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Seasonal and ocean basin-scale assessment of amino acid δ**15N trends in a Southern Ocean marine predator**

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ABSTRACT: The Southern Ocean exhibits substantial spatio-temporal variation in biogeochemical processes that shape interactions and productivity across food webs. Stable isotopes in marine predators provide an opportunity to capture such variations, yet few studies have accounted for variability in the isotopic baseline when interpreting predator isotope values. Using bulk $\delta^{15}N$ and δ^{13} C values and the δ^{15} N values of amino acids (AAs) of blood from female Antarctic fur seals (AFSs) *Arctocephalus gazella*, we investigated spatial and seasonal variation in baseline $\delta^{15}N$ ($\delta^{15}N_{\text{baseline}}$) values across 3 Southern Ocean basins (Indian, Pacific and Atlantic) to facilitate robust comparison of consumer trophic ecology. We detected spatial and seasonal differences in $\delta^{15}N_{\text{baseline}}$ values across the basins, using the source AAs phenylalanine (Phe) and lysine (Lys), consistent with the latitudinal gradient of AFS colonies and seasonal changes in seal foraging movement. The $\delta^{15}N$ values of source AAs from Marion Island and Cape Shirreff were representative of particulate organic matter $\delta^{15}N$ values in the Indian and southwest Atlantic sector, respectively, whereas more complex patterns were observed in the Atlantic sector around Bird Island. Variations in bulk $\delta^{15}N$ values can also be attributed to changes in AFS diet, with females foraging in the Atlantic and Pacific targeting higher trophic level prey in winter. Trophic position estimation using Phe and leucine (Leu) suggested that females encompass more than 2 trophic levels. Our study highlights the utility of using Lys alongside Phe to assess seasonal and ocean basin-level variations in the isotopic baseline and Leu/Phe for AFS trophic position estimation.

KEY WORDS: Compound-specific isotope analysis · Trophic position · Nitrogen · Southern Ocean · Antarctic fur seal · *Arctocephalus gazella* · Isotopic baselines

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1. INTRODUCTION

Marine ecosystems are inherently spatially and temporally complex. Accounting for these dynamics is crucial for understanding their functioning and to inform effective resource management in the context of rapid anthropogenic climate change (Pecl et al. 2017, Cavanagh et al. 2021). From the tropics to the poles, variations in physical (e.g. temperature, currents, fronts, sea ice cover; Sokolov & Rintoul 2009, Abraham et al. 2013, Moore et al. 2013) and chemical (e.g. oxygen, nutrient availability; Somes et al. 2010, Moore et al. 2013, Breitburg et al. 2018) processes create distinct oceanographic conditions. These conditions support a wide array of open pelagic and coastal marine ecosystems characterized by specific compositions and abundances of species and unique food web structures (Crowder & Norse 2008, Constable et al. 2014, Poloczanska et al. 2016). Seasonality plays an important role in shaping the networks of interactions among species that underpin these ecosystems by driving fluctuations in productivity and resource availability, which can propagate through the entire food web, from microbes to top predators (Constable 2003, Asch 2019). The Southern Ocean holds particular importance in this context, as it is one of the most highly seasonally productive environments globally (Sarmiento et al. 2004), and variation in the physical and chemical environment influences variation in food web structure at multiple scales (Constable 2003, De Broyer et al. 2014, McCormack et al. 2021). Approaches that consider variation across biogeographic regions and seasons are particularly important to provide a comprehensive view of the structural and functional complexity of Southern Ocean marine ecosystems at particular spatiotemporal scales. How ever, such integrative approaches are deficient for the Southern Ocean, because of constraints on data availability (Bonnet-Lebrun et al. 2023).

Within this context, marine predators serve as valuable indicators to better understand ecosystem functioning and for monitoring ecosystem responses to changes in the marine environment (Carpenter-Kling et al. 2019, Hazen et al. 2019, Bestley et al. 2020). Through their ability to integrate trophic information from the bottom to the top of the food web, higher trophic level predators can be used to assess energy flow and baseline productivity underpinning food webs (Pethybridge et al. 2018a, Seyboth et al. 2018, MacKenzie et al. 2019, Carpenter-Kling et al. 2020, de la Vega et al. 2022). Using retrospective biogeochemical techniques, such as stable isotope analysis, it is feasible to study trophodynamics through wide-ranging predators that migrate across broad geographic regions and through seasons (Trueman et al. 2012, Trueman & St John Glew 2019, Walters et al. 2020). Two of the most used isotopes are δ^{13} C and δ^{15} N measured in consumer protein that can be matched to an isotope gradient across the animal's foraging range (McMahon et al. 2013, Trueman & St John Glew 2019). Consumer proteins are enriched in $15N$ relative to the proteins of their prey in a predictable manner (DeNiro & Epstein 1981). Consequently, δ^{15} N provides an indicator of consumer trophic position (TP) and nitrogen sources fueling the food web (Post 2002). In contrast, δ^{13} C only slightly increases along the food web and is thus commonly used to trace the origin of the production supporting the food web (Kelly 2000).

However, interpreting tissue bulk isotope compositions at higher trophic levels is challenging due to various factors, particularly the spatial and temporal variability in the isotopic baseline, making it difficult to determine the causes of observed variations in predator tissues (Boecklen et al. 2011). Significant spatiotemporal variability in $\delta^{15}N$ values in primary producers (e.g. phytoplankton), consumers and particulate organic matter have been observed across the global oceans, including the Southern Ocean (Jennings & Warr 2003, Somes et al. 2010, Espinasse et al. 2019, St John Glew et al. 2021). Variations in $\delta^{15}N$ values in primary producers can be influenced by community composition, nutrient sources (e.g. nitrate, nitrite, ammonium), nutrient pool size and isotopic fractionation during nitrogen fixation, uptake, assimilation, nitrification and denitrification processes (Somes et al. 2010, Sigman & Fripiat 2019). The $\delta^{15}N$ values in phytoplankton tend to be higher in productivity hot spots like upwelling regions around coastlines and lower in pelagic oceans (i.e. areas of nitrogen fixation; Somes et al. 2010). In the Southern Ocean, there is a poleward decrease in phytoplankton $\delta^{15}N$ values, along with variations between basins and across seasons (DiFiore et al. 2010, Espinasse et al. 2019, St John Glew et al. 2021). These spatial $\delta^{15}N$ gradients at the base of the food web are still discernible in higher trophic levels, allowing the study of predator trophic ecology across varying temporal and spatial scales (Graham et al. 2010, McMahon et al. 2013, Pethybridge et al. 2018a, McMahon & Newsome 2019).

