

The coevolutionary mosaic of *Betacoronavirus* spillover risk from bat hosts

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Driven by the need to understand the ecological factors involved in the emergence of *Betacoronavirus* (the genus causing the 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 reservoir 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 system may originate novel viruses in humans.

Keywords:
bats
betacoronavirus
disease ecology
geographic mosaic theory of coevolution
phylogenetic diversity
viral sharing
SARS-CoV-2

Spillover risk is complex and, even within a pool of susceptible wildlife hosts, driven by a multiplicity of factors (Plowright et al. 2017). Although host richness is often used as a coarse proxy for hotspots of emergence risk (Anthony et al. 2017, Ruiz-Aravena et al. 2022), these approaches deliberately oversimplify interspecific heterogeneity in immunology, behavior, and other traits. Global maps of spillover risk often struggle to distill these features into interpretable risk maps, and overlook highly-unique host pools that allow for the rapid evolution of highly divergent viruses (Agosta et al. 2010). In the case of generalist pathogens like betacoronaviruses, there is conceptual and empirical support to the idea that these community-level mechanisms are even more important in driving hotspots of overall risk (Power and Mitchell 2004).

These kinds of dynamics lend themselves to interpretation through the lens of the Geographic Mosaic Theory of Coevolution (GMTC; Thompson 2005), which connects microevolutionary dynamics in symbiotic interactions to macroecological dynamics in host communities. The GMTC posits that coevolutionary processes between pairs (Thompson 1994) or complexes (Janzen 1980) of species are structured in space by the rippling effects of abiotic conditions onto evolutionary mechanism, resulting in spatially fragmented evolutionary dynamics, coupled only by dispersal-related processes (Gomulkiewicz et al. 2000). In turn, these spatially fragmented processes can lead taxonomically homogeneous systems to have different structure and dynamics over large spatial extents (see e.g. Price 2002). The GMTC predicts a spatial fragmentation of coevolutionary dynamics under the joint action of three processes (see

notably Gomulkiewicz et al. 2007), which all have the potential to act on outbreak potential, pathogen transmission, and disease virulence (Parratt et al. 2016, Turner et al. 2021). First hot- and coldspots of coevolution can appear when the intensity of *interaction* (in terms of reciprocal fitness consequences) varies spatially, because of e.g. partial range overlap between organisms (Nuismer et al. 2003). Second, the GMTC supposes the existence of selection mosaics, wherein the intensity of *selection* varies across space; the strength of reciprocal selection responds to the biotic complexity of the community (locally diverse hosts and viruses are more biotically complex; Thrall et al. 2007) and to the local favorability of the environment (Hochberg and Baalen 1998). Finally, trait remixing occurs when coevolutionary dynamics are driven by the arrival (or departure) of functional traits, through changes in community composition due to invasions, meta-community dynamics, and dispersal.

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

Here,

We turn the processes on the GMTC into definitions of spillover risk from viruses to hosts (focusing on the bats-betacoronavirus complex), with a specific emphasis on the potential to create independent coevolutionary dynamics (and therefore spatial fragmentation in the risk) through heterogeneity.

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Methods

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

1.2. Bats occurrences We downloaded the rangemap of every current bat species that was classified as an empirically documented host of *Betacoronavirus* from the previous step, according to recent IUCN data (IUCN 2021). The range maps were subsequently rasterized using the `rasterize` function from GDAL (Rouault et al. 2022) at a resolution of approximately 100kmx100km. For every pixel in the resulting raster where at least one bat host of *Betacoronavirus* was present, we extract the species pool (list of all competent bat hosts), which was used to calculate the following risk assessment components: bat phylogenetic diversity, bat compositional uniqueness, and predicted viral sharing risk.

1.3. Bats phylogenetic diversity For every pixel, we measured Faith’s Phylogenetic Diversity (Faith 1992) based on a recent synthetic tree with robust time calibration, covering about 6000 mammalian species (Upham et al. 2019). Faith’s PD measures the sum of unique branches from an arbitrary root to a set of tips, and comparatively larger values indicate a more phylogenetic diverse species pool. We measured phylogenetic diversity starting from the root of the entire tree (and not from Chiroptera); this bears no consequences on the resulting values, since all branches leading up to Chiroptera are only counted one per species pool, and (as we explain when describing the assembly of the composite risk map), all individual risk components are ranged in [0,1]. This measure incorporates a richness component, which we chose not to correct for; the interpretation of the phylogenetic diversity is therefore a weighted species richness, that accounts for phylogenetic over/under-dispersal in some places.

1.4. Bats compositional uniqueness For every species pool, we measured its Local Contribution to Beta-Diversity (Legendre and De Cáceres 2013); LCBD works from a species-data matrix (traditionally noted as \mathbf{Y}), where species are rows and sites are columns, and a value of 1 indicates occurrence. We extracted the \mathbf{Y} matrix assuming that every pixel represents a unique location, and following best practices (Legendre and Condit 2019) transformed it using Hellinger's distance to account for unequal bat richness at different pixels. The correction of raw community data is particularly important for two reasons: first, it prevents the artifact of richer sites having higher importance; second, it removes the effect of overall species richness, which is already incorporated in the phylogenetic diversity component. High values of LCBD indicate that the pixel has a community that is on average more dissimilar in species composition than what is expected knowing the entire matrix, i.e. a more unique community. Recent results by Dansereau et al. (2022) shows that LCBD measures are robust with regards to spatial scale, and are therefore applicable at the global scale.

