

**Table S1.** Correlation matrix showing Spearman Correlation’s coefficients (r) of the variables included in the models.

<b>Parameters</b>	Temperature	Precipitation	Population size
<b>Bd prevalence (GLMM)</b>			
Temperature	1		
Precipitation	0.271	1	
Population size	-0.024	-0.238	1
<b>Bd infection intensity (GLM)</b>			
Temperature	1		
Precipitation	0.269	1	
Population size	-0.253	-0.631	1
<b>Scaled mass index (GLMM)</b>			
Temperature	1		
Precipitation	0.322	1	
Population size	0.119	-0.508	1

**Table S2.** *Batrachochytrium dendrobatidis* prevalence and number of *Melanophryniscus montevidensis* sampled individuals, by sex and life stage. Prevalence is the proportion of infected toads out of the total number of toads sampled.

<b>Life stage and sex</b>	<b>Prevalence</b>
Adult males	43 % (70/162)
Adult females	36 % (21/58)
Juveniles of undetermined sex	47 % (9/19)
Adult undefined	0 % (0/2)
Total	41 % (100/241)

**Table S3.** *Batrachochytrium dendrobatidis* infection intensity in recaptured *M. montevidensis* individuals. Bd infection intensity is presented as the log of zoospore genomic equivalents (g.e.).

<b>First Capture</b>	<b>Days</b>	<b>Recapture 1</b>	<b>Days</b>	<b>Recapture 2</b>
Bd infection intensity		Bd infection intensity		Bd infection intensity
0.28	65	0	16	0
0.34	116	0		
0	181	0		
0	96	0		
1.37	112	0		
1.78	112	0.44		
0.25	598	0		
0.34	598	0		
2.15	377	0.59		
0	762	0		
0	499	1.14		
0	320	0		
0.51	113	0		
0	320	0	150	0
0.25	263	0		
0.55	150	0		
0	354	0		

**Table S4.** Summary of the variables used in statistical models assessing the variation in *Batrachochytrium dendrobatidis* infection prevalence, infection intensity and toads body condition. Variation in Bd prevalence in warm and cold season; prevalence is the proportion of infected toads out of the total number of toads sampled. Mean infection intensity in *M. montevidensis* in warm and cold season; Bd infection intensity is represented with the mean, standard deviation and range of zoospore genomic equivalents (g.e.). Mean of temperature and median of precipitation of the 15 days before sampling in Laguna de Rocha, Uruguay in warm and cold season; temperature and precipitation (mm<sup>3</sup>) are represented with the mean, minimum and maximum values.

	Prevalence	Mean g.e.	Temperature (°C)	Precipitation (mm <sup>3</sup> )
<b>Warm</b>	50.67 % (75/148)	18.56 ± 35.34 (1.03 – 194.86)	20.12 (15.35 – 22.18)	29.75 (5.30 – 191.50)
<b>Cold</b>	26.88 % (25/93)	5.27 ± 7.32 (1.13 – 28.36)	11.43 (8.73 – 18.41)	25.40 (4.90 – 47.00)
<b>Total</b>	41.00 % (100/241)	15.24 ± 31.31 (1.03 – 194.86)	17.72 (8.735 – 22.18)	26.15 (4.90 – 191.50)

**Table S5.** Estimates of the Generalized Linear Mixed Model (GLMM) showing parameter estimates for each predictor variable regarding their effect on *Batrachochytrium dendrobatidis* prevalence in *M. montevidensis*. For a model in the form  $y = a + b_1x_1 + \dots + b_nx_n + c_1u_1 + \dots + c_nu_n$ ;  $y$  is the estimated effect on prevalence in a logit scale (link function scale), the “intercept” is the coefficient  $a$  of the model (intercept of the model in the  $y$  axis); “ $b$ ” are the parameter estimates of the fixed effects of each variable  $x$ ; “ $c$ ” are the random effects of each variable  $u$ ; “SE” are the standard errors of the parameter estimates  $b$ ; “ $z$ ” value are the z-statistic values of each coefficient  $b$ ; “ $P$ ” are the significance values of the z-test of each coefficient  $b$ . In bold are the predictive variables with a significant effect.

Predictor	$b$	SE	$z$	$P$
Intercept (cold season)	-0.2187	0.5790	-0.378	0.705
Warm season	-0.0158	0.5449	-0.029	0.976
Temperature	0.3359	0.2572	1.306	0.191
Precipitation	-0.3327	0.2166	-1.536	0.124
<b>Population size</b>	1.0080	0.2632	3.830	<b>&lt;0.001</b>

**Table S6.** Estimates of the Generalized Linear Model (GLM) showing parameter estimates for each predictor variable regarding their effect on *Batrachochytrium dendrobatidis* infection intensity in *M. montevidensis*. For a model in the form  $y = a + b_1x_1 + \dots + b_nx_n$ ;  $y$  is the estimated effect on infection intensity in the inverse scale (link function scale), “intercept” is the coefficient  $a$  of the model (intercept of the model in the  $y$  axis); “ $b$ ” are the parameter estimates of each variable  $x$ ; “SE” are the standard errors of the estimates  $b$ ; “ $t$ ” value are the t-statistic values of each coefficient  $b$ ; “ $P$ ” are the significance values of the t-test of each coefficient  $b$ . In bold are the predictive variables with a significant effect.

Predictor	$b$	SE	$t$	$P$
<b>Intercept (cold season)</b>	2.6055	0.4040	6.449	<b>&lt;0.001</b>
<b>Warm season</b>	-1.4726	0.4411	-3.339	<b>0.001</b>
Temperature	0.2768	0.1527	1.812	0.073
<b>Precipitation</b>	0.3499	0.1452	2.411	<b>0.017</b>
<b>Population size</b>	0.3859	0.1357	2.843	<b>0.005</b>

**Table S7.** Estimates of the Generalized Linear Mixed Model (GLMM) showing parameter estimates for each predictor variable regarding their effect on the scaled mass index of *M. montevidensis*. For a model in the form  $y = a + b_1x_1 + \dots + b_nx_n + c_1u_1 + \dots + c_nu_n$ ;  $y$  is the logit link of prevalence, “intercept” is the coefficient  $a$  of the model (intercept of the model with the  $y$  axis); “ $b$ ” are the estimates of the fixed effects of each variable  $x$ ; “ $c$ ” are the random effects of each variable  $u$ ; “SE” are the standard errors of the estimates  $b$ ; “ $t$ ” value are the t-statistic values of each coefficient  $b$ ; “ $P$ ” are the significance values of the t-test of each coefficient  $b$ . In bold are the predictive variables with a significant effect.

Predictor	$b$	SE	$t$	$P$
<b>Intercept (cold season, Bd<sup>+</sup>)</b>	0.9748	0.0717	13.566	<b>&lt;0.001</b>
<b>Warm season</b>	0.0990	0.0443	2.234	<b>0.025</b>
Temperature	-0.0041	0.0178	-0.235	0.814
Precipitation	0.0225	0.0134	1.675	0.093
Population size	-0.0316	0.0247	-1.282	0.199
Bd <sup>+</sup> incidence	0.0375	0.0259	1.448	0.147