Compound-specific isotope analysis of amino acids (CSIA-AA) is a valuable tool that facilitates better identification of trophic effects due to the integration of underlying variation in primary production sources (Chikaraishi et al. 2009, McMahon & Newsome 2019, Magozzi et al. 2021). The $\delta^{15}N$ values of amino acids $(\delta^{15}N_{AA})$ provide information about the 'source' amino acids (e.g. phenylalanine), which are directly routed from the prey into the predator tissues, reflecting the δ^{15} N values of primary producers, and 'trophic' amino acids (e.g. glutamic acid), which undergo transformations during assimilation, showing stepwise enrichments with each trophic level (McClelland & Montoya 2002, Chikaraishi et al. 2007, 2009, Popp et al. 2007, McMahon & McCarthy 2016, McMahon & Newsome 2019). This approach provides information about the trophic position of a consumer while accounting for the nitrogen isotopic value at the base of the food web, using a single organism (Chikaraishi et al. 2009, Nielsen et al. 2015, McMahon & McCarthy 2016). Analysing bulk $\delta^{13}C$ ($\delta^{13}C_{\text{bulk}}$) and $\delta^{15}N$ ($\delta^{15}N_{\text{bulk}}$) and $\delta^{15}N_{AA}$ values of wide-ranging predators can provide a powerful tool to study both trophic structure and nitrogen sources supporting production within and across ecosystems (Pethybridge et al. 2018b, McMahon & Newsome 2019). Several studies have validated this approach to infer the migration patterns and trophic ecology of marine predators (Ruiz-Cooley et al. 2014, Lorrain et al. 2015, Feddern et al. 2022, Rita et al. 2024) and to detect temporal environmental changes (de la Vega et al. 2022, 2023). In the Southern Ocean, only a limited number of studies have successfully incorporated spatial variations in the isotopic baseline when interpreting predator isotope values (Lorrain et al. 2009, Brault et al. 2019, Lübcker et al. 2021) and none, to our knowledge, has incorporated seasonal variation. Here, we investigated seasonal variation in baseline $\delta^{15}N$ ($\delta^{15}N_{\text{baseline}}$) values across 3 ocean basins (Indian, Pacific and Atlantic sectors of the Southern Ocean) using $\delta^{15}N_{AA}$ values of a highly mobile, circumpolar species, the female Antarctic fur seal (AFS) *Arctocephalus gazella* to facilitate robust comparisons of consumer trophic ecology.

The AFS is an important and numerous Southern Ocean predator, with breeding colonies located from various sub-Antarctic islands to the northern tip of the Antarctic Peninsula (Forcada & Staniland 2009, Ropert-Coudert et al. 2014). The diet of females varies with the location of the colony due to differences in the local conditions and the availability and accessibility of prey species, notably due to the large latitudinal gradient in breeding range. For Bird Island and Cape Shirreff colonies in the Atlantic sector, which encompass the core southern distribution of the species, their summer diet contains a high proportion of Antarctic krill *Euphausia superba*, followed by fish and cephalopods (Reid & Arnould 1996, Casaux et al. 2003, 2016, Osman et al. 2004, Harrington et al. 2017, Abreu et al. 2019). In contrast, females predominantly feed on myctophid fishes and squid at colonies in the Indian sector (such as Marion Island) located at the northern edge of their breeding range, and further north of the Polar Front (PF) where Antarctic krill does not occur (Klages & Bester 1998, Makhado et al. 2008, Reisinger et al. 2018). However, those studies analysed scat and stomach contents, focusing primarily on the breeding period, when female AFS are accessible as they forage close to their colonies to regularly provide milk to their pups. During the inter-breeding period (May– November), female AFSs occupy a greater geographical range (sub-Antarctic to Antarctic zones, SAZ and AZ, respectively) due to long-distance movements (Guinet et al. 2001, Bailleul et al. 2005, Arthur et al. 2017). Recent bulk stable isotope analyses have provided additional insight into the trophic ecology of female AFSs (Tarroux et al. 2016, Jones et al. 2020, Walters et al. 2020); however, none of these studies incorporated variations in the isotopic baseline when interpreting AFS isotope values. Understanding food web baseline dynamics and changes in the seal trophic ecology is essential, especially given the overlap with intensified krill fishing activities and the recent documented changes in AFS populations in the Atlantic sector (Forcada et al. 2023, Krause et al. 2024).

Here, we combined $\delta^{13}C_{\text{bulk}}$ and $\delta^{15}N_{\text{bulk}}$ values and $\delta^{15}N_{AA}$ values of whole blood collected from adult female AFSs from breeding sites in the southern Indian and Atlantic sectors during the pre- and post-breeding periods. We focus on 2 key questions: (1) What is the seasonal and spatial variation in $\delta^{15}N_{\text{baseline}}$ across the 3 Southern Ocean basins? (2) How do these baseline variations influence the trophic ecology of female AFSs, using trophic amino acid $\delta^{15}N$ values and trophic position (TP) estimations? This approach will enhance our understanding of the spatiotemporal patterns in the Southern Ocean food webs on which these seals depend. We hypothesized significant spatial variations in the isotopic baseline, with strong differences expected in summer, when female AFSs forage in localised areas around their colonies. Specifically, we expected higher $\delta^{15}N_{\text{baseline}}$ values for females from Marion Island foraging in the SAZ compared to those from Bird Island and Cape Shirreff (Table 1). In contrast, we expected reduced spatial variation in the isotopic baseline in winter, when female seals exhibit wide-ranging foraging behaviour, thus integrating isotopic information across various food web baselines. Furthermore, we predicted spatial variation in AFS trophic ecology, particularly in summer, when dietary preferences diverge significantly between colonies and there is marked seasonal variation in trophic ecology of the females within each colony, due to long-distance movements of females during the winter period.

Breeding site	- Foraging habitat – Breeding season Non-breeding season		$Diet-$ Breeding season Non-breeding season		References
Marion Island	Sub-Antarctic Zone Open ocean	Sub-Antarctic Zone Polar Frontal Zone Antarctic Zone Open ocean	Myctophids Cephalopods	Myctophids Cephalopods Krill spp.	Klages et al. (1998), Makhado et al. (2008), Arthur et al. (2017) , Reisinger et al. (2018), Wege et al. (2019), Walters et al. (2020)
Bird Island	Antarctic Zone Open ocean	Sub-Antarctic Zone Polar Frontal Zone Antarctic Zone Open ocean Patagonian Shelf	Antarctic krill Myctophids Nototheniids	Antarctic krill Myctophids Nototheniids Cephalopods	Brown et al. (1999), Boyd et al. (2002), Staniland et al. (2010), Waluda et al. (2010), Arthur et al. (2017), Jones et al. (2020), Walters et al. (2020)
Cape Shirreff	Southern Zone Sea ice zone	Sub-Antarctic Zone Polar Frontal Zone Antarctic Zone Southern Zone Open ocean	Antarctic krill Fish	Fish Cephalopods Antarctic krill	Polito & Goebel (2010), Arthur et al. (2017). Hinke et al. (2017), Borrás-Chávez (2020), Walters et al. (2020)

Table 1. Foraging ecology of female Antarctic fur seals *Arctocephalus gazella* during the breeding and non-breeding periods at Bird Island, Cape Shirreff and Marion Island

2. MATERIALS AND METHODS

2.1. Study sites and sample collection

Whole blood samples were collected from female AFSs breeding at 3 circumpolar sites in the Southern Ocean: (1) Marion Island (46° 52' S, 37° 51' E), in the Indian sector, (2) Bird Island $(54^{\circ}00' \text{ S}$, $38^{\circ}02' \text{ W})$, off the northwest tip of South Georgia in the southwest Atlantic sector and (3) Cape Shirreff (62° 28' S, 60° 48' W), on the north coast of Livingston Island, in the South Shetland Islands, near the tip of the Antarctic Peninsula on the edge of the Pacific sector (Fig. 1). These 3 colonies encompass a large latitudinal and longitudinal range. Marion Island is located in the SAZ, between the sub-Antarctic Front (SAF) and the PF (Treasure et al. 2015); Bird Island lies in the AZ, between the PF and the Southern Antarctic Circumpolar Current Front (SACCF), while Cape Shirreff is located within the seasonal ice zone south of the Southern Boundary Front (Fig. 1; Park et al. 2019). The 3 colonies are part of the Convention on the Conservation of Antarctic Marine Living Resources (CCAMLR) convention areas: Sub-area 48.1 for Cape Shirreff, 48.3 for Bird Island and 58.7 for Marion Island. The AFS is a key indicator species for resource management in the Southern Ocean ecosystem within the CCAMLR framework. In particular, the CCAMLR Ecosystem Monitoring Program (CEMP) designates Bird Island and Cape Shirreff as crucial

monitoring sites for AFS, emphasizing their importance in tracking ecosystem changes and informing sustainable management practices for harvested species like Antarctic krill.

