

1 **SUPPORTING INFORMATION**

2 The following Supporting Information is available for this article:

3

4 **Appendix S1.** References cited for estimation of host minimum residence times.

5 **Appendix S2.** References cited for the construction of the phylogenetic tree.

6 **Table S1.** Parameter estimates and tests for the global model of native range pathogen richness.

7 **Table S2.** Parameter estimates and tests for the global model of introduced range pathogen richness.

8 **Table S3.** Parameter estimates and tests for the global model of pathogen release.

9 **Figure S1.** The hypothesized phylogenetic relationship of the 124 host species.

10 **Figure S2.** Biological and historic / geographic factors explaining pathogen species richness in hosts'  
11 native range.

12 **Figure S3.** Analysis of all data available for each response variable, rather than their intersection.

13 **Figure S4.** Analysis of introduced range data using host habitat richness as an explanatory variable  
14 instead of residence time.

15

16 Additional Supporting Information may be found in the online version of this article.

17

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21

22 **Appendix S1.** References cited for estimation of host minimum residence times.

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- 196

197 Table S1. Parameter estimates (with asymptotic standard errors) and Type III quasi-likelihood Wald  
 198 tests for the global model of native range pathogen richness. Shown  $\chi^2$  values were scaled by the  
 199 model's residual deviance divided by its degrees of freedom.

Parameter	Estimate $\pm$ Std Error	DF	$\chi^2$	p-value
Intercept	1.236 $\pm$ 0.4228	1	8.55	0.0035
Sampling effort [ln(native range cites)]	0.1206 $\pm$ 0.0398	1	9.16	0.0025
Stress tolerance (yes)	-0.3317 $\pm$ 0.1274	1	6.78	0.0092
Height [ln(m)]	-0.000177 $\pm$ 0.000512	1	0.119	0.73
Leaf type (thickened epidermis and cuticle)	0.2303 $\pm$ 0.1247	1	3.41	0.065
History of agricultural use (yes)	0.3085 $\pm$ 0.1291	1	5.71	0.017
Native geographic range size ( $10^6$ km <sup>2</sup> )	0.0214 $\pm$ 0.0324	1	0.437	0.51
Habitat richness (number of types)	0.0169 $\pm$ 0.0040	1	17.6	<0.0001

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202 Table S2. Parameter estimates (with asymptotic standard errors) and Type III quasi-likelihood Wald  
 203 tests for the global model of introduced range pathogen richness. Shown  $\chi^2$  values were scaled by the  
 204 model's residual deviance divided by its degrees of freedom.

Parameter	Estimate $\pm$ Std Error	DF	$\chi^2$	p-value
Intercept	-1.255 $\pm$ 0.6478	1	3.76	0.053
Sampling effort [ln(introduced range cites)]	0.1238 $\pm$ 0.0600	1	4.25	0.039
Stress tolerance (yes)	-0.5192 $\pm$ 0.3149	1	2.72	0.099
Height [ln(m)]	-0.000818 $\pm$ 0.000857	1	0.911	0.34
Leaf type (thickened epidermis and cuticle)	0.2985 $\pm$ 0.2280	1	1.71	0.19
History of agricultural use (yes)	1.263 $\pm$ 0.2407	1	27.5	<0.0001
Introduced geographic range size ( $10^6$ km <sup>2</sup> )	0.2333 $\pm$ 0.0515	1	20.5	<0.0001
Residence time (centuries)	0.5240 $\pm$ 0.1197	1	19.1	<0.0001

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207 Table S3. Parameter estimates (with asymptotic standard errors) and Type III quasi-likelihood Wald  
 208 tests for the global model of introduced range proportional pathogen release. Shown  $\chi^2$  values were  
 209 scaled by the model's residual deviance divided by its degrees of freedom.

