

A semi-quantitative framework to prioritize the zoonotic risks of invasive alien species

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Research Article

Keywords: Invasive alien mammals, Zoonotic diseases, Risk assessment, One Health, Europe, Biosecurity

Posted Date: October 27th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-11299195/v1>

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Additional Declarations: No competing interests reported.

Abstract

Invasive alien species (IAS) contribute to zoonotic disease emergence, yet human health impacts are rarely incorporated into IAS prioritization frameworks. This study presents a semi-quantitative tool to evaluate zoonotic risk from invasive mammals in Europe by integrating epidemiological and spatial information. The framework combines four parameters: pathogen prevalence, disease severity based on the biosafety level of associated pathogens, geographic distribution, and potential human exposure derived from spatial overlap between IAS distributions and human population density. Parameters were standardized using a five-point ordinal scale and combined into a human health impact score.

The framework was applied to eight EU-regulated invasive mammal species. Six species were classified as having a Major potential impact on human health, one as Moderate, and one as Minor. No species reached the Minimal or Massive categories. Comparison with impact assessment systems revealed partial agreement, with the strongest association observed between the proposed score and the Generic Impact Scoring System (GISS) overall score. Weaker correlations with EU biodiversity impact scores and the GISS human health category suggest that existing assessments provide useful but incomplete information on zoonotic risk.

At country level, variation was observed in potential human exposure to invasive mammals and public health preparedness. Some highly exposed countries showed high preparedness, whereas others combined high exposure with lower preparedness. The framework provides a quantitative and replicable tool for identifying IAS and regions where zoonotic risk may require greater attention, supporting management and public health preparedness under a One Health perspective.

Introduction

Zoonotic diseases originating from wildlife account for over 40% of global emerging infectious disease (EID) events since 1940 (Jones et al., 2008). Among the drivers of zoonotic disease emergence, Invasive Alien Species (IAS) are increasingly recognized for their role in introducing pathogens into new regions where host populations lack prior immunity (Keesing et al., 2010; Roy et al., 2023). The ability of IAS to harbor pathogens asymptotically and thrive in diverse habitats enables them to act as reservoirs, amplifiers, and vectors of zoonotic diseases, increasing opportunities for spillover to humans (Vilà et al., 2021; Zhang et al., 2022).

Invasive mammals are of particular concern because their phylogenetic proximity to humans increases the likelihood of cross-species transmission (Zhang et al., 2022). Many invasive mammals also occur at relatively high local abundances in human-modified environments, potentially increasing opportunities for direct or indirect contact with people and domestic animals. In parallel, the number of people living within mammal species' ranges has been identified as a predictor of zoonotic viral richness, likely reflecting greater opportunities for human–wildlife contact (Olival et al., 2017). In Europe, invasive mammals of Union concern are still expanding their ranges, and most have been implicated in the epidemiological cycle of zoonotic pathogens (Tedeschi et al., 2022). More broadly, habitat disturbance

and land-use change can intensify contact among wildlife, domestic animals, and humans, thereby increasing opportunities for pathogen spillover. This has been illustrated by the 1998 Nipah virus outbreak in Malaysia, where agricultural intensification facilitated transmission from bats to humans via livestock (Parashar et al., 2000).

Climate change may further amplify these processes by altering species distributions and patterns of contact among wildlife, domestic animals, and humans. For example, the risk of Hendra virus spillover in Australia is predicted to expand southwards as environmental conditions and interactions among flying foxes, horses, and humans change (Martin et al., 2018). Similarly, rising temperatures and altered precipitation patterns may allow IAS to expand into previously unsuitable regions, increasing contact with new host species and human populations (Bradley et al., 2024; Gu et al., 2023). Warmer conditions can also facilitate the expansion and establishment of disease vectors, particularly mosquitoes, increasing the risk of mosquito-borne infections in newly suitable areas (Epstein, 2001; Pabst et al., 2026; Patz et al., 1996). Together, these changes may further increase zoonotic disease incidence across different regions. Despite this, public health strategies currently focus on outbreak control through quarantine, vaccination, and treatment, while early detection and prevention remain limited (Allen et al., 2017). Likewise, despite the public health risks associated with IAS, current management strategies focus mainly on ecological and economic impacts, often overlooking their role in zoonotic disease transmission.

Risk assessment frameworks have proven highly effective for identifying and prioritizing major threats posed by IAS to biodiversity and ecosystem services (Peyton et al., 2026; Roy et al., 2018). However, these tools are not specifically designed to assess risks to human health. Given the large number of IAS with zoonotic potential, specific tools are needed to prioritize management of the species incurring the greatest biosecurity risks. Previous work compiled epidemiological and spatial information for invasive mammals in Europe, including pathogen prevalence, disease severity, potential distribution, and human exposure (Monguilod & Gallardo, 2026). However, these data had not yet been integrated into a standardized framework for comparing zoonotic risk across species.

To address this gap, the objectives of the present study are to (1) develop a semi-quantitative risk assessment framework to evaluate the zoonotic risks posed by invasive species; (2) apply the framework to a case study focused on invasive mammals in Europe; and (3) rank these invasive species according to their relative risk to human health; (4) compare the resulting human health scores with existing IAS impact assessment systems; and (5) explore whether potential human exposure to invasive mammals aligns with national public health preparedness across European countries. The resulting framework integrates four key parameters: pathogen prevalence in IAS populations, disease severity, potential distribution, and human exposure. Although the framework is illustrated here using invasive mammals in Europe, it can be adapted for application to other IAS and study areas.

