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Modelling regional impact risk combining land-use-informed habitat suitability and potential impact assessment: Case study of *Sorghum halepense* in Switzerland

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ABSTRACT

Effective management of emerging invasive alien species requires spatially explicit tools that translate standardized impact assessments into regionally relevant information for guiding surveillance and proactive management measures. To address this need, we introduce a land-use-informed regional impact risk classification (RIRC) framework that integrates two distinct components: (1) a hierarchical species distribution model (SDM) – comprising a global climatic model and a nested regional model that incorporates high-resolution land use/land cover (LU/LC) data to refine local habitat suitability - and (2) a LU/LC-based (S)EICAT impact assessment. By combining these components, the RIRC framework generates spatially explicit estimates of impact risk that disentangle potential impacts into distinct ecological and socio-economic mechanisms, mapped at a fine regional scale according to the LU/LC types where each mechanism is most likely to occur. This approach differentiates areas of likely establishment according to both the nature and magnitude of the expected impacts.

We illustrate this framework using *Sorghum halepense* (Johnsongrass), a rhizomatous weed of global concern expanding in Central Europe, with Switzerland serving as a regional case study. Our results show that while suitable habitats are primarily concentrated in lowland regions – including the Swiss Plateau, the Lake Geneva basin, and central and southern valley bottoms in Valais and Ticino - the potential impact risk is not uniformly distributed across these projected suitable areas. Instead, risk is concentrated in lowland agro-urban mosaics where multiple impact mechanisms co-occur. Based on the land-use-informed RIRC, main impacts are expected on pastures (toxicity to livestock), arable land (competition with crops, disease transmission), urban green spaces (allergenic effects on human health and management costs), transportation areas (management costs), and natural environments (competition with and chemical inhibition of native flora, ecosystem structural changes in meadows).

Ultimately, the land-use-informed RIRC framework offers a transparent, transferable, and scalable workflow. By combining modelled habitat suitability with the potential impacts associated with different land uses in a precautionary and conservative way, the framework identifies high-risk areas that should be prioritized for surveillance and the early detection of new and emerging problematic invasive species.

1. Introduction

Biological invasions are among the most economically damaging natural threats worldwide, causing economic losses and management expenditures comparable in magnitude to those of natural hazards (Diagne et al., 2020, 2021; Glaser et al., 2024; Turbelin et al., 2023). In recent decades, the rate of alien species introductions into new regions has markedly increased due to growing global interconnectedness (Seebens et al., 2017). This trend underscores the need for prospective assessments of the potential impact of species' invasion to proactively guide management strategies and mitigate ecological and socio-economic consequences (Bradshaw et al., 2016). Such predictions are

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crucial not only for addressing recently introduced species but also for anticipating those likely to arrive in the future (Díaz Cando et al., 2025; Robertson et al., 2020).

Existing impact assessment frameworks, including the Environmental Impact Classification for Alien Taxa (EICAT) and the Socio-economic Impact Classification for Alien Taxa (SEICAT), provide systematic approaches for evaluating the environmental and socio-economic threats posed by invasive alien species (Bacher et al., 2018; Blackburn et al., 2014). These frameworks enable global comparisons, facilitate the identification of high-risk taxa, and ensure that assessments and management decisions are consistent and comparable across regions (IUCN, 2020). While these impact assessment frameworks are scale-independent and can potentially be applied at global, national or regional levels, their reliability largely depends on the availability of published evidence quantifying impacts. Such documentation is often limited or entirely lacking in many regions (Canavan et al., 2025; Probert et al., 2020; Vimercati et al., 2022). Consequently, global impact assessments can often be conducted using these standardized frameworks; however, effective management depends on a thorough understanding of regional contexts. As a result, the development and application of regional-scale impact assessments continue to represent a major challenge.

Species Distribution Models (SDMs) are a powerful tool that can be used to estimate the likelihood of a species becoming established and its potential for spreading, based on occurrence data and environmental variables (Elith, 2017; Elith and Leathwick, 2009; Guisan et al., 2013). By capturing and quantifying complex species-environment relationships, SDMs can produce spatially explicit estimates of habitat suitability, allowing inferences about regions where alien invasive species may establish and potentially exert negative ecological or socio-economic impacts.

To address the need for regional-scale impact assessments to inform local decision-making, the capabilities of SDMs and (S)EICAT can be integrated to predict the potential impacts of invasive alien species. To operationalize this concept, we build upon the recently developed Regional Impact Risk Classification (RIRC) framework proposed by Oveisi et al. (2026). RIRC integrates climate suitability derived from SDMs with standardized global impact scores to generate spatially explicit predictions of impact risk. However, because habitat suitability is strongly shaped by land use and land cover (LU/LC), we refined the climatic SDM by incorporating high-resolution regional LU/LC data and developed a LU/LC-based EICAT/SEICAT impact assessment. Together, these refinements allow the RIRC framework to generate impact predictions that are tailored to individual regions, capturing local environmental conditions and land use patterns to better inform surveillance and management strategies. Such an approach is particularly valuable for emerging invasive species or species expanding into new regions, for which local impacts are often poorly documented despite substantial evidence from other parts of their invaded range, and proactive risk assessment is needed to support early detection and management.

In the present study, we selected *Sorghum halepense* (L.) Pers. as a case study to illustrate the framework. This highly invasive, perennial C_4 grass is considered one of the world's most persistent rhizomatous weeds in crops and grasslands (Warwick and Black, 1983; Fanfarillo et al., 2022; Peerzada et al., 2023, review). Native to the Mediterranean region, Western Asia, and North Africa, *S. halepense* has been introduced outside its native range, where it readily invades anthropogenic and agricultural habitats (Holm et al., 1977; Warwick and Black, 1983; Follak and Essl, 2013; Follak et al., 2017). It reduces biodiversity and crop yields, particularly for maize and soybeans (Andújar et al., 2012, 2013; Barroso et al., 2016; Follak and Essl, 2013; Güneş et al., 2008; Nikolić et al., 2021). In Central Europe, *S. halepense* is expanding rapidly, particularly in Italy, Austria and southern Switzerland, where it has become established primarily in Canton Ticino (FOEN, Federal Office for the Environment, 2022; Follak and Essl, 2013; Gentilini et al., 2021, 2026). Its northward spread from the Po Valley, compounded by projected climate warming, is expected to further increase habitat suitability and facilitate its establishment across Switzerland and neighbouring regions (Fanfarillo et al., 2022; Follak and Essl, 2013; Kleinbauer et al., 2010; Yang et al., 2023). In Switzerland, the Federal Office for the Environment has officially listed the species among the potentially invasive taxa of Switzerland, acknowledging its invasive potential (FOEN, Federal Office for the Environment, 2022). So far there are only qualitative evaluations and no quantitative empirical data on its ecological and socio-economic impacts within the national context (Gentilini et al., 2021, 2026). We applied the refined, land-use-informed RIRC framework to *S. halepense* to generate spatially explicit predictions of the relevant invasion mechanisms and identify high-risk areas for early detection and targeted management. More broadly, this framework provides a transferable tool for predicting regional-scale, mechanism-specific impacts for any invasive alien species.

2. Methods

2.1. Framework

The enhanced framework and corresponding analysis workflow we propose is illustrated in Fig. 1 and consists of the following steps: 1a) *Habitat Suitability Modelling*: calibration of a spatially-nested hierarchical SDM that incorporates global-scale climate information and high-resolution regional land use information to (1b) produce spatial projections of habitat suitability in the target region; 2a) *Potential Impact Assessment*: expert-based assessment involving the identification of key impact mechanisms and the evaluation of the magnitude of their potential impacts; (2b) the assessment is performed according to standard EICAT/SEICAT frameworks and is contextualized by land use type, enabling a differentiated spatial mapping of the different potential impacts across the region; 3) *land-use-informed RIRC*: integration of Habitat Suitability and land-use-specific Impact Potential to produce a map, that spatially predicts the mechanism and class of impact risk. The analysis has been performed with R and a script with the R code is archived at Zenodo and accessible via https://doi.org/10.5281/zenodo.23235356.

2.2. Hierarchical habitat suitability modelling

2.2.1. Global climate suitability model

Global occurrence records of *Sorghum halepense* were downloaded from the Global Biodiversity Information Facility (GBIF; https://gbif.org) on 25 July 2026 (https://doi.org/10.15468/dl.sky3a2) and subsequently consolidated into a single geodatabase for analysis. The downloaded dataset initially contained 69,089 records. Records were retained for further analysis only if they were collected from 1950 onward, had a coordinate uncertainty $\leq$1000 m (in agreement with the resolution of the climatic data used for the modelling), fell within valid WGS84 coordinate bounds (longitude −180 to 180, latitude −90 to 90°), did not contain null coordinates or correspond to country/province centroids, and were not duplicate coordinate pairs. Sequential record filtering reduced the dataset from 69,089 records to 57,234 after applying the temporal filter, to 55,801 after validating coordinates, to 52,419 after removing records with coordinate uncertainty greater than 1000 m, and finally to 51,673 after removing duplicate coordinates pairs.

To reduce spatial autocorrelation, the records were spatially thinned to one occurrence point per 1-km (30-arcsec) grid cell, matching the resolution of the bioclimatic variables used for the modelling. This spatial thinning procedure resulted in 29,150 global presence records that were retained for further analysis.

