 <p>Agreement on the Conservation of Albatrosses and Petrels</p>	<p>Joint Thirteenth Meeting of the Seabird Bycatch Working Group and Ninth Meeting of the Population and Conservation Status Working Group</p> <p><i>Swakopmund, Namibia, 26 May 2026</i></p> <p>ACAP Secondment S2022-03 Report. Multi-fishery interactions of sympatric black-browed and grey-headed albatrosses from the Diego Ramírez Islands: An isotopic and tracking approach</p> <p><i>Cristián G. Suazo, Javier E. Ciancio, Paula Plaza, Luis Adasme & Petra Quillfeldt</i></p>
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1. Background

Previous work has focused on improving knowledge of the non-breeding distribution of Black-browed (BBA) and Grey-headed albatrosses (GHA) from sub-Antarctic Chile, as well as their interactions with fisheries through the consumption of discards and offal. To address these objectives, tracking datasets (BirdLife International tracking database; <https://www.seabirdtracking.org/>) were explored to understand the distribution dynamic of albatrosses in response to their phenology performed by adult individuals (incubation, guard, and postguard).

These datasets included records from the 2001, 2010, and 2011 breeding seasons at the Diego Ramírez Islands, located approximately 113 km southwest of Cape Horn. In addition, banding data from adults and juveniles collected since the 2010 breeding season were incorporated to complement movement and demographic information.

To further investigate trophic ecology, intrinsic markers were analysed through stable isotope techniques. Specifically, nitrogen ($\delta^{15}\text{N}$) and carbon ($\delta^{13}\text{C}$) isotopic compositions were measured to infer trophic level and food web structure, in collaboration with Dr. Petra Quillfeldt (JLU Giessen, Department of Animal Ecology and Systematics). Baseline isotopic values were established using dietary samples collected during previous campaigns, including natural prey such as krill (Quillfeldt et al. 2005), as well as reference dietary material obtained from both albatross species at the Diego Ramírez Islands during 2010, 2011, and 2014.

In parallel, prey items associated with fisheries discards were collected in situ during fishing operations along the Chilean continental shelf (central and southern Chile), as well as in oceanic islands and sub-Antarctic fishing grounds. These samples represented both industrial and small-scale fisheries, including longline, trawl, purse seine, and gillnet operations, across

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three study areas. These reference samples, together with data compiled from the literature, were used to assess the relative contribution of natural versus fisheries-derived food in albatross diets.

Stable isotope signatures from potential natural and fisheries-derived food sources were compared with those obtained from multiple tissue types, including tail feathers (long-term dietary integration), chick down (reflecting the incubation period), adult blood samples collected during incubation, and back feathers from pre-fledging individuals (reflecting the post-guard period). These analyses were conducted in relation to the breeding phenology of both albatross species at the Diego Ramírez Islands.

The integration of tracking and isotopic approaches enabled the identification of seasonal distribution patterns of albatrosses, including spatial and temporal hotspots of interaction with natural prey and fisheries-derived food, particularly during the non-breeding period. Distribution patterns were described based on the frequency of use of regional areas within the Humboldt Current System, as well as sub-Antarctic and oceanic islands, following approaches like those described by Arata et al. (2014).

Finally, modelling approaches were applied to evaluate the relative importance of different fisheries as sources of supplementary food, considering both percentage contribution and frequency (Mariano-Jelicich et al. 2014). These analyses incorporated information on fishing effort across the three study areas in Chilean waters, supported by data from the national fisheries monitoring programme developed by IFOP for SUBPESCA.

2. Material and Methods

On February 3, 2023, the development of this secondment was approved in collaboration with ACAP, including Chile and Argentina. Due to scheduling issues for the visit to Dr. Javier E. Ciancio (CENPAT-Puerto Madryn, Argentina), this work began in 2023 through 2024 with the collection, analysis, and curation of reference diet samples from the two albatross species that breed in Chile for isotopic fingerprint analysis towards the interpretation of results at the end of 2024-early 2025.

During this process, we collected tissue samples from various target species in industrial and small-scale fisheries, based on the context in which these foods are available to albatrosses (e.g. muscle from discards, offal). The sample collection was supported by the IFOP fisheries observer program and the Albatross Task Force in Chile (BirdLife International-RSPB), covering both pelagic fisheries in oceanic islands (pelagic longline for swordfish) and demersal fisheries in southern Chile (demersal trawl for Austral hake). Overall, fisheries included in this sample set represented the full gradient of fisheries in Chile, from the border with Peru (18°S) to the southern Diego Ramírez Islands (56°S) in the Drake Passage also covering longline (pelagic, demersal), trawl (pelagic, demersal), and purse seine fisheries (industrial and small-scale).

