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Assessing threats of non-native species to native freshwater biodiversity: Conservation priorities for the United States

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ABSTRACT

Non-native species pose one of the greatest threats to native biodiversity, and can have severe negative impacts in freshwater ecosystems. Identifying regions of spatial overlap between high freshwater biodiversity and high invasion pressure may thus better inform the prioritization of freshwater conservation efforts. We employ geospatial analysis of species distribution data to investigate the potential threat of non-native species to aquatic animal taxa across the continental United States. We mapped non-native aquatic plant and animal species richness and cumulative invasion pressure to estimate overall negative impact associated with species introductions. These distributions were compared to distributions of native aquatic animal taxa derived from the International Union for the Conservation of Nature (IUCN) database. To identify hotspots of native biodiversity we mapped total species richness, number of threatened and endangered species, and a community index of species rarity calculated at the watershed scale. An overall priority index allowed identification of watersheds experiencing high pressure from non-native species and also exhibiting high native biodiversity conservation value. While priority regions are roughly consistent with previously reported prioritization maps for the US, we also recognize novel priority areas characterized by moderate-to-high native diversity but extremely high invasion pressure. We further compared priority areas with existing conservation protections as well as projected future threats associated with land use change. Our findings suggest that many regions of elevated freshwater biodiversity value are compromised by high invasion pressure, and are poorly safeguarded by existing conservation mechanisms and are likely to experience significant additional stresses in the future.

1. Introduction

Biodiversity is in decline globally, with little indication of improving trends despite broad international consensus on conservation needs (Ceballos et al., 2015; Pimm et al., 2014; Tittensor et al., 2014). This decline is associated with a variety of human drivers ranging from habitat fragmentation and degradation to overexploitation (Murphy and Romanuk, 2014; Tilman et al., 2017). With limited resources available, prioritization of conservation action has become a necessary component of biodiversity science (Tulloch et al., 2015). Due to the uneven spatial distribution of diversity and the drivers of decline, many researchers have focused efforts to map locations that may be especially vulnerable to diversity loss, at multiple spatial scales, across taxonomic groups, and over terrestrial, freshwater, and marine ecosystems (Brum et al., 2017; Collen et al., 2014; Dobson et al., 1997; Jenkins et al., 2013; Mokany et al., 2014; Selig et al., 2014). They have also adopted a variety of diversity metrics to assess vulnerability and determine conservation priority, including species range size and protection coverage (Jenkins et al., 2015a), threatened status (Wickham et al., 2013), and phylogenetic, taxonomic, and trait diversity (Brum et al., 2017; Moorhouse and Macdonald, 2015).

Such prioritization of conservation needs is acutely important for freshwater systems. These systems support a disproportionate share of global diversity; at the same time, the insular nature of freshwater habitat and growing demands by human populations for services derived from freshwater ecosystems suggest that concerted action will be required to prevent considerable future losses of freshwater biodiversity (Chester and Robson, 2013; Collen et al., 2014; Dudgeon, 2014; Garcia-Moreno et al., 2014). Freshwater diversity has generally been underrepresented in efforts to map conservation priorities at broad spatial scales (Abell et al., 2011). A number of studies have identified priority regions for freshwater biodiversity conservation with particular emphasis on amphibian and fish taxa (Abell et al., 2011; Grenyer et al., 2006; Jenkins et al., 2015b; Wake and Vredenburg, 2008), but relatively few prioritization studies examine freshwater invertebrate or microbial diversity (Collen et al., 2014; Stomp et al., 2011).

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Biological invasions have been implicated in the decline of biodiversity across virtually all ecological systems and taxonomic groups (Doherty et al., 2016; Galiana et al., 2014; Vila et al., 2011), and remain the most common threat associated with the extinction of vertebrate species worldwide (Bellard et al., 2016a). But freshwater systems may, in fact, be especially susceptible to the negative impacts of species introductions (Moorhouse and Macdonald, 2015). Indeed, invasive species have been associated with decline in diversity of freshwater shrimps (De Grave et al., 2015), crayfish (Richman et al., 2015), mussels (Haag and Williams, 2013), and fish (Liu et al., 2017) at both national and global scales. The importance of non-native species as a driver of native diversity loss has led to an increased interest in mapping non-native diversity. The availability of data on the distribution of non-native species provides opportunity to ascertain spatially explicit areas of high native biodiversity experiencing anthropogenic stress of known relevance to diversity decline. Such overlay analysis has been employed to inform conservation prioritization based on broad suites of factors associated with human impact (Selig et al., 2014); only few studies, however, have explored this approach to specifically identify potential conflict areas between native and non-native biodiversity (Carpio et al., 2017; Padalia and Bahuguna, 2017; Thalmann et al., 2015), and these mapping efforts have rarely targeted freshwater systems (Dawson et al., 2017; Dyer et al., 2017; Stohlgren et al., 2006).