1.5. Viral sharing between hosts For all bat hosts of *Betacoronavirus*, we extracted their predicted viral sharing network, generated from a previously published generalized additive mixed model of virus sharing by a tensor function of phylogenetic distance and geographic range overlap (Albery et al. 2020). This network stores pairwise values of viral community similarity. To project viral sharing values into a single value for every pixel, we averaged the pairwise scores. High values of the average sharing propensity means that this specific extant bat assemblage is likely to be proficient at exchanging viruses.

1.6. Composite risk map To visualize the aggregated risk at the global scale, we combine the three individual risk components (phylogenetic diversity, compositional uniqueness, and viral sharing) using an additive color model (Seekell et al. 2018). In this approach, every risk component gets assigned a component in the RGB color model (phylogenetic diversity is green, compositional uniqueness is red, and viral sharing is blue). In order to achieve a valid RGB measure, all components are re-scaled to the [0,1] interval, so that a pixel with no sharing, no phylogenetic diversity, and no compositional uniqueness is black, and a pixel with maximal values for each is white. This additive model conveys both the intensity of the overall risk, but also the nature of the risk as colors diverge towards combinations of values for three risk components. Out of the possible combinations, the most risky in terms of rapid diversification and spillover potential is high phylogenetic diversity and low viral sharing (Gomulkiewicz et al. 2000, Cavender-Bares et al. 2009), in that this allows multiple independent host-virus coevolutionary dynamics to take place in the same location. In the colorimetric space, this correspond to yellow – because the HSV space is more amenable to calculations for feature extraction (see e.g. Keke et al. 2010), we measured the risk level by calculating the angular distance of the hue of each pixel to a reference value of 60, and weighted this risk level by the value component. Specifically, given a pixel with colorimetric coordinates (h, s, v) , its ranged weighted risk value is

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

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

1.7. Viral phyogeography and evolutionary diversification To next represent phylogeography of betacoronaviruses in bats, we aggregated and analyzed betacoronavirus sequence data. We used the following query to pull all *Betacoronavirus* sequence data from the GenBank Nucleotide database except SARS-CoV-2; ("Betacoronavirus"[Organism] OR betacoronavirus[All Fields]) NOT ("Severe acute respiratory syndrome coronavirus 2"[Organism] OR sars-cov-2[All Fields]). We added a single representative sequence for SARS-CoV-2 and manually curated to remove sequences without the RNA-dependent RNA polymerase (RdRp) sequence or that contained words indicating recombinant or laboratory strains including "patent," "mutant," "GFP," and "recombinant." We filtered over-represented taxa including betacoronavirus 1, hCoV-OC43, Middle East respiratory syndrome coronavirus, Murine hepatitis virus, and hCoV-HKU1. Curated betacoronavirus RdRp sequences were then aligned using MAFFT v 1.4.0 [Katoh and Standley (2013); Algorithm FFT-NS-2, Scoring matrix 200PAM / k=2, gap open penalty 1.53m offset value 0.123] and a maximum likelihood tree reconstructed in IQ-TREE v 1.6.12 (Nguyen et al. 2015) with ModelFinder (Kalyaanamoorthy et al. 2017) ultrafast bootstrap approximation (Hoang et al. 2018) with a general time reversible model with empirical base frequencies and the 5-discrete-rate-category FreeRaye model of nucleotide substitution (GTR+F+R5).

We first tested the hypothesis that hotspots of viral diversification would track hotspots of bat diversification. To do so, we plotted the number of known bat hosts (specifically only those included in the phylogeny, so there was a 1:1 correspondence between data sources) against the “mean evolutionary distinctiveness” of the associated viruses. To calculate this, we derived the fair proportions evolutionary distinctiveness (Isaac et al. 2007) for each of the viruses in the tree, then averaged these at the bat species level, projected these values onto their geographic distributions, and averaged across every bat found in a given pixel. As such, this can be thought of as a map of the mean evolutionary distinctiveness of the known viral community believed to be associated with a particular subset of bats present.

1.8. Co-distribution of hosts and viral hotspots Subsequently, we tested the hypothesis that the biogeography of bat betacoronaviruses should track the biogeography of their hosts. To test this idea, we loosely adapted a method from (Kreft and Jetz 2007, 2010), who proposed a phylogenetic method for the delineation of animal biogeographic regions. In their original method, a distance matrix - where each row or column represents a geographic raster’s grid cell, and the dissimilarity values are the “beta diversity similarity” of their community assemble - undergoes non-metric multidimensional scaling (NMDS); the first two axes of the NMDS are projected geographically using a four-color bivariate map. Here, we build on this idea with an entirely novel methodology. First, we measure the phylogenetic distance between the different viruses in the betacoronaviruses tree by using the cophenetic function in ape (Paradis and Schliep 2019); subsequently, we take a principal components analysis of that distance matrix (readily interchangeable for NMDS in this case) to project the viral tree into an n-dimensional space. We then take the first two principal components and, as with the evolutionary distinctiveness analysis, aggregated these to a mean host value and projected them using a four-color bivariate map.