Methods

This study developed a semi-quantitative risk assessment framework to prioritize IAS according to their potential impact on human health. The framework integrates four parameters: pathogen prevalence, disease severity, geographic distribution, and human exposure. It builds upon previously published epidemiological and distributional analyses of invasive mammal species in Europe (Monguilod & Gallardo, 2026). While earlier work was descriptive, here we quantify and integrate these key parameters into a standardized risk prioritization framework directed to support prevention and early detection. The framework is illustrated using eight invasive mammal species of concern in Europe as a case study.

Data sources

To demonstrate the application of the framework, eight invasive mammal species were selected for this study: *Herpestes javanicus* (É. Geoffroy Saint-Hilaire, 1818), *Myocastor coypus* (Molina, 1782), *Nasua nasua* (Linnaeus, 1766), *Nyctereutes procyonoides* (Gray, 1834), *Ondatra zibethicus* (Linnaeus, 1766), *Procyon lotor* (Linnaeus, 1758), *Sciurus carolinensis* (Gmelin, 1788), and *Tamias sibiricus* (Laxmann, 1769). Species selection followed a two-step process: first, invasive mammals included in the EU Union List were retrieved, as these IAS are considered priorities for management in Europe; second, species with evidence of zoonotic potential were retained, based on the review conducted by Roy et al. (2023)

For each selected species, four parameters were obtained to assess potential impacts on human health:

- **Pathogen prevalence**, defined as the proportion of individuals infected with zoonotic pathogens within invasive mammal populations. This information was obtained from the literature review conducted by Monguilod & Gallardo, (2026), which compiled zoonotic pathogens reported in invasive mammal populations. In that study, prevalence values were extracted from published studies and expressed as the proportion of infected individuals within invasive mammal populations. When multiple prevalence estimates were available for the same pathogen in a given invasive mammal, these estimates were first averaged to obtain a single pathogen-specific prevalence value. When an invasive mammal species was associated with multiple zoonotic pathogens, the pathogen-specific prevalence values were then averaged to obtain a single mean prevalence value for that invasive mammal.
- **Disease severity**, calculated as the mean biosafety level (BSL) of pathogens associated with each invasive mammal. BSL indicates the containment level required for handling microorganisms and biological materials in laboratory settings (Centers for Disease Control and Prevention, 2020; WHO, 2005). BSL-1 pathogens are considered non-pathogenic or of minimal risk; BSL-2 pathogens may cause treatable human disease but generally present low transmission risk; BSL-3 pathogens can cause serious disease and may present a higher risk of spread; and BSL-4 pathogens cause severe, often untreatable diseases with high transmission potential. When pathogens belonging to the same genus or family had different BSL classifications, the highest BSL was retained following a precautionary approach. For each invasive mammal species, disease severity was calculated as the mean BSL score of the associated zoonotic pathogens.

Pathogen prevalence and BSL values used in the analysis are provided in Supplementary Table S1.

- **Geographic distribution**, defined as the proportion of European territory suitable for each invasive mammal according to the Species distribution models (SDMs) developed by Monguilod & Gallardo (2026). In brief, SDMs were calibrated at a global scale using occurrence records from both native and introduced ranges, allowing the models to capture the range of environmental conditions suitable for each species. All known occurrence records of the focus species were compiled, cleaned for incorrect values, and thinned to a maximum of one record per 10 × 10 km grid cell (Sillero, 2011). The occurrence data sources and the total numbers of records used for each mammal are provided in Supplementary Table S2. A set of uncorrelated climatic, topographic, and anthropogenic variables was used as potential predictors. SDMs were developed using an ensemble of four modelling algorithms in BIOMOD2 (Thuiller et al., 2009). Model performance was evaluated using the True Skill Statistic (TSS). The final ensemble models were projected onto Europe to generate continuous suitability maps for each species, where 0 indicates no suitability for invasion and 1000 optimum conditions for establishment based on the current spread of the species. The cut-off thresholds, sensitivity, specificity, and validation values obtained for each algorithm and invasive mammal species are provided in Supplementary Table S3. Maps were converted into binary suitable/unsuitable maps using a TSS-based threshold (Barbet-Massin et al., 2012). Binary maps were then clipped using a European mask, and geographic distribution (%) was calculated as the proportion of suitable pixels (value = 1) relative to the total number of pixels within the European mask, multiplied by 100.
- **Human potential exposure**, estimated as the percentage of the European population residing within suitable areas for the IAS. It reflects the potential of direct or indirect contact between humans and the IAS. It was estimated by intersecting invasive mammal suitability maps with human population density data from the Gridded Population of the World, Version 4 (GPWv4) dataset (CIESIN, 2018).

Development of the human risk assessment framework

The extent of the impacts linked to any particular hazard depends on two major factors: the degree of vulnerability and the level of exposure to the hazards (Cardona et al., 2012). In our case, exposure to zoonotic hazards was represented by two variables: the potential geographic distribution of invasive mammals and the prevalence of associated zoonotic pathogens. Vulnerability was represented by the potential human exposure to these mammals and the severity of the associated diseases, estimated using the biosafety level (BSL) classification.

The proposed framework classifies IAS into five human health impact categories, ranging from Minimal (1) to Massive (5). The classification was based on standardized thresholds for the four parameters included in the assessment (Table 1). Thresholds for geographic distribution and human exposure were defined using equal 20% intervals, whereas pathogen prevalence and disease severity were grouped according to epidemiological relevance and BSL classification.

Table 1. Semi-quantitative framework for assessing IAS impacts on human health. Values falling exactly on the boundary between two intervals were assigned to the higher impact category.

Each parameter was standardized using a semi-quantitative five-point ordinal scale (1–5), consistent with established IAS impact classification systems such as Environmental Impact Classification for Alien Taxa (EICAT) of the IUCN (Hawkins et al., 2015) and related frameworks (González-Moreno et al., 2019; Peyton et al., 2019).

