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1 **Using citizen science monitoring data in species distribution models to inform isotopic**  
2 **assignment of migratory connectivity in wetland birds**

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11 **Abstract**

12 Stable isotopes have been used to estimate migratory connectivity in many species. Estimates are often  
13 greatly improved when coupled with species distribution models (SDMs), which temper estimates in  
14 relation to occurrence. SDMs can be constructed using from point locality data from a variety of sources  
15 including extensive monitoring data typically collected by citizen scientists. However, one potential issue  
16 with SDM is that these data oven have sampling bias. To avoid this potential bias, an approach using  
17 SDMs based on marsh bird monitoring program data collected by citizen scientists and other participants  
18 following protocols specifically designed to maximize detections of species of interest at locations  
19 representative of the species range. We then used the SDMs to refine isotopic assignments of breeding  
20 areas of autumn-migrating and wintering Sora (*Porzana carolina*), Virginia Rails (*Rallus limicola*), and  
21 Yellow Rails (*Coturnicops noveboracensis*) based on feathers collected from individuals caught at  
22 various locations in the United States from Minnesota south to Louisiana and South Carolina. Sora were  
23 assigned to an area that included much of the western U.S. and prairie Canada, covering parts of the  
24 Pacific, Central, and Mississippi Flyways. Yellow Rails were assigned to a broad area along Hudson and  
25 James Bay in northern Manitoba and Ontario, as well as smaller parts of Quebec, Minnesota, Wisconsin,  
26 and Michigan, including parts of the Mississippi and Atlantic Flyways. Virginia Rails were from several  
27 discrete areas, including parts of Colorado, New Mexico, the central valley of California, and southern  
28 Saskatchewan and Manitoba in the Pacific and Central Flyways. Our study demonstrates extensive data  
29 from organized citizen science monitoring programs are especially useful for improving isotopic  
30 assignments of migratory connectivity in birds, which can ultimately lead to better informed management  
31 decisions and conservation actions.

32 **Keywords:** Autumn Migration, Hydrogen, Sora, Stable Isotopes, Virginia Rail, Wetlands, Yellow Rail

### 33 **Introduction**

34 Determining links among breeding, migratory stopover, and wintering areas for different populations of  
35 migratory birds (hereafter ‘migratory connectivity’) is critically important for conserving species  
36 throughout their annual cycle (Webster et al. 2002, Hobson et al. 2014). Knowledge on migratory  
37 connectivity informs full life cycle conservation by associating populations with areas that they inhabit.  
38 Connecting populations and habitat is essential to identifying limiting factors and can permit more  
39 effective responses to threats by targeting the most affect parts of populations or the annual cycle (Norris  
40 and Taylor 2006, Taylor and Norris 2010, Rushing et al. 2016). Most studies examine migratory  
41 connectivity between wintering and breeding areas, but connectivity with stopover habitat during  
42 migration is also important in understanding factors that limit populations throughout their annual cycle  
43 (e.g., Hobson et al. 2014; 2015).

44 There are a variety of effective methods for estimating migratory connectivity of birds including mark-  
45 recapture (Ryder et al. 2011), archival biologgers (Ryder et al. 2011, Salewski et al. 2013, Hallworth et al.  
46 2013), collaborative radio tracking networks (Taylor et al. 2017), and satellite transmitters (Krementz et  
47 al. 2011). Despite a diversity of methods, these techniques will not work with all species. When a  
48 transmitter is too heavy relative to the weight of the species it is unsafe to attach the device. When a  
49 species has low site fidelity among years it becomes impractical to relocate and recapture individuals to  
50 retrieve the archival biologgers and the data the devices contain. In addition, collaborative radio-tracking  
51 networks, although extremely promising in the near-future for broad scale studies, are currently  
52 unavailable in most areas. In situations when the above approaches are ineffective, isotopes can be used  
53 because individuals need to be captured only once to obtain samples (e.g., feathers, toenails, blood), and  
54 no tracking devices need to be attached. In North America, the ratio of hydrogen isotopes ( $\delta^2\text{H}$ ) follows a  
55 spatial gradient from northwest to southeast and has been widely used to examine migratory connectivity  
56 of many species (Hobson and Wassenaar 2008, Guillemain et al. 2014a, Butler et al. 2016). One  
57 disadvantage of stable hydrogen isotopes is the resulting coarse geographic assignments, which can limit

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58 the level of inference, but even this limited inference can inform conservation if it's the only information  
59 available (Hobson and Wassenaar 2008). The incorporation of additional data, such as environmental  
60 variables, genetic information, band recovery data, and predictions from species distribution models  
61 (SDMs), can improve geographic assignment because populations are not equally spread over space  
62 (Royle and Rubenstein 2004, Hobson et al. 2013, Rushing et al. 2014, Ruegg et al. 2016). The results lead  
63 to assignments that are more informative for conservation and management purposes (Haig et al. 1998,  
64 Webster et al. 2002, Hobson 2005).