Additionally, we considered samples of natural prey from the diet repertoire of the Diego Ramírez albatrosses, including tissues from regurgitated squid from the subantarctic waters, as well as fish like Fuegian sprat *Sprattus fuegensis* from the Chilean fjords, and Antarctic krill *Euphausia superba* off the Antarctic Peninsula (60°S).

In total, we obtained 126 processed tissue samples with $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ readings, representing the described endemic areas for seabirds in Chile, such as the Humboldt Current System, Oceanic Islands, Fjords and Channels in Southern Chile, and Antarctica.

Regarding the albatrosses, blood and feather samples ($n= 171$) were analysed for adult and chick Black-browed albatross (*Thalassarche melanophris*; $n= 125$; BBA) and Grey-headed albatross (*T. chrysostoma*; $n= 46$; GHA) from the Diego Ramírez Islands.

To assess differences in carbon and nitrogen enrichment patterns between BBA and GHA, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values were compared. Normality was examined using the Shapiro-Wilk test. Where assumptions were not met, non-parametric tests were applied. Tissue sample type (blood or feather) and age class (chick and adult) were considered as categorical factors.

Multivariate differences in isotopic composition were evaluated separately for each species using permutational multivariate analysis of variance (PERMANOVA) implemented in the vegan package. Isotopic variation was first tested using a factorial model including the interaction term (Tissue \times Age). When interaction terms were non-significant, reduced models including only main effects (Age + Tissue) were fitted to evaluate their independent contributions. Statistical significance was assessed using 999 permutations, and effect sizes were estimated using R^2 . Homogeneity of multivariate dispersion was assessed and differences among groups were tested using ANOVA followed by Tukey HSD post-hoc comparisons where appropriate. The significance level was set at $\alpha= 0.05$ for all tests.

Isotopic niche width was estimated using the Stable Isotope Bayesian Ellipses in R (SIBER) framework (Jackson et al. 2011). Species were treated as groups within a single community. Total convex hull area (TA) and standard ellipse area (SEA) were calculated to quantify total and core isotopic niche width, respectively. To account for small sample sizes, small sample corrected ellipse areas (SEAc) were also computed. Moreover, the Bayesian approximation of the standard ellipse area (SEAb) was employed to compare niche widths between species, using 95% of the data as a measure of isotopic partitioning.

Albatross species and fishery resource groups were treated as a community within a single food web. For Subantarctic waters, sample-size corrected standard ellipse area (SEAc) was calculated using maximum likelihood estimation. Isotopic niche overlap between groups was quantified using the percentage of overlap in SEAc ellipses. Isotopic niche overlap was quantified separately for each albatross tissue type (feather and blood).

Dietary proportions of BBA and GHA were estimated using the Bayesian mixing model framework MixSIAR in R. Separate models were implemented for feathers ($n= 153$) and blood ($n= 75$) to evaluate dietary integration across distinct temporal windows: the non-breeding/molt period and the recent breeding/foraging period, respectively. For both tissues, 'Species' was incorporated as a fixed effect. Five potential prey sources were identified based on isotope signal: Demersal fish (AH) or Austral hake, Demersal fish (PT) or Patagonian toothfish, Pelagic cephalopods, Pelagic fish (FS) or Fuegian sprat and Demersal crustaceans. Trophic discrimination factors (TDF) were tissue-specific to account for physiological fractionation.

For feathers, following Cherel et al. (2005): $\Delta^{13}\text{C} = 1.1 \pm 0.2\text{‰}$, $\Delta^{15}\text{N} = 3.6 \pm 0.4\text{‰}$. For blood, following Phillips & Eldridge (2006): $\Delta^{13}\text{C} = 0.1 \pm 0.2\text{‰}$, $\Delta^{15}\text{N} = 2.3 \pm 0.3\text{‰}$. Models were executed including both residual and process error terms. Posterior distributions were estimated via Markov Chain Monte Carlo (MCMC) simulations in JAGS. Prior to inference, isospace plots were visually inspected to ensure appropriate consumer-source geometry. Convergence was validated through Gelman-Rubin and Geweke diagnostics. Dietary shifts

between tissues were analysed by comparing posterior mean proportions and their associated standard deviations.

3. Results

The distribution of albatrosses in Chile shows different spatial patterns for the BBA, with a stronger association with more continental waters during the incubation and guard stages, as well as foraging incursions toward the Antarctic Peninsula at the end of the breeding cycle during the post-guard period (Fig. 1). In contrast, the GHA is distributed in more oceanic waters, showing a strong association with the Antarctic Circumpolar Current and the Antarctic Peninsula (Fig. 1).