Equal weighting was applied to all four parameters to avoid introducing subjective prioritization among criteria. The final human health impact score was calculated as the sum of the four parameter scores, resulting in a total possible score ranging from 4 to 20. Final scores were then assigned to five impact categories: Minimal (4–6), Minor (7–9), Moderate (10–12), Major (13–16), and Massive (17–20).

Comparison with existing impact assessment systems

To evaluate whether the human health impact score developed in this study was consistent with existing IAS impact assessments, we compared our scores with three impact metrics: (i) biodiversity impact scores from the EU Union List Risk Assessments, (ii) overall scores from the Generic Impact Scoring System (GISS) and (iii) the specific GISS human health score.

Biodiversity impact scores were obtained from the official EU risk assessments supporting species inclusion in the List of Invasive Alien Species of Union concern under Regulation (EU) No 1143/2014 (<https://ec.europa.eu/>). EU biodiversity impacts were reported using five qualitative categories: Minimal concern, Minor, Moderate, Major, and Massive. To facilitate comparison with our proposed framework, these categories were converted to an ordinal scale from 1 to 5, with Minimal, Minor, Moderate, Major, and Massive concern assigned scores of 1, 2, 3, 4, and 5, respectively. GISS scores were obtained from a European alien species assessment in which impacts were evaluated across 12 environmental and socio-economic categories scored from 0 to 5; the specific GISS human health category was also extracted for comparison (Nentwig et al., 2016, 2018).

Because the impact scores compared in this study were expressed on different numerical ranges, all scores were converted to a common 0–100 scale. For the human health impact score developed here, rescaling accounted for its theoretical range from 4 to 20, as the score was obtained by summing four parameters scored from 1 to 5. Therefore, human health scores were rescaled using:

$$\text{Rescaled score} = \frac{\text{observed score} - 4}{20 - 4} \times 100$$

For the remaining indicators, scores were expressed as a percentage of their maximum possible value: EU biodiversity impact score over 5, GISS overall score over 60, and GISS human health score over 5. This rescaling was used only for comparison purposes and did not modify the original classifications.

Associations between the human health impact score developed in this study and existing impact assessment metrics were evaluated using Kendall's rank correlation coefficient (τ). Kendall's τ was selected because all variables were measured on ordinal scales and the number of species evaluated was small ($n = 8$). Positive values of τ indicate that species receiving higher scores in one assessment system also tend to receive higher scores in the other.

Comparison with public health preparedness

To evaluate whether countries potentially exposed to zoonotic risks from invasive mammals are adequately prepared to respond to emerging health threats, national levels of human exposure were compared with public health preparedness scores. Preparedness was assessed using the 2025 State Party Self-Assessment Annual Reporting (SPAR) framework developed by the World Health Organization under the International Health Regulations (WHO, 2025). The SPAR framework evaluates national capacities to prevent, detect and respond to public health emergencies and provides an overall preparedness score ranging from 0 (lowest preparedness) to 100 (highest preparedness).

For each European country, potential human exposure was calculated separately for each invasive mammal as the percentage of the population living within areas suitable for that mammal. The eight mammal-specific values were then averaged to obtain a single human exposure value per country. Human exposure does not necessarily imply zoonotic transmission or disease occurrence but rather indicates potential spatial overlap between human populations and invasive mammals with zoonotic potential.

Countries were subsequently classified according to their relative levels of exposure and preparedness. Mean values of human exposure and SPAR scores across all countries were used as thresholds to divide countries into four categories: (i) low exposure–high preparedness, (ii) high exposure–high preparedness, (iii) low exposure–low preparedness, and (iv) high exposure–low preparedness. The same classification was also performed using median values and is presented in the Supplementary Information. This classification was used to identify countries where potential zoonotic exposure associated with invasive mammals may not be matched by corresponding levels of public health preparedness.

Differences in public health preparedness between countries classified as having high and low potential human exposure were evaluated using a two-sided Mann–Whitney U test, also known as the Wilcoxon rank-sum test. This non-parametric test was selected because the two groups were independent and SPAR scores showed some deviation from normality. Countries with exposure values equal to or above the mean exposure across countries were assigned to the high-exposure category.

Results

The framework was applied to the eight invasive mammal species in the Union List to demonstrate how epidemiological and spatial information can be integrated into a standardized human health risk classification. Although this study focuses on invasive mammals in Europe, the framework can be adapted to other species groups or geographic regions.

Zoonotic pathogens associated with invasive mammals

The 8 focus invasive mammal species differed in the number and prevalence of zoonotic pathogens associated with them (Figure 1). Some species, such as *Myocastor coypus*, *Nyctereutes procyonoides*, *Procyon lotor*, and *Ondatra zibethicus*, were linked to multiple zoonotic pathogens, while others showed fewer reported associations. Most pathogens showed low or intermediate prevalence within the invasive mammal species in which they were reported, although high prevalence values were observed for some pathogens, including *Toxoplasma*, *Giardia*, *Cryptosporidium*, *Mycoplasma*, *Strongyloides*, and *Clostridium*. These results indicate that both pathogen diversity and prevalence vary considerably among invasive mammal species.

Disease severity showed relatively limited variation among the invasive mammals assessed. Mean BSL values across the pathogens potentially transmitted by each mammal ranged from 1.86 for *Myocastor coypus* to 3.00 for *Tamias sibiricus*, with most species showing mean values between BSL-2 and BSL-3.

The complete list of zoonotic pathogens associated with each invasive mammal species, together with the pathogen-specific prevalence and BSL values, is provided in Supplementary Table S1. Mean prevalence and mean BSL, together with their corresponding standard deviations, were subsequently calculated for each invasive mammal and are presented in Supplementary Table S4.