Background sample definition – both in terms of size and spatial distribution - critically determines fitted response shapes (Merow et al., 2013). Restricting background selection to the accessible area and weighting sampling probability by estimated survey bias improves model robustness when using opportunistic occurrence data (Fourcade

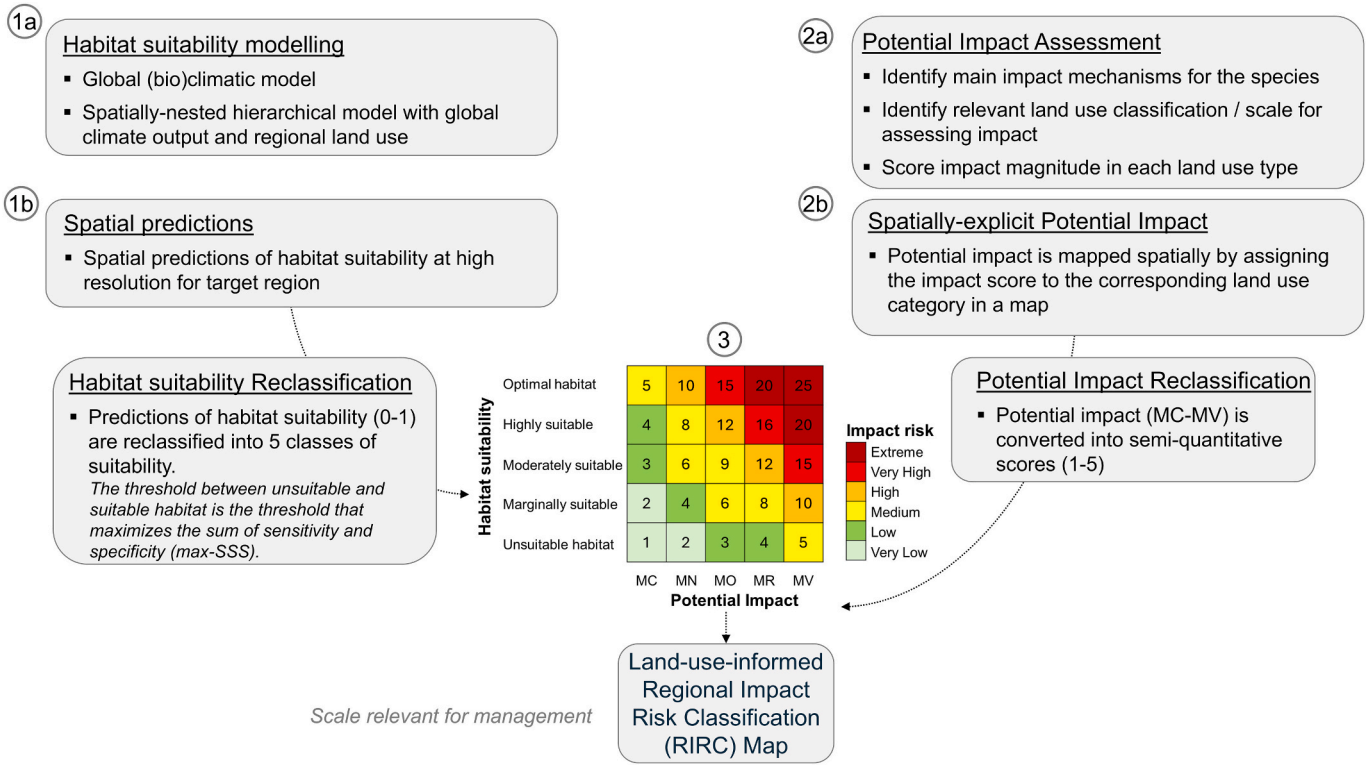


Fig. 1. Schematic illustration of the analysis workflow for spatially predicting the risk of potential impact from invasive alien species and producing a land-use-informed Regional Impact Risk Classification.

et al., 2014; Kramer-Schadt et al., 2013; Phillips et al., 2009). The accessible area (M sensu Barve et al., 2011) was delineated by buffering each spatially thinned occurrence record by 100 km, dissolving overlapping buffers, and rasterizing the result within the extent of valid environmental coverage. According to the BAM framework (Biotic, Abiotic, and Movement factors that determine geographic distributions; Barve et al., 2011; Soberón and Peterson, 2005), this constrains calibration to areas plausibly reachable by dispersal over relevant biological and biogeographic timescales, thereby avoiding unrealistically large background and improving inferential relevance. Also, because performance metrics like AUC improve as the modelling extent expands beyond a species' occupied range (Anderson and Raza, 2010; Lobo et al., 2008), the modelling extent was empirically selected rather than assumed and buffers of different radii were tested. Following VanDerWal et al. (2009), background/pseudo-absence data were drawn from buffers of increasing radii (50, 100, 200, 500, and 1000 km) around thinned occurrence records. The number of occurrences and background points remained constant across radii. Models calibrated with these candidate radii were all evaluated on a single, fixed, spatially blocked test dataset to ensure AUC values were comparable across extents (Lobo et al., 2008). The 100-km buffer yielded the best model performance and was adopted as the hypothesized accessible area for the species (M). Buffers of this type are widely used to constrain background sampling and limit overfitting in plant and animal SDMs (Chowdhury et al., 2025; de Lima et al., 2025; Diengdoh, 2025; Méndez et al., 2024).

To account for spatial heterogeneity in sampling effort, a bias surface was generated from the spatially thinned occurrences using Gaussian kernel density estimation (*spatstat::density.ppp*) with a 200-km smoothing distance normalized within the extent of the accessible area M. The smoothing bandwidth was set to 200 km following a sensitivity analysis across 50–400 km, which indicated that model predictions were insensitive to bandwidth within this range; smaller bandwidths reproduce the occurrence pattern itself and provide no effective bias correction. Background points were sampled without replacement from cells within M (excluding occupied presence cells), and with selection probabilities proportional to the bias surface. The target number of background points was set equal to the number of environmentally thinned presence records, resulting in 29,150 background (pseudo-absence) points.

Climatic predictors used for the modelling were obtained from CHELSA v2.1 database (www.chelsa-climate.org), which provides high-resolution climatological data for the terrestrial environments worldwide that were produced using the statistical downscaling framework described by Karger et al. (2017). The dataset includes monthly-aggregated temperature- and precipitation-related variables for the 1981–2010 reference period at a spatial resolution of approximately 1 km (30 arcsec). To reduce multicollinearity among the 19 initial candidate bioclim predictors (CHELSA-bioclim), pairwise Spearman rank correlations were calculated and one variable was excluded from each highly correlated pair ($|\rho| \geq 0.80$). The remaining variables were subsequently screened using variance inflation factors (VIF), and predictors were iteratively removed until all retained predictors exhibited VIF values ≤ 10.

Nine variables were finally retained for the modelling representing thermal limits and variability, overall water availability, and seasonal moisture constraints: maximum temperature of the warmest month (BIO5), minimum temperature of the coldest month (BIO6), isothermality (BIO3), temperature seasonality (BIO4), annual precipitation (BIO12), precipitation of the driest month (BIO14), precipitation seasonality (BIO15), precipitation of the driest quarter (BIO17), and precipitation of the warmest quarter (BIO18).

Random Forest models (Breiman, 2001) were fitted in probabilistic mode using the ranger implementation (Wright and Ziegler, 2017) with 1000 trees. This algorithm was chosen for its ability to accommodate non-linear responses and interactions among predictors while maintaining strong predictive performance in ecological classification problems (Cutler et al., 2007). Hyperparameters were optimized through a grid search across alternative values for the number of variables

randomly sampled at each split of the tree (*mtry* = 2, 3, 4, 5, and 6), the smallest number of data points allowed in a terminal node (*min.node.size* = 1, 3, 5, and 10), and the fraction of training observations randomly sampled to build each individual decision tree (*sample.fraction* = 0.50, 0.632, and 0.80). Permutation-based variable importance was also calculated (Wright and Ziegler, 2017).

Model performance was assessed using geographically structured cross-validation based on spatial blocking. This approach mitigates inflated performance estimates caused by spatial autocorrelation in training and test data (Roberts et al., 2017; Valavi et al., 2019). Presence and background observations were therefore partitioned into spatially distinct folds. Block sizes of 75, 100, and 125 km were tested, and the optimal configuration was subsequently used in a five-fold cross-validation procedure.

Predictive performance was evaluated from pooled out-of-fold predictions using the area under the receiver operating characteristic curve (AUC), the true skill statistic (TSS), sensitivity, and specificity. Climate suitability was classified using the threshold that maximized the sum of sensitivity and specificity (max-SSS), a criterion shown to perform reliably for presence-only and presence–background models (Allouche et al., 2006; Liu et al., 2005). The final model was refit on the full global dataset to generate global climatic-suitability predictions and variable-importance estimates.

2.2.2. Nested regional land-use-refined suitability model

To refine habitat-suitability predictions within Switzerland, we implemented a spatially nested species distribution model incorporating the global climatic-suitability predictions as a covariate alongside regional land use/land cover (LU/LC) information at a resolution of 25 m. LU/LC data originate from the Swiss Land Use Statistics, which follow the NOAS04 standard nomenclature and categorize land into 72 base categories from aerial imagery interpreted on a 100 m grid (FSO (Federal Statistical Office), 2018). These categories are typically aggregated into four main domains (urban, forested, agricultural and unproductive areas) with either 17 (AS17) or 27 (AS27) thematic classes. For this study, we developed a hybrid land use/land cover classification that retained coarse AS17 classification for main LU/LC types (e.g., industrial, built-up and transportation areas, green spaces, forests, lakes, glaciers) while using detailed AS27 classification to differentiate agricultural areas (e.g., vineyards, orchards, arable land, farm and alpine pastures). This resulted in a total of 22 LU/LC categories for analysis: 'industrial areas', 'built-up areas', 'transportation areas', 'special urban areas', 'green spaces and recreational areas', 'forests' (except brush forests), 'brush forests', 'other wood surfaces', 'lakes', 'rivers and river shores', 'unproductive vegetation', 'bare land', 'glaciers and snowfields', 'orchards', 'vineyards', 'horticulture', 'arable land', 'natural meadows', 'farm pastures', 'mountain meadows', 'alpine pastures', and 'built-up agricultural area' (that were treated separately from the other built-up areas). All categories were mapped at a 25-m spatial resolution using the downscaled LU/LC map for Switzerland developed by Giuliani et al. (2022). For modelling, the land use classes were encoded as one-hot dummy variables, with one category omitted as it can be inferred from the others to avoid redundancy. The final regional predictor set therefore comprised one continuous climatic-suitability variable (1-km global model predictions were resampled at 25 m resolution using bilinear interpolation) and 21 binary land use dummy variables.

