

1 **Stable isotope analyses of feather amino acids identify penguin migration**
2 **strategies at ocean basin scales.**

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4 Michael J. Polito^{1-2*}, Jefferson T. Hinke³, Tom Hart⁴, Mercedes Santos⁵⁻⁶, Leah A. Houghton²,
5 Simon R. Thorrold²

6

7 ¹Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge,
8 LA 70803,

9 ²Biology Department, Woods Hole Oceanographic Institution, Woods Hole, MA 02543, U.S.A.

10 ³Antarctic Ecosystem Research Division, Southwest Fisheries Science Center, National Marine
11 Fisheries Service, National Oceanic and Atmospheric Administration, La Jolla, California 92037,
12 U.S.A. 1.

13 ⁴Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK

14 ⁵Departamento Biología de Predadores Tope, Instituto Antártico Argentino, 25 de Mayo 1143,
15 B1650CSP, San Martín, Buenos Aires, Argentina

16 ⁶Laboratorios Anexos, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La
17 Plata, Calle 64 N° 3, B1904AMA, La Plata, Buenos Aires, Argentina

18

19 *Author for correspondence: Michael J. Polito mpolito@lsu.edu

20 **Abstract:** Identifying the at-sea distribution of wide ranging marine predators is critical to
21 understanding their ecology. Advances in electronic tracking devices and intrinsic
22 biogeochemical markers have greatly improved our ability to track animal movements on ocean-
23 wide scales. Here we show that, in combination with direct tracking, stable carbon isotope
24 analysis of essential amino acids in tail feathers provides the ability to track the movement
25 patterns of two, wide-ranging penguin species over ocean basin scales. In addition, we use this
26 isotopic approach across multiple breeding colonies in the Scotia Arc to evaluate migration
27 trends at a regional scale that would be logistically challenging using direct tracking alone.

28

29 **Keywords:** migration, geolocation (GLS), seabird, stable isotopes

30 **1. Introduction**

31 Identifying the at-sea distribution of wide ranging marine animals is critical to aid in their
32 conservation [1] and advances in electronic tracking devices have revolutionized our ability to
33 track animal movements on ocean-wide scales [2]. However, tracking studies can be limited in
34 scale due to logistical, financial and ethical constraints. Intrinsic biogeochemical markers that
35 retain spatial information, including stable isotope analysis (SIA), have therefore been used to
36 complement direct tracking [3]. SIA can increase the scale of tracking studies by examining a
37 greater number of individuals and/or locations to better generalize population-level movements
38 [4]. However, interpreting bulk tissue SIA can be challenging because it is often difficult to
39 distinguish the influence of a consumer's diet (i.e. what it eats) from geographic differences in
40 isotopic values (i.e. where it is eating) [3, 5].

41 Compound-specific SIA of amino acids (CSIA-AA) may offer a solution to the bulk SIA
42 problem of distinguishing between diet and geographic differences as some individual amino
43 acids (AAs) faithfully reflect ecosystem baseline isotopic values that can be used to
44 independently evaluate animal movement [5]. However, few studies have applied CSIA-AA at
45 ocean basin scales and most have focused on nitrogen isotopes [5, 6]. Carbon isotope values
46 ($\delta^{13}\text{C}$) of essential AA are also likely to be useful for estimating movement patterns of wide-
47 ranging marine species. This is because essential AAs transfer from diet without alteration and
48 reflect primary producer community composition at the base of geographically distinct food
49 webs [7-9]. For example, one recent study found geographic variation in penguin chick AA $\delta^{13}\text{C}$
50 values with latitude, though they cautioned that using AA $\delta^{13}\text{C}$ to track foraging
51 locations may not be possible [9].

52 The goal of this research is to test the ability of $\delta^{13}\text{C}$ CSIA-AA to discriminate among
53 three migrations strategies identified by archival geolocation tags (GLS) [10] in two wide-
54 ranging species, the Adélie (*Pygoscelis adeliae*) and Chinstrap (*P. antarctica*) penguin. We then
55 use this technique to assign migration strategies to untracked individual Chinstrap penguins from
56 multiple breeding colonies to evaluate regional migration trends at population-level scales.

