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O IMPACTO DA SÍNDROME DO NARIZ-BRANCO NO ESTADO DE CONSERVAÇÃO DOS MORCEGOS NORTE-AMERICANOS

Orientador: Dr. Daniel Brito

Goiânia ï GO

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Dissertação apresentada à Universidade Federal Goiás como parte das exigências do Programa de Pós-graduação em Ecologia e Evolução para obtenção do título de Mestre.

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SUMÁRIO

Eu dedico esse trabalho a todos aqueles que acreditam em mim, principalmente minha família.

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V., S. e A.

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MATERIAIS SUPLEMENTARES

APRESENTAÇÃO

A ecologia tem como interesse entender como as interações dos organismos afetam suas distribuições ecológico-espaciais e abundâncias. Essas interações podem ser tanto com componentes abióticos, quanto bióticos. Entretanto, o interesse em compreender a interação entre organismos e seus patógenos dentro de um contexto conservacionista é bastante recente dentro da agenda de pesquisa ecológica. Em outras palavras, estudos de doenças que afetam a biodiversidade não é uma tradição entre os ecólogos. Nem faz sentido dizer em relação aos conservacionistas, já que essa área do conhecimento tem cerca de trinta anos de história. A partir da observação de doenças recentes como a chytridiomycosis em anfíbios e o tumor facial nos diabos-da-tasmânia, esse processo vêm despertando o interesse da comunidade científica ecológica.

Nessa dissertação, nós predizemos o impacto de uma nova doença infecciosa que afeta a comunidade de morcegos neárticos. Essa doença é conhecida como a Síndrome do Nariz-Branco (SNB), um processo que já matou cerca de seis milhões de morcegos e já expandiu mais de 2000 quilômetros desde o seu epicentro. A SNB foi detectada pela primeira vez no inverno de 2006-2007 em uma caverna no estado de Nova Iorque, no nordeste dos Estados Unidos da América. A doença possui esse nome devido ao fato do patógeno colonizar o ñfocinhoò dos seus hospedeiros. Entretanto, ele pode colonizar outros locais em que não há pelos, como orelhas e asas. O patógeno é um fungo tolerante ao frio conhecido como *Geomyces destructans*, e só afeta indivíduos que possuem o comportamento de hibernar em cavernas e/ou minas durante os períodos em que as condições ambientais são muito severas (i.e. baixas temperaturas e escassez de alimentos).

O mecanismo mais aceito para explicar a mortalidade causada pelo patógeno é o gasto da energia que deveria ser utilizada para sobreviver ao intervalo de tempo em que as condições ambientais não são adequadas. Os morcegos de altas latitudes armazenam energia durante os períodos antecedentes à hibernação, mas durante a hibernação eles ñacordamò algumas vezes para satisfazerem necessidades fisiológicas, como urinar e se hidratar. Cada interrupção equivale a um alto consumo de energia, já que o organismo retorna à sua temperatura corporal pré-hibernação. Entretanto, essa demanda conflitante (ñtradeoffò) entre a quantidade certa de energia gasta para armazenamento e necessidades fisiológicas foi selecionada durante a história evolutiva desses organismos. O problema é que o fungo incomoda os hospedeiros, aumentando a frequência de interrupções durante a hibernação e ocasionando a morte de fome.

O nosso objetivo foi utilizar uma forma de quantificar o possível impacto que a SNB poderia causar sobre a comunidade de quirópteros do Neártico. Para isso, nós produzimos um mapa de adequabilidade ambiental para a ocorrência do fungo, e sobrepusemos com a extensão de ocorrência de todos os morcegos hibernantes do os critérios da União Internacional para a Naturais (IUCN) para classificar os possíveis hospedeiros em alguma categoria de estado de conservação. As categorias da IUCN são uma informação transparente e intuitiva do estado conservacionista em que a biodiversidade se encontra, e, portanto são uma boa opção para alertar as autoridades sobre os potenciais impactos da SNB. Nós esperamos que os resultados dessa dissertação possam auxiliar os planos de ações no sentido de indicar as localidades mais suscetíveis à ocorrência da doença e as espécies que possivelmente serão mais impactadas.

MANUSCRITO

THE IMPACT OF WHITE-NOSE SYNDROME ON THE CONSERVATION STATUS OF NORTH-AMERICAN BATS

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Abstract: The White-Nose syndrome is an emergent infectious disease that had already killed almost six millions North American bats and spread more than two thousand kilometers. Even so, studies about their possible impacts upon hosts are still lacking, principally upon all the susceptible North American bats. We predicted the consequences of the WNS spread in the North American hosts by generating an environmental suitability map for the disease, and then, we overlaid with the extension of occurrence of all hibernating bats in North America. We assumed that all intersection localities will somehow negatively affect batôs local populations, and we reassessed their conservation status based on their potential population reduction. 16% of the North American hibernating bat fauna were considered threatened under this WNS potential spread. We believe our results could contribute with governments conservation actions.

