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RESEARCH ARTICLE

Global redistribution of major disease vectors under high-emissions climate scenario SSP-8.5: implications for emerging public health risks

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ABSTRACT

Climate change under the high-emissions scenario SSP5–8.5 is expected to substantially reshape the global distribution of disease vectors, creating emerging environmental and public health risks. While previous studies have largely focused on individual vectors, integrated multi-species assessments remain limited. In this study, we modelled the future distributions of more than 20 globally important vector species across four periods (2021–2040, 2041–2060, 2061–2080, 2081–2100) using logistic regression and 19 bioclimatic variables. The selected taxa span multiple biomes and include vectors of major zoonotic pathogens. The results indicate pronounced climate-driven redistribution, characterized by poleward expansion of tropical and subtropical vectors into temperate regions such as Europe, North America, and East Asia, alongside declining suitability in parts of the equatorial zone due to increasing thermal stress. Persistent hotspots are projected in Sub-Saharan Africa and Southeast Asia, while temperate regions face increasing exposure to vector-borne diseases. These findings highlight climate change as a key driver of ecological reorganization and transboundary health risks, emphasizing the need for climate-sensitive surveillance and adaptive public health strategies.

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Climate change; vector-borne diseases; zoonoses; future projections; environmental management

Introduction

Zoonotic diseases, including vector-borne neglected infections, represent a significant and growing global health threat, affecting millions of people worldwide (Noguera et al. 2022). These diseases are closely linked to climate change and broader sustainability challenges, particularly in regions such as Africa (Schwerhoff and Sy 2017) and South America (Leal Filho et al. 2018), where environmental and socioeconomic vulnerabilities intersect. In addition, inadequate waste management in urban environments contributes substantially to disease transmission, as improperly disposed waste creates breeding grounds for vectors such as mosquitoes and other arthropods. For example, discarded tires and organic waste can support mosquito development and increase the risk of vector-borne diseases, while poorly managed wastewater has been associated with outbreaks such as dengue (Abdullah et al. 2024).

The situation is further exacerbated by the widespread and often excessive use of pesticides in agriculture. Such practices can disrupt ecosystems, alter vector–pathogen interactions, and promote the emergence of pesticide-resistant vector populations (Sutherst 2004). Resistance in species such as *Aedes aegypti* has made the control of diseases like dengue and Zika increasingly difficult (Dusfour et al. 2019). These dynamics highlight the complex and non-linear relationships between environmental, ecological, and socioeconomic factors that influence the spread of mosquito-borne diseases (Li et al. 2021). At the same time, some mosquito species, including *Anopheles gambiae* and *Aedes aegypti*, can serve as bioindicators of water quality and environmental contamination, underscoring their dual role in both public health risk and environmental monitoring (Kinga et al. 2022).

Zoonotic diseases account for approximately 60% of all human infectious diseases and 75% of emerging infections, making them a dominant component of the global infectious disease burden (Di Bari et al. 2023). They are caused by a wide range of pathogens maintained in animal hosts such as rodents, non-human primates, and bats, and are transmitted either directly or via vectors (Munjita et al. 2024). Globally, zoonotic

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diseases contribute significantly to morbidity and mortality, accounting for an estimated 60 million disability-adjusted life years and approximately 700,000 deaths annually, many of which are linked to mosquito vectors such as *Aedes* and *Anopheles* species (Hossain et al. 2023). Their distribution is uneven, with higher prevalence in regions where climatic, ecological, and socioeconomic risk factors converge (Ferraguti et al. 2023).

The burden of zoonotic diseases is particularly severe in low-income countries, where limited healthcare infrastructure and resources hinder effective disease prevention and control (Lv et al. 2024). Moreover, the transmission dynamics of these diseases are highly variable across space and time due to the complex interactions among hosts, vectors, and environmental conditions (Mishra et al. 2021). Zoonotic pathogens also possess high pandemic potential, as demonstrated by recent outbreaks of diseases such as COVID-19, SARS, and MERS (Shanmugaraj et al. 2024). Frequent host-switching events between animals and humans further accelerate the evolution and emergence of novel pathogens (Joseph et al. 2024).

Climate change is expected to play a critical role in shaping the future distribution and transmission of zoonotic diseases. Rising global temperatures, changing precipitation patterns, and increasing human population density are likely to enhance disease spread, particularly because many vectors are ectothermic and highly sensitive to environmental conditions (de Souza and Weaver 2024). Even endothermic hosts such as fruit bats exhibit strong climate sensitivity (Diengdoh et al. 2022). Environmental changes, including habitat fragmentation and biodiversity loss, alter ecological niches and facilitate the expansion of disease vectors into previously unsuitable regions, including temperate zones (Chikezie et al. 2024). These shifts not only increase transmission risks but also expose naïve populations to new infectious diseases and raise the likelihood of disease re-emergence (Ma et al. 2022).

In addition to climate factors, land-use changes such as deforestation, urbanization, and agricultural intensification are driving increased contact between wildlife, livestock, and human populations. These interactions heighten the risk of pathogen spillover events and the emergence of new zoonotic diseases (Ferraguti et al. 2023). Cultural practices, including bushmeat consumption in some tropical regions, combined with growing food insecurity, further increase the likelihood of host-switching and disease transmission (Tajudeen et al. 2022).

Beyond their direct health impacts, zoonotic diseases pose significant risks to sustainable development. They can disrupt food production systems, strain healthcare infrastructure, and contribute to social instability, particularly in resource-limited settings (Kruidbos 2022). Globalization and increased human mobility also accelerate the spread of infectious diseases across borders, amplifying their global impact (Lessani et al. 2024). The interconnected effects of climate change, environmental degradation, biodiversity loss, and anthropogenic disturbances collectively intensify the risks associated with zoonotic diseases (Wilke et al. 2021).