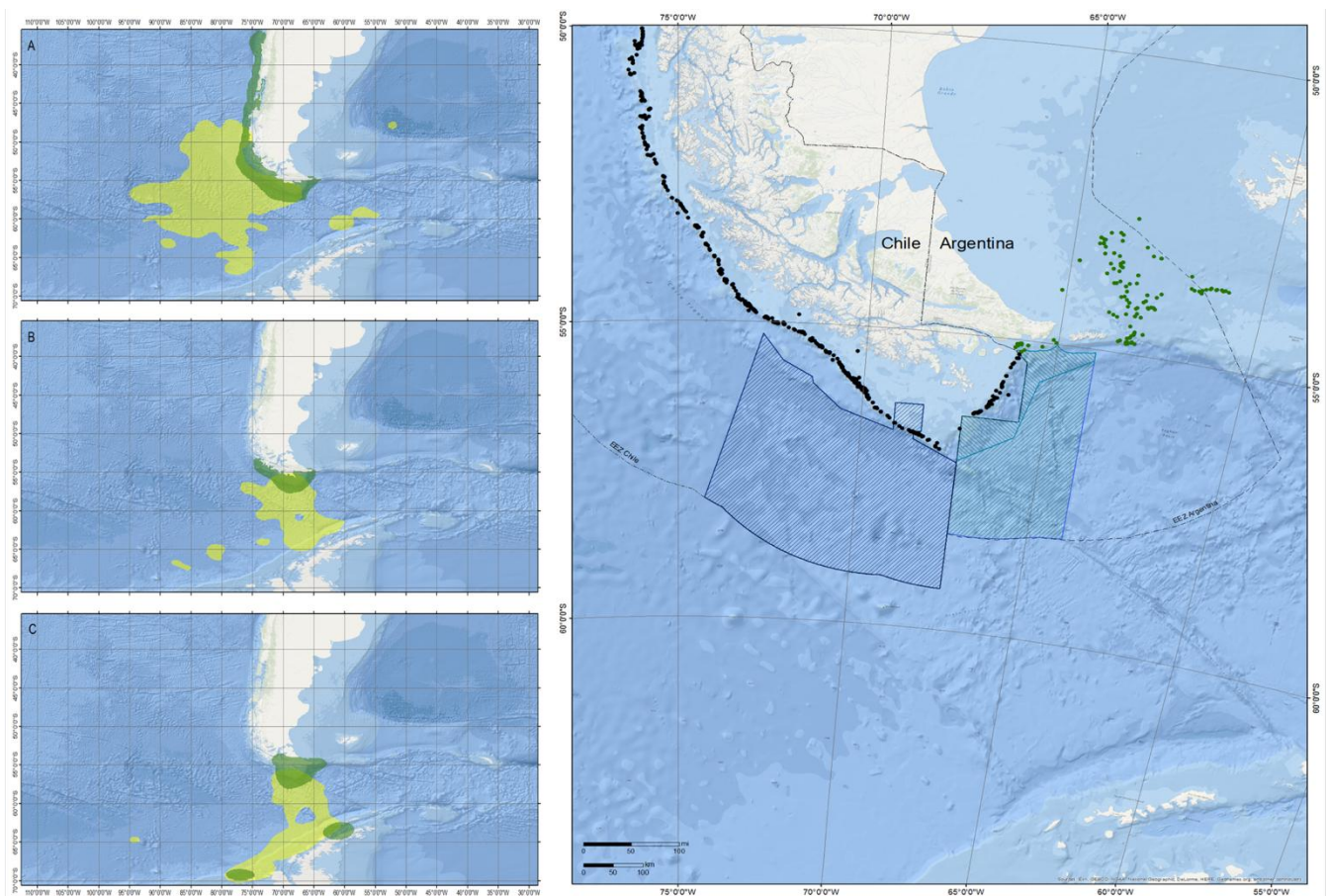


Figure 1. Left: Accumulate breeding distribution for the Grey-headed albatross (GHA, light green) and the Black-browed albatross (BBA, dark green) during the incubation (A), guard (B), and postguard (C). Right: Distribution of interaction events between albatrosses and demersal longline and trawl fisheries beyond the borders of Diego Ramírez islands.

Within the distribution of both albatross species, it is possible to identify a greater overlap of the BBA with a diverse range of fisheries, including both industrial and small-scale operations in the Humboldt Current System. These include pelagic fisheries, such as purse seine, and demersal fisheries, such as trawl, operating as far south as the Diego Ramírez Islands.