Keywords: Emerging infectious disease, ecological niche model, IUCN, conservation actions, MAXENT.

INTRODUCTION

Diseases are an inherent component of natural wildlife communities. However, anthropogenic activities may disrupt the natural dynamics and distribution of diseases (Daszak et al. 2000; 2001). Such disruptions might result in population declines and range contractions, jeopardizing the long-term persistence of wildlife species (Daszak et al. 2000; 2001; McCallum & Dobson 2002; Altizer et al. 2003). The negative effects of diseases are particularly worrisome for wildlife populations when the pathogen is an invasive species (Baillie et al. 2004). As a consequence, several vertebrate species are listed as threatened due to the impacts of both of disruptions in native disease dynamics and the invasion of pathogens into new ecological communities (Baillie et al. 2004; Brito et al. 2012), which is also known as pathogen pollution (Daszak et al. 2000). Traditionally, the issue of wildlife diseases only draw attention when human welfare and/or interests were involved (Daszak et al. 2000; Jones et al. 2008). However, this scenario has changed recently, and disease effects on wildlife have come to the forefront of the conservation agenda (Daszak et al. 2000; Cunningham et al. 2012).

Chytridiomycosis, a disease caused by the invasive fungus *Batrachochytrium dendrobatidis*, is a major driver of amphibian population declines and extinctions worldwide (Daszak et al. 2003; Johnson 2006; Lips et al. 2006; Norris 2007; Skerrat et al. 2007). Several New World bird populations are suffering severe die-offs from the invasion of the West Nile Virus (Marra et al 2004; Kilpatrick 2011), with the recorded death of millions of individual and population declines of more than 50% and local extinctions recorded for several species (LaDeau et al. 2007). Until recently, diseases were not a widespread threat for mammals (Brito et al. 2012). A few mammal species were particularly threatened by the emergence of infectious diseases, such as the Tasmanian devil and the onset of the Tasmanian devil facial tumor disease (Dennis 2006; Hawkins et al. 2006; McCallum et al. 2007; 2009; McCallum 2008).However, this picture may change for North-American bats.

The White-Nose Syndrome (WNS) is an emergent disease that affects hibernating bats in North America and was first detected in a cave in the state of New York in the winter of 2006-2007 (Foley et al. 2011). WNS is caused by the psychrophilic fungus *Geomyces* d (Warnecke et al. 2012), which colonizes the open skin mortality mechanism is associated to the increase in batôs arousals during the hibernation period, expending prematurely the energy that should be stored to maintain bats alive during the winter (Warnecke et al. 2012). The WNS has already killed almost six million bats, and expanded its distribution more than two thousand kilometers within North America (BCI 2012; Maher et al. 2012). The United States Fish and Wildlife Service (USFWS) produced a national plan to manage the disease, comprising research and management actions on epidemiology and wildlife management (USFSW 2011) and important advances have already been made on comprehending the epidemiology of WNS (Blehert 2012). Even though severe population declines have already been documented due to the WNS (e.g. Frick et al. 2010; Brooks et al. 2011; Dzal et al. 2011; Thogmartin et al. 2012) , there is still an important knowledge gap, which is the impact of the disease in the conservation status of all North American bat species.

Therefore, our objective is to estimate if the invasion of *G. destructans* and the onset of WNS will cause population declines and or extinctions severe enough to affect the current conservation status of North-American hibernating bats.

METHODS

Modeling the invasion of WNS in the New World

We used a model based on the niche theory to predict the potential geographic spread of WNS in North America. The ecological niche model used was MaxEnt (version 3.3.3e), which basically uses a maximum entropy method to correlate presence records of an organism with environmental variables to predict potential localities for occurrence (Elith et al. 2006; 2011, Phillips & Dudík 2008). *Geomyces destructans* is likely an invasive species from Europe (Warnecke et al. 2012), therefore, we used the occurrence points of the fungus native (Europe) and invaded area (North America) to better identify its niche and the potential area susceptible to the occurrence of the WNS (Broennimann et al. 2008). We only used presence records, with 60 confirmed sites in Europe (Puechmaille et al. 2011a), and 114 records from North American (White-Nose Syndrome.org, 2012) (confirmed sites database updated until 30/03/2012) (see

