

The coevolutionary mosaic of bat betacoronavirus emergence risk

Norma Forero Rocio Munoz^{1,2,‡} Renata L. Muylaert³ Stephanie N. Seifert⁴ Gregory F. Albery⁵

Daniel J. Becker⁶ Colin J. Carlson^{7,8,9,‡} [Timothée Poisot](#)^{1,2,‡}

¹ Université de Montréal ² Québec Centre for Biodiversity Sciences ³ Molecular Epidemiology and Public Health Laboratory, School of Veterinary Science, Massey University, New Zealand ⁴ Paul G. Allen School for Global Health, Washington State University, Pullman, WA, United States ⁵ Department of Biology, Georgetown University, Washington, DC, USA ⁶ Department of Biology, University of Oklahoma, Norman, OK, USA ⁷ Department of Biology, Georgetown University, Washington, DC,

⁸ Center for Global Health Science and Security, Georgetown University Medical Center, Washington, DC, USA ⁹ Department of Microbiology and Immunology, Georgetown University Medical Center, Washington, DC, USA

[‡] These authors contributed equally to the work

Correspondance to:

Timothée Poisot — timothee.poisot@umontreal.ca

Driven by the need to understand the ecological factors involved in the emergence of *Betacoronavirus* (the genus causing SARS, MERS, and COVID-19 in human) through bat hosts, we develop an approach to the assessment of spillover risk based on the Geographic Mosaic Theory of Coevolution. In doing so, we provide a global mapping of the spillover risk posed by betacoronaviruses, reflecting the fact that this risk is best understood through the multi-faceted prism of ecological and evolutionary mechanisms. Our framework reveals that host richness alone, although a component of viral hazard, is not a sufficiently integrative predictor of risk. We offer alternative insights based on viral sharing, host compositional uniqueness, and host phylogenetic diversity and phylogeographic regions. By comparing our aggregated measure of risk to a proxy for human density, namely the proportion of each pixel that is covered by urban or built land, we provide a synthetic risk map, allowing the identification of hotspots where the bat-betacoronavirus interaction network may facilitate the emergence of novel viruses and their spillover into human populations.

1 Disease emergence is complex, and is driven not only by animal-human contact, but also by the
2 underlying evolutionary dynamics in viral reservoirs.¹ Although host richness is often used as a superficial
3 proxy for spillover risk,^{2,3} these approaches oversimplify the relevant interspecific heterogeneity in
4 immunology, behavior, and other traits, and therefore overlook unique host pools that allow for the rapid
5 evolution of highly divergent viruses.⁴ In the case of generalist pathogens like betacoronaviruses, there is
6 conceptual and empirical support to the idea that these community-level mechanisms are even more
7 important,⁵ particularly given that cross-species transmission may, as a rule, structure viral evolution
8 more than co-divergence with hosts.⁶ This creates a disconnect between coevolutionary theory and most
9 existing ecological frameworks for mapping spillover risk.

10 The geographic mosaic theory of coevolution (GMTC) attempts to explicitly connect microevolutionary
11 dynamics to the macroecology and biogeography of symbiotic interactions.⁷ The GMTC posits that
12 coevolutionary processes among pairs⁸ or complexes⁹ of species are structured in space by the rippling
13 effects of abiotic conditions onto evolutionary mechanisms, giving rise to fragmented systems with
14 different ecologies over large spatial extents.¹⁰ The GMTC predicts a spatial fragmentation of
15 coevolutionary dynamics under the joint action of three processes:¹¹ coevolutionary hot- and coldspots,
16 which appear when the intensity of *interaction* (in terms of reciprocal fitness consequences) varies
17 spatially; selection mosaics, wherein the intensity of *selection* varies across space, driven by both the biotic
18 complexity of the community (locally diverse hosts and viruses are more biotically complex) and the local
19 favorability of the environment;¹² and trait remixing, which occurs when coevolutionary dynamics change
20 when community-level *functional traits* change through meta-community dynamics.

21 Here, we apply the GMTC to explore and explain the global biogeography of betacoronaviruses, the group
22 that includes SARS-CoV, MERS-CoV, and SARS-CoV-2. In their bat reservoirs, coronaviruses evolve
23 through a mix of host jumps, recombination among disparate lineages, and, to a lesser degree,
24 co-divergence with their hosts—²a mix of mechanisms that creates a complex and nonlinear relationship
25 between host diversity and viral emergence. Working from a recently published database of bat hosts of
26 betacoronaviruses, we test whether spatial structure in bat-betacoronavirus coevolution is identifiable at a
27 global scale. Aiming to explain these patterns, we develop a generalized framework for applying the
28 GMTC to host-virus interactions, with a specific emphasis on the potential to create independent
29 coevolutionary dynamics (and therefore spatial fragmentation in risk) through heterogeneity. We develop
30 a trivariate risk assessment system that connects each GMTC mechanism to a quantifiable aspect of

31 host-virus interactions: (i) viral sharing rates in host communities, representing the strength of potential
32 interaction between viruses and any one host (i.e., places where viruses undergo constant host switching
33 may be coevolutionary coldspots); (ii) the phylogenetic diversity of hosts, as a proxy for variation in the
34 immunological mechanisms that antagonize viruses (i.e., the selection mosaic); and (iii) the local
35 uniqueness of the bat community, representing the potential for viruses to be exposed to novel host traits
36 (e.g., variation in receptor sequences). Together, we argue that these can be used to identify and map the
37 evolutionary drivers that—in conjunction with transmission processes (e.g., viral prevalence in reservoirs
38 and animal-human contact rates)—determine disease emergence risk.

