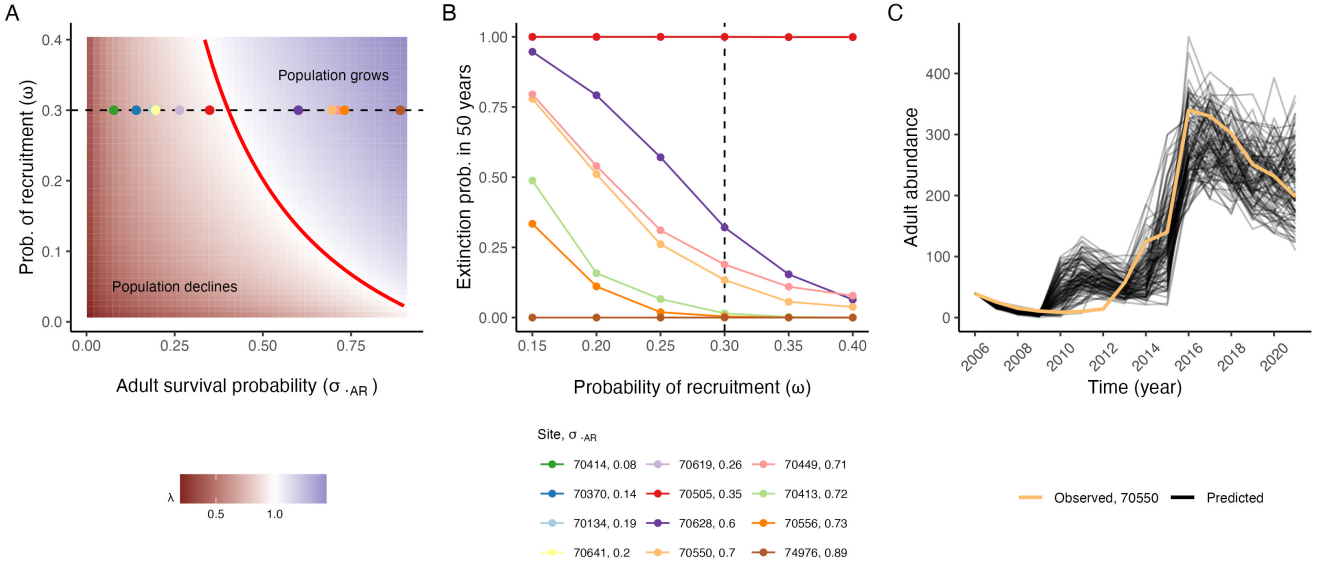

Fig. 5. Population viability analysis of translocated MYL frogs quantified the long-run growth rate and extinction probability of frog populations: (A) Predicted long-run growth rate λ for different values of yearly adult survival probability σ_{A_R} and probability of recruitment ω, given the parameterized, deterministic model. Colored points show the predicted λ values for the twelve translocated populations when probability of recruitment into the adult class is $\omega = 0.3$ (indicated by the dashed line). The red line shows where $\lambda = 1$. Note that the point for 70413 is mostly hidden behind other points. (B) Predicted 50-year extinction probabilities of the 12 translocated populations, given demographic stochasticity, environmental variability in ω, and different mean values of ω. The dashed line shows where $\omega = 0.3$, for comparison to (A). There are 6 lines at extinction probability = 1, 5 of which (70414–70619) are hidden beneath the line for 70505. (C) 100 simulated trajectories (black lines) from the population viability model that most closely matched the observed abundance trajectory of adult amphibians at site 70550 (light orange).

Supporting Information for

Evolutionary rescue and reintroduction of resistant frogs allows recovery in the presence of a lethal fungal disease

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This PDF file includes:

Supporting text
Figs. S1 to S8
Tables S1 to S2
Legends for Dataset S1 to S4
SI References

Other supporting materials for this manuscript include the following:

Datasets S1 to S4

Supporting Information Text

1. Frog evolution in response to Bd

A. Methods. We compared frog genomes sampled in naive versus recovering populations. Bd-exposure histories of these populations are based on a decade or more of data from visual encounter surveys and Bd surveillance using skin swabbing (e.g., 1). Comparing populations with different infection histories allowed larger sample sizes and replication across the landscape. The alternative approach of comparing samples from the same populations before and after Bd exposure isn't feasible in this system because Bd arrived in most MYL frog populations decades ago and population persistence/recovery is rare and unpredictable. As a result, samples from recovering populations collected from before and after Bd exposure are not available and are unlikely to be available in the future.