Potential geographic distribution of selected invasive mammals

Species distribution models showed marked differences in the current potential geographic distribution of the selected invasive mammals across Europe (Figure 2). These maps were used to calculate the geographic distribution parameter included in the risk assessment framework. Species with broader suitable areas, such as *Myocastor coypus*, *Nyctereutes procyonoides*, and *Ondatra zibethicus*, showed extensive potential distributions across Europe, whereas *Nasua nasua* and *Herpestes javanicus* showed more restricted suitable areas.

Potential human exposure also varied considerably among species. Species with broader suitable areas, particularly *Nyctereutes procyonoides*, *Ondatra zibethicus*, and *Myocastor coypus*, overlapped with a larger proportion of the European population. In contrast, *Nasua nasua* and *Herpestes javanicus* showed lower human exposure, consistent with their more restricted suitable distributions.

Applying the human risk assessment framework

Because each of the four parameters was scored from 1 to 5, total human health impact scores could range from 4 to 20. Final scores were assigned to five impact categories: Minimal (4–6), Minor (7–9), Moderate (10–12), Major (13–16), and Massive (17–20). Based on this classification, six of the eight invasive mammal species were classified as having Major potential impact on human health: *Myocastor coypus*, *Nyctereutes procyonoides*, *Ondatra zibethicus*, *Procyon lotor*, *Sciurus carolinensis*, and *Tamias sibiricus*. *Nasua nasua* was classified as Moderate, whereas *Herpestes javanicus* was classified as Minor. No species were assigned to the Minimal or Massive categories. The highest scores were obtained for *Nyctereutes procyonoides* and *Ondatra zibethicus* (16/20), followed by *Myocastor coypus* (15/20), reflecting the combined contribution of pathogen prevalence, disease severity, geographic distribution, and human exposure (Table 2).

Table 2. Human health risk classification of invasive mammal species. The raw values calculated for each parameter are provided. For disease severity and pathogen prevalence, values are shown as mean $\pm$ standard deviation. Values in parentheses indicate the ordinal impact score assigned to each parameter according to the semi-quantitative framework, ranging from 1, minimal impact, to 5, massive impact. Cell colours represent the ordinal impact score, from low impact in green to higher impact in red. The final impact score was calculated as the sum of the four parameter scores, with possible values ranging from 4 to 20.

Comparison with biodiversity impact scores

Table 3. Standardized comparison of human health, biodiversity, and GISS impact scores for the invasive mammal species assessed. Cell colours indicate the standardized score category: green for values from 0 to <25, yellow for values from 25 to <50, orange for values from 50 to <75, and red for values from 75 to 100. Interval limits were assigned to the upper category, so values equal to 25, 50, and 75 were classified as yellow, orange, and red, respectively.

After standardization to a common 0–100 scale, the comparison among impact assessment systems showed several agreements and discrepancies. *Sciurus carolinensis*, *Ondatra zibethicus* and *Myocastor coypus* showed consistently high standardized scores across the different assessments. Table 3 presents only the rescaled values, while the original scores together with their corresponding rescaled values are provided in Supplementary Table S5.

However, some mismatches became clearer after standardization. *Herpestes javanicus* had the maximum standardized EU biodiversity score but a low standardized human health score and no GISS human health impact. Similarly, *Nyctereutes procyonoides* had one of the highest standardized human health scores in our framework and the maximum EU biodiversity score, but a GISS human health score of zero. *Procyon lotor* also showed a relatively high standardized human health score despite having no GISS human health score.

Table 4. Kendall’s rank correlations between the human health impact score developed in this study and existing impact assessment scores.

Kendall's rank correlation analysis indicated only partial agreement between our human health impact score and existing impact assessment systems (Table 4). The strongest association was found with the GISS overall score ($\tau = 0.583$, $p = 0.063$), suggesting a moderate positive relationship between general invasion impact and the human health score proposed here. In contrast, weaker correlations were observed with the EU biodiversity impact score ($\tau = 0.369$, $p = 0.282$) and the GISS human health score ($\tau = 0.333$, $p = 0.288$).

Comparison with public health preparedness

Countries were classified into four exposure–preparedness scenarios using the mean values of SPAR score and human potential exposure across all countries (mean SPAR = 74.03; mean human exposure = 64.43%). The SPAR scores and human exposure values for each country are provided in Supplementary Table S6. The same classification was repeated using median thresholds and is presented in the Supplementary Information (median SPAR = 76.00; median human exposure = 66.93%, Figure S1).

The mean and median-based classifications produced very similar results, with only three countries changing quadrant between the two approaches: Bulgaria, Italy, and Serbia. These changes occurred because these countries had SPAR scores or human exposure values close to the threshold values, indicating that the classification was not strongly affected by the choice of mean or median thresholds.

Substantial variation was observed among European countries in both public health preparedness and estimated human exposure to invasive mammals (Figure 3). SPAR scores ranged from 29 to 95, whereas mean human potential exposure varied from approximately 25% to more than 90% of the population.

Several countries, including Denmark, the Netherlands, France, Switzerland and UK, combined high levels of human potential exposure with high preparedness scores, therefore having a great capacity to detect and respond to zoonotic threats associated with invasive mammals. In contrast, countries such as Bosnia and Herzegovina, Slovakia, Montenegro and San Marino exhibited high exposure but low preparedness scores, indicating greater vulnerability to zoonotic disease emergence.

Countries including Norway, Sweden, Finland, Lithuania and Portugal showed high preparedness levels despite lower human exposure. Conversely, Greece, Malta, Moldova and Estonia showed both low exposure and lower preparedness levels.

