Where are Canada's species-at-risk? Identifying hotspots for conservation

Marie Hardouin

Supervised by Dr. Anna Hargreaves

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Biology Department, McGill University

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TABLE OF CONTENTS **Page**

1. ABSTRACT

Canada is committed to protecting both 25% of its land by 2025 and its taxa deemed nationally at-risk. Both mandates could be powerfully furthered if future protected areas simultaneously protect habitat that is important for multiple groups of imperilled taxa. Using the range maps of 9 terrestrial taxonomic groups' at-risk taxa, I identified areas where the ranges of Canada's at-risk taxa overlapped the most (i.e. hotspots, using 100 x 100 km grid cells). I also asked how the national threat status of Canada's at-risk taxa relates to the size and peripherality of their distribution. Total at-risk hotspot cells clustered along Canada's southern regions, and together encompassed more than half of the at-risk taxa in each taxonomic group and 80% of the 462 total at-risk taxa in our data. Hotspot cell overlap between taxonomic groups ranged from 2 to 70%. Additionally, I found that 71% of nationally imperilled taxa occurred at the northmost ≤ 20% of their western hemisphere range in Canada, and that the most imperilled taxa were significantly more peripheral with a median of 2.0%. My results highlight key areas of high taxonomic overlap on which future conservation efforts could potentially focus to reach Canada's biodiversity protection targets.

2. INTRODUCTION

Global biodiversity is rapidly declining due to increasing anthropogenic pressures such as habitat loss and fragmentation (Butchart et al., 2010; Haddad et al., 2015). Building on its previous targets as a signatory to the Convention of Biological Diversity, Canada is committed to protecting 25% of its land and 25% of its oceans by 2025 (Government of Canada, 2020). This target can help combat biodiversity declines by protecting habitat and increasing habitat connectivity. Indeed, protected areas are a key tool to reduce the extent and intensity of anthropogenic pressures on taxa (Coristine et al., 2018), although their benefits strongly rely on effective and committed management (Watson et al., 2014). Additionally, land protection can provide crucial corridors across degraded landscapes as species adjust their ranges to follow suitable climates (Thomas et al., 2012). With widespread range shifts already occurring under climate change, maintaining habitat connectivity will be key to maintaining biodiversity, particularly as species move toward high-latitude countries such as Canada (Chen et al., 2011; Littlefield et al., 2019).

In addition to its land protection targets, Canada considers its at-risk species for legal protection under the Species at Risk Act (SARA, 2002) after they have received a recommended threat status by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC, 2014). Consequently, an “at-risk” (defined here as Special Concern, Threatened, or Endangered) designation by COSEWIC does not automatically translate to a species’ habitat protection (Favaro et al., 2014). In fact, many of Canada’s at-risk species have very little range overlap with protected areas, as found both around (Kerr & Chilar, 2004; Deguise & Kerr, 2006) and more than a decade after (Coristine et al., 2018; Kraus & Hebb, 2020) SARA’s enactment in 2002. At-risk vascular plants’ protected range fraction even tends to be lowest for the most imperilled taxa, with a median of merely 3.7% overall (Caissy et al., 2020). This scarce protection can hinder imperilled species' recovery, with COSEWIC reassessments finding more than twice as many declines as improvements (Favaro et al., 2014). If future protected areas also protect at-risk species' habitat, Canada's protection mandates could both be furthered at the same time.

A promising strategy to select areas for protection could be to identify biodiversity hotspots, which are areas of high species richness, endemism, or threat (Ceballos & Ehrlich, 2006). While the coarse mapping of Canada's terrestrial at-risk taxa has shown their aggregation along the southern border (Coristine et al., 2018; Gibson et al., 2009), the distribution of all at-risk taxa has not been quantified into hotspots and the range overlap across different taxonomic groups remains unclear. Although at-risk vascular plants also cluster southward, this contrasts with hotspots of at-risk terrestrial mammals in northwestern Canada (Cameron & Hargreaves, 2020; Caissy et al., 2020). The clustering of at-risk taxa in southern Canada could thus potentially be driven by highly abundant taxonomic groups such as vascular plants, which have three times as many assessed taxa as almost any other terrestrial group (Government of Canada, 2021), and could be unrepresentative of the distribution of less abundant groups such as mammals. Using hotspots to explore the range overlap across Canada's at-risk taxa would highlight key regions for multiple taxonomic groups on which future conservation efforts could potentially focus.

Canada's at-risk hotspots may be driven by taxa occurring at their range's northern edge, as do >75% of its nationally at-risk vascular plants and 50% of its terrestrial mammals (henceforth "peripheral" taxa; Caissy et al., 2020; Cameron & Hargreaves, 2020). This may focus Canada's conservation efforts on edge populations that are globally secure (Raymond et al., 2018). While some argue that Canada must protect its most endemic species, others suggest that protecting locally at-risk edge populations is important for diversification and distribution shifts (Gibson et al., 2009; Hunter & Hutchinson, 1994; Lesica & Allendorf, 1995). Although estimated (Gibson et al. 2009), the proportion of peripheral at-risk taxa in Canada has not been measured across taxonomic groups. It also remains unclear whether peripheral taxa are more at-risk due to smaller ranges and proximity to human activity, as with vascular plants (Caissy et al., 2020), or whether peripheral taxa are simply prevalent in Canada, as with mammals (Cameron and Hargreaves 2020). Assessing Canada's at-risk taxa's peripherality would not only inform how to best protect its current populations, but how to potentially welcome future ones shifting towards a new home.