Parameter	Estimate $\pm$ Std Error	DF	$\chi^2$	p-value
Intercept	2.801 $\pm$ 0.9339	1	9.00	0.0027
Sampling effort [ln(native)-ln(introduced)]	0.1901 $\pm$ 0.1135	1	2.80	0.094
Stress tolerance (yes)	-0.4114 $\pm$ 0.4124	1	0.995	0.32
Height [ln(m)]	0.000991 $\pm$ 0.001317	1	0.567	0.45
Leaf type (thickened epidermis and cuticle)	-0.2720 $\pm$ 0.3261	1	0.700	0.40
History of agricultural use (yes)	-1.166 $\pm$ 0.3052	1	14.6	0.0001
Introduced geographic range size ( $10^6$ km <sup>2</sup> )	-0.2649 $\pm$ 0.0713	1	13.8	0.0002
Residence time (centuries)	-0.6234 $\pm$ 0.1680	1	13.8	0.0002

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211 Figure S1. The hypothesized phylogenetic relationship of the 124 host species. The scale bar unit is  
212 millions of years ago.

213 Figure S2. Biological and historic / geographic factors explaining pathogen species richness in hosts'  
214 native range. Gray symbols indicate stress tolerant hosts, and black symbols indicate hosts that are not  
215 stress tolerant. Diamonds indicate hosts with a history of agricultural use, and circles indicate hosts with  
216 no history of agricultural use. Symbols with cross-hairs indicate hosts with a thickened leaf cuticle and  
217 epidermis, and symbols without cross-hairs indicate hosts without this leaf anatomy. Shown  $\chi^2$  values  
218 are from quasi-likelihood Wald tests and were scaled by the model's residual deviance divided by its  
219 degrees of freedom. Statistics are from the AIC best model, which included only sampling effort  
220 (log-transformed citation count) and the five explanatory variables shown. Results were similar in all  
221 models analyzed. Pathogen species richness was greater on hosts that occupied a greater number of  
222 habitat types ( $\chi^2_1 = 18.0$ ;  $p < 0.0001$ ), on hosts that were not stress tolerant ( $\chi^2_1 = 6.74$ ;  $p = 0.0094$ ), and on  
223 hosts with a history of agricultural use ( $\chi^2_1 = 5.65$ ;  $p = 0.017$ ). Pathogen species richness also tended to  
224 be greater on hosts with a thickened leaf cuticle and epidermis ( $\chi^2_1 = 3.44$ ;  $p = 0.064$ ), and on hosts with a  
225 larger native geographic range size ( $\chi^2_1 = 0.65$ ;  $p = 0.42$ ).

226 Figure S3. Historic / geographic factors explaining pathogen species richness and proportional release  
227 from pathogens in hosts' introduced range. (A) Pathogen richness was greater on hosts that had a  
228 larger introduced geographic range size ( $\chi^2_1 = 45.5$ ;  $p < 0.0001$ ). (B) Pathogen richness was greater on  
229 hosts that had a longer residence time in the introduced range ( $\chi^2_1 = 9.99$ ;  $p < 0.0016$ ). (C) Release from  
230 pathogens was lesser on hosts that had a larger introduced geographic range size ( $\chi^2_1 = 40.2$ ;  $p < 0.0001$ ).  
231 (D) Release from pathogens was lesser on hosts that had a longer residence time in the introduced  
232 range ( $\chi^2_1 = 5.11$ ;  $p = 0.024$ ). (A-D) When points had identical x and y coordinates, the x-coordinate was  
233 jittered to render all points visible.

234 Figure S4. The relative importance (on a scale from 0 to 1) of biological (black bars) and historic /  
235 geographic (gray bars) variables in explaining (A) pathogen richness in hosts' native ranges (n=218), (B)  
236 pathogen richness in hosts' introduced ranges (n=175), (C) pathogen release in hosts' introduced ranges  
237 (n=158). These results use all available data for each of the three response variables. Results were  
238 similar to those in Fig. 1, which were based on the intersection of these three expanded data sets.

