Ornithological Applications, 2024, 127, 1–9
https://doi.org/10.1093/ornithapp/duae064
Advance access publication 15 November 2024
Research Article

Ornithological Applications
OXFORD

Migratory mixing of *Gallinago delicata* (Wilson's Snipe) in wintering areas highlights the need for international coordination for monitoring and management

Bobbi G. Carpenter,[1,*] Caitlin J. Campbell,[2,3,4] Andrew Fanning,[5] and Mark McBride[5,6]

[1]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, Gainesville, Florida, USA
[2]Department of Biology, University of Florida, Gainesville, Florida, USA
[3]University of Florida Biodiversity Institute, Gainesville, Florida, USA
[4]Bat Conservation International, Austin, Texas, USA
[5]Florida Fish and Wildlife Conservation Commission, Tallahassee, Florida, USA
[6]Tennessee Wildlife Resources Agency, Nashville, Tennessee, USA

[*]Corresponding author: bobbi.carpenter@myfwc.com

ABSTRACT

Determining migratory connectivity is essential to understanding population dynamics and managing and conserving migratory species. *Gallinago delicata* (Wilson's Snipe) is a widely hunted wetland bird distributed throughout North America and parts of South America with little known regarding migratory strategy, connectivity, or population trends. Here, we used stable hydrogen isotope analysis of feathers to identify breeding areas and determine the degree of migratory mixing of 323 *G. delicata* harvested in Florida during the nonbreeding season. Our results demonstrate a high degree of migratory mixing between breeding and nonbreeding seasons and provide evidence that breeding birds from throughout Canada and the northwestern United States migrate to Florida. We also found evidence of long-distance migration across both latitudinal and longitudinal bands, with 104 individuals traveling from breeding grounds in western Canada or Alaska to nonbreeding habitat in Florida; the farthest-traveling individual likely migrated at least 4,270 km. Our findings highlight the crucial role of active and coordinated monitoring and management of the widely harvested *G. delicata*, which as long-distance migrants are disproportionately vulnerable to global environmental change.

Keywords: game birds, migratory mixing, migratory connectivity, nonbreeding, shorebirds

How to Cite

Carpenter, B. G., C. J. Campbell, A. Fanning, and M. McBride (2024). Migratory mixing of *Gallinago delicata* (Wilson's Snipe) in wintering areas highlights the need for international coordination for monitoring and management. Ornithological Applications 127:duae064.

LAY SUMMARY

- Migratory wetland birds face unique pressures from habitat change, harvest, and other human-caused factors.
- The degree that populations "mix" between breeding and nonbreeding habitats, and how far individuals travel between those habitats, is important to understand population dynamics and to monitor and manage populations.
- We used the chemical signatures in the feathers of *Gallinago delicata* (Wilson's Snipe) harvested in Florida in the nonbreeding season to determine breeding origins.
- Breeding habitat of *G. delicata* found in Florida extends from eastern Canada to Alaska. Many of the *G. delicata* we studied may have spent the breeding season in central Canada, an area associated with recent population declines.
- Because *G. delicata* mix widely between breeding and nonbreeding habitats, it is essential to better coordinate monitoring and conservation efforts among stakeholder agencies.

Migración mixta de Gallinago delicata en áreas de invernada destaca la necesidad de coordinación internacional para el monitoreo y la gestión

RESUMEN

Determinar la conectividad migratoria es esencial para comprender la dinámica poblacional y gestionar y conservar las especies migratorias. *Gallinago delicata* es un ave de humedales ampliamente cazada, distribuida por América del Norte y partes de América del Sur, sobre la cual se sabe poco en cuanto a estrategia migratoria, conectividad o tendencias poblacionales. Aquí, utilizamos el análisis de isótopos estables de hidrógeno en plumas para identificar áreas de reproducción y determinar el grado de migración mixta de 323 individuos de *G.*

Submission Date: June 20, 2024. Editorial Acceptance Date: October 29, 2024

delicata cazados en Florida durante la temporada no reproductiva. Nuestros resultados demuestran un alto grado de migración mixta entre las temporadas reproductivas y no reproductivas, y proporcionan evidencia de que aves reproductoras de todo Canadá y el noroeste de Estados Unidos migran a Florida. También encontramos evidencia de migración de muy larga distancia a través de bandas latitudinales y longitudinales, con 104 individuos viajando desde lugares de cría en el oeste de Canadá o Alaska hasta hábitats no reproductivos en Florida; el individuo que viajó más lejos probablemente migró al menos 4.270 km. Nuestros hallazgos resaltan el papel crucial del monitoreo y la gestión activa y coordinada de *G. delicata*, que, como migrantes de larga distancia, son desproporcionadamente vulnerables al cambio ambiental global.

Palabras clave: aves de caza, aves playeras, conectividad migratoria, migración mixta, no reproductivo

INTRODUCTION

Management and population trends of long-distance migratory organisms are often not considered across the entire annual cycle (Marra et al. 2015). Populations are vulnerable to impacts year-round, and monitoring and management efforts must consider seasonal dynamics to assess population trends and changing conditions effectively (Morrison et al. 2013). Understanding migratory connectivity (MC), particularly the degree of mixing of individuals between breeding and nonbreeding seasons, is crucial to informing conservation and management (Webster et al. 2002, Martin et al. 2007, Kramer et al. 2018, Knight et al. 2021). Species with low connectivity due to broad mixing of individuals are theoretically more resilient to a changing climate than low-mixing species because some individuals are more likely to encounter and use newly suitable nonbreeding habitats (Finch et al. 2017). Impacts during the nonbreeding season might have widespread but diffuse effects on breeding populations due to high levels of mixing, particularly when breeding populations spread out into extensive nonbreeding habitats (Finch et al. 2017). Conversely, population trends in low-mixing, high-connectivity species are more detectable, because impacts on nonbreeding populations are directly linked to impacts affecting breeding season populations (Kramer et al. 2018).

Monitoring the population dynamics of migratory species with low connectivity may require additional effort and extensive coordination compared to those with high connectivity. The population dynamics of high-mixing migrant species with low connectivity are often unknown and may change across the annual cycle (Marra et al. 2015; Piironen et al. 2023) requiring more extensive surveys (Finch et al. 2017). Surveys of multiple habitats are essential, because variable trends on distinct breeding grounds may result in “averaged” trends in nonbreeding grounds for high-mixing species (Cresswell 2014). This consideration, compounded with challenges facing long-distance migrants driven by habitat loss and global environmental change (Møller et al. 2008, Both et al. 2010), makes it critical to monitor population trends across the geographic range and annual cycle of long-distance migrants. However, for many migratory species, populations are subject to limited monitoring and management, often not coordinated among management agencies. Conversely, status and trends obtained from large-scale unstructured citizen-science data collection, such as eBird status, may not yet be sufficiently sensitive to detect declines within and across populations of the world’s bird species, particularly cryptic species (Neate-Clegg et al. 2020).