In this context, the present study provides a comprehensive global assessment of the potential impacts of climate change on the distribution of major disease vectors. Unlike previous research that has typically focused on individual species, this study models more than 20 key vectors across multiple future climate scenarios using a wide range of bioclimatic variables. By integrating both tropical and temperate species, it identifies potential hotspots, expansion zones, and regions where extreme conditions may limit vector survival. These findings offer valuable insights for public health planning, vector control strategies, and climate change adaptation efforts worldwide.

Materials and methods

Logical outline of the study

This study evaluates the impact of climate change under the high-emission SSP5-8.5 scenario on the global distribution of zoonotic diseases and related environmental management strategies between 2021 and 2100. This scenario represents a worst-case pathway, enabling the identification of regions most vulnerable to severe climate change and supporting proactive disease prevention (Xu et al. 2021). The analysis focuses on 45 pathogen, vector, and host taxa representing zoonotic transmission chains, using statistically downscaled CMIP6 climate projections.

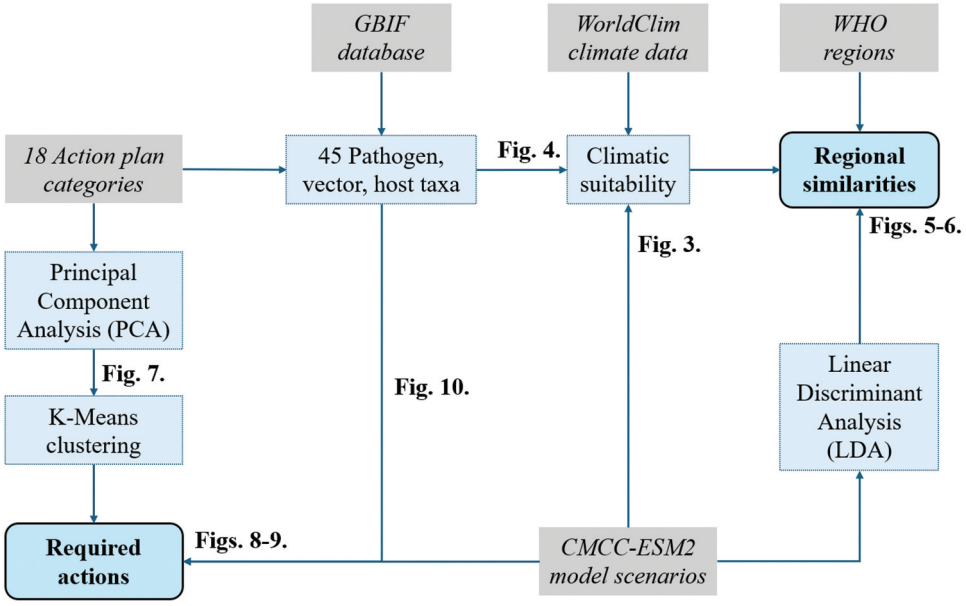

Figure 1. Workflow of the climate change – driven alteration management framework.

Occurrence data for pathogens, vectors, and hosts were obtained primarily from the Global Biodiversity Information Facility (GBIF), with additional sources for specific taxa such as henipaviruses (Luo et al. 2021). Vector-borne disease systems include interactions among hosts, vectors, and pathogens, though some zoonoses involve non-arthropod transmission routes (Trájer 2019). Four invasive mosquito species (*Aedes aegypti*, *Aedes albopictus*, *Aedes japonicus*, *Aedes koreicus*) were analysed separately due to their global epidemiological importance (Miranda et al. 2022).

Given the large number of zoonotic pathogens, selected taxa were used as climatic indicators, including viruses, protozoa, mammals, snails, crustaceans, ticks, and insects (Madewell 2020). Emphasis was placed on bats due to their role as reservoirs of major zoonotic viruses and their sensitivity to environmental change (Ranjan 2021).

Climatic suitability was modeled for four future periods (2021–2040, 2041–2060, 2061–2080, 2081–2100). Suitability values were extracted for major global cities and interpolated using inverse distance weighting, with cities grouped by WHO regions. Linear Discriminant Analysis (LDA) was used to assess regional differences, while K-means clustering and Principal Component Analysis (PCA) were applied to classify management strategies and link them to zoonosis indicator taxa. The workflow is presented in Figure 1, which is an overview of the overarching climate change-induced alteration management framework.

Data

Climatic data

Baseline climate data (1979–2003) were obtained from WorldClim v2.1 at 2.5 arc-minute resolution (Fick and Hijmans 2017). Future projections were based on the CMIP6 CMCC-ESM2 model under SSP5-8.5 for four future periods, chosen for its detailed representation of biogeochemical processes (Lovato et al. 2022). Model sensitivity values are consistent with CMIP multi-model means (Song et al. 2022).

Vector, parasite and host occurrence data

Species occurrence data were sourced from GBIF, which aggregates global biodiversity records from multiple institutions and observation systems (Gaiji et al. 2013). Supplementary Table S1 provides a summary of the data sources used for each zoonosis-indicator taxon.

Modelling of climatic suitability patterns

A rule-based additive approach was applied to estimate large-scale climatic suitability rather than species-specific occurrence probabilities. Climatic variables were processed in Python and QGIS, with outliers removed. Suitability was calculated using Boolean logic, where each satisfied climatic condition contributed to a cumulative score, later normalized between 0 and 1 (Whitesitt 2010). This approach enables consistent comparison across diverse taxa and scenarios.