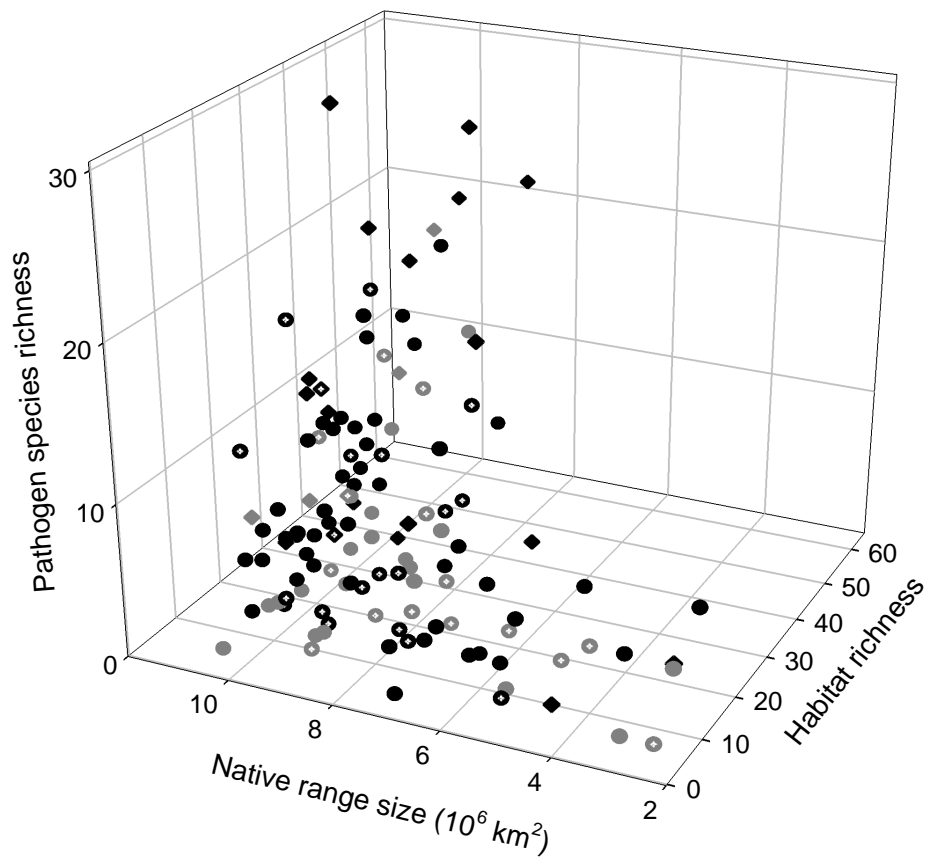
239 Figure S5. The relative importance (on a scale from 0 to 1) of biological (black bars) and historic /  
240 geographic (gray bars) variables in explaining (A) pathogen richness in hosts' introduced ranges, and (B)  
241 pathogen release in hosts' introduced ranges. Host habitat richness was used as an explanatory variable  
242 instead of residence time. Results were similar to the analogous main analyses (Fig. 1.B,C).