57

58 **2. Material and methods**

59 Breeding adult Chinstrap and Adélie penguins from Cape Shirreff, Livingston Island and
60 Admiralty Bay, King George Island (Table 1 and 2) were tagged during 2011/12 breeding
61 season with Lotek Nano-Lat 2900-series GLS (Lotek Wireless, Inc.) and recaptured the
62 following year (2012/13). Tags provided daily estimates of latitude and longitude over the
63 austral winter. At recapture a central tail feather was collected, a proximal section of which
64 reflected a late-March to early-June growth period when penguins were migrating to or
65 inhabiting their winter foraging areas [10]. We restricted our spatial analyses to penguins that
66 had GLS data within the window of tail-feather synthesis and isotopic incorporation (i.e. 40-
67 100 days following the onset of molt; Adélie penguins: 25 March - 24 May; chinstrap
68 penguins: 10 April - 9 June). Details on GLS data processing, feather growth rates, and bulk
69 $\delta^{13}\text{C}$ values are provided in Hinke et al. [10]. In 2012/13 we collected tail feathers from
70 additional, untracked breeding adult Chinstrap penguins from five breeding sites (Table 2).

71 Tail feather sections (20 mg each) were acid hydrolyzed, derivatized and analyzed for
72 CSIA-AA following the methods outlined McMahon et al. [11]. Samples were analyzed in
73 duplicate with AA and fish muscle standards of known isotopic composition (mean
74 reproducibility: AA standard: ± 0.2 ‰; internal fish standard: ± 0.6 ‰). We focused on bulk

75 feather $\delta^{13}\text{C}$ and five essential AAs (threonine, isoleucine, valine, phenylalanine, and
76 leucine) and used linear discriminant analyses (LDA) in program R (ver. 2.15.3) [12] with
77 leave-one-out cross-validation to differentiate among the three migration strategies observed
78 by Hinke et al. [10]: Adélie penguins migrating eastward from their breeding sites into the
79 Weddell Sea, Chinstrap penguins migrating eastward into the Scotia Sea, and Chinstrap
80 penguins migrating westward to the Pacific sector of the Southern Ocean (Table 1, Fig. 1).
81 We then used LDA to discriminate between the two Chinstrap penguin migration strategies
82 in isolation and assign untracked individuals to specific migration strategies. We evaluated
83 regional migration trends using only Chinstrap penguins with known migration patterns
84 (GLS) and those that were assigned based on CSIA-AA with $\geq 80\%$ probability of group
85 membership [4, 5].

86 We also applied a Bayesian mixing-model approach [13] in program R [12] to obtain a
87 probability distribution of migration strategies at the five Chinstrap penguins breeding sites
88 examined. We used essential AAs $\delta^{13}\text{C}$ values of GLS tracked Chinstrap penguin as source
89 end-members (eastward vs. westward), and values of all penguins by breeding site regardless
90 of if their migration status was known. We used a small non-zero trophic discrimination
91 factor in the model ($0.1 \pm 0.1\%$) [7] and ran 1 million iterations, thinned by 15, with an
92 initial discard of 40,000 resulting in 64,000 posterior draws.

93

94 **3. Results**

95 LDA classification using AA $\delta^{13}\text{C}$ out-performed bulk $\delta^{13}\text{C}$ and provided clear separation
96 in canonical multivariate space (Wilk's lambda = 0.16, $P < 0.001$; Table 1, Fig. 1).
97 Individuals misclassified by AA $\delta^{13}\text{C}$ were assigned as Chinstrap penguins migrating

98 eastward. AA $\delta^{13}\text{C}$ LDA accuracy was $\geq 89.3\%$ for Chinstrap penguins only (Wilk's lambda
99 = 0.34, $P < 0.001$) and out-performed bulk $\delta^{13}\text{C}$ (Table 1).