Whole blood samples (1–5 ml) were collected from a hind flipper interdigital vein from adult female AFSs in 2008, 2009 and 2010 ($n = 127$) (Table S1). Blood was sampled as soon as possible after females arrived at the breeding colony (mean \pm SD, Bird Island: 9.07 \pm 11.5 d after arrival; Cape Shirreff: 5.5 ± 8.8 d after arrival; Marion Island: 10.2 ± 9.6 d after arrival), and again at the end of the breeding season. Whole blood provides an indication of the consumer trophic ecology over the past 2–3 mo (Hilderbrand et al. 1996, Vander Zanden et al. 2015). Samples collected at the start of the breeding season thus represent the last few months of the inter-breeding period, while samples collected at the end of the breeding season reflect foraging during the summer breeding period.

2.2. Stable isotope analysis

Samples were stored at -20° C until isotopic analysis. Blood samples were dried at 60°C for at least 24 h prior to bulk and compound-specific stable isotope analyses (Walters et al. 2020). Dried blood samples were analysed for bulk $\delta^{13}C$ and $\delta^{15}N$ values ($\delta^{13}C_{bulk}$ and $\delta^{15}N_{bulk}$) by combusting them in a Carlo-Erba EA1100 (CE Instruments) and passing

Fig. 1. Locations where female Antarctic fur seal blood samples were collected in the Atlantic and Indian sectors of the Southern Ocean. Samples were collected during the summer and winter seasons in 2008, 2009 and 2010. Coloured lines indicate mean frontal position (Park et al. 2019), from lighter to darker colour: STF: Sub-tropical Front; SAF: Sub-Antarctic Front; PF: Polar Front; SACCF: Southern Antarctic Circumpolar Current Front; SBDY: Southern Boundary of the Antarctic Circumpolar Current

the separated gases produced to an Isoprime (Elementar) continuous-flow isotope ratio mass spectrometer (IRMS). All samples were processed at the Farquhar Laboratory, Australian National University (ANU), Canberra. Replicate measurements of internal laboratory standards for $\delta^{15}N$ (qlycine, cysteine) and δ^{13} C (glycine, cane sugar and beet sugar) indicated internal precisions better than 0.15‰, for both. Internal standards were previously calibrated against interlaboratory comparison standards distributed by the International Atomic Energy Agency (IAEA) and the USGS (L-glutamic acid, USGS 40 and USGS 41), except for ANU cane sugar, which was also the source of IAEA CH-6. Stable isotope ratios were reported using standard δ notation in parts per thousand $(\%_0)$ deviation from the international standards Vienna PeeDee belemnite for $\delta^{13}C$ and atmospheric nitrogen for $\delta^{15}N$ as follows:

$$
\delta X = \left[(R_{\text{sample}} / R_{\text{standard}}) - 1 \right] \times 1000 \tag{1}
$$

where *X* is ¹³C or ¹⁵N, and *R* is the corresponding ratio of ${}^{13}C/{}^{12}C$ or ${}^{15}N/{}^{14}N$.

Dried blood samples were analysed for individual amino acid $\delta^{15}N$ values $(\delta^{15}N_{AA})$ using a modified method described by Meekan et al. (2022) at the Commonwealth Scientific and Industrial Research Organisation (CSIRO) laboratories in Hobart, Australia. The modification was the temperature and duration of the initial hydrolysis; we used 20 h at 110°C. The $\delta^{15}N$ compositions of the individual amino acids were measured with a Trace GC Ultra gas chromatograph coupled to a Delta V Plus IRMS through a GC-C combustion furnace (980°C), reduction furnace (650°C) and liquid $N₂$ cold trap. Each sample was analysed at least in duplicate. To normalize the $\delta^{15}N$ values, a set of amino acid standards with known $\delta^{15}N$ values was used to bracket the 2 distinct IRMS analyses. The slope and intercept of known vs. measured values were then used to correct the measured values for the sample set. The reproducibility of the isotopic analysis of individual amino acids calculated from the bracketing standards was $\pm 0.48\%$ (1 SD) and ranged from ± 0.10 to $\pm 0.71\%$ ₀.

Through acid hydrolysis, glutamine (Gln) was converted to glutamic acid (Glu) and asparagine (Asn) was converted into aspartic acid (Asp). As a result, the final measurements combine $G\ln + G\ln$ (Glx) and Asn + Asp (Asx). Amino acids were categorized into 4 groups: (1) source AAs, lysine (Lys) and phenylalanine (Phe), reflecting $\delta^{15}N_{\text{baseline}}$ as they are not significantly affected by trophic transfer; (2) trophic AAs, alanine (Ala), valine (Val), Asx, leucine (Leu), proline (Pro) and Glx, which tend to become more enriched in ¹⁵N through deamination and transamination as they move up the food web; (3) the metabolic AA threonine (Thr), often involved in transamination, with decreases in values of $\delta^{15}N$ with each trophic level, leading to negative values; and (4) source/trophic AAs, glycine (Gly) and serine (Ser), which are challenging to classify, with values often similar within an organism but varying widely between organisms (McMahon & McCarthy 2016, Cherel et al. 2019, Whiteman et al. 2019).

2.3. Data analysis

2.3.1. TP and relative TP (RTP)

Individual TP was calculated using a multi-trophic discrimination factor (TDF) equation and a combination of source and trophic AAs (Germain et al. 2013, McMahon et al. 2019):

 $TP_{Tr-Sr} = [(\delta^{15}N_{Tr} - \delta^{15}N_{Sr} - TDF_2 - \beta) / TDF_1] + 2$ (2)

where $\delta^{15}N_{Tr}$ and $\delta^{15}N_{Sr}$ represent the nitrogen isotopic values of the trophic and source AAs in the consumer, respectively; TDF_1 represents the trophic discrimination for lower trophic levels, $TDF₂$ represents the TDF_{Tr-Sr} for higher trophic levels, and β is the difference between the $\delta^{15}N$ values of trophic and source AAs in primary producers (Table S2), taken from Nielsen et al. (2015) and Germain et al. (2013). Borrell et al. (2012) suggested that TDFs remain relatively consistent among taxonomically closely related species, thus we selected the TDF values of the harbour seal *Phoca vitulina* (Germain et al. 2013) due to the absence of a species-specific TDF for AFSs (Text S1). We selected Glx-Phe, as it is the most commonly used amino acid pair in marine predator isotope ecology, and Leu-Phe, which provided the most ecologically realistic TP estimation for AFSs, based on previous dietary information (Table 1, Text S1). Alternative TPs were also calculated using a combination of other trophic (Ala, Asx, Pro, Val) and source (Lys) AAs (Table S3), which gave similar trends in TP between the colonies (Fig. S1). Following the recommendation of Ramirez et al. (2021), propagation of analytical and methodological error was accounted for using the 'propagate' package in R (Spiess 2018), to improve the accuracy of TP estimation.

