**Extinction and loss of genetic diversity in a pantropical seabird population in the southwestern Atlantic Ocean**

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**SUPPORTING INFORMATION 1**

## DNA extraction and microsatellite amplification

Amplifications were performed with primers described for *Sula nebouxii* and *Sula variegata* (Taylor et al. 2010). Fluorescences labeled with the M13 (-21) tail were incorporated into the Polymerase Chain Reaction (PCR; Schuelke 2000). For blood samples, reactions were performed with a final volume of 20 µl, containing approximately 50 ng of DNA, 0.1 µM of the forward primer, 0.2 µM of the reverse primer and HEX or FAM fluorescence, 0.2 mM of each dNTP, 1.5 mM of MgCl2, 1× buffer, and 1 unit of Taq DNA Polymerase. The PCR programs were used according to Nunes and Bugoni (2017), with the following PCR profile: 94°C for 5 min, followed by 35 cycles of 94°C for 30 s, annealing temperature for 30 s, and 72°C for 30 s, with final extension at 72°C for 10 min. The primer-specific annealing temperature was adjusted as follows: 50°C for Sv2A-95, Sv2A-47, and Sv2B-27; 52°C for Sv2A-2 and Sn2A-123; 54°C for Sn2B-100; and 56°C for Sv2A-26 and Sn2B-83.

For interdigital membrane samples, PCR reactions were performed using the same protocol described above, except for the quantity of template DNA used, which was approximately 30 ng. The PCR programs also followed Nunes and Bugoni (2017), only with the following change for the amplification of these samples: 40 amplification cycles and 45 s of extension within each cycle.

* 1. **Microsatellite analysis**

The peaks resulting from genotyping were checked manually using the Peak Scanner program (Applied Biosystems). The presence of null alleles was checked with MICRO-CHEKER 2.2.3 (van Oosterhout et al. 2004). For the two sampled sites, genetic diversity indices were calculated, such as observed and expected heterozygosity, deviations from Hardy-Weinberg equilibrium (Nei 1978), and allelic richness using Arlequin 3.5 (Excoffier and Lischer 2010), FSTAT (Goudet 1995) and GenePop 4.4 (Rousset 2008) programs. Linkage disequilibrium tests between pairs of loci were performed with the Arlequin 3.5 program. The population structure between the two colonies studied was tested using two techniques: a multivariate and a Bayesian. The Principal Coordinate Analysis (PCoA), a multivariate technique, was performed in the GenAlEx 6.5 program (Peakall and Smouse 2012) with standardized data to identify the similarity and clustering between the colonies. A Bayesian cluster analysis was also performed in the STRUCTURE 2.3.4 program, which determines the most plausible number of genetic groups represented by K (Pritchard et al. 2000). The numbers of K from 1 to 5 were tested through 5 independent iterations for each K with 50,000 burn-in steps and 500,000 Markov chains. K was determined from 1 to 5 to consider the possibility of subpopulations on the sampled islands. The calculation of ΔK (Evanno et al. 2005) was used to detect the best K through STRUCTURE HARVESTER Web 0.6.94 (Earl and vonHoldt 2012). The five independent runs for the best K were merged with the CLUMPP 1.1.2 program (Jakobsson and Rosenberg 2007). The DISTRUCT 1.1 program (Rosenberg 2004) was used to generate the bar graph of the assignment of individuals to different clusters to demonstrate the percentage of shared ancestry between organisms, in which each bar represents an individual and the colors represent distinct lineages. For comparison, the Puechmaille (2016) method was also used to detect the best number of K, through STRUCTURE SELECTOR (Li and Liu 2018). The BOTTLENECK 1.2.02 program (Piry et al. 1999) was used to test whether the populations are in equilibrium between mutation and genetic drift, according to the methodology described by Cornuet and Luikart (1996).

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**SUPPORTING INFORMATION 2**

**Table S1** Number of red-footed boobies (*Sula sula*)*,* sampled on tree sites of Fernando de Noronha Archipelago (*n* = 34; Sancho Beach, Rata Island, and Meio Island) and Trindade Island (*n* = 30), in different years.

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| **Sampling year** | **Trindade Island (*n* = 30)** | **Fernando de Noronha Archipelago (*n* = 34)** | | |
| **Sancho Beach** | **Rata Island** | **Meio Island** |
| **1914** | 1 | 0 | 0 | 0 |
| **1916** | 19 | 0 | 0 | 0 |
| **1919** | 1 | 0 | 0 | 0 |
| **1921** | 2 | 0 | 0 | 0 |
| **<1941** | 2 | 0 | 0 | 0 |
| **1950** | 4 | 0 | 0 | 0 |
| **1988** | 1 | 0 | 0 | 0 |
| **2011** | 0 | 10 | 1 | 0 |
| **2016** | 0 | 0 | 0 | 12 |
| **2018** | 0 | 0 | 0 | 11 |