

Table S1: Information summary on species and their genetic diversity (GD), fitness proxies and correlations between both as well as interpretation of the results							
Species, study country, region, no. and size of SS	Molecular marker / method	Genetic diversity	Proxy for fitness	Statistical model	Correlation Bold = significant	Remarks / Interpretation of results	Citation
Bufo bufo UK, TE 12 SS: 1) 8 small urban pop, N = 6 - 200 adults; 2) 4 large rural pop, N = 500 – 5000 adults	27 allozymes (12 SS) 3 minisats (5 SS)	Urban Rural F _{ST} = 0.53 0.29 P = 14.8% 25% Na/l= 1.18 1.36 F _{ST} = 0.23 0.066 H _O = 0.035 0.017 Na/l= 3.89 5.00 H _O = 0.36 0.43	Tad survival Tad deformity	Correlation analyses	Survival Deformity P: r = 0.74 Na/l: r = 0.67 Na/l: r = 0.85 H _O : r = -0.65	Higher GD in large rural pops than in smaller urban pops. GD is pos. correlated with tadpole survival, but neg. with developmental abnormalities; reduction in GD and fitness in urban toads	Hitching & Beebee 1998 [36]
Bufo calamita UK, TE 38 SS (34 in UK) variable N	8 microsats 33 SS	P = 38-75% Na/l = 1.5 – 2.8 H _E = 0.19-0.34 H _O = 0.22-0.38	Tad survival Tad growth rate In 6 test SS	Correlation analyses	No correlation between survival and GD ; growth rate was correlated with H _E (r=0.6 - 0.9 , P< 0.01), H _O , P, Na/l; low hatch rate in pop with lowest GD	H _E lower in range edge pops; H _E pos. correlated with fitness (growth rate); tad from smallest and isolated pop exhibited lowest fitness and H _E	Rowe et al. 1999 [49]
Hyla arborea Sweden, TE 10 SS (ponds)	18 allozymes	Mean GD : 1.06 alleles per locus	Egg hatch rate Tadpole survival	Correlation analyses	Very low GD ; no correlation with fitness	Survival was lower in isolated ponds compared to more central ponds	Edenham et al. 2000 [54]
Bufo calamita UK, TE 1 SS: large natural population, N ~ several thousand adults	5 microsats Experiment: high & low food regime	For individual tadpoles: H = 0.42 – 0.73 Mean d ² = 5.76-14.02 Outbreeding d ² = 12.2 – 25.5 Scaled d ² = 0.13 – 0.19	Tad survival Tad growth rate Tad develop. rate Tad time to metamor.	Correlation analyses	No correlation between fitness and genetic measures; but fitness better under high food condition	No relationship between fitness related traits and individual genetic diversity	Rowe & Beebee 2001 [32]
Rana temporaria UK, TE 1SS: large natural population with immigration, N ~ tens of adults	7 microsats Experiment: high & low food regime	For individual tadpoles: H = 0.50 – 0.65 Mean d ² = 26.5 – 62.4 Outbreeding d ² = 36.1 – 134.0 Scaled d ² = 0.01 – 0.067	Tad survival Tad growth rate Tad develop. rate Tad time to metamor.	Correlation analyses	No correlation between fitness and genetic measures, but fitness better under high food condition	No relationship between fitness related traits and individual genetic diversity	Rowe & Beebee 2001 [32]
Bufo calamita UK, TE 2 SS: 1) large pop several hundred toads	8 microsats Experiment: Pop X predation X competition X	No data: lower GD in small compared to large pop (extracted from Rowe et al. 1999)	Tad survival Tad growth rate	Correlation analyses	Survival and growth rate (during first 10 days) higher in large than small pop. Predation & desiccation reduced survival; predation	Lower fitness in small than large pop; best explained by increased genetic load in small isolated pop; pop at risk due to small N _E	Rowe & Beebee 2003 [48]