). The diseaseôs niche was constructed using six (2) mean temperature of the wettest quarter; (3) precipitation of the wettest month; (4) precipitation of the driest month; (5) elevationôs standard deviation; and (6) land classes (variables 1-4 obtained from Hijmans et al. 2005 and WORLDCLIM 2012; variable 5 obtained from USGS 2012a; and variable 6 obtained from ESA 2012). The rationale for the choice of variables used to model the disease distribution followed Flory et al. (2012), which quantified the environmental factors that best explained the WNS actual geographic distribution. We only used the six main variables because we prefer a simpler ecological space that predicts a higher quantity of area invaded in the geographic space than a more complex one that predicts a smaller quantity of area (the Hucthinsonôs duality; Colwell & Rangel 2009), since our objective is to generate a potential distribution. This rationale also fits well with the conservation precautionary perspective. All the environmental layers were on a global scale and had different resolutions, so we rescaled them for North America and Europe with a resolution of 0.5^0. We used this extension to decrease the background effect in modelôs performance (Barve et al. 2011).

We used the area under the curve (AUC) of the receiver operating characteristics (ROC) as the performance metric. We divided the occurrence points in training (70%) and test (30%) with a random sample with replacement (also known as bootstrap; 100 iterations), which generated a frequency distribution of AUC values. We used the map that had the highest quantity of suitable area for the disease to account for the most pessimistic scenario of spread.

Evaluating the impact of WNS spread on batôs conservation status

We used the predicted potential distribution of *G. destructans* to estimate the potential impact of WNS upon the North American susceptible hosts. All the North American hibernating bats (25 species) were considered as susceptible hosts (USGS 2012b). We transformed the extension of occurrence (EOO) of the 25 bat species (obtained from IUCN 2012) into polygons of 0.5^o of resolution. Then, we overlapped the WNS environmental suitability map with the EOO map of each bat species. We assumed that the environmental suitability value of each quadrant for the fungus constitutes a proxy for population decline to each host. In other words, tial relative decline for the local population of each bat A in cell Z = 1; environmental suitability for disease in cell Z = 0.7; local population for species A in cell Z under disease effect = 1 ï 0.7 = 0.3). This corresponded to a relation of 1:1 between the environmental suitability for the disease and the hostsô population reduction. To account for more optimistic scenarios, we calculated suitability-population reduction in another two scenarios: (1) a relation of 1:0.75 (intermediate scenario), and (2) a relation of 1:0.5 (optimistic scenario; see Appendix S2 for the results of both the intermediate and the optimistic scenarios). We included the two scenarios because there is evidence that some infected populations were not extirpated by the disease (Thogmartin et al. 2012). The relation between environmental suitability and local population abundance is a new topic in science, but some studies have demonstrated that a correlation exists (more specifically a wedge-shaped pattern; VanDerWall et al. 2009, Tôrres et al. 2012). Therefore, we summed the relative local population of each quadrant to infer the fraction of the total population of the species that would be under the WNSô spread. In order to quantify the impact of WNS upon the conservation status of bat species, we used the potential population reduction caused by the disease (see above) to assess the species against criteria A of the Red List of Threatened Species of the International Union for the Conservation of Nature and Natural Resources (IUCN 2011).

RESULTS

Our map of the potential spread of *G. destructans* and the onset of WNS in the New World showed the current distribution of the disease (mostly in the Appalachian Mountains), and predicted its invasion towards North America northeastern coastal areas, towards the Mississippi basin and towards the Rocky Mountains (Fig. 1; median AUC 0.95; range 0.92-0.98; Appendix S3 for AUC frequency distribution; Appendix S4 and S5 for average and standard deviation environmental suitability maps, respectively).