We also calculated the relative TP (RTP) of each seal (Cherel et al. 2019):

$$
RTP = \delta^{15}N_{Tr} - \delta^{15}N_{Sr}
$$
 (3)

expressed in ‰. Contrary to the TP estimation, the RTP does not necessitate *a priori* assumptions about the β and TDF values, thus emphasizing relative differences in food web position (Choy et al. 2015, Cherel et al. 2019).

2.3.2. Statistical analysis

All statistical analyses were performed using R version 4.2.1 (R Core Team 2022). Ocean-basin scale variation in $\delta^{15}N_{bulk}$, $\delta^{13}C_{bulk}$, $\delta^{15}N_{AA}$, TP and RTP within each season were investigated using a linear mixed-effects model with site as a fixed effect and year as a random effect followed by a Tukey's post hoc test to identify significant differences between specific sites. Within-location differences between seasons in $\delta^{15}N_{\text{bulk}}$, $\delta^{13}C_{\text{bulk}}$, $\delta^{15}N_{AA}$, TP and RTP were examined using another linear mixed-effects model with season as a fixed effect and year as a random effect, followed by a Tukey's post hoc test for pairwise comparisons to test significant differences between seasons. All linear mixed-effects models were fitted using the R package 'lme4'. To determine the general differences in AA compositions between colonies, we performed a multivariate analysis of variance (MA-NOVA) on $\delta^{15}N_{AA}$ values, considering the interaction effect of site, season and year, followed by a principal component analysis (PCA). We used linear regressions to investigate if variation in $\delta^{15}N_{bulk}$ can be attributed to variation in the isotopic baseline $(\delta^{15}N_{\text{Phe}})$ $\delta^{15}N_{\text{Leu}}$) and/or trophic effects $(\delta^{15}N_{\text{Glu}};\delta^{15}N_{\text{Leu}})$.

The $\delta^{15}N$ values of particulate organic matter $(\delta^{15}N_{\text{POM}})$ are typically used to represent the food web isotopic baseline (Espinasse et al. 2019). To evaluate if our $\delta^{15}N_{\text{baseline}}$ values are representative of the food web isotopic baseline, we compared our $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{Lys}$ values to $\delta^{15}N_{\text{POM}}$ (Seyboth et al. 2018, Espinasse et al. 2019, Stirnimann et al. 2024) and $\delta^{15}N$ of particulate organic nitrate $(\delta^{15}N_{PON})$ values (only available for the Indian sector; Smith et al. 2022). Values from Cape Shirreff were compared only with Atlantic values in winter, as, to our knowledge, no $\delta^{15}N_{POM}$ values are available for the Pacific sector region.

3. RESULTS

3.1. Blood $\delta^{15}N_{bulk}$ and $\delta^{13}C_{bulk}$ values

The $\delta^{13}C_{\text{bulk}}$ and $\delta^{15}N_{\text{bulk}}$ values varied between seasons and across the 3 ocean basins (Table 2; Fig. S2 in the Supplement at [www.int-res.com/articles/suppl/](https://www.int-res.com/articles/suppl/m747p151_supp.pdf) [m747p151_supp.pdf\)](https://www.int-res.com/articles/suppl/m747p151_supp.pdf). The $\delta^{15}N_{bulk}$ values at Marion Island were significantly higher than both Cape Shirreff and Bird Island in summer (Tukey HSD, both p < 0.0001; Table 2; Table S4). Seasonal comparisons within each colony showed higher $\delta^{15}N_{bulk}$ values in winter for Bird Island (Tukey HSD, $p = 0.034$) and Table 2. Bulk and individual amino acid δ15N values of whole blood from female Antarctic fur seals *Arctocephalus gazella*. Values are means ± SD. Linear mixed effect modelling followed by Tukey pairwise comparisons was performed to compare bulk and compound-specific stable isotope values, trophic position and relative trophic position between sites or seasons (see Tables S4 & S5 for the models used). Values in the same row with differing superscript letters or signs differ statistically (p < 0.05). Superscript letters indicate significant differences between sites within each season (a,b,c for summer; A,B,C for winter), while superscript signs $(\star,^{\dagger})$ show significant differences between seasons within each site

Cape Shirreff (Tukey HSD, p < 0.0001), but no significant differences between seasons for Marion Island females. We did not observe spatial variation in δ¹⁵N_{bulk} in winter.

3.2. $\delta^{15}N_{AA}$ values

The $\delta^{15}N_{AA}$ values of 11 AAs were quantified, including 6 trophic AAs (Ala, Val, Asx, Leu, Glx, Pro), 2 source AAs (Phe, Lys), 2 trophic/source AAs (Ser, Gly) and 1 metabolic AA (Thr). The MANOVA revealed significant differences in $\delta^{15}N_{AA}$ values among sites and seasons (Table S5).

The $\delta^{15}N_{AA}$ values varied among the 3 colonies and between seasons (Table 2, Fig. 2). The PCA revealed that the trophic AAs, in particular Pro, and the meta-

bolic AA Thr were driving most of the differences among colonies and seasons (Fig. 3). All trophic AAs, the trophic/source AA Gly and the source AA Lys showed significantly higher $\delta^{15}N$ values in females from Marion Island compared to females from Bird Island and Cape Shirreff in summer (Table 2, Fig. 2; Table S5). Females from Marion Island exhibited significantly higher $\delta^{15}\rm{N}_{\rm{Phe}}$ values in comparison to females from Bird Island in summer (Tukey's HSD, p = 0.003). In contrast, females from Bird Island exhibited higher $\delta^{15}N_{Lvs}$ values compared to females from Cape Shirreff and Marion Island in winter (Tukey's HSD, $p = 0.019$ and 0.016, respectively). No differences in $\delta^{15}N_{\text{Phe}}$ values were detected in winter (Table 2, Fig. 2; Table S5).

The trophic AA Leu and metabolic AA Thr were the only AAs with $\delta^{15}N$ values significantly different

Fig. 2. Mean and SD δ15N values of amino acids for adult female Antarctic fur seal *Arctocephalus gazella* whole blood samples from Bird Island, Cape Shirreff and Marion Island during the (a) summer and (b) winter period. Significant differences (p < 0.05) in δ¹⁵N values of amino acid between sites among a season are indicated with asterisks (*). Ala: alanine; Val: valine; Asx: aspartic acid; Leu: leucine; Glx: Glutamic acid; Pro: proline; Ser: serine; Gly: glycine; Phe: phenylalanine; Lys: lysine; Thr: threonine. Amino acids are divided into trophic, trophic/source, source and metabolic (Meta) groups

Fig. 3. Principal component analysis of δ15N values of amino acids in female Antarctic fur seal *Arctocephalus gazella* whole blood samples from Bird Island, Cape Shirreff and Marion Island (a) among colonies and (b) between seasons. Abbreviations as in Fig. 2

among all 3 colonies in summer (Table 2, Fig. 2; Table S5). Values of $\delta^{15}N_{\text{Leu}}$ were higher for Marion Island, followed by Cape Shirreff and lower for Bird Island, while Thr showed the opposite trend. In winter, δ^{15} N values of the metabolic AA Thr were higher for Bird Island females compared to those from Cape Shirreff and Marion Island (Tukey's HSD, p = 0.002 and <0.0001, respectively).