100 Migration strategies for 59 of the 66 untracked Chinstrap penguins were assigned with \geq
101 80% probability. When combined with individuals of known migration status, a majority of
102 Chinstrap penguins exhibited "Pacific" isotopic signatures, consistent with a westward
103 migration (81.7%). However, we also observed a relatively higher number of individuals
104 exhibiting a "Scotia Sea" signature at sites located farther north and east (Table 2; Fig. 2).
105 This was confirmed by our mixing-model approach, with 95% credibility intervals around
106 the contribution of eastward vs. westward migrants overlapping only at the most northeastern
107 breeding site (Table 2; Fig. 2).

108

109 **4. Discussion**

110 Essential AA $\delta^{13}\text{C}$ values in tail feathers successfully discriminated between the winter
111 migrations strategies observed in Adélie and Chinstrap penguins. This approach provided more
112 accurate classifications than bulk $\delta^{13}\text{C}$ and successfully differentiated species-specific habitat
113 niches between eastward moving Adélie and Chinstrap penguins (into the ice-covered Weddell
114 Sea vs. ice free Scotia Sea, respectively) [10]. In addition, our results were unaffected by trophic
115 biases [5, 8] as essential AA in penguin tail feathers most likely reflect only the baseline $\delta^{13}\text{C}$
116 values in their specific wintering area [8]. Differences in baseline $\delta^{13}\text{C}$ values across wintering
117 areas in this study may be driven by differences in the phytoplankton and/or sea-ice algae
118 community composition and sources of inorganic carbon [14, 15].

119 Differences in essential AA $\delta^{13}\text{C}$ values among eastward vs. westward migrating
120 Chinstrap penguins also provided a basis for assignment of untracked individuals. This allowed

121 us to expand the overall sample sizes (i.e. number of individuals) and spatial scope (i.e. number
122 and range of breeding sites) of our study to confirm that the dominant migration strategy of
123 chinstrap penguins from the Antarctic Peninsula region and southern Scotia Sea is westward.
124 One possible hypothesis for this trend is competitive avoidance as the Scotia Sea is home to large
125 wintering populations of Macaroni (*Eudyptes chrysolophus*) and southern rockhopper (*E.*
126 *chrysocome chrysocome*) penguins [16]. In addition, we identified a spatial trend with a
127 relatively higher number of eastward migrating individuals at sites located farther northwards
128 and eastwards (Fig. 2). This may suggest that the location of breeding sites influences migration
129 patterns. Following this trend, one might expect individuals breeding in the South Sandwich
130 Islands to remain in the Scotia Sea during winter, as this archipelago is the farthest northeast and
131 contains the largest Chinstrap penguin breeding population [17]. If so, this might serve as a
132 source of intra-specific competition and further explain dominance of westward migration
133 strategies of Chinstrap penguins from our study sites. An alternate explanation is some
134 individuals from northeastern colonies may obtain a “Scotia Sea” isotopic signature while
135 migrating westward towards the Pacific.

136 In summary, to our knowledge this research represents the first use of essential AA $\delta^{13}\text{C}$
137 values to track the migration routes and at-sea distribution of a wide-ranging marine predator.
138 While the spatial resolution of essential AA $\delta^{13}\text{C}$ is coarse compared to direct tracking, this
139 approach can significantly expand the scope of studies and help facilitate inference about
140 individual and population processes in far-ranging marine species. Future studies that elucidate
141 spatial gradients in oceanic isotopic baselines will further refine our ability to track marine
142 animal movements over ocean basin scales.

143

144 **Ethics.** Field work was conducted via an Antarctic Conservation Act permit (ACA 2013-007)
145 and animal use approved by WHOI (27071382) and UCSD (S05480) IACUC.