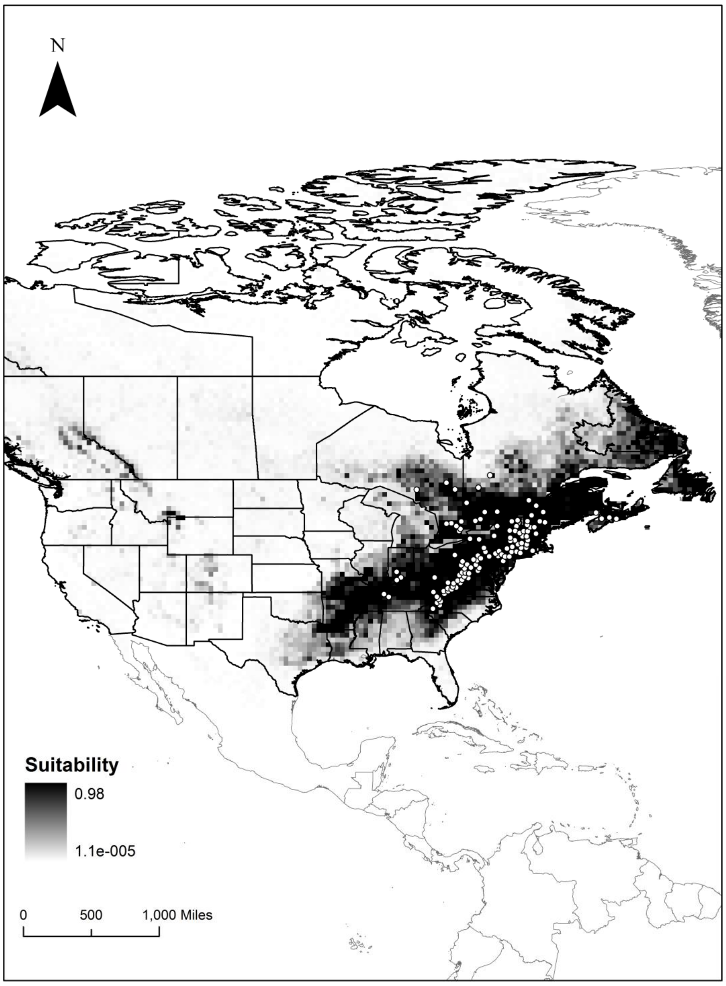

Figure 1. The potential spread of White-Nose Syndrome and their current presence sites (white dots; until march of 2012).

The spread of the WNS distribution in the New World showed that 30% of the native hibernating bats (8 species) are expected to lose more than 25% of their entire population. Among these, four bat species (*Corynorhinus rafinesquii*, *Myotis grisescens*, *Myotis leibii* and *Myotis sodalis*) would suffer population decline rates severe enough to be classified into one of IUCNôs threat categories (Tab. 1; species list of the intermediate and optimistic scenarios in Appendix S2). Even though the absolute number of species becoming threatened due to the invasiveness of WNS may seem low (four species), this represents 16% of the hibernating bat fauna of North America.

Species	Population reduction (%)	Actual status	Expected status	Criteria
Myotis leibii	58.6	LC	EN	A4ce
Myotis sodalis[b]	47.2	EN	EN	A4ce
Myotis grisescens	43.3	NT	VU	A4ce
Corynorhinus rafinesquii	30.3	LC	VU	A4ce
Pipistrellus subflavus	28.2	LC	LC	-
Myotis austroriparius	27.8	LC	LC	-
Nycticeius humeralis	26.5	LC	LC	-
Myotis septentrionalis	25.4	LC	LC	-
Myotis lucifugus	13.1	LC	LC	-
Eptesicus fuscus	11.5	LC	LC	-
Corynorhinus townsendii	4.0	LC	LC	-
Myotis evotis	2.5	LC	LC	-
Myotis ciliolabrum	2.1	LC	LC	-
Myotis volans	2.1	LC	LC	-
Euderma maculatum	2.0	LC	LC	-
Myotis keenii	1.7	LC	LC	-
Myotis yumanensis	1.5	LC	LC	-
Myotis vellifer	1.2	LC	LC	-
Myotis californicus	1.1	LC	LC	-
Myotis thysanodes	0.9	LC	LC	-
Antrozous pallidus	0.9	LC	LC	-
Myotis occultus	0.8	LC	LC	-
Pipistrellus hesperus	0.6	LC	LC	-
Idionycteris phyllotis	0.3	LC	LC	-
Myotis auriculus	0.3	LC	LC	-

Table 1. The expected conservation status of the North American bats susceptible to the White-Nose syndrome spread (calculated by their potential population reduction according to IUCN[a] criteria).

[a] International Union for Conservation of Nature and Natural Resources.

[b]The expected conservation status of *Myotis sodalis* was not solely based on the estimated population decline caused by the potential White-Nose syndrome spread. It was also based on an estimated population decline of 50% calculated before 2008 by the IUCN, which the mainly cause was human disturbance at the caves. This represents an overall population decline of 73.6%.

DISCUSSION

Our predicted expansion of WNS in North America is similar to other modeling exercises (Flory et al. 2012), even though our results show a somewhat larger expansion of the disease. Such differences are because they modeled just for the Northeast of the United State of America (USA) and because they used the occurrence data only from the invaded range. For the attempt to model potential distributions, is preferable to use data both from the native and y capture more from the organismô niche (Broennimann et al. 2006). [...] climate change and others modeling approaches, WNS spread towards the western USA might be greater than predicted (Maher et al. 2012). However, to our knowledge, this is the first study to couple predictions of WNS spread and population declines with the conservation status of host species.