Gallinago delicata (Wilson’s Snipe) is an elusive shorebird found in inland freshwater habitats including marshes, pasturelands, wetlands, rivers, and rice fields (Tuck 1972). From 1945 to 2002, *G. delicata* was classified as a subspecies of *G. gallinago* (Common Snipe) until Banks et al. (2002) determined that it was a distinct species based on morphology and display vocalizations. *Gallinago delicata* breed in Canada and the northern United States and spend the nonbreeding season in the southern United States, Caribbean, Central America, and northern South America (Banks et al. 2002), with high concentrations in southern California, Florida, Texas, and the Lower Mississippi Alluvial Valley (Fink et al. 2022). They are a popular game bird that is harvested in Canada, Alaska, and all over the continental United States (Richkus et al. 2008). Despite being a widely harvested species, knowledge about *G. delicata* migration and seasonal distributions is limited (Cline and Haig 2011). One of the U.S. Fish and Wildlife Service’s (USFWS) research priorities is to identify the breeding regions of *G. delicata* harvested in nonbreeding states with high harvest rates (Case and McCool 2009). Limited banding and recapture data from the early 1900s linked breeding regions from the northeastern U.S. and eastern Canada with nonbreeding locations throughout the southeastern U.S. and Caribbean (Tuck 1972). Tuck (1972) speculated that populations breeding in Alaska and Canada likely mix widely between breeding and nonbreeding ranges; however, it has never been formally evaluated or confirmed at a broad scale. Understanding whether *G. delicata* move as populations or subpopulations between distinct breeding and nonbreeding habitats or mix widely between seasonal ranges would inform both natural history and management.

There is no coordinated range-wide monitoring effort of *G. delicata* population trends, although eBird data suggest the abundance of the species has declined sharply between 2007 and 2021 along the shores of Hudson Bay and southern Manitoba (Fink et al. 2022). Range-wide breeding bird survey estimates, which have challenges in monitoring trends of infrequently observed wetland species including snipe (Link and Sauer 1998), do not show significant changes in abundance from 1966 to 2021 (trend estimate: 0.5; 95% CI: –0.1 to 1.1), but region-specific negative trends were observed during that period (Sauer et al. 2023). Much less is known about nonbreeding regional abundance trends. Declines have not been documented in sections of the nonbreeding range including the southeastern U.S., although extremely limited monitoring has been undertaken there (Cooper 2010). Declining population trends have been documented in other snipe species (e.g., *G. gallinago*) in Europe (Henderson et al. 2002).

To evaluate key elements of MC between breeding and nonbreeding habitats of *G. delicata*, we used stable hydrogen isotope analysis to assess the geographic breeding origins of birds overwintering in Florida. We generated probabilistic maps of the likely origins of 323 individuals and used these maps to estimate the minimum distance traveled and general longitude of origin (< 100°W or > 100°W). Our primary aim was to assess MC between breeding and nonbreeding habitat. Specifically, we explored the degree of breeding population mixing within Florida that might thus be subject to disparate population pressures. We anticipated that *G. delicata* overwintering in Florida would represent diverse breeding origins and have low connectivity with nonbreeding regions, highlighting the need for additional monitoring and interagency collaboration.

METHODS

Study Sampling and Stable Isotope Analysis

Feather samples were collected during the 2020–2021 and 2021–2022 snipe hunting seasons (November 1 to February 15) throughout Florida from legally harvested *G. delicata* brought to hunter check stations or mailed to designated locations. The first primary feather from the right wing was removed and stored in an envelope labeled with the collection date, location harvested, and unique identifier. Samples were stored at room temperature. At the end of the hunting season, samples were sent to the Center for Environmental Science Central Appalachians Stable Isotope Facility (CASIF) at the University of Maryland Center for Environmental Science Appalachian Laboratory (Frostburg, MD) for preparation and analysis.

Stable hydrogen isotope analysis is a low-cost and broadly scalable approach to animal movement studies that relies on geographic variation in the stable isotope values of precipitation, which is reflected by animal tissues that synthesize hydrogen from local water sources. By measuring the stable hydrogen isotope composition of feathers, relating these measurements to spatial models of the stable hydrogen isotope values of precipitation allows for inference of the location of formation of those feathers (Hobson et al. 2012). As *G. delicata* grow fresh primary feathers during the breeding season (Tuck 1972), sampling primary feathers during the nonbreeding season allows inference of recent movements between seasons.

Stable hydrogen isotope analysis of feathers was conducted using a standard protocol (Katzner et al. 2017, Vander Zanden et al. 2018a), briefly described below. Feathers were subsampled by cutting along the length, from tip to base, of each feather 2 to 3 times as described by Wassenaar and Hobson (2006). The subsamples from each feather were cleaned and dried (Coplen and Qi 2012) before applying a comparative equilibration approach to measure nonexchangeable stable hydrogen isotope values (δ^2H; Waassenaar and Hobson 2003). Approximately 0.2 mg of cleaned feather subsamples were allowed to equilibrate in ambient air for 72 hr prior to analysis alongside matrix-matched international standards with known values of non-exchangeable hydrogen (USGS42, –72.9‰; USGS43, –44.4‰; CBS [Caribou Hoof Standard], –157.0‰; and KHS [Kudu Horn Standard], –35.3‰; Wassenaar and Hobson 2010, Coplen and Qi 2012) and an internal standard (porcine keratin product #K3030; Spectrum Chemicals, New Brunswick, NJ, USA; –59.5 ± 2.3‰ as by Nelson et al. 2015). The δ^2H of each feather subsample was then measured using a ThermoFisher high-temperature conversion/elemental analyzer pyrolysis unit interfaced with a ThermoFisher Delta V+ isotope ratio mass spectrometer. The resulting δ^2H values were reported on the Vienna Standard Mean Ocean Water-Standard Light Antarctic Precipitation (VSMOW-SLAP) scale, which were calculated using a 2-point normalization curve using CBS and KHS and are reported in units per mil (‰).

