

The coevolutionary mosaic of bat betacoronavirus emergence risk

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Pathogen evolution is one of the least predictable components of disease emergence, particularly in nature. Here, building on principles established by the geographic mosaic theory of coevolution, we develop a quantitative, spatially-explicit framework for mapping the evolutionary risk of viral emergence. Driven by interest in diseases like SARS, MERS, and COVID-19, we examine the global biogeography of bat-origin betacoronaviruses, and find that coevolutionary principles suggest geographies of risk that are distinct from the hotspots and coldspots of host richness. Further, our framework helps explain patterns like a unique pool of merbecoviruses in the Neotropics, a recently-discovered lineage of divergent nobecoviruses in Madagascar, and—most importantly—hotspots of diversification in southeast Asia, sub-Saharan Africa, and the Middle East that correspond to the site of previous zoonotic emergence events. Our framework may help identify hotspots of future risk that have also been previously overlooked, like west Africa and the Indian subcontinent, and may more broadly help researchers understand how host ecology shapes the evolution and diversity of pandemic threats.

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,^{2–4} 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.⁵ 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,⁶ particularly given that cross-species transmission may, as a rule, structure viral evolution
8 more than co-divergence with hosts.⁷ 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.⁸ The GMTC posits that
12 coevolutionary processes among pairs⁹ or complexes¹⁰ 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.¹¹ The GMTC predicts a spatial fragmentation of
15 coevolutionary dynamics under the joint action of three processes:¹² 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;¹³ 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 broadly consistent at a global scale; perfect matching between the biogeographic regions would have
56 indicated that the signal of virus distribution is fully predicted by bat hosts ranges. Areas for which the

57 biogeographic regions for bats and betacoronaviruses differ are primarily (i) southeast Asia and southern
58 China, and (ii) the Arabian peninsula, which are both regions where zoonotic transmission has been
59 documented (potentially driving a unique level of viral sampling effort that generates these patterns).
60 These spatially limited mismatches notwithstanding, the large level of congruence may be surprising,
61 given that cross-species transmission may play a stronger role in coronavirus diversification than
62 cospeciation—²a property that would theoretically allow for substantial broad divergence in their
63 biogeography. However, host jumps at the family level or higher are relatively rare and significant events
64 in coronavirus evolutionary history;^{2,14} as a result, the mosaic of betacoronavirus phylogeography is
65 assembled from a set of overlapping smaller coevolutionary systems, superimposed in space and filtered
66 by the importance of different subgroups in local host communities. For example, the most speciose and
67 cosmopolitan family of bats, the vesper bats (Vespertilionidae), are considered the primary hosts of the
68 subgenus *Merbecovirus* (MERS-like viruses);^{3,14} but in the Americas, where merbecoviruses are the only
69 lineage present, they have only been found in other bat taxa (e.g., Molossidae, Phyllostomidae).^{15–18} At the
70 coarsest scale, these heterogeneities are lost, and betacoronavirus biogeography tracks the deep rifts in bat
71 evolutionary history—but within broad regions, the component coevolutionary systems may have very
72 different dynamics.

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

74 Bats, the second most diverse group of mammals, are found worldwide; gradients in their species
75 richness generally track broader patterns of mammal diversity,¹⁹ with a striking Neotropical hotspot
76 (especially in the Amazon basin) and a secondary hotspot centered in Indochina. These hotspots of bat
77 diversity are generally presumed to be hotspots of viral adaptive radiation, and therefore areas of concern
78 for human health.^{2,20} However, the hotspots of known bat betacoronavirus hosts show a distinct pattern,
79 with primary hotspots (both in terms of area and higher values) of host richness situated in southeast
80 Asia, parts of southern Europe, and to a lesser extent parts of Africa in the -25-0 range of latitudes (fig. 2;
81 top). Although hundreds of species likely host undiscovered betacoronaviruses, machine learning
82 predictions have suggested that these undiscovered reservoirs should follow the same diversity gradient.²¹
83 In principle, these hotspots of locally-diverse, virus-rich bat communities should drive more adaptive
84 diversification in their viruses.

86 However, we find that the global pattern of betacoronavirus phylogenetic distinctiveness is quite distinct
87 from both bat host richness and phylogenetic distinctiveness (fig. 2; bottom). In contrast to the sparsity of
88 Neotropical betacoronavirus hosts, South and Central America have the most evolutionary distinct hosts
89 and viruses, followed by secondary hotspots in southeast Asia and the Rift Valley region have mostly
90 distinct viruses. Some degree of sampling bias may contribute to these patterns: for example, the
91 Neotropics are one of the places where the fewest bat betacoronavirus sequences have been generated,^{22–24}
92 resulting in a sparser phylogenetic tree, and artificially inflating distinctiveness; conversely,
93 disproportionate research effort in eastern China²⁵ may have led to a more complete inventory of the local
94 diversity of coronaviruses, again inflating these metrics relative to underlying patterns. Even accounting
95 for these potential biases, though, there is obvious heterogeneity in betacoronavirus evolutionary
96 distinctiveness that is distinct from overall bat diversity.