Each satisfied condition contributed 1 to the raw suitability score:

$$B_i(x) = \begin{cases} 1, & \textit{if the condition is satisfied at location } x \\ 0, & \textit{otherwise} \end{cases}$$

The total suitability score was calculated as:

$$S(x) = \sum_{i=1}^{n} B_i(x)$$

These raw suitability scores were then normalized to the range [0,1] to enable comparison between species with varying numbers of climatic constraints.

Action categories and their processing

Environmental management and disease control action plans were obtained from literature sources, including vector control recommendations by the World Health Organization (2017) and other related literature (Lawler et al. 2007; Morzillo and Mertig 2011; Roth 2011; Bardosh et al. 2017; Otranto et al. 2017; Salerno et al. 2017; Matilla et al. 2018; Shaukat et al. 2019; Tsao et al. 2021; Friani et al. 2022; McKee et al. 2022; Tourapi and Tsioutis 2022; Wong et al. 2023; Eddy et al. 2024).

A total of 18 action plan categories were established, covering all possible zoonotic agents ranging from wildlife reservoirs to fresh water intermediate hosts and mosquito vectors. K-Mean clustering and PCA were used to classify the species according to their corresponding action categories. A brief description of the action plans for each species is given in Supplementary Table S2.

Linear discriminant analysis

LDA was employed to analyse the expected changes in the multivariate climatic suitability indices for the WHO regions. Convex hulls were generated in the LDA space, and the distances between the centroids of the hulls were calculated to measure the divergence of the regions for the periods 2041–2060, 2061–2080, and 2081–2100. The distances were plotted as heatmaps to enable comparison of the regional courses of zoonotic risk.

Results

Invasive aedine species

During 2021–2040, the four invasive *Aedes* species (*Aedes aegypti, Aedes albopictus, Aedes japonicus*, and *Aedes koreicus*) are mainly confined to tropical and subtropical regions, including South America, Africa, Southeast Asia, and parts of Australia. By 2041–2060, a clear northward expansion emerges, with increasing suitability in the Mediterranean, southeastern United States, Central Asia, and parts of China.

This expansion intensifies by 2061–2080 and 2081–2100, with large areas of Europe, North America, and Asia becoming suitable. While the highest species richness remains concentrated in tropical regions, the progressive spread into temperate zones is evident (Figure 2).

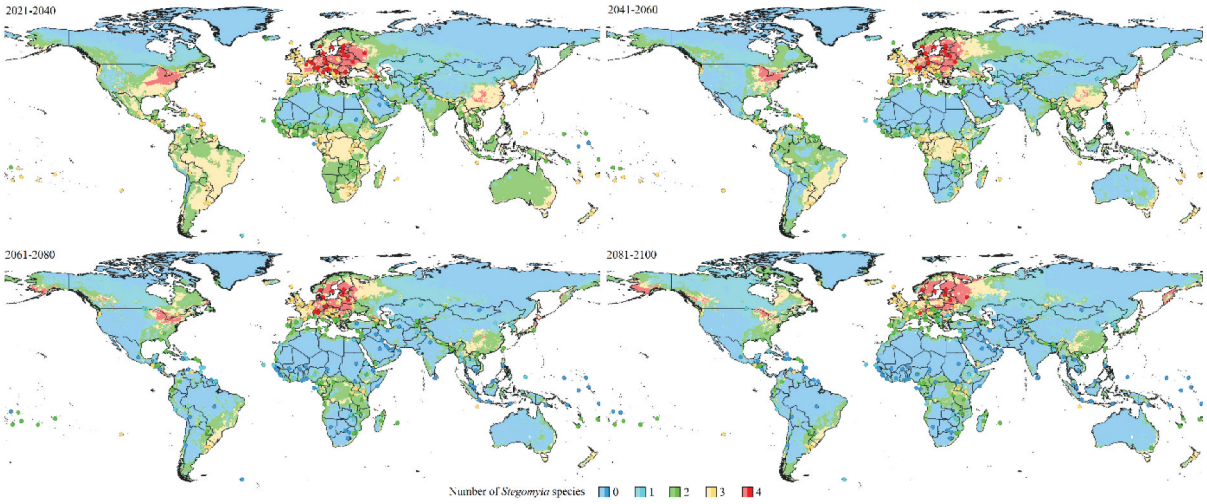

Figure 2. The modelled number of the selected four important invasive aedine mosquito species based on the 90% threshold of the projected climatic suitability values of *Aedes aegypti, Aedes albopictus, Aedes japonicus* and *Aedes koreicus* in the future periods of 2021–2040, 2041–2060, 2061–2080, and 2081–2100.

Zoonoses-related indicators

Projected number of occurrences

The number of zoonosis-indicator taxa with high climatic suitability (≥0.9) shows strong regional variation. Europe initially exhibits high suitability, which expands northward into Eastern Europe and northern Asia by the end of the century.

In Africa and South America, high suitability in equatorial regions declines over time due to warming and aridification, while southern South America shows increasing suitability. North America displays rising suitability in northern regions, whereas South and Southeast Asia show an overall decline. In contrast, northern Asia shows a strong increase, and Australia remains largely unsuitable except for limited northern expansion (Supplementary Figure S1).

Modelled changes in occurrences

Compared to the 2021–2040 baseline, results indicate a general poleward shift in climatic suitability. Europe and northern Asia experience consistent increases, while tropical regions (e.g. Amazon Basin, Central Africa, Southeast Asia) show marked declines. North America exhibits mixed trends, with increases in northern areas and decreases in southern and western regions (Figure 3).