In contrast, the GHA shows lower overlap with fisheries within Chile's Exclusive Economic Zone (EEZ), except for its association with fisheries located outside the southern fjord system of the country, including demersal trawl and demersal longline fisheries targeting hake and Patagonian toothfish (Table 1).

Table 1. Fisheries, target resources, and observer coverage during different studies carried out on seabird bycatch in Chilean waters.

Fishery	Fisheries' general latitudinal range	Fishing depth (m)	Seabird endemism area	Period covered	Source
Industrial demersal longline for Patagonian toothfish <i>Dissostichus eleginoides</i>	South of 47° S	168-2,250	sub-Antarctic (SA)	2001 (Exploratory); 2002-2003 (Study)	Moreno <i>et al.</i> , (2003)
Industrial demersal longline for austral hake <i>Merluccius australis</i> and ling <i>Genypterus blacodes</i>	45°-57° S	200-600	SA	Oct-Nov 2003; Mar 2004	Unpublished data from Moreno <i>et al.</i> , (2003); Moreno and Arata (2004) cited by Robertson <i>et al.</i> , (2014)
Artisanal demersal longline for austral hake <i>Merluccius australis</i> and ling <i>Genypterus blacodes</i>	41°-45° S	100-500	SA	1999	Moreno <i>et al.</i> , (2006)
Artisanal demersal longline for Patagonian toothfish	41°-47° S	1,000-2,000	SA; Humboldt Current system (HCS)	2002	Moreno <i>et al.</i> , (2006)
Industrial pelagic longline for swordfish <i>Xiphias gladius</i>	29°-32° S	4-10	HCS; Oceanic islands (OI)	Feb 2007-Oct 2009	Azócar <i>et al.</i> , (2010)

Industrial demersal trawl for austral hake, southern blue whiting <i>Micromesistius australis</i> and hoki <i>Macruronus magellanicus</i>	43°-53°S	200-500	SA	2 nd half of 2012	Céspedes et al. (2012)
Industrial demersal trawl for South Pacific hake <i>Merluccius gayi gayi</i>	34°-39°S	150-800	HCS	Jun 2011-Aug 2012	ATF - Chile (2013)

Stable isotope values differed significantly between species (Kruskal-Wallis: $\delta^{13}\text{C}$ $\chi^2= 89.83$, $p < 0.001$; $\delta^{15}\text{N}$ $\chi^2= 70.65$, $p < 0.001$), indicating segregation in both trophic position and basal carbon sources (Table 2). BBA exhibited significantly more enriched $\delta^{13}\text{C}$ values ($-17.87 \pm 0.82\text{‰}$) compared to GHA ($-20.34 \pm 1.12\text{‰}$), indicating differences in basal carbon sources. Similarly, $\delta^{15}\text{N}$ values were significantly higher in BBA ($15.92 \pm 0.72\text{‰}$) than in GHA ($13.81 \pm 1.55\text{‰}$), suggesting a higher trophic position.

Table 2. Summary of stable isotope values (mean \pm SD) for Black-browed Albatross (BBA) and Grey-headed Albatross (GHA).

Species	n	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$
BBA	140	-17.87 (0.821)	15.92 (0.72)
GHA	49	-20.34 (1.12)	13.81 (1.55)

In the BBA, the factorial PERMANOVA model (Tissue \times Age) showed no significant interaction between factors ($p > 0.05$). Reduced models including only main effects indicated that both Age and Tissue significantly influenced isotopic composition. Tissue type explained a substantially larger proportion of variation ($R^2= 0.43$) than age class ($R^2= 0.28$; $p = 0.001$ for both).

Analysis of multivariate dispersion revealed significant heterogeneity among Age \times Tissue groups ($F= 22.85$, $p= 0.001$). Post-hoc pairwise comparisons indicated that adult feathers differed significantly from all other groups ($p \leq 0.005$), exhibiting the highest isotopic variability. In contrast, no significant differences in dispersion were detected among adult blood, chick blood, and chick feather groups, suggesting more consistent dietary composition during the breeding period across age classes (Table 3).

In GHA, the interaction term could not be estimated due to incomplete factorial combinations (absence of adult feather samples in the dataset; Table 2). Therefore, models including only main effects were fitted. Isotopic composition differed significantly between tissues ($F= 58.89$, $R^2= 0.39$, $p= 0.001$) and, to a lesser extent, between age classes ($F= 5.19$, $R^2= 0.03$, $p= 0.012$). Tissue type explained substantially more variation than age. Multivariate dispersion differed marginally among groups (PERMDISP: $F= 3.13$, $p= 0.047$). Pairwise comparisons indicated that only chick blood and chick feather groups differed significantly in dispersion ($p= 0.024$), whereas no other comparisons were significant.