2) small isolated pop $N_C < 50$	desiccation treatment				& competition reduced growth rate		
<i>Rana temporaria</i> Finland, TE 4 SS In all pops females $N < 100$	8 microsats Experiment: 3 temp. treatm: 14°C, 18°C, 22°C Low & high food	Individual Measures: Parents: H_0 , d^2 , r_{xy} Tad: H_{EST} and d^2_{EST} for tadpoles	Tad survival Tad develop. rate Tad growth rate	GLMM	Survival neg. correlated with r_{xy} , pos. correlated with H_{EST} , (d^2_{EST} n.s.), develop. rate pos. correlated to d^2_{EST} , growth rate neg. correlated with d^2_{EST}	GD interacts with food and temperature; GFCs are present for survival, seem to be sensitive to environment, more pronounced in stressful condition	Lesbarrères et al. 2005 [50]
<i>Rana latastei</i> Italy, Slovenia, TE 6 SS: embryos from 10 clutches per pop	6 microsats Experiment: high and low exposure of tad to <i>Ranavirus</i>	AR HS P	Tad survival	GEE, Regression analyses	Better survival in population with higher GD in low exposure treatment ($P > 0.0001$); high exposure led to high mortality	Lower survival in western isolated pops with low GD when exposed to novel pathogen; eastern pops have higher potential to evolve resistance	Pearman & Garner 2005 [55]
<i>Rana sylvatica</i> Connecticut, TE 1 SS: $N \sim 110$ adults, 292 metamorphs (+ 1 SS with too low sample size)	9 microsats	Parental r_{xy} Eggs / Tad: MLH	<u>In the wild</u> Sibship survival to metamorphosis Indiv. tadpole weight <u>In the lab</u> Egg survival Tadpole survival Tadpole weight Tadpole devel.stage	Linear regression	Sibship survival pos. correlated with MLH ($R^2 = 0.30$) and neg. correlated with r_{xy} ($R^2 = 0.29$), weight not correlated with GD no correlation of fitness proxies with MLH or r_{xy} in the lab	Inbreeding (measured as MLH or r_{xy}) negatively affects survival in the wild, but not in the lab	Halverson et al. 2006 [56]
<i>Rana sylvatica</i> Ohio, TE 12 SS	RAPD Experiment: 3 UV-B radiation treatm. of eggs: sun light, filter, acetat sheet	GSI for each population (no data)	Egg survival Tad survival Tad deformity	MANOVA	All 3 fitness traits neg. correlated with GD ; Low GD correlated with higher larval mortality and deformity when exposed to UV-B light (both $P > 0.0001$)	Fragmented populations with low GD might be at increased risk of mortality when interacting with environmental stressors like direct sun radiation	Weyrauch & Grubb 2006 [57]
<i>Rana latastei</i> Italy, TE 10 SS: 4 isolated, 6 non-isolated pops	6 microsats	Non-isolated / Isolated Mean $p_w F_{ST} = 0.18 / F_{ST} = 0.34$ Estimate of GD : PCA score including AR, P, H_0 AR = 1.4 – 2.6 $H_0 = 0.12 – 0.23$ $H_E = 0.16 – 0.24$	Egg hatch rate	Correlation analyses	No correlation between GD and hatch rate ($r=0.14$, $P=0.75$), correlation ($r=0.82$, $P=0.023$) when controlling for distance from glacial refugium; Hatch rate higher in continuous (0.77-0.98) than isolated (0.38-0.54) pops.	Overall GD is low; GD lost through recent isolation had negative effect on fitness; habitat restoration is recommended	Ficetola et al. 2007 [39]

<i>Rana temporaria</i> Sweden, TE 6 areas with 9 SS each; 3 fragmented (F) and 3 continuous (C) areas: N _F = 6-154, N _C = 25-1470	7 microsats Experiment: 4 fragmented & 4 continuous SS with low vs. high GD	Fragmented / Continuous Global F _{ST} = 0.071 F _{ST} = 0.02 AR = 3.3 – 3.7 AR = 4.3 – 5.0 H _O = 0.50-0.62 H _O = 0.71-0.78 HS = ??	Tad body size Tad survival probab.	Correlation analyses	Body size Survival probab. Ho: r = 0.73 Ho: r = 0.77 Hs: r = 0.70 Hs: r = 0.88 AR: r = 0.31 AR: r = 0.70	Higher GD in continuous habitat; positively correlated with fitness traits; larvae from frag. habitat were smaller and survived less	Johansson et al. 2007 [37]