The original set of occurrence records were restricted inside Switzerland (country boundary obtained from geoBoundaries, Runfola et al., 2020; country: Switzerland, type: ADM0), temporally filtered (1950 onward), screened for valid geographic coordinates and for coordinate uncertainty $\leq$25 m (resolution of land use data used for modelling) and deduplicated, resulting in 1755 presence records for analysis. An equal number of background points were generated from the area where valid global climatic suitability predictions overlapped with complete land use data coverage, excluding a 1000-m buffer around presence points. Alternative radii of 500, 1000, and 2000 m were evaluated for the exclusion buffer in a sensitivity analysis, and 1000 m was finally retained because it yielded the best model performance. All spatial processing and final outputs were standardized to the official Swiss projected coordinate reference system CH1903+ / LV95 (EPSG:2056).

The nested regional model was fitted using the ranger package (Wright and Ziegler, 2017). Model evaluation employed five-fold spatial block cross-validation to reduce estimate inflation caused by spatial autocorrelation (Roberts et al., 2017; Valavi et al., 2019). Candidate block sizes ranging from 1 to 10 km were evaluated during preliminary analyses, and a 5-km block structure was finally retained for the main analysis. Hyperparameter optimization tested *mtry* values of 1–4, *ntree* values of 300, 500 and 1000, and *nodesize* values of 1, 5, 10. Candidate models were ranked according to mean cross-validation AUC, with mean TSS and mean accuracy (total number of correct predictions over total number of evaluated data points in the model) used as a secondary criterion. The optimal hyperparameter combination was then used to train the final regional model on the full national dataset. Model performance was assessed across spatial folds using AUC, accuracy, sensitivity, specificity, and TSS (Allouche et al., 2006). The final calibrated regional model was applied across Switzerland to produce a continuous raster of predicted habitat suitability. For mapping purposes, predictions were reclassified into five ordered suitability classes using *terra::classify*, with the threshold separating unsuitable and suitable habitat defined by the maximum sensitivity plus specificity criterion (max-SSS; Liu et al., 2005).

2.3. Assessment of impact mechanisms and potential magnitude

The potential environmental and socio-economic impacts of *S. halepense* in Switzerland were evaluated using standardized frameworks that classify negative impacts and associated mechanisms (Bacher et al., 2018;Blackburn et al., 2014; IUCN, 2020). This assessment followed a structured methodology consistent with international standards for invasive species risk evaluation, incorporating both ecological and socio-economic dimensions. Impact analysis was conducted across the same 22 LU/LC categories used for the modelling, with a particular focus on agricultural systems given the species' well-documented negative impacts on crop production (Peerzada et al., 2023, review).

Impact classification followed the EICAT (Blackburn et al., 2014; IUCN, 2020) and SEICAT (Bacher et al., 2018) protocols, which provide semi-quantitative scoring systems for evaluating the effects of alien species on ecological aspects (i.e., native biodiversity) and socio-economic aspects (i.e., human well-being), respectively. As both (S)EICAT protocols typically requires country-specific evidence, the procedure was adapted to estimate potential impacts in Switzerland using literature from regions with comparable eco-climatic conditions. This approach enabled a preliminary assessment despite the absence of quantitative local data. Evidence from Switzerland and neighbouring countries (Austria, Italy, France, Germany and Liechtenstein) was considered directly transferable (*** literature from neighbouring countries in Fig. 4). Evidence from more distant regions was considered potentially transferable (* literature from distant countries in Fig. 4) when environmental conditions were similar to those of the study area. Transferability was evaluated based on eco-climatic similarity, primarily using the Köppen-Geiger climate classification (Beck et al., 2018; see also EPPO (European and Mediterranean Plant Protection Organization), 2012), together with documented ecological responses of *S. halepense* in the study region. Information from other regions was therefore considered relevant only when these factors indicated a reasonable degree of environmental comparability with the Swiss context (see 'Transferability' in Supplementary material - Table). Peer-reviewed publications, official reports and authoritative databases were prioritized, while gray literature was used only when issued by recognized scientific institutions or government agencies (Collaboration for Environmental Evidence, 2022; IUCN, 2020).

Ecological impact mechanisms were identified from the standardized list of 12 EICAT mechanisms (Blackburn et al., 2014; IUCN, 2020): 'competition', 'predation', 'hybridization', 'transmission of disease', 'parasitism', 'poisoning/toxicity', 'bio-fouling', 'grazing/herbivory/browsing', 'chemical', 'physical' or 'structural impacts on ecosystems', as well as 'interaction with other species'. For socio-economic impacts, the SEICAT framework (Bacher et al., 2018) considers that alien species can affect different so-called constituents of human well-being, e.g., 'safety', 'material and immaterial assets', 'health', as well as 'social, spiritual and cultural relations'. We identified the following socio-economic mechanisms within these categories to infer impact magnitude in SEICAT assessments: management and control costs, crop and livestock losses, human health effects, infrastructure damage, loss of ecosystem services, restrictions on recreation or tourism, loss of income, market or trade disruptions, and social or cultural impacts. The more severe an impact's effect – whether in terms of management cost, crop loss or consequences on human health – the greater its magnitude and, consequently, the higher the SEICAT score.

The magnitude of impacts described by the studies were scored using EICAT and SEICAT impact categories (Blackburn et al., 2014, and Bacher et al., 2018, respectively): Minimal Concern (MC), Minor (MN), Moderate (MO), Major (MR), Massive (MV), and Data Deficient (DD). EICAT categories reflect impact magnitude at different biological scales, from MN meaning that the alien taxon "causes reduction in individual performance" up to MV meaning that it "causes local or subpopulation extinction of at least one native taxon" that is naturally irreversible (Table 1 in IUCN, 2020). Similarly, SEICAT categories are based on the magnitude of observed changes in people's activities, with MN meaning that there are "negative effect on people's well-being, such that the alien taxon makes it difficult for people to participate in their normal activities. Individual people in an activity suffer in at least one constituent of well-being […]", up to MR meaning "local disappearance of an activity from all or part of the area invaded by the alien taxon. Collapse of the specific social activity, switch to other activities, or abandonment of activity without replacement, or emigration from region." (Table 2 in Bacher et al., 2018). A Data Deficient (DD) classification was assigned when no suitable evidence was available to assess a given impact mechanism within a LU/LC category. DD categories were treated separately from scored impact categories in the RIRC calculation and risk mapping and were interpreted as reflecting uncertainty due to insufficient information rather than an absence of impact. Consequently, DD classifications were not assigned a numerical impact magnitude and were excluded from risk score classification, while being retained as an indicator of knowledge gaps and priorities for future research and monitoring.

An impact category was assigned to each impact mechanism identified for each LU/LC category, and final scores for each LU/LC category were based on the highest documented impact magnitude. The scoring involved a structured expert elicitation process in which experts attributed impact categories independently from each other, followed by a consensus discussion to resolve discrepancies (a two-round Delphi-style process; Collaboration for Environmental Evidence, 2022; IUCN, 2020). Initial scoring was conducted independently by three experts (co-authors A. Jousson, S. Buholzer, B. Marazzi), and consensus scores were assigned only after discussion of cases where scores differed (see also Supplementary material - Table). Given the limited availability of impact data for Switzerland, uncertainty was addressed using independent expert scoring, transparent documentation of evidence sources, and explicit evaluation of evidence transferability across regions.

2.4. Regional impact risk classification

To assess regional impact risk, we combined the SDM-derived habitat suitability, representing the likelihood of species establishment at each location, with the potential impact magnitude expected for the local LU/LC type. First, habitat suitability was rescaled into a five-level ordinal scale, ranging from unsuitable (1) to optimal habitat (5). Impact severity was likewise classified on a five-level ordinal scale, from Minimal Concern (MC = 1) to Massive (MV = 5), following the standardized magnitude framework of (S)EICAT protocols. Cell-level score of impact risk was calculated as the product of the reclassified habitat suitability and impact-severity scores, resulting in values ranging from 1 to 25. The resulting risk score reflects the combined contribution of establishment likelihood and impact severity. Multiplicative risk matrices are commonly used in risk assessment because they transparently integrate the likelihood and consequences of adverse events within a single framework (Duijm, 2015; Kovačević et al., 2019; Oveisi et al., 2026). Compared to additive formulations, multiplicative approaches place greater emphasis on interactions that simultaneously exhibit high likelihood and high consequence, thereby supporting the identification and prioritization of areas with most critical risks.

Because the product of two ordinal scores ranging from 1 to 5 produces a limited set of discrete values, not all integer values between 1 and 25 can occur (e.g., 7, 11, 13, 14, and 17–19 are impossible). Accordingly, product scores were aggregated into six risk categories: Very Low (1, 2), Low (3, 4), Medium (5, 6, 8, 9), High (10,12), Very High (15, 16), and Extreme (20, 25) (Fig. 1). These risk categories were defined based on the attainable multiplicative scores and the ecological interpretation of suitability-impact interactions, providing an ecologically meaningful framework for risk prioritization. Specifically, 'Very Low' included unsuitable or marginally suitable areas combined with MC impact or unsuitable areas with MN impact; 'Low' included marginally suitable × MN, unsuitable × MO or MR, or moderately or highly suitable × MC; 'Medium' included unsuitable × MV, marginally suitable × MO or MR, moderately suitable × MN or MO, highly suitable × MN, or optimal suitability × MC; 'High' included marginally suitable × MV, moderately suitable × MR, highly suitable × MO, or optimal suitability × MN; 'Very High' included moderately suitable × MV, highly suitable × MR, or optimal suitability × MO; and finally 'Extreme' included highly suitable × MV or optimal suitability × MR or MV.

2.5. Hotspots of impact risk

To characterize the spatial patterns of regional impact risk associated with invasive alien species, we derived four cell-level indices based on alternative aggregation of the spatial distribution of the individual impact mechanisms and their magnitude. These indices summarize complementary dimensions of cumulative impact, including total and mean impact magnitude, mechanism co-occurrence (overlap), and risk hotspots.