Linear discriminant analysis results

Linear Discriminant Analysis (LDA) reveals patterns of multivariate climatic suitability across World Health Organization regions, quantified by distances between convex hulls (Supplementary Figure S2-S3) . In 2021–2040, the smallest distances occur between the American and Western Pacific regions, followed by Western Pacific – Southeast Asian and African – Southeast Asian pairs, while the largest distance is between the Western Pacific and Eastern Mediterranean regions. Europe and Africa show intermediate distances (Supplementary Figure S2a). In 2041–2060, strong divergence persists between the Eastern Mediterranean and both Western Pacific and Southeast Asian regions. European – African and European – Western Pacific distances remain moderate, whereas American – Southeast Asian and African – Southeast Asian distances are small (Supplementary Figure S2b).

By 2061–2080, the Eastern Mediterranean continues to diverge markedly from the Western Pacific and Africa, while decreasing distances between the American and Southeast Asian regions indicate increasing similarity. In 2081–2100, a general decrease in distances suggests convergence of climatic suitability patterns across regions. However, the Eastern Mediterranean – Western Pacific pair remains the most distinct, while American – Southeast Asian and African – Southeast Asian regions show increasing similarity.

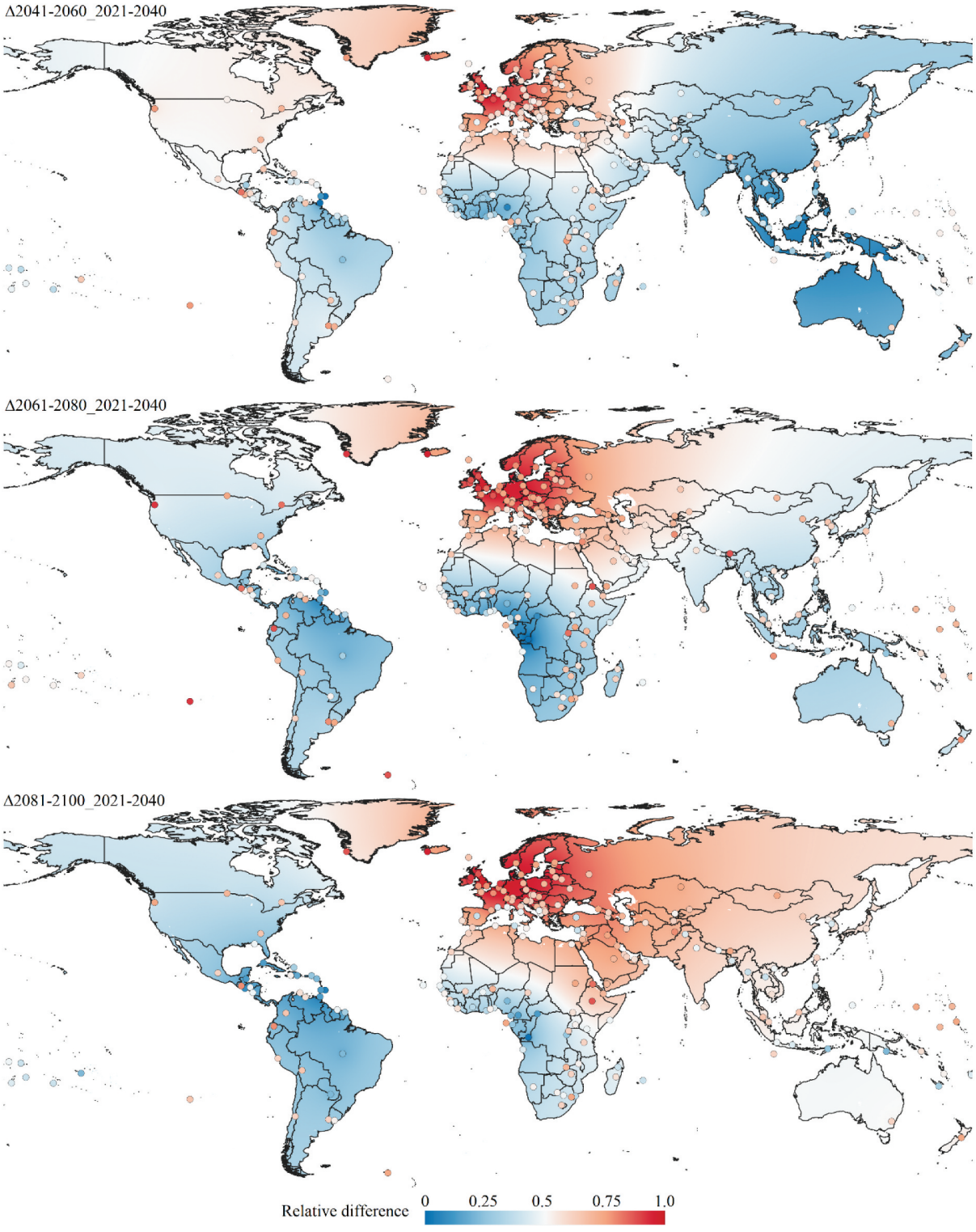

Figure 3. Change in the relative number of zoonosis-indicator taxa reaching climatic suitability ≥0.9 compared to the 2021–2040 period (IDW-interpolated).