65 Of the many options for refining isotopic assignments of migratory connectivity, SDMs show excellent  
66 utility. The models can be used to predict species occurrence or abundance across vast unsampled areas,  
67 often with reasonable precision and accuracy based on existing data (Elith and Leathwick 2009). This  
68 information can then be coupled with isotopic assignments to produce refinements in relation to species  
69 occurrence or abundance. The most useful SDMs for this purpose are ones based on extensive  
70 representative datasets through space and time.

71 Species abundance data at broad scales are easily obtained from citizen science monitoring programs.

72 These programs operate by engaging volunteers and training them to follow standardized survey  
73 protocols to collect reliable monitoring data. Due to the volunteer nature of the programs combined with  
74 widespread engagement of participants, they often produce large sample sizes over broad spatial  
75 distributions that benefit SDM development. For instance, Fournier et al. (2016) used haphazard  
76 presence-only citizen science data from eBird (Sullivan et al. 2009) to refine stable isotope assignments of  
77 migratory connectivity in the Virginia Rail (*Rallus limicola*). The approach was successful and  
78 substantially improved the refinement of isotopic assignments. However, the authors noted challenges  
79 due to potential biases caused by factors driving where and how observers conduct surveys.

80 One way to overcome perceived bias associated with haphazard presence-only data is to use data  
81 collected by formal monitoring programs. In these programs, participants collect data at locations  
82 regardless of whether the species of interest was detected or not, following established protocols designed

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83 to maximize detection probability (e.g. Conway 2011). Organized monitoring programs typically collect  
84 data at pre-determined randomly-chosen survey locations, making the data representative of entire  
85 populations. Therefore, data from organized bird monitoring programs is more suitable than presence  
86 only data for developing SDMs to refine isotopic assignments of migratory connectivity.

87 In this paper, we demonstrate the use of SDMs to refine isotopic assignments of migratory connectivity in  
88 Sora (*Porzana carolina*), Virginia Rail, and Yellow Rail (*Coturnicops noveboracensis*) using data  
89 collected by citizen scientists and other participants in organized marsh bird monitoring programs and  
90 feathers collected from individuals caught at autumn migration and wintering locations in the United  
91 States ranging from Minnesota to Louisiana and South Carolina. We chose these three rail species, in  
92 part, because they are elusive wetland birds that breed across a wide swath of North America, but are  
93 poorly studied (Eddleman et al. 1988). The species are of concern because they stopover in highly  
94 modified landscapes where wetland loss ranges 60-90%, and their populations are thought to be declining,  
95 but are not clearly understood (Reid 1989, Case and McCool 2009, Ducks Unlimited Canada 2010, Dahl  
96 2011). In addition, the Sora and Virginia Rail are game bird species in some jurisdictions (Tacha and  
97 Braun 1994), while the Yellow Rail is a species of special concern in Canada (Alvo and Robert 2009).  
98 Knowledge of migratory connectivity in these three rail species is only now beginning to emerge (Butler  
99 et al. 2016, Fournier et al. 2016), and is needed to inform conservation and management efforts. Studying  
100 broad scale migratory connectivity in the three species is also currently unsuitable with any of the  
101 methods listed above, except isotopes. Together, these characteristics made the species worthy candidates  
102 with which to demonstrate the method and approach.

## 103 **Methods**

### 104 *Field*

#### 105 *Migrating and Wintering Individuals*

106 Sora, Yellow Rail, and Virginia Rail were captured using dipnets from all-terrain vehicles during autumn  
107 migration between August and October 2015 at 10 sites in Missouri, USA (Perkins et al. 2010). Sora,

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108 Virginia Rail and Yellow Rail feathers from other migratory locations (Minnesota, Michigan, South  
109 Carolina, Ohio, and Arkansas, USA) and wintering locations (Louisiana and Mississippi, USA) were  
110 collected opportunistically by hunters and researchers from August through December 2015 (Table S2).  
111 The first primary feather, which is grown on the breeding grounds (Pyle 2008) and therefore has the  
112 isotopic signature of that location, was removed from each individual. Previously collected Yellow Rail  
113 feathers from another project were included to increase sample size and these feathers were collected in  
114 Missouri during autumn migration in 2013 and 2014.