146

147 **Data accessibility.** GLS and isotope data are available online at [https://swfsc.noaa.gov/AERD-](https://swfsc.noaa.gov/AERD-Data/)
148 [Data/](https://swfsc.noaa.gov/AERD-Data/)

149 **Authors' contributions.** Study design: M.J.P, J.T.H, S.R.T.; Fieldwork: M.J.P, J.T.H, T.H.,
150 M.S.; Data analysis: M.J.P, J.T.H, T.H., L.H.; Manuscript: M.J.P; All authors revised and gave
151 final approval for publication and agree to be held accountable for the work performed therein.

152

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154

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209 **Table 1.** Mean±SD $\delta^{13}\text{C}$ values and classification accuracies from GLS tracked penguins
210 exhibiting three differing winter migration strategies. Parentheses identify individuals from
211 either Admiralty Bay or Cape Shirreff, and LDA classifications excluding Adélie penguins.

212

213 **Table 2.** Mean±SD essential AA $\delta^{13}\text{C}$ values and assigned winter migration strategies of
214 Chinstrap penguins from five breeding locations. Parentheses identify GLS tracked individuals at
215 each site.

216

217 **Figure 1.** Indices of A) geographic habitat utilization and B) multivariate discrimination based
218 on essential AA $\delta^{13}\text{C}$ values of C) Adélie and Chinstrap penguins. Habitat utilization data
219 modified from Hinke et al. [10]. Dotted lines represent 50% probability of assignment.

220

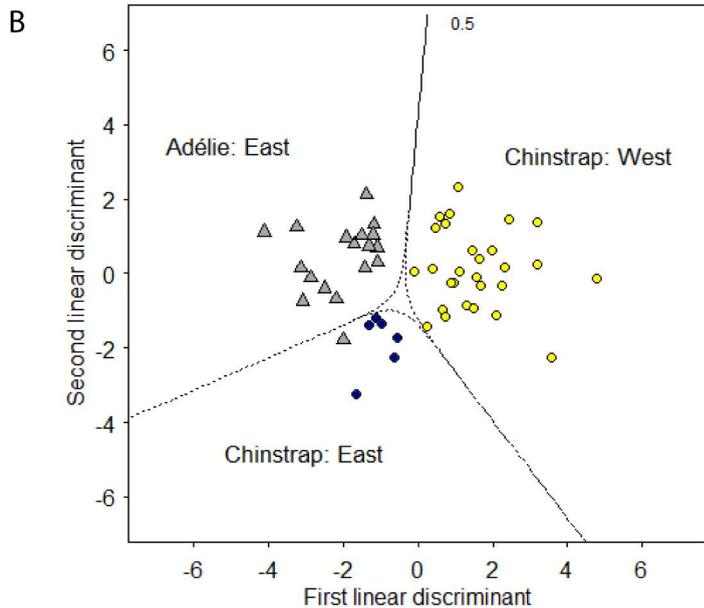
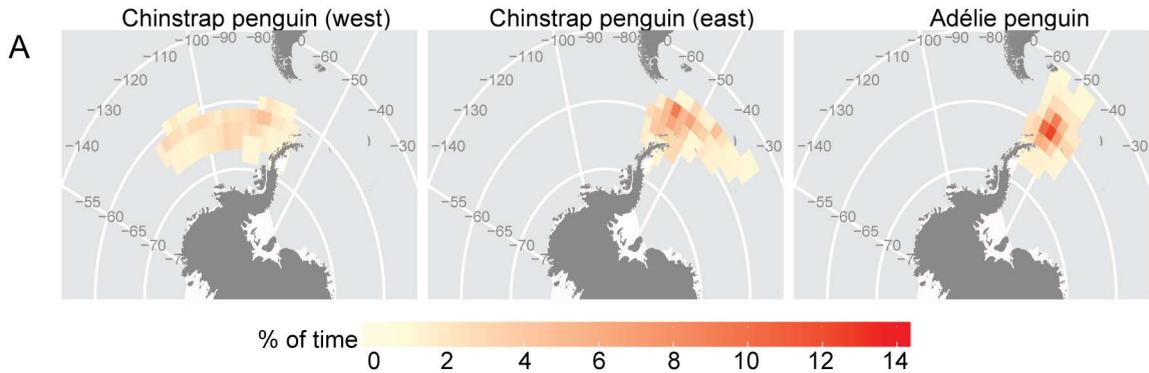
221 **Figure 2.** A) Multivariate discrimination of tracked (colored points) and untracked (white points)
222 Chinstrap penguins based on essential AA $\delta^{13}\text{C}$ values and B) assigned winter migration
223 strategies (eastward or westward) in Chinstrap penguins from five breeding locations using LDA
224 (pie charts) and stable isotope mixing-models (histograms). Dotted line represents 50%
225 probability of assignment.