39 Results and Discussion

40 Bat and betacoronavirus biogeography are broadly consistent

41 Most previous work has assumed that the presence or richness of key groups of bat hosts are predictive of
42 coronavirus diversity.^{2,3} Projecting bat and betacoronavirus phylogeny over space (fig. 1), we find support
43 for the idea that bat community assembly is directly responsible for a global mosaic of viral evolution. The
44 distinct groupings (represented by different colors, symbolizing positions in a subspace formed by the first
45 two phylogenetic principal components) are essentially equivalent between the two groups, and can be
46 coarsely delineated as (1) south and southeast Asia; (2) east Asia (including northern China), west Asia,
47 and the Mediterranean coast; (3) Eurasia above a northing of 40; and (4) Africa and Latin America. In
48 some cases, this diverges from expectations about coronavirus biogeography: for example, previous work
49 has rarely flagged India as a region of interest, but for both bats and betacoronaviruses, the subcontinent
50 falls into the same regions as the southeast Asian peninsula (and indeed, the region is home to known bat
51 hosts of multiple betacoronavirus subgenera, including nobecoviruses, sarbecoviruses, and
52 merbecoviruses).³

53 [Figure 1 about here.]

54 Overall, these results suggest that the boundaries of bat and betacoronavirus biogeographic regions are
55 largely consistent. This may be surprising, given that cross-species transmission may play a stronger role
56 in coronavirus diversification than cospeciation—²a property that would theoretically allow for

57 substantial broad divergence in their biogeography. However, host jumps at the family level or higher are
58 relatively rare and significant events in coronavirus evolutionary history;^{2,13} as a result, the mosaic of
59 betacoronavirus phylogeography is assembled from a set of overlapping smaller coevolutionary systems,
60 superimposed in space and filtered by the importance of different subgroups in local host communities.
61 For example, the most speciose and cosmopolitan family of bats, the vesper bats (Vespertilionidae), are
62 considered the primary hosts of the subgenus *Merbecovirus* (MERS-like viruses);^{3,13} but in the Americas,
63 where merbecoviruses are the only lineage present, they have only been found in other bat taxa (e.g.,
64 Molossidae, Phyllostomidae).^{14–17} At the coarsest scale, these heterogeneities are lost, and betacoronavirus
65 biogeography tracks the deep rifts in bat evolutionary history—but within broad regions, the component
66 coevolutionary systems may have very different dynamics.

67 **Hotspots of bat and betacoronavirus biodiversity are distinct**

68 Bats, the second most diverse groups of mammals, are found worldwide; gradients in their species
69 richness generally track broader patterns of mammal diversity, with a striking Neotropical hotspot
70 (especially in the Amazon basin) and a secondary hotspot centered in the southeast Asian peninsula.
71 These hotspots of bat diversity are generally presumed to be hotspots of viral adaptive radiation, and
72 therefore areas of concern for human health.^{2,18} However, the hotspots of known bat betacoronavirus
73 hosts show a distinct pattern, with primary hotspots (both in terms of size and higher values) of host
74 richness situated in southeast Asia, parts of southern Europe, and to a lesser extent parts of Africa in the
75 -25-0 range of latitudes (fig. 2; top). Although hundreds of species likely host undiscovered
76 betacoronaviruses, machine learning predictions have suggested that these undiscovered reservoirs should
77 follow the same diversity gradient.¹⁹ In principle, these hotspots of locally-diverse, virus-rich bat
78 communities should drive more adaptive diversification in their viruses.

79 [Figure 2 about here.]

80 However, we find that the global pattern of betacoronavirus phylogenetic distinctiveness is quite distinct
81 from both bat host richness and phylogenetic distinctiveness (fig. 2; bottom). In contrast to the sparsity of
82 Neotropical betacoronavirus hosts, South and Central America have the most evolutionary distinct hosts
83 and viruses, followed by secondary hotspots in southeast Asia and the Rift Valley region have mostly
84 distinct viruses. Some degree of sampling bias may contribute to these patterns: for example, the

85 Neotropics are one of the places where the fewest bat betacoronavirus sequences have been generated
86 (cite2), resulting in a sparser phylogenetic tree, and artificially inflating distinctiveness; conversely,
87 disproportionate research effort in eastern China²⁰ may have led to a more complete inventory of the local
88 diversity of coronaviruses, again inflating these metrics relative to underlying patterns. Even accounting
89 for these potential biases, though, there is obvious heterogeneity in betacoronavirus evolutionary
90 distinctiveness that is distinct from overall bat diversity.

91 Overall, these patterns recapitulate the evolutionary history of both the order Chiroptera and the genus
92 *Betacoronavirus*. Horseshoe bats (Rhinolophidae) include the reservoirs of the SARS-like viruses
93 (subgenus *Sarbecovirus*), the group of pandemic threats that have been of the greatest interest to
94 researchers¹³ (and so have been sampled most intensively).²⁰ The hotspots of host richness and viral
95 diversity in southeast Asia—both of which are disproportionately high, considering the global landscape
96 of bat species richness—are almost entirely driven by viral adaptive radiation through host switching
97 within this clade^{3,19}. In contrast, the Neotropical hotspot of viral distinctiveness is driven by isolation by
98 host vicariance. Out of the four main groups of betacoronaviruses, only merbecoviruses have been found
99 in animals in the Americas—an introduction that is generally presumed to be ancient.^{3,21} While
100 comparatively understudied, New World merbecoviruses have been found in the ghost-faced bats
101 (Mormoopidae), Neotropical leaf-nosed bats (Phyllostomidae), and free-tailed bats (Molossidae).^{14–17} The
102 former two groups and a clade of the latter are endemic to the Neotropics, while the explosive adaptive
103 radiations of the phyllostomids are responsible for the hotspot of bat diversity in the Amazon.²² Together,
104 these clades of New World bats play host to a distinct regime of betacoronavirus coevolution.