#### 115 *Breeding Individuals*

116 Sora, Yellow Rail and Virginia Rail were captured on foot during night using call broadcast lures and a  
117 dipnet in late-June and July 2015 near Foam Lake, Saskatchewan, Canada (51.6601, -103.5538). Captures  
118 began at dusk and ran until dawn. Similar to migrants, the first primary feather was removed from each  
119 individual.

#### 120 *Laboratory*

121 Feathers were cleaned with phosphate-free detergent and 2:1 chloroform methanol solution, rinsed them  
122 in deionized water, and dried them at 50 °C for 24 hours. A total of 0.350 mg of material was weighed  
123 into silver capsules (Elemental Microanalysis, part# d2302) and analyzed by coupled pyrolysis/isotope-  
124 ratio mass spectrometry using a thermo-chemical elemental analyzer (TC/EA) (Thermo Scientific)  
125 interfaced to a Thermo Scientific Delta V Plus configured through a CONFLO IV for automated  
126 continuous flow gas-isotope ratio mass spectrometer (CF-IRMS) at the Colorado Plateau Stable Isotope  
127 Laboratory at Northern Arizona University.

128 Given that ~20% of the  $\delta^2\text{H}$  in feathers exchanges freely with ambient water vapor (Wassenaar & Hobson  
129 2003), we analyzed feathers concurrently with three calibrated keratin standards (Keratin – SC Lot SJ  
130 (powdered) mean =  $-120.7 \pm 1.1$  ‰, expected =  $-121.6$  ‰, n=32; CBS – caribou hoof (powdered) mean=  
131  $-198.5 \pm 1.1$  ‰, expected =  $-197.0$  ‰, n=10; KHS – Kudo horn (powdered) mean=  $-55.1 \pm 1.0$  ‰,  
132 expected =  $-54.1$  ‰, n=10) to allow for future comparison across laboratories (Wassenaar & Hobson

133 2003). We report the non-exchangeable  $\delta^2\text{H}$  fraction in parts per mil (‰) normalized to the Vienna  
134 Standard Mean Ocean Water-Standard Light Antarctic Precipitation (VSMOW-SLAP) standard.

135 *Species Distribution Models*

136 We used count data from 7,146 100-m-radius plots surveyed largely by citizen scientists and other  
137 participants in Bird Studies Canada's Great Lakes, Québec, and Prairie marsh monitoring programs (Bird  
138 Studies Canada 2017a; Tozer 2013, 2016) available through Nature Counts (Bird Studies Canada 2017b),  
139 and by observers in the North American Marsh Bird Monitoring Program at various National Wildlife  
140 Refuges available from the Midwest Avian Data Center (Figure 1; Koch et al. 2010) to construct SDMs.  
141 These data spanned 1995-2015 and were collected under a slightly modified version of the Standardized  
142 North American Marsh Bird Monitoring Protocol (e.g., Tozer et al. 2016), which included the use of  
143 standardized call broadcasts of Sora, Yellow Rail, and Virginia Rail during point counts to increase  
144 detection probability (Conway 2011). We collapsed the dataset so the response was the highest count at  
145 each point across all years. We did this instead of formally modeling detection probability to keep the  
146 models simple and more manageable, and to overcome challenges with modeling detection across points  
147 surveyed in different years and in different numbers of years. Selecting the maximum count across all  
148 years surveyed gives a conservative estimate of abundance of each species at each point. This yielded 929  
149 Sora, 695 Virginia Rail, 39 Yellow Rail points where at least one individual was detected and 4,056 Sora,  
150 4,290 Virginia Rail, and 4,946 Yellow Rail points where each species was not detected in any year.