Our results clearly show the potential impact of WNS on bat populations in North America. Empirical evidence of severe population declines due to the spread of WNS have already been recorded for the three *Myotis* species we predicted will become threatened (Brooks et al. 2011; Dzal et al. 2011; Thogmartin et al. 2012). For example, significant population reductions were detected for the already endangered *M. sodalis* in the localities closest to the diseaseœ epicenter, in the northeast USA (Thogmartin et al. 2012). Even though our three scenarios depicted a lower number of threatened species (see table 1 and Appendix S2), such results could underestimate the real impact of WNS on bat populations. This because a recent study predicted a high extinction probability for the abundant and widely distributed little brown bat *M. lucifugus* in less than 20 years (Frick et al. 2010), even though this species did not appeared within the most impacted group in our study.

Since the outbreak of WNS in 2006, the scientific community directed its efforts to identify the etiological agent (Blehert et al. 2009), to uncover the disease origin (Puechmaille et al. 2011b; Warnecke et al. 2012), to understand the mortality mechanism (Cryan et al. 2010; Warnecke et al. 2012), and to understand the risk factors associated with the disease (Wilder et al. 2011, Flory et al. 2012; Langwig et al. 2012). Recently, due to the widespread and high mortality levels of the disease, part of the scientific efforts were directed towards understanding the disease impacts on host populations (Frick et al. 2010, Dzal et al. 2011; Brooks et al. 2011; Thogmartin et al. 2012), however none of them comprehended all the North American bat fauna, and only one (see Frick et al. 2010) had a predictive approach such as ours.

The use of niche theory to predict sites for disease outbreaks is not new (Ron 2005). However, the use of niche theory to infer disease pathogenicity upon hosts is (Murray et al. 2011). The rationale behind this inference is that areas with optimal environmental conditions for a given pathogen will permit higher intensity of infection (Murray et al. 2011). However, the relationship between environmental suitability and an organismôs abundance may not be as straightforward as previously thought, whereas suitable sites can show low abundances due to dispersal barriers, microclimates, stochastic effects and/or biotic interactions (VanDerWall et al. 2009; Tôrres et al. 2012). Even so, we preferred to use values closer to the upper limit of the pathogen local abundances (based on a 1:1 relationship) to account for a more pessimistic scenario.

Until recently, the mammal groups most affected by diseases were those that comprehended higher proportions of domesticated species (i.e. Artiodactyla and Carnivora; Pedersen et al. 2007). Unfortunately our results suggest that this picture will change for North American bats. We believe conservation efforts should be directed to the four bat species identified as potentially becoming threatened, however, the population reduction of the remnant species should not be neglected. Even though our results contribute to predict the diseaseôs consequences to the conservation status of the North-American bats, further advances need to be made to understand if there is a phylogenetic signal in host susceptibility to WNS, and also to better understand the relationship between environmental suitability and pathogen abundance. North American bats play key roles in ecosystem processes (Boyles et al. 2011) and the severe population declines predicted to occur due to WNS may even have serious consequences for the economy, as ecosystem services provided by them are compromised.

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Supporting information 1. Geographic coordinates for sites confirmed with White-Nose Syndrome. For North American sites were used the central points of the counties confirmed for disease and were compiled from Fort Collins (2012; 30/03/2012). European sites were compiled from Puechmaille et al. (2011).

Local	Latitude	Longitude
North America	36.8	-87.9
North America	36.5	-87.4
North America	35.3	-82.7
North America	35.6	-82.0
North America	35.9	-82.3
North America	36.0	-81.9
North America	36.3	-82.1
North America	36.5	-82.3
North America	37.0	-82.7
North America	36.8	-81.5
North America	37.1	-81.6
North America	37.1	-81.1
North America	37.4	-81.1
North America	37.3	-80.7
North America	37.5	-80.2
North America	37.6	-80.6
North America	37.9	-80.5
North America	38.0	-81.1
North America	38.6	-82.5
North America	38.6	-86.1
North America	38.3	-86.6
North America	39.2	-86.6
North America	38.0	-79.8
North America	38.2	-80.1
North America	38.3	-79.6
North America	38.8	-79.9
North America	38.5	-79.0
North America	38.7	-79.4
North America	39.1	-79.6
North America	39.1	-79.3
North America	39.0	-78.9
North America	39.5	-79.4
North America	39.9	-79.7
North America	41.0	-80.4
North America	40.3	-79.6
North America	40.0	-79.1
North America	39.6	-78.7
North America	39.3	-77.9
North America	39.6	-77.8
North America	39.9	-78.2
North America	40.4	-78.0
North America	40.5	-78.4