These results reveal substantial variation among European countries and show that higher levels of human exposure to invasive mammals are not always matched by higher levels of public health preparedness.

Public health preparedness did not differ significantly between countries classified as having high and low potential human exposure to invasive mammals (two-sided Wilcoxon rank-sum test, $W = 172.5$, $p = 0.652$). Median SPAR scores were 73.5 and 77.0 for the low- and high-exposure groups, respectively.

Discussion

This study presents a semi-quantitative framework to assess the potential human health impact of IAS and demonstrates its application using eight invasive mammal species of concern in Europe: *Nyctereutes procyonoides*, *Ondatra zibethicus*, *Myocastor coypus*, *Procyon lotor*, *Sciurus carolinensis*, *Tamias sibiricus*, *Nasua nasua*, *Herpestes javanicus*. By integrating pathogen prevalence, disease severity, geographic distribution, and human exposure, the framework provides a standardized approach for comparing zoonotic risk across species. This builds on previous descriptive work that compiled epidemiological and spatial information for invasive mammals in Europe (Monguilod & Gallardo, 2026) but goes further by converting these data into comparable human health impact scores. In doing so, the framework provides a practical tool to support the prioritization of invasive mammals from a public health perspective.

Applying the human risk assessment framework

The application of the framework showed that most assessed invasive mammals were classified as having Major potential impact on human health. The highest scores were obtained for *Nyctereutes procyonoides* and *Ondatra zibethicus*, followed by *Myocastor coypus*, while *Procyon lotor*, *Sciurus carolinensis*, and *Tamias sibiricus* also received relatively high scores. The high scores of this group are largely explained by the combination of broad suitable areas, high potential exposure of human populations, and the presence of zoonotic pathogens of public health relevance. Across these species, previous studies have documented multiple zoonotic or potentially zoonotic pathogens, including *Toxoplasma gondii*, *Echinococcus multilocularis*, *Giardia*, *Cryptosporidium*, *Clostridium*, and *Leptospira*, with some pathogens reaching high prevalence in the populations examined (Duscher et al., 2017; Ganoe et al., 2020, 2021; Kjær et al., 2021; Martino et al., 2014; Nardoni et al., 2011; Umhang et al., 2013). Other mammals classified as having a Major potential impact have also been reported to host pathogens of potential public health relevance. *Procyon lotor* has been associated with *Giardia duodenalis*, *Cryptosporidium*, *Leptospira*, and *Borrelia* spp. (Duncan et al., 2012; Inoue et al., 2011; Leśnińska et al., 2016; Solarczyk et al., 2021), while *S. carolinensis* has been reported to host *Bartonella* spp. and *Borrelia burgdorferi* sensu lato (Bown et al., 2002; Millins et al., 2015). *Nasua nasua* showed one of the highest mean prevalences of zoonotic pathogens, consistent with previous reports of highly prevalent filarial nematodes and multiple vector-borne agents (Moraes et al., 2017; Perles et al., 2023). Nevertheless, its overall human health impact was classified as Moderate because its predicted geographic distribution and potential human exposure in Europe were comparatively limited.

Pathogen prevalence and disease severity variables contributed to differences among mammals. Although disease severity showed comparatively limited variation across mammals, most were associated with pathogens requiring BSL-2 or BSL-3 containment. This highlights their potential relevance for human health and reinforces the importance of including invasive mammals in zoonotic surveillance and early detection strategies. Overall, these findings are consistent with previous work showing that zoonotic risk depends not only on pathogen presence, but also on ecological context, host distribution, and opportunities for contact between wildlife and humans (Allen et al., 2017; Jones et al., 2008; Keesing et al., 2010). Previous evidence indicates that infection rates in wildlife can vary with host

density, although the form of this relationship differs among host–pathogen systems (Smith et al., 2009). Host density and stress were not explicitly incorporated into the present framework but could represent a relevant additional parameter in future refinements.

Geographic distribution and human exposure are especially relevant for IAS, as biological invasions are closely linked to human-mediated transport, habitat disturbance, and anthropogenic environments (Gallardo et al., 2015). Invasive mammals that occupy broad areas of Europe and overlap with densely populated regions may create more opportunities for direct or indirect contact with humans. This is consistent with previous studies showing that IAS can influence zoonotic pathogen dynamics by acting as reservoirs, amplifiers, or facilitators of pathogen transmission, particularly in human-modified areas (Roy et al., 2023; Vilà et al., 2021). Therefore, incorporating human exposure to the invasive mammals allows the framework to capture the spatial context in which potential human exposure may occur.

At the same time, species with more restricted potential distributions should not be considered irrelevant from a public health perspective. *Herpestes javanicus* and *N. nasua* obtained the lowest scores in the framework, mainly because their potential geographic distribution was more restricted and overlapped with a smaller proportion of the European human population. However, this does not exclude the possibility of localized risk in areas where suitable habitat, pathogen presence, and human populations overlap. Therefore, the framework should be interpreted as a tool for broad-scale prioritization, rather than as an indication that lower-scoring species cannot generate local public health concerns.