97 Overall, these patterns recapitulate the evolutionary history of both the order Chiroptera and the genus
98 *Betacoronavirus*. Horseshoe bats (Rhinolophidae) include the reservoirs of the SARS-like viruses
99 (subgenus *Sarbecovirus*), the group of pandemic threats that have been of the greatest interest to
100 researchers¹⁴ (and so have been sampled most intensively;).²⁵ The hotspots of host richness and viral
101 diversity in southeast Asia—both of which are disproportionately high, considering the global landscape
102 of bat species richness—are almost entirely driven by viral adaptive radiation through host switching
103 within this clade^{3,21}. In contrast, the Neotropical hotspot of viral distinctiveness is driven by isolation by
104 host vicariance. Out of the four main groups of betacoronaviruses, only merbecoviruses have been found
105 in animals in the Americas—an introduction that is generally presumed to be ancient.^{3,26} While
106 comparatively understudied, New World merbecoviruses have been found in the ghost-faced bats
107 (Mormoopidae), Neotropical leaf-nosed bats (Phyllostomidae), and free-tailed bats (Molossidae).^{15–18} The
108 former two groups and a clade of the latter are endemic to the Neotropics, while the explosive adaptive
109 radiations of the phyllostomids are responsible for the hotspot of bat diversity in the Amazon.²⁷ Together,
110 these clades of New World bats play host to a distinct regime of betacoronavirus coevolution.

111 Our approach is potentially limited by sampling bias: key hotspots identified by our model have, indeed,
112 been sampled intensely following major zoonotic emergence events. In these areas, more betacoronavirus
113 hosts will have been discovered, leading to higher overall diversity and potentially higher sharing.

114 Similarly, hotspots of evolutionary uniqueness - as in the Arabian peninsula - could reflect much broader
115 lineages that have only been sampled in focal areas for public health. While the discovery of new branches
116 of bat-betacoronavirus coevolution is certainly likely, and might change some of the observed patterns, our
117 framework is likely to be fairly robust: the 126 hosts in our study capture nearly 10% of global bat diversity,
118 and the underlying evolutionary patterns they represent are much less sensitive to new information than
119 any inferences about viral evolution.

120 **Coevolutionary regimes structure evolutionary potential for zoonotic emergence**

121 The existence of well-defined cophylogenetic regions suggests that the bat-betacoronavirus system is
122 spatially fragmented enough to create divergent coevolutionary trajectories; in turn, this coevolutionary
123 mosaic may alter the risk of zoonotic emergence. These ideas are, respectively, supported by the existence
124 of hotspots of viral uniqueness and the diverse origins of human betacoronaviruses. Together, this
125 framework points to a predictable relationship between host community structure and coevolutionary
126 pressure: phylogeographic structure in bat hosts (and their diverse immune strategies);²⁸ creates a
127 landscape of selective pressure; the trajectory of viruses' coevolutionary response is, in turn, constrained
128 by their opportunities for either specialization or diversification through host jumps and recombination.

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

140 [Figure 3 about here.]

141 The greatest evolutionary potential for zoonotic emergence exists where pathogen pools have a high

142 genetic diversity and high propensity for cross-species transmission. In our framework, emergence risk is
143 therefore maximized under higher phylogenetic diversity (viruses are exposed to different host clades),
144 higher host uniqueness (viruses are experiencing novel, heterogeneous host traits combinations), and low
145 to medium viral sharing (host-virus pairs can coevolve independently, but divergent viruses may still have
146 opportunities for recombination). In fig. 3, this corresponds to yellow areas (dynamics dominated by low
147 viral sharing, with equal contributions of selection mosaics and trait remixing; southeast Asia, and the
148 Indian sub-continent), green-yellow areas (dynamics with low viral sharing but dominated by the
149 selection mosaic effect of host diversity; sub-Saharan Africa), and red-yellow areas (dynamics with low
150 viral sharing but dominated by trait remixing in host communities; the Middle East). Translating this axis
151 of variation back into a univariate risk map (fig. 4) highlights that this evolutionary landscape has a
152 striking correspondence to regions where zoonotic betacoronaviruses have previously emerged. Our
153 findings align with predictions regarding the spatial location of cross-species transmission. These
154 locations not only pose a potential risk of viral jumps that could endanger human health but also provide
155 valuable information for monitoring wildlife health. This could guide us to determine where and what
156 measures to implement for effectively monitoring wildlife and human betacoronavirus outbreaks before
157 they escalate to critical levels. Nevertheless, there are actually very few documented cases of emergence
158 events, and similarities could be some degree of coincidental.

159 Compared to approaches that map emergence risk based only on the number of known bat hosts of
160 betacoronaviruses, our framework suggests regions where high viral sharing dominates coevolutionary
161 dynamics—such as Latin America, or Eurasia above a northing of 30—would pose less of a relative risk of
162 zoonotic emergence. Nevertheless, areas of high host uniqueness coupled with high viral sharing
163 (red-to-pink in fig. 3) could create hotspots facilitated by viral codivergence. Our framework identifies
164 Madagascar, where most bat species are endemic following evolutionary divergence from sister species in
165 both African and Asian continents,²⁹ as one such hotspot; interestingly, a recent study³⁰ reported a novel
166 and highly divergent lineage of nobecoviruses from Madagascar-endemic pteropid bat species (*Pteropus*
167 *rufus* and *Rousettus madagascariensis*), again supporting the predictive power of the coevolutionary
168 framework.

169

[Figure 4 about here.]

170 **Human landscapes filter the geography of emergence risk**

171 The relationship between the underlying pathogen pool and emergence risk is mediated by both
172 human-wildlife interfaces (the probability of spillover) and opportunities for onward horizontal
173 transmission (the probability that spillovers become epidemics)¹. It must be noted that the assessment of
174 risk based on the GMTC mechanisms does not account for human presence; for this reason, it represents
175 “potential” level of risk, which must be re-evaluated in the light of human presence. As a proxy for both,
176 we finally overlaid the risk component from the composite map (see above) with the proportion of built
177 land, as a proxy for a mix of habitat disturbance, potential for bat synanthropy or contact with bridge hosts
178 like livestock,^{31,32} and human population density and connectivity^{1,33,34} (fig. 5). Accounting for these
179 factors, most of South America and Europe are at comparatively lower risk, as—although densely
180 populated—settlements tend to be in areas with lower potential risk. Conversely, regions like Malaysia and
181 the northern coast of Australia have a high evolutionary risk component, but should represent a relatively
182 lower effective risk due to low human density. However, southeast Asia, the Indian subcontinent, and
183 scattered hotspots in sub-Saharan Africa are at high risk due to the overlap between human populations
184 and natural opportunities for cross-species transmission of betacoronaviruses.