I addressed two questions using the range maps of the 9 terrestrial taxonomic groups assessed by COSEWIC. Q1) How much do hotspots of different at-risk taxonomic groups overlap? I predicted that most at-risk hotspots would occur in southern Canada, where at-risk species cluster (Coristine et al., 2018; Kraus & Hebb, 2020), but their overlap across taxonomic groups was unclear based on the distinct distributions of at-risk mammals and vascular plants (Caissy et al., 2020; Cameron & Hargreaves, 2020). Q2) Do more nationally at-risk taxa have smaller or more peripheral ranges in Canada? Does this vary among taxonomic groups? Since COSEWIC uses Canadian range area as a risk assessment criterion (COSEWIC, 2014), and since Canada's range-edge populations may be under higher threat by being near high human activity (Caissy et al., 2020), I predicted that more imperilled taxa would have smaller and more peripheral ranges in Canada. I predicted a stronger association between peripherality and higher threat status in less dispersive or more temperature-limited groups, as their peripheral taxa would be distributed in Canada's highly modified southern areas, than in groups with ranges extending further North.

3. METHODS

3.1 Data Collection: Range Map Digitization

COSEWIC assessment and status reports are publicly available as PDF documents and generally include a range map of the assessed species (Government of Canada, 2021). Pascale Caissy digitized the COSEWIC range maps available between November 2017 and November 2018 (depending on the taxonomic group) using the Quantum GIS 2.18 geographic information software (QGIS Development Team, 2021; methods outlined in Caissy et al. 2020). To update this database, I digitized the global range maps from reports released by COSEWIC after those dates. These reports were either updated reports of taxa that had previously been assessed (n = 17 taxa) or reports of newly assessed taxa (n = 12 taxa). I also digitized the range maps of taxa whose global range maps were not properly digitizable (maps were either incomplete, imprecise, or in a projection that could not be digitized), but whose Canadian range maps were digitizable (n = 34 taxa). These taxa were excluded from the peripherality analysis (Q2) but were included in the hotspot analysis (Q1), where only the Canadian ranges were needed (Table 1).

To keep new range maps consistent with those in the database, I followed the map digitization methods created by Pascale Caissy (Caissy et al., 2020), but updated them for QGIS 3.16 (QGIS Development Team, 2021). I first saved a cropped image of the range maps from each COSEWIC assessment report as a PDF and imported each PDF in the georeferencer in QGIS. I then associated ≥15 (generally 40-60) specific points on the PDF map with their corresponding coordinates on a base map of the world; these points were clear landmarks such as sharp land mass corners, waterbody edges, roads, or jurisdictional boundaries. The maps then went through a thin plane spline transformation, which introduced local deformations. This

Table 1. Sample sizes for each terrestrial taxonomic group assessed by COSEWIC. At-risk taxa are those designated as Special Concern, Threatened or Endangered. Marine birds and mammals are excluded from this study. Bird range maps in columns C and D were obtained from BirdLife International rather than COSEWIC and are therefore independent of the sample sizes in columns A and B.

	A. Populations with a COSEWIC status	**B. Taxa with a COSEWIC report and range map**	**C. At-risk taxa with a digitized Canadian range map (Q1)**	**D. At-risk taxa with a digitized global range map (Q2)**
Birds	124	82	56	54
Mammals	78	50	37	36
Reptiles	59	40	32	26
Amphibians	54	26	21	17
Arthropods	81	71	60	54
Molluscs	52	45	34	32
Vascular Plants	242	223	184	171
Mosses	26	23	17	10
Lichens	27	25	21	14

A. Note: COSEWIC only assesses taxa that are deemed potentially at risk. The number of populations in Column A does not correspond to the total number of populations present in Canada.

B. Column B excludes taxa from A) that either have no available COSEWIC report, or whose report does not provide a range map as of January 2021. If a species in A) contained multiple populations with the same range map, they were merged into one.

C. Column C excludes taxa from B) who are not at-risk and/or whose Canadian range maps were not properly digitizable (maps were either incomplete, imprecise, or in a projection that could not be digitized) as of January 2021.

D. Column D excludes taxa from C) who are not at-risk and/or whose global range maps were not properly digitizable (maps were either incomplete, imprecise, or in a projection that could not be digitized) as of January 2021. If the populations merged in B) did not have the same COSEWIC status, they were excluded.

projected all maps in the World Geodetic System 1984 projection (WGS 84, EPSG:4326), a common global latitude and longitude-based coordinate reference system (Caissy et al., 2020; Kennedy & Kopp, 2004). Lastly, I verified that the output raster map layer was precisely aligned with the base map (vector layer) I used for georeferencing, and I readjusted my points if needed.