2

Results and discussion

2.1. Host richness does not predict virus distinctiveness Bats, the second most diverse group of mammals, are found worldwide and serve as the main animal reservoir for different strains of betacoronaviruses (Drexler et al. 2014). This has attracted attention to areas where high diversity of bats, and therefore presumably high diversity of betacoronaviruses, can be an important issue for human health (Calisher et al. 2006, Moratelli and Calisher 2015). By overlaying the IUCN range maps for confirmed bat hosts of betacoronaviruses [fig. 1; top], we see that the main hotspots (both in terms of size and higher values) of host richness are primarily South-Eastern Asia, parts of Southern Europe, and to a lesser extent parts of Africa in the -25-0 range of latitudes. The description of host richness is an important first step towards understanding risk, as previous research (Anthony et al. 2017, Mollentze and Streicker 2020) states that locally diverse bat communities could maintain more viruses and hence, a higher probability of having a pathogen that could represent a risk for human health.

Nevertheless, locally diverse and virus-rich bat communities could represent an increased risk of spillover under climate change through the creation of novel interactions (Carlson et al. 2022), and therefore the diversity of *Betacoronavirus* strains should similarly be accounted for. In fig. 1 (bottom), we contrast the evolutionary distinctiveness of bats and viruses – this reveals a slightly different portrait than bat richness alone. Chiropterans can be classified, from a macro-evolutionary standpoint, as Yangochiroptera and Yinpterochiroptera elsewhere (Teeling et al. 2005, Springer 2013). Specifically, we would expect that the so-called “New World” group of bats, being more evolutionary distinct, would also have evolutionary distinct viruses. Indeed fig. 1 (bottom) reveals it to be the case, and this region harbors a distinct bat-betacoronaviruses complex. This can be explained by the fact that Yangochiroptera, although not limited to the western hemisphere, contain the highly diverse adaptive radiation in the Phyllostomidae (Villalobos and Arita 2010), which is restricted to the western hemisphere. By contrast, South-Eastern Asia has a lot of non-evolutionary distinct bats, who nevertheless hosted evolutionary-distinct viruses.

It is noteworthy that outside of South America, viral evolutionary distinctiveness does not accurately track host diversity, with some areas having over-distinct viruses (eastern China but, oddly, not the rest of southeast Asia). There are a number of likely explanations. First, given the richness of bats in southeast Asia, many betacoronaviruses likely remain to be discovered in this region. Indeed, global predictions by Becker et al. (2022) highlight that southeast Asia is a likely hotspot of unconfirmed hosts of betacoronaviruses, which would likely result in additional viral discoveries. This idea is unsurprising given the growing realization, especially since the emergence of SARS-CoV-2, that unique