B. Results. In the Results section of the main paper, we describe the stringent set of outlier SNPs (identified using a Bonferroni-corrected p-value of 0.01). The liberal set, identified using a Bonferroni-corrected p-value of 0.05, included 38 outliers (35 SNPs and 3 INDELS) from 30 distinct genes across 16 contigs. Our analysis found no significantly over-represented GO terms in this set of 30 genes, or in the set of 38 outlier regions identified with the splined window analysis.

In the comparison of individual outlier variants between naive and recovering populations, we detected consistent allele frequency changes across all genetic clusters for only 1 of 7 of the associated genes (RIN3; Fig. 1). However, for the other 6 genes we still found a statistically significant signal of selection in 2 of the 3 genetic clusters (containing populations 6–9; Fig. 1, Figure S1 A). Therefore, although some outlier variant associations have a more limited geographic extent than RIN3, they still describe parallel evolutionary changes following Bd exposure and are therefore interesting candidates for future studies.

2. Frog population recovery

A. Methods. Swab extracts were analyzed using standard Bd DNA extraction and qPCR methods (2), and extracts were analyzed singly instead of in triplicate (3). For analysis of swabs collected during 2005–2014, we used standards developed from known concentrations of zoospores (2), and after 2014, we used standards based on single ITS1 PCR amplicons (4). Based on paired comparisons between samples analyzed using both types of standards, Bd in the study area has an average of 60 ITS1 copies per zoospore. To express all qPCR results as the number of ITS1 copies, starting quantities obtained using the zoospore standard (measured as "zoospore equivalents") were multiplied by 60. In addition, all qPCR quantities (regardless of standard) were multiplied by 80 to account for the fact that DNA extracts from swabs were diluted 80-fold during extraction and PCR (5).

3. Population viability modeling

A. Methods.

Incorporating yearly variability in vital rates We extracted yearly survival probabilities for translocated adults σ_{A_T} and naturally recruited adults σ_{A_R} from the CMR model used to estimate population-level parameters of translocated populations (see "Materials and Methods - Estimation of frog survival and abundance" in main paper). Although we observed yearly variability in adult survival within a population, the magnitude of this variability was small compared to among-population variability (Fig. 3). Thus, we did not include yearly within-population variability in adult survival in this analysis. However, within a population there was substantial yearly variability in the successful recruitment of adults, greater than what we would expect from Poisson variability around a mean value. Therefore, we allowed for yearly variability in the probability of successful recruitment ω (additional details provided in "Estimating model parameters" below).

Estimating model parameters The baseline parameter values for the model and how they were estimated are given in Table S2. Parameters σ_{A_T} and σ_{A_R} were extracted directly from our CMR models (see "Materials and Methods - Estimation of frog survival and abundance" in main paper). For populations where we had a sufficient number of PIT-tagged, naturally-recruited adults, we observed that σ_{A_T} and σ_{A_R} could be notably different, with $\sigma_{A_R} > \sigma_{A_T}$ (Figure S7). For populations lacking sufficient numbers of naturally-recruited adults, we were unable to directly estimate σ_{A_R}, and instead set $\sigma_{A_R} = \sigma_{A_T}$.

Model analysis and simulation We performed four analyses on our model. First, we considered a deterministic version of our model with no yearly heterogeneity in probability of successful recruitment ω, and calculated the predicted long-run growth rate λ of a population for different values of σ_{A_R} and ω. We then fixed $\omega = 0.3$ and calculated the predicted growth rate of our 12 populations.