Once the map was accurately georeferenced, I created a polygon shapefile and traced the shaded area(s)' outline by hand for ranges that were represented as such. For ranges represented as point occurrences, I created a point shapefile and added each point. If there were at least 4 points on each continent in which the taxon was present, I then generated a convex polygon (the smallest polygon shape encompassing all the points), which is generally equivalent to the taxon's extent of occupancy reported by COSEWIC. If there were less than 4 point occurrences on a continent and I was unable to generate a convex polygon (n = 10 taxa), I generated a buffer around each point instead. To do so, I projected the point shapefile to the World Mollweide equal area projection (WGS 84, ESRI:54009), which is an equal area projection in which all mapped areas have the same relative size as they do on Earth (Kennedy & Kopp, 2004). Using this projection, I was able to set the buffer radius to a distance in kilometers. I specifically set this distance for each taxon to ensure that the taxon's total buffer area would be equivalent to the extent of occupancy reported in its COSEWIC report.

I performed a quality check on all the maps that had been digitized as convex polygons in the database by visualizing them in QGIS 3.16 (QGIS Development Team, 2021). I cut out the Great Lakes from the ranges of all taxa with convex polygons except for the mollusc taxa that were present in these lakes, as specified by COSEWIC. All coastal water bodies would get cut out during the data extraction. Additionally, I found 9 convex polygon maps that linked the point occurrences of taxa with a distribution across multiple continents. The COSEWIC reports for these taxa explained that they consisted of small, disjunct populations, and their range maps only represented their occurrence in each country by a coarse point without specifying their extent of occurrence in each continent. In these cases, I excluded the global range map and only digitized the Canadian range map provided in the COSEWIC report, since a convex polygon would have grossly overestimated these taxa's ranges by linking points across different continents.

These methods were used for all taxonomic groups apart from birds, whose range maps were obtained using a different process. Since the majority of bird species with a COSEWIC assessment report are migratory, their range maps had to be divided between their resident, breeding, non-breeding and passage ranges to meaningfully compare their Canadian and global distributions (Supplementary Table 1). To obtain range maps with this information, we contacted BirdLife International, the IUCN Red List Authority for global bird distributions. In November 2020, BirdLife International provided us with an ESRI File Geodatabase containing distribution polygons of bird species across the world, from which I extracted the polygon shapefiles of any species assessed by COSEWIC using QGIS 3.14.16 (BirdLife International and Handbook of the Birds of the World, 2019; QGIS Development Team, 2021).

For each species, the Geodatabase provided a separate polygon shapefile for each seasonal range (Supplementary Table 1). In QGIS 3.14.16, I intersected these polygons with a polygon shapefile of Canada (QGIS Development Team, 2021). I then dissolved the polygons that intersected with Canada into a single polygon shapefile for each species, and I used this shapefile for all future analyses. Thus, my future analyses would only be comparing each species' Canadian range with their corresponding seasonal global range. For instance, for a species that is only found in Canada during its breeding season, I compared its Canadian breeding season range to its global breeding season range.

There were 8 COSEWIC species listed under a different name in the Geodatabase, and 4 COSEWIC species that were either not present in the Geodatabase or whose ranges were uncertain. In some cases, the range maps in the Geodatabase represented an entire species' distribution while the COSEWIC report only assessed a particular subspecies. In such cases, I cut out the subspecies' range myself if the demarcation between subspecies was very clear based on the COSEWIC report (i.e. the subspecies' global range was entirely located on a Canadian island, or there were disjunct Eastern and Western populations; n = 3 taxa). Otherwise, the subspecies was excluded from the analysis (n = 9 taxa). Since this study mainly focuses on terrestrial taxa, I also excluded birds whose ranges were largely or completely marine (n = 14 taxa).

3.2 Data Extraction

All data extraction was done in the statistical platform R (version 4.0.3, R Core Team, 2020). To calculate range areas, I projected all digitized range maps in the World Mollweide equal area projection (WGS 84, ESRI:54009) to accommodate for taxa with worldwide ranges. To calculate Canadian, Western Hemisphere (henceforth "Hemisphere"), and global range areas (km^2), I intersected each digitized map with a Canada, North and South America, or world boundary map respectively (Natural Earth, 2020), thus cropping all maps to land only. To extract a measure of peripherality, I divided each taxon's Canadian range area by its Hemisphere range area. I defined peripheral taxa as those with ≤ 20% of their Hemisphere range in Canada, as per Caissy et al., 2020 and Cameron and Hargreaves, 2020. I deemed Hemisphere range proportion to be a more biologically relevant measure of peripherality than global range proportion, since the difficulty of moving between hemispheres would likely prevent other continents' populations from substantially impacting Canadian populations. Indeed, many COSEWIC reports explained that populations in other continents were quite disjunct from their Canadian counterparts.