Results of combined PCA and K-Means clustering

Based on the results obtained from the joint analysis using the PCA and K-Means clustering, five different clusters of action policy were found, which were related to the zoonosis-indicator taxa. The first cluster contains terrestrial mammals, such as fruit bats and wild canids. The second cluster contains freshwater snails and mosquitoes. The third cluster contains flies, fresh and brackish water-dwelling crustaceans, biting

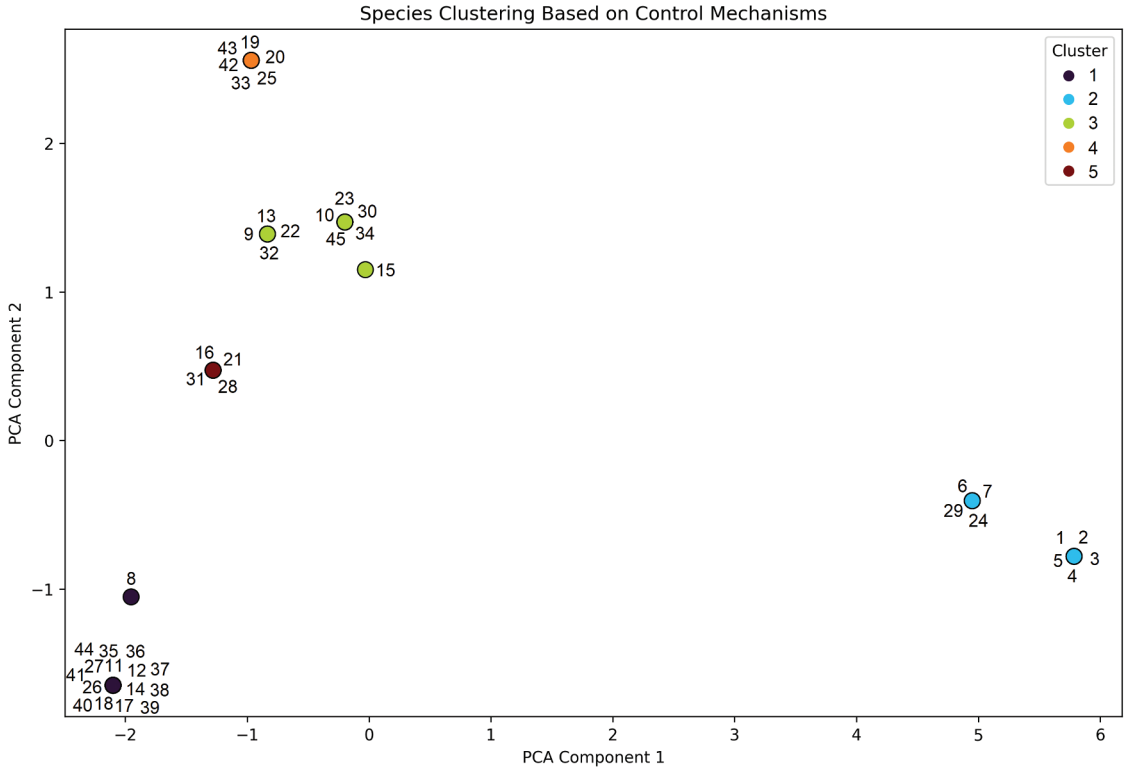

Figure 4. PCA – k-means clustering of action strategy profiles for zoonosis-indicator taxa. 1: *Anopheles stephensi*, 2: *Aedes aegypti*, 3: *Aedes albopictus*, 4: *Aedes koreicus*, 5: *Aedes japonicus*, 6: *Biomphalaria*, 7: *Bulinus*, 8: *Canis lupaster*, 9: *Chrysomyia*, 10: *Culicoides*, 11: *Eidolon dupreanum*, 12: *Eidolon helvum*, 13: *Eirocheir sinensis*, 14: *Epomops franquetti*, 15: *Eucyclops*, 16: *Hendra virus*, 17: *Hipposideros larvatus*, 18: *Hypsignathus monstrosus*, 19: *ixodes ricinus*, 20: *ixodes persulcatus*, 21: Langya henipavirus, 22: *Leptotrombidium*, 23: *Lutzomyia*, 24: *Lymnaea*, 25: *Meriones*, 26: *Miniopterus schreibersii*, 27: *Myonycteris torquata*, 28: Nipah virus, 29: *Oncomelania*, 30: *Phlebotomus similis*, 31: *Plasmodium*, 32: *Procavia*, 33: *Psammomys*, 34: *Psychodopygus*, 35: *Pteropus alecto*, 36: *Pteropus lyelli*, 37: *Pteropus policephalus*, 38: *Pteropus rufus*, 39: *Pteropus conspicillatus*, 40: *Pteropus medius*, 41: *Pteropus vampyrus*, 42: *Rattus tazerumi*, 43: *Rhipicephalus sanguineus*, 44: *Rousettus aegyptiacus*, 45: *Sergentomyia*.

midges, mites, and sand flies. The fourth cluster contains ticks and rodents (Figure 4). The fifth cluster contains pathogenic species. The cluster assignments of all the taxa are presented in Supplementary Table S3.

Projected global distribution of required actions

Interpolated patterns of the five action policy clusters reveal marked spatial and temporal differences between 2021–2040 and 2081–2100. The first cluster shows initially moderate, regionally concentrated activity, followed by increasing intensity in some areas and decreases in others by the end of the century. The second cluster exhibits a similar trend, with an initially more uniform distribution that later contracts or expands regionally. High-frequency activity increases in some areas, while others show declining activity levels.

In the third cluster, early spatial fragmentation with moderate to high activity shifts toward region-specific increases or decreases, with formerly high-activity areas often declining while others intensify. The fourth cluster undergoes substantial reorganization, with initially high activity patterns giving way to pronounced regional shifts, where some areas become dominant and others diminish. The fifth cluster shows relatively stable, widespread activity in the early period, followed by spatial expansion or contraction in the late century, indicating dynamic changes in activity distribution (Supplementary Figure S4).