105 Host landscapes generate a coevolutionary mosaic

106 The existence of well-defined cophylogenetic regions suggests that the bat-betacoronavirus system is
107 spatially fragmented enough to create differential coevolutionary processes; in turn, the coevolutionary
108 mosaic contributes to heterogeneity in emergence risk. These ideas are, respectively, supported by the
109 existence of hotspots of viral uniqueness and the diverse origins of human betacoronaviruses. Together,
110 these ideas point to a predictable relationship between host community structure and coevolutionary
111 pressure: phylogeographic structure in bat hosts—and their diverse immune strategies—²³ creates a
112 landscape of selective pressure; the trajectory of viruses' coevolutionary response is, in turn, constrained
113 by the opportunities they have for either coevolutionary specialization or diversification through host

114 jumps and recombination.

115 Based on the geographic mosaic theory of coevolution, we developed a trivariate map of three facets of
116 coevolutionary pressure (see Methods): (1) *host phylogenetic diversity*: a high diversity of evolutionary
117 histories should expose viruses to more variation in host immune traits; (2) *host community uniqueness*:
118 exposure to greater host trait heterogeneity can drive viral diversification, and coevolving with more
119 unique host communities should create more unique branches of viral evolution; and (3) propensity for
120 *viral sharing*: frequent cross-species transmission may act as a buffer on selective pressure, while lower
121 rates of exchange may enable more simultaneous trajectories of viral specialization to coexist within a
122 given community. We combine global maps of all three to generate a map of coevolutionary regimes,
123 where close colors represent similar risks, and paler pixels represent overall higher risk (fig. 3). We find
124 that these regions do not neatly overlap with those defined in fig. 1 or fig. 2, reinforcing the notion that
125 local-scale coevolutionary mosaics can form within cophylogenetic regions.

126 [Figure 3 about here.]

127 The greatest evolutionary potential for zoonotic emergence exists where pathogen pools have a high
128 genetic diversity and high propensity for cross-species transmission. In our framework, emergence risk is
129 therefore maximized under higher phylogenetic diversity (viruses are exposed to different host clades),
130 higher host uniqueness (viruses are experiencing novel, heterogeneous host traits combinations), and low
131 to medium viral sharing (host-virus pairs can coevolve independently, but divergent viruses may still have
132 opportunities for recombination). In fig. 3, this corresponds to yellow areas (dynamics dominated by low
133 viral sharing, with equal contributions of selection mosaics and trait remixing; southeast Asia, and the
134 Indian sub-continent), green-yellow areas (dynamics with low viral sharing but dominated by the
135 selection mosaic effect of host diversity; Africa below the Sahara desert), and red-yellow areas (dynamics
136 with low viral sharing but dominated by trait remixing in host communities; the Middle East). Translating
137 this axis of variation back into a univariate risk map (fig. 4) highlights that this evolutionary landscape has
138 a striking correspondence to regions where zoonotic betacoronaviruses have previously emerged.

139 Under this framework, other regions where high viral sharing dominates coevolutionary dynamics—such
140 as Latin America, or Eurasia above a northing of 30—would pose less of a risk of zoonotic emergence.
141 Nevertheless, areas of high host uniqueness coupled with high viral sharing (red-to-pink in fig. 3) could
142 create hotspots facilitated by viral codivergence. Our framework identifies Madagascar, where most bat

143 species are endemic following evolutionary divergence from sister species in both African and Asian
144 continents,²⁴ as one such hotspot; interestingly, a recent study²⁵ reported a novel and highly divergent
145 lineage of nobecoviruses from Madagascar-endemic pteropid bat species (*Pteropus rufus* and *Rousettus*
146 *madagascariensis*), again supporting the predictive power of the coevolutionary framework.

147 [Figure 4 about here.]

148 Human landscapes filter the geography of emergence risk

149 The relationship between the underlying pathogen pool and emergence risk is mediated by both
150 human-wildlife interfaces (the probability of spillover) and opportunities for onward transmission (the
151 probability that spillovers become epidemics)¹. As a proxy for both, we finally overlaid the risk component
152 from the composite map (see above) with the proportion of built land, as a proxy for a mix of habitat
153 disturbance, potential for bat synanthropy or contact with bridge hosts like livestock,^{26,27} and human
154 population density and connectivity^{1,28,29} (fig. 5). Accounting for these factors, most of South America and
155 Europe are at comparatively lower risk, as—although densely populated—settlements tend to be in areas
156 with lower potential risk. Conversely, regions like Malaysia and the northern coast of Australia have a
157 high evolutionary risk component, but should represent a relatively lower effective risk due to low human
158 density. However, southeast Asia, the Indian subcontinent, and scattered hotspots in sub-Saharan Africa
159 are at high risk due to the overlap between human populations and natural opportunities for cross-species
160 transmission of betacoronaviruses.

161 [Figure 5 about here.]