North America	40.6	-77.6
North America	41.3	-77.1
North America	41.7	-77.3
North America	40.8	-76.7
North America	40.3	-75.2
North America	40.9	-75.8
North America	41.1	-76.1
North America	41.4	-75.7
North America	41.0	-75.4
North America	40.8	-75.0
North America	40.8	-74.6
North America	41.7	-74.8
North America	41.3	-74.3
North America	41.3	-73.8
North America	41.2	-73.4
North America	41.4	-72.1
North America	41.8	-72.8
North America	41.8	-73.3
North America	41.8	-74.3
North America	42.1	-73.7
North America	42.2	-73.3
North America	42.1	-72.7
North America	42.5	-72.6
North America	42.9	-73.2
North America	42.5	-74.0
North America	42.5	-74.5
North America	42.8	-74.5
North America	43.6	-74.5
North America	43.0	-76.2
North America	42.6	-77.8
North America	42.7	-78.8
North America	43.5	-79.9
North America	43.7	-79.8
North America	44.5	-79.7
North America	44.0	-80.2
North America	44.4	-80.8
North America	44.3	-81.3
North America	44.6	-78.2
North America	44.8	-77.7
North America	45.5	-77.2
North America	45.6	-75.9
North America	44.0	-75.9
North America	44.6	-74.3
North America	44.0	-73.8
North America	43.5	-74.0
North America	43.3	-73.5
North America	44.7	-73.7
North America	43.5	-73.1

North America	43.0	-72.7
North America	43.2	-71.7
North America	43.9	-72.4
North America	44.2	-72.7
North America	44.6	-72.6
North America	43.9	-71.9
North America	45.2	-72.2
North America	44.6	-71.3
North America	44.4	-70.8
North America	45.5	-71.0
North America	46.2	-71.7
North America	44.8	-63.2
North America	45.0	-63.9
North America	44.8	-64.7
North America	45.5	-65.3
North America	46.8	-72.5
North America	49.5	-76.6
North America	48.1	-77.9
North America	46.5	-79.1
North America	47.9	-80.4
North America	48.7	-81.3
North America	47.9	-84.5
Europe	49.9	4.1
Europe	50.6	2.5
Europe	47.7	-2.1
Europe	49.8	5.3
Europe	50.8	5.6
Europe	50.8	5.6
Europe	52.0	5.8
Europe	52.1	4.3
Europe	49.7	7.4
Europe	49.8	9.6
Europe	50.7	13.7
Europe	50.9	7.5
Europe	51.2	8.1
Europe	52.3	9.5
Europe	52.3	9.4
Europe	47.1	17.6
Europe	50.8	16.7
Europe	59.3	24.6
Europe	48.7	26.6
Europe	44.8	1.6
Europe	42.6	2.2
Europe	47.7	-2.1
Europe	45.0	2.0
Europe	47.3	6.2
Europe	50.4	3.5
Europe	47.2	1.4

Europe	50.3	5.9
Europe	50.8	5.7
Europe	52.1	4.3
Europe	52.0	5.7
Europe	56.4	9.1
Europe	51.8	10.8
Europe	51.6	10.5
Europe	51.7	10.3
Europe	52.3	9.5
Europe	52.1	8.2
Europe	52.2	8.0
Europe	46.8	16.0
Europe	47.1	17.6
Europe	46.2	18.1
Europe	48.5	20.5
Europe	47.1	17.6
Europe	50.8	16.7
Europe	48.8	26.6
Europe	46.8	22.6
Europe	45.4	25.2
Europe	41.9	27.9
Europe	49.1	6.6
Europe	48.5	6.9
Europe	48.3	7.1
Europe	48.3	5.7
Europe	47.9	6.8
Europe	49.5	5.2
Europe	48.9	0.3
Europe	47.2	5.7
Europe	52.1	4.3
Europe	50.9	13.3
Europe	49.9	7.4
Europe	48.8	26.6
Europe	47.0	22.4

Supporting information 2. The intermediate and optimistic expected conservation status (see footnotes below for explanations) of the North American bats susceptible to the White-Nose syndrome spread (according to IUCN[a] criteria).