Table 3. Stable isotope values (mean \pm SD) for BBA and GHA by age class and tissue type.

Specie	Age	Tissue	n	$\delta^{13}\text{C}$	$\delta^{15}\text{N}$
BBA	Adult	Blood	46	-18.11 (0.64)	15.87 (0.54)
BBA	Adult	Feather	10	-16.41 (1.20)	16.93 (1.61)
BBA	Chick	Blood	10	-19.43 (0.45)	14.79 (0.31)
BBA	Chick	Feather	74	-17.71 (0.37)	15.97 (0.42)
GHA	Adult	Blood	9	-20.97 (0.48)	11.68 (0.79)
GHA	Chick	Blood	10	-21.67 (0.47)	12.57 (0.47)
GHA	Chick	Feather	30	-19.71 (0.90)	14.87 (0.82)

Across all metrics, the isotopic niche was substantially larger in the GHA compared to the BBA, indicating a broader overall isotopic niche in the former. Analysis of tissue-specific niche metrics revealed that feathers exhibited larger isotopic niches than blood for both species (Figs. 2-3). Bayesian estimates of isotopic niche width corroborated these findings with high statistical confidence, the posterior distribution of SEAb for GHA was consistently larger than that of BBA across all MCMC iterations in both tissues. Interspecific niche overlap was moderate in feathers (overlap= 1.81 ‰) and low in blood (overlap= 0.78 ‰), indicating significant resource segregation in isotopic space during the breeding season, with partial overlap persisting during the non-breeding period (moult).

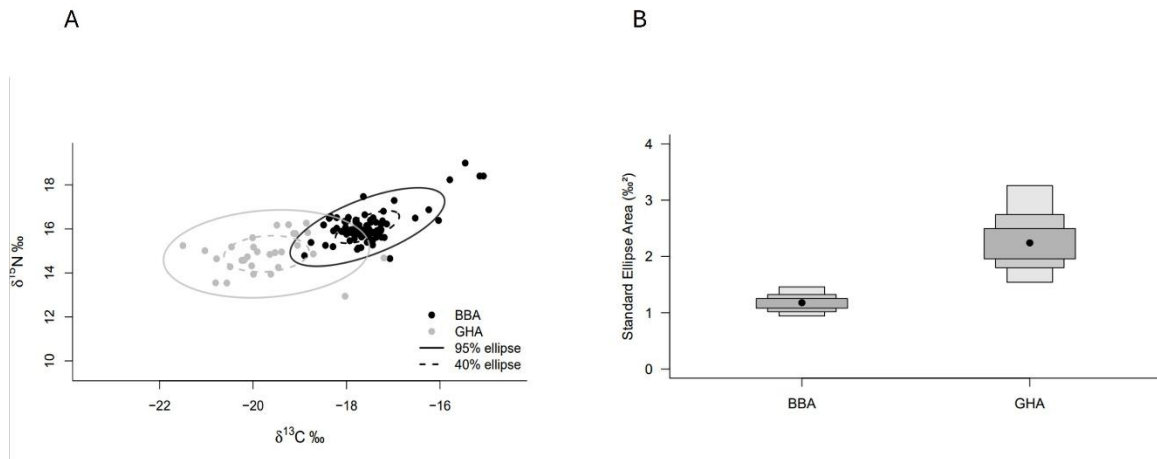


Figure 2. Isotopic niche metrics for BBA and GHA in feather samples. **(A)** Biplot of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values showing standard ellipse area corrected for small sample sizes (SEAc, solid lines representing) and total convex hull area (TA, dashed lines). **(B)** Bayesian estimates of isotopic niche width (SEAb) derived from 10,000 MCMC iterations. Violin plots show posterior distributions, with horizontal lines indicating median values.