Let x_{ij} denote the risk score associated with mechanism j in raster cell i, where $j = 1, 2, \ldots, m$, and m is the total number of impact mechanisms considered; in this study, $m = 7$.

Cumulative severity in cell i was calculated as the sum of the risk scores across all mechanisms:

$$SS_i = \sum_{j=1}^{m} x_{ij} \tag{1}$$

where SS_i represents the total combined impact in cell i.

Mechanism overlap was defined as the number of mechanisms with non-null risk scores co-occurring in each cell:

$$O_i = \sum_{j=1}^{m} I(x_{ij} > 0) \tag{2}$$

where O_i is the overlap count in cell i, and $I(x_{ij} > 0)$ is an indicator function taking the value 1 when mechanism j is present and exerting an impact in cell i, and 0 otherwise.

To distinguish cells affected by many low-intensity mechanisms from those affected by fewer but stronger mechanisms, mean mechanism severity was calculated as:

$$SM_i = \frac{SS_i}{O_i}, O_i > 0 \quad (3)$$

Cells with $O_i = 0$ were assigned no-data values.

To identify risk hotspots, we classified cells according to whether cumulative severity and mechanism overlap exceeded the upper quartile of their positive values. Thresholds were defined as:

$$T_{SS} = Q_{0.75}(SS_i | SS_i > 0) \quad (4)$$

$$T_O = Q_{0.75}(O_i | O_i > 0) \quad (5)$$

where $Q_{0.75}$ denotes the 75th percentile. Each cell was then assigned to one of five hotspot classes:

$$HC_i = \begin{cases} 0, & \text{if } SS_i = 0 \text{ or } O_i = 0 \\ 1, & \text{if } SS_i > 0, SS_i < T_{SS}, O_i < T_O \\ 2, & \text{if } SS_i < T_{SS}, O_i \geq T_O \\ 3, & \text{if } SS_i \geq T_{SS}, O_i < T_O \\ 4, & \text{if } SS_i \geq T_{SS}, O_i \geq T_O \end{cases} \quad (6)$$

These classes represent, respectively, no impact, low severity with low overlap, low severity with high overlap, high severity with low overlap, and high severity with high overlap. Cells classified as $HC_i = 4$ were interpreted as risk hotspots.

In addition, pairwise spatial associations among impact mechanisms were quantified using Spearman rank correlation coefficients calculated from the rasters with risk score for each mechanism. Pairwise correlations were computed across raster cells with positive values in at least one mechanism. The resulting correlation matrix was visualized as a lower-triangular heatmap to summarize the direction and strength of inter-mechanism spatial associations.

3. Results

3.1. Habitat suitability modelling

The global climatic suitability model showed moderate to strong discriminatory performance under spatially structured evaluation. Employing five-fold spatial block cross-validation with a 75-km block size, the final model achieved an out-of-fold AUC of 0.813 and a TSS of 0.466. At the optimal threshold (0.386) identified by SSS maximisation, sensitivity was 0.774 and specificity was 0.692, indicating a reasonable ability in discriminating suitable and unsuitable environments. Variable relative importance was highest for the minimum temperature of the coldest month (BIO6; mean importance = 0.130 ± 0.0036 s.d.), followed by the maximum temperature of the warmest month (BIO5; 0.125 ± 0.0039), isothermality (BIO3; 0.118 ± 0.0016), and precipitation of the warmest quarter (BIO18; 0.105 ± 0.0032). Lower contributions were observed for precipitation seasonality (BIO15; 0.0971 ± 0.0046), precipitation of the driest quarter (BIO17; 0.0938 ± 0.0034), and annual precipitation (BIO12; 0.0847 ± 0.0028). Sensitivity analyses revealed that model performance remained broadly stable across alternative calibration settings, with AUC ranging from 0.789 to 0.814 and TSS from 0.425 to 0.473. Performance was highest under the smaller block scenario (AUC = 0.814; TSS = 0.473) and lowest under the larger block scenario (AUC = 0.789; TSS = 0.425), suggesting limited sensitivity to validation stringency and overall robustness of the climatic suitability signal.

The nested regional model for Switzerland further refined the broad-scale climatic suitability by integrating fine-resolution land use information. Using five-fold spatial block cross-validation with a 5-km block size, the nested model achieved a mean AUC of 0.960 ± 0.010 and a mean TSS of 0.819 ± 0.039, indicating substantially improved regional suitability discrimination.

Predicted habitat suitability for *S. halepense* across Switzerland revealed clear spatial patterns (Fig. 2). Moderate to optimal suitability was concentrated primarily in low-elevation areas, such as parts of the Swiss Plateau, the Lake Geneva basin, valley bottoms in the Chablais and Central Valais and in southern Switzerland, particularly in Ticino. Additional suitable patches were found along major valley corridors, while higher-elevation areas were classified as unsuitable or only marginally suitable.

Analysis of the predicted habitat suitability across LU/LC categories showed (Fig. 3) that the highest median suitability was predicted for industrial areas, special urban areas, vineyards, and horticultural land. High values were also predicted for transportation areas, as well as green spaces and recreational areas. Built-up areas and orchards were predicted with relatively high median suitability, albeit with broader interquartile ranges. In contrast, lakes, rivers and river shores, arable land, natural meadows and farm pastures were characterized by low suitability values. Several categories, including unproductive vegetation, bare land, mountain meadows, alpine pastures and brush forests, showed very low median values but a wide spread in the predictions, indicating substantial within-class variation.

3.2. Assessment of impact mechanism and impact magnitude

Among the 22 LU/LC categories considered, six were identified as relevant for assessing the environmental and socio-economic impacts of *S. halepense* based on the availability of impact evidence in the literature: transportation areas, green spaces and recreational areas, arable land, farm pastures, natural meadows, and unproductive vegetation (Fig. 4). Expert-based identification of impact mechanisms and impact assessments relied on 11 information strings (snippets) extracted from seven independent literature sources, yielding a total of 16 impact scores (Fig. 4; Supplementary material - Table).

In transportation areas, as well as in green spaces and recreational areas, impacts are primarily driven by management costs (Massone, 2018) and allergenic effects on humans (Esch et al., 2001). Both management costs and allergenic effects are rated as MN impacts across literature sources from both neighbouring and distant countries, respectively. From literature of neighbouring countries, arable land is affected by several impact mechanisms: competition with crops is rated as a MO impact, particularly affecting spring-sown crops such as maize (Follak and Essl, 2013). *Sorghum halepense* also serves as a reservoir for crop pathogens, with disease transmission rated as a MN impact. Based on literature from distant countries, management costs in arable fields are rated as MN impacts. Management costs, whether through herbicide applications or the additional use of site-specific weed-management techniques, can significantly increase with the infestation, but do not prevent agricultural use (Nikolić et al., 2021). Farm pastures exhibit the most severe impacts: toxicity to livestock is rated as a MR impact, supported by documented cow mortalities in neighbouring countries associated with grazing or consumption of contaminated hay containing *S. halepense* (Giantin et al., 2024). As reported in literature from distant countries, additional MO impacts are expected from chemical and allelopathic effects as well as competition with native species (Rout et al., 2013). In natural meadows, impacts are rated as MO across several mechanisms, including competition, structural changes, and chemical or allelopathic effects. Invaded prairies in distant regions showed decreased species richness, altered community evenness, and allelopathic root exudates affecting soil biogeochemistry (Rout et al., 2013; Rout and Chrzanowski, 2009). Unproductive vegetation is similarly affected, with MO impacts from competition, structural changes, and chemical or allelopathic mechanisms. *Sorghum halepense* can form near-monocultures in nutrient-poor soils, alter nutrient cycling, and influence microbiota, including probable rhizome-associated N_2-fixation, thereby driving ecosystem-level changes (Rout et al., 2013; Rout and Chrzanowski, 2009).

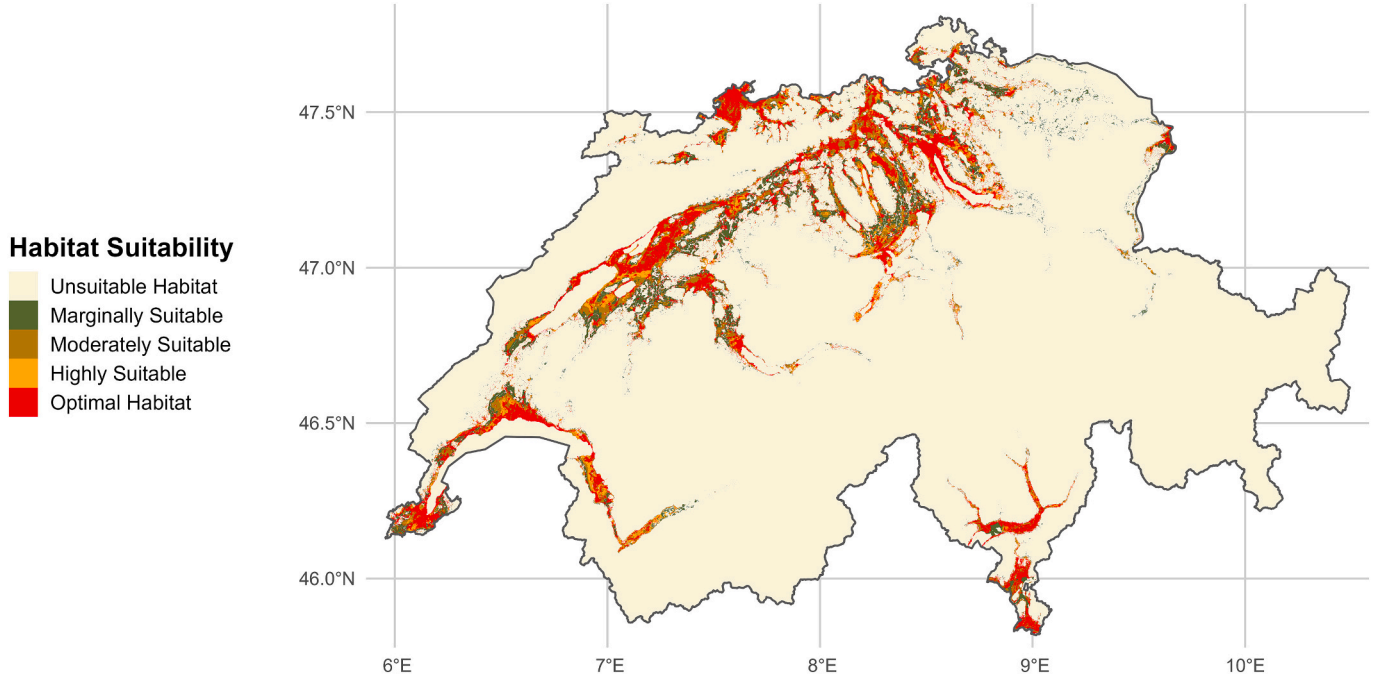


Fig. 2. Habitat suitability for *S. halepense* in Switzerland predicted by a spatially nested hierarchical model integrating global-scale climatic suitability with high-resolution national land use/land cover data. Predicted probabilities were reclassified into five suitability classes: unsuitable, marginally suitable, moderately suitable, highly suitable, and optimal habitat.