Second, we performed a local elasticity analysis on λ with respect to parameters ω, σ_{A_R}, and F to determine how small changes in these parameters could influence the long-run deterministic growth rate of populations (Figure S8).

Third, we defined a version of the model with demographic and environmental stochasticity, where environmental stochasticity was represented by among-year variability in ω. We used this model to simulate a one-time introduction of 40 translocated adult frogs. We ran this simulation 1000 times for each population and computed the probability of a population becoming extinct after 50 years given the observed parameter values and environmental stochasticity in ω. We varied the mean recruitment

probability ω from 0.15 and 0.4 and drew values of ω each year from a beta distribution with a dispersion parameter of $\phi = 2$ (when $\omega = 0.5$ and $\phi = 2$ the beta distribution is uniform between 0 and 1).

Finally, we assessed whether our stochastic model could reproduce observed trajectories of population recovery. We focused on population 70550 because this was our longest CMR time series for a translocated population and because this population shows evidence of substantial post-translocation increases in adult abundance associated with population establishment and recovery. We simulated our model for 16 years, repeating the simulation 50,000 times. For each run and each year, we drew ω from a uniform distribution between 0 and 1 (or equivalently a beta distribution with mean 0.5 and $\phi = 2$). Using Approximate Bayesian Computing and rejection sampling (6), we identified the top 2% of trajectories (i.e., 1000 trajectories) that minimized the sum of squared errors between the observed and predicted data. The ω values associated with these "best" trajectories represented an approximate posterior distribution (7). Using these best fit trajectories, we assessed whether our model could qualitatively describe the patterns of recovery in the observed data for population 70550.

