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Dispersal of green turtles from Africa's largest rookery assessed through genetic markers

Running page head: **Green turtle connectivity in the Atlantic**

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Abstract

Marine turtles are highly migratory species that establish multiple connections among distant areas, through oceanic migration corridors. To improve the knowledge on the connectivity of Atlantic green turtles, we analysed the genetic composition and contribution to juvenile aggregations of one of the world's largest rookeries at Poilão Island, Guinea-Bissau. We amplified 856bp mitochondrial DNA (mtDNA) control region sequences of this population (n=171) containing the ~490bp haplotypes used in previous studies. Haplotype CM-A8 was dominant (99.4%) but it divided in two variants when the whole 856 bp was considered: CM-A8.1 (98.8%) and CM-A8.3 (0.6%). We further identified the haplotype CM-A42.1 (0.6%), found previously only in juvenile foraging grounds at Argentina, Brazil and Equatorial Guinea. The Poilão breeding population was genetically different from all others in the Atlantic (F_{ST} range 0.016-0.961, $P< 0.001$). An extensive 'Many-to-many' mixed-stock analysis (MSA) including 14 nesting populations (1,815 samples) and 17 foraging grounds (1,686 samples) supported a strong contribution of Poilão to West Africa (51%) but also to Southwest Atlantic (36%). These findings, in particular the strong connectivity within West Africa, where illegal harvesting is still common, should motivate conservation partnerships, so that population protection can be effectively extended through all life-stages. Our study expands the knowledge on migration patterns and connectivity of green turtles in the Atlantic, evidences the importance of larger sample sizes and emphasises the need to include more finely resolved markers in MSAs and more genetic sampling from West African foraging grounds to further resolve the connectivity puzzle for this species.

Key-words: connectivity, dispersal, green turtle, migration, mitochondrial DNA (mtDNA), mixed-stock analysis (MSA), population genetics, West Africa

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Introduction

Many marine species undertake migratory movements among distant geographic areas and across distinct habitats, for feeding, reproduction or development. As a result they may be subject to a diverse range of threats during their extensive movements. Sea birds (Catry et al., 2011), marine mammals (Rasmussen et al., 2007), large fish (Bonfil et al., 2005, Rooker et al., 2014) and sea turtles (Hays and Scott, 2013) undertake such movements and are known to play important ecological roles. Understanding their dispersal patterns and the links they establish among different areas is critical to contextualize threats and inform effective management strategies (Rees et al., 2016).

Marine turtles are long-lived organisms and their life histories are marked by ontogenic habitat shifts and large-scale migrations (Bowen & Karl, 2007). Green turtles (*Chelonia mydas* L*)* associate with oceanic currents after hatching and undergo an oceanic pelagic stage, which is thought to last *ca.* 3 – 5 years (Reich et al., 2007). After this period, often referred to as 'the lost years', as the whereabouts of the turtles at this phase are poorly known, they generally recruit to coastal habitats, which may change seasonally (Fukuoka et al., 2015), and shift into benthic foraging at a straight-carapace-length of 25 – 35 cm (Bolten, 2003). These neritic zones are used as developmental habitats and turtles may spend several years foraging in the same area until reaching a size or maturity stage that triggers them to migrate to additional foraging areas (Patrício et al., 2011, Patrício et al., 2014, Shimada et al., 2015). Upon reaching maturity, adults make periodic migrations between their neritic foraging areas and natal rookeries (Bowen and Karl, 2007). This complex migratory behaviour creates multiple connections among distant coastal areas through oceanic migration corridors (Velez-Zuazo et al., 2008). Genetic studies have been critical in enlightening such connectivity (Encalada et al., 1996; Naro-Maciel et al., 2007; Prosdocimi et al., 2012).

Most studies have used sequences of the control region of the mitochondrial DNA (mtDNA), a maternally inherited genetic marker (Bowen and Karl, 2007). This marker shows generally high levels of genetic structuring among marine turtle nesting populations worldwide, supporting the natal homing hypothesis, in which the females of marine turtles return to the beaches were they were born to reproduce as a consequence of philopatry (Meylan et al., 1990). In contrast, foraging aggregations are usually mixed stocks composed of individuals from different rookeries (Bowen and Karl, 2007). The high genetic structuring of nesting populations allows the use of mixed stock analysis (MSA, Millar, 1987), to estimate contributions of rookeries (stocks) to mixed foraging grounds (mixed stocks). A Bayesian MSA (Pella and Masuda, 2001) has been widely applied, allowing the incorporation of informative priors, such as rookery size or geographic distance. Bolker et al (2007) subsequently developed a 'many-to-many' mixed stock analysis (m2m MSA), aiming to simultaneously answer the questions 1) where do the individuals from a given source population go? and 2) where do individuals from a given mixed foraging ground originate? Limitations of MSAs have been pointed out however, in particular the assumption that all source populations and mixed aggregations have been adequately sampled (Proietti et al., 2012). The existence of orphan haplotypes at juvenile foraging grounds indicates that some stocks still lack genetic assessment or have not yet been adequately sampled; hence estimates should be interpreted cautiously and along with meaningful ecological data.

One controversial result of recent MSAs of the Atlantic green turtles is the suggested potential connectivity between Guinea-Bissau, West Africa, and the Southwest Atlantic. Although MSAs have supported this migration (Bolker et al., 2007; Monzón-Argüello et al., 2010; Naro-Maciel et al., 2012), the fact that the population at Poilão, Guinea-Bissau, was found to be fixed for the common South Atlantic haplotype (CMA-8, Encalada et al., 1996; Formia et al., 2006; Godley et al., 2010) has limited the interpretations of these results. Notably, the discovery of exclusive haplotypes at low frequency is highly dependent on sample size. This putative migration seems to involve movements greater than expected, according to the ‘closest to home’ hypothesis where immature turtles tend to move to and settle in foraging grounds closest to their natal beach after recruiting to neritic habitats (Bolker et al., 2007). Additionally, studies using particle dispersal modelling with major oceanic currents did not support this connectivity (Godley et al., 2010; Putman and Naro-Maciel 2013). However, when Putman and Naro-Maciel (2013) estimated the origins of the green turtle Atlantic mixed stocks, tracking particles back through time, this crossing