Species	IPR[b] (%)	OPR[c] (%)	Actual status	IES[d]	OES[e]	Criteria
Myotis leibii	43.9	29.3	LC	VU	LC	A4ce
Myotis sodalis[f]	35.4	23.6	EN	EN	EN	A4ce
Myotis grisescens	32.5	21.6	NT	VU	LC	A4ce
Corynorhinus rafinesquii	22.7	15.1	LC	LC	LC	-
Pipistrellus subflavus	21.1	14.1	LC	LC	LC	-
Myotis austroriparius	20.9	13.9	LC	LC	LC	-
Nycticeius humeralis	19.9	13.3	LC	LC	LC	-
Myotis septentrionalis	19.0	12.7	LC	LC	LC	-
Myotis lucifugus	9.8	6.5	LC	LC	LC	-
Eptesicus fuscus	8.6	5.8	LC	LC	LC	-
Corynorhinus townsendii	3.0	2.0	LC	LC	LC	-
Myotis evotis	1.9	1.3	LC	LC	LC	-
Myotis ciliolabrum	1.5	1.0	LC	LC	LC	-
Myotis volans	1.5	1.0	LC	LC	LC	-
Euderma maculatum	1.5	1.0	LC	LC	LC	-
Myotis keenii	1.3	0.9	LC	LC	LC	-
Myotis yumanensis	1.1	0.7	LC	LC	LC	-
Myotis vellifer	0.9	0.6	LC	LC	LC	-
Myotis californicus	0.8	0.6	LC	LC	LC	-
Myotis thysanodes	0.7	0.5	LC	LC	LC	-
Antrozous pallidus	0.7	0.4	LC	LC	LC	-
Myotis occultus	0.6	0.4	LC	LC	LC	-
Pipistrellus hesperus	0.5	0.3	LC	LC	LC	-
Idionycteris phyllotis	0.3	0.2	LC	LC	LC	-
Myotis auriculus	0.2	0.1	LC	LC	LC	-

[a] International Union for Conservation of Nature and Natural Resources.

[b] Intermediate Population Reduction correspond to a relation of 1 : 0.75 between the environmental suitability for the disease and the hosts' population reduction, respectively.

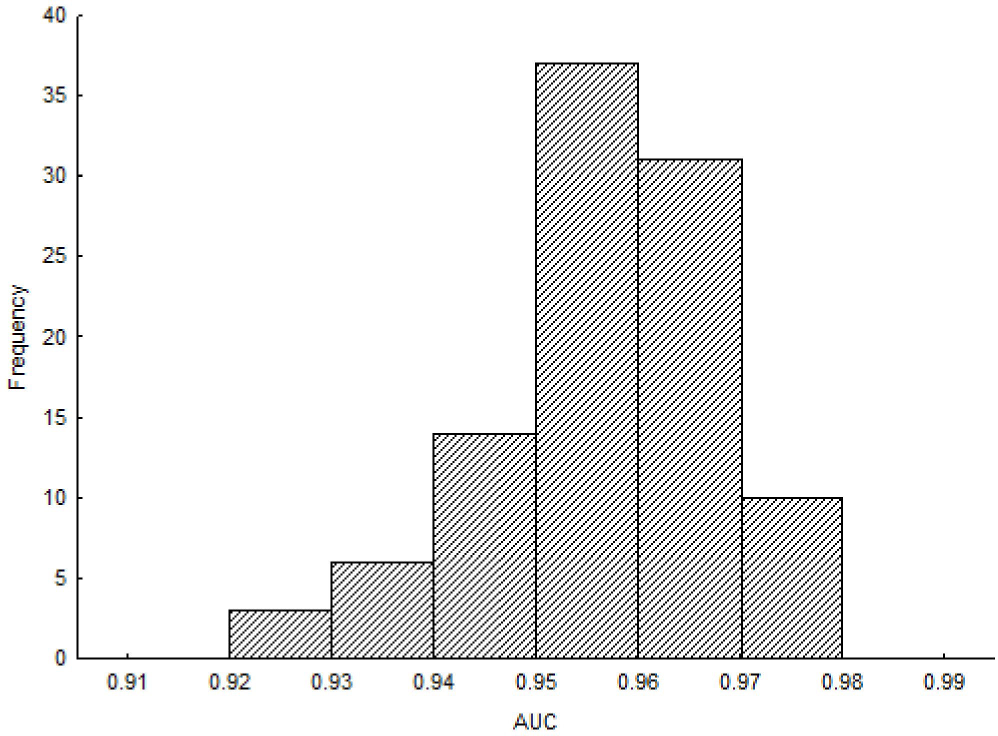
[c] Optimistic Population Reduction correspond to a relation of 1 : 0.5 between the environmental suitability for the disease and the hosts' population reduction, respectively.

[d] Intermediate Expected Status correspond to the conservation status based on IPR.