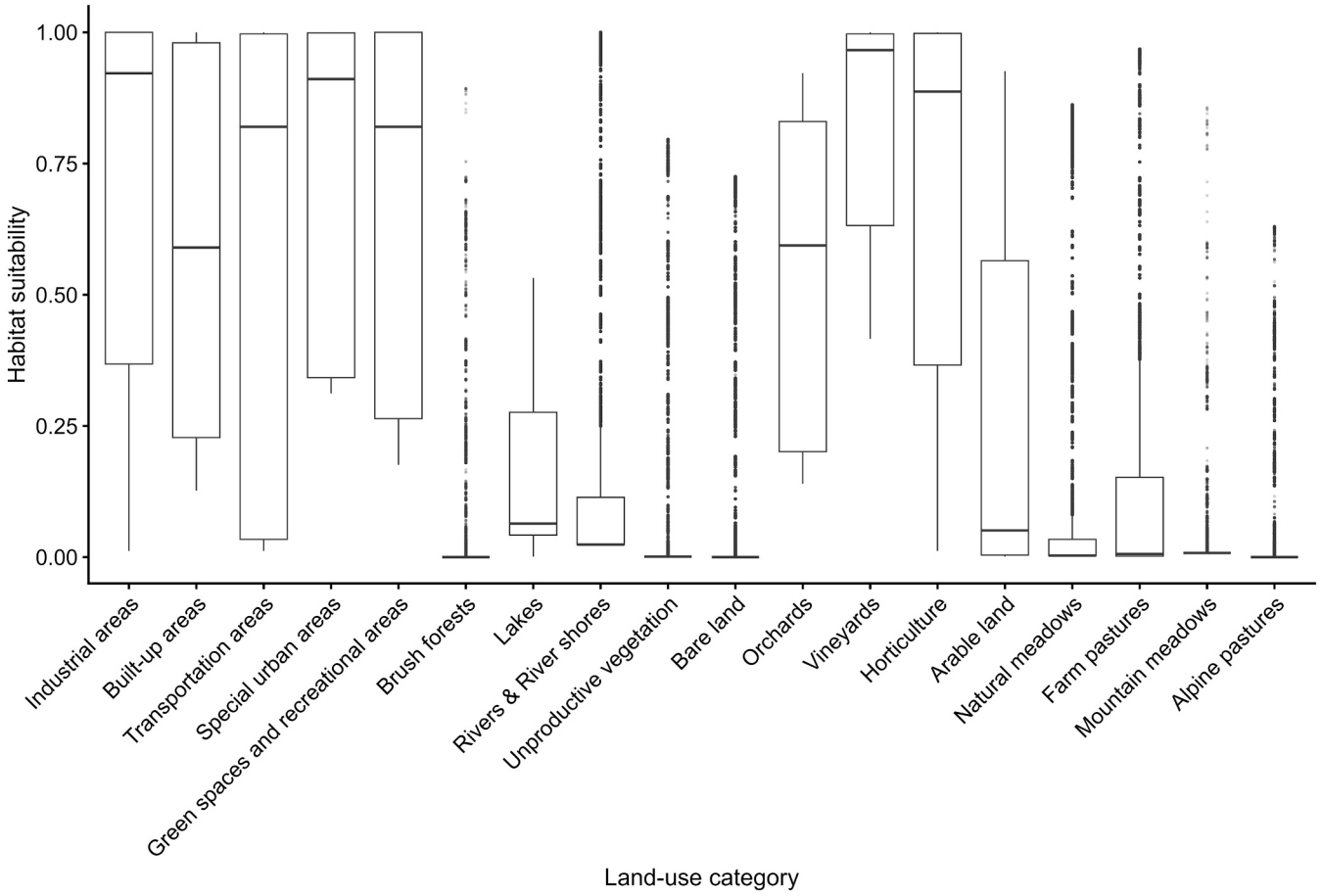


Fig. 3. Predicted habitat (climate + land use) suitability of *Sorghum halepense* across land use/land cover categories in Switzerland. Boxplots show the distribution of suitability values within each category, including the median, interquartile range, and outliers.

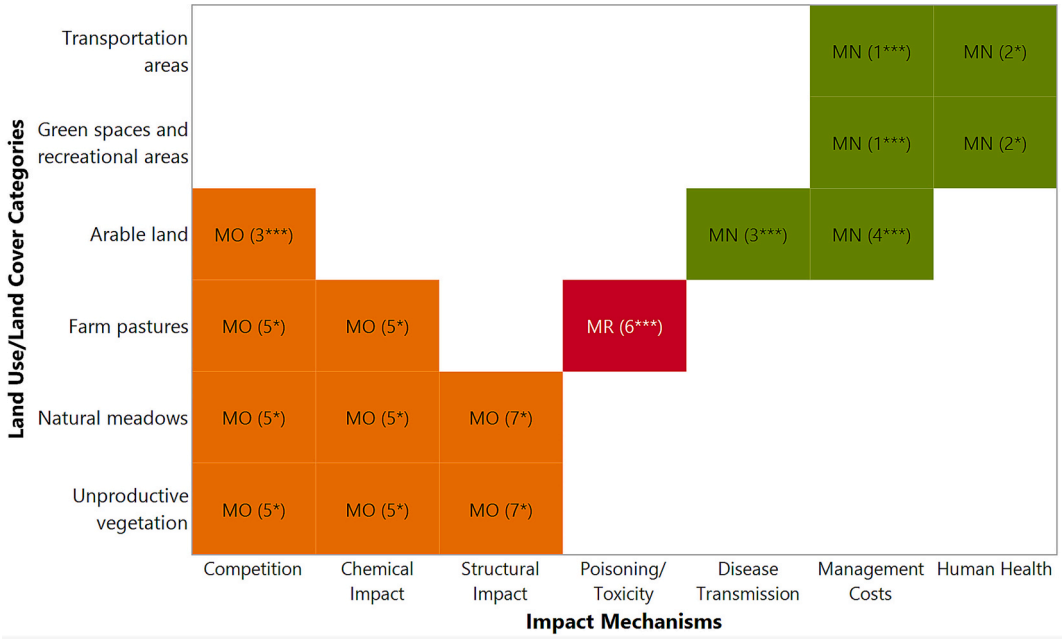


Fig. 4. Potential impact of *S. halepense* across different land use/land cover categories in Switzerland. Impact categories and mechanisms follow (S)EICAT protocols (Bacher et al., 2018; Blackburn et al., 2014; IUCN, 2020). The x-axis represents impact mechanisms, and the y-axis indicates land use / land cover categories. Colors illustrate potential impact categories (red = MR; orange = MO; green = MN). Symbols indicate primary sources of evidence: *** literature from neighbouring countries (transferable), * literature from distant countries (potentially transferable). Sources: 1) Massone (2018); 2) Esch et al. (2001); (3) Follak and Essl (2013); 4) Nikolić et al. (2021); 5) Rout et al. (2013); 6) Giantin et al. (2024); 7) Rout and Chrzanowski (2009). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

3.3. Regional impact risk classification

The Regional Impact Risk Classification (RIRC) maps (Fig. 5) reveal distinct spatial patterns in the potential impacts of *S. halepense* across Switzerland, with clear differences among impact mechanisms.

Competition is the impact mechanism that operates across the largest spatial extent. Medium to very-high risk areas are scattered across the Swiss Plateau, along a partially connected belt extending from the Lake Geneva region through central Switzerland to the northeastern Plateau. Very high to extreme impact cells occur mainly as elongated patches within this lowland belt, with additional clusters in thermophilus central and southern valley systems, including the Chablais in Valais and Magadino Plain in Ticino. In contrast, alpine and subalpine regions are dominated by low or very low risk.

Chemical impact is more fragmented and localized. Medium- to very high-risk cells occur mainly as discrete clusters across the Pre-Alps, with additional small patches in the Plateau and Jura Mountains, as well as in the lowland areas of southern valleys in Ticino.

Disease transmission ranges from low to high and is more spatially confined to the central Plateau, with local high-risk clusters embedded within this zone, especially in the central and western parts of the country. Additional smaller patches of moderate risk occur in valley areas, including Valais and Ticino. In contrast, most alpine and higher-elevation regions are mainly classified as data-deficient/non-applicable.

Human health risk (allergenicity) displays a pervasive, interconnected, and dendritic network pattern across the lowlands. High-risk and medium-risk cells form a dense, continuous web stretching from the Lake Geneva basin, extending eastward across the central Swiss Plateau, and continuing toward the northeastern regions. A separate, elongated network of similar risk intensity is also visible within the southern valley systems of Ticino. Outside these lowland networks, risk intensity diminishes rapidly, with the vast majority of alpine and pre-alpine regions characterized by data deficiency or very low risk.

Management cost shows a broad but spatially heterogeneous distribution across the Plateau. Moderate-risk areas are widespread, while high-risk areas are more concentrated in elongated patches, particularly in the central-western Plateau and in the Jura Mountains. Additional moderate- to high-risk patches occur in southern valley systems, including Ticino.