151 We created species distribution models describing Sora, Yellow Rail and Virginia Rail abundance using  
152 11 raster layers (1 km<sup>2</sup> resolution) representing land cover (Latifovic et al. 2002), wetland presence  
153 (Lehner & Döll 2004), and bioclimatic parameters. We chose these layers because they likely influence  
154 precipitation, and thus stable isotope ratios across North America, as well as the distribution and  
155 abundance of the three species we considered. We removed variables which were correlated (Pearson's  
156 correlation coefficient  $\geq 75\%$ , See Table S1). We constrained predictions to each species' summer range  
157 (BirdLife International & NatureServe 2015). Within each species' summer range, our goal, similar to

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158 Fournier et al. (2016), was to generate a SDM with the greatest predictive accuracy (see details below),  
159 but not necessarily informative for inferring environmental relationships (Merow, Smith and Silander  
160 2013). We included all 11 environmental covariates in the analysis and used leave-one-out jackknifing to  
161 identify covariates that reduced the predictive power of the model, which were then removed. All  
162 modeling took place in R (R Core Team 2016, version 3.3.2).

163 *Spatially explicit assignment of geographic origins*

164 We used the methods and code of Van Wilgenburg and Hobson 2011 to perform our spatially explicit  
165 isotopic assignments for each individual. Below is a summary of those methods. We used a likelihood-  
166 based assignment that incorporated estimates of uncertainty (Royle and Rubenstein 2004). Expected  
167  $\delta^2\text{H}_{\text{feather}}$  values were calculated by regressing raw  $\delta^2\text{H}$  feather values of sampled feathers on mean annual  
168 growing season  $\delta^2\text{H}$  in precipitation at the site of collection. This calibration was necessary to account for  
169 systematic differences between the  $\delta^2\text{H}$  of sampled feathers and  $\delta^2\text{H}$  in precipitation. Because we only  
170 had feathers from one breeding ground location, we included data from other projects in our linear  
171 regression of  $\delta^2\text{H}$  of flight feathers to mean annual growing season  $\delta^2\text{H}$  across North America ( $\sim 37 \times 37$   
172 km resolution; Bowen et al. 2005). This known-origin dataset included feathers from Foam Lake  
173 Saskatchewan (45 Sora feathers, 30 Yellow Rail Feathers and 4 Virginia Rail), and 10 Virginia Rail  
174 feathers from one location from Fournier et al. (2016), along with 44 King Rail feathers from Perkins  
175 (2007), including 13 museum specimens from 11 different localities and 31 live captured King Rail  
176 specimens. In total we had 133 feathers from 14 different localities (for additional detail on the feathers  
177 from locations outside of Saskatchewan see Appendix S1 in Fournier et al. (2016)). Because of small  
178 sample size for Yellow Rails in 2015, we also included feathers from autumn migration in 2013 and 2014.  
179 We did not find a significant difference between the median  $\delta^2\text{H}$  values in Yellow Rails among years  
180 (ANOVA  $F = 0.11$ ,  $df = 21$ ,  $p = 0.91$ ; Figure 2), suggesting that inter-annual variability in feather  $\delta^2\text{H}$   
181 was unlikely to be a significant source of variation for our analysis so we combined annual samples. We



182 regressed our data of known-origin feathers against  $\delta^2\text{H}$  precipitation to derive the calibration equation

183  $(\delta^2\text{H}_{\text{corrected}} = -52.36 + 0.83[\delta^2\text{H}_{\text{precipitation}}]).$

184 For each feather we assessed the probability that any cell within the expected values was the origin of that

185 individual using a normal probability density function as follows:

186 
$$f(y^* | \mu_c \sigma_c) = \left( \frac{1}{\sqrt{2\pi}\sigma_c} \right) \exp \left[ -\frac{1}{2\pi\sigma_c^2} (y^* - \mu_c)^2 \right]$$

187 Where  $f(y^* | \mu_c \sigma_c)$  represents the probability that a given cell (c) within the  $\delta^2\text{HF}$  isoscape represents a

188 potential origin for an individual of unknown origin ( $y^*$ ), given the expected mean  $\delta^2\text{HF}$  for that cell ( $\mu_c$ )

189 from the calibrated  $\delta^2\text{HF}$  isoscape and the expected standard deviation ( $\sigma_c$ ) of  $\delta^2\text{HF}$  between individuals

190 growing their feathers at the same locality. To assign probable breeding areas to samples within a

191 particular state, we summed the assignments from each feather sample in units of the number of rails with

192 origins consistent with a given pixel and converted to proportions to enable comparisons with other states,

193 which we report only in the supplementary material. For each individual we produced a surface of

194 spatially explicit probability densities (i.e., one surface per bird in a sample). We then incorporated the

195 prior probabilities from our SDM by applying Bayes's Rule (Van Wilgenburg and Hobson 2011). To

196 depict these origins across the entire sample size we assigned each feather to the base map individually by

197 determining the odds that any given assigned origin was correct relative to the odds it was incorrect.