Statistical Analyses

We projected the likely origin where the feather was grown (hereafter, "origin") of each sample based on the measured δ^2H values using the *isotopeAssignmentModel* function of the R package *isocat* 0.2.6 (Campbell 2020, Campbell et al. 2020) in R (4.4.1). This approach applies Bayes' Theorem to estimate the posterior probability of a normal distribution representing the probability that a given sample originated at a particular location. To generate these predictions, we leveraged a first-order predicted relationship between feather and local precipitation δ^2H values. As this relationship has not been measured explicitly for *G. delicata*, we used an equation from a related species with similar foraging substrate and migration distance. These characteristics are key factors indicating similarity in the relationship between local precipitation and feathers (Hobson et al. 2012) and are commonly used to identify species for which such equations are expected to be similar (Hobson et al. 2012, Vander Zanden et al. 2018b). We selected an equation from another Scolopacidae, *Scolopax minor* (American Woodcock), a long-distance migrant that also feeds primarily on ground-dwelling invertebrates: $\delta^2H_{feather} = 1.16\ \delta^2H_{precip} + 23.57$ (standard deviation 12.6‰), as by Sullins et al. (2016). Maps of precipitation δ^2H and standard error were sourced from Bowen et al. (2005).

We extracted several key metrics summarizing the origins of each feather sample to contextualize the movements of individual *G. delicata* from their breeding range to eventual sampling in Florida during their nonbreeding period. First, we estimated the minimum distances traveled by individuals by measuring the shortest distance on an ellipsoid between the sample location and potential origins with probabilities of origin that represented cumulative sum probabilities ≥0.25 (Campbell et al. 2020), reporting to the nearest 5 km. We also categorized each sample as likely originating east of the 100°W longitudinal line, west of the line, or could not be determined. This line was selected to represent an approximate longitudinal midpoint of the breeding season range for *G. delicata*, and empirical evidence strongly suggested some individuals grew feathers either east or west of the 100°W longitudinal line. This is made possible because of the strong effect of elevation on the stable hydrogen isotope composition of precipitation in the breeding range of *G. delicata*, wherein ~95% of precipitation values ≥ –65‰ within that range fall east of 100°W and ~98% of precipitation values < –130‰ fall west of 100°W (Supplementary Material Figure 1). We next drew probability-weighted points from each surface over 1,000,000 iterations. If more than 80% of the points drawn were from either side of the line, individuals were assigned to "easterly" or "westerly" origins accordingly (similar approaches were used to assign the likely direction of origins by Smith et al. 2022). Finally, we clustered individual maps into 4 groups arranged by the relative latitude of their likely origins. This approach relies on pairwise comparisons of individual probability surfaces, which are then assembled into a distance matrix used in a clustering analysis (Campbell et al. 2020). We divided surfaces into 4 groups using *k*-means clustering, relying on the within-cluster sum of squares to identify an informative number of clusters by selecting a *k* near the elbow. Clusters were arranged by the mean latitude of the probability of origin, and individual samples were assigned to ordinal clusters. To visualize the cumulative origins of clusters, we summed binarized 2:1 odds ratio surfaces for all origins represented in each cluster.

We used minimum estimated distance traveled and longitudinal assignment (easterly, westerly, undetermined) in conjunction with sampling metadata and $\delta^2\text{H}_{\text{feather}}$ measurements to conduct exploratory analyses describing variation in geographic origin and migratory linkages. First, we checked for any temporal relationships in the origins of *G. delicata* included in our study by testing for differences in δ^2H values with respect to collection year using Welch's *t*-test (*stats* package v. 3.6.2). Next, we explored potential relationships between breeding origin and sampling locations and timing by checking for correlations between δ^2H values (which would reflect any fundamental differences in breeding origins) and sampling latitude, and then between δ^2H values and sampling day of the year, using univariate linear regression. Next, we explored how migration distance and region of origin varied within our study and with respect to sampling location by dividing samples according to their grouped origins, and qualitatively mapped the sampling regions of those origins. We used mapping as a preliminary to check for the presence of strong spatial structuring in nonbreeding habitats used by individuals originating in different breeding habitats. We also reported the minimum distances traveled among those groups. Finally, we quantitatively estimated the degree of MC within the sampled population. Similar to the methods established in Cohen et al. (2018, 2019), we incorporated the uncertainty of stable isotope-based maps of breeding origins into multiple empirical direct estimates of MC for the population using the *calcMC* function of the *MigConnectivity* R package (Cohen et al. 2018). We estimated potential origins by sampling potential cells of origin for each individual's breeding origin map, weighted by probability of origin and with replacement for 1,000 iterations, and calculated a bootstrapped MC for each iteration. We report the median estimate and 95% confidence interval of MC estimates for the sampled population.

RESULTS

We collected feather samples from 323 *G. delicata* harvested during the winters of 2020–2021 ($n = 117$) and 2021–2022 ($n = 206$). Feathers were obtained from 25 locations in 13 counties, across a latitudinal gradient ranging from 26.50°W to 30.52°W (Figure 1). Samples were obtained from right primaries when available ($n = 315$), and from left primaries when not ($n = 8$). The exploratory Welsh's *t*-test indicated no differences among δ^2H feather values with respect to sampling year ($P = 0.31$; 95% CI: –0.11, 0.34; $n = 323$); we then proceeded with generating the probability of origin maps. We also found no significant relationship between δ^2H feather values and sampling latitude using linear regression ($P = 0.81$; 95% CI: –2.2, 2.9), nor between δ^2H feather values and sampling day of the year ($P = 0.88$; 95% CI: –0.05, 0.06).

We were able to distinguish easterly vs. westerly origins confidently in 38% of samples ($n = 119$; Figure 2). Most samples ($n = 104$) represented westerly origins. We observed no qualitative evidence of structure among longitudinal origins with respect to sample site location (Figure 3).