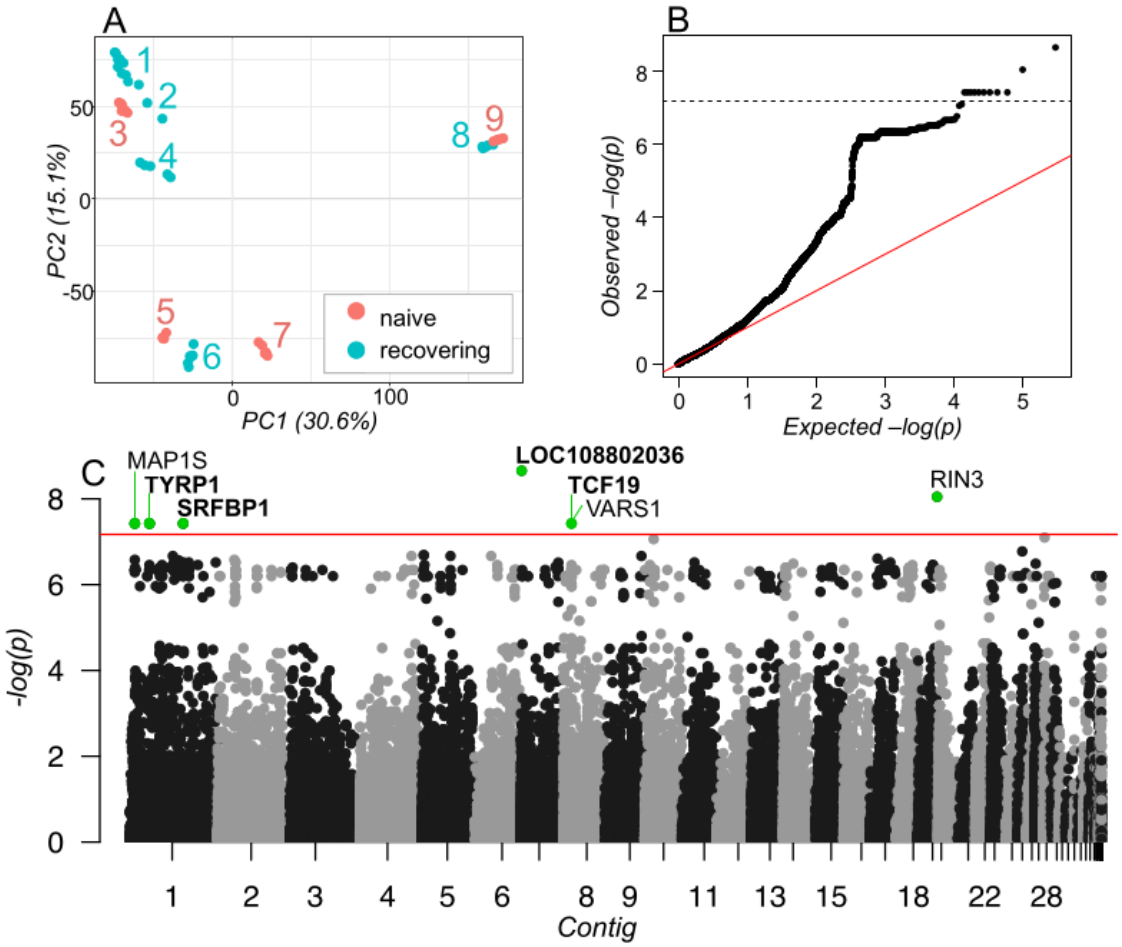

Fig. S1. Evidence for selection on individual variants in recovering MYL frog populations. (A) PCA calculated from binary SNPs showing the genomic relationship of samples. Numeric labels and colors match those in Fig. 1A. Populations 1-7 are *R. sierrae* and populations 8 and 9 are *R. muscosa*. (B) qqplot showing observed and expected p-values for 148,307 SNPs and INDELS. Dashed line shows p-value that identifies outliers. (C) Manhattan plot showing p-value for each SNP. SNPs are sorted by genomic position and contigs are sorted by size. Red line shows p-value that identifies outliers. Outlier SNPs above this threshold are highlighted and labeled. Bold labels indicate the presence of at least one non-synonymous SNP in that gene.

Roland A. Knapp, Mark Q. Wilber, Allison Q. Byrne, Maxwell B. Joseph, Thomas C. Smith, Andrew P. Rothstein, Robert L. Grasso, Erica Bree Rosenblum

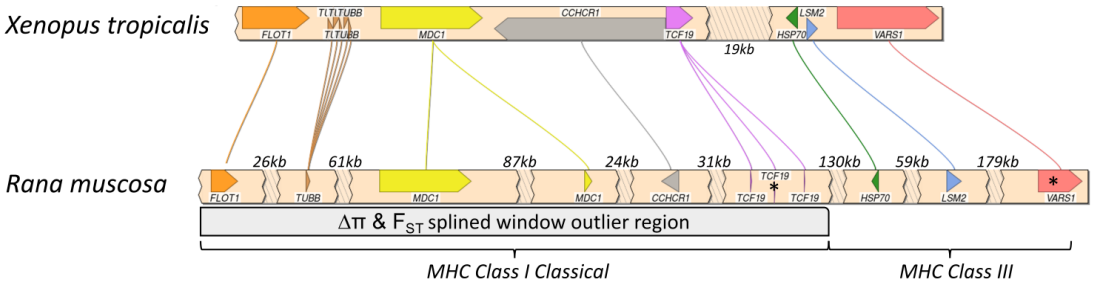

Fig. S2. Synteny plot showing conserved gene order in *Xenopus tropicalis* and *Rana mucosa* for the outlier region containing MHC Class I Classical and MHC Class III gene regions. The plot was created with SimpleSynteny (8) using *Xenopus tropicalis* Chromosome 8 (NC_030684.2, genbank accession GCA_000004195.4) and *Rana mucosa* Contig19. Asterices indicate the location of SNP outliers in the TCF19 and VARS1 genes. Gap sizes for each contig representation are labeled.