198 Based on 3:1 odds that a given bird had originated from within the range we recorded the set of raster

199 cells that defined the upper 75% of estimated origins and coded them as 1, all others as 0. We choose 3:1

200 odds based on Van Wilgenburg and Hobson (2011) where this ratio provided a compromise between the

201 possibility of being incorrect and the bird assignment geographic resolution. The results of the individual

202 assignments were then summed over all individuals, by addition of the surfaces. We facilitated this step

203 by rescaling the posterior probabilities ( $f_x$ ) relative to the maximum value within the posterior probability

204 surface prior to applying the odds-ratio-based reclassification.

205 We made assignments using functions within the R statistical computing environment (R Core Team  
206 2016, version 3.3.2) using the ‘raster’ package (Hijmans 2016, version 2.5-8). To make our results even  
207 more relevant for conservation, we also visually inspected assignments to determine broad overlap with  
208 traditional flyways used as administrative units by migratory game bird managers (US Fish and Wildlife  
209 Service 2017).

## 210 **Results**

### 211 *Captures*

212 We captured 142 southbound autumn migrating and wintering rails across the southern U.S., and 79  
213 breeding rails at a wetland complex in Saskatchewan, Canada. Sora comprised the bulk of migrant and  
214 wintering samples (88%; 117 individuals; 8 states) followed by Virginia Rails (7%; 9 individuals; 2  
215 states) and Yellow Rails (5%; 11 individuals; 2 states). Sora also comprised the bulk of breeder samples  
216 (57%; 45 individuals) followed by Yellow Rails (38%; 30 individuals) and Virginia Rails (5%, 4  
217 individuals). See Table S2 for more details.

### 218 *Species Distribution Models*

219 All three species distribution models fit the data (Homer-Lemeshow Goodness of Fit Test, Sora  $\chi^2 = 4.7$ ,  
220  $df = 8$ ,  $p = 0.7$ ; Virginia Rail  $\chi^2 = 4.7$ ,  $df = 8$ ,  $p = 0.7$ ; Yellow Rail  $\chi^2 = 4.4$ ,  $df = 8$ ,  $p = 0.8$ ). The top  
221 species distribution model for Yellow Rail contained mean temperature of driest quarter ( $\beta = -0.30$ ,  $SE =$   
222  $0.09$ ,  $p = 0.002$ ), mean temperature of warmest quarter ( $\beta = 0.28$ ,  $SE = 0.14$ ,  $p = 0.008$ ), mean diurnal  
223 range (mean of monthly (max temp-min temp)) ( $\beta = 0.60$ ,  $SE = 0.16$ ,  $p < 0.001$ ) and a significant  
224 interaction between latitude and longitude ( $\beta = 2.09$ ,  $SE = 0.59$ ,  $p < 0.001$ ). The top species distribution  
225 model for Virginia Rail contained temperature seasonality ( $\beta = -0.002$ ,  $SE = 0.0007$ ,  $p = 0.002$ ). The top  
226 species distribution model for Sora included annual mean temperature ( $\beta = 0.07$ ,  $SE = 0.02$ ,  $p = 0.003$ ),  
227 mean temperature of the warmest quarter ( $\beta = -0.09$ ,  $SE = 0.02$ ,  $p < 0.001$ ) and temperature seasonality ( $\beta$   
228  $= 0.001$ ,  $SE = 0.0002$ ,  $p < 0.001$ ).

229 *Isotopic Assignments*

230 Sora were assigned to an area that included much of the western U.S. and prairie Canada, covering parts  
231 of the Pacific, Central, and Mississippi flyways (Figure 3). Yellow Rails were assigned to a broad area  
232 along Hudson and James Bay in northern Manitoba and Ontario, as well as smaller parts of Quebec,  
233 Minnesota, Wisconsin, and Michigan, including parts of the Mississippi and Atlantic flyways (Figure 3).  
234 Virginia Rails were from several discrete areas, including the southern part of their breeding range in  
235 parts of Colorado, New Mexico, the central valley of California, and southern Saskatchewan and  
236 Manitoba in the Pacific and Central flyways (Figure 3). Due to small sample size (Table S2), we do not  
237 include comparison of breeding ground assignments among states, although for the interested reader we  
238 include maps of these assignments in the supplementary material (Figure S2, S3, S4).