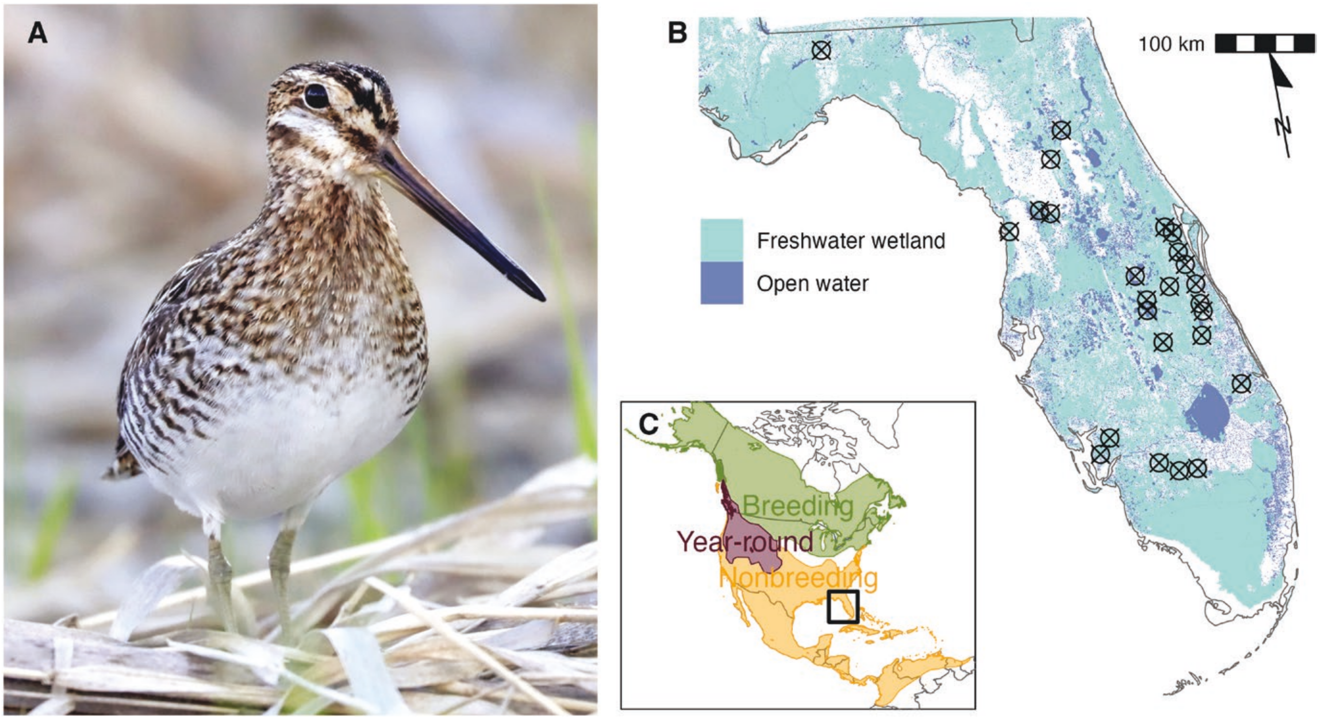

FIGURE 1. (**A**) *Gallinago delicata* (Wilson's Snipe) were sampled during the nonbreeding season throughout Florida (photo credit to Andrew Thomas). (**B**) Sample locations in *x*-marked circles where birds were harvested in freshwater wetland and open water habitats (USFWS National Wetlands Inventory; wetland habitats include freshwater emergent wetland and freshwater forested/shrub wetlands, open water includes lake, freshwater pond, and riverine habitats). (**C**) Inset map highlights the study region (black box) located within the nonbreeding range of the species (lower portion of the map), while feather samples reflect habitat occupied during the breeding season (green and purple regions). Seasonal range maps were sourced from eBird (Fink et al. 2022).

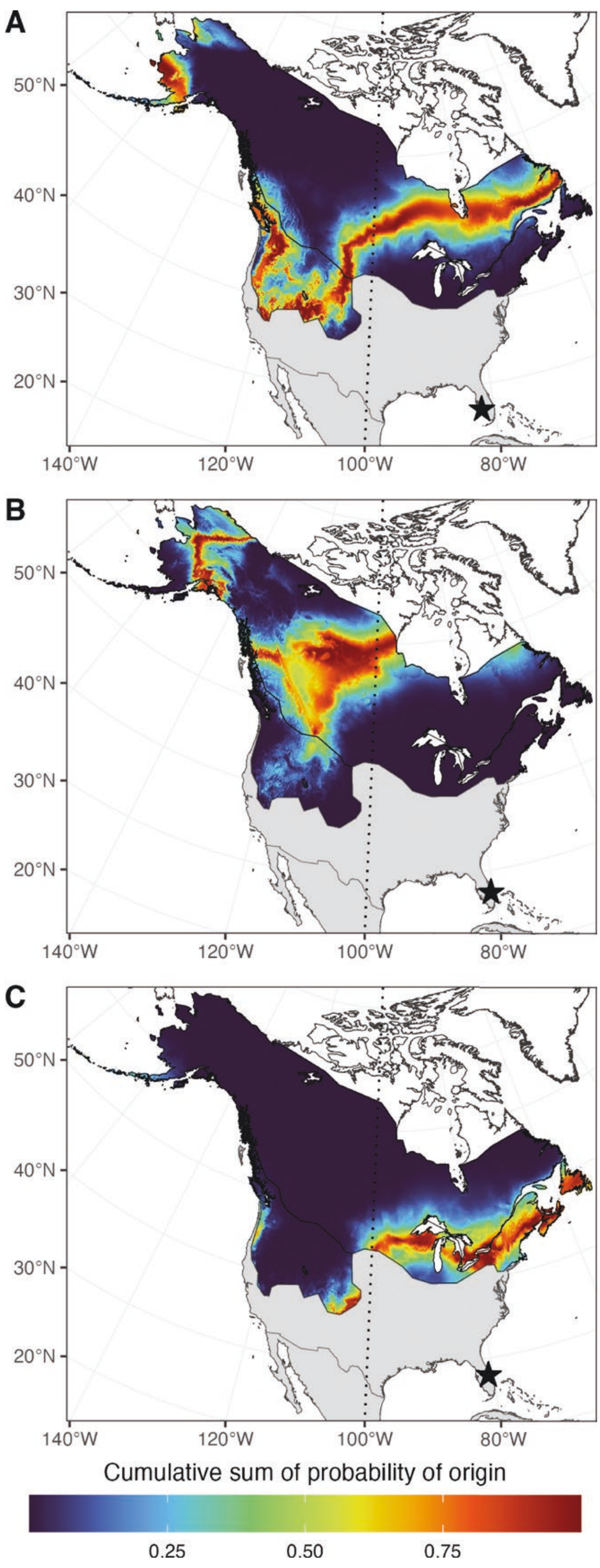

FIGURE 2. We assigned feather samples of *G. delicata* to breeding season geographic origins, including delineation of likely eastern or western origins when possible. Three examples of breeding season origin maps are highlighted here, with warmer colors indicating higher cumulative sums of probabilities of origin. Many maps showed a longitudinally indeterminate origin (**A**), while some indicate a clear westerly (**B**) or easterly (**C**) origin. The nonbreeding sampling location is indicated by a star; light gray areas show the nonbreeding range. We quantified the confidence in assignment to easterly or westerly origins using a simulation approach and indicated the 100°W meridian with a dashed line.

The range of minimum distances traveled between breeding grounds and nonbreeding season grounds sampled in Florida ranged from 1,060 to 4,270 km, with a mean (SD = 688) minimum distance traveled of 2,541 km (Figure 3). The longest distances traveled were associated with westerly origins (mean = 3,212 km, n = 104), with the shortest associated with easterly origins (mean = 1,278 km, n = 15). Clustering broadly aligned with longitudinal assignments, with all westerly originated individuals representing the most northerly origins and all easterly originating individuals generally representing more southerly origins (Figure 3). Our estimates of MC were low, with a median estimate of 0.002 (95% CI: –0.03, 0.05; n = 1000).