<i>Rana temporaria</i> Finland, TE, 2 SS = 2 ponds, small N	8 microsats	Individual H _O of tad, father(sire) and dam (mother)	Tad weight Tad age at metamorphosis	GLMM	Tad weight was influenced by H _O (Linear Model); P<0.001) and dam H _O (P<0.047); no genetic but “pond” influence on age at metamorph.	Since weight is correlated with fitness in amphibians, GD might be an important component of individual fitness in <i>R. temporaria</i>	Lesbarrères et al. 2007 [58]
<i>Bufo calamita</i> Sweden, TE 6 SS all pops are large	105 AFLPs Experiment: 3 temp. treatm: 27°, 19°C, variable	Global F _{ST} = 0.16 Pairwise F _{ST} = 0.06-0.27 47-91% variable AFLP loci	Tad survival	GLMM	GD positively correlated with survival in cold treatment (19°C) where survival was highest (P = 0.016)	Low genetic variation does not seem to cause a fitness cost under stressful condition (variable temp.)	Rogell et al. 2010 [38]
<i>Rana temporaria</i> UK, TE 8 SS Urban (4 SS) and rural (4SS) habitats	9 microsats MHC II β exon 2 Experiment: 3 temperature regimes: 10°C, 14°C, 21°C	Mean pw Msat F _{ST} = 0.051, Mean pw MHC F _{ST} = 0.099 Microsats: Rural Urban AR = 6.3-6.9, AR = 5.8-6.8 H _O = 0.62-0.74 H _O = 0.68-0.84 H _E = 0.68-0.72, H _E = 0.68-0.73	Tad growth rate Tad survival	Correlation analyses, Chi ² -Test	No correlation between GD (both markers) and fitness; Dying vs. surviving tad: MHC allele C was over- represented, allele H was underrepresented in dead tad	No differences in GD or survivorship between rural and urban pops; growth rate higher in urban areas. Functional loci are important when assessing pop genetic health	Zeisset & Beebee 2010 [40]
<i>Hyla arborea</i> France, TE 4 SS: 2 large and 2 small, isolated & genetically eroded pops	15 microsats Experiment: inter- and intrapopulational crosses	Estimates of H _{EST} per family	Tad body mass, Tad length Tad stage at day 23	Linear model	Tad performances better in non-frag. pops than isolated pops; correlated with H _{EST} : Stage: F = 14.19, P < 0.001; Mass: F = 9.18, P = 0.003; Length: F = 10.77, P = 0.001 Stage and length increased in interpop. crosses in isolated pops; mass increased in crosses from isolated and non-frag. pops	Inbreeding depression (within) vs fixation load (among pops)? Support for genetic drift leading to fixation of slightly deleterious alleles; translocating individ. from moderately divergent pops might increase fitness in tadpole stage	Luquet et al. 2011 [59]
<i>Bufo calamita</i> UK, TE Region 1: uninfected, N _C = 140	8 microsats MHC II β exon 2	<u>Microsats</u> : Region 1 Region 2 H _E = 0.1 H _E = 0.41 AR = 1.33 AR = 3.14 5 <u>MHC</u> allele frequency	Tad growth rate Tad develop. time Tad survival	KW-ANOVA, Chi ² -Test	Microsat GD not correlated to fitness. No differences in fitness between infected and uninfected region; toads in both areas equally healthy.	Certain MHC alleles might be associated with infection. Directional selection favouring alleles conferring resistance to Bd	May et al. 2011 [52]

Region 2: infected with <i>Bd</i> , N _c = 282					MHC diversity higher in uninfected region.		