Comparison with biodiversity impact scores

The comparison with existing IAS impact assessments showed only partial agreement between the proposed human health framework and biodiversity or general impact scores. Some species, particularly *O. zibethicus*, *M. coypus*, and *S. carolinensis*, scored highly across different assessment systems, suggesting that certain invasive mammals represent priorities from both biodiversity and public health perspectives. However, several discrepancies were observed. *H. javanicus* had a high biodiversity impact score in the EU Union List Risk Assessment but received the lowest human health impact score in our framework and low GISS scores. In addition, *N. procyonoides* and *P. lotor* obtained high scores in both the EU biodiversity assessment and our human health framework, despite having a GISS human health score of zero. GISS scores human health impacts based on published evidence of effects such as disease transmission, pathogen contamination, injuries, and associated health costs (Nentwig et al., 2016). Importantly, a score of zero may indicate that no data were available, no impacts were known or detectable, or the category was not applicable. Therefore, a zero GISS score does not necessarily demonstrate an absence of zoonotic potential. Consequently, differences may reflect the fact that our framework evaluates potential zoonotic concern by combining pathogen prevalence, disease severity, geographic distribution, and potential human exposure, whereas GISS focuses on documented impacts (Nentwig et al., 2016, 2018). These differences were also reflected in the Kendall correlation analysis. The strongest association was observed between our human health impact score and the GISS overall score, although the relationship was only moderate and not statistically significant. Weaker correlations were found with the EU biodiversity impact score and the GISS human health score. Together, these

results suggest that existing impact scores provide useful but incomplete information on the zoonotic risks posed by invasive mammals. This is particularly relevant because most IAS risk assessment tools have traditionally focused more on ecological and economic impacts than on human health (González-Moreno et al., 2019), reinforcing the need to assess human health impacts explicitly rather than assuming that biodiversity-based assessments fully capture public health concerns. By integrating pathogen prevalence, disease severity, geographic distribution, and human exposure, the proposed framework provides a more targeted approach for identifying invasive mammals of potential zoonotic concern.

Comparison with public health preparedness

The exposure–preparedness analysis provides an additional perspective by comparing potential human exposure with national public health preparedness. Several countries, including Denmark, the Netherlands, France, Switzerland, and the United Kingdom, combined high exposure with high SPAR scores, suggesting that potential exposure to invasive mammals is accompanied by relatively strong public health preparedness capacity. However, other countries, including Bosnia and Herzegovina, Slovakia, Montenegro, and San Marino, showed high exposure but lower preparedness scores. These countries may therefore represent priority areas for monitoring, as relatively high potential exposure to invasive mammals coincides with lower public health preparedness. Importantly, the overall classification remained similar when using either mean or median thresholds, with only Bulgaria, Italy, and Serbia changing quadrant between the two approaches.

These findings highlight the importance of integrating biological invasion data into public health planning. Our results suggest that countries potentially more exposed to zoonotic risks associated with invasive mammals are not always the most prepared to respond to them. Incorporating information on IAS distributions, pathogen prevalence, and human exposure into preparedness planning could help identify areas where targeted surveillance or early detection may be particularly valuable to support biosecurity strategies. This connection between biological invasions and disease risk is not limited to mammals. For example, recent work on invasive mosquitoes showed that the introduction and establishment of non-native mosquito vectors can increase the risk of mosquito-borne diseases in areas where these diseases were previously absent or less common (Pabst et al., 2026). This is especially relevant under a One Health–One Biosecurity approach, which emphasizes the interconnection between biodiversity conservation, ecosystem change, animal health, and human health in the mitigation of health risks associated with biological invasions (Hulme, 2021).

Methodological considerations and limitations

While the framework offers a standardized approach to risk prioritization, several limitations should be acknowledged. First, equal weighting was assigned to all four parameters to avoid introducing subjective prioritization among criteria. However, alternative weighting schemes could produce different classifications. Second, the framework depends on the availability and quality of prevalence and distribution data. Pathogen prevalence estimates are based on reported studies and may vary across

regions, sampling methods, host populations, and diagnostic approaches. This is a common limitation in wildlife disease monitoring, where uneven sampling and differences in surveillance methods can affect pathogen detection and prevalence estimates (Barroso et al., 2024). As a result, prevalence values may underestimate true infection levels in wildlife populations, especially for poorly monitored species or pathogens. Similarly, geographic distribution and human exposure values rely on species distribution models, which estimate potential suitability rather than confirmed presence in every suitable area. Human exposure was estimated as the proportion of the European population living within areas suitable for each IAS. This provides a useful broad-scale indicator of potential contact between humans and invasive mammals, but it does not represent confirmed contact or actual transmission events (Monguilod & Gallardo, 2026). Therefore, the framework should be interpreted as a prioritization tool rather than as a direct estimate of spillover probability.

Despite these limitations, the framework integrates open access ecological, epidemiological, and biogeographic information and can be applied to a broad range of invasive organisms and geographic contexts. It can also be expanded to incorporate additional factors relevant to zoonotic spillover, such as host population density, as more detailed data become available. Its spatial component further allows future applications to explore how potential human health impacts may change under climate change scenarios or shifts in human population distribution.

Conclusions

This study presents a semi-quantitative framework for assessing zoonotic risks posed by IAS and demonstrates its application using invasive mammals of concern in Europe. By integrating pathogen prevalence, disease severity, spatial distribution, and human exposure, the framework allows IAS to be compared and prioritized according to their potential impact on human health.

The results show that several invasive mammals already recognized as priorities for biodiversity management may also pose relevant risks from a public health perspective. Incorporating zoonotic risk into IAS assessment and management can therefore support more preventive and integrated biosecurity strategies under a One Health framework.

Declarations

Funding

This study has received funding from the Spanish National Research Council (CSIC), through its program JAE-Intro 2022, as part of the training plan JAEINT22_EX_0788.