185 [Figure 5 about here.]

186 Reassuringly, these predictions correspond to the geographic origins of the three bat-origin coronaviruses
187 that have recently emerged in human populations. While available information puts the spillover of
188 SARS-CoV-2 in a live animal market in Wuhan, China, the ultimate origin of the virus is almost certainly
189 in a divergent lineage of sarbecoviruses from Indochina that was poorly characterized prior to the
190 pandemic.^{22–24} Similarly, the SARS-CoV outbreak began in Guangdong province in 2002, reaching
191 humans through small carnivore bridge hosts, but was eventually traced back to a set of likely progenitor
192 viruses found in cave-dwelling horseshoe bats in Yunnan province;³⁵ nearby, antibody evidence has
193 indicated human exposure to SARS-like viruses.³⁶ MERS-CoV was first detected in Jordan, but is
194 widespread in camels in East Africa and the Middle East, and may have reached its bridge host decades
195 earlier than originally supposed;³⁷ as a result, the geography of the original bat-to-camel transmission is
196 still widely regarded as uncertain. All of these are broadly consistent with the risk factors we identify.
197 Notably, India and west Africa are additional hotspots that have yet to experience the emergence of a bat
198 coronavirus into human populations, but may still be at risk—particularly given known gaps in bat

199 surveillance,²⁵ and a dense population in both regions with global connectivity. In any of these regions,
200 surveillance on viral reservoirs can be paired with targeted monitoring of high-risk human populations
201 (i.e., those with regular wildlife contact)³⁸ for maximum impact.

202 Conclusion

203 Bats emerged around 64 million years ago, and are one of the most diverse mammalian orders, with more
204 than 1,400 estimated species.^{Peixoto2018SynEco?, Simmons2020BatSpe?} They exhibit a broad variety of habitat use,
205 behaviour, and feeding strategies, putting them at key positions in the delivery and provisioning of several
206 ecosystem services, tied to important ecosystem-derived benefits to humans.³⁹ Over two-thirds of bats are
207 known to be either obligate or facultative insectivores, therefore actively contributing for agricultural pest
208 control,^{40,41} and vectors of pathogens that put a risk on human health;^{42,43} some other species are essential
209 links in many seed-dispersal networks.⁴⁴ However, many of these species face a high risk of extinction,
210 particularly given persecution and killings that sometimes follows from messaging about their role in
211 disease emergence. Areas where bats, viruses, and humans co-occur are not always hotspots of risk for
212 human health; as such, developing more precise ways to map zoonotic hazards can help bats and humans
213 coexist safely, and support the conservation of these important and unique animals.

214 Here, we propose a simple framework with broad explanatory power that helps contextualize discoveries
215 like highly divergent nobecoviruses in Madagascar and the once-neglected adaptive radiation of
216 sarbecoviruses in the Indochinese peninsula. In doing so, it advances ecological theory beyond the current
217 state of the art for global maps of emergence risk. For example, previous studies that have used host
218 richness as a proxy have predicted a high diversity of unsampled bat viruses,²⁰ bat coronaviruses,² and
219 even specifically betacoronaviruses²¹ in both the Amazon and southeast Asia. While we find that both
220 regions are characterized by unique and diverse communities of both hosts and viruses, our framework is
221 able to identify key differences between the two systems. We find that the merbecovirus complex in Latin
222 America has been a unique branch of evolution separate from the rest of the global pool, but with limited
223 potential for viral diversification—a finding that is supported by previous work indicating a higher rate of
224 codivergence in Latin America.^{2,45} In contrast, in southeast Asia, host richness and viral distinctiveness
225 are high but sharing is low; this suggests a different type of evolutionary dynamics that could generate
226 high local diversity of viruses through host switching and viral recombination (see e.g.,¹⁴ as well as the

227 discovery of recombinant viruses with genetic material from both the SARS-CoV and SARS-CoV-2
228 branches of the Sarbecovirus lineage).⁴⁶ Both of these regions are priority areas for sampling, especially
229 given predictions that they contain many bat hosts of undiscovered betacoronaviruses.^{21,25} However, both
230 the evolutionary and ecological aspects of emergence risk are higher in southeast Asia—a fact that will
231 only become more relevant, as bats track shifting climates and exchange viruses with other species,
232 creating a hotspot of elevated cross-species transmission unique to the region.^{33,47}

233 Our trivariate additive mapping of components of risk (fig. 3) aims to elicit the complexity of spatial
234 cross-species transmission risk beyond the mere presence or absence of the pathogen host in a specific
235 location. By considering coevolutionary factors such as viral sharing and host uniqueness, we suggest
236 insights that can aid in identifying potential locations for surveillance of betacoronavirus circulation and
237 assessing the risk of cross-species transmission to other mammals. In communities characterized by
238 diverse but unique host populations, with limited viral sharing between them, we could encounter viruses
239 that specialize in targeting the immune system of specific hosts. This implies a low likelihood of infecting
240 novel hosts but, once locally introduced into a new host (either a new species, or an immunologically
241 naïve population), the specialized virus could spread relatively easily due to encountering little immune
242 resistance.⁴⁸ With the right combination of viral traits, such as low disease-induced mortality or high
243 transmission rate, this could lead to successfully spread within the new host community. However, while
244 high adaptation to a specific host can be advantageous, it may also lead to maladaptation when the
245 pathogen encounters a new unsuitable host, potentially resulting in its extinction.