Stirnimann et al. (2024); ^bEspinasse et al. (2019); ^cSmith et al. (2022); ^dSeyboth et al. (2018); ^eδ¹⁵N values from particulate organic nitrogen $(\delta^{15}N_{PON})$

Seasonal variations in $\delta^{15}N_{AA}$ values were detected for females from Bird Island and Cape Shirreff. Specifically, $\delta^{15}N$ values from all trophic AAs, in addition to $\delta^{15}N_{\rm Ser}$ and $\delta^{15}N_{\rm Lvs}$ values, were significantly higher in winter, and $\delta^{15}N_{\text{Thr}}$ values were higher in summer (Table 2; Table S5). For Cape Shirreff, we also ob served a seasonal variation in $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Glv}}$ values, with higher values in winter compared to summer (Tukey's HSD, $p = 0.014$ and 0.019).

During the summer season, $\delta^{15}N$ values of Phe and Lys were similar to those of $\delta^{15}N_{\text{POM}}$ at Marion Island and Cape Shirreff, but significantly higher (p < 0.0001) than $\delta^{15}N_{\text{POM}}$ at Bird Island (Table 3). In winter, $\delta^{15}N$ values of Phe and Lys remained similar to $\delta^{15}N_{\text{POM}}$ at Marion Island, while $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ values were aligned with $\delta^{15}N_{\text{POM}}$ at Cape Shirreff. However, at Bird Island, $\delta^{15}N_{\text{Phe}}$ values were similar to $\delta^{15}N_{\text{POM}}$, whereas $\delta^{15}N_{Lvs}$ values were significantly lower (Table 3).

Positive relationships between $\delta^{15}N_{bulk}$ values and $\delta^{15}N_{\text{Phe}}$ (*y* = -8.071 +0.779*x*, r² = 0.125, p = 0.001), $\delta^{15}N_{\text{Glx}}$ (*y* = -8.204 +2.538*x*, r^2 = 0.375 p < 0.0001), $\delta^{15}N_{Lys}$ (*y* = -9.021 + 0.825*x*, *r*² = 098, *p* = 0.001) and $\delta^{15}N_{\text{Leu}}$ values (*y* = -11.945 + 2.795*x*, r² = 0.45, p < 0.0001) were observed (Fig. 4).

3.3. TP and RTP

The estimated TP of females varied from 2.7 to 4.7 for $TP_{Glx-Phe}$ and 3.0 to 5.3 for $TP_{Leu-Phe}$ (Table 2, Fig. 5; Table S3).Variations in TPLeu-Phe among colonies were observed in summer, with females from Marion Island having higher TP_{Leu-Phe} than females from Bird Island and Cape Shirreff (Tukey's HSD, both $p < 0.0001$, and females from Cape Shirreff occupying a higher TP_{Leu-Phe} compared to females from Bird Island (Tukey's HSD, p < 0.0001; Table 2, Fig. 5; Table S4). During the winter, female seals from Marion Island and Cape Shirreff occupied a higher TP_{Lepb} compared to females from Bird Island (Tukey's HSD, $p < 0.0001$ and $p = 0.002$, respectively; Table 2, Fig. 5; Table S4), but no difference in TP_{Leu-Phe} was detected between females from Marion Island and Cape Shirreff. Within-colony seasonal differences were detected for females from Bird Island and Cape Shirreff, with seals occupying a higher average TPLeu-Phe in winter (Tukey's HSD, both p < 0.0001; Table 2, Fig. 5; Table S4). A statistically significant positive relationship was detected between $\delta^{15}N_{bulk}$ values and

Fig. 4. Bulk $\delta^{15}N$ values plotted against source (phenylalanine) and trophic (glutamic acid and leucine) amino acids and the derived trophic position obtained from female Antarctic fur seal *Arctocephalus gazella* whole blood. (a) δ¹⁵N values of phenylalanine $(\delta^{15}N_{\text{Phe}})$, glutamic acid $(\delta^{15}N_{\text{Glx}})$ and their derived trophic position (TP_{Glx-Phe}); (b) $\delta^{15}N$ values of phenylalanine $(\delta^{15}N_{\text{Phe}})$ and leucine ($\delta^{15}N_{\text{Leu}}$) and their derived trophic position (TP_{Leu-Phe}). The dotted lines indicate the linear regression between $\delta^{15}N_{\text{bulk}}$ and $\delta^{15}N_{\text{AA}}$ or TP

Fig. 5. Density distributions, boxplots (median, first and third quartile) and individual data points indicating the trophic position and relative trophic position of female Antarctic fur seals *Arctocephalus gazella* from Bird Island (summer n = 41, winter $n = 8$), Cape Shirreff (summer $n = 12$, winter $n = 26$) and Marion Island (summer $n = 21$, winter $n = 19$) during the summer and winter period. Estimated trophic position and relative trophic position were calculated using the glutamic acid or leucine (trophic) and phenylalanine (source) δ^{15} N values of whole blood samples

 $TP_{\text{Glx-Phe}}$ (*y* = 0.963 + 0.279*x*, r^2 = 0.473, *p* < 0.0001) and $TP_{Leu-Phe}$ (*y* = 0.794 + 0.354*x*, r^2 = 0.571, p < 0.0001; Fig. 4). RTP varied from 10.5 to 23.4‰ for $RTP_{Glx-Phe}$ and from 8.7 to 21.8‰ for $RTP_{\text{Leu-Phe}}$ and followed the same trends as $TP_{\text{Glx-Phe}}$ and TP_{Leu-Phe}, respectively.

4. DISCUSSION

We used CSIA-AA to determine large-scale and seasonal variation in the food web baseline and trophic ecology of a wide-ranging Southern Ocean marine predator, the female AFS. We measured $\delta^{15}N_{AA}$ from 11 AAs, aligning with findings from prior CSIA-AA studies on Southern Ocean pinnipeds, in cluding Weddell seals *Lepto nychotes weddellii*, crabeater seals *Lobodon carcinophaga*, Ross seals *Ommatophoca rossii* (Brault et al. 2019) and southern elephant seals *Mirounga leonina* (Lübcker et al. 2020). Our results indicated that variations in bulk δ^{15} N values can be primarily attributed to changes in female AFS trophic ecology, with a smaller influence from changes in the isotopic baseline ($\delta^{15}N_{\text{baseline}}$). We demonstrated that $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{Lvs}$ values of females from Marion Island are representative of the isotopic baseline in the Indian sector during both seasons, as compared to $\delta^{15}N_{\text{POM}}$ and $\delta^{15}N_{\text{PON}}$ values. Similarly, values of AFS females from Cape Shirreff are representative of the isotopic baseline of the northern Antarctic Peninsula in summer and of the southwest Atlantic sector in winter, as compared to $\delta^{15}N_{\text{POM}}$ values. In contrast, $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ of females from Bird Island were more ¹⁵N-depleted than $\delta^{15}N_{\text{POM}}$ in summer. This suggests that our values may not accurately represent the isotopic baseline in this area in summer, whereas $\delta^{15}N_{\text{Phe}}$ values were comparable to $\delta^{15}N_{\text{POM}}$ in winter. These differences are likely due to complex biogeophysical processes around South Georgia, which are reflected in POM and seal blood due to their different isotopic turnover rate. Our compound-specific isotope approach to trophic dynamics revealed significant spatial and temporal differences in the trophic ecology of the AFS, consistent with previous diet studies. Notably, we observed a seasonal shift in the trophic ecology of females from Bird Island and Cape Shirreff, targeting higher trophic level prey in winter. Our results also highlight the utility of additional amino acids, such as Lys, alongside Phe for investigating isotopic baselines, and Leu for more accurate ecological TP estimations.