162 Reassuringly, these predictions correspond to the geographic origins of the three bat-origin coronaviruses
163 that have recently emerged in human populations. While available information puts the spillover of
164 SARS-CoV-2 in a live animal market in Wuhan, China, the ultimate origin of the virus is almost certainly
165 in a divergent lineage of sarbecoviruses from the Indochinese peninsula that was poorly characterized
166 prior to the pandemic.^{30–32} Similarly, the SARS-CoV outbreak began in Guangdong province in 2002,
167 reaching humans through small carnivore bridge hosts, but was eventually traced back to a set of likely
168 progenitor viruses found in cave-dwelling horseshoe bats in Yunnan province;³³ nearby, antibody
169 evidence has indicated human exposure to SARS-like viruses.³⁴ MERS-CoV was originally detected in

170 Saudi Arabia, accompanied by a nearly identical virus sequenced from an Egyptian tomb bat (*Taphozous*
171 *perforatus*),³⁵ but is widespread in camels in East Africa and the Middle East, and may have reached its
172 bridge host decades earlier than originally supposed;³⁶ as a result, the geography of the original
173 bat-to-camel transmission is still widely regarded as uncertain. All of these are broadly consistent with the
174 risk factors we identify. Notably, India and west Africa are additional hotspots that have yet to experience
175 the emergence of a bat coronavirus into human populations, but may still be at risk—particularly given
176 known gaps in bat surveillance,²⁰ and a dense population in both regions with global connectivity. In any
177 of these regions, surveillance on viral reservoirs can be paired with targeted monitoring of high-risk
178 human populations (i.e., those with regular wildlife contact)³⁷ for maximum impact.

179 Conclusion

180 Bats are important reservoir hosts for different classes of microorganisms, many of which a threat to
181 human health.^{38,39} Chiropterans emerged around 64 million years ago and are one of the most diverse
182 mammalian orders, with an estimated richness of more than 1400 species.^{40,41} They exhibit a broad variety
183 of habitat use, behaviour, and feeding strategies, putting them at key positions in the delivery and
184 provisioning of several ecosystem services, tied to important ecosystem-derived benefits to human.⁴² For
185 example, bats are an essential component of many seed-dispersal networks.⁴³ Over two-thirds of bats are
186 know to be either obligate or facultative insectivores, therefore actively contributing for agricultural pest
187 control,^{44,45} and vectors of pathogens that put a risk on human health.^{46,47} Because bats are globally
188 distributed and have a long evolutionary history, phylogeographic and biogeographic approaches are
189 required to shed light on the contemporary distribution of coevolutionary processes between bats and the
190 pathogens they host. Not all areas in which bats, viruses, and human are co-occurring are facing a risk of
191 spillover towards human populations, and the areas in which this risk exist may not be facing risks of the
192 same nature and magnitude.

193 Here, we propose a simple framework with broad explanatory power that helps contextualize discoveries
194 like highly divergent nobecoviruses in Madagascar and the previously-neglected adaptive radiation of
195 sarbecoviruses outside of southern China and throughout southeast Asia. In doing so, it advances
196 ecological theory beyond the current state of the art for global maps of emergence risk. For example,
197 previous studies that have used host richness as proxy have predicted a high diversity of unsampled bat

198 viruses,¹⁸ bat coronaviruses,² and even specifically betacoronaviruses¹⁹ in both the Amazon and southeast
199 Asia. While we find that both regions are characterized by highly divergent host and viral communities,
200 our framework identifies key differences between the regions. We find that Latin America is a hotspot of
201 both host and viral distinctiveness, suggesting that this branch of the bat-betacoronavirus complex may be
202 undergoing independent evolutionary dynamics from the rest of the global pool, but with limited potential
203 for viral diversification—a finding that is supported by previous work indicating a higher rate of
204 codivergence in Latin America.² In contrast, in southeast Asia, host richness and viral distinctiveness are
205 high but sharing is low; this suggests a different type of evolutionary dynamics that could generate high
206 local diversity of viruses through host switching and viral recombination (see e.g.,¹³ as well as the
207 discovery of recombinant viruses that share genetic material from both the SARS-CoV and SARS-CoV-2
208 branches of the Sarbecovirus lineage).⁴⁸ Both of these regions are priority areas for sampling, especially
209 given predictions that they contain many bat hosts of undiscovered betacoronaviruses.^{19,20} However, both
210 the evolutionary and ecological aspects of emergence risk are likely higher in southeast Asia—a fact that
211 will only become more relevant, as bats track shifting climates and exchange viruses with other species,
212 creating a hotspot of cross-species transmission unique to the region.⁴⁹

213 The diversity and diversification potential of bats responds to anthropogenic factors others than shifting
214 climates.⁵⁰ Land use changes could significantly decrease bat suitability, notably through effects on diet
215 and availability of habitats.⁵¹ As our results establish that the diversification of bats betacoronaviruses
216 happens on top of processes affecting hosts, biogeographic variation in human population density and
217 anthropogenic disturbances may feed into co-evolutionary dynamics. Increase in humans-hosts contacts
218 also increase the risk of emergence of novel diseases,⁵² so does the changes in landscape connectivity at
219 local/regional scales.⁵³ This represents a challenge for both conservation strategies and disease ecology:
220 some areas can a high emergence risk and more potential for the acquisition of zoonotic viruses through
221 bat-human encounters.⁵⁴ In particular, the challenge ahead lies in the need to quantify actual exposure
222 (and risk) accounting for several transmission scenarios, including both direct and indirect bat - human
223 interactions, and feeding back into the provision of ecosystem services by bats.