246 Bats—and the spillover of their viruses—are also sensitive to anthropogenic factors others than climate
247 change, including deforestation and other kinds of habitat loss, increased stress, and greater contact with
248 potential bridge hosts like domesticated species.^{31,49–51} This represents a challenge for both conservation
249 strategies and pandemic prevention,⁵² but identifying areas at risk, and protecting the health of bats and
250 ecosystems within those zones, can be a win-win intervention for both.^{53–55} As we scale these predictions
251 down in space to finer spatial resolutions to guide public health actions,³³ the incorporation of human
252 activity predictors will become more importyant.⁵⁶

253 **Acknowledgements:** We acknowledge that this study was conducted on land within the traditional
254 unceded territory of the Saint Lawrence Iroquoian, Anishinabewaki, Mohawk, Huron-Wendat, and
255 Omàmiwininiwak nations. This work was supported by funding to the Viral Emergence Research
256 Initiative (VERENA) consortium including NSF BII 2021909 and a grant from Institut de Valorisation des

257 Données (IVADO). This research was enabled in part by support provided by Calcul Québec
258 (www.calculquebec.ca) and Compute Canada (www.computecanada.ca). NF is funded by the NSERC
259 BIOS² CREATE program. TP and NF are funded by the Courtois Foundation. RLM was supported by
260 Bryce Carmine and Anne Carmine (née Percival), through the Massey University Foundation. DJB was
261 supported by the National Institute of General Medical Sciences of the National Institutes of Health
262 (P20GM134973).

263 **Methods**

264 **Known *Betacoronavirus* hosts**

265 We downloaded the data on bats hosts of *Betacoronavirus* from
266 <https://www.viralemergence.org/betacov> on Apr. 2022,²¹ and filtered it to “known” hosts (established
267 before the emergence of SARS-CoV-2) and “novel” hosts (confirmed through sampling and competence
268 assays since the initial data collection). The original database was assembled by a combination of data
269 mining and literature surveys, including automated alerts on the “bats” and “coronavirus” keywords to
270 identify novel empirical evidence of bats-betacoronaviruses associations; this yielded a total of 126 known
271 hosts, 47 of which were novel hosts. This host–virus list of interactions was obtained through a
272 comprehensive aggregation of GenBank data as well as systematic literature searches,^{21,25} such that we
273 have high confidence in its fitness for the purpose of inference at a large spatial scale.

274 **Bat occurrences**

275 We downloaded the rangemap of every current bat species that was classified as an empirically
276 documented host of *Betacoronavirus* from the previous step, according to recent IUCN data.⁵⁷ The IUCN
277 data have been assembled to support wildlife conservation efforts, and therefore we do not expect that they
278 are biased by wildlife disease sampling efforts or priority. The range maps were subsequently rasterized
279 using the `rasterize` function from GDAL⁵⁸ at a resolution of approximately 100kmx100km at the equator.
280 For every pixel in the resulting raster where at least one bat host of *Betacoronavirus* was present, we extract
281 the species pool (list of all known bat hosts), which was used to calculate the following risk assessment
282 components: bat phylogenetic diversity, bat compositional uniqueness, and predicted viral sharing risk.

283 **Bat phylogenetic diversity**

284 For every pixel, we measured Faith’s Phylogenetic Diversity⁵⁹ based on a recent synthetic tree with robust
285 time calibration, covering about 6000 mammalian species.⁶⁰ Faith’s PD measures the sum of unique
286 branches from an arbitrary root to a set of tips, and comparatively larger values indicate a more
287 phylogenetic diverse species pool. We measured phylogenetic diversity starting from the root of the entire
288 tree (and not from Chiroptera); this bears no consequences on the resulting values, since all branches

289 leading up to Chiroptera are only counted once per species pool, and (as we explain when describing the
290 assembly of the composite risk map), all individual risk components are ranged in [0,1]. This measure
291 incorporates a richness component, which we chose not to correct for; the interpretation of the
292 phylogenetic diversity is therefore a weighted species richness, that accounts for phylogenetic
293 over/under-dispersal in some places.

294 **Bat compositional uniqueness**

295 For every species pool, we measured its Local Contribution to Beta-Diversity;⁶¹ LCBD works from a
296 species-data matrix (traditionally noted as \mathbf{Y}), where species are rows and sites are columns, and a value of
297 1 indicates occurrence. We extracted the \mathbf{Y} matrix assuming that every pixel represents a unique location,
298 and following best practices⁶² transformed it using Hellinger's distance to account for unequal bat
299 richness at different pixels. The correction of raw community data is particularly important for two
300 reasons: first, it prevents the artifact of richer sites having higher importance; second, it removes the effect
301 of overall species richness, which is already incorporated in the phylogenetic diversity component. High
302 values of LCBD indicate that the pixel has a community that is on average more dissimilar in species
303 composition than what is expected knowing the entire matrix, i.e. a more unique community. Recent
304 results by⁶³ shows that LCBD measures are robust with regards to spatial scale, and are therefore
305 applicable at the global scale.

306 **Viral sharing between hosts**

307 For all bat hosts of *Betacoronavirus*, we extracted their predicted viral sharing network, generated from a
308 previously published generalized additive mixed model of virus sharing by a tensor function of
309 phylogenetic distance and geographic range overlap across mammals.⁶⁴ This network stores pairwise
310 values of viral community similarity, measured for all hosts (to maintain consistency with teh
311 phylogenetic diversity measure) across all viruses; therefore, we consider that it accounts for some overall
312 similarity in the way hosts deal with viruses, and not only betacoronaviruses. There is empirical evidence
313 that capacity for cross-species transmission even between divergent species is generally high,⁶⁵ especially
314 for beta-coronaviruses.¹⁴ To project viral sharing values into a single value for every pixel, we averaged the
315 pairwise scores. High values of the average sharing propensity means that this specific extant bat

316 assemblage is likely to be proficient at exchanging viruses.