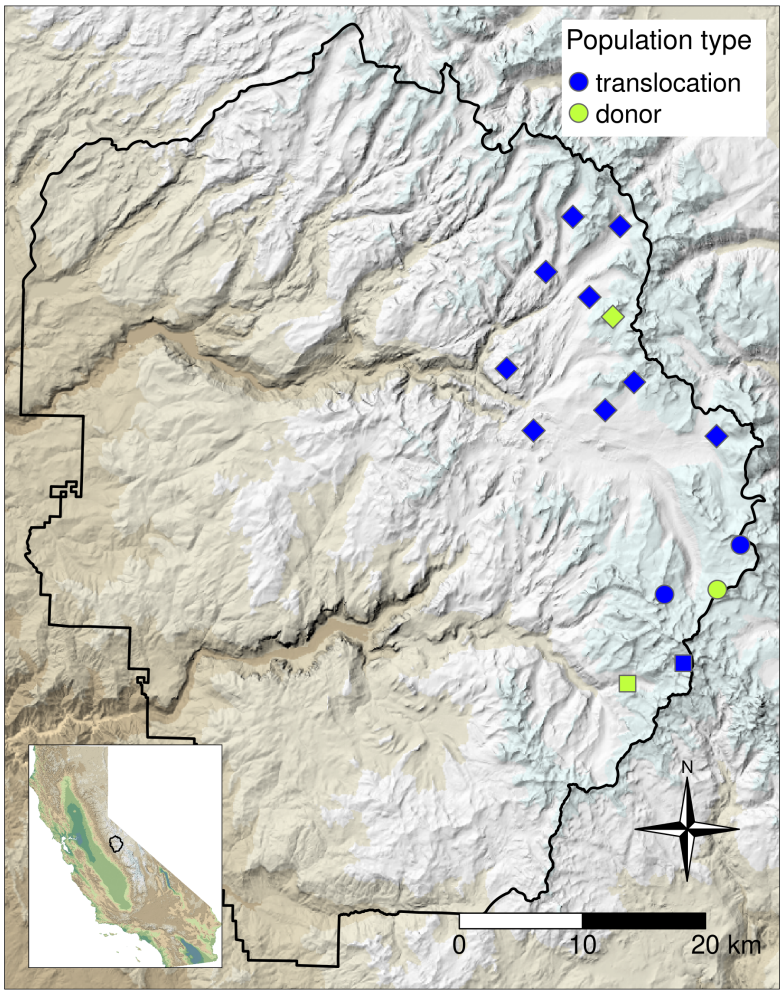

Fig. S3. Map showing the locations of translocated and donor MYL frog populations in Yosemite National Park (park boundary indicated by black polygon). Symbol shapes indicate the donor population used for each translocation site. To obscure the exact locations of populations, random noise was added to all point coordinates. Inset map shows the location of Yosemite within California. In both maps, elevation is indicated by the colored hillshade layer (dark green = lowest elevation, white = highest elevation).

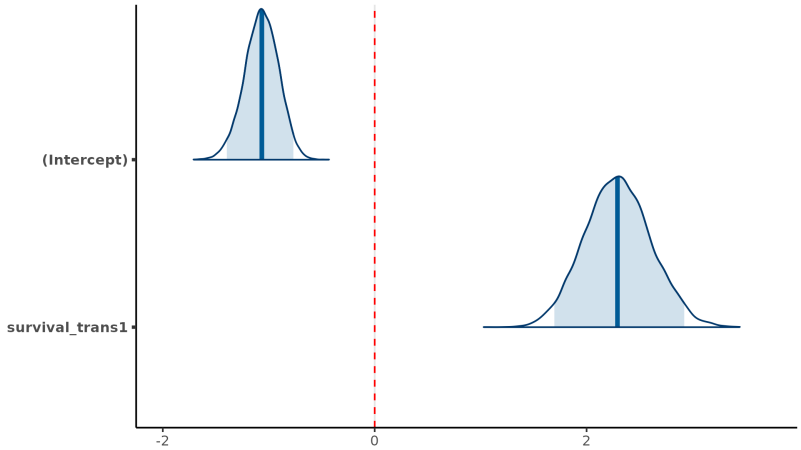

Fig. S4. For the best model describing the average 1-year survival of frogs in the first translocation to a site as a predictor of survival of frogs in all subsequent translocations to that site, estimated posterior density curves and shaded 95% uncertainty intervals for the intercept and single predictor variable. In the Bayesian framework in which the model was developed, a variable is considered an important predictor if the associated uncertainty interval does not overlap zero (indicated by the dashed red line).