3.3 Data Analyses

All data analyses were done in R 4.0.3 (R Core Team, 2020).

3.3.1 Q1) How much do hotspots of different at-risk taxonomic groups overlap?

To divide the distribution of Canada's at-risk taxa into cells of equal area, I projected the digitized range maps in the Albers equal area conic projection. This projection is commonly used for Canada, while the Mollweide equal area projection is only recommended for world maps (Kennedy & Kopp, 2004). I then overlaid these digitized range maps on a map of Canada divided into 100 x 100 km grid cells and counted the total number of at-risk species in each grid cell. I identified "hotspot" cells for each taxonomic group, which I defined as the cells with the highest number of at-risk species up to a maximum of 5% (63 cells) of the total 1276 grid cells. This method follows Cameron and Hargreaves (2020) and was adapted from Prendergast et al. (1993) and Reid (1998). This yielded different numbers of hotspot cells for each taxonomic group, ranging from 42 to 62 hotspots. Lastly, I generated a matrix of overlap to count the proportion of coinciding hotspot cells for each taxonomic group, and averaged corresponding cells in the matrix into a single cell for easier interpretation (e.g., I averaged the number of bird hotspots that overlap with moss hotspots with the number of moss hotspots that overlap with bird hotspots).

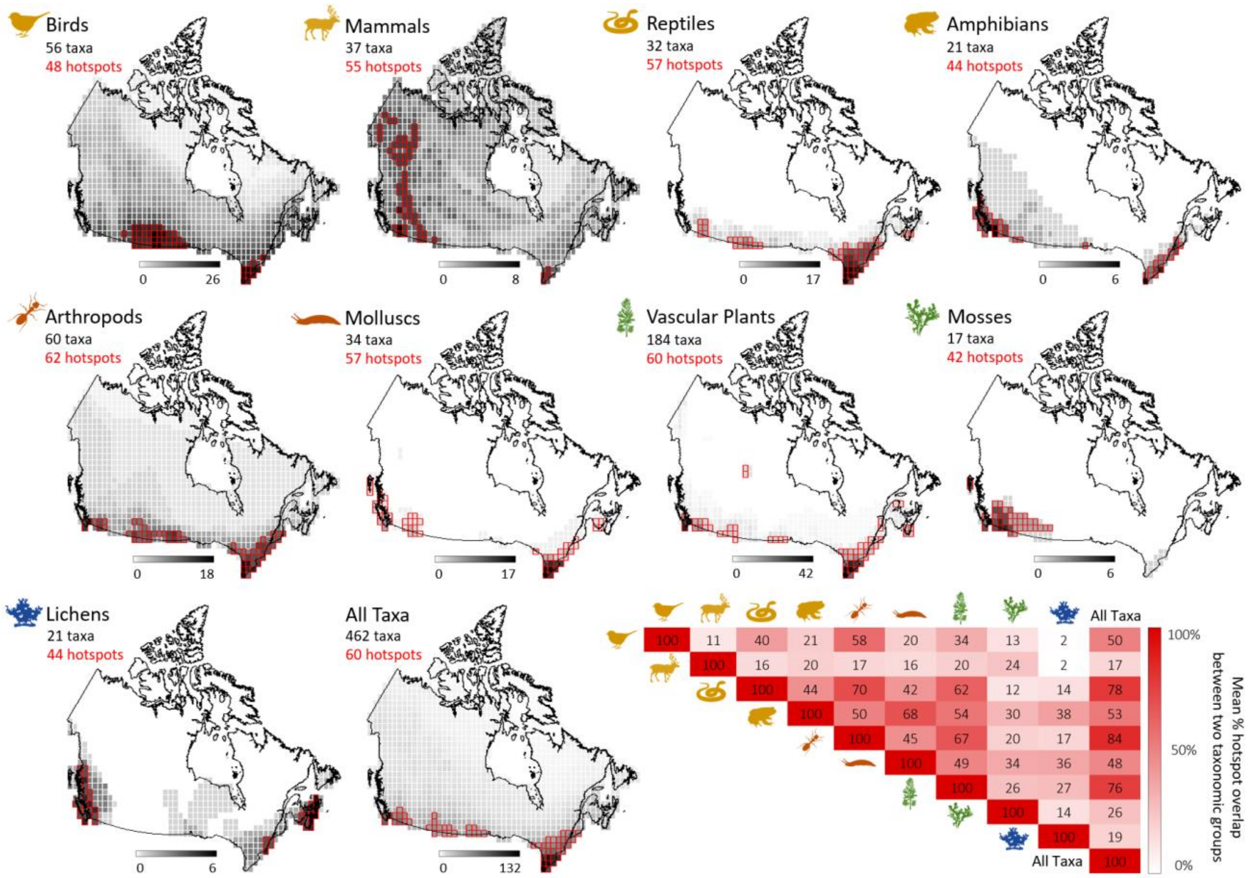
3.3.2 Q2) Do more nationally at-risk taxa have smaller or more peripheral ranges in Canada? Does this vary among taxonomic groups?