317 Composite risk map

318 To visualize the aggregated risk at the global scale, we combine the three individual risk components
319 (phylogenetic diversity, compositional uniqueness, and viral sharing) using an additive color model.⁶⁶ In
320 this approach, every risk component gets assigned a component in the RGB color model (phylogenetic
321 diversity is green, compositional uniqueness is red, and viral sharing is blue). In order to achieve a valid
322 RGB measure, all components are re-scaled to the [0,1] interval, so that a pixel with no sharing, no
323 phylogenetic diversity, and no compositional uniqueness is black, and a pixel with maximal values for
324 each is white. This additive model conveys both the intensity of the overall risk, but also the nature of the
325 risk as colors diverge towards combinations of values for three risk components. Out of the possible
326 combinations, the most risky in terms of rapid diversification and spillover potential is high phylogenetic
327 diversity and low viral sharing,⁶⁷ in that this allows multiple independent host-virus coevolutionary
328 dynamics to take place in the same location. In the colorimetric space, this correspond to yellow – because
329 the HSV space is more amenable to calculations for feature extraction,⁶⁸ we measured the risk level by
330 calculating the angular distance of the hue of each pixel to a reference value of 60 (yellow), and weighted
331 this risk level by the value component. Specifically, given a pixel with colorimetric coordinates (h, s, v) , its
332 ranged weighted risk value is

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

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

334 Viral phyogeography and evolutionary diversification

335 To next represent phyogeography of betacoronaviruses in bats, we aggregated and analyzed
336 betacoronavirus sequence data. We used the following query to pull all *Betacoronavirus* sequence data
337 from the GenBank Nucleotide database except SARS-CoV-2; (“Betacoronavirus”[Organism] OR
338 betacoronavirus[All Fields]) NOT (“Severe acute respiratory syndrome coronavirus 2”[Organism] OR
339 sars-cov-2[All Fields]). We added a single representative sequence for SARS-CoV-2 and manually curated

340 to remove sequences without the RNA-dependent RNA polymerase (RdRp) sequence or that contained
341 words indicating recombinant or laboratory strains including “patent”, “mutant”, “GFP”, and
342 “recombinant”. We filtered over-represented taxa including betacoronavirus 1, hCoV-OC43, Middle East
343 respiratory syndrome coronavirus, Murine hepatitis virus, and hCoV-HKU1. Curated betacoronavirus
344 RdRp sequences were then aligned using MAFFT⁶⁹ v1.4.0 (Algorithm FFT-NS-2, Scoring matrix 200PAM /
345 k=2, gap open penalty 1.53m offset value 0.123) and a maximum likelihood tree reconstructed in
346 IQ-TREE⁷⁰ v1.6.12 with ModelFinder⁷¹ ultrafast bootstrap approximation⁷² with a general time reversible
347 model with empirical base frequencies and the 5-discrete-rate-category FreeRaye model of nucleotide
348 substitution (GTR+F+R5).

349 We first tested the hypothesis that hotspots of viral diversification would track hotspots of bat
350 diversification. To do so, we plotted the number of known bat hosts (specifically only those included in the
351 phylogeny, so there was a 1:1 correspondence between data sources) against the “mean evolutionary
352 distinctiveness” of the associated viruses. To calculate this, we derived the fair proportions evolutionary
353 distinctiveness⁷³ for each of the viruses in the tree, then averaged these at the bat species level, projected
354 these values onto their geographic distributions, and averaged across every bat found in a given pixel. As
355 such, this can be thought of as a map of the mean evolutionary distinctiveness of the known viral
356 community believed to be associated with a particular subset of bats present.

357 Co-distribution of hosts and viral hotspots

358 Subsequently, we tested the hypothesis that the biogeography of bat betacoronaviruses should track the
359 biogeography of their hosts. To test this idea, we loosely adapted a method from,^{74,75} who proposed a
360 phylogenetic method for the delineation of animal biogeographic regions. In their original method, a
361 distance matrix - where each row or column represents a geographic raster’s grid cell, and the dissimilarity
362 values are the “beta diversity similarity” of their community assemble - undergoes non-metric
363 multidimensional scaling (NMDS); the first two axes of the NMDS are projected geographically using a
364 four-color bivariate map. Here, we build on this idea with an entirely novel methodology. First, we
365 measure the phylogenetic distance between the different viruses in the betacoronaviruses tree by using the
366 cophenetic function in ape;⁷⁶ subsequently, we take a principal components analysis of that distance
367 matrix (readily interchangeable for NMDS in this case) to project the viral tree into an n-dimensional
368 space. We then take the first two principal components and, as with the evolutionary distinctiveness

369 analysis, aggregated these to a mean host value and projected them using a four-color bivariate map.

370 **Data availability statement**

371 The code to reproduce these analyses, as well as the data (with the exception of the IUCN rangemaps,
372 which must be downloaded from their website) are available in the [viralemergence/betemap](#) repository
373 on GitHub.