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234 **Methods**

235 **Known *Betacoronavirus* hosts**

236 We downloaded the data on bats hosts of *Betacoronavirus* from
237 <https://www.viralemergence.org/betacov> on Apr. 2022,¹⁹ and filtered it to “known” hosts (established
238 before the emergence of SARS-CoV-2) and “novel” hosts (confirmed through sampling and competence
239 assays since the initial data collection). The original database was assembled by a combination of data
240 mining and literature surveys, including automated alerts on the “bats” and “coronavirus” keywords to
241 identify novel empirical evidence of bats-betacoronaviruses associations; this yielded a total of 126 known
242 hosts, 47 of which were novel hosts.

243 **Bat occurrences**

244 We downloaded the rangemap of every current bat species that was classified as an empirically
245 documented host of *Betacoronavirus* from the previous step, according to recent IUCN data.⁵⁵ The range
246 maps were subsequently rasterized using the rasterize function from GDAL⁵⁶ at a resolution of
247 approximately 100kmx100km. For every pixel in the resulting raster where at least one bat host of
248 *Betacoronavirus* was present, we extract the species pool (list of all known bat hosts), which was used to
249 calculate the following risk assessment components: bat phylogenetic diversity, bat compositional
250 uniqueness, and predicted viral sharing risk.

251 **Bat phylogenetic diversity**

252 For every pixel, we measured Faith’s Phylogenetic Diversity⁵⁷ based on a recent synthetic tree with robust
253 time calibration, covering about 6000 mammalian species.⁵⁸ Faith’s PD measures the sum of unique
254 branches from an arbitrary root to a set of tips, and comparatively larger values indicate a more
255 phylogenetic diverse species pool. We measured phylogenetic diversity starting from the root of the entire
256 tree (and not from Chiroptera); this bears no consequences on the resulting values, since all branches
257 leading up to Chiroptera are only counted one per species pool, and (as we explain when describing the
258 assembly of the composite risk map), all individual risk components are ranged in [0,1]. This measure
259 incorporates a richness component, which we chose not to correct for; the interpretation of the

260 phylogenetic diversity is therefore a weighted species richness, that accounts for phylogenetic
261 over/under-dispersal in some places.

262 **Bat compositional uniqueness**

263 For every species pool, we measured its Local Contribution to Beta-Diversity;⁵⁹ LCBD works from a
264 species-data matrix (traditionally noted as \mathbf{Y}), where species are rows and sites are columns, and a value of
265 1 indicates occurrence. We extracted the \mathbf{Y} matrix assuming that every pixel represents a unique location,
266 and following best practices⁶⁰ transformed it using Hellinger's distance to account for unequal bat
267 richness at different pixels. The correction of raw community data is particularly important for two
268 reasons: first, it prevents the artifact of richer sites having higher importance; second, it removes the effect
269 of overall species richness, which is already incorporated in the phylogenetic diversity component. High
270 values of LCBD indicate that the pixel has a community that is on average more dissimilar in species
271 composition than what is expected knowing the entire matrix, i.e. a more unique community. Recent
272 results by⁶¹ shows that LCBD measures are robust with regards to spatial scale, and are therefore
273 applicable at the global scale.

274 **Viral sharing between hosts**

275 For all bat hosts of *Betacoronavirus*, we extracted their predicted viral sharing network, generated from a
276 previously published generalized additive mixed model of virus sharing by a tensor function of
277 phylogenetic distance and geographic range overlap across mammals.⁶² This network stores pairwise
278 values of viral community similarity. To project viral sharing values into a single value for every pixel, we
279 averaged the pairwise scores. High values of the average sharing propensity means that this specific extant
280 bat assemblage is likely to be proficient at exchanging viruses.

281 **Composite risk map**

282 To visualize the aggregated risk at the global scale, we combine the three individual risk components
283 (phylogenetic diversity, compositional uniqueness, and viral sharing) using an additive color model.⁶³ In
284 this approach, every risk component gets assigned a component in the RGB color model (phylogenetic
285 diversity is green, compositional uniqueness is red, and viral sharing is blue). In order to achieve a valid

286 RGB measure, all components are re-scaled to the [0,1] interval, so that a pixel with no sharing, no
287 phylogenetic diversity, and no compositional uniqueness is black, and a pixel with maximal values for
288 each is white. This additive model conveys both the intensity of the overall risk, but also the nature of the
289 risk as colors diverge towards combinations of values for three risk components. Out of the possible
290 combinations, the most risky in terms of rapid diversification and spillover potential is high phylogenetic
291 diversity and low viral sharing,⁶⁴ in that this allows multiple independent host-virus coevolutionary
292 dynamics to take place in the same location. In the colorimetric space, this corresponds to yellow – because
293 the HSV space is more amenable to calculations for feature extraction,⁶⁵ we measured the risk level by
294 calculating the angular distance of the hue of each pixel to a reference value of 60 (yellow), and weighted
295 this risk level by the value component. Specifically, given a pixel with colorimetric coordinates (h, s, v), its
296 ranged weighted risk value is

$$v \times \left[1 - \frac{|\text{atan}(\cos(\text{rad}(h)), \sin(\text{rad}(h))) - X|}{2\pi} \right],$$

297 where X is $\text{atan}(\cos(\text{rad}(60)), \sin(\text{rad}(60)))$, a constant approximately equal to 0.5235.