I ran three generalized linear models (GLM) to test the relationship between each of three response variables (Hemisphere range area, Canadian range area, and % of Hemisphere range in Canada) and two categorial predictors (COSEWIC status and taxonomic group). The model structure was response ~ COSEWIC status + taxonomic group. I used a negative binomial GLM for range area and a binomial GLM for % of range. Predictors were tested for significance using likelihood ratio χ^2 tests to compare models with and without the predictor (*anova* function in R; R Core Team, 2020). If the effect of predictor(s) was significant, I contrasted least squared means to determine which COSEWIC statuses within each taxonomic group differed (*lsmeans* package version 2.30-0; Length, 2016). If the interaction effect of COSEWIC status and taxonomic group on the response variable was not significant (as with % of range), the interaction was dropped. For all three models, I grouped vascular plants and mosses into a single taxonomic group category called “plants” due to the mosses’ small sample size (Table 1, n = 10).

4. RESULTS

4.1 Q1) How much do hotspots of different at-risk taxonomic groups overlap?

When all of Canada’s at-risk taxa from our data were combined, their hotspots clustered along the southern borders of British-Columbia, the Prairies, Ontario and Quebec (Figure 1). Hotspot cells of all at-risk taxa each contained 47 to 132 at-risk species, and together encompassed 372 (80%) of the 462 taxa in our data. Together, they were home to 97% of the reptile taxa in our data, 95% of the amphibians, 92% of the arthropods, 89% of the birds, 85% of the molluscs, 76% of the plants, 65% of the molluscs, 65% of the mammals and 62% of the lichens.



	🐦	🦌	🐍	🐸	🐜	🐌	🌿	🌱	🪸	All Taxa
🐦	100	11	40	21	58	20	34	13	2	50
🦌		100	16	20	17	16	20	24	2	17
🐍			100	44	70	42	62	12	14	78
🐸				100	50	68	54	30	38	53
🐜					100	45	67	20	17	84
🐌						100	49	34	36	48
🌿							100	26	27	76
🌱								100	14	26
🪸									100	19
All Taxa										100

Figure 1. Canadian range maps of Canada’s at-risk taxa separated by taxonomic group and ordered biologically (yellow icons = vertebrates; orange icons = invertebrates; green icons = photosynthesizers; blue icon = lichens). The maps of Canada are divided into 1276 100 km by 100km grid cells, which are shaded in a greyscale according to the number of taxa they contain. The greyscale is indicated below each map, with black corresponding to the highest number of taxa found in a cell. Hotspot cells (i.e. those with the highest number of at-risk species up to a maximum of 5% of the total grid cells) are outlined in red. The matrix of overlap indicates the percentage of hotspot cells that coincide for each pairwise combination of taxonomic groups. These are the results for Q1), with sample sizes shown in Table 1C).

When at-risk taxa were separated by taxonomic group, different distribution patterns emerged. At-risk arthropod, reptile and vascular plant hotspots were clustered in similar southern areas to the at-risk hotspots of all taxa, with new hotspots in Southern Nova Scotia for reptiles and vascular plants. New vascular plant hotspots were also found in the Gaspé Peninsula and in the Athabasca Plain ecoregion of Northern Saskatchewan, which is home to many endemics. The distribution of at-risk bird hotspots also mirrored that of the at-risk hotspots of all taxa, but with a notable northward extension of hotspots along the Southern Prairies. At-risk amphibian, mollusc and lichen hotspots were largely concentrated along the Western and Eastern Canadian coasts and extended further North than the at-risk hotspots of all taxa. Interestingly, at-risk moss and mammal hotspots were almost entirely located in Western Canada, with at-risk moss hotspots extending westward from Southern Saskatchewan to the BC islands of Haida Gwaii, and at-risk mammal hotspots extending northward from the montane to the taiga cordillera, with only four hotspots in Southern Ontario.

The overlap among the hotspots of taxonomic groups ranged from 2% to 70% of hotspots coinciding (Figure 1). More than three-quarters of at-risk reptile, arthropod and vascular plant hotspots overlapped with the at-risk hotspots of all taxa (78%, 84%, and 76%, respectively). Conversely, at-risk mammal and lichen hotspots only coincided with the at-risk hotspots of all taxa in 17% and 19% of cases, respectively. The highest overlap between taxonomic groups was between reptiles and arthropods, whose hotspots coincided with each other in 70% of cases, while the hotspot overlap between birds and lichens and between mammals and lichens was only 2%. Taxonomic groups that are more closely related phylogenetically did not necessarily have a higher hotspot overlap. Hotspot overlap between vertebrate groups ranged from 11% to 44%, compared to 2% to 70% overlap between vertebrates and other groups. Hotspot overlap between the two invertebrate groups was 45%, compared to 16% to 70% overlap between invertebrates and other groups, and hotspot overlap between the two photosynthesizer groups was 26%, compared to 12% to 67 % overlap between photosynthesizers and other groups.