239 **Discussion**

240 We demonstrated the use of SDMs to inform isotopic assignments of migratory connectivity in wetland  
241 birds, based on organized marsh bird monitoring program data collected by citizen scientists and other  
242 participants. We found these data to be especially useful for this purpose for reasons related to sample  
243 size, search effort, detection probability, and ease of obtaining data, which we elaborate further below.

244 Use of SDMs to refine isotopic assignments of migratory connectivity should be based on extensive  
245 datasets through space and time. Such data are most easily obtained by researchers from citizen science  
246 monitoring programs. These programs normally involve careful training of participants to follow well-  
247 established and tested field protocols that produce reliable data. They also typically engage impressive  
248 numbers of participants to survey numerous locations throughout large portions of the range of  
249 occurrence of species of interest. These characteristics produce datasets with large sample sizes that are  
250 amenable for capturing the range of conditions and circumstances under which species occur, leading to  
251 better predictions based on SDMs for refining isotopic assignments of migratory connectivity than from  
252 isotopes alone.

253 Various extensive citizen science datasets suitable for SDM development are freely-available to  
254 researchers. Most of these and other useful sources of data are easily obtained through the various  
255 information nodes of the Avian Knowledge Network (2017), such as the ones used to obtain data for this  
256 paper: Nature Counts (Bird Studies Canada 2017b) and Midwest Avian Data Center (Koch et al. 2010).

257 Some available datasets, however, are more useful or easier to implement than others for developing  
258 SDMs. Like the programs that produced data for this paper, some monitoring programs pre-select survey  
259 locations so they are representative of larger areas of inference, typically by using various randomization  
260 procedures (e.g., Johnson et al. 2009). Many of these programs also record data regardless of whether  
261 certain species were detected or not, following protocols specifically designed to maximize detections of  
262 species of interest (e.g., Conway 2011). Such protocols include restrictions on the time of day and season,  
263 type of weather, and the amount of background noise that is acceptable during surveys (e.g., Tozer et al.  
264 2016). They also include requirements on the minimum number of visits per survey location, and the total  
265 duration of each survey, plus some use standardized call broadcasts to increase the probability of  
266 detection of especially elusive species. All of these characteristics provide more reliable information on  
267 the presence or absence or abundance of species of interest at a particular point. These programs, which  
268 are dedicated to generating reliable, representative data on occurrences or counts of species across  
269 specific areas of inference may be the best choice, when available, for developing SDMs to refine isotopic  
270 assignments of migratory connectivity.

271 By contrast, monitoring programs that lack the standardized restrictions and guidelines noted above can  
272 pose challenges for SDM development. This was shown by the additional bias-correction analysis that  
273 Fournier et al. (2016) were required to perform during their use of SDMs based on eBird data to refine  
274 isotopic assignments of migratory connectivity in the Virginia Rail. The bias was thought to occur  
275 because there are no restrictions on where and how eBird participants observe rails or other species, and  
276 because of the nature of eBird data it did not meet the assumption that presence data points were  
277 randomly distributed (Yackulick et al. 2012). While this flexibility is a major advantage of eBird and

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278 other programs like it for numerous other applications, the lack of organized standardization of surveys  
279 can cause challenges for SDM development (Yackulic et al 2012).

280 Our SDMs might have provided better assignment resolution if finer-scale habitat covariates, especially  
281 wetland cover, were available in a consistent format across Canada and the U.S. Our analysis might also  
282 have been improved by simultaneously considering another isotope, such as Sulphur ( $\delta^{34}\text{S}$ ). Some rails  
283 use brackish or saline habitats during the breeding season, and this would be reflected in their  $\delta^{34}\text{S}$  feather  
284 signatures, potentially helping to further refine assignments (Hobson et al. 2012, Butler et al. 2016). The  
285 incorporation of genetic information could have been beneficial, though currently, to our knowledge, such  
286 information is not available for rails.