298 **Viral phyogeography and evolutionary diversification**

299 To next represent phyogeography of betacoronaviruses in bats, we aggregated and analyzed
300 betacoronavirus sequence data. We used the following query to pull all *Betacoronavirus* sequence data
301 from the GenBank Nucleotide database except SARS-CoV-2; (“Betacoronavirus”[Organism] OR
302 betacoronavirus[All Fields]) NOT (“Severe acute respiratory syndrome coronavirus 2”[Organism] OR
303 sars-cov-2[All Fields]). We added a single representative sequence for SARS-CoV-2 and manually curated
304 to remove sequences without the RNA-dependent RNA polymerase (RdRp) sequence or that contained
305 words indicating recombinant or laboratory strains including “patent”, “mutant”, “GFP”, and
306 “recombinant”. We filtered over-represented taxa including betacoronavirus 1, hCoV-OC43, Middle East
307 respiratory syndrome coronavirus, Murine hepatitis virus, and hCoV-HKU1. Curated betacoronavirus
308 RdRp sequences were then aligned using MAFFT⁶⁶ v1.4.0 (Algorithm FFT-NS-2, Scoring matrix 200PAM /
309 k=2, gap open penalty 1.53m offset value 0.123) and a maximum likelihood tree reconstructed in
310 IQ-TREE⁶⁷ v1.6.12 with ModelFinder⁶⁸ ultrafast bootstrap approximation⁶⁹ with a general time reversible
311 model with empirical base frequencies and the 5-discrete-rate-category FreeRaye model of nucleotide

312 substitution (GTR+F+R5).

313 We first tested the hypothesis that hotspots of viral diversification would track hotspots of bat
314 diversification. To do so, we plotted the number of known bat hosts (specifically only those included in the
315 phylogeny, so there was a 1:1 correspondence between data sources) against the “mean evolutionary
316 distinctiveness” of the associated viruses. To calculate this, we derived the fair proportions evolutionary
317 distinctiveness⁷⁰ for each of the viruses in the tree, then averaged these at the bat species level, projected
318 these values onto their geographic distributions, and averaged across every bat found in a given pixel. As
319 such, this can be thought of as a map of the mean evolutionary distinctiveness of the known viral
320 community believed to be associated with a particular subset of bats present.

321 **Co-distribution of hosts and viral hotspots**

322 Subsequently, we tested the hypothesis that the biogeography of bat betacoronaviruses should track the
323 biogeography of their hosts. To test this idea, we loosely adapted a method from,^{71,72} who proposed a
324 phylogenetic method for the delineation of animal biogeographic regions. In their original method, a
325 distance matrix - where each row or column represents a geographic raster’s grid cell, and the dissimilarity
326 values are the “beta diversity similarity” of their community assemble - undergoes non-metric
327 multidimensional scaling (NMDS); the first two axes of the NMDS are projected geographically using a
328 four-color bivariate map. Here, we build on this idea with an entirely novel methodology. First, we
329 measure the phylogenetic distance between the different viruses in the betacoronaviruses tree by using the
330 cophenetic function in ape;⁷³ subsequently, we take a principal components analysis of that distance
331 matrix (readily interchangeable for NMDS in this case) to project the viral tree into an n-dimensional
332 space. We then take the first two principal components and, as with the evolutionary distinctiveness
333 analysis, aggregated these to a mean host value and projected them using a four-color bivariate map.

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Figure 1: Phylogeographic regions of bats (top) and viruses (bottom) based on the joint analysis of their occurrence and phylogenetic relatedness. The different colors show tendencies to separate alongside the first two components of a PCoA. Note that the PCoA for the bats and viruses are independent, and so cannot be compared directly – that being said, the regions can be compared across maps.