<i>Lithobates yavapaiensis</i> Arizona, ST 5 SS	MHC II β exon 2 14 microsats <i>Bd</i> infection experiments: yes or no	Individual and population MHC heterozygosity and MHC allele frequencies Population structure (microsats): K = 6	Adult frog survival	Cox proportional hazard model, Fishers exact test	MHC heterozygotes & MHC allele Q associated with survival	Variation among pops in <i>Bd</i> infection and MHC alleles. Fitness advantage conveyed by MHC heterozygosity & allele Q	Savage & Zamudio 2011 [67]
<i>Hyla arborea</i> France, TE 5SS: 3 large and 2 small, isolated & genetically eroded pops	Intrapopul. Crosses: 5 – 9 clutches Low & high <i>Bd</i> dose	<i>GD</i> known from previous studies	Tad stage at metamorphosis Tad mass Tad time to metamor. Survival of froglets	GLMM, ANOVA, ANCOVA	No <i>Bd</i> detection in adults or tad; Longer time to metamor. in isolated pops exposed to high <i>Bd</i> ; Mass higher in isolated pops, but more reduced when exposed to high <i>Bd</i>	Tad seem to prevent or clear infections rapidly; At high <i>Bd</i> dose survival of froglets from nonfragmented pops. slightly higher, but survival higher & higher mass of isolated tadpoles in control group	Luquet et al. 2012 [47]
<i>Hyla arborea</i> France, TE 4 SS: 2 large and 2 small, isolated & genetically eroded pops	15 microsats n = 150 females, 296 males	Na/I = 3.6 – 5.6 AR = 3.6 – 5.5 H _E = 0.37-0.46 H _O = 0.38 -0.46 F _{IS} = -0.08 – 0.04 Indiv. MLH	Adult body size Body condition Reproductive investment: males: chorus attendance; females: clutch mass & egg size	Linear models	No correlation between fitness measurements and indiv. MLH; larger frogs invested more in reproduction.	Lack of <i>GFC</i> on adult traits probably because inbreeding is low in these populations; (<i>inbreeding avoidance by female mate choice?</i>); or selection against unfit genotypes in tad	Luquet et al. 2013 [60]
<i>Lithobates sevosus</i> Mississippi, ST 1 SS, isolated and small pop size, probably inbred and bottlenecked	8 microsats	Individuals: eggs metamorphs, adults: MLH IR	Egg mortality Tad survival to metamorphosis	Regression analyses	MLH positively correlated with survival of egg clutches ($r^2 = 0.15$); Metamorphs had lower F _{IS} , lower IR and greater MLH than adults and eggs!	Conclusion: most inbred tad did not survive to metamorphosis; survival of individual with greater <i>GD</i> might prolong persistence of isolated pop	Richter & Nunziata 2013 [61]
<i>Anaxyrus boreas</i> USA, Montana, TE One large sample area: Glacier National Park	11 microsats <i>Bd</i> : n =199	AR = 9.9-13.0 (for 3 groups) H _O = 0.62-0.71 H _E = 0.68-0.74 F _{IS} = 0.04-0.09 Indiv. MLH Population structure: K=2	Adults (> 1year old) <i>Bd</i> presence	Hierarchical logistic regression model	Overall toads have high genetic diversity MLH was positively related to <i>Bd</i> infection (P=0.03)	Population effect: immigration might increase heterozygosity as well as greater exposure to <i>Bd</i>	Addis et al. 2015 [45]
<i>Lithobates yavapaiensis</i> Arizona, ST 12 SS	14 microsats 19 bioclimatic variables	pw F _{ST} = 0.17-0.60 (mean = 0.32) AR, F _{IS} , H _O = 0.38 – 0.68	Adults <i>Bd</i> intensity <i>Bd</i> prevalence	GLMs	AR + H _O highest in <i>Bd</i> tolerant pops, intermediate in susceptible, and lowest in uninfected pops; Host <i>GD</i>	Warmer temp. associated with higher <i>Bd</i> prevalence & intensity; Mortality lower in pops with higher	Savage et al. 2015 [41]