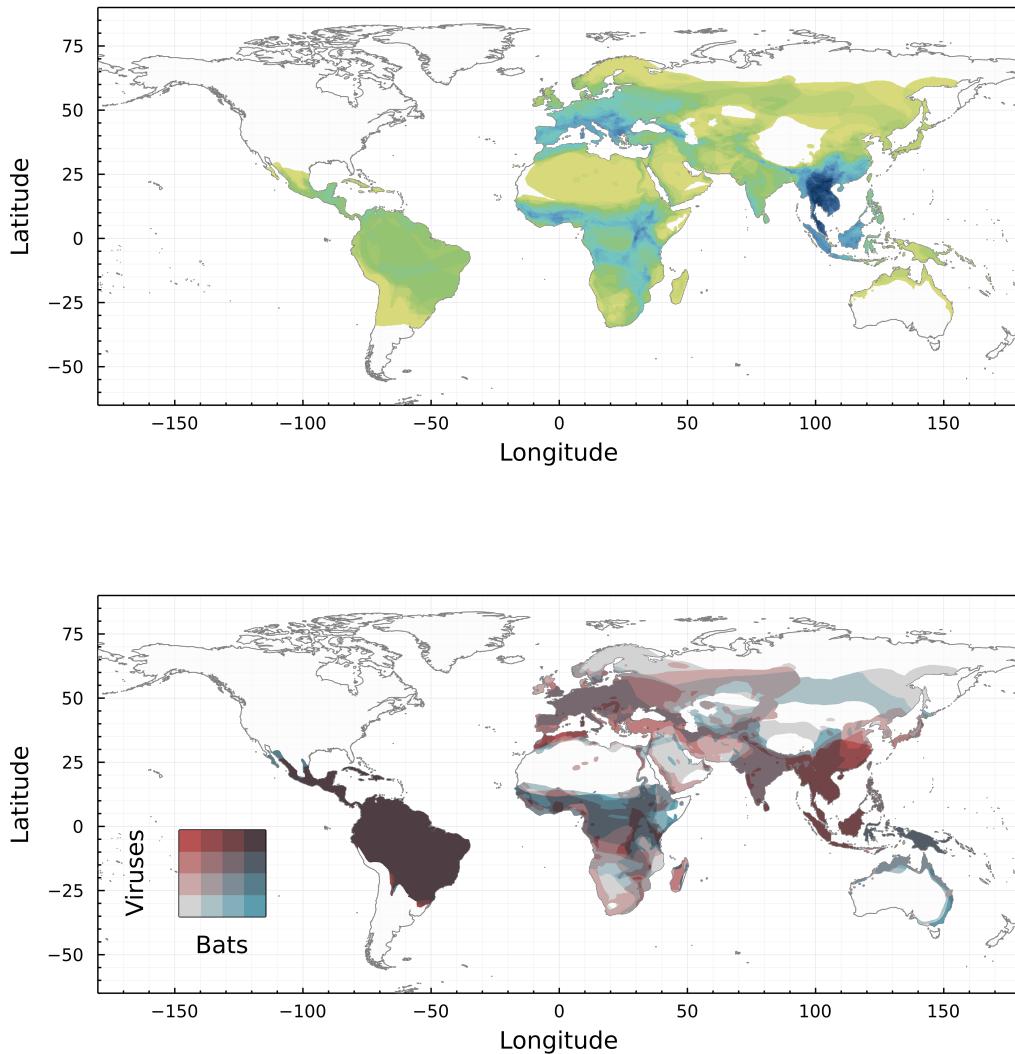


Figure 1 Top panel: relative diversity of known bat hosts of betacoronaviruses. This map shows that the region with the largest number of possible hosts is South-Eastern Asia. Bottom panel: congruence between the evolutionary distinctiveness of the hosts (grey to blue) and the viruses (grey to red). By contrast to the richness map, this reveals that South America has the most evolutionary distinct hosts *and* viruses, whereas South-Eastern Asia and the Rift Valley region have mostly distinct viruses. This is congruent with known results about New World bats being evolutionary distinct, and suggests that they similarly have distinct viruses.

lineages of similar viruses are widespread in bats but still mostly undescribed. The most distinct bat-betacoronaviruses complex is found in South America, a region with a comparatively lower number of hosts; this matches with the isolation through variance of the host group, and may highlight a different co-evolutionary dynamic. Alternatively, this distinctiveness hotspot may be a product of undersampling: South-America is one of the places where the fewest *Betacoronavirus* sequences have been discovered (Anthony et al. 2017, Olival et al. 2017, Allen et al. 2017), resulting in sparser phylogenetic tree, thereby artificially inflating distinctiveness. Adding more viruses would bring the distinctiveness of known sequences down. Finally, South-America is the range of Phyllostomidae, a group of bats that underwent explosive diversification events (Villalobos and Arita 2010), which may drive the emergence of multiple viral lineages.

2.2. The phylogeographic regions of hosts and their viruses overlap Despite the difference in evolutionary distinctiveness globally, there are reasons to expect that the phylogeography of bats and betacoronaviruses should show some degree of congruence (Letko et al. 2020, Van Brussel and Holmes 2022). In particular, this should be the case if viruses can circulate among hosts and co-evolve with local hosts communities, making their evolutionary process more than a byproduct of host evolution. High density of hosts sharing the same virus (albeit possibly different strains) can drive or result from evolution of the bat antiviral immune system, resulting in spatially distinct immunological responses, as evidenced in several bat species (Banerjee et al. 2020). Immune characteristics that allow bats to be better adapted to infection by emerging viruses (Gorbunova et al. 2020, Irving et al. 2021), in addition to being hardcoded in their genome (Jebb et al. 2020), may be related to a wide variety of diets (Banerjee et al. 2020, Moreno Santillán et al. 2021), themselves likely to be driven by spatial effects, especially at the local scale – bats, indeed, occupy a variety of environments, and therefore display a variety of adaptations to these environments (Muylaert et al. 2022).

In fig. 2, we show a projection of the phylogeographic signal of bats (top) and viruses (bottom) in space; the distinct groupings (represented by different colors symbolizing positions in the subspace formed by the first two axes of the PCoA) are essentially equivalent between the two groups, and can be coarsely delineated as southeast Asia, Eurasia above a northing of 25, and Africa and south America. These results suggest that, although the evolutionary distinctiveness of the bat-betacoronaviruses complex varies spatially, the system shows an important degree of spatial consistency, with a reduced number of bioregions. Available information describing the spillover of zoonotic betacoronaviruses of bat origin where data was available before and up through the COVID-19 pandemic puts spillover events of SARS-CoV-2 in Wuhan, China; SARS-CoV in Guangdong, China based on the presence of closest known viruses circulating in nature, and a nearby location where serological (antibody) evidence has indicated human exposure to SARS-like viruses (Wang et al. 2018); MERS-CoV in Saudi Arabia based on index cases available from a recently-published compendium of cases (Ramshaw et al. 2019). For the latest event, most if not all index cases are presumed to be camel-to-human transmission, and the precise origin point (if it exists) of MERS-CoV in bats is uncertain. Recent recombinant canine coronavirus spillover events in Haiti (Lednicky et al. 2021) and Europe (Vlasova et al. 2022) are not relevant here, as bats' involvement in these cycles of transmission have been supposed to be non-existent. These index cases fall within different phylogeographic bioregions (fig. 2), which further highlight the issue that different host-virus sub-systems may lead to widespread emergence.