Table 1.

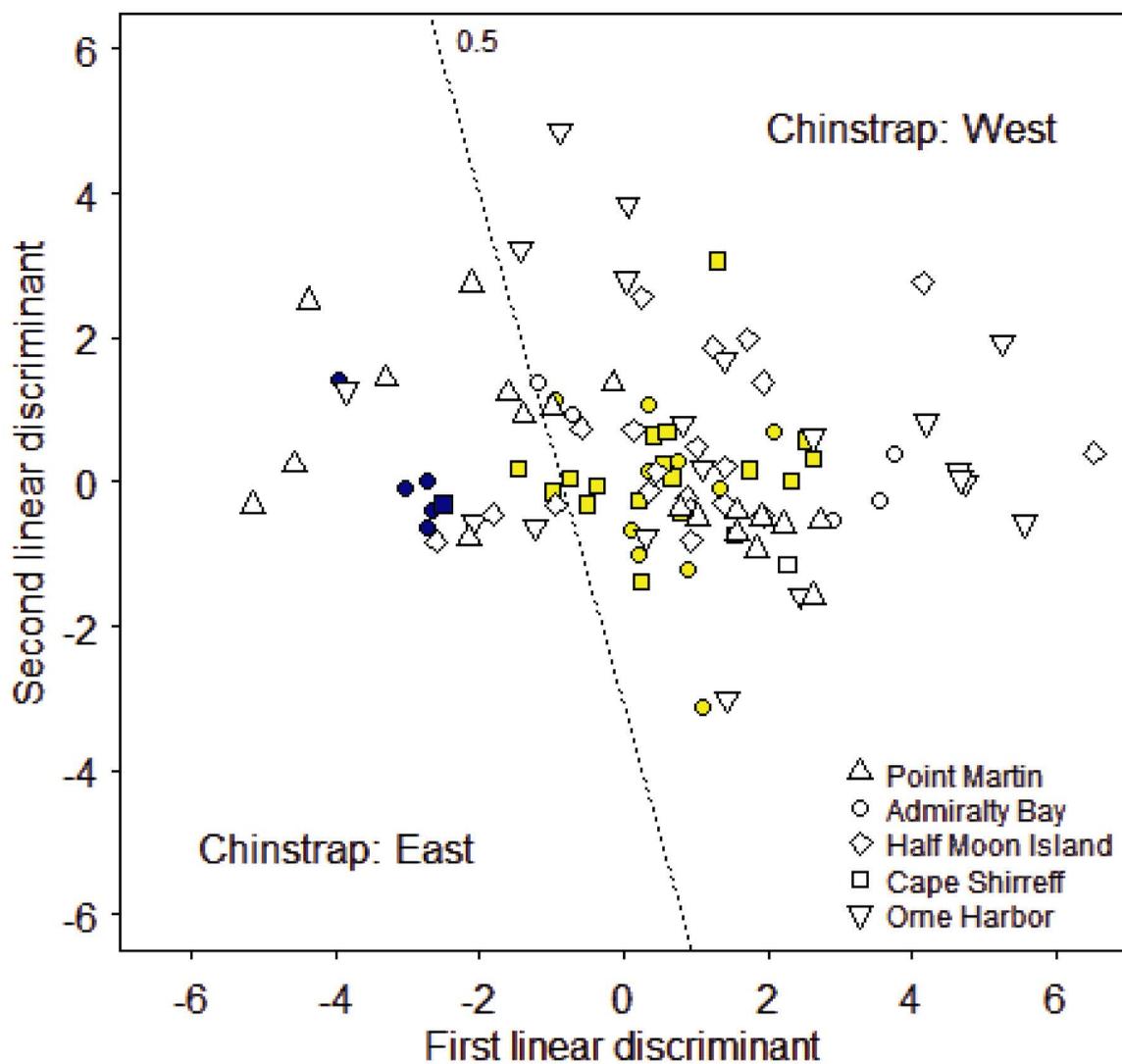
GLS tracked penguins	Adélie penguin	Chinstrap penguin	
	East, Weddell Sea	East, Scotia Sea	West, Pacific sector
<i>n</i>	18 (18,0)	6 (5,1)	28 (10,18)
$\delta^{13}\text{C}$ (‰)			
<i>Bulk feather</i>	-24.3±0.3	-24.5±0.5	-22.8±0.6
<i>Valine</i>	-30.7±0.7	-29.7±0.4	-27.9±0.9
<i>Isoleucine</i>	-20.4±2.1	-17.7±0.9	-19.4±1.5
<i>Leucine</i>	-34.9±0.7	-33.4±1.7	-33.4±1.7
<i>Threonine</i>	-14.1±1.7	-11.4±1.5	-11.7±2.6
<i>Phenylalanine</i>	-30.2±0.7	-30.1±0.4	-28.7±1.5
LDA (%)			
<i>Bulk $\delta^{13}\text{C}$</i>	66.7	33.3 (83.3)	82.1 (82.1)
<i>Essential AA $\delta^{13}\text{C}$</i>	94.4	100.0 (100.0)	96.4 (89.3)