287 We combined isotopic signatures of the largest sample of autumn-migrating and wintering rails with  
288 SDMs based on organized marsh bird monitoring data to produce the most extensive estimates of  
289 migratory connectivity of three rail species currently available. We found that the migratory connectivity  
290 of the three species included wide-ranging breeding areas, including more than one migratory game bird  
291 flyway in the two hunted species—results useful for improving conservation of these poorly-studied  
292 species—although additional work is needed to fully establish patterns. Extensive data from organized  
293 citizen science monitoring programs are especially useful for improving isotopic assignments of  
294 migratory connectivity in birds, which will ultimately lead to better management and conservation of  
295 species.

296

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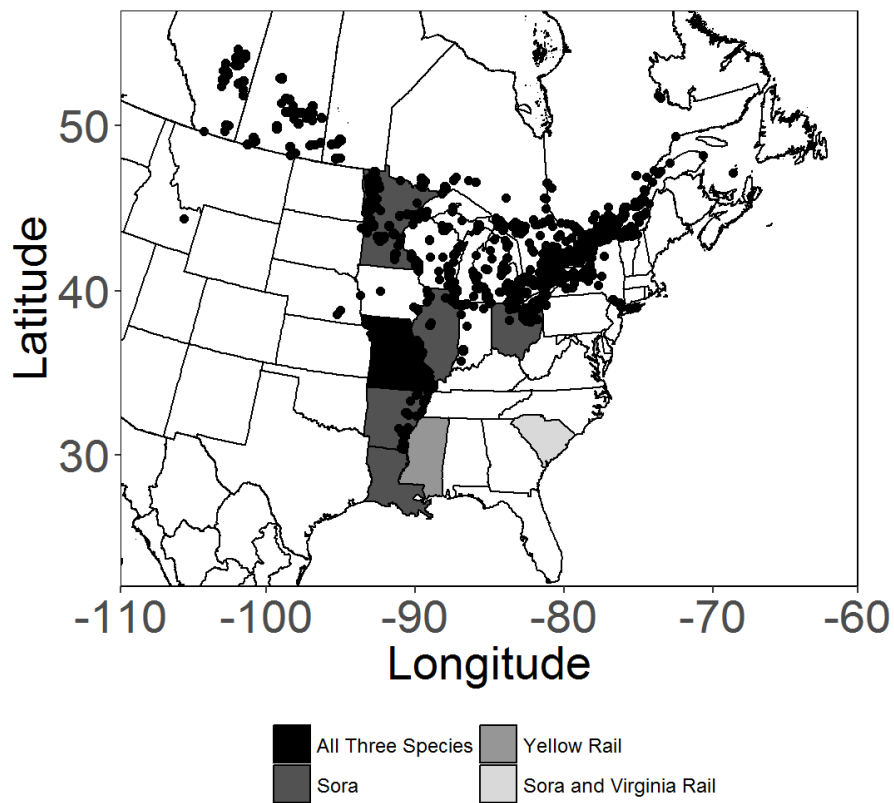
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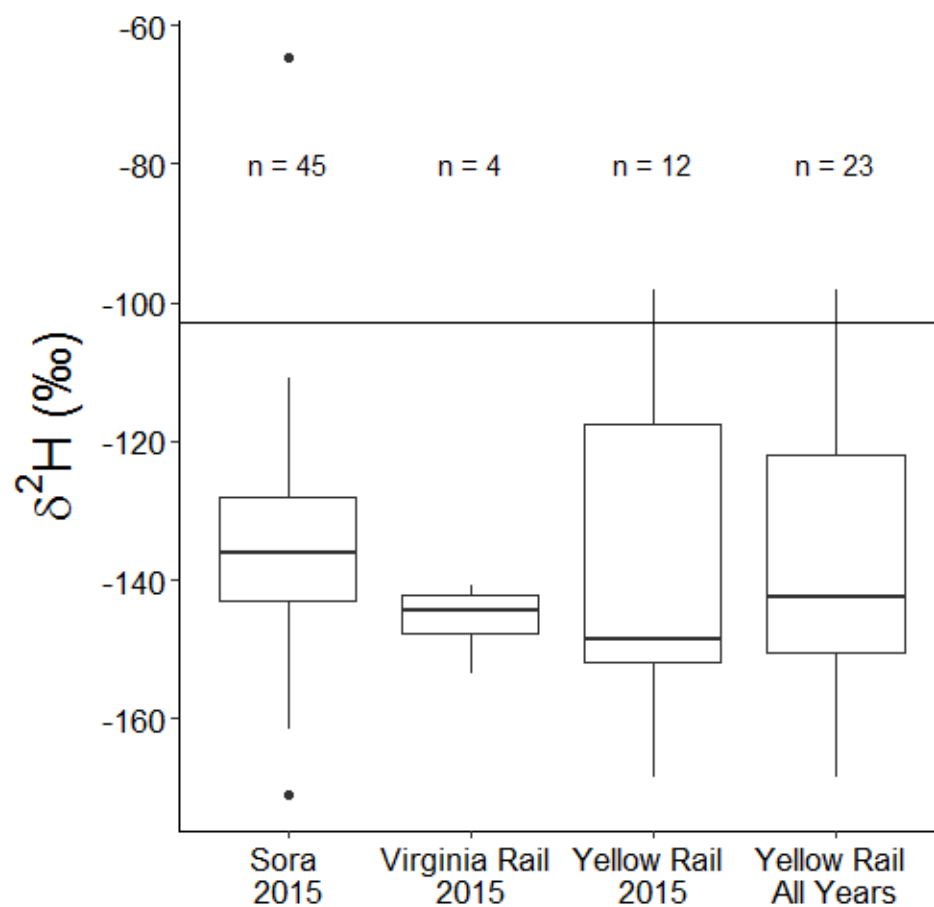
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452 **Figure 1.** Locations of marsh bird monitoring program survey points used to develop species distribution  
453 models, and states where autumn-migrating and wintering rails were captured and sampled or isotopic  
454 analysis.