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Tables

Tables 1 to 4 are available in the supplementary files section

Figures

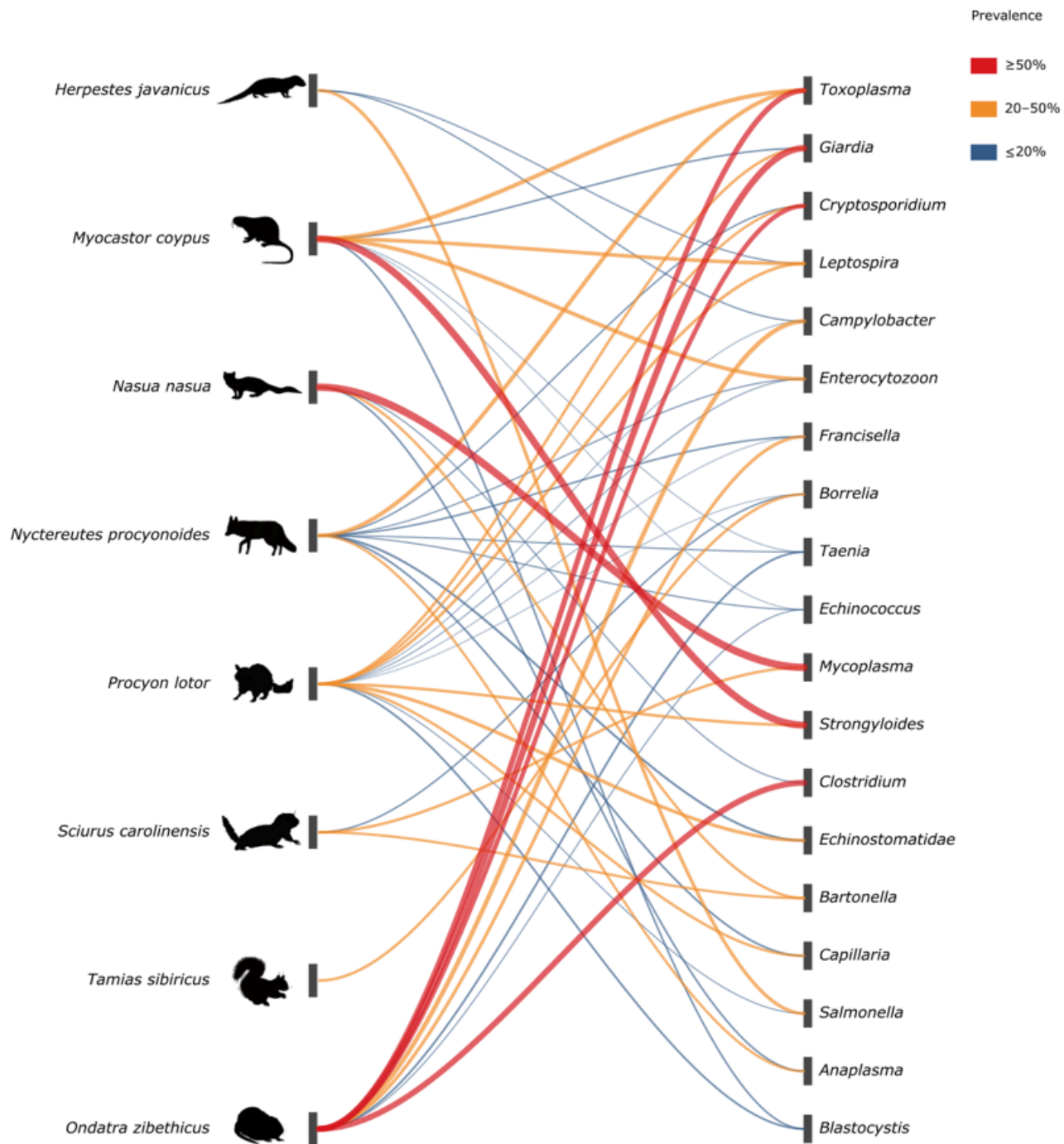


Figure 1

Associations between invasive mammals and zoonotic pathogens reported in two or more of the mammals assessed. The complete list of mammal–pathogen associations is provided in Supplementary Table S1. Line colour indicates prevalence categories: blue, $\leq 20\%$; orange, 20–50%; and red, $\geq 50\%$, while line width is proportional to prevalence.