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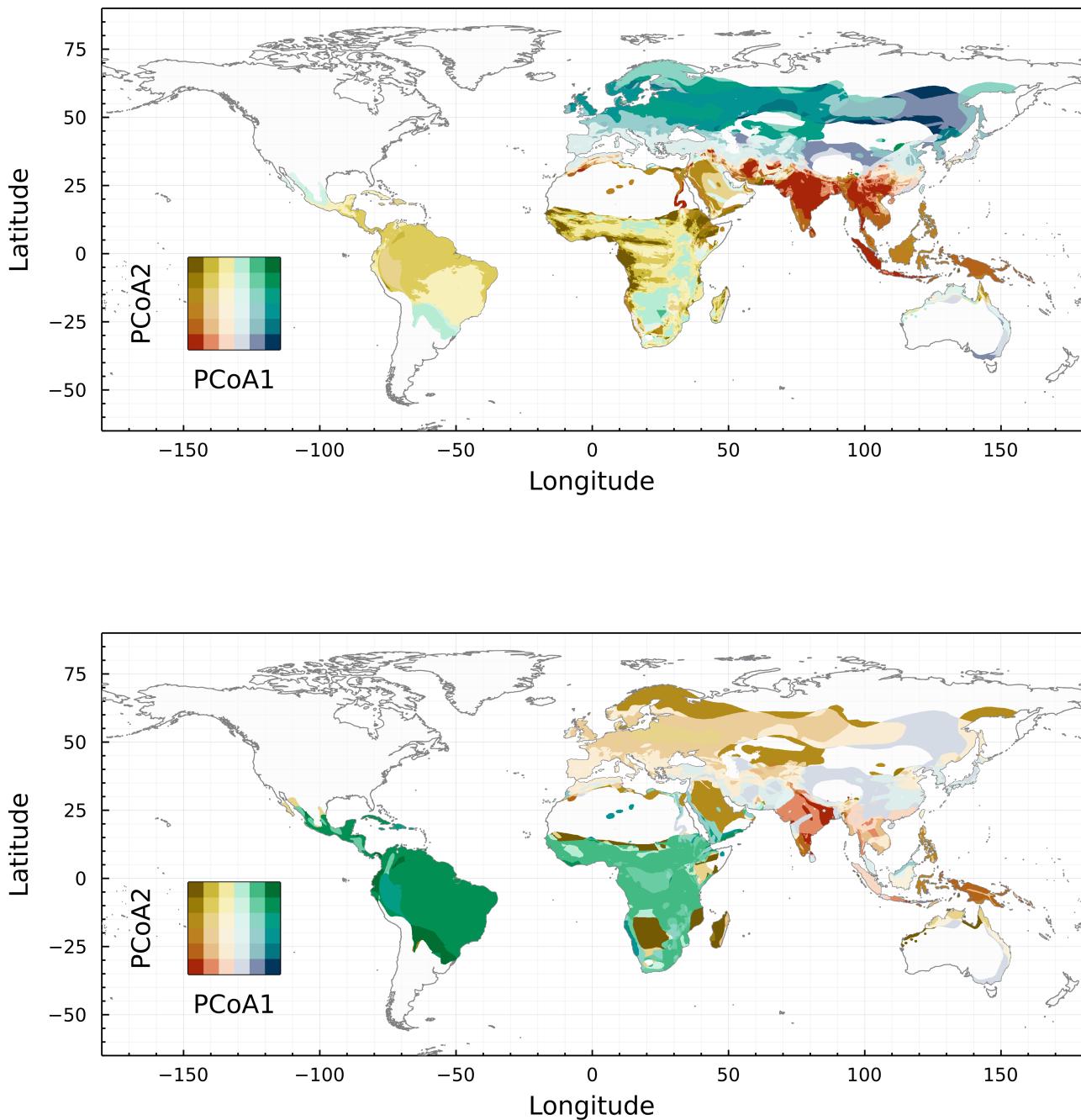


Figure 1: Bat and betacoronavirus biogeographic regions. Phylogeography of bats (top) and viruses (bottom) is categorized based on an analysis of bat distributions, paired with bat or virus phylogeny. The different colors show tendencies to separate alongside the first two components of a PCoA. Note that the PCoA for the bats and viruses are independent, and so cannot be compared directly – that being said, the fact that different regions cluster in the same way across maps be directly compared.