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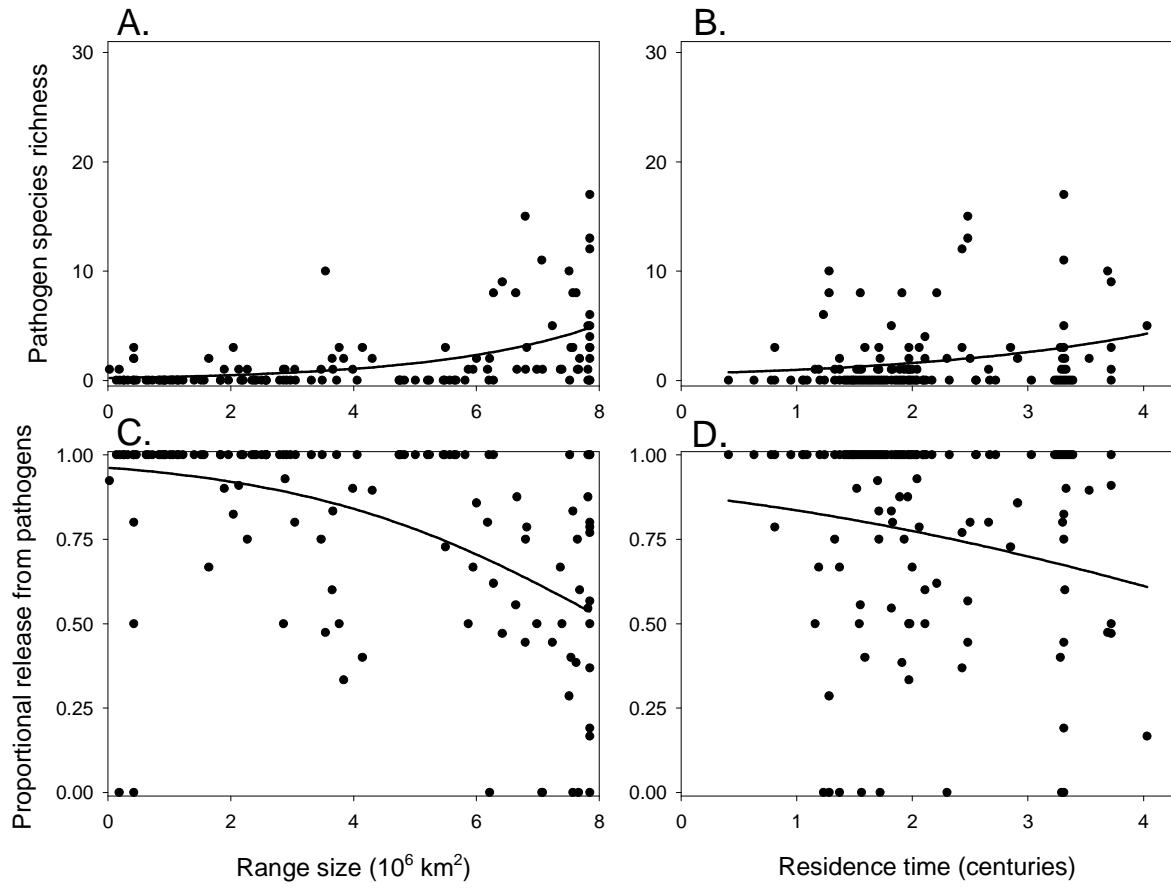
248 Figure S2.