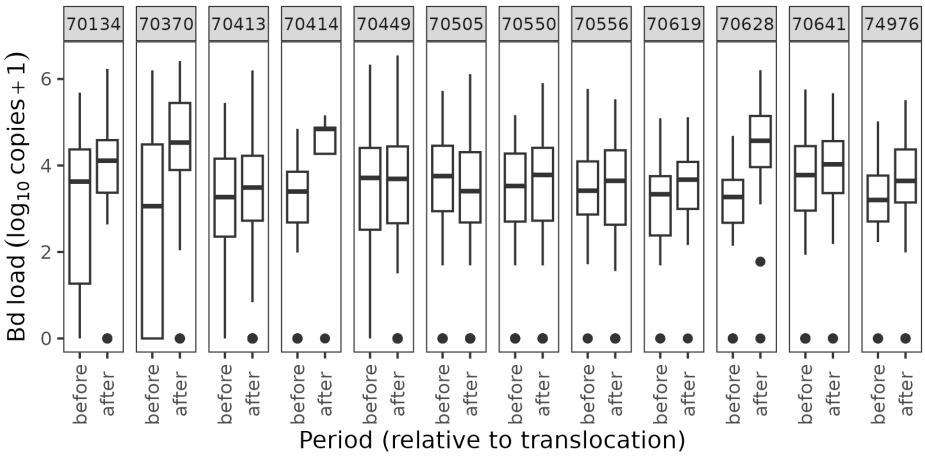

Fig. S5. Evidence that frogs translocated from recovering populations can maintain the benefits of resistance/tolerance in non-natal habitats. For frogs translocated to each of the 12 recipient sites, Bd loads for the period immediately prior to translocation versus during the 1-year period after translocation. Bd loads are expressed as the number of ITS1 copies per skin swab, as estimated by qPCR of the Bd ITS1 region. Box plots show medians, first and third quartiles, largest and smallest values within 1.5x interquartile range, and values outside the 1.5x interquartile range. Loads indicative of severe disease are > 5.8 ITS copies (on a $\log_{10}$ scale).