	(related to temp. & precipitation)	Population structure: K=10	Mortality prevalence per population		(PC calculated from Ho, Fis, AR) alone explained mortality $r^2 = 0.499$, $P=0.015$	GD measures; GD lowers Bd susceptibility, important to preserve GD for species persistence	
<i>Physalaemus pustulosus</i> , Panama, TR 3 SS: 2 lowland, 1 highland, sampled 2010 & 2103	5 microsats MHC II β 1	High genetic diversity: $H_E = 0.57 - 0.93$ (across loci) MHC II β 1 allele frequency	Adults Bd infection	?	Lowland frogs less infected than highland frogs; higher frequency of MHC II β 1 P9 alleles associated with resistance to Bd in highland populations	Strong selection on MHC II β 1 P9 alleles in highly infected populations. Potential fitness cost: Homozygosity at this loci may decrease capacity to bind antigens of other pathogens	Kosch et al. 2016 [68]
<i>Pseudacris ornata</i> SE USA, ST 15 SS	7 microsats n = 327	AR H_E	Adults Bd infection 11 (out of 15) pops. infected with Bd	GLMs	Pop average H_E correlated with Bd prevalence; Decreasing temperature correlated with increasing Bd prevalence and Bd intensity	Possibly in pop. with now low prevalence, selection has pushed tolerant genotypes towards fixation resulting in decreased heterozygosity	Horner et al. 2017 [51]
<i>Bombina variegata</i> Germany, TE 19 SS $N_E = 24-128$	6 microsats n = 274	Indiv. MLH H_E	Adults Bd infection 14 out of 19 pops infected with Bd	GLMs	No correlation between indiv. MLH or pop level H_E with Bd infection	Bd presence did not influence survival or body condition; no evidence that genetic diversity or environmental variables affect Bd infection probability	Wagner et al. 2017 [62]
<i>Plethodon cinereus</i> Virginia, TE 1SS	7 microsats n = 109 adults n = 35 juveniles	Indiv. MLH	Adult home range size Juvenile growth	GLM, GLMM	MLH pos. correlated with home range size; tendency that MLH pos. affects growth, no effect of MLH on survival	GD might influence behaviour and growth via foraging	Liebgold et al. 2018 [63]
<i>Hynobius tokyoensis</i> Japan, ST 32 SS $N_C = 1 - 117$	Cytb 5 microsats	$\pi = 0.00 - 0.04$ $H_E = 0.10 - 0.51$	Hatchability of clutches in the field	Path analysis	For both species: Temperature, altitude & land-use explained GD		Okamiya & Kusano 2018 [33]
<i>Rana ornativentris</i> Japan, ST 38 SS $N_C = 2 - 500$	Cytb 4 climatic, 3 topographic & 4 land-use variab.	$\pi = 0.00-0.24$	Hatchability of clutches in the field	Path analysis	GD positively affected mean hatchability (path analysis coefficient = 0.27, for both species together)	Forested area ratio positively affected population size (n.s.), GD and mean hatchability	

<p><i>Pseudophryne corroboree</i> Australia, ST 4 SS, small census size N_C = 13 males</p>	<p>SNPs n = 16 - 22</p> <p>MHC IA n = 16 - 22 Experiment: Bd infection</p>	<p>Indiv. genome-wide H H_E = 0.33 - 0.37 H_O = 0.36 - 0.40 F_{IS} = -0.050 - -0.073 AR = 1.34 - 1.38 F_{ST} = 0.106 - 0.191 Population structure K=2</p>	<p>Adult frogs Infection load Number of days survived</p>	<p>GWAS</p>	<p>Indiv. genome-wide H pos. correlated with survival; 1 MHC allele associated with high infection load; 2 MHC alleles more common in susceptible pops, one MHC allele neg. associated with survival; some putative adaptive SNPs associated with survival (n.s.)</p>	<p>GD associated with survival; the resistant pop M had highest level of GD; Adaptive SNP and MHC variants important for breeding more resistant individuals.</p>	<p>Kosch et al. 2019 [42]</p>