The maximum number of overlapping taxa in a hotspot also varied by taxonomic group, generally according to their sample sizes (Figure 1). At-risk plant hotspot cells had a maximum of 42 overlapping taxa, while also being the most abundant taxonomic group in our data with 184 taxa. Conversely, the least abundant taxonomic groups (mosses, amphibians and lichens) each had at most 6 overlapping taxa in a hotspot. When accounting for the total number of taxa in each group, birds, reptiles, and molluscs each had a maximum number of taxa in a hotspot of around half of their total sample size (46%, 53% and 50% of their total taxa in our data respectively). For the other six taxonomic groups, the maximum number of taxa in a hotspot ranged from 22% to 35% of their total taxa.

4.2 Q2) Do more nationally at-risk taxa have smaller or more peripheral ranges in Canada? Does this vary among taxonomic groups?

Taxa given an at-risk (Special Concern, Threatened or Endangered) threat status by COSEWIC had very similar global (median = 728,753 km^2) and Hemisphere (median = 725,676 km^2) ranges. Their Canadian distributions were generally much smaller (median = 13,042 km^2; Figure 2A). At-risk taxa in Canada largely occurred at the edge of their Hemisphere range, with 71% of them having 20% or less of their range in Canada. The median and mean percentage of their global in Canada were 4.26% and 23.11% respectively; the median and mean percentage of their Hemisphere range in Canada were 4.38% and 23.82% respectively.

Hemisphere range area differed with COSEWIC status depending on the taxonomic group (Hemisphere range area ~ COSEWIC status + taxonomic group, $\chi^2_{df14} = 30.0$, $P = .0077$; Figure

2B). The Hemisphere range areas of threatened arthropods were significantly smaller than those of special concern (*P* < .0001) or endangered (*P* < .0001) arthropods, while the Hemisphere range areas of special concern plants were significantly smaller than those of threatened plants (*P* = .0085). The Hemisphere range areas of the other taxonomic groups did not change significantly with COSEWIC status.

Canadian range area differed with COSEWIC status depending on the taxonomic group (Canadian range area ~ COSEWIC status + taxonomic group, $\chi^2_{df14} = 56.4$, $P < .0001$; Figure 2C). Among birds, amphibians and arthropods, the most imperilled taxa had significantly smaller Canadian range areas than less imperilled taxa ($P < .005$). Among plants, threatened taxa had significantly greater Canadian range areas than special concern ($P = .0028$) or endangered ($P < .0001$) taxa. The Canadian range areas of the other taxonomic groups did not change significantly with COSEWIC status.

As predicted, the percentage of Hemisphere range in Canada (i.e. peripherality) differed among COSEWIC statuses, with the most imperilled taxa (endangered) having a significantly smaller proportion of their range in Canada than the least imperilled taxa (special concern) (% of Hemisphere range in Canada ~ COSEWIC status, $\chi^2_{df2} = 15.2$, $P = .0005$; Figure 2D). Peripherality also differed among taxonomic groups, with mammals having a significantly greater proportion of their range in Canada than reptiles or plants (% of Hemisphere range in Canada ~ taxonomic group, $\chi^2_{df7} = 23.1$, $P = .0016$; Figure 2D). The percentage of Hemisphere range in Canada did not differ significantly with COSEWIC status depending on the taxonomic group, so the interaction was dropped (% of Hemisphere range in Canada ~ COSEWIC status + taxonomic group, $\chi^2_{df14} = 14.4$, $P = .42$).