DISCUSSION

We report migratory mixing of *G. delicata* from a broad diversity of breeding origins and probable migratory routes to a common nonbreeding region. Likely breeding origins ranged from Alaska to southeastern Canada and the northeastern United States, with several individuals representing clearly easterly or westerly origins (Figures 2 and 3). We found no evidence of migratory or demographic structure between breeding and nonbreeding habitats, which strongly supports widespread mixing of breeding populations in shared nonbreeding habitats. We also report a low level of MC (0.002), as is expected in a high-mixing species (Cohen et al. 2018). This is the first study to evaluate MC in a large number of *G. delicata* (n = 323), and our findings confirm Tuck's (1972) speculation that nonbreeding *G. delicata* populations are made up of individuals from a dispersed breeding range. High mixing is likely common among migratory birds generally (Finch et al. 2017) but has not previously been documented in snipe (Lindström et al. 2016).

This study also presents the first direct evidence of an impressively long-distance migration in many *G. delicata*, with minimum estimated distances traveled by all individuals ranging from 1,060 to 4,270 km. The longest distance traveled by *G. delicata* in this study (4,270 km) linked a nonbreeding location of Lake Panasoffkee WMA in Sumter County, FL, with a breeding location in the Yukon, Northwest Territories, or Alaska. This distance is similar to that reported in Canadian banding studies (n = 9; Tuck 1972). We also identified a surprising proportion of longitudinal movements, as a third of our sampled birds likely spent the breeding season in western North America and some individuals likely traveled from as far as northwest Alaska, presumably crossing several mountainous regions including the Rocky Mountains. As long-distance migrants, *G. delicata* are likely subject to increasing pressure from widespread habitat loss and conversion, as well as navigational impediments including light and noise pollution as well as increased risk of collision with anthropogenic structures along their migratory routes (Thaxter et al. 2010, Davy et al. 2017). Long-distance migrants are potentially

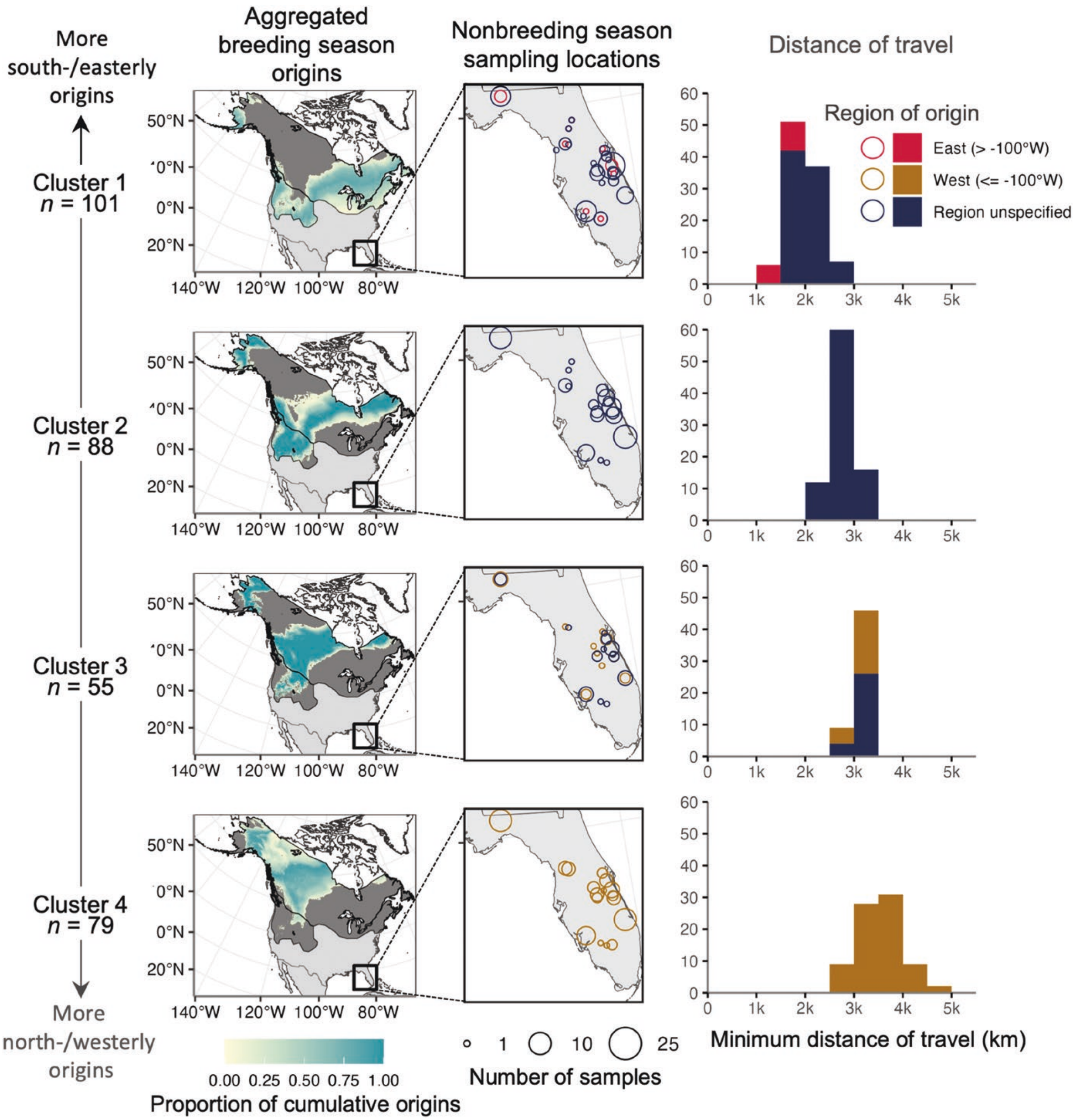

FIGURE 3. Nonbreeding *G. delicata* sampled throughout Florida had diverse breeding season origins. We show grouped breeding season origins, sampling locations, and distances traveled for all samples, grouped by clusters based on the similarity of breeding season origins (vertical arrangement of panels). At the far left, labels indicate cluster group sizes and relative regions of origin for each cluster. North American maps summarize the aggregated regions of origin for each group: darker blues indicate more common origins within each group. Dark gray shows the breeding range, and light gray the nonbreeding range. The middle panels show the sampling locations for each group within Florida, with larger circles indicating more samples taken at a location. The circle colors indicate the longitude of the breeding origin of samples, with confidently easterly (< –100°W), confidently westerly (≥ –100°W), and no confident assignment to a particular longitudinal region of origin. The rightmost panels show histograms indicating the minimum distances of travel associated with each sample.

vulnerable to increased loss of breeding habitat caused by climate change (Møller et al. 2008, Both et al. 2010), which can compound the pressure posed by other forms of global environmental changes (e.g., delayed vegetation green-up) leading to phenological mismatch (Zurell et al. 2018, Youngflesh et al. 2021).