Table 2.

Breeding site	South Orkney Islands	South Shetland Islands			Western Antarctic Peninsula
	Point Martin, Laurie Is.	Admiralty Bay, King George Is.	Cape Shirreff, Livingston Is.	Half Moon Is., Livingston Is.	Orne Harbour, Arctowski Peninsula
Lat., Long.	60.76°S, 44.68°W	62.17°S, 58.45°W	62.47°S, 60.78°W	62.58°S, 62.58°W	64.62°S, 62.53°W
<i>n</i>	20 (0)	20 (15)	20 (19)	20 (0)	20 (0)
$\delta^{13}\text{C}$ (‰)					
<i>Valine</i>	-27.9±1.8	-28.5±1.1	-27.8±1.0	-27.2±1.3	-27.2±2.1
<i>Isoleucine</i>	-18.8±1.9	-19.5±2.0	-19.1±1.5	-19.5±2.6	-21.0±1.6
<i>Leucine</i>	-32.7±2.1	-33.3±1.7	-33.5±1.6	-32.4±1.8	-33.9±1.6
<i>Threonine</i>	-12.1±3.4	-11.6±2.7	-11.5±2.2	-12.1±2.7	-10.5±4.6
<i>Phenylalanine</i>	-30.2±1.9	-29.1±1.2	-28.6±1.6	-30.7±1.6	-30.5±1.6
LDA (%)					
<i>East</i>	38.9	26.3	5.0	10.5	11.8
<i>West</i>	61.1	73.7	95.0	89.5	88.2
Mixing-model (%)					
<i>East</i>	32.6 (2.1-58.7)	23.8 (5.9-41.3)	9.0 (0.0-19.9)	10.0 (0.0-28.5)	11.5 (0.0-32.7)
<i>West</i>	67.4 (41.3-97.9)	76.2 (58.7-94.1)	91.0 (80.1-100)	90.0 (71.5-100)	88.5 (67.3-100)



A



B