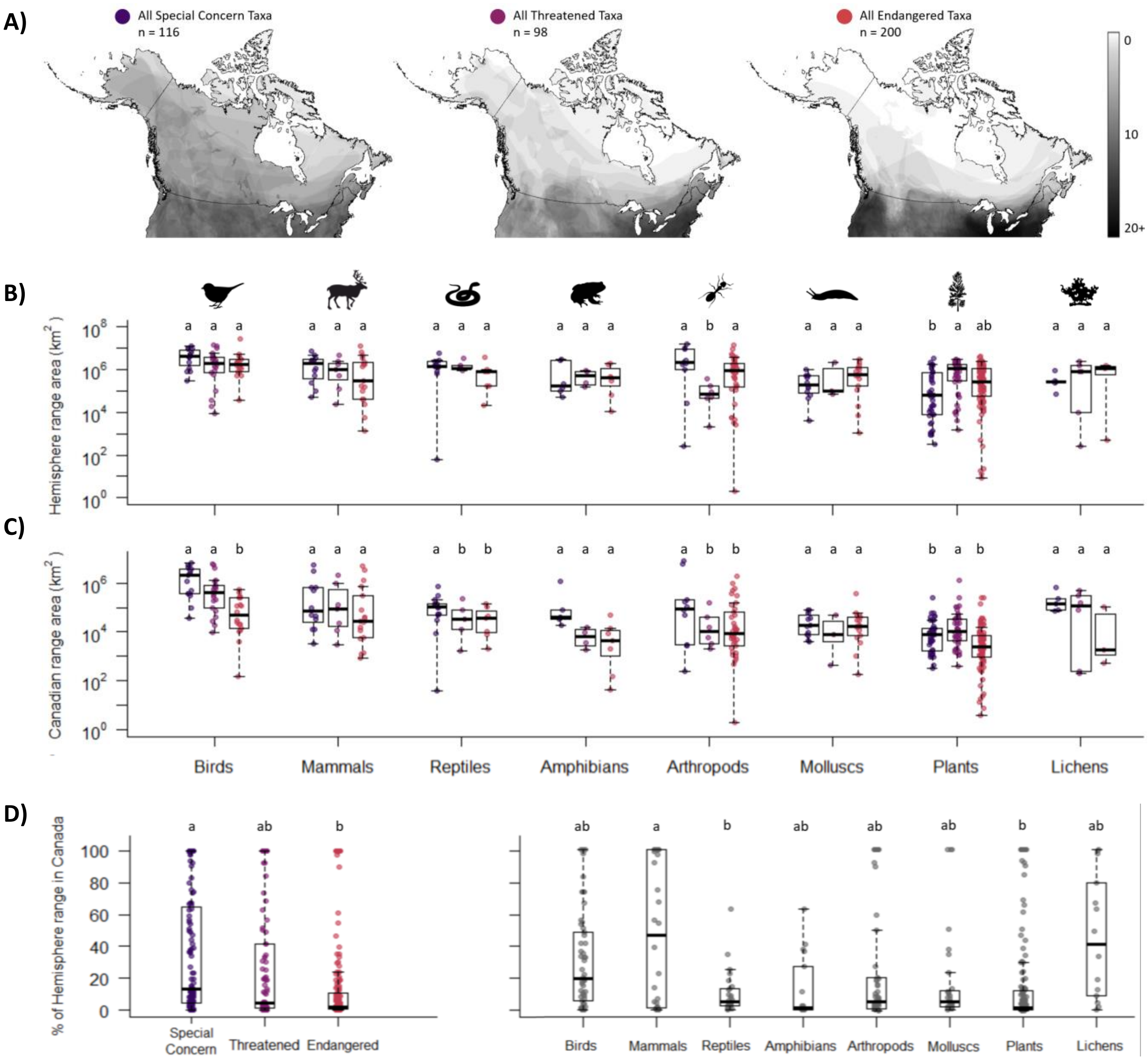


Figure 2. A) Canadian distributions of the terrestrial at-risk taxa assessed by COSEWIC with digitizable global maps. Taxa are separated by their COSEWIC threat status, with coloured dots describing the colour scheme used in all four panels. **B-C)** Hemisphere range area and Canadian range area, separated by COSEWIC threat status for each taxonomic group. Differing letters represent significant differences among COSEWIC statuses within each taxonomic group. **D)** Percentage of Hemisphere range area in Canada. Differing letters in panel D (left) represent significant differences among COSEWIC statuses; those in panel D (right) represent significant differences among taxonomic groups. **B-D)** Vascular plants and mosses were grouped into a single taxonomic group called "plants". In each box plot, the lower horizontal line represents the 25th percentile, the middle line represents the median, and the upper line represents the 75th percentile. Whiskers extend from the 25th or 75th percentile to the lowest value between either the extreme points or 1.5 times the interquartile range. Raw data is indicated by horizontally jittered coloured points. These are the results for Q2), with sample sizes shown in Table 1D).

5. DISCUSSION

By exploring the spatial distribution of Canada's at-risk taxa, I found two key results. First, the areas with the highest numbers of at-risk taxa were clustered along Canada's southern border, which is consistent with the patterns found by previous studies (Caissy et al., 2020; Coristine et al., 2018; Gibson et al., 2009). Together, these hotspots of at-risk taxa were taxonomically diverse and were not solely driven by the most abundant groups (Figure 1). Second, almost three-quarters (71%) of the at-risk taxa in our data have 20% or less of their range in Canada (Figure 2), aligning with the findings of previous works on peripherality (Caissy et al., 2020; Cameron & Hargreaves, 2020; Gibson et al., 2009). The most imperilled taxa had a significantly smaller percentage of their range in Canada than the least imperilled taxa, as well as a significantly smaller Canadian range area in some taxonomic groups, which supports a real relationship between higher threat status and peripheral populations as proposed by Caissy et al., 2020.

While hotspot overlap was particularly high among taxonomic groups that clustered along the southern border (e.g., between reptiles, arthropods, and vascular plants; between amphibians and molluscs), birds, mammals, mosses, and lichens had relatively unique distributions patterns and lower overlap (Figure 1). Variation in hotspot overlap could be due to certain groups being threatened by similar pressures or sharing similar habitat requirements, such as amphibians and molluscs depending on water. Birds and mammals' higher dispersal ability could be driving their more extensive distribution (Howard et al., 2020), while groups such as reptiles may be clustering southward by being more temperature-limited at their northern range edge (Cunningham et al., 2016). This variation could also reflect sampling biases. Birds and mammals appear to be more extensively mapped in remote areas than other less readily identifiable groups, whose mapped ranges along the southern border might simply reflect higher research resources in these areas. However, the typically understudied arthropods (Titley et al., 2017) also appear to be widely mapped (Figure 1), suggesting that these patterns could also be biologically driven.