Structural impact displays a predominantly low-risk background across lowlands and valleys of the northern and southern flank of the Alps, punctuated by highly localized, high-impact hotspots in central-western Switzerland and small patches scattered across the Plateau, Jura Mountains and southern valley systems of Ticino. Outside these specific lowland and valley zones, the high-elevation alpine regions are dominated by very low risk or data-deficient/non-applicable areas.

Finally, toxicity exhibits a spatially widespread but mostly moderate impact across the Swiss Plateau and the Jura Mountains. It shows a discontinuous speckling extending from the Lake Geneva basin north-eastward to Lake Constance. High- to extreme-risk cells are sparse and highly restricted, appearing as isolated points across the Plateau and a single distinct linear feature in southern Ticino.

3.4. Hotspots of impact risk

The spatial synthesis of impact risk revealed pronounced geographic heterogeneity in the distribution of the multi-mechanism potential impact patterns of *S. halepense* across Switzerland (Fig. 6). The risk hotspot map (Fig. 6a) shows that low-severity/low-overlap areas are widely distributed across the main mapped areas, particularly throughout the Swiss Plateau and adjacent lowland and valley systems. High-severity/low-overlap areas also occur across these regions but are more localized. Low-severity/high-overlap hotspots form extensive, spatially connected patterns, especially in the Plateau region (from Lake Geneva basin to north-eastern Switzerland) and the Jura Mountains. In contrast, high-severity/high-overlap hotspots are highly localized, occurring mainly as narrow patches across the Plateau and in the lowland areas of valley systems, including the Chablais in Valais and Magadino Plain in Ticino.

The map of mechanism overlap (Fig. 6b) indicates substantial spatial

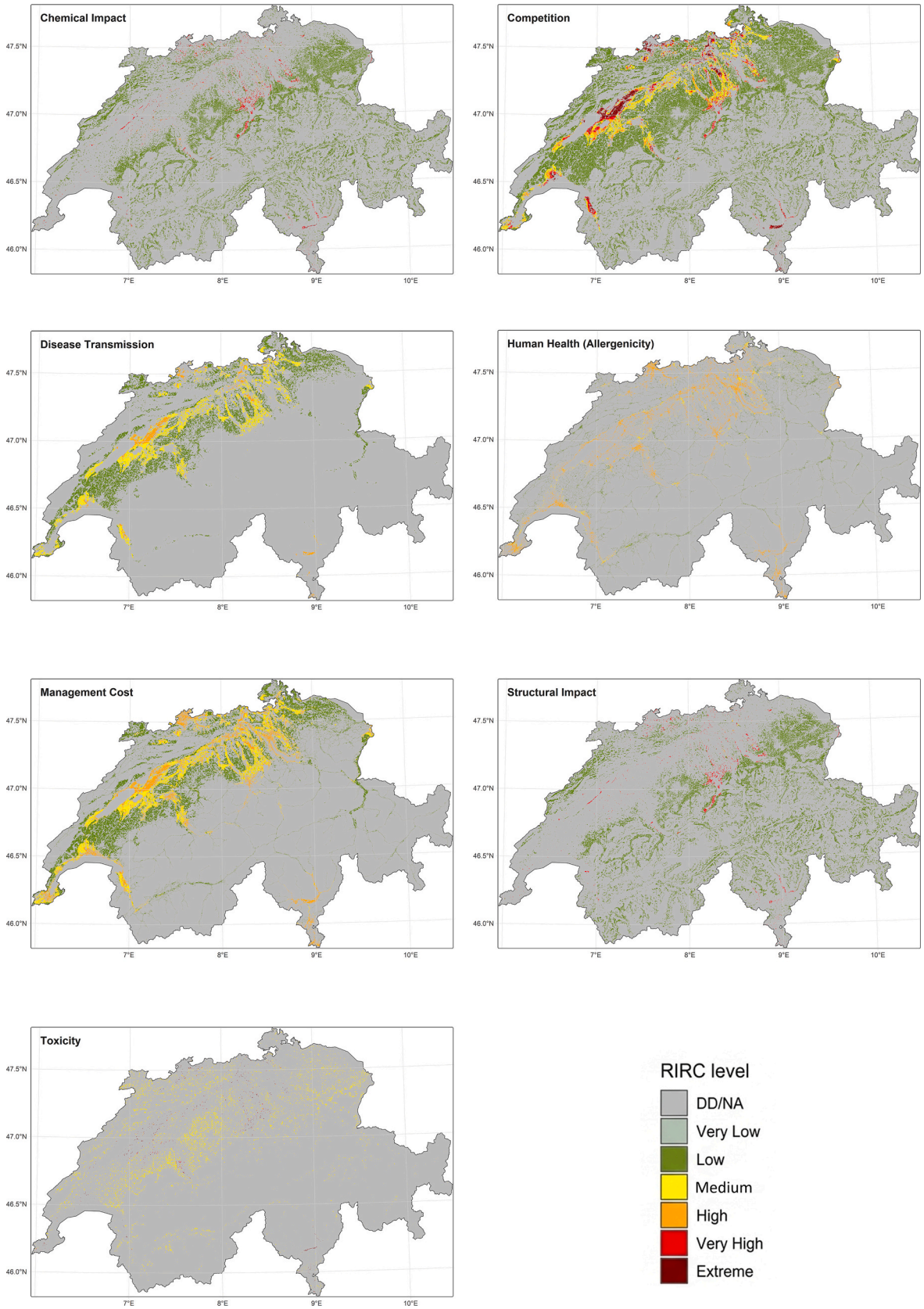


Fig. 5. Regional Impact Risk Classification (RIRC) maps for *Sorghum halepense* across Switzerland under multiple impact mechanisms. Colors represent risk intensity from Very Low to Extreme, while DD/NA areas are shown in gray.

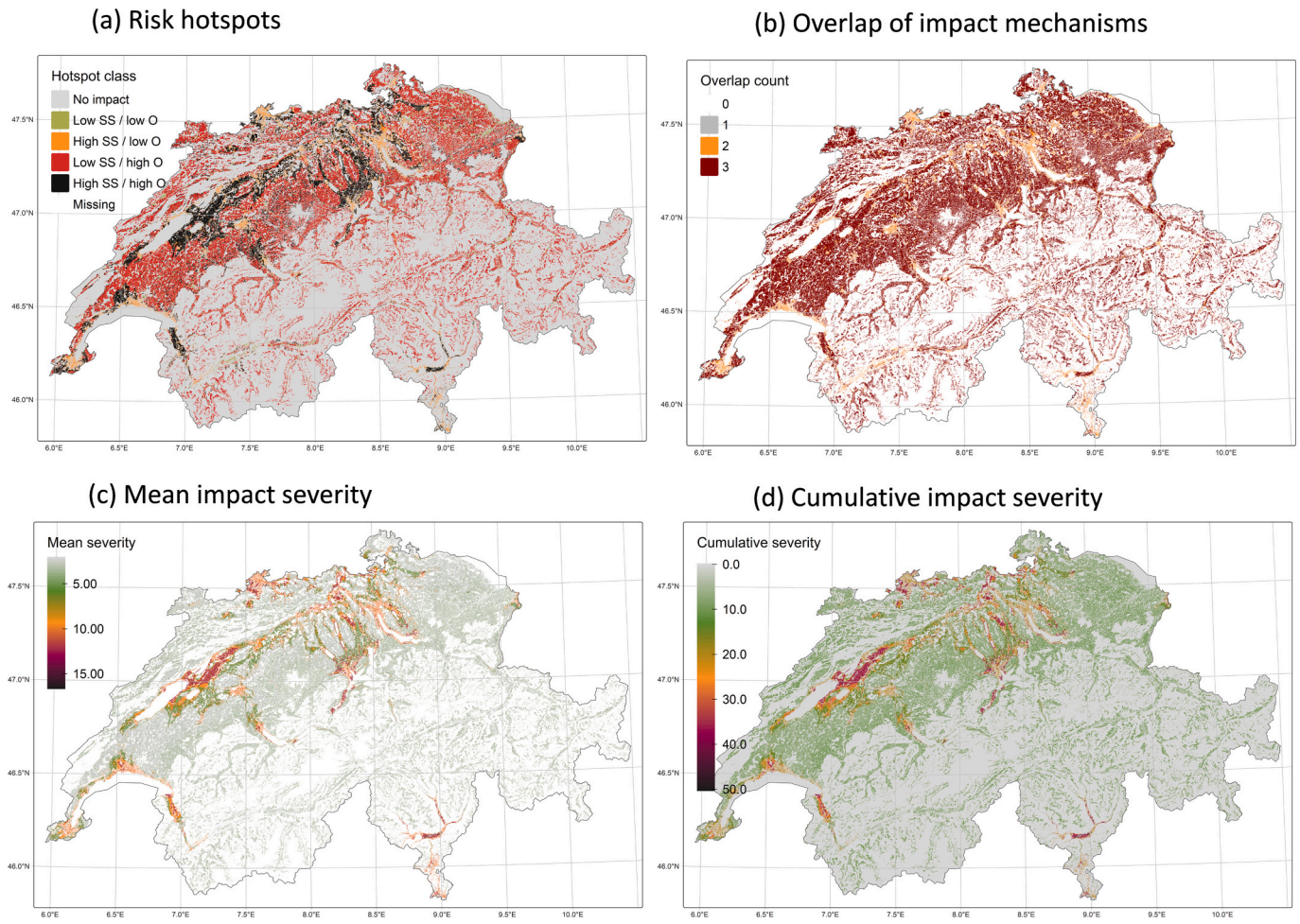


Fig. 6. Spatial synthesis of potential impacts risk of *S. halepense* across Switzerland: (a) hotspot identification based on cumulative severity (SS) and mechanism overlap (O); (b) mechanism overlap, expressed as the number of active impact mechanisms per cell; (c) mean active severity, expressed as the average severity of active mechanisms per affected cell; and (d) cumulative severity, expressed as the summed severity of all active mechanisms per cell.

variation in the number of co-occurring impact mechanisms across Switzerland. Areas with three overlapping mechanisms are widespread across Swiss lowland regions, forming dense and relatively continuous patterns across much of the Swiss Plateau, particularly in western, northwestern, and northern Switzerland. Areas with two overlapping mechanisms are more spatially fragmented and occur mainly as localized patches and linear features within lowland and valley systems. Areas with a single overlapping mechanism are also scattered throughout the territory, including lowland parts of the alpine and southern valley regions. Overall, the map indicates that multiple impact mechanisms frequently co-occur in lowland regions, whereas they are more spatially dispersed and less concentrated in mountainous and southern areas.