4.1. Basin-scale and seasonal variation in δ**15N baseline**

Prior investigations into $\delta^{15}N_{\text{POM}}$ values in the Southern Ocean have identified complex seasonal and spatial variations compared to variation in $\delta^{13}C_{POM}$ (Espinasse et al. 2019, St John Glew et al. 2021). Our study, done on a seasonal and multi-basin scale, supports these findings. Collectively, our results indicate seasonal and spatial variations in the isotopic $\delta^{15}N$ baseline across the 3 ocean basins. In summer, we detected significant differences in $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lvs}}$ values between the Atlantic and Indian basins, with higher values for females from Marion Island, reflecting the local foraging behaviour of female AFSs in different water masses. Previous studies have identified differences in $\delta^{15}N_{\text{POM}}$ between Southern Ocean water masses, linked to variation in sea surface temperature, nitrogenous nutrients supporting net primary productivity, mixed layer depth and sea ice concentration, and delineated 2 major distinct biogeochemical regimes, i.e. north and south of the PF (Espinasse et al. 2019, St John Glew et al. 2021). During the summer season, females from Marion Island forage primarily within the SAZ (Wege et al. 2019), while females from higher-latitude Bird Island and Cape Shirreff forage south of the PF (Table 1). These differences in foraging zone use could explain the significantly higher $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{Lys}$ values for females from Marion Island. Moreover, as the Antarctic Circumpolar Current flows eastward, it transports essential nutrients like iron to phytoplankton communities, enhancing primary productivity in regions downstream of landmasses (Sergi et al. 2020). Phytoplankton preferentially take up ^{14}N nitrate, causing the residual pool to become progressively enriched in ${}^{15}N$ in productive areas (Lara et al. 2010, Sigman & Fripiat 2019). Consequently, observed differences in summer may also be explained by female AFS from Marion Island foraging preferentially south to southeast of the island (mostly downstream; Wege et al. 2019), while females from Bird Island and Cape Shirreff forage north–northwest of their island (upstream; Boyd et al. 2002, Staniland et al. 2010, Waluda et al. 2010, Borrás-Chávez 2020). We detected spatial differences in $\delta^{15}N_{Lys}$ values in winter, with $\delta^{15}N_{Lys}$ values from Bird Island significantly higher compared to the 2 other colonies, likely resulting from the wide-ranging movements of females (Fig. S3). Espinasse et al. (2019) also observed latitudinal variations in $\delta^{15}N_{\text{POM}}$ values in winter, but they noted a general decrease in values with increasing latitude in the Atlantic section. Our observed difference in this study may reflect variations in foraging locations rather than a clear latitudinal gradient. Indeed, variation can be attributed to the females that fed over the Patagonian shelf break (Fig. S3). This region is recognized for its higher $\delta^{15}N_{\text{baseline}}$ values (Lara et al. 2010, Espinasse et al. 2019, Stirnimann et al. 2024), contributing to the overall increase in $\delta^{15}N_{Lys}$ values in winter.

Regarding seasonal variation within basins, the higher values of $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ in winter for females from Cape Shirreff can be attributed to females travelling west to the Pacific basin, and/or along the Chilean coast to the north of the SAF and the sub-Tropical Front (Fig. S3; Arthur et al. 2017, Hinke et al. 2017, Walters et al. 2020). Additionally, this variation may be explained by changes in the productivity of primary producers, as higher $\delta^{15}N_{POM}$ values have been predicted for the Chilean coast and near the Antarctic Peninsula between May and December (St John Glew et al. 2021). The absence of seasonal variation in $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ for seals from Marion Island aligns with seasonally stable $\delta^{15}N_{\text{POM}}$ values, found between 40° and 55° S (Espinasse et al. 2019), where most female AFSs foraged (Fig. S3).

The potential for using $\delta^{15}N$ values from source AAs of marine predators to monitor long-term changes in marine food web baselines has been highlighted by de la Vega et al. (2022). The $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lvs}}$ values for female AFS from Marion Island and Cape Shirreff are consistent with $\delta^{15}N_{\text{POM}}$ and $\delta^{15}N_{\text{PON}}$ values in their respective foraging areas (Seyboth et al. 2018, Espinasse et al. 2019, Smith et al. 2022, Stirnimann et al. 2024). The summer $\delta^{15}N_{\text{Phe}}$ values of females from Marion Island also align with those found in the lower beaks of Dana octopus squid *Taningia danae* (0.8 ± 1.6‰; Cherel et al. 2019) and whole blood samples of southern rockhopper penguins *Eudyptes chrysocome chrysocome* (–0.2 to 1.8‰; Lorrain et al. 2009) sampled in the southern Indian Ocean. Taken together, our results suggest that $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ values can be used as reliable source AAs in the foraging regions of the Marion Island and Cape Shirreff AFS colonies and highlight their potential to monitor spatial and seasonal changes in the isotopic baseline of the Southern Ocean. It is important to note that the comparison for Cape Shirreff winter values was conducted using only $\delta^{15}N_{\text{POM}}$ data from the Atlantic sector. For a more precise comparison, it would be beneficial to include winter data from the Pacific sector, as some females also forage in this area (Fig. S3). However, to our knowledge, $\delta^{15}N_{\text{POM}}$ values for the Pacific sector in winter are unavailable at present.