Gallinago delicata mix broadly between breeding and nonbreeding seasons, a finding that highlights that harvest pressure in one state or province might cause substantial declines in other regions without clear cause at the local level. This factor makes *G. delicata* harvest challenging to manage at local and regional scales. Particularly in the context of potential population declines in the central nonbreeding range (Fink et al. 2022), understanding the migratory linkages between breeding and nonbreeding regions is key to both managing harvest and conserving *G. delicata* populations. A key research priority is further studies of MC in *G. delicata* focused on other high-harvest nonbreeding states, which include California, Louisiana, and Texas (Raftovich et al. 2023). As *G. delicata* appear to have at least regional breeding site fidelity (Tuck 1972, Cline and Haig 2011), we expect a genetic structure that reflects those breeding regions. Further studies across the nonbreeding range might benefit from linking movement studies with genetic analyses to test this hypothesis.

Our study highlights the need for standardized, coordinated local and regional monitoring to detect population trends of long-distance, low-connectivity migrants. eBird status and trend data from 2007 to 2021 for breeding populations show declines of over 30% throughout Manitoba and Ontario (Fink et al. 2022); the likely origins of the majority of individuals we sampled in Florida overlapped with that region ($n = 143$ from clusters 2 to 3; Figure 3). The high-spreading migratory strategy would make declines driven by changes to breeding habitat more challenging to detect in the nonbreeding season, particularly because the nonbreeding range of this species is less surveyed overall, particularly through the Caribbean, Central America and northern South America. As the species is elusive and challenging to observe (Mueller 2020), current eBird status and trends data (Fink et al. 2022), and the harvest data reported to the USFWS (Raftovich et al. 2023) appear insufficient to estimate population trends during the nonbreeding season. *Gallinago delicata* is also likely negatively impacted by anthropogenic pressures throughout the nonbreeding range that should be carefully monitored. For example, reflecting widespread degradation and loss of wetland habitat worldwide (Fluet-Chouinard et al. 2023), Florida's wetlands have declined by 51% between 1936 and 1995 (Kautz 1998), and remaining wetland habitat is affected by altered hydrology, pollution, and fragmentation (Kingsford et al. 2016).

A collective effort is needed between the management agencies and stakeholders throughout the range of *G. delicata* that could be modeled after recent coordination to manage research and monitoring of *S. minor* in the eastern United States and Canada (Eastern Woodcock Migration Research Cooperative; www.woodcockmigration.org). The *S. minor* effort leverages coordination between federal agencies in Canada and the United States as well as 15 states and 3 provincial agencies across the species range (Berigan et al. 2022). Efforts to coordinate monitoring and coordination of *G. delicata*, in contrast, would necessitate federal agency involvement from throughout its 21-country range, as well as 49 U.S. states and all 13 Canadian provinces and territories. Research areas should align with the Webless Migratory Game Bird Research Program's priority research list for *G. delicata*, including a national monitoring program, improved harvest and wing collection surveys, and vital rate estimates to support population monitoring (Case and McCool 2009).

A more informed harvest management approach would be useful for *G. delicata* but requires collaboration between managers and researchers across the range to create management objectives, and develop relevant predictive models, management actions, and monitoring programs (Nichols et al. 2007). Similar efforts have been undertaken with other species; for example, for the past 4 decades, waterfowl management and research in the mid-continental administrative flyways (Central and Mississippi Flyways) have coordinated their efforts to create a harvest management strategy that implements management tools on a continental scale to achieve a sustainable population and adequate habitat using *Anas platyrhynchos* (Mallards) as the representative species (Nichols et al. 1995, 2007). Regional efforts to monitor *G. delicata*, like the Carroll and Krementz (2014) survey conducted in the Lower Mississippi Flyway, should be scaled and coordinated across the nonbreeding range. High-priority research should explore migratory phenology and identify priority habitats across breeding and nonbreeding seasons as well as key stopover sites. Such studies might leverage tracking with band recovery and/or GPS transmitters in conjunction with endogenous markers (e.g., stable hydrogen, genetic analysis as in Chabot et al. 2018), allowing for high-resolution tracking data of live individuals to be combined with low-cost endogenous marker analysis of many harvested *G. delicata* (Hobson et al. 2014). A concerted, international partnership would yield valuable ecological and behavioral insights that could lead to scientifically informed management of the *G. delicata*.

Supplementary material

Supplementary material is available at *Ornithological Applications* online.

Acknowledgments

We thank Tammy Sapp and Carol Davis for their work on advertising the call for wing collection and all the hunters who contributed wings for feather sampling. Thanks to Michael Belitz, Andrew Cox, Lisa Smith, and Mark Seamans who provided feedback on the manuscript.

Funding statement

Our research was funded by the Florida Fish and Wildlife Conservation Commission through the State Game Trust Fund. C.J.C. was supported by a University of Florida Biodiversity Institute Fellowship and by a Threadgill Dissertation Fellowship.

Conflict of interest statement

The authors declare they have no competing interests.

Author contributions

A.F. and M.M. conceived the idea. B.C. designed the study. M.M. collected feather samples. B.C. cataloged and coordinated with the isotope analysis lab. C.C. conducted the statistical analysis for the isotope results. C.C. and B.C. contributed equally to writing the manuscript. All authors read and approved the final manuscript.

Data availability

The datasets generated during and/or analyzed during the current study are available in the Zenodo repository, https://zenodo.org/doi/10.5281/zenodo.10680881.

LITERATURE CITED

Banks, R. C., C. Cicero, J. L. Dunn, A.W. Kratter, P. C. Rasmussen, J. V. Remsen Jr., J. D. Rising, and D. F. Stotz (2002). Forty-third supplement to the *American Ornithologists' Union Check-list of North American Birds*. *The Auk* 119:897–906.

Berigan, L., A. Fish, R. Darling, S. Clements, C. Slezak, K. Filkins, E. Blomberg, A. Roth, S. McWilliams, and J. Straub (2022). *American Woodcock (Scolopax minor) migration ecology in eastern North America—2022 Annual Report. Eastern Woodcock Migration Research Cooperative*. https://www.woodcockmigration.org/uploads/1/2/2/8/122821366/year_5_report_2.pdf

Both, C., C. A. Van Turnhout, R. G. Bijlsma, H. Siepel, A. J. Van Strien, and R. P. Foppen (2010). Avian population consequences of climate change are most severe for long-distance migrants in seasonal habitats. *Proceedings of the Royal Society B: Biological Sciences* 277:1259–1266.