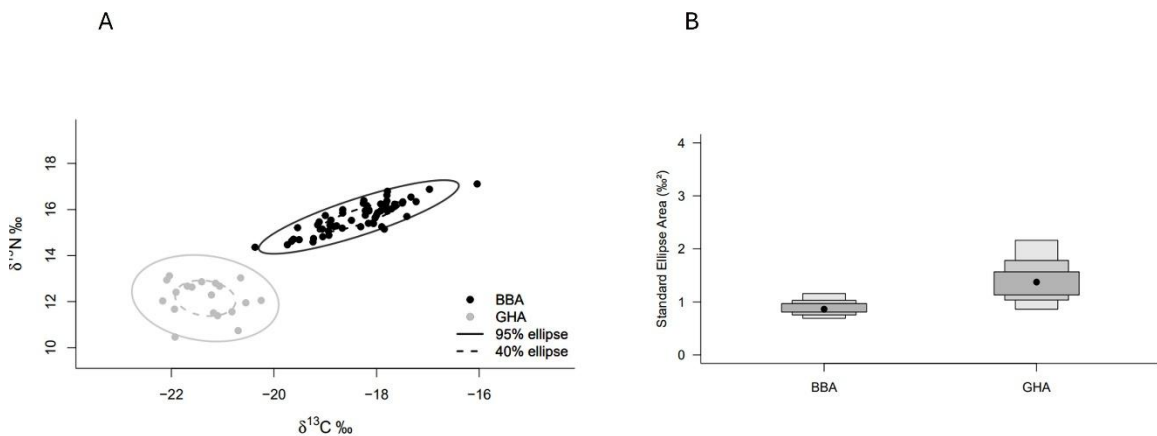


Figure 3. Isotopic niche metrics for BBA and GHA in blood samples. **(A)** Biplot of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values showing standard ellipse area corrected for small sample sizes (SEAc, solid lines) and total convex hull area (TA, dashed lines). **(B)** Bayesian estimates of isotopic niche width (SEAb) showing posterior distributions from MCMC simulations.

Stable isotope signatures of potential prey items and fishery-associated resources varied significantly across geographic areas and marine strata (Fig. 4). In the Humboldt Current System (HCS), pelagic and demersal target species such as Sardine *Strangomera bentincki* and South Pacific hake *Merluccius gayi gayi* exhibited enriched $\delta^{15}\text{N}$ values (15.96 -17.65, respectively) and relatively higher $\delta^{13}\text{C}$ values (ca.-15.0‰). In contrast, resources from the Sub-Antarctic (SA) and Antarctic (AN) regions showed a marked depletion in $\delta^{13}\text{C}$, with values reaching -24.33 ‰ for Lobster krill and -23.50 ‰ for Antarctic krill.

Within the sub-Antarctic (SA) region, a mixed isotopic signal was observed for $\delta^{15}\text{N}$: pelagic fish (Fuegian sprat) was enriched (14.85 ‰) compared to deeper demersal or mid-water species like Hoki *Macruronus magellanicus* (13.45 ‰) and Squid (7.79 ‰). Finally, high-trophic-level pelagic predators from Oceanic Islands (OI), including Swordfish *Xiphias gladius* and Mako shark *Isurus oxyrinchus*, exhibited the most enriched $\delta^{15}\text{N}$ signatures (>19.0‰), while maintaining intermediate $\delta^{13}\text{C}$ values (mean -16.6 ‰), reflecting their position as top predators within the pelagic food web.