During the winter, only $\delta^{15}N_{\text{Phe}}$ values were consistent with $\delta^{15}N_{POM}$ for females from Bird Island in the southern Atlantic basin. Differences between $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{Lys}$ values may be due to differences in AA turnover (McMahon & McCarthy 2016). In summer, $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ values of females from Bird Island were more ¹⁵N-depleted than $\delta^{15}N_{POM}$, suggesting that our values may not accurately represent the isotopic baseline in this area. Although higher terrestrial inputs from Bird Island are unlikely to be significant in this context, nitrogen uptake processes on 15 Ndepleted sources could be a contributing factor (Espinasse et al. 2019). Additionally, the observed differences might result from the different years in which samples were collected. Changes in water masses can influence $\delta^{15}N_{\text{baseline}}$ values (de la Vega et al. 2022), and the pelagic system around South Georgia is complex, characterized by considerable inter-annual variability (Hill et al. 2009). The complex patterns observed during summer may be attributed to disparate isotopic turnover, with POM exhibiting a fast isotopic turnover (Espinasse et al. 2019), while whole blood of marine predators has a longer turnover rate (several months; Cherel & Hobson 2007). Post-weaning of their pups, females are free from the constraints of lactation (Boyd et al. 2002) and forage across multiple frontal zones (Staniland et al. 2012, Arthur et al. 2017, Hinke et al. 2017, Wege et al. 2019) so that blood integrates isotopic compositions across multiple food web baselines. Consequently, $\delta^{15}N_{POM}$ and $\delta^{15}N_{AA}$ values from blood integrate baseline temporal variation over different time scales. To detect changes in the isotopic baseline in a specific area, it is important to consider the foraging range of the predator when using $\delta^{15}N_{AA}$ blood values. An alternative method would be to use $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lvs}}$ values from sequentially sampled keratinous tissues like whiskers that enable the reconstruction of an isotopic timeseries that can be directly related to foraging areas at sea (Walters et al. 2020). Another explanation for the differences between $\delta^{15}N_{\text{Phe}}$, $\delta^{15}N_{\text{Lys}}$ and $\delta^{15}N_{\text{POM}}$ values could be that $\delta^{15}N_{\text{POM}}$ values may not accurately represent the $\delta^{15}N$ values of primary producers. Stable isotope data from POM have been used to provide isotopic baselines, but its suitability has been debated (St John Glew et al. 2021). Particulate organic matter comprises particles from various sources, not only phytoplankton, including faecal pellets of grazers (Soares et al. 2015), and therefore may not accurately represent what primary consumers are feeding on. Moreover, the composition of POM can vary significantly over time due to various processes such as microbial and grazing activity or water column stratification, raising questions about the reliability of POM as a food web baseline over large areas and medium- to long-term changes in

marine ecosystems (St John Glew et al. 2021, Espinasse et al. 2022). Finally, despite recent publications on $\delta^{15}N_{\text{POM}}$ in the Southern Ocean (Espinasse et al. 2019, Stirnimann et al. 2024), there is still a lack of reference data available for some regions (e.g. Pacific) and seasons (especially winter), which limited our comparisons and conclusions in this study.

4.2. Basin-scale and seasonal variation in the trophic ecology of AFS

We observed spatial differences in $\delta^{15}N_{\text{Glx}}\,\delta^{15}N_{\text{Leur}}$ TPGlx-Phe, TPLeu-Phe, RTPGlx-Phe and RTPLeu-Phe during both seasons. Our results suggest that, in summer, females from Marion Island feed on higher trophic level prey compared to females from Bird Island and Cape Shirreff. Marion Island AFSs had TP values indicative of predation on myctophids (average TP value of 2.9; Choy et al. 2012) and squids, likely including *Filippovia knipovitchi* (average TP value of 4.1; Woods et al. 2022). In contrast, TP values of females from Bird Island indicate a diet predominantly consisting of Antarctic krill (average TP value of 2.3; Conroy et al. 2024). These findings are consistent with previous scat analysis studies (Table 1; Reid & Arnould 1996, Klages & Bester 1998, Brown et al. 1999, Makhado et al. 2008, Polito & Goebel 2010, Reisinger et al. 2018, Borrás-Chávez 2020). Fur seals from Cape Shirreff had TP values in summer consistent with predation on krill as expected, but also on myctophids and squids, likely including *Martialia hyades* (TP values ranging from 2.7 to 3.7; Woods et al. 2022). AFSs from Cape Shirreff primarily rely on Antarctic krill as their main food source in summer, but there are indications of a dietary shift towards myctophids and squid prior to parturition and when krill availability is limited (Polito & Goebel 2010, Krause et al. 2022). Interestingly, in winter, Cape Shirreff females showed higher TP compared to Bird Island females but were comparable to that of Marion Island females. The higher TPs may result from females incorporating more myctophids and squids into their diet, due to a decrease in krill availability. Additionally, a shift in the diet of krill, which feed at higher trophic levels in autumn/winter (Zhu et al. 2018), could also result in higher TP values. Another factor that needs consideration is the vertical foraging of AFS, as this can influence δ^{15} N values in their tissues. However, previous studies have shown that females are relatively shallow divers, with an average dive depth within the first 20 m and maximum diving depth of 200 m (Arthur et al. 2016).

Regarding seasonal variations, our results indicate no significant differences in $\delta^{15}N_{\text{Leu}}$, TP_{Leu-Phe} and RTPLeu-Phe between summer and winter for females from Marion Island. During mid-winter, some female AFSs from Marion Island have been reported foraging south of the PF near the ice edge (Fig. S3; Arthur et al. 2017, Wege et al. 2019). Corresponding bulk stable isotope values in whiskers revealed that they are targeting lower trophic level prey, likely Antarctic krill (Walters 2014, Walters et al. 2020). In our study, one female in winter showed a TP below 4, which is consistent with feeding on krill (average TP value of 2.3 for Antarctic krill; Conroy et al. 2024). The absence of seasonal differences could be due to only a small portion of females feeding on krill, or as whole blood reflects seal diet only at the end of the inter-breeding foraging trip, it limits the ability to detect long-term dietary trends, such as mid-winter krill consumption. The TPs of females from Marion Island are in the same range as those calculated for Dana octopus squid (4.8 ± 0.3) and colossal squid *Mesonychoteuthis hamiltoni* (4.7 ± 0.3) beaks sampled in the southern Indian Ocean (Cherel et al. 2019), indicating that female AFSs likely occupy a similar position in the food web.

Significant seasonal differences in $\delta^{15}N_{\text{Leu}}$, TP_{Leu-Phe} and RTP_{Leu-Phe} were detected for females from Bird Island in the south Atlantic sector, indicating that females occupied a higher $TP_{Leu-Phe}$ in winter. This is consistent with tracking studies (Boyd et al. 2002) and scat analysis (Reid 1995, Reid & Arnould 1996). A study analysing scats of female AFSs from Bird Island during the same years as this study (2008–2010) re vealed a higher frequency of krill in their diet during summer (79%) when most of our females had a TP_{Leu} -Phe between 3 and 4 (Coleman 2022). In contrast, during winter, fish made an increased contribution to their diet (57%), with half of the females having a TP_{Leu-Phe} below 4 and the other half a TP_{Leu-Phe} above 4 (Coleman 2022). A seasonal shift in $TP_{Leu-Phe}$ is consistent with a change in diet composition as observed from scat analysis.

The distribution of TP_{Leu-Phe} and RTP among females from Bird Island indicates the existence of several predominant feeding strategies within the population. In summer, one group exhibits RTP between 8 and 12‰, another between 12 and 16‰, and in winter, a third group between 16 and 20‰ (Fig. 4). Previous studies using stable isotope analysis on whiskers revealed niche partitioning among females from the same colony (Jones et al. 2020, Walters et al. 2020). Jones et al. (2020) estimated during winter that approximately 30% foraged to the north of the PF, primarily consuming squid, myctophids and other fishes, while the remaining 70% foraged to the south of the PF, feeding on large quantities of Antarctic krill. In addition, in warmer years with reduced krill availability, females from Bird Island tend to consume more squid (McCafferty et al. 1998, Abreu et al. 2019). The large population of AFSs at South Georgia (Bird Island), accounting for 95% of the global population, may lead to intra-specific competition and resource partitioning among females to relax competition (Jones et al. 2020). Intra-population niche partitioning also appears to be present among females from Cape Shirreff (Fig. 4). Borrás-Chávez (2020) de scribed 2 distinct dietary clusters among these females in summer: one was characterized by a krilldominated diet and the other by a fish-dominated diet. Our results confirm these findings and further reveal that, in winter, the TP and RTP distributions also indicate 2 main groups. One group has RTP_{Leu-Phe} between 15 and 16, indicative of primarily feeding on myctophids, while the other larger group has RTP_{Leu} . _{Phe} values between 17 and 21, which suggest a diet more focused on squid.