Bowen, G. J., L. I. Wassenaar, and K. A. Hobson (2005). Global application of stable hydrogen and oxygen isotopes to wildlife forensics. *Oecologia* 143:337–348.

Campbell, C. (2020). *isocat: Isotope Origin clustering and assignment tools*. https://cran.r-project.org/web/packages/isocat/index.html

Campbell, C. J., M. C. Fitzpatrick, H. B. Vander Zanden, and D. M. Nelson (2020). Advancing interpretation of stable isotope assignment maps: Comparing and summarizing origins of known-provenance migratory bats. *Animal Migration* 7:27–41.

Carroll, J. M., and D. G. Krementz (2014). Density and abundance of Wilson's Snipe Gallinago delicata in winter in the Lower Mississippi Flyway, USA. *Wildlife Biology* 20:108–114.

Case, D. J., and D. D. McCool (2009). Priority information needs for rails and snipe: A funding strategy. U.S. Fish and Wildlife Publications 381. https://digitalcommons.unl.edu/usfwspubs/381

Cline, B. B., and S. M. Haig (2011). Seasonal movement, residency, and migratory patterns of Wilson's Snipe (*Gallinago delicata*). *The Auk* 12:543–555.

Chabot, A. A., K. A. Hobson, S. L.V. Wilgenburg, G. E. Pérez, and S. C. Lougheed (2018). Migratory connectivity in the Loggerhead Shrike (*Lanius ludovicianus*). *Ecology and Evolution* 8:10662–10672

Cohen, E. B., J. A. Hostetler, M. T. Hallworth, C. S. Rushing, T. S. Sillett, and P. P. Marra (2018). Quantifying the strength of migratory connectivity. *Methods in Ecology and Evolution* 9:513–524.

Cohen, E. B., C. R. Rushing, F. R. Moore, M. T. Hallworth, J. A. Hostetler, M. G. Ramirez, and P. P. Marra (2019). The strength of migratory connectivity for birds en route to breeding through the Gulf of Mexico. *Ecography* 42:658–669.

Cooper, T. R. (Compiler) (2010). *Webless Migratory Game Program, Project Abstracts–2009*. U.S. Department of the Interior, Fish and Wildlife Service, Fort Snelling, MN, USA.

Coplen, T. B., and H. Qi (2012). USGS42 and USGS43: Human-hair stable hydrogen and oxygen isotopic reference materials and analytical methods for forensic science and implications for published measurement results. *Forensic Science International* 214:135–141.

Cresswell, W. (2014). Migratory connectivity of Palaearctic–African migratory birds and their responses to environmental change: The serial residency hypothesis. *Ibis* 156:493–510.

Davy, C. M., A. T. Ford, and K. C. Fraser (2017). Aeroconservation for the fragmented skies. *Conservation Letters* 10:773–780.

Finch, T., S. J. Butler, A. M. Franco, and W. Cresswell (2017). Low migratory connectivity is common in long-distance migrant birds. *Journal of Animal Ecology* 86:662-673.

Fink, D., T. Auer, A. Johnston, M. Strimas-Mackey, S. Ligocki, O. Robinson, W. Hochachka, L. Jaromczyk, A. Rodewald, C. Wood, I. Davies, and A. Spencer (2022). *eBird Status and Trends, Data Version: 2021*. Cornell Lab of Ornithology, Ithaca, NY, USA. https://doi.org/10.2173/ebirdst.2021

Fluet-Chouinard, E., B. D. Stocker, Z. Zhang, A. Malhotra, J. R. Melton, B. Poulter, J. O. Kaplan, K. K. Goldewijk, S. Siebert, T. Minayeva, and G. Hugelius (2023). Extensive global wetland loss over the past three centuries. *Nature* 614:281–286.

Henderson, I. G., A. M. Wilson, D. Steele, and J. A. Vickery (2002). Population estimates, trends and habitat associations of breeding Lapwing *Vanellus vanellus*, Curlew *Numenius arquata* and Snipe *Gallinago gallinago* in Northern Ireland in 1999. *Bird Study* 49:17–25.

Hobson, K. A., S. L. Van Wilgenburg, L. I. Wassenaar, and K. Larson (2012). Linking hydrogen (δ^2H) isotopes in feathers and precipitation: Sources of variance and consequences for assignment to isoscapes. *PloS One* 7:4, e35137.

Hobson, K. A., S. L. Van Wilgenburg, J. Faaborg, J. D. Toms, C. Rengifo, A. L. Sosa, Y. Aubry, and R. B. Aguilar (2014). Connecting breeding and wintering grounds of Neotropical migrant songbirds using stable hydrogen isotopes: A call for an isotopic atlas of migratory connectivity. *Journal of Field Ornithology* 85:237–257.

Katzner, T. E., D. M. Nelson, M. A. Braham, J. M. Doyle, N. B. Fernandez, A. E. Duerr, P. H. Bloom, M. C. Fitzpatrick, T. A. Miller, R. C. E. Culver, L. Braswell, and J. A. DeWoody (2017). Golden Eagle fatalities and the continental-scale consequences of local wind-energy generation. *Conservation Biology* 31:406–415.

Kautz, R. S. (1998). Land use and land cover trends in Florida 1936–1995. *Florida Scientist* 6:171–187.

Kingsford, R. T., A. Basset, and L. Jackson (2016). Wetlands: Conservation's poor cousins. *Aquatic Conservation: Marine and Freshwater Ecosystems* 26:892–916.

Knight, E. C., A. Harrison, A. L. Scarpignato, S. L. Van Wilgenburg, E. M. Bayne, J. W. Ng, E. Angell, R. Bowman, R. M. Brigham, B. Drolet, W. E. Easton, T. R. Forrester, J. T. Foster, S. Haché, K. C. Hannah, K. G. Hick, J. Ibarzabal, T. L. Imlay, S. A. Mackenzie, A. Marsh, L. P. McGuire, G. N. Newberry, D. Newstead, A. Sidler, P. H. Sinclair, J. L. Stephens, D. L. Swanson, J. A. Tremblay, and P. P. Marra (2021). Comprehensive estimation of spatial and temporal migratory connectivity across the annual cycle to direct conservation efforts. *Ecography* 44:665–679.

Kramer, G. R., D. E. Andersen, D. A. Buehler, P. B. Wood, S. M. Peterson, J. A. Lehman, K. R. Aldinger, L. P. Bulluck, S. Harding, J. A. Jones, J. P. Loegering, C. Smalling, R. Vallender, and H. M. Sereby (2018). Population trends in *Vermivora* warblers are linked to strong migratory connectivity. *Proceedings of the National Academy of Sciences USA* 115:E3192–E3200

Lindström, Å., T. Alerstam, P. Bahlenberg, R. Ekblom, J. W. Fox, J. Råghall, and R. H. Klaassen (2016). The migration of the Great Snipe *Gallinago media*: Intriguing variations on a grand theme. *Journal of Avian Biology* 4:321–334.