2.3. Coevolution-informed spillover risk is different in space As host richness, joint distinctiveness, or phylogeographic structure suggest that the bat-betacoronaviruses complex is globally fragmented enough to give rise to both different levels of risk (as evidenced by the spatial location of spillover events) and different types of co-evolutionary dynamics, we turn to the Geographic Mosaic Theory of Coevolution (Thompson 2005) to provide a measure of risk accounting for multiple processes. In fig. 3, we overlapped three components of spillover risk: viral sharing, i.e. the chance that two bats will share viruses overall; Local Contribution to Beta Diversity, i.e. the fact that a bat community is compositionally unique compared to the average compositional similarity across the entire system; finally, host phylogenetic diversity, i.e. how dispersed the bats in a location are within the tree of life. This approach leads to the definition of broad biogeographic regions of risk, where the same color represents the same type of risk. By way of contrast to figures fig. 1 and fig. 2, these regions do not necessarily overlap with previous spatial partitions of the bat-betacoronaviruses complex.

From the perspective of spillover risk, the most important combination of factors is a high phylogenetic diversity of hosts with low viral sharing; this, essentially, means that very different betacoronaviruses could co-exist within the same place. This is particularly the case given that betacoronaviruses often

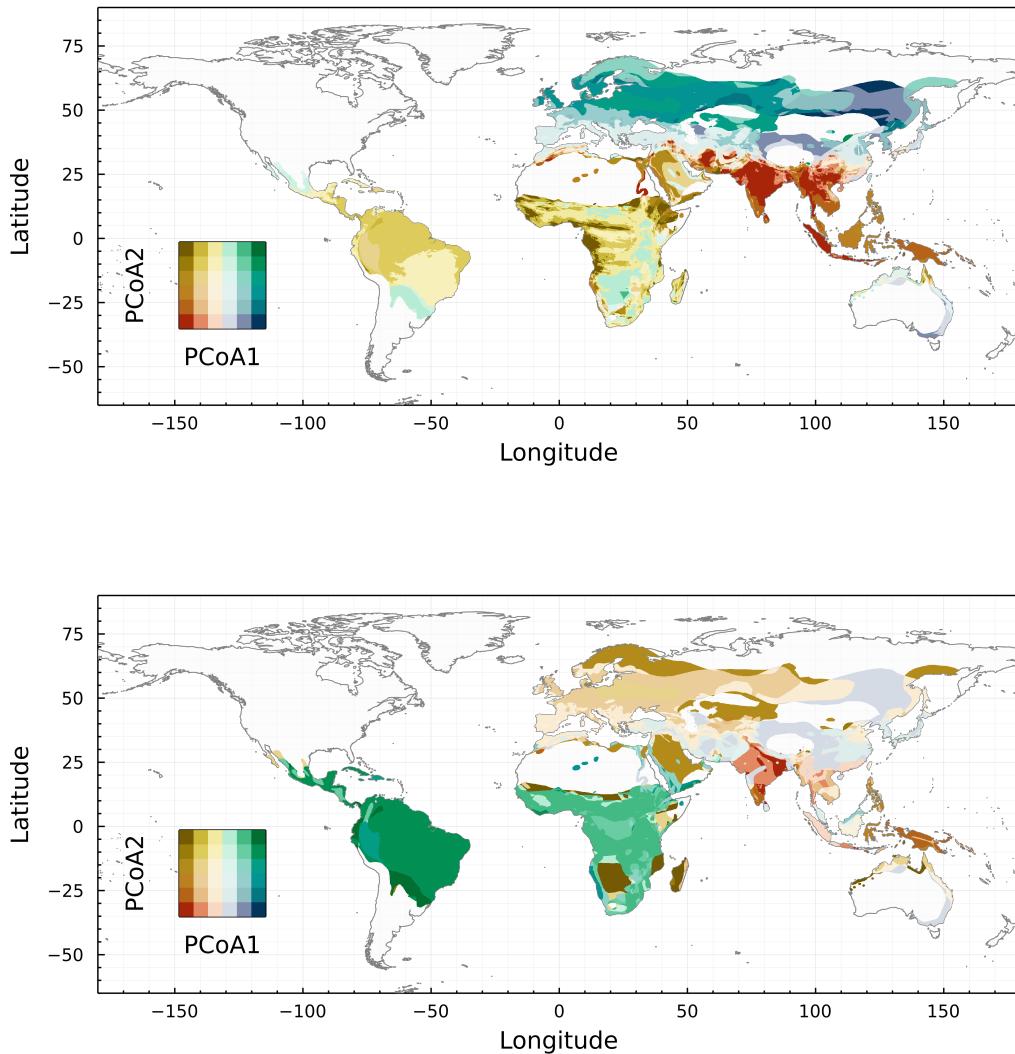


Figure 2 Phylogeographic regions of bats (top) and viruses (bottom) based on the joint analysis of their occurrence and phylogenetic relatedness. The different colors show tendencies to separate alongside the first two components of a PCoA. Note that the PCoA for the bats and viruses are independent, and so cannot be compared directly – that being said, the regions can be compared across maps.