The unique distribution of at-risk mammals is particularly important as conservation interest is often heavily biased towards them (Davies et al., 2019; Titley et al., 2017). Since many charismatic at-risk mammals are found in northwestern Canada's at-risk mammal hotspots (e.g., caribou *Rangifer tarandus*; grizzly bear *Ursus arctos*), using one as a flagship species may focus conservation efforts away from other at-risk taxonomic groups' southern clusters. However, my analysis' at-risk hotspots do not necessarily equate to other types of biodiversity hotspots. While at-risk mammal hotspots significantly coincide with total mammal richness in Canada (Cameron & Hargreaves, 2020), we cannot assume this holds true for all taxa. In fact, no significant congruence among at-risk and total richness hotspots has been found when assessing global birds (Orme et al., 2005) or plants in China (Feng et al., 2012). At-risk mammals may thus overlap poorly with other at-risk taxa but could still be valuable umbrella species for Canada's overall biodiversity. Either way, future conservation efforts should remain aware of this potential disparity in at-risk taxa distributions if a diversity of Canada's imperilled taxa is to be protected.

Despite variations, hotspot overlap among Canada's taxonomic groups is promising for the planning of diverse protected areas. Protecting Canada's total at-risk hotspots would encompass more than half of the at-risk taxa in each taxonomic group and 80 % of the total at-risk taxa in our data. Unfortunately, the 100x100 km grid scale at which I found this high overlap is much coarser than the scale at which land is usually protected (Cameron & Hargreaves, 2020). Species ranges do not always cover an entire hotspot grid cell, which can make overlaps scale dependent (McKerrow et al., 2018). Even so, coarsely mapping Canada's at-risk hotspots provides a useful starting point for future, more local-scale analyses. This also speaks to delineating larger areas for protection to encompass the full suite of overlapping taxa in a hotspot grid cell. Additionally, species range shifts are already changing cross-taxonomic overlap in dynamic landscapes (Yong et al., 2016), which will likely be the case in southern Canada's highly human modified areas where our at-risk hotspots are located (Coristine et al., 2018; Coristine & Kerr, 2011). Coarse scale protection could therefore turn out to be the best way to keep pace with shifting species.

Potential species range shifts are particularly important to consider in light of the finding that 71% of Canada's at-risk taxa are peripheral. As expected, smaller Canadian range area was associated with more imperilled taxa in birds, reptiles, and arthropods, while the most imperilled taxa had a significantly smaller percentage of their range in Canada (i.e. were more peripheral) than the least imperilled taxa. Once again, the distribution of mammals stood out by being significantly less peripheral than that of reptiles and plants, which is likely due to their comparatively less southward-bound distribution pattern (Figure 1). Overall, this corroborates the idea that range-edge populations are associated with higher risk, as found by Caissy et al., 2020. This could be due to these populations' smaller Canadian range area and therefore smaller numbers, and to their proximity to clusters of anthropogenic pressures such as human population density and agriculture along Canada's southern border (Caissy et al., 2020; Coristine & Kerr, 2011).

The prevalence of peripherality among Canada's at-risk taxa suggests that the at-risk hotspots I identified are likely also the home of many range-edge taxa. Thus, these areas not only key to protecting a taxonomically diverse set of at-risk populations, but they could also provide essential corridors at a time when species are shifting toward higher latitudes to follow a changing climate (Chen et al., 2011). Indeed, leading-edge peripheral populations may be the best suited to lead the northward range shifts of larger populations farther south and thus contribute to their species’ persistence under climate change, which makes protection along Canada’s southern at-risk hotspots particularly important (Gibson et al., 2009). While this study revealed large scale variation in the distribution patterns of Canada’s at-risk fauna and flora, it also highlighted promising hotspots with highly diverse overlap, which I hope will provide a useful starting point as Canada leads its biodiversity into the future.

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8. SUPPLEMENTARY MATERIAL

Supplementary Table 1. Seasonal bird range categories. Table taken from the dataset provided by BirdLife International and Handbook of the Birds of the World 2019.

Season	**Definition**
Resident	The species is/was known or thought very likely to be resident throughout the year
Breeding Season	The species is/was known or thought very likely to occur regularly during the breeding season and to breed and capable of breeding
Non-breeding Season	The species is/was known or thought very likely to occur regularly during the non-breeding season. In the Eurasian and North American contexts, this encompasses 'winter'.
Passage	The species is/was known or thought very likely to occur regularly during a relatively short period(s) of the year on migration between breeding and non-breeding ranges.
Seasonal Occurrence Uncertain	The species is/was present, but it is not known if it is present during part or all of the year.

* Note: No species used in this study had a range in Canada with a season defined as "Seasonal Occurrence Uncertain".