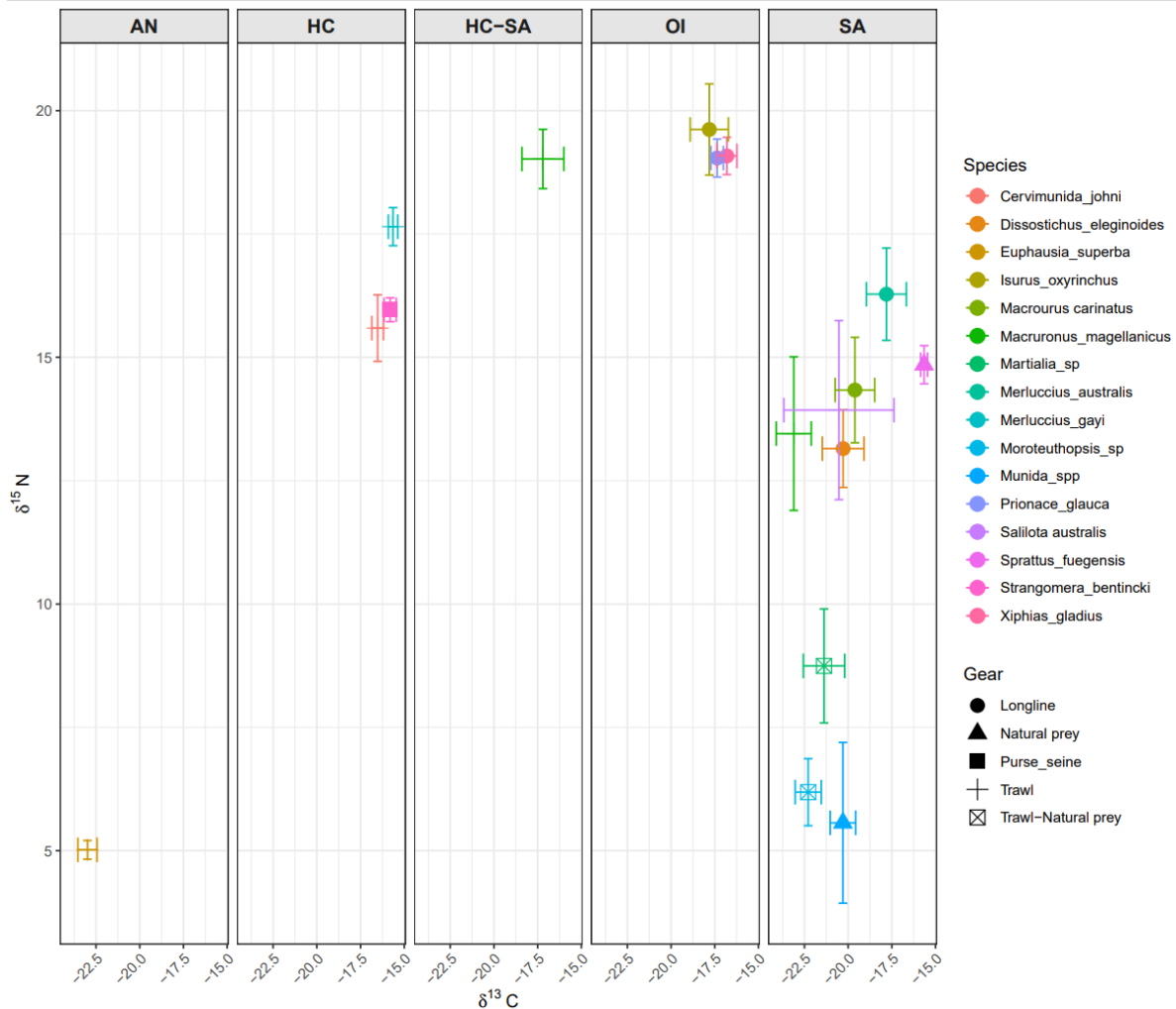


Figure 4. Biplot of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values for fishery resources across four regional zones: Humboldt Current System (HCS), sub-Antarctic (SA), Antarctic (AN), and Oceanic Islands (OI). Colors distinguish resource types: pelagic fish (blue), demersal fish (green), invertebrates (orange), and large predators (red). The wide range of isotopic values (-23 to -16‰ for $\delta^{13}\text{C}$ and 5 to 20‰ for $\delta^{15}\text{N}$).

The integration of niche metrics and Bayesian mixing models for the SA region revealed distinct foraging strategies and resource partitioning between BBA and GHA across different temporal scales (feathers vs. blood). During the non-breeding period (recorded in feathers), interspecific niche overlap was moderate (1.21 ‰²). MixSIAR results indicate that this overlap is largely driven by a similar utilization of demersal fish resources by both species (BBA: 25.1% for PT and GHA: 23.1% for PT).

This suggests that during the molt and post-breeding dispersal, both albatrosses interact similarly with demersal fishery discards, leading to a more shared isotopic space. Interspecific niche overlap between BBA and GHA decreased in blood samples (0.80 ‰²), suggesting a marked increase in resource segregation during the chick-rearing period. In contrast, GHA demonstrated an increasing specialization in pelagic resources. Pelagic cephalopods (squid) remained the dominant prey, with their contribution increasing from 64.7% in feathers to 81.5% in blood (Figure 5). This dietary focus is further reflected in the GHA extensive overlap with the squid isotopic ellipse (2.36 ‰² in feathers and 2.06 ‰² in blood), confirming its role as a specialized oceanic predator.