Here we employ geospatial analyses to determine conservation priorities for native freshwater biodiversity across five taxonomic groups, by better understanding the distribution of pressures from non-native aquatic species (NAS) on rare and imperiled native species across the continental US (CONUS). We describe the spatial distributions of both native and non-native diversity across the CONUS using distribution information drawn from multiple publicly available databases and develop a prioritization metric based on native species richness, threatened and endangered status, and rarity, as well an index designed to estimate cumulative stress associated with NAS at the watershed scale. We used prioritization scores to identify regions exhibiting overlap of elevated native biodiversity value and high levels of NAS colonization. In keeping with a number of recent studies highlighting the inadequacy of existing protected lands to preserve vulnerable biodiversity (Brum et al., 2017; Jenkins et al., 2015b; Quan et al., 2017), we also explored the degree to which our priority regions overlapped known conservation areas in the US. To assess potential for multiple and cumulative future threats to biodiversity in these priority areas we further investigated trends in projected land use change, as increases in urbanization are likely to bring not only increased pressure from non-native species but also additional anthropogenic stressors to freshwater systems (Martinuzzi et al., 2014). Our results recognize regions of conservation need that may be ignored by other prioritization methods focused exclusively on the distribution of native species.

2. Materials and methods

2.1. Data acquisition and database development

We compiled a database of native aquatic species distributions across the CONUS by reallocating ranges from the International Union for Conservation of Nature (IUCN) Red List spatial database (IUCN, 2014) to watersheds using ArcGIS (v. 10.3.1) and R (v. 3.3.3). We selected the US Geological Survey (USGS) eight-digit hydrologic unit code (HUC8), which represent surface drainage basins, as the unit of spatial analysis. The hydrologic unit code system is a system of hierarchically nested watersheds delineated by topographic and hydrological features. There were a total of 2106 HUC 8 watersheds in our study extent, with an average size of 1821 km^2. Our native biodiversity database contains 1510 species, including fish, mollusks, amphibians, turtles, and crustaceans (shrimps and crayfish).

To generate non-native richness estimates, we curated a list of non-native freshwater aquatic species (192 plant species and 287 animal species), where "non-native" was defined as introduced to the continental US during or after European settlement (~1500 CE). The plants list was compiled initially using the USDA Natural Resources Conservation Service's (NRCS) plants database (https://plants.usda.gov). Candidate species were identified by searching for species non-native to the lower 48 states and listed with a National Wetland Indicator Status of "obligate wetland" in at least some part of that range. This list was later extended to include several species (e.g. *Lythrum salicaria* and others) that are widely considered to be "aquatic" invasive species by management groups throughout the US despite not being listed as obligate wetland species by the NRCS. These additional species were identified based on existing lists of invasive aquatic plants maintained by the USDA's National Invasive Species Information Center (https://www.invasivespeciesinfo.gov), the University of Georgia's Center for Invasive Species and Ecosystem Health (https://www.invasive.org), and regional databases such as the Great Lakes Non-indigenous Species Information System (GLANSIS, https://www.glerl.noaa.gov/glansis) and the University of Florida Center for Aquatic and Invasive Plants (https://plants.ifas.ufl.edu). The plant data analyzed here expand considerably on those utilized in previous studies (Davis et al., 2017). Species included in the NAS animal list were obtained from the USGS Non-Indigenous Aquatic Species program (USGS-NAS; https://nas.er.usgs.gov/). While we recognize that species translocated within the continental US ("native transplants") can also have considerable negative impacts in freshwater systems, we have excluded them from the current analysis. The difficulty of defining precisely the non-native range of native transplants can lead to uncertain ascription of non-native occurrences nearby, bordering, or even sometimes within the described native range of these species. This, in turn, raises the possibility of overestimating non-native richness. Excluding these species avoids such overestimation, resulting in what we consider to be justifiably conservative estimate of that richness.

Using these lists, we assembled species occurrence data from USGS-NAS, the Early Detection and Distribution Mapping System (EDDMaps), and the USGS Biodiversity Serving Our Nation (BISON) databases, which is a curated US data repository for the Global Biodiversity Information Facility (GBIF). We used the Integrated Taxonomic Information System (ITIS) to ensure that species were not double counted, or that synonymous taxa were accidentally excluded. Duplicate occurrence records, centroids, records with missing spatial coordinates, and occurrence data outside of the conterminous US were removed. Despite the fact that our native biodiversity data is exclusive to animal species, we included plants and animals in our analysis of non-native species because they are both important indicators of overall invasion pressure and significant drivers of general ecological impairment, including native animal species decline (Vilà et al., 2011).

For the overlay analyses, we acquired datasets from the USGS Gap Analysis Program's (USGS-GAP) Protected Areas Database of the United States (PAD-US, version 1.4) (DellaSala et al., 2001; USGS, 2016), which includes the boundaries for national parks, national forests, private conservation easements, and other protected areas. We used lands with any level of permanent protection, which are designated with GAP status codes 1, 2, and 3 according to the definitions provided by Scott et al. (1993). GAP status code 1 signifies the strictest protection, with lands maintained in their natural state, while 3 means land is permanently protected but subject to resource extraction. We also acquired 250-meter resolution land cover maps for the years 2000 and projected 2060 from FORE-SCE (Sohl et al., 2014). From the Intergovernmental Panel on Climate Change Special Report on Emissions Scenarios (IPCC-SRES), we used the year 2060 projection of the A2 scenario, which is characterized by moderate economic growth, very high population increase, and a focus on self-reliance and local identity.

2.2. Calculation and mapping of diversity metrics

We employed geospatial analyses to derive metrics associated with