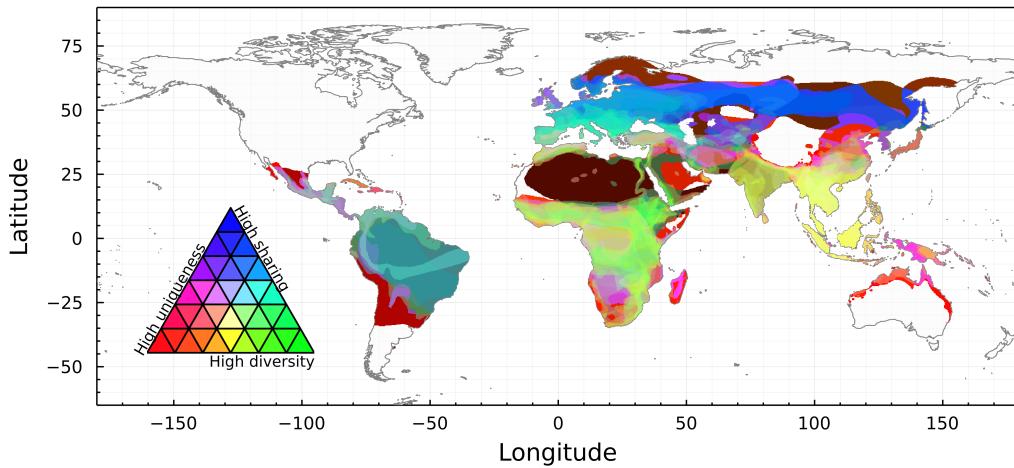


Figure 3 Trivariate additive mapping of the components of risk in the red/green/blue, where high virus sharing is encoded in the blue channel, host phylogenetic diversity in the green channel, and compositional uniqueness in the red channel. A pixel that would maximize all measures (highest possible risk) would be a pure white (specifically RGB(1.0, 1.0, 1.0)), and a pixel with the lowest possible values would be pure black (specifically RGB(0.0, 0.0, 0.0)). Therefore, lighter values (the sum of the three channels gets closer to 3) indicate higher risk, and the color indicates the proportional distribution of the factors making up the total risk.

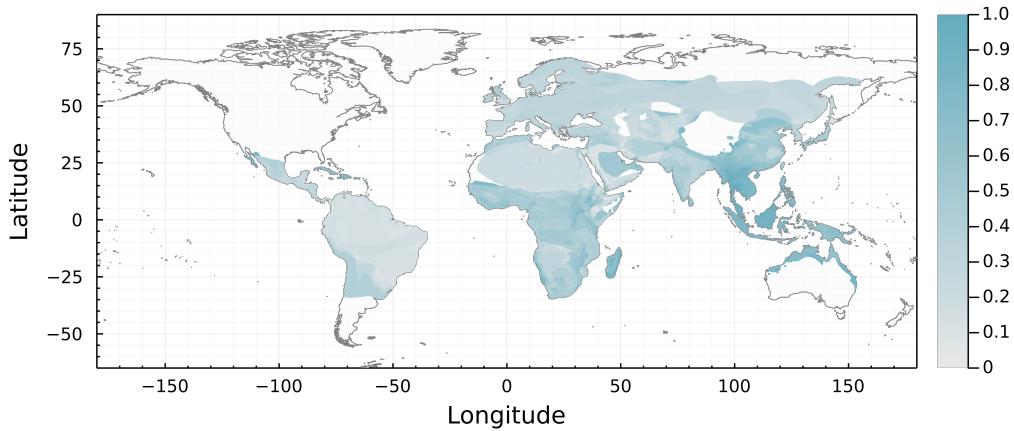


Figure 4 Extraction of a measure of *Beta-coronavirus* spillover risk from bat hosts based on the colorimetric space from fig. 3. The risk is a composite measure of the color value and angular distance to the yellow hue, as defined in the methods, ranged in the unit space. Based on this analyses, regions at high risk of spillover are southeast Asia and Madagascar.

evolve and even achieve host shifts through recombination, which requires the co-occurrence of sufficiently distinct viruses to be a major driver of emergence. In fig. 3, this corresponds to yellow to pale green areas, which are essentially limited to South-Eastern Asia, and to some part of Sub-Saharan Africa. Adopting a geographic mosaic theory perspective on risk, other regions of the world are of lesser concern fig. 4. Our risk decomposition does not account for viral diversity or distinctiveness. The simple rationale behind it is that the acquisition of viral data is rarely disconnected from the acquisition of host data. There are more sources of information on hosts than on viruses, allowing to develop a host-centric perspective on risk (although this estimate would more accurate with viral traits related to e.g. ability to switch hosts or pathogenic potential). Areas with high bat diversity and high turnover *may* facilitate the evolutionary radiation of viruses, matching previous findings that the diversification of bat coronaviruses is driven largely by host shifts (inter-genus or higher levels of cross-species transmission) and, to a lesser degree, cospeciation and sharing (intra-genus cross-species transmission; Anthony et al. 2017). This diversification is not an actual risk factor for spillover itself, but acts downstream of a spillover event by increasing the random chance of the emergence of a virus with the raw genomic components required for the potential to infect humans.