The spatial distribution of dominant action policy clusters shows distinct regional patterns and marked changes between 2021–2040 and 2081–2100. In 2021–2040, clusters are broadly distributed across continents. Cluster 2 (light blue) is widespread across Europe, North America, and parts of Asia, while Cluster 1

(dark blue) is also globally present but concentrated in South America, Africa, and Southeast Asia. Cluster 3 is less prevalent overall, and Clusters 4 and 5 occur sparsely in localized hotspots. By 2081–2100, the spatial structure shifts substantially. Cluster 5 (deep purple) expands notably, especially in Africa, South Asia, and parts of South America, indicating a growing dominance in these regions. Cluster 2 remains common but becomes more spatially concentrated, while Cluster 1 persists with slightly reduced density in some areas. Clusters 3 and 4 show redistribution, with localized gains and losses across regions.

Overall, the comparison indicates a dynamic reorganization of policy dominance over time, with an increasing role of Cluster 5—particularly in the Global South – while Cluster 2 remains influential in developed regions, reflecting evolving regional priorities in response to long-term global drivers (Figure 5).

Based on the spatial distribution of taxa (Figure 5), the effectiveness of environmental management interventions can be assessed by linking taxa to action plan categories via k-means cluster membership. Figure 6 presents a multipartite graph mapping relationship among taxa, five clusters, and recommended management actions, enabling targeted disease risk reduction strategies.

Three main groups of action categories emerge. Blue nodes represent vector-focused interventions, including surveillance, larviciding, and vector control targeting arthropods such as *Aedes* and *Anopheles*. Deep purple nodes correspond to public health surveillance, monitoring of bat-associated pathogens, and reduction of human–wildlife contact, linked to bat- and virus-dominated taxa (e.g. Pteropus spp., Nipah virus, Hendra virus). Orange nodes focus on rodent and tick control, habitat management, and reservoir host reduction strategies.

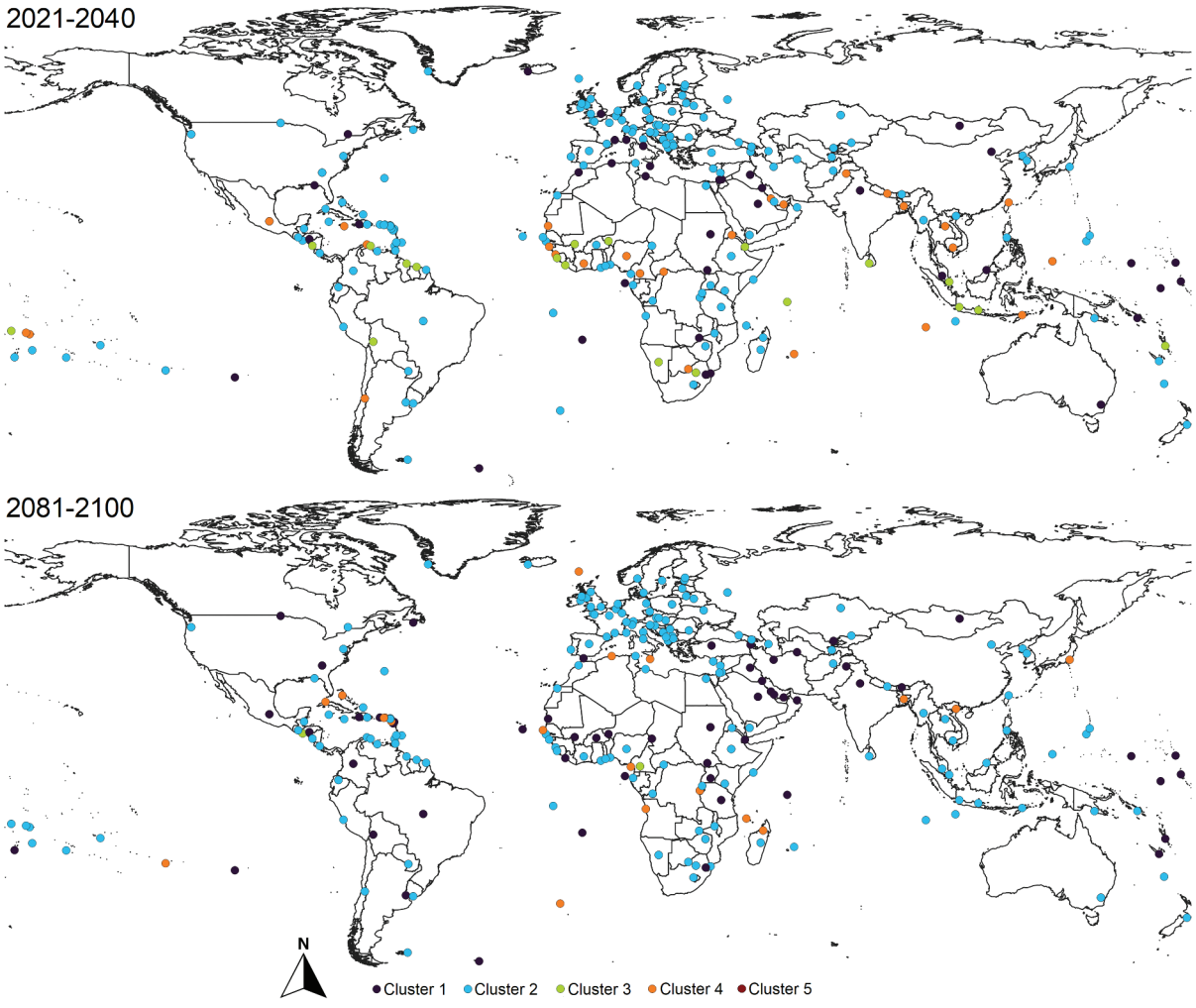

Figure 5. Distribution of dominant action activity clusters in the future periods 2021–2040 and 2081–2100.