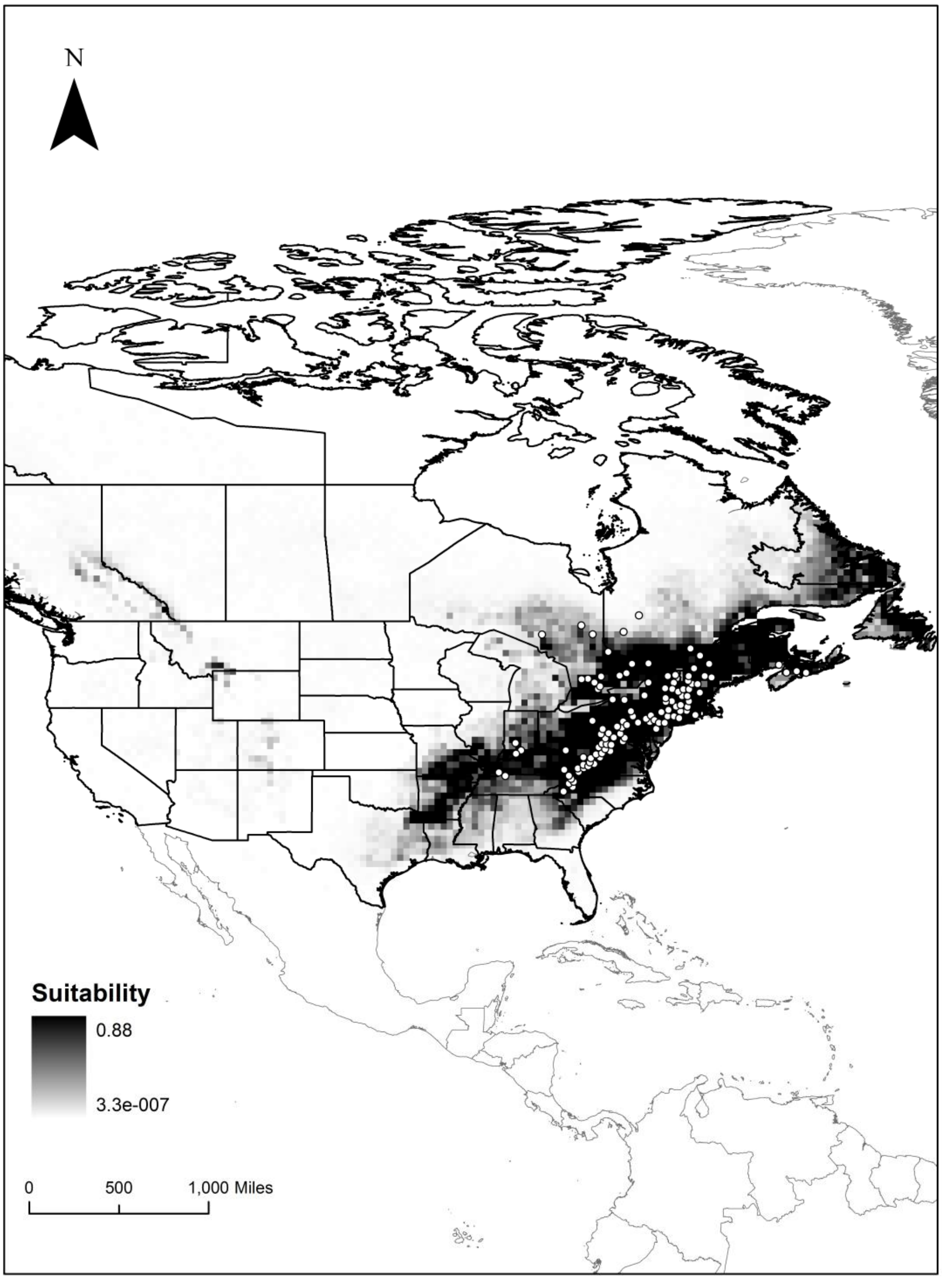
[e] Optimistic Expected Status correspond to the conservation status based on OPR.

[f] The two expected conservation status of *Myotis sodalis* was not solely based on the estimated population decline caused by the potential White-Nose syndrome spread. It was also based on an estimated population decline of 50% calculated before 2008, which the mainly cause was human disturbance at the caves. This represents an overall population decline of 67.7% (intermediate scenario) and 61.8% (optimistic scenario).

Supporting information 3. Frequency distribution of the area under the receiver operating characteristics values (AUC) from 100 iterations.



Supporting information 1. The average environmental suitability map for White-Nose Syndrome. White dots represent the confirmed sites for the disease until march of 2012.



Supporting information 5. The standard deviation environmental suitability map for White-Nose Syndrome. White dots represent the confirmed sites for the disease until march of 2012.