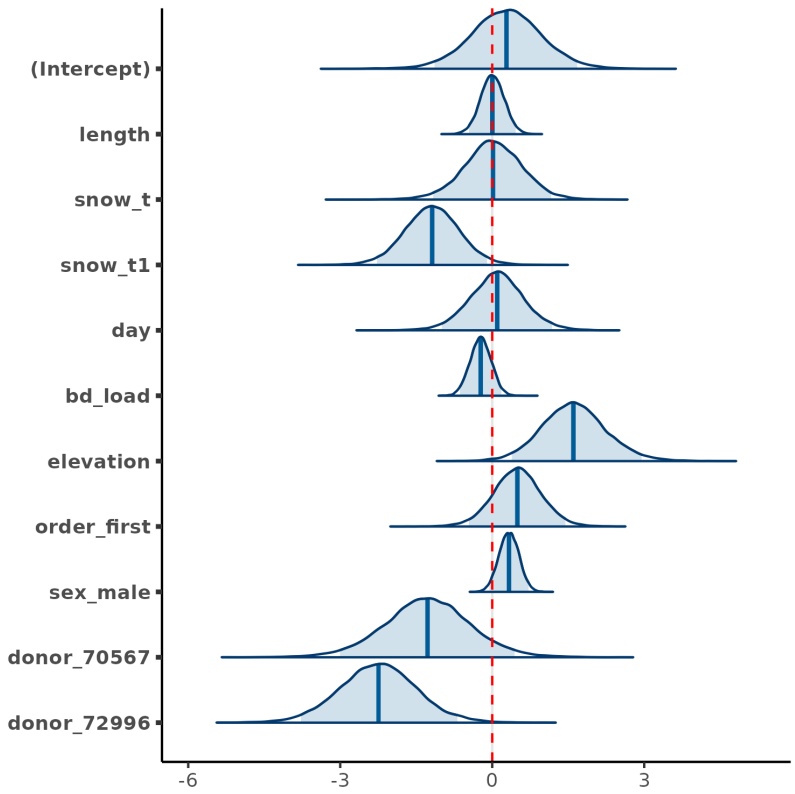

Fig. S6. Evidence that Bd load is not an important predictor of post-translocation frog survival. For the best model identifying predictors of 1-year frog survival following translocation, estimated posterior density curves and shaded 95% uncertainty intervals for the intercept and all predictor variables. In the Bayesian framework in which the model was developed, variables are considered important predictors if the associated uncertainty interval does not overlap zero (indicated by the dashed red line). Predictor variables shown on the y-axis are defined as follows: length = frog size, snow_t = winter severity in the year of translocation (measured on April 1), snow_t1 = winter severity in the year following translocation (measured on April 1), day = day of year on which a translocation was conducted, bd_load = Bd load, elevation = site elevation, order_first = within-site translocation order, sex_male = frog sex, donor_70567 and donor_72996 = donor population.

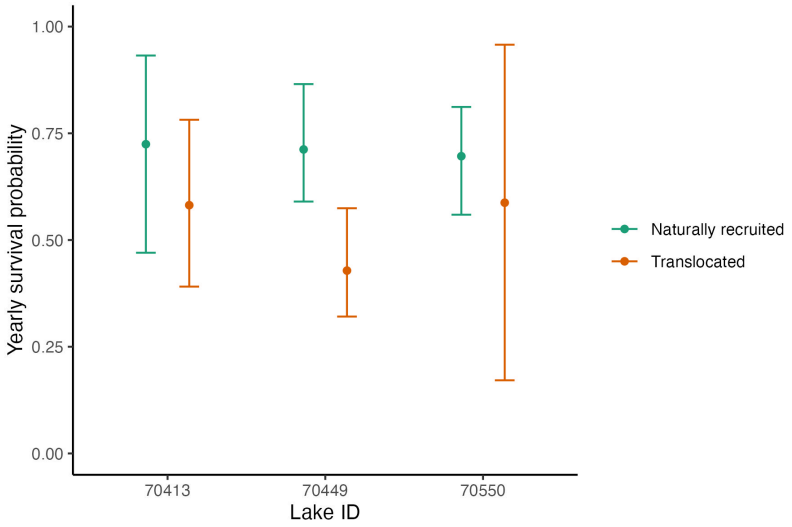

Fig. S7. Evidence that frog resistance/tolerance in non-natal habitats is maintained across generations. Comparison of the average yearly adult survival probabilities for adults translocated to each of 3 sites versus adults that were naturally recruited at each site (as a result of reproduction by translocated frogs). In contrast to Fig. 3, these are not survival probabilities from the first year following translocation, but instead represent averaged survival probabilities across multiple years and cohorts. Points are median estimates and error bars give the 95% uncertainty intervals around the estimates, accounting for yearly variation in survival probabilities. All estimates were derived using the mrmr package.