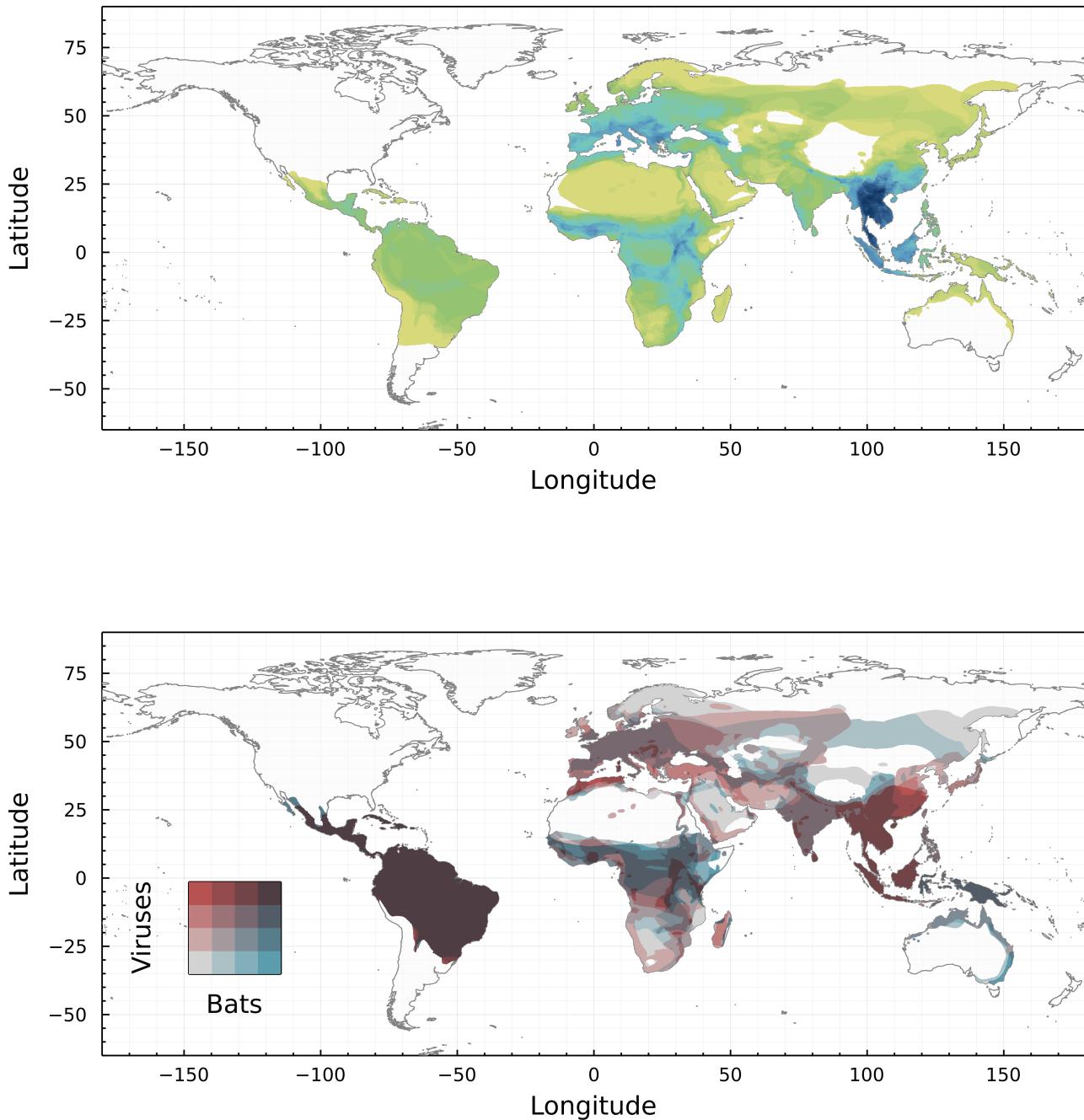


Figure 2: Top panel: relative diversity of known bat hosts of betacoronaviruses. This map shows that the region with the largest number of possible hosts is South-Eastern Asia. Bottom panel: congruence between the evolutionary distinctiveness of the hosts (grey to blue) and the viruses (grey to red).

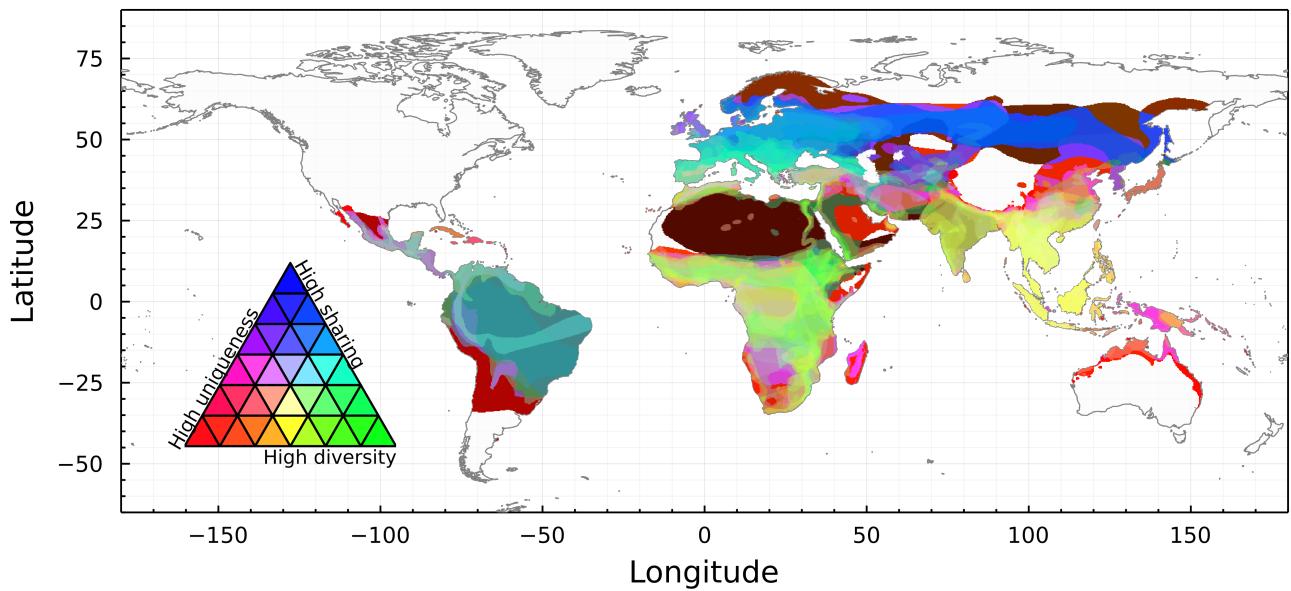


Figure 3: Trivariate additive mapping of the components of risk in the red/green/blue, where high virus sharing is encoded in the blue channel, host phylogenetic diversity in the green channel, and compositional uniqueness in the red channel. The main driver of emergence risk (possibility of spatially overlapped but coevolutionarily independent host-viral dynamics) corresponds to low viral sharing, *i.e.* pixels around yellow.