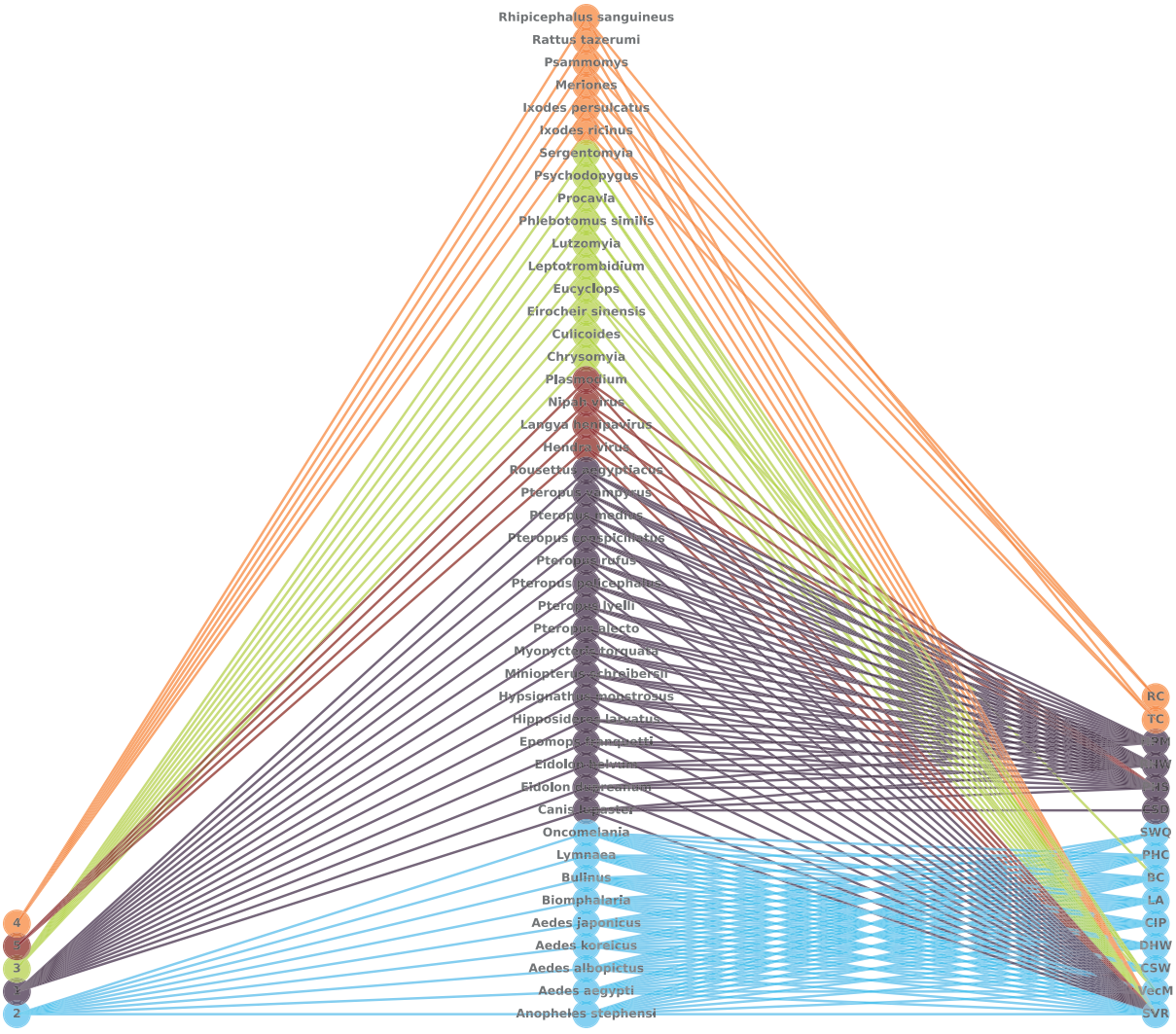

Figure 6. Bipartite representation of clusters, taxa, and action categories. Action categories are: SVR: Surveillance of vector and reservoir populations, EE: Environmental education, VecM: Vector management, CSD: Control of stray dog populations, VVC: Vaccination and veterinary care, RC: Rodent control in urban and rural settings, TC: Tick control in livestock and wildlife, HPM: Habitat protection and monitoring, PHS: Public health surveillance (incl. monitor bat-related diseases and their transmission pathways to humans or livestock), RHW: reduce human–wildlife contact, CSW: Control of stagnant water sources eliminating breeding sites, DHW: Draining shallow water bodies, CIP: Control of irrigation practices (irrigation canals to avoid stagnant water), LA: larviciding (using safe larvicides), BC: Biological control (by introducing natural predators), VegM: Vegetation management, PHC: Public health campaigns/public awareness (water containers and using bed nets or insect repellents), SWQ: Danitation and water quality. The affiliation of the studied vector chain element vector and host animal taxa is given in Supplementary Table S3.

Overall, the framework integrates taxa distribution, cluster structure, and intervention types to support prioritization of high-impact taxa, linkage to actionable strategies, and spatially explicit planning. This integrated approach improves resource allocation and supports proactive mitigation of climate-driven shifts in zoonotic and vector-borne disease risks (Figure 6).

Discussion

Although several models have projected future occurrences of specific vector species (Laporta et al. 2023), this study provides a broader global perspective on projected changes. A key finding is that Europe and the Mediterranean emerge as particularly vulnerable, contrasting with earlier studies emphasizing tropical–subtropical regions of the Americas and Africa (Aliaga-Samanez et al. 2024). This pattern is already evident,

as the Eastern Mediterranean WHO region currently accounts for 40% of the global population in need of humanitarian assistance (Fazaludeen Koya et al. 2023), while diseases such as dirofilariasis (Morchón et al. 2022), leishmaniasis (Tunalı and Özbilgin 2023), and West Nile fever (Lu et al. 2024) are increasingly reported across Europe.