From another perspective, areas of high host uniqueness and virus sharing (red-to-pink) could provide

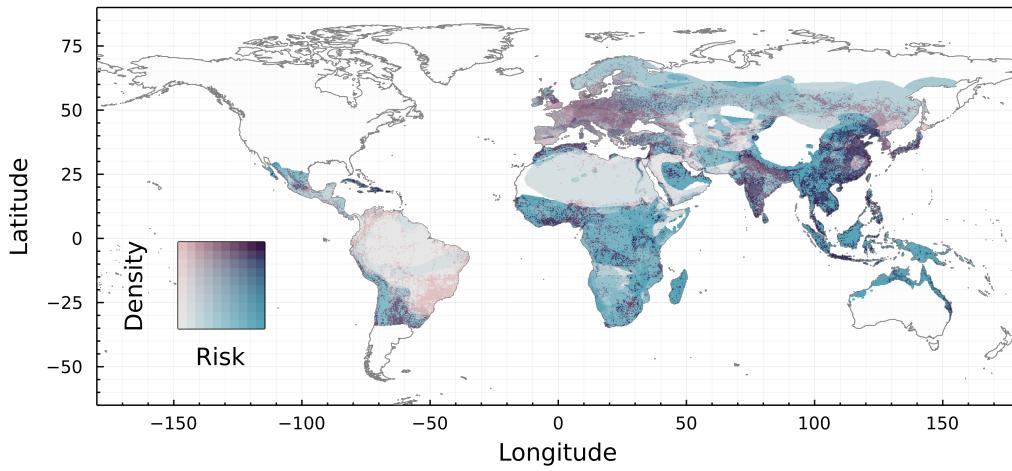


Figure 5 Overlap of the percent of each pixel occupied by urbanized structures, representing the degree of settlement, on the spillover risk map (where the risk comes only from wildlife, and ignores multi-hosts chains of transmissions including non-bats hosts). Darker pixels correspond to more risk, 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.

hotspots of *Betacoronavirus* risk through mixing of unique viruses (via codivergence) and in turn recombination. Under our framework, such a hotspot was identified in Madagascar, where most bat species are endemic following evolutionary divergence from sister species in both African and Asian continents (e.g. Shi et al. 2014). Recent surveillance (Kettenburg et al. 2022) has identified a novel *Betacoronavirus* (in the subgenus *Nobcovirus*) in Madagascar-endemic pteropid bat species (*Pteropus rufus*, *Rousettus madagascariensis*), emphasizing strong proof of principle in model predictions.

2.4. Human occupancy drives different levels of effective risk globally Based on the previous result, we extracted the risk component from the composite map (see Methods), to provide a single measure of risk varying between 0 and 1. This measure is presented in fig. 4. As this map represents the potential risk, it must be weighed by the potential for contacts with humans. As a proxy for this measure, we used the proportion of build/urban land from the EarthEnv dataset: this is a reasonable proxy for the density of humans per unit area, which increases the probability of pathogen spread more widely (Hazarie et al. 2021). Since human activity is required to amplify the frequency of virus encounters and thus create areas of viral amplification, mapping the potential risk against measures of land use is required to generate a more actionable assessment of risk. This map is presented in fig. 5. Most of South America and Europe are at comparatively lower risk, as although densely populated, settlements tend to be in areas with lower potential risk. Regions like Malaysia and the North coast of Australia have a high risk component, but should represent a relatively lower effective risk due to low human density. However, this mapping reveals that South-East Asia, the Indian subcontinent, and parts of sub-Saharan Africa, are at high risk due to the overlap between built areas and bat communities representing more opportunities for cross-species transmission of betacoronaviruses. In looking for the origins of SARS in China, Xu et al. (2004) present serological evidence that strongest human-animal contact results in higher risk of virus exposure, regardless of the animal species, but that different types of contact had different impacts. Ideally, finer-grained information about human activity (rather than human presence through anthropisation) could allow to partition this risk further, albeit at the cost of more hypotheses required to estimate the amount of risk represented by each activity. Our map of risk overlays with recent results from Cohen et al. (2022) – areas of purported high risk/diversitification potential (Madagascar, South-America) overlay with sampling gaps for *Betacoronavirus*, stressing the need for spatially targeted monitoring and discovery.

Conclusion

RELOCATE: Indeed, it only assumes the action of well described evolutionary mechanisms. The benefit of this approach is to provide the potential for a more dynamic and nuanced understanding of risk: not

only on ecological timescales, but also by providing clues about which areas can change over micro-evolutionary timescales.