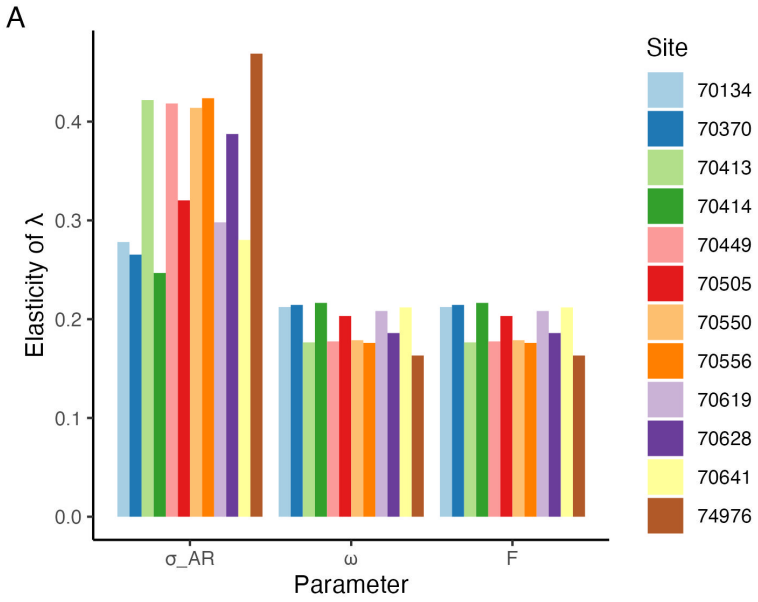

Fig. S8. Sensitivity analysis of the stage-structured MYL frog model. Elasticity of λ with changes in 3 parameters: σ_{A_R} (yearly survival probability of naturally recruited adults), ω (yearly probability of successful recruitment from juveniles to adults), and *F (*number of eggs produced by a female frog in a year that successfully hatch). Elasticity is calculated at the default parameter values for each population and ω = 0.3.

A.1. Tables.

Table S1. Association between the proportion of populations translocated early versus late in the study period (< 2013 or $\geq$ 2013, respectively) and probability of survival (< 0.5 or $\geq$ 0.5). Based on the viability analysis, survival probabilities < 0.5 and $\geq$ 0.5 produced 50-year extinction probabilities of 1 and < 0.5, respectively.

Period	Survival probability	Number of translocations	Total translocations	Proportion of translocations
early	< 0.5	4	5	0.800
early	≥ 0.5	1	5	0.200
late	< 0.5	2	7	0.286
late	≥ 0.5	5	7	0.714

Table S2. Description and values of parameters used in the model. All survival probabilities are in the presence of the fungal pathogen Bd.

Parameter	Value	Source
σ_{L_1}, Yearly survival probability of year 1 tadpoles	0.7	Estimated from field data, observations, natural history knowledge
σ_{L_2}, Yearly survival probability of year 2 tadpoles	0.7	Estimated from field data, observations, natural history knowledge
σ_{L_3}, Yearly survival probability of year 3 tadpoles	0.7	Estimated from field data, observations, natural history knowledge
σ_{J_1}, Yearly survival probability of year 1 juveniles	0.25	Estimated from field data, observations, natural history knowledge
σ_{J_2}, Yearly survival probability of year 2 juveniles	0.5	Estimated from field data, observations, natural history knowledge
σ_{A_R}, Yearly survival probability of naturally recruited adults	Varies by population	Estimated from mark-recapture studies
σ_{A_T}, Yearly survival probability of translocated adults	Varies by population	Estimated from mark-recapture studies
p_{L_1}, Probability of a year 1 tadpoles remaining as a tadpoles	1	Estimated from field data, observations, natural history knowledge
p_{L_2}, Probability of a year 2 tadpoles remaining as a tadpoles	0.25	Estimated from field data, observations, natural history knowledge
p_{J_1}, Probability of a year 1 juvenile remaining as a juvenile	0.25	Estimated from field data, observations, natural history knowledge
p_F, Probability of a adult female reproducing in a year	0.5	Could be as high at 1, based on field observations
F, Number of surviving eggs produced by an adult female	100	From observations of captive frogs
ω, Probability of juvenile successfully recruiting to an adult	Varies yearly	Explored different values of this parameter

SI Dataset S1 (gemma_outliers_all.csv)

Set of liberal SNP and INDEL outlier variants (Bonferroni corrected p-value < 0.05), identified via GEMMA.

SI Dataset S2 (gemma_outliers_strict_freq.csv)

Set of strict SNP and INDEL outlier variants (Bonferroni corrected p-value < 0.01), identified via GEMMA. Additional information includes variant location within the gene (predicted_gene_loc) and whether the variant is synonymous or nonsynonymous (predicted_effect_AA).

SI Dataset S3 (spline_window_shared_outliers.csv)

Description of overlapping F_{ST} and π_{diff} outlier windows, as identified in the splined window analysis.

SI Dataset S4 (spline_window_gene_details.csv)

Annotation information for all genes within each of the overlapping outlier windows in dataset S3

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