<p><i>Rana sylvatica</i> Maryland, TE 15 SS (ponds)</p>	<p>MHC IIB exon sequencing and supertyping n = 381</p>	<p>π = 0.059 TD = 1.72</p>	<p>Tad <i>Ranavirus</i> prevalence <i>Ranavirus</i> infection intensity</p>	<p>Hurdle model</p>	<p>Infection intensity was associated with MHC heterozygosity (P<0.001), lowest in indiv. with MHC genotype ST1/ST7; prevalence without genetic association</p>	<p>MHC heterozygotes have a 23fold lower infection intensity compared to homozygotes; MHC functional genetic variation is important for <i>Ranavirus</i> susceptibility</p>	<p>Savage et al. 2019 [64]</p>
<p><i>Litoria verreauxii</i> Australia, alpine, ST 10 SS: 2 with & 8 without Bd</p>	<p>Genomic DNA: SNPs (GBS) 6 SS n = 50 each site</p>	<p>Indiv. H_O mean number of alleles: 1.37-1.91 mean H_O = 0.12-0.26, mean H_E = 0.11-0.23 Population structure: K=10</p>	<p>Adult frogs Bd infection presence Bd infection intensity</p>	<p>GLMs, Fishers exact test</p>	<p>No differences in GD between sample sites with and without Bd; No relationship between indiv. infection intensity and H_O; but frogs with higher H_O were less likely to be infected</p>	<p>Large pop effect on infection rate; No Bd in isolated pops; Maintenance of genetic diversity is crucial in pops infected with Bd</p>	<p>Banks et al. 2020 [46]</p>
<p><i>Bombina variegata</i> Germany, TE 16 SS (7 focal sample sites, including 2 inbred subpops)</p>	<p>9 microsats n =300 Bd infection n =577</p>	<p>Indiv. MLH H_E = 0.49-0.65, H_O = 0.34-0.73 HS = 0.44-0.55 F_{IS} = -0.4 - 0.26 AR = 1.48-1.59 N_{pa} = 0-6 Population structure: K = 3</p>	<p>Adult toads Bd prevalence per pop Bd presence / indiv. Bd intensity/ indiv. Bd in 15 out of 16 SS Prevalence: 7.1 - 85.7% Intensity: 0 - 570 GE</p>	<p>GLMs</p>	<p>Infection presence correlated with indiv. MLH; No correlation between MLH and infection intensity</p>	<p>No Bd associated mortality; Bd infection prob. highest in toads with low genetic diversity and isolated, inbred pops.</p>	<p>Oswald et al. 2021 [65]</p>
<p><i>Rana pipiens</i> Northamerica, TE 14 SS N_E = 37 - 4861</p>	<p>7 microsats n = 428 mtDNA haplotypes n = 94</p>	<p>H_E = 0.59 - 0.92 H_O = 0.67 - 0.89 AR = 5.5 - 13.9 H_E = 0.00 - 0.76 TD = -2.03 - 0.77 H_E = 0.00 - 0.90</p>	<p>Adult frogs Bd prevalence Bd intensity Bd in 8 out of 14 SS Prevalence : 5.0 - 100%</p>	<p>GLMs</p>	<p>Bd prevalence neg. correlated with MHC H_E MHC allele <i>Rapi*03</i> associated with reduced risk of infection (n.s); MHC <i>supertype 4</i> associated with</p>	<p>Populations (2SS) with smallest N_E also had lowest MHC diversity; MHC GD correlated with prevalence; neutral GD not correlated with Bd.</p>	<p>Trujillo et al. 2021 [53]</p>

	MHC IIB exon 2 N=272 Environmental predictors	$H_0 = 0.00 - 0.86$ $AR = 1.0 - 6.5$ $TD = -0.35 - 3.19$	Intensity: 40.7 – 35706 GE		increased risk of infection (P=0.03). Bd intensity was affected only by environm. variables: rainfall, temperature, latitude	Most measures of neutral and adaptive GD not correlated. Adaptation to disease seems possible though selection on MHC genes.	