Mean severity (Fig. 6c) exhibited a highly localized spatial pattern. Most of the mapped area was characterized by low severity values, whereas high values (exceeding 10.0) were concentrated in narrow, fragmented corridors and compact clusters, particularly in the Plateau region, with additional localized features in the thermophilus valleys (Chablais, Magadino Plain).

The cumulative severity map (Fig. 6d) shows a strongly skewed distribution of aggregate impact. The highest cumulative values are concentrated in distinct linear features and compact patches, mainly across the Swiss Plateau and in selected southern and thermophilus valley segments, including Ticino. In contrast, much of the study area

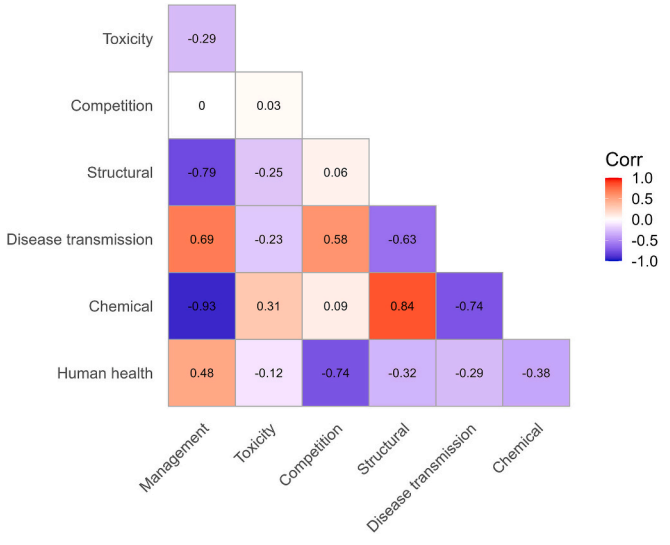


Fig. 7. Heat map of pairwise spatial correlations between the RIRC values of the seven main impact mechanisms. The correlation indicates the amount of spatial overlap between areas at risk by the different mechanisms.

remains within the lowest cumulative-severity classes, indicating that high aggregate impact was localized rather than widespread across the species' distribution.

Spearman correlations calculated to capture spatial associations among impact mechanisms (Fig. 7) show several strong positive and negative correlations among impact mechanisms. The strongest positive correlation was observed between chemical and structural impacts ($r = 0.84$), followed by management and disease transmission ($r = 0.69$), and competition and disease transmission ($r = 0.58$). In contrast, the analysis also highlighted several strong negative associations, particularly between management and chemical impacts ($r = -0.93$), management and structural impacts ($r = -0.79$), human health and competition ($r = -0.74$), and chemical and disease transmission ($r = -0.74$). Structural impacts were negatively associated with disease transmission ($r = -0.63$), while management showed a moderate positive correlation with human health impacts ($r = 0.48$). Most other pairwise correlations were weak to negligible. Overall, the matrix indicates that some impact mechanisms tend to co-occur spatially, whereas others are distributed in contrasting geographic patterns.

4. Discussion

Predicting the potential impacts of invasive alien species at a regional scale is essential for translating global risk assessments into operational management strategies (Díaz Cando et al., 2025; Hulme, 2022; Robertson et al., 2020). While continental or global models capture broad climatic envelopes that delineate the potential species distributions, regional models capture the finer-scale heterogeneity in environmental conditions, land cover and human activity that ultimately determine invasion success (Liu et al., 2023; Pyšek et al., 2010; Thuiller et al., 2004). For decision-makers and practitioners, spatially-explicit regional predictions thus provide the precision needed to support surveillance, target prevention and implement control activities where these are most cost-effective (Cuthbert et al., 2022; Robertson et al., 2020). For *Sorghum halepense*, a rhizomatous perennial grass characterized by strong vegetative regeneration, high dispersal capacity, and broad environmental tolerance, regional-scale assessment is especially valuable for distinguishing between climatically suitable but low-risk landscapes and those where ecological or socio-economic impacts are most likely (Follak and Essl, 2013; Peerzada et al., 2023, review; Yang et al., 2023). Switzerland, with its steep environmental gradients and fine mosaic of agricultural, urban, and (semi-)natural habitats, serves as an ideal case study for identifying invasion hotspots and integrating invasive alien species management into land use and agri-environmental policy frameworks (Early et al., 2016; FOEN, Federal Office for the Environment, 2022).

Frameworks like EICAT and SEICAT provide a transparent, standardized method for ranking the magnitude of alien species impact based on empirical evidence (Volery et al., 2021). These schemes are increasingly used in regional evaluations of invasive alien species (Bacher et al., 2018; Blackburn et al., 2014; Kumschick et al., 2024; Volery et al., 2021). However, their utility for regional management planning is limited by their primarily descriptive and non-spatial character, which can entail a high degree of uncertainty (Probert et al., 2020). Indeed, spatial heterogeneity (in terms of topography, land use, environmental gradients, etc.) across the landscape can significantly influence the outcome of invasions. Integrating this spatial dimension is therefore essential for providing assessments that are useful at a scale where management of invasive species is implemented (Christie et al., 2019). The land-use-informed RIRC framework addresses this issue by combining (S)EICAT-derived impact scores with the SDM-derived likelihood that a species will become established, thereby producing spatially-explicit risk maps that highlight areas where the highest impact is expected. In other words, habitat suitability models assess the suitability of environmental conditions for a given species, converting climatic and other landscape characteristics into spatially-explicit predictions of establishment potential (Elith and Leathwick, 2009). By combining these predictions of potential distribution with information on potential impact, the land-use-informed RIRC generates impact risk maps that go beyond a simple descriptive categorization to provide spatially-explicit projections. This approach enables decision-makers and practitioners to identify areas that are most likely to experience ecological or socio-economic impacts even before local establishment actually occurs, thereby bridging the gap between broad-scale assessments and regional management needs. This capability is particularly relevant for emerging species, as it supports anticipatory risk assessment in regions where establishment is recent and impacts have not yet been fully realized.

While able to capture the full climatic niche, global climate suitability models have intrinsic limitations in predicting species' distributions. They set the broad climatic constraints within which the species can potentially occur and they assume environmental homogeneity, which prevents them from capturing fine-scale habitat characteristics (e.g. edaphic characteristics, land cover or anthropogenic activities) that may either amplify the likelihood or completely prevent establishment and invasion outcomes (Elith, 2017; Elith and Leathwick, 2009; Perez-Navarro et al., 2022). As an example, Seuren et al. (2025) showed that country-level ensemble SDMs transferred poorly to municipal extents, and El-Gabbas and Dormann (2018) found that range-wide data do not necessarily improve regional models under biased sampling. The use of a nested approach – where climate determines broad-scale suitability and land use defines fine-scale habitat suitability - produces more realistic predictions of species' potential distributions (Fournier et al., 2017; Goicolea et al., 2025). Although the metrics resulting from the two models developed here are not fully comparable due to differences in settings, the global model showed moderate discrimination (AUC = 0.813, TSS = 0.466 under 75-km blocks cross-validation) and sensitivity to calibration settings (AUC 0.789–0.814). In contrast, the regional nested model performed strongly and consistently (AUC = 0.960 ± 0.010; TSS = 0.819 ± 0.039). This result is consistent with other hierarchical applications (Fournier et al., 2017; Goicolea et al., 2025) and is more defensible than single-stage extrapolation for a species unlikely to be at equilibrium (Yang et al., 2023).

Similarly, generic impact assessments are only partially useful in guiding management strategies at the regional level. For these to be effective, differentiation by habitat type and anthropogenic activity is necessary. To address these limitations, we incorporated land use and land cover information as a common spatial context for both habitat suitability modelling and impact predictions within the RIRC framework. Land use is not a passive background variable; it actively shapes disturbance regimes, propagule pressure, and competitive dynamics, which are key determinants of invasion success (Díaz Cando et al., 2025; Manzoor et al., 2021; Pellegrini et al., 2021). Our LU/LC-informed potential impact risk assessment of *S. halepense* demonstrates that, although climate suitability defines its broad potential range, the fine-scale habitat suitability and the mechanism and magnitude of impact are determined by land use context. This integration significantly enhances projections' realism and allows for differentiation among areas of similar habitat suitability but contrasting risk levels due to anthropogenic land use.

Sorghum halepense is currently recognized as a potentially invasive species in Switzerland (FOEN, Federal Office for the Environment, 2022; InfoFlora, 2022). However, there are only qualitative and no quantitative empirical data on its ecological and socio-economic impacts within the national context (Gentilini et al., 2021, 2026). Thanks to the approach proposed by the land-use-informed RIRC, we identified potential high-risk zones for *S. halepense* in lowlands of the Swiss Plateau, the Lake Geneva basin, the Chablais, and the central valley bottoms of Ticino, mainly in correspondence with transportation, industrial, urban and recreational areas, as well as agricultural land and (semi-)natural ecosystems. This pattern matches the species' ruderal and disturbance-dependent ecology in Central Europe (Follak and Essl, 2013; Fanfarillo

et al., 2022; Peerzada et al., 2023, review) and may reflect broader changes in land-use and management intensity across European landscapes, which have reshaped disturbance regimes and the availability and distribution of suitable habitats (Colling et al., 2025; Kuemmerle et al., 2016). The observed pattern may also partly reflect survey bias toward roads and settlements (Phillips et al., 2009). However, previous studies have shown that the number of occurrence records often has a greater influence on model performance than spatial sampling bias alone (Fourcade et al., 2014; Gaul et al., 2020). Although sampling bias may have led to an overestimation of suitability in easily accessible land-use classes, the large number of occurrence records available suggests that its influence is likely to represent a bounded source of uncertainty rather than a critical limitation. Also, low median habitat suitability does not necessarily imply low sampling, as arable land and grasslands dominate large portions of the Swiss lowlands.