This does not imply a reduction of tropical zoonotic burden, but rather an expansion of vector and host diversity into Western Eurasia (see Figure 2 and Supplementary Figure S1). Invasive vectors such as *Aedes* mosquitoes further increase future risk in Europe, with complex, non-linear effects within vector transmission chains (Garrido et al. 2023). Overall, projections indicate a redistribution of suitability, with declines in tropical regions and increases in temperate and boreal zones (Figure 3), driven by temperature rise, precipitation shifts, and habitat change (Yadav and Upadhyay 2023).

Persistent high convex hull distances between the Eastern Mediterranean and Western Pacific regions (Supplementary Figure S2–S3) indicate distinct pathogen emergence pathways, likely due to differing climatic responses. The Western Pacific, Southeast Asian, and American regions form a closely related cluster, while the Eastern Mediterranean is the most distinct. Europe and Africa occupy intermediate positions, whereas decreasing distances among Southeast Asian, African, and American regions suggest increasing similarity, potentially linked to converging climate drivers, including monsoon variability (Tierney and Russell 2007) and El Niño dynamics (Alizadeh 2022).

Over the 21st century, vector suitability patterns are projected to shift substantially, with simultaneous regional divergence and homogenization, consistent with broader climate-driven trends in zoonotic diseases (Thomson and Stanberry 2022). This underscores the need for region-specific interventions, as heterogeneous impacts can worsen inequality, reduce productivity, and strain healthcare systems (Ryan et al. 2021). For example, in Europe and other temperate regions where *Aedes* spp. are projected to expand (Abbasi 2025; Radici et al. 2025), surveillance systems, early detection programs, and targeted mosquito control measures may become increasingly important. In Sub-Saharan Africa and Southeast Asia, where climatic suitability remains high for multiple vector and reservoir taxa, integrated vector management, habitat reduction, and strengthened disease monitoring may remain priorities. Regions characterized by increasing suitability for bat-associated pathogens may benefit from enhanced wildlife surveillance and measures aimed at reducing human–wildlife contact (Davy et al. 2023). The selection of interventions was guided by the dominant action-policy clusters identified through the PCA and K-means analyses, which link projected taxa distributions to specific management categories (Figure 5–6).

The implementation of these regionally tailored measures is particularly important because the consequences of zoonotic disease emergence extend well beyond public health, affecting economic stability, livelihoods, and broader sustainability outcomes. Zoonotic diseases thus have broader economic consequences, as demonstrated by the 2015–2016 Zika virus epidemic across Latin America and the Caribbean, which imposed substantial public health and economic burdens (Kim and Liu 2024), with additional impacts on household finances (Patikorn et al. 2024), macroeconomic stability (Immurana et al. 2024), and ecosystem services (Habibullah et al. 2022). They can also hinder sustainable development goals related to water, food, and energy security (Linderhof et al. 2021), particularly in regions with limited adaptive capacity (Leal Filho et al. 2021), while livestock outbreaks and ecosystem degradation further amplify food insecurity and systemic vulnerability (Yin et al. 2021).

As shown in Supp. Figure S4 and Figure 5, required interventions may evolve and sometimes conflict with broader goals. For example, vegetation removal can reduce mosquito habitats but increase heat stress, creating trade-offs in urban greening (Yang et al. 2019). Conversely, green roofs and green – blue infrastructure may reduce mosquito presence under certain conditions (Rhodes et al. 2022).

These findings highlight the need for integrated strategies combining vector control, urban planning, and climate adaptation (Umar 2024). Spatial design and plant selection can help balance ecosystem benefits with reduced vector suitability (Reisen 2010), while multi-sector interventions reduce risk without undermining environmental or social objectives (Trout Fryxell et al. 2022), as also reflected in Figure 6.

Policy conflicts may also arise between desertification control and mosquito habitat reduction. Aridification does not necessarily reduce risk (Khezzani et al. 2023). For example, the Danube – Tisza Interfluve has undergone strong aridification due to river regulation (Kovács et al. 2017) and may become semi-arid by late century (Kovács et al. 2017), while hydrological restoration could increase mosquito habitat availability. Historically, the Hungarian Great Plain was malaria-endemic prior to river regulation

(Trájer and Hammer 2016). Similarly, wetland management in urban areas may reduce biodiversity but increase mosquito risk (Hanford et al. 2020), while also affecting other disease vectors such as *Bulinus* spp., hosts of *Schistosoma haematobium* (Wepnje et al. 2023).

Conclusion

Projected climatic shifts are expected to substantially reshape the global distribution of zoonotic disease risk, with increasing suitability in temperate and boreal regions and a relative decline in tropical areas. These changes highlight the need for targeted surveillance, vector control, and adaptive health policies in emerging risk zones. Future work should integrate additional ecological and socioeconomic variables to improve prediction accuracy and strengthen preparedness. A broader set of climatic and ecological drivers will further refine pathogen distribution forecasts and support more effective interventions, which is critical for global health resilience. Our results also indicate a redistribution of *Aedes* and high-diversity *Anopheles* habitats, particularly across tropical lowlands, with a shift toward more humid and climatically stable regions. These trends may significantly affect malaria transmission dynamics, reinforcing the need for adaptive public health responses.

Overall, the findings emphasize the importance of region-specific monitoring, proactive intervention strategies, and climate-informed health planning to mitigate the evolving risks of zoonotic diseases.

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Author contributions

CRediT: **Attila J. Trájer:** Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing; **Viktor Sebestyén:** Conceptualization, Funding acquisition, Investigation, Methodology, Supervision, Validation, Visualization, Writing – review & editing.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

All data supporting this study are available in the supplementary materials and in the referenced open-access datasets.

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