Our study focuses largely on the biogeography of hosts. Specifically, we identify the Amazon and South-Eastern Asia as hotspots where the phylogenetic distinctiveness of *Betacoronavirus* is the highest (Anthony et al. 2017); surprisingly, current data suggest that viral sharing between hosts is high in the Amazon and low in South-Eastern Asia, which has the potential to result in different evolutionary dynamics between these two regions, hinting at different futures for their viral communities. This work is important both as a description of the bats-betacoronaviruses complex, but also because more broadly, bats are known reservoirs for a variety of emerging viruses and other pathogens (Calisher et al. 2006, Melaun et al. 2014), making balancing the needs for bat conservation and disease prevention most likely very difficult and a source of human-wildlife conflicts, especially in more densely populated areas (Stone et al. 2015, Rego et al. 2015).

Yet, we know that viruses with high host plasticity, that is, the ability of a given virus to adapt to various taxonomic orders and ecological groups (Kreuder Johnson et al. 2015), are more likely to amplify viral spillover, followed by secondary human-to-human transmission, and geographical spread (Hazarie et al. 2021). High viral host plasticity is an especially important trait for RNA viruses like betacoronaviruses (Haddad et al. 2021). Indeed, our analysis of viral sequences reveals that Latin America is a hotspot of viral distinctiveness, suggesting that this part of the bats-betacoronaviruses complex may be undergoing independent evolutionary dynamics (related species sharing viruses that are different from the rest of the global pool). The other hotspot of viral distinctiveness is S.E. Asia, in which richness is high but sharing is low; this suggests a different type of evolutionary dynamics (unrelated viruses coevolving with evolutionarily distinct hosts, generating high diversity locally, see e.g. Latinne et al. 2020). Both of these areas should be priority areas for sampling, especially since Becker et al. (2022) advance that they harbor undiscovered hosts of beta-coronaviruses. This diversity of hosts, and the mechanisms by which the exchange of viruses occurs between species, is largely affected by the local environmental conditions and environmental change.

Bats are important reservoir hosts for different classes of microorganisms, many of which a threat to human health (Letko et al. 2020, Van Brussel and Holmes 2022). Chiropterans emerged around 64 million years ago and are one of the most diverse mammalian orders, with an estimated richness of more than 1400 species (Peixoto et al. 2018, Simmons and Cirranello 2020). They exhibit a broad variety of habitat use, behaviour, and feeding strategies, putting them at key positions in the delivery and provisioning of several ecosystem services, tied to important ecosystem-derived benefits to human (Kasso and Balakrishnan 2013). For example, bats are an essential component of many seed-dispersal networks (Mello et al. 2011). Over two-thirds of bats are known to be either obligate or facultative insectivores, therefore actively contributing for agricultural pest control (Williams-Guillén et al. 2008, Voigt and Kingston 2016), and vectors of pathogens that put a risk on human health (Gonsalves et al. 2013a, b). Because bats are globally distributed and have a long evolutionary history, phylogeographic and biogeographic approaches are required to shed light on the contemporary distribution of coevolutionary processes between bats and the pathogens they host. Not all areas in which bats, viruses, and humans are co-occurring are facing a risk of spillover towards human populations, and the areas in which this risk exist may not be facing risks of the same nature and magnitude.

There are several factors that drive changes in the diversity of bats (Alves et al. 2018), but human activities' effects on the ecosystem (like modifications of land use) could significantly decrease it. Therefore, it can be suggested that changes in the diversity of betacovs in bats are linked to their biogeographic variation, and human population density and other anthropogenic factors are decisive moderators for its implications in public health. With the increase of contact between humans and potential hosts, we also increase the risk of emergence of novel diseases (Johnson et al. 2020), as previous studies on RNA viruses suggest the importance of host phylogeography at the time of virus dispersal (Gryseels et al. 2017). One of these scenarios where interaction between bats and humans can occur can be seed dispersal in tropical agroecosystems. It opens the discussion of whether the fruits thrown by bats not only disperse seeds but could also be a source of indirect interaction between viruses of bat origin and humans (Deshpande et al. 2022). This represents a challenge for conservation strategies and disease ecology since some areas can have both potential for the acquisition of zoonotic viruses and bat-human interactions; in particular, the challenge lies in the fact that actual exposure must then be quantified accounting for several transmission scenarios, including both direct and indirect bat - human interaction.

Acknowledgements: We acknowledge that this study was conducted on land within the traditional unceded territory of the Saint Lawrence Iroquoian, Anishinabewaki, Mohawk, Huron-Wendat, and Omàmiwininiwak nations. This work was supported by funding to the Viral Emergence Research

Initiative (VERENA) consortium including NSF BII 2021909 and a grant from Institut de Valorisation des Données (IVADO). This research was enabled in part by support provided by Calcul Québec (www.calculquebec.ca) and Compute Canada (www.computecanada.ca). NF is funded by the NSERC BIOS² CREATE program. TP and NF are funded by the Courtois Foundation. RLM was supported by Bryce Carmine and Anne Carmine (née Percival), through the Massey University Foundation.

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