4.3. Advances and challenges in using AAs for studying wide-ranging marine predators

Accurate dietary assessment of marine predators is needed to detect spatial and temporal variations in predator–prey relationships in the Southern Ocean. Our study highlights the importance of using CSIA-AA for detecting spatial trophic variations in trophic ecology of marine predators. While spatial differences in the AFS trophic ecology between Bird Island and Cape Shirreff in summer, and between Marion Island and Bird Island in winter, were detected with $\delta^{15}N_{AA}$ values, they were not observed with $\delta^{15}N_{bulk}$ values. The metabolic AA Thr, along with Leu, were the only AAs to differentiate between the 3 colonies in summer, and Bird Island from the 2 other colonies in winter, suggesting that Thr is a useful ecological biomarker to support robust comparisons of spatial and temporal variability in consumer trophic ecology (Lübcker et al. 2020).

While Glu and Phe have traditionally been the primary AAs used in studies, we show the potential value of incorporating additional AAs into isotopic baseline and trophic ecology investigations of marine predators (McMahon et al. 2015b). Lys could also serve as an informative source AA (Nielsen et al. 2015), as $\delta^{15}N_{Lys}$ values revealed differences in baselines between Marion Island and Cape Shirreff in summer, as well as between Bird Island and the 2 other colonies in winter, which were non-detected by $\delta^{15}N_{\text{Phe}}$ values. Additionally, we showed that $\delta^{15}N_{Lvs}$ is more representative of the isotopic baseline compared to $\delta^{15}N_{\text{Phe}}$ during this season for Marion Island AFSs. The differences in $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lys}}$ values can be attributed to their distinct metabolic pathways. Lys metabolism is unique due to the presence of 2 nitrogen groups. While there are several pathways for Lys catabolism, the primary pathway in mammals involves irreversible transamination. In contrast, Phe has 2 potential catabolic routes: a minor pathway involving transamination, and a dominant pathway involving hydroxylation to tyrosine (McMahon & McCarthy 2016, O'Connell 2017).

Additionally, we found that TP_{Leu-Phe} (as opposed to the widely used TP_{Glx-Phe}) provided the most ecologically realistic TP estimation for female AFSs, given that, as secondary and tertiary consumers (depending on their diet), it is ecologically impossible for AFSs to have a TP below 3.0. Moreover, average TP_{Leu-Phe} estimates for Marion Island (4.7 in summer and 4.8 in winter) are close to TP_{bulk} estimated for females from the Kerguelen Islands (4.8 ± 0.1) ; Cherel et al. 2010), which have a similar diet and forage within the same ocean basin. In contrast, 33% of females from Bird Island exhibited $TP_{Glu-Phe}$ below 3.0, a TP unrealistically low for AFSs. Previous studies on crabeater seals and squids have also documented TPs below 3.0 (Brault et al. 2019, Woods et al. 2020, 2022). These findings underscore the persistent challenges in relying on absolute TP values and in the parameterization of TP equations. Additionally, we observed low TPs (<4.0) for some female AFSs from Marion Island in summer, which are thought to primarily feed on myctophid fish during this season (Makhado et al. 2008). These low TP estimates may also be due to the TP estimation method used, or alternatively, it may suggest that those females predated on organisms at lower trophic levels than previously assumed during the summer. However, as scat analysis is known to be biased to prey with hard parts, alternative genetic (DNA) metabarcoding analysis of scat samples from females from Marion Island could provide valuable insights into prey consumption (Augé et al. 2012, McInnes et al. 2017, Cavallo et al. 2018).

Another challenge is the absence of an AFS-specific TDF; however, Borrell et al. (2012) suggested that TDFs remain relatively consistent among taxonomically closely related species, making the harbour seal the most suitable option for our study. This underscores the need for TDF and β estimates specific to AFS or at least for more closely related species. While the inclusion of RTP values can provide a more standardized approached, it does not eliminate the issue of unknown TDF variability.

5. PERSPECTIVES AND CONCLUSIONS

Long-term studies encompassing spatiotemporal variability in the structure and function of the Southern Ocean ecosystem across all of its sectors are essential (Constable et al. 2023). Considering the recent major changes in AFS populations (Krause et al. 2022, 2024, Forcada et al. 2023), and the pronounced inter-annual and intra-colony variability (Trathan et al. 2021), exploring long-term variability in the food web baseline and trophic ecology of AFSs across Southern Ocean sectors can provide insight into the environmental changes happening in Southern Ocean food webs (Huang et al. 2011, de Lima et al. 2022). Recent long-term studies have highlighted changes in phytoplankton phenology and bloom duration in the Southern Ocean (Thomalla et al. 2023, Antoni et al. 2024). For example, Antoni et al. (2024) revealed significant changes in phytoplankton communities in the western Antarctic Peninsula region between 2010 and 2020, including the detection of a nanoplankton species from temperate waters (Antoni et al. 2024). Changes in the food web baseline can impact the overall food web structure, and such changes have been detected in marine predator isotopic signatures (de la Vega et al. 2022, 2023). Our study provides valuable baseline data for the detection of future changes in local food webs.

Our findings provide further evidence of the complex spatial and seasonal variations in the $\delta^{15}N$ baseline in the Southern Ocean and highlight both the advantages and limitations of using δ^{15} N from source AAs of a marine predator to detect them. While $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Lvs}}$ values from Marion Island and Cape Shirreff females were consistent with $\delta^{15}N_{\text{POM}}$ Abreu J, Staniland I, Rodrigues CF, Queirós JP, Pereira JM, and $\delta^{15}N_{PON}$ values in the Indian and Atlantic sector during both seasons, the area of the Atlantic sector around Bird Island exhibited a more complex pattern. The wide range of foraging behaviours of AFSs in winter, complex spatial and seasonal variations in processes influencing $\delta^{15}N$ at the base of the food web, possible discrepancies between $\delta^{15}N$ of source AAs, $\delta^{15}N_{\rm POM}$ and $\delta^{15}N_{\rm baseline}$, and the lack of data in winter and in the Pacific basin suggest the need for cautious interpretation and further research to improve the reliability of $\delta^{15}N_{\text{baseline}}$ estimates. Nonetheless, our method provides greater insight into variations in the isotopic baseline in the Southern Ocean and the foraging ecology of the AFS, including the poorly sam-

pled winter season, emphasizing the importance of a comprehensive understanding of seasonal dynamics in the region, and providing a baseline for future CSIA-AA studies. AFSs occupy a diverse range of TPs, encompassing more than 2 trophic levels. This highlights the intra- and inter-colony flexibility in the diet and trophic role of female AFSs, and the importance of considering individual and regional variability in populations for management, conservation, and ecosystem models of the Southern Ocean.

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