In these areas, potential impacts can result from multiple and often co-occurring mechanisms, including chemical and structural impacts on ecosystems and competition with native species (Rout et al., 2013; Rout and Chrzanowski, 2009), crop yield reduction through competition for resources (Follak and Essl, 2013), transmission of plant pathogens (Follak and Essl, 2013) and toxicity for livestock in farm pastures (Giantin et al., 2024). Additionally, *S. halepense* may be allergenic to humans (Esch et al., 2001) and increase management costs in urban (Massone, 2018) and agricultural systems (Nikolić et al., 2021). The land-use-informed RIRC framework therefore enables spatially targeted surveillance by linking ecological processes with management needs for *S. halepense* in Switzerland. For instance, allergenicity risk maps support urban health planning, toxicity profiles inform livestock management, and structural or chemical impacts guide conservation strategies. In addition, estimates of economic costs help prioritize resources, while competition metrics provide insights for agricultural decision-making.

The land-use-informed RIRC framework decomposes impact into its principal mechanisms. Evaluating these mechanisms separately clarifies the main impact pathways, reveals areas where multiple impact mechanisms concentrate (overlap), and provides a precautionary overview for early applied management, allowing for specific, rather than generic and often ineffective, control efforts. Importantly, the overlap among mechanism-specific risks does not necessarily indicate interactions between mechanisms; rather, it arises from the structural nature of land use categories that can simultaneously support multiple impact pathways and multi-mechanism risk in each location. It is also important to note the spatial decoupling between mechanism overlap and impact severity. While the overlap of three mechanisms is widespread, areas of high mean and cumulative severity are concentrated in limited corridors and patches within the Plateau and the thermophilus valleys of Switzerland (Chablais and central Ticino). This pattern suggests that extensive areas require routine monitoring because multiple impact pathways may occur simultaneously, whereas targeted proactive management efforts should be directed toward a smaller number of high-severity risk locations.

In anthropogenic and urban habitats (transportation areas and green spaces), *S. halepense*'s impacts are primarily related to management costs and allergenic effects. However, *S. halepense* exerts its greatest ecological and socio-economic impacts in agricultural systems (farm pastures and arable land), and semi-natural ecosystems (natural grasslands), where toxicity, competition, disease transmission, and chemical or allelopathic effects reduce crop productivity, but also biodiversity. The competitive effects of *S. halepense* on cultivated crops are pronounced, driven by dense rhizome networks, rapid growth rates, and elevated resource uptake (Barroso et al., 2016; Güneş et al., 2008; Travlos et al., 2019). Surveys in southern Austria found that approximately 41% of maize fields and 40% of oil-pumpkin fields are at risk (Follak and Essl, 2013), while studies in Romania reported yield losses of 30–70% in maize and sugar beets (Chiriţa et al., 2008). Management should therefore prioritize crop rotation, early-season mechanical or chemical control, and vigilant edge monitoring (Andújar et al., 2012, 2013; Frans et al., 1991; Nikolić et al., 2021; Travlos et al., 2019). Management should address both aboveground competition and belowground soil impacts through integrated mechanical and restoration measures, strategically targeted to high-risk areas to maximize management efficiency. *Sorghum halepense* releases indeed allelochemicals – such as p-hydroxybenzoic, vanillic, syringic, p-coumaric, and ferulic acids, along with the lipophilic compound sorgoleone - that inhibit neighbouring plant growth and alter soil microbial communities (Rout and Chrzanowski, 2009; Rout et al., 2013; Majumdar et al., 2017; Hussain et al., 2021). Rhizome extracts of *S. halepense* have also shown significant germination inhibition on other species in bioassays (Nestorović Živković et al., 2025). Early detection and containment are therefore essential for supporting habitat resilience and preventing cascading effects on the structure and functioning of the entire agro-ecosystem. The species can also harbour pathogens such as *Bipolaris sorghicola* and *Clavibacter michiganensis* subsp. *nebraskensis*, that infect cereals and fruit crops (Ahn et al., 2021). Management should integrate weed and crop health surveillance in landscapes where infested stands are located in the vicinity of orchards, vineyards, or cereal fields. *Sorghum halepense* contains the cyanogenic glycoside dhurrin, which releases hydrogen cyanide (HCN) under stress (e.g., drought or frost). A notable case of poisoning in northwest Italy involved the deaths of 66 cattle after they grazed on *S. halepense* under drought conditions (Giantin et al., 2024). Management should adjust grazing timing to avoid grazing during drought stress periods, fence infested pastures, and alert producers in risk zones. Additional concerns include allergenic pollen that may affect human populations; implementing phenologically relevant mowing regimes and municipal awareness campaigns are recommended in this case (Davies, 2014; Velez-Gavilan, 2024).

Overlaying mechanism-specific risk maps reveals cumulative hotspots of potential impacts by *S. halepense*, i.e. locations where multiple impact mechanisms (e.g., competition, toxicity, and disease transmission) co-occur. These hotspots are typically lowland agro-urban mosaics with moderate to high climatic suitability and diverse LU/LC configurations. By identifying where particular impact mechanisms dominate, the LU/LC-informed RIRC framework supports proactive, context-sensitive management across agricultural, conservation, and urban sectors. However, once established, *S. halepense* is difficult to eradicate, because of its phenotypic plasticity and ability to adapt its reproductive strategies following mechanical disturbance, including regrowth and seed production even under frequent cutting regimes (Peerzada et al., 2023, review; Schantz, 2025). Prevention hence remains the most cost-effective strategy, as *S. halepense* spreads mainly through seeds and rhizome fragments in soil or machinery. Therefore, enforcement of strict guidelines to prevent soil displacement and ensure machinery hygiene are essential, as well as the use of certified seeds (Barroso et al., 2012; Peerzada et al., 2023, review). Coupling agricultural and environmental instruments – such as linking subsidy compliance to weed control obligations - can strengthen national policy leverage. In urban areas, where the use of herbicide is generally restricted (e.g. Federal Act on the Protection of Waters, *Swiss Confederation*, 1991), mechanical control, mulching, and public awareness campaigns remain crucial. Finally, integrating RIRC outputs into land use and infrastructure planning can further reduce future spread along transport corridors.

5. Conclusions

Our study illustrates how integrating land use-contextualized habitat suitability modelling and mechanism-specific impact assessment allows moving away from suggestions of generic approaches for invasive species management toward spatially-explicit, context-specific and sector-relevant actionable measures. By mapping *S. halepense*'s potential for establishment alongside its multiple impact mechanisms, we provide a detailed overview of impact risk that enables targeted, mechanism-specific management. The hierarchical two-stage SDM, combining a

global model with a nested regional model evaluated under spatially blocked cross-validation, confirmed that land use stratification substantially improves regional discrimination and that the distinction between broad climatic suitability and fine-scale habitat opportunity is operationally meaningful. The six-class risk scheme, ranging from "Very Low" to "Extreme," translates the combined suitability and impact dimensions into interpretable, sector-differentiated priorities. This approach also reveals where different ecological and socio-economic impact threats converge and where coordinated, multi-sector strategies are most urgent.

The applicability and accuracy of the land-use-informed RIRC framework depend on the availability, quality, and spatial resolution of the data, as well as the dynamic interplay between climate, anthropogenic activities and impacts, particularly for emerging invasive species. The realized (actual) impact patterns may diverge from projections as landscapes, land use, and management practices evolve. Propagule pressure, dispersal dynamics, and management intensity were not incorporated explicitly, although each can strongly influence establishment and realized impact. Also, some impact evidence was transferred from other regions and may require validation under Swiss ecological, agricultural, and public-health conditions. Therefore, risk classes should be interpreted as structured decision support rather than exact probabilities.

Looking ahead, the predictive power and operational relevance of regional impact risk assessments can be enhanced by coupling the land-use-informed RIRC approach with several key advancements. Specifically, future assessments should integrate indicators of seed and propagule dispersal (such as road network density and citizen-science reporting), economic cost evaluations derived from global databases like InvaCost, and formal statistical methods to trace and communicate model uncertainty. Incorporating these elements alongside dynamic land use projections and climate-change scenarios will enable managers to more accurately identify future hotspots and dominant impact mechanisms. Consequently, proactive and context-specific management strategies can be implemented to safeguard biodiversity, sustain agricultural productivity, and protect human and livestock health.

CRediT authorship contribution statement

Mostafa Oveisi: Conceptualization, Formal analysis, Data curation, Methodology, Writing – original draft, Writing – review & editing. **Antoine Jousson:** Formal analysis, Data curation, Methodology, Writing – original draft, Writing – review & editing. **Serge Buholzer:** Formal analysis, Writing – review & editing. **Brigitte Marazzi:** Formal analysis, Writing – review & editing. **Ramona Maggini:** Conceptualization, Formal analysis, Methodology, Writing – original draft, Writing – review & editing, Supervision, Project administration, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ecoinf.2026.104149.

Data availability

Reproducible R code for the analysis presented in this study is archived at Zenodo and accessible via https://doi.org/10.5281/zenodo.23235356. Global occurrence records of *Sorghum halepense* were downloaded from the Global Biodiversity Information Facility (GBIF; https://gbif.org) on 25 July 2026 and are available at https://doi.org/10.15468/dl.sky3a2. Country boundary for study region (Switzerland) was obtained from geoBoundaries, an open database of political administrative boundaries (https://www.geoboundaries.org/; Runfola et al., 2020). Finally, downscaled land use / land cover (LU/LC) map for Switzerland at 25 m resolution (Giuliani et al., 2022) was retrieved from Yareta Digital Repository (University of Geneva, Switzerland), at: https://doi.org/10.26037/yareta:dlx3hu54jfa3ne3c2xjfcnqpxm.

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