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457 **Figure 2** – Distribution of  $\delta^2\text{H}$  values of feathers from rails caught at Foam Lake, Saskatchewan, Canada.

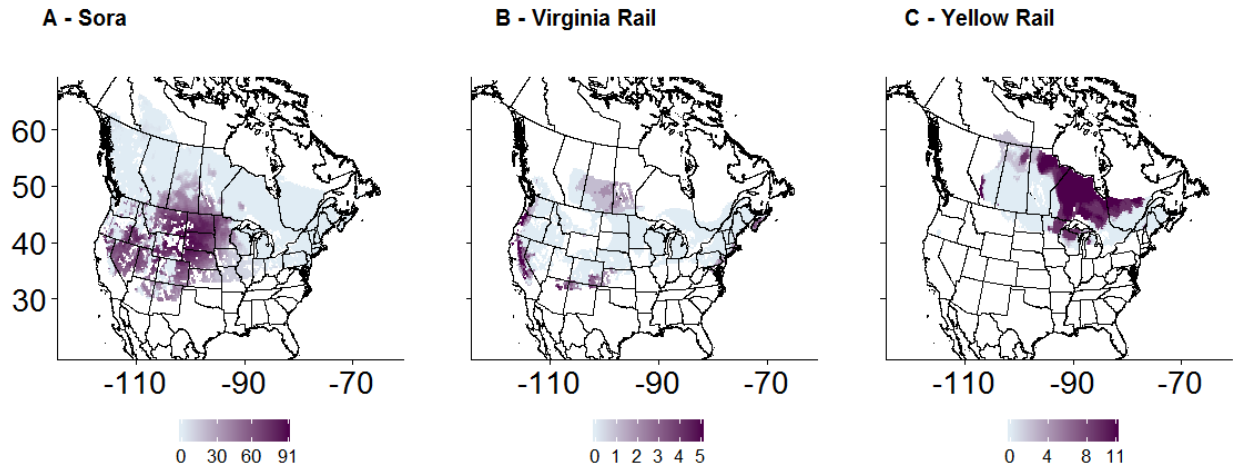
458 The horizontal line represents  $\delta^2\text{H}$  in precipitation from Bowen et al. (2005).

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463 **Figure 3** – Cumulative assignment of breeding areas of autumn migrating and wintering Sora (*Porzana*  
464 *carolina*), Virginia Rails (*Rallus limicola*) and Yellow Rails (*Corturnicops noveboracensis*) based on  
465 expected  $\delta^2\text{H}_{\text{feather}}$  values using regional monitoring data in a species distribution model as an informative  
466 prior. Each individual bird’s assignment surface represents the area where the bird is like from with 3:1  
467 odds and then those surfaces are summed to form the cumulative assignment for all individuals from that  
468 species.