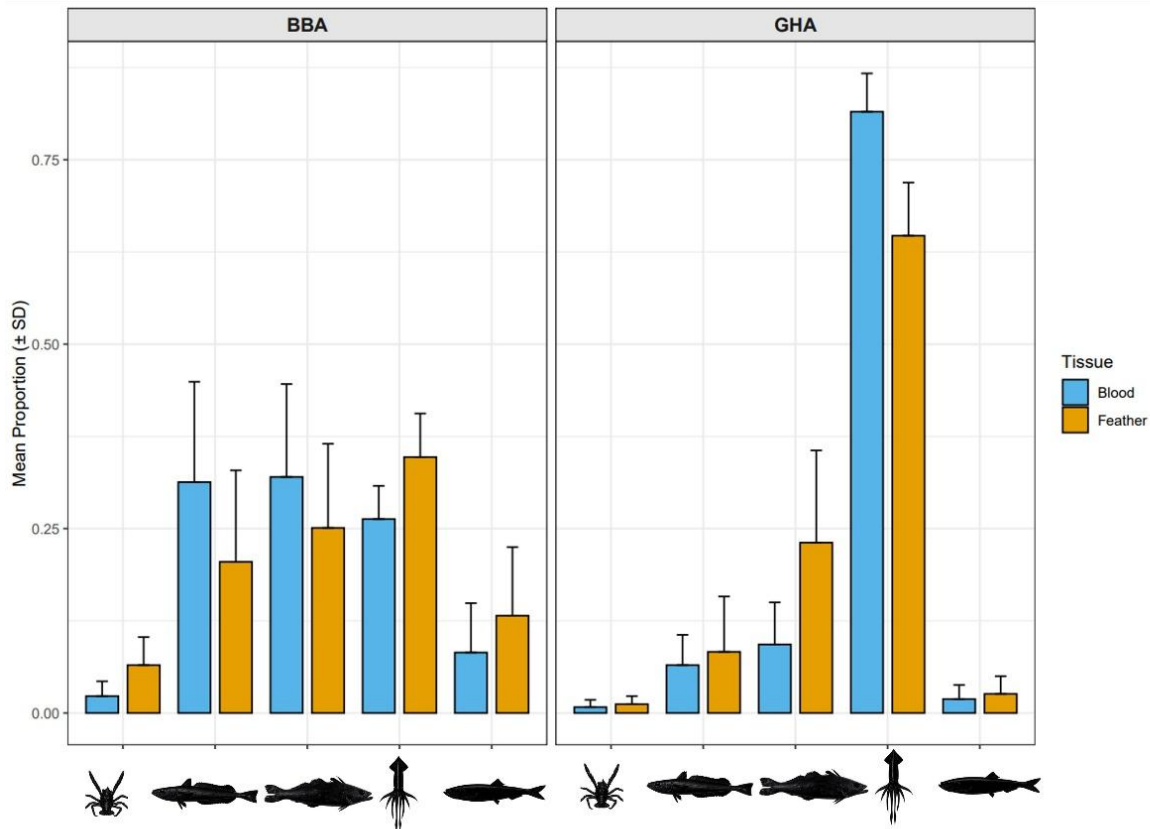


Figure 5. Comparison of dietary proportions between tissue types (feather vs. blood) for BBA and GHA. Stacked bar plots show median posterior estimates from MixSIAR models. Differences between feather (orange) and blood (blue) proportions.

4. Concluding remarks

This study provides an integrative assessment of the spatial distribution and trophic ecology of sympatric Black-browed and Grey-headed albatrosses breeding at the Diego Ramírez Islands, highlighting clear differences in habitat use, trophic position, and interactions with fisheries across temporal scales. By complementing tracking information with stable isotope analyses and fishery-derived prey sampling, this work establishes a baseline to date on how these ACAP-listed species exploit natural and anthropogenic food resources in Chilean waters.

A key finding is the contrasting degree of interaction with fisheries between species. The Black-browed Albatross shows broad overlap with multiple industrial and small-scale fisheries within the Humboldt Current System and sub-Antarctic waters, reflecting a more generalist and opportunistic trophic strategy. In contrast, the Grey-headed albatross remains more oceanic and specialized, with more limited but still relevant interactions with specific demersal fisheries. These differences reinforce the importance of species-specific approaches when evaluating bycatch risk and mitigation strategies.

Importantly, this study underscores the critical need to generate robust baseline information on trophic relationships under diverse fisheries scenarios. The integration of isotopic signatures from both natural prey and fishery-derived resources allows for a quantitative understanding of the relative contribution of subsidies from fisheries, which is essential for

interpreting ecological responses to changing fishing practices. In dynamic systems such as the Humboldt Current and sub-Antarctic regions, where multiple fisheries operate across spatial and temporal gradients, such baselines are indispensable.

Looking forward, the continuation and expansion of these approaches will be fundamental to monitor changes in trophic interactions and distribution patterns over time. This is particularly relevant in the context of shifting fishing effort, climate variability, and evolving management measures. Long-term monitoring combining tracking, isotopic analyses, and observer-based fishery data will enable the detection of changes in reliance on fisheries-derived food, potential increases in bycatch risk, and shifts in foraging ecology.

Ultimately, this work contributes to the conservation and management of sympatric albatross species in Chile by providing fundamental knowledge to inform ecosystem-based fisheries management. Strengthening baseline datasets and maintaining consistent monitoring frameworks will be essential to anticipate future changes and to support effective mitigation strategies for these globally threatened seabirds.

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