Link, W. A., and J. R. Sauer (1998). Estimating population change from count data: Application to the North American Breeding Bird Survey. *Ecological Applications* 8:258–268.

Marra, P. P., E. B. Cohen, S. R. Loss, J. E. Rutter, and C. M. Tonra (2015). A call for full annual cycle research in animal ecology. *Biology Letters* 11:20150552.

Martin, T. G., I. Chadès, P. Arcese, P. P. Marra, H. P. Possingham, and D. R. Norris (2007). Optimal conservation of migratory species. *PloS One* 2:e751.

Møller, A. P., D. Rubolini, and E. Lehikoinen (2008). Populations of migratory bird species that did not show a phenological response to climate change are declining. *Proceedings of the National Academy of Sciences USA* 105:16195–16200.

Morrison, C. A., R. A. Robinson, J. A. Clark, K. Risely, and J. A. Gill (2013). Recent population declines in Afro-Palaearctic migratory birds: The influence of breeding and non-breeding seasons. *Diversity and Distributions* 19:1051–1058.

Mueller, H. (2020). Wilson's Snipe (*Gallinago delicata*), version 1.0. In *Birds of the World* (A. F. Poole and F. B. Gill, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA. https://doi.org/10.2173/bow.wilsni1.01

Neate-Clegg, M. H., J. J. Horns, F. R. Adler, M. Ç. K. Aytekin, and Ç. H. Şekercioğlu (2020). Monitoring the world's bird populations with community science data. *Biological Conservation* 248:108653.

Nelson, D. M., M. Braham, T. A. Miller, A. E. Duerr, J. Cooper, M. Lanzone, J. Lemaître, and T. Katzner (2015). Stable hydrogen isotopes identify leapfrog migration, degree of connectivity, and summer distribution of Golden Eagles in eastern North America. *The Condor: Ornithological Applications* 117:414–429.

Nichols, J. D., F. A. Johnson, and B. K. Williams (1995). Managing North American waterfowl in the face of uncertainty. *Annual Review of Ecology and Systematics* 26:177–199.

Nichols, J. D., M. C. Runge, F. A. Johnson, and B. K. Williams (2007). Adaptive harvest management of North American waterfowl populations: A brief history and future prospects. *Journal of Ornithology* 48:S343–S349.

Piironen, A., A. D. Fox, H. Kampe-Persson, U. Skyllberg, O. R. Therkildsen, and T. Laaksonen (2023). When and where to count? Implications of migratory connectivity and nonbreeding distribution to population censuses in a migratory bird population. *Population Ecology* 65:121–132.

Raftovich, R. V., K. K. Fleming, S. C. Chandler, and C. M. Cain (2023). *Migratory bird hunting activity and harvest during the 2021–22 and 2022–23 hunting seasons*. U.S. Fish and Wildlife Service, Laurel, MD, USA. https://fws.gov/library/collections/migratory-bird-hunting-activity-and-harvest-reports

Richkus, K. D., K. A. Wilkins, R.V. Raftovich, S. S. Williams, and H. L. Spriggs (2008). *Migratory bird hunting activity and harvest during the 2006 and 2007 hunting seasons: Preliminary estimates*. U.S. Fish and Wildlife Service, Laurel, MD, US. https://digitalcommons.unl.edu/usfwspubs/356/

Sauer, J. R., W. A. Link, and J. E. Hines (2023). The North American Breeding Bird Survey, Analysis Results 1966–2019: U.S. Geological Survey data release. https://doi.org/10.5066/P9SC7T11

Smith, L. M., J. A. Gore, T. J. Doonan, and C.J. Campbell (2022). Tricolored bats at a southern range edge exhibit partial migration northward in autumn. *Movement Ecology* 10:56.

Sullins, D. S., W. C. Conway, D. A. Haukos, K. A. Hobson, L. I. Wassenaar, C. E. Comer, and I. K. Hung (2016). American Woodcock migratory connectivity as indicated by hydrogen isotopes. *The Journal of Wildlife Management* 80:510–526.

Thaxter, C. B., A. C. Joys, R. D. Gregory, S. R. Baillie, and D. G. Noble (2010). Hypotheses to explain patterns of population change among breeding bird species in England. *Biological Conservation* 143:2006–2019.

Tuck, L. M (1972). *The Snipes: A Study of the Genus Capella*. Canadian Wildlife Service, Ottawa, Canada.

Vander Zanden, H. B., A. Reid, T. Katzner, and D. M. Nelson (2018a). Effect of heat and singeing on stable hydrogen isotope ratios of bird feathers and implications for their use in determining geographic origin. *Rapid Communications in Mass Spectrometry* 32:1859–1866.

Vander Zanden, H. B., D. M. Nelson, M. B. Wunder, T. J. Conkling, and T. Katzner (2018b). Application of isoscapes to determine geographic origin of terrestrial wildlife for conservation and management. *Biological Conservation* 228:268–280.

Wassenaar, L. I., and K. A. Hobson (2003). Comparative equilibration and online technique for determination of non-exchangeable hydrogen of keratins for use in animal migration studies. *Isotopes in Environmental and Health Studies* 39:211–217.

Wassenaar, L. I., and K. A. Hobson (2006). Stable-hydrogen isotope heterogeneity in keratinous materials: Mass spectrometry and migratory wildlife tissue subsampling strategies. *Rapid Communications in Mass Spectrometry* 20:2505–2510.

Wassenaar, L. I., and K. A. Hobson (2010). Two new keratin standards (δ^2H, δ^{18}O) for daily laboratory use in wildlife and forensic isotopic studies. In *The 7th International Conference on Applications of Stable Isotope Techniques to Ecological Studies*. University of Alaska, Fairbanks, AK, USA.

Webster, M. S., P. P. Marra, S. M. Haig, S. Bensch, and R. T. Holmes (2002). Links between worlds: Unraveling migratory connectivity. *Trends in Ecology & Evolution* 17:76–83.

Youngflesh, C., J. Socolar, B. R. Amaral, A. Arab, R. P. Guralnick, A. H. Hurlbert, R. LaFrance, S. J. Mayor, D. A. W. Miller, and M. W. Tingley (2021). Migratory strategy drives species-level variation in bird sensitivity to vegetation green-up. *Nature Ecology and Evolution* 5:987–994.

Zurell, D., C. H. Graham, L. Gallien, W. Thuiller, and N. E. Zimmermann (2018). Long-distance migratory birds threatened by multiple independent risks from global change. *Nature Climate Change* 8:992–996.