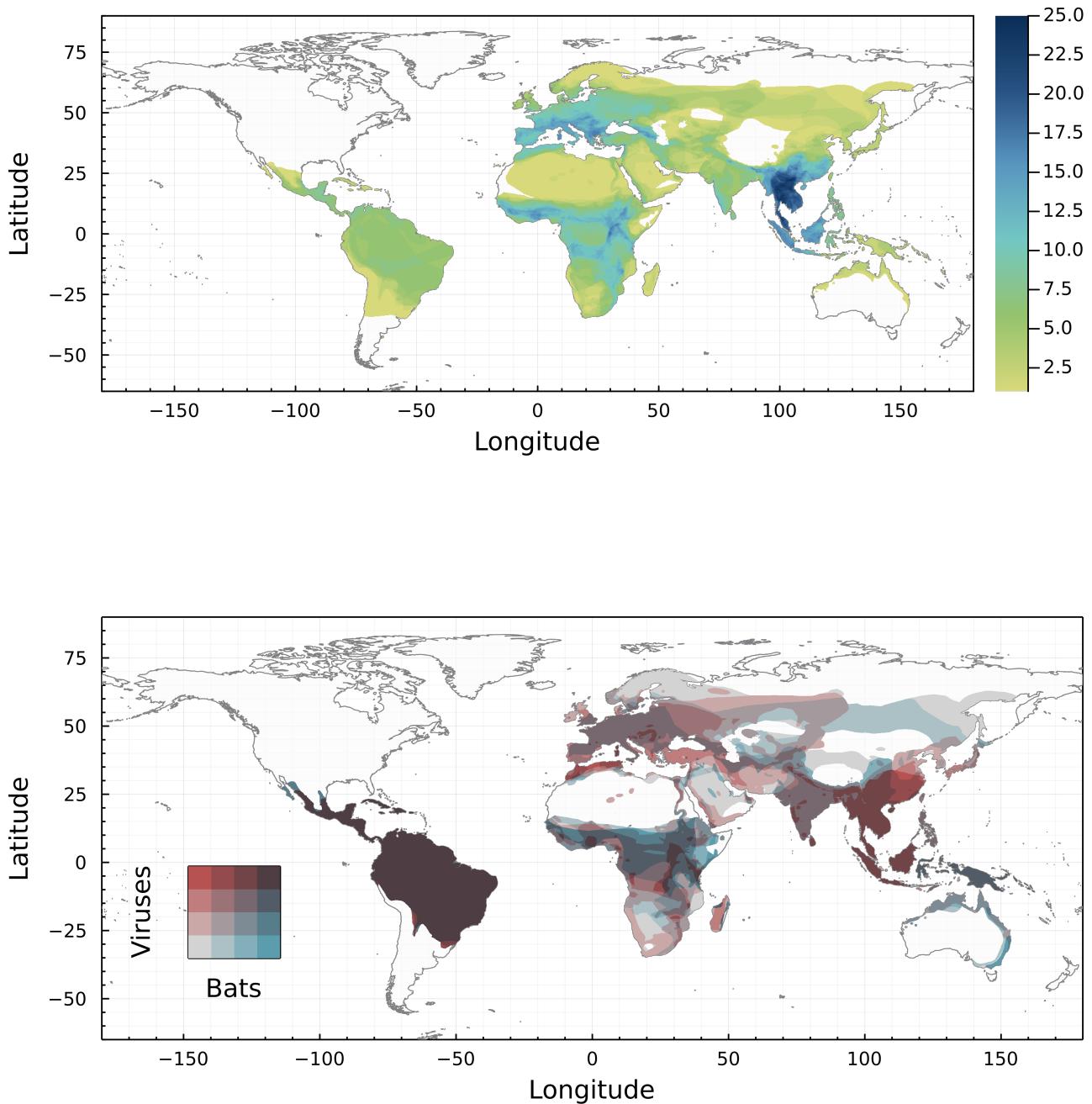


Figure 2: **Bat and betacoronavirus diversity.** Top panel: diversity of known bat hosts of betacoronaviruses in our dataset. This map shows that the region with the largest number of possible hosts is South-Eastern Asia. Bottom panel: congruence between the *evolutionary* distinctiveness of the hosts (grey to blue) and the viruses (grey to red). Darker areas have higher combined evolutionary distinctiveness for the entire bat-virus system.

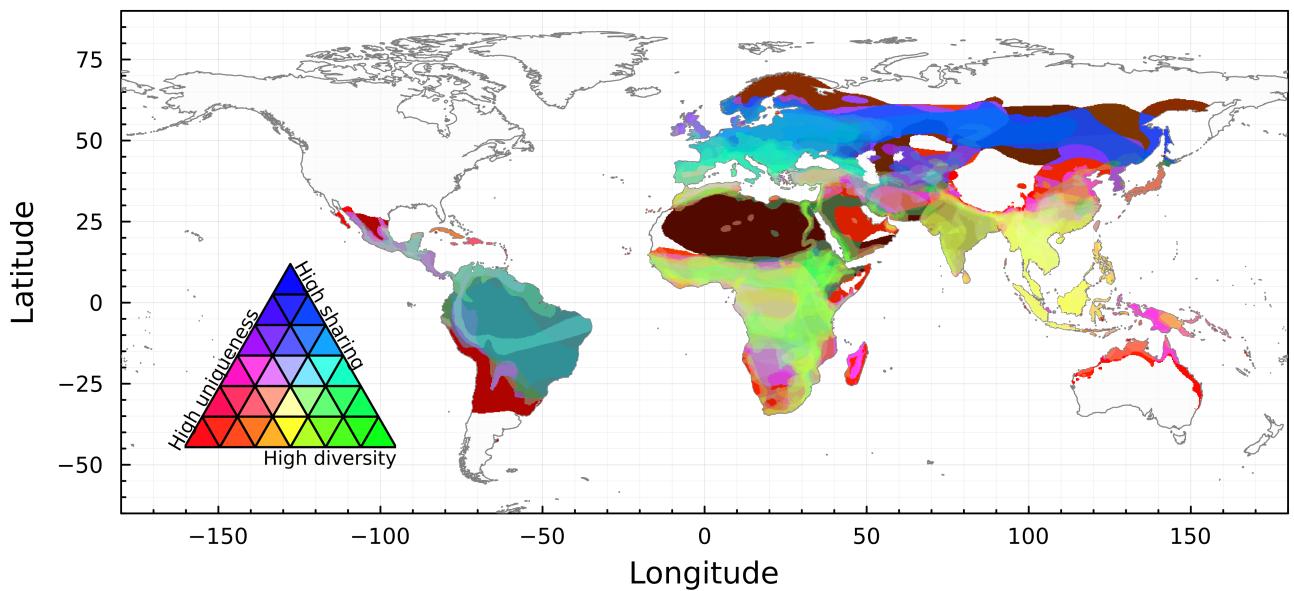


Figure 3: Trivariate additive mapping of the components of risk. Viral sharing runs from yellow (low) to blue (high); host phylogenetic diversity runs from pink (low) to high (green); and host compositional uniqueness runs from cyan (low) to red (high). The GMTC suggests that the highest evolutionary potential for emergence exists in unique and diverse host communities with low viral sharing, *i.e.* pixels around yellow. All components within bat host ranges are scaled in brightness so that a pixel with no sharing, no phylogenetic diversity, and no compositional uniqueness would be black, and a pixel with maximal values for each would be white. The individual layers that compose this figure are given in supplementary material.