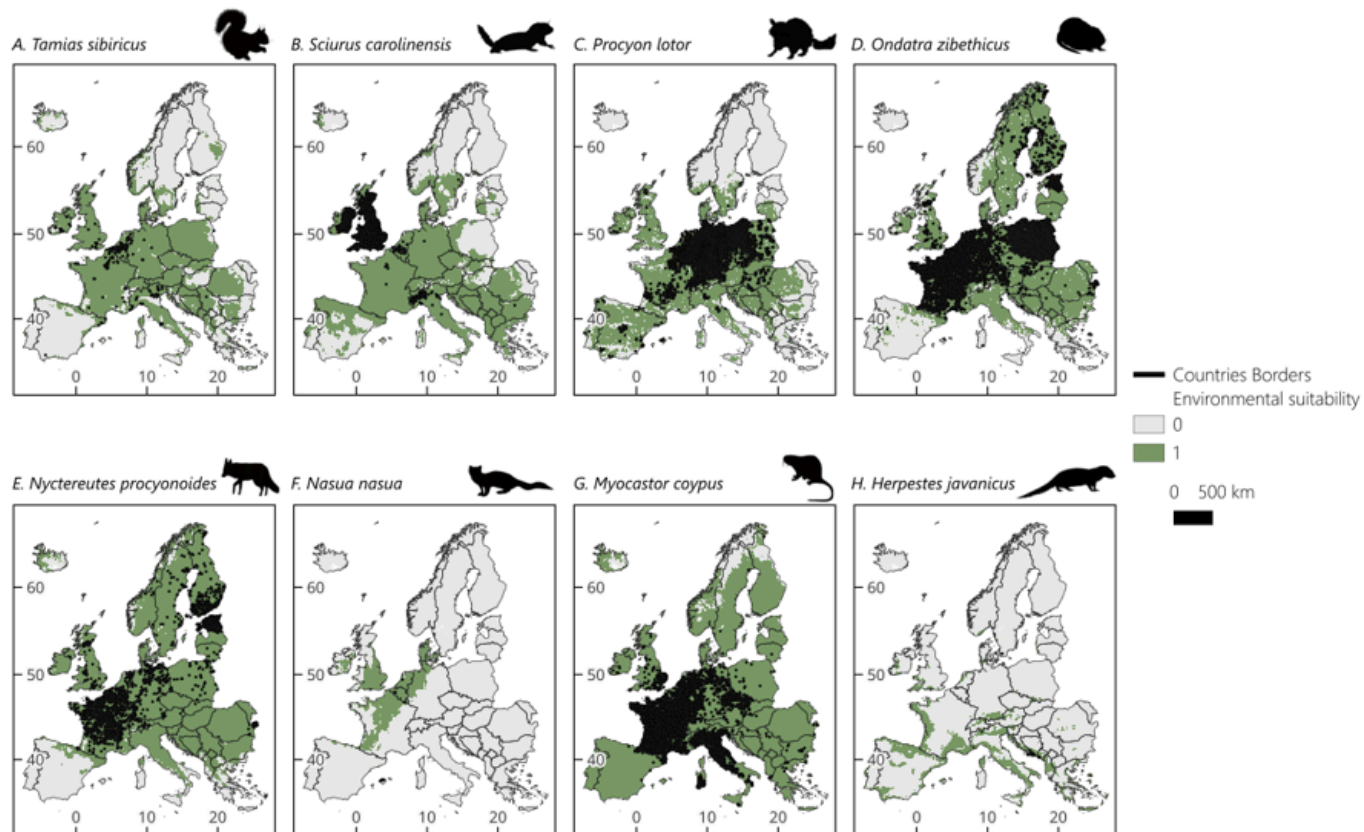


Figure 2

Binary species distribution maps for the invasive mammal species included in the risk assessment (adapted from Monguilod & Gallardo, 2026). Green areas indicate environmentally suitable regions, whereas light grey areas indicate unsuitable regions. Black points represent real occurrence records used to build the models.

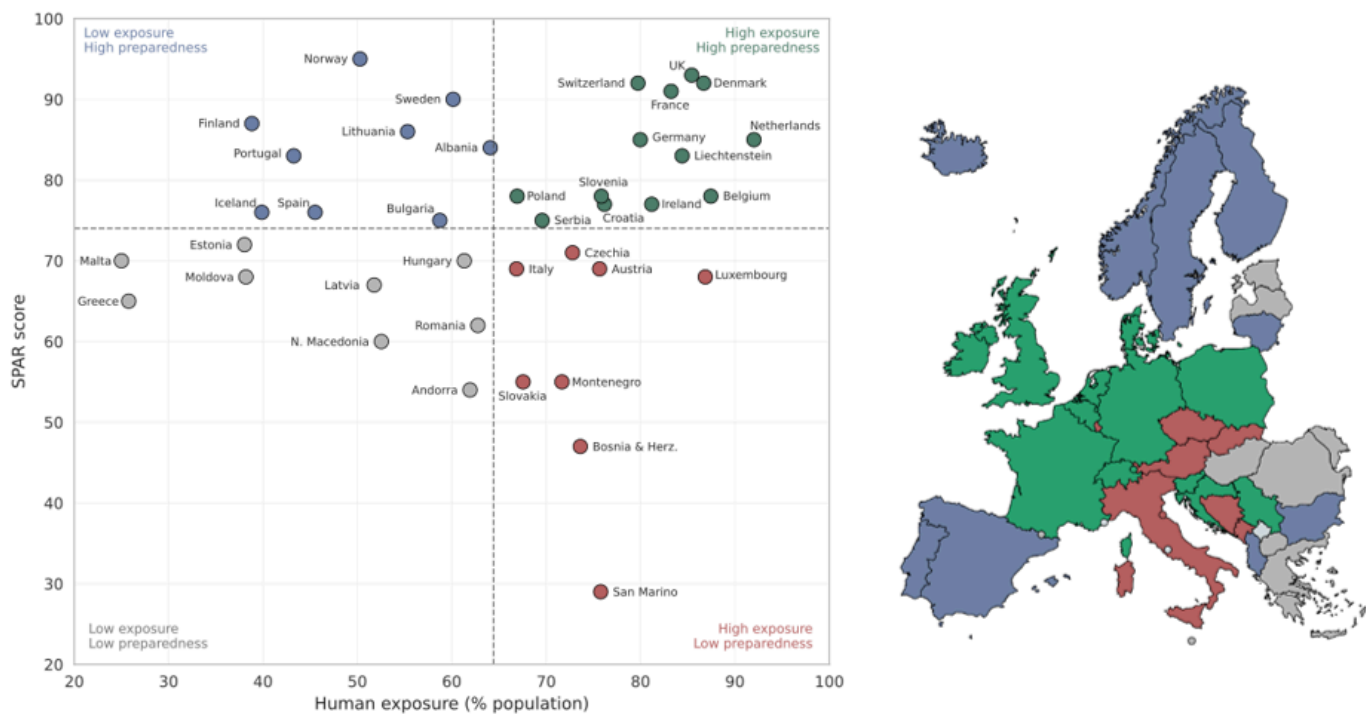


Figure 3

Relationship between human exposure to invasive mammals and public health preparedness across European countries. A) Relationship between mean human exposure and public health preparedness. Dashed lines show the mean thresholds used to define the four exposure–preparedness scenarios. B) Map showing the same classification across Europe. Countries not included in the analysis are shown in light grey.

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