<i>Atelopus varius & zeteki</i> Panama, TR 8 SS with declining or extinct pops, small N_E	Transcriptome sequencing, exome –capture assay to sequence coding regions Decrease in genetic diversity Pop. Structure K=8, no clear separation between <i>A. varius</i> and <i>zeteki</i> (but <i>zeteki</i> pops extinct)		Adult frogs Survival after Bd infection	Fishers exact test	Immune related gene variants (outlier SNPs) associated with contemporary survivors after Bd caused declines (e.g. toll-like receptor genes)	The study uncovered candidate genes related to immune system and skin integrity. Admixture in one pop point to potential of genetic rescue	Byrne et al. 2021 [69]
Six species Brasil, TR 3 forest specialists <i>Aplastodiscus leucopygius</i> <i>Ischnocnema henselii</i> <i>Boana semmilineata</i> & 3 habitat generalists <i>Dendrosophus minutus</i> <i>Boana polytaenia</i> <i>Dendrosophus branneri</i> 6 areas, 2SS / species	MHC IIB Exon2 genotyping; Genomic data: SNPs (ddRAD seq.)	N_A , H_E , H_0 , π Indiv: heterozygosity Lower MHC H_E in fragmented forest compared to continuous forest; MHC diversity was inversely related to ddRAD diversity NO DATA FOR SINGLE SPECIES	Adult frogs Bd infection	GLMs, T-Test, Chi ² -Test	Reduced pop level MHC diversity (H_E , H_0 , but not π) correlated with increased Bd infection; no correlation with neutral genetic diversity (ddRAD); MHC IIB heterozygote indiv. tended to be less infected than homozygotes (n.s.)	Bd prevalence highest in fragmented forest and forest specialist; Habitat fragmentation increases Bd infection susceptibility mediated through erosion of immunogenetic diversity	Belasen et al. 2022 [34]
<i>Eleutherodactylus coqui</i> Puerto Rico, TR 1 SS, $N_c = 141$; Bottlenecked pop. Probably in decline	Genomic data: SNPs (GBS) n = 77 Anti- Bd bacterium Microbiome	F_{IS} : 0.04-0.72 HR: 0.57-4.38	Adults frogs Bd infection	Structural equation models	Frogs with low HR were more likely to be infected; no correlation between microbiome diversity and HR Abundance of anti- Bd bacterium higher in infected frogs	Offsetting effect: frogs with higher HR were less likely to be infected; but frogs with higher HR and infected frogs showed higher bacterium abundance; study highlights importance to study multiple interactions	Torres-Sanchez & Longo 2022 [66]

Abbreviations: **SS** = sample site, **TE** = Temperate region, **ST**= Subtropical region, **TR** = Tropical region, **n** = no. of individual investigated, **Pop** = population, **Tad** = tadpoles, **K** = no. of genetic cluster according to Bayesian assignment analysis (pop. Structure); **N** = pop size; **N_c**= census pop size, **N_E** = effective pop size, **Bd** = Chytrid fungus (*Batrachochytrium dendrobatidis*); **pw** = pairwise

Genetic diversity (**GD**) estimates: **P** = % polymorphic loci, **Na/I** = no. of alleles /locus, **H_E** = expected heterozygosity, **H_O** = observed heterozygosity, **H** = individual heterozygosity, **F_{IS}** = inbreeding coefficient; mean **d²** = squared distance (in repeat units) between the two alleles within a locus, averaged over all loci analysed in an individual (Coulson et al. 1998); **H_{EST}** and **d²_{EST}** estimated from parental genotypes, **r_{xy}**, a pairwise relatedness estimator which measures the relatedness of the parents used in the common garden experiment (Queller & Goodnight 1989), **AR** = allelic richness, **HS** = gene diversity (microsats), **Npa** = no. of private alleles, **F_{ST}** = fixation index (population structure), **MLH** = indiv. multilocus heterozygosity, **IR** = ind. internal relatedness, **N_A** = allelic diversity (MHC alleles), **GSI** = Gini-Simpson Index (RAPD), **Nh** = Number of haplotypes, **h** = haplotype diversity, **π** = nucleotide diversity, **NE** = Effective number of alleles, **TD** = Tajima's D, **HR** = Heterozygous/homozygous ratio, **HFC** = heterozygosity – fitness correlation, **GFC** = Genetic variability fitness correlations