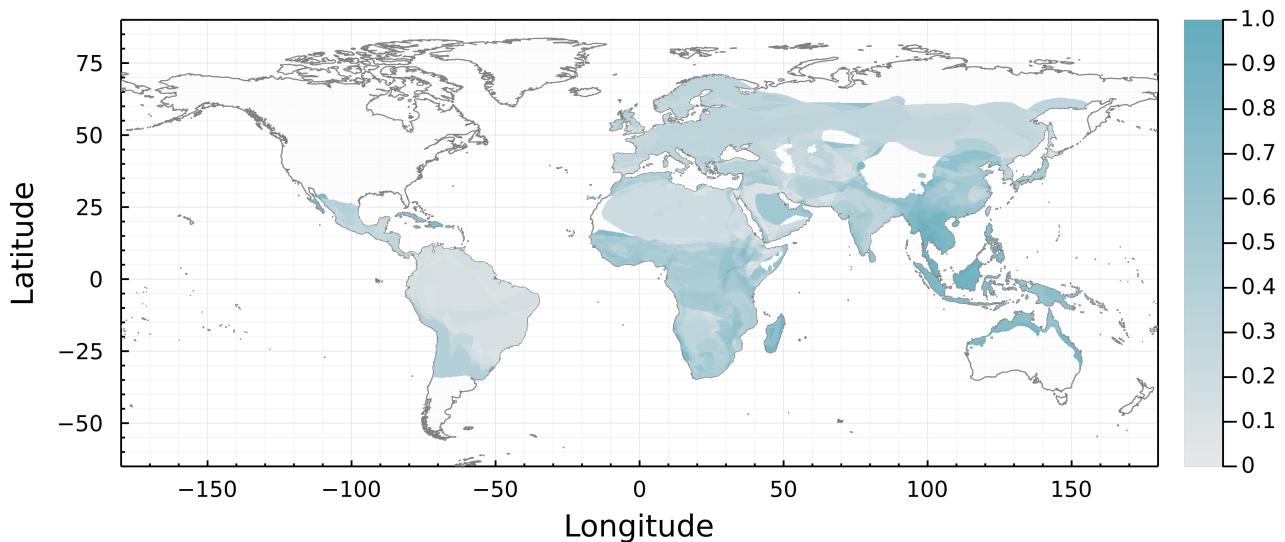


Figure 4: Extraction of a measure of *Betacoronavirus* emergence risk from bat hosts based on the colorimetric space from fig. 3. The risk is a composite measure of the color value and angular distance to the yellow hue, as defined in the methods, ranged in the unit space. Based on these analyses, South-Eastern Asia, Madagascar, the Middle-East, and Africa below the Sahara desert have the highest relative risk of emergence.

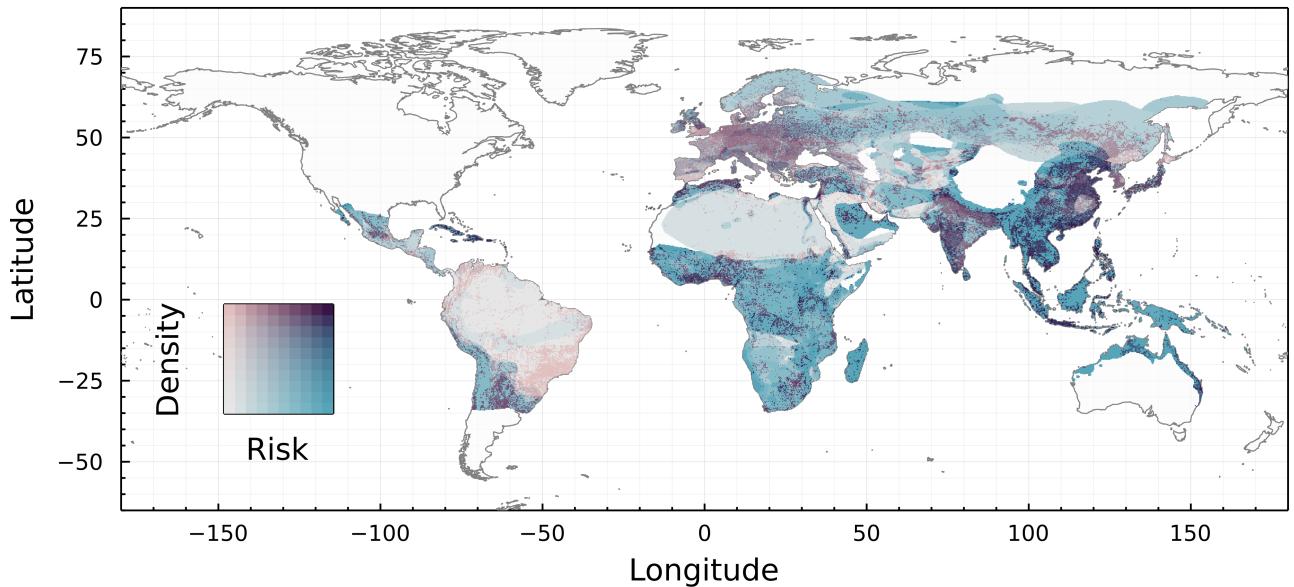


Figure 5: Overlap of the percent of each pixel occupied by urbanized structures, representing the degree of settlement, on the spillover risk map (where the risk comes only from wildlife, and ignores multi-hosts chains of transmissions including non-bats hosts). Darker pixels correspond to more risk, in that the GMTC-derived risk of fig. 4 is high *and* the pixel is densely occupied by human populations. This approach increases the relative risk of several regions in Africa, and highlights the risk in India, southeast China, and the Arabian peninsula where areas of high to moderate risk overlap with areas of denser population.