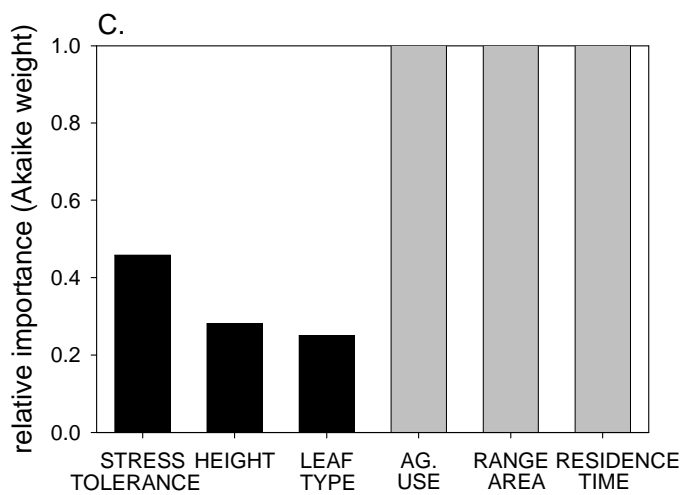
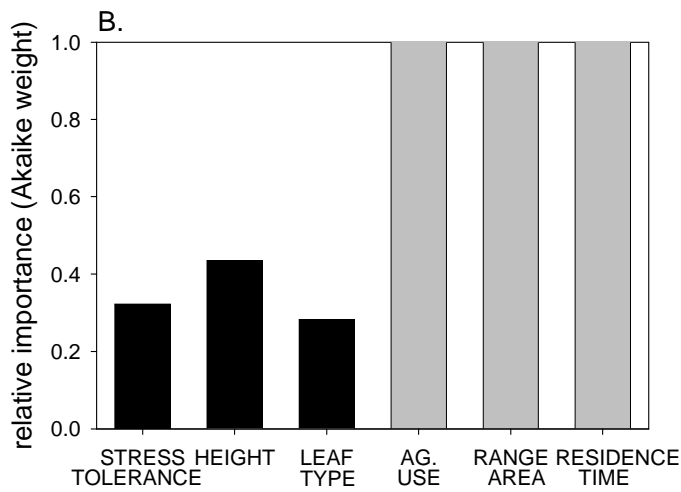
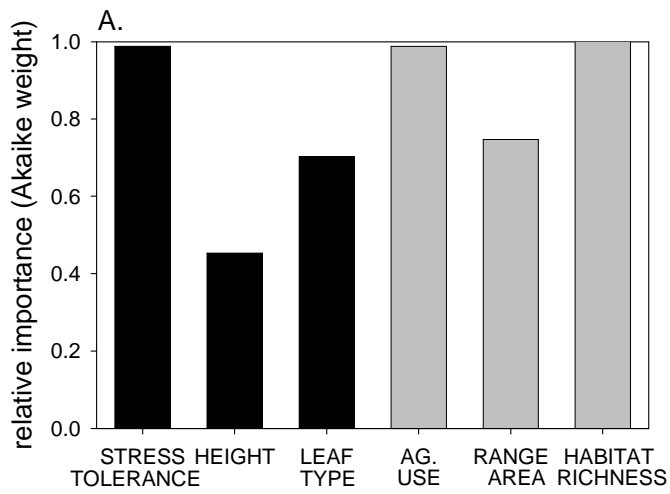
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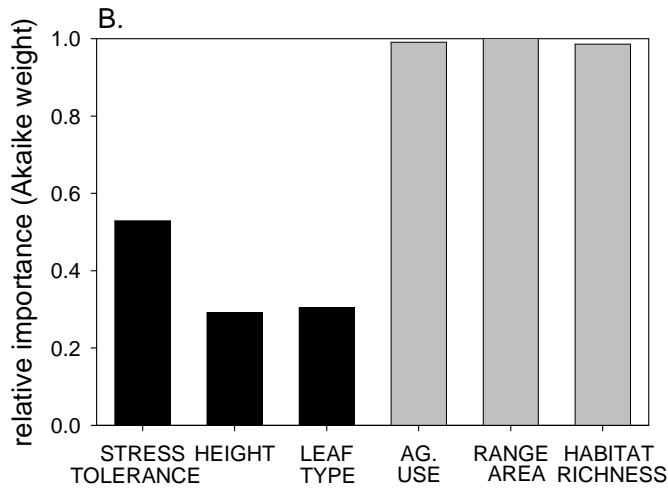
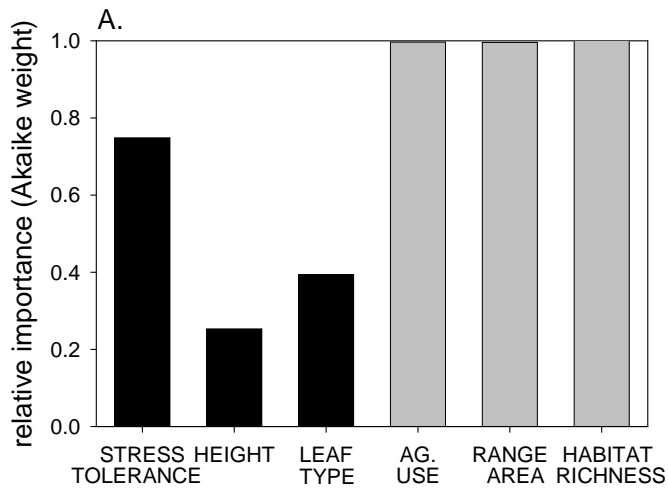


253 Figure S4.



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258 Figure S5.



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