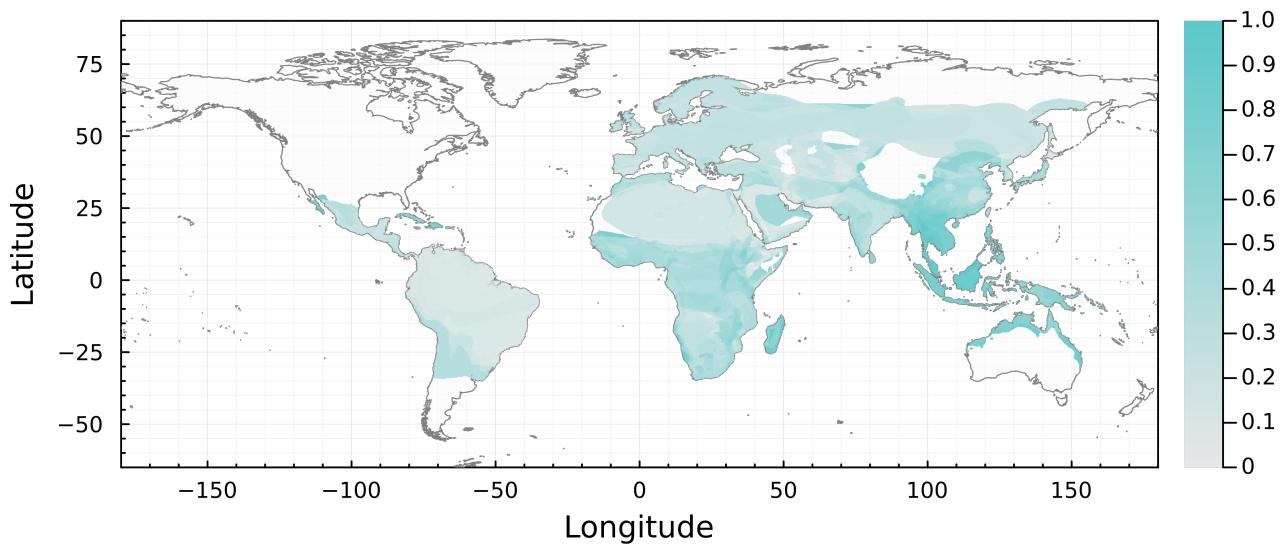


Figure 4: Evolutionary potential for zoonotic emergence of bat-origin betacoronaviruses. Risk is a composite measure of the color value and angular distance to the yellow hue in fig. 3 (see Methods). Darker pixels represent areas where the co-evolutionary mechanisms are likely to introduce a strong risk of emergence.

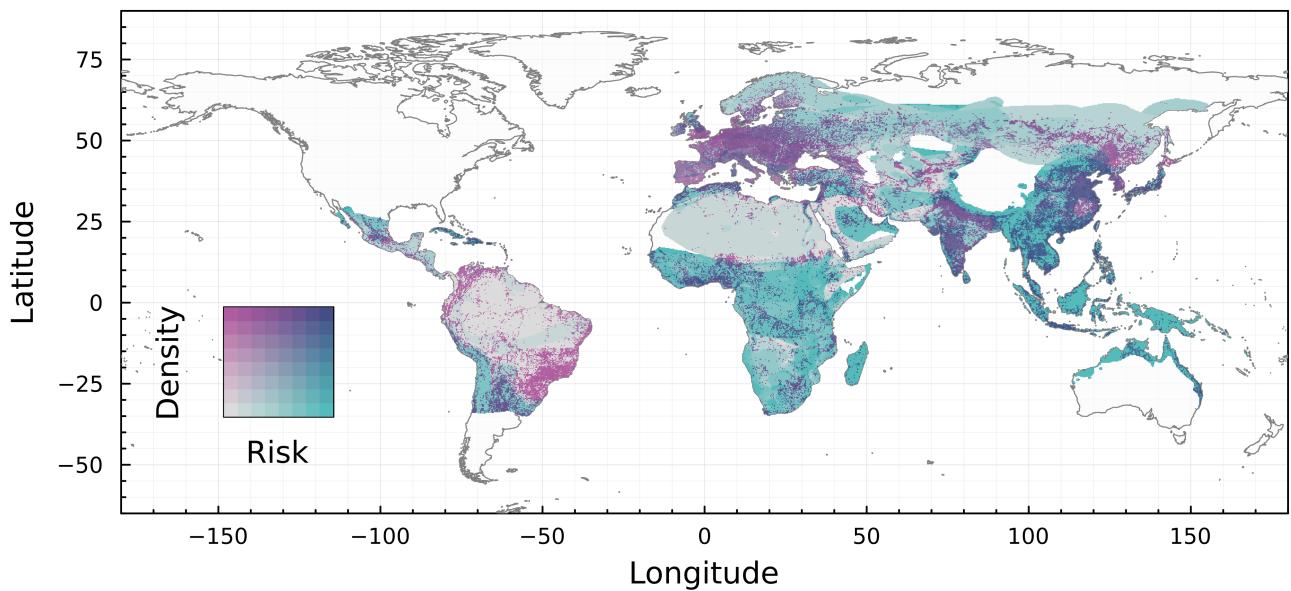


Figure 5: **Overlap between evolutionary potential and ecological opportunity for zoonotic emergence.** Overlap of the percent of each pixel occupied by urbanized structures, representing the degree of settlement, on the spillover risk map (where the risk comes only from wildlife, and ignores multi-hosts 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.