**SUPPLEMENTARY METHODS**

**Resource partitioning influences levels of toxic trace elements in sympatric tropical seabirds**

**Bruno de Andrade Linhares, Guilherme Tavares Nunes, Adalto Bianchini, Luísa Bertolini, Fiorella Vilela, Márcio Amorim Efe, Fábio Lameiro Rodrigues, Sophie Lanco, Yuri Dornelles Zebral, Patrícia Gomes Costa, Leandro Bugoni**

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**Bio-logging analysis**

Hidden Markov Models (HMMs) were fitted from step length and turning angle values estimated from the regularized GPS data using the Gamma and von Mises distributions, respectively. Calculations were performed using the ‘moveHMM’ package (Michelot et al., 2016). The initial values of the step length and turning angle distributions for the HMMs were determined with clustering analysis based on Gaussian mixture models (Scrucca et al., 2016). Potential foraging areas were estimated using locations interpreted as ‘foraging’ from HMMs. From this, autocorrelation kernel densities (AKDE) were applied using the ‘ctmm’ package in R (Fleming and Calabrese, 2016). The Bhattacharyya coefficient was calculated to estimate overlap in foraging areas, using the ‘ctmm’ R package (Winner et al., 2018).

**Analysis of regurgitates**

For the analysis of regurgitates, at family level, the estimated body mass was calculated as the average of all species representing the family. When obtaining measures of certain species and/or family was not possible due to digestion level, and the prey was shared with other seabird, the reconstituted mass from the other predator was used. For *Ablennes hians* regurgitated by *S. dactylatra*, morphometric values of specimens from *S. leucogaster* were used. In cases where specimens were identified only at the genus level, the mean mass of species belonging to that same genus was used.

 The percentage of prey-specific index of relative importance (%PSIRI) for the diet of seabirds was obtained using the equation 1, adapted from Brown et al. (2012):

 eq. 1

where %FO*i* is the percent frequency of occurrence (the number of regurgitates containing prey category *i* divided by the total number of regurgitates *n*); %PN*i* is the number of each prey category *i* divided by the total number of prey items in the regurgitates in which it occurred; and %PM*i* is the total mass of each prey category *i* divided by the total mass of prey items in the regurgitates in which it occurred.

**Stable isotope analysis**

For stable isotope analysis, blood samples were freeze-dried and homogenized and 0.7–1 mg was placed in tin capsules and then analyzed for carbon (*δ*13C) and nitrogen (*δ*15N) stable isotopes. Fish and squid muscle samples had lipids washed out using a 2:1 chloroform:methanol solution in three 6 h cycles in a Soxhlet apparatus, given that uneven lipid content in these tissues may alter *δ*13C values (Post et al., 2007). Stable isotope ratios are determined by equation 2:

*δ*X (‰) = (Rsample/Rstandard) -1 (eq. 2)

where R represents the ratio 13C/12C and 15N/14N of the sample and the analytical standard, and X is 13C/12C or 15N/14N. Stable isotope abundances are expressed in delta (*δ*) in parts per thousand (‰). Standards used for carbon and nitrogen were Vienna Pee Dee belemnite and atmospheric air, respectively. Internal laboratory standards cafein, acetinilide and glutamic acid were interspersed between samples. These standards yielded accuracy of 0.07‰ and 0.3‰, for carbon and nitrogen, respectively.

 Prey with greater dietary importance based on %PSIRI were selected to compose stable isotope mixing models, being squids (order Cephalopoda) and the following fish families: Hemiramphidae (halfbeaks), Dorosomatidae (sardines and herrings), Exocoetidae (flying fish), Scombridae (tunas and bonitos) and Belonidae (needlefish). Squids were only included in the models of red-billed tropicbirds to avoid potential spurious estimations for boobies, as it was not detected in the regurgitates of boobies (see Phillips et al., 2014 for a review on best practices using mixing models).

 Informative priors were set in Bayesian mixing models for red-billed tropicbirds and masked boobies in order to refine model estimations for prey contributions, based on results from the regurgitate analysis (Phillips et al., 2014). Proportions detected in %PSIRI in the diet of seabird species were used as priors, considering standard deviation of 0.1 and shape and rate set as 4 and 3/50, respectively. HDB (Hemiramphidae, Dorosomatidae and Belonidae fish families) prior proportions were the sum of %PSIRI of each fish family detected in the regurgitates. For brown boobies, informative priors were not set because only HDB fish families were detected in regurgitates, and mixing model results responded in accordance (see Results).

**Seabird metal(loid) analysis**

Digested samples and standard solutions were diluted with high purity deionized water (resistivity of 18.2 MΩ/cm). Metal(loid) concentrations were determined based on calibration curves built for each metal using a serial dilution prepared from a multi-elementary standard solution (1000 mg.L-1; Merck®). Quality control and assurance procedures for metals and As determinations were based on regular analysis of blanks and spiked matrices, as well as through the evaluation of a certified reference material (National Research Council Canada, Canada). Mean (± SD) recovery rates for As, Cd, Hg and Pb corresponded to 81.7 ± 2.2, 81.7 ± 2.0, 88.0 ± 8.0 and 84.3 ± 7.1%, respectively. The limit of detection (LOD) was three times the standard deviation (SD) of the blank signals (3×SD; *n* = 7) and the LOQ was ten times the SD of the blank signals (10×SD; *n* = 7). The LOQ for the elements analyzed in blood samples were 0.0435, 0.0050, 0.0182 and 0.0100 mg.kg-1 dry mass, respectively. For feathers, they corresponded to 0.0087, 0.5535, 0.0036 and 0.0020 mg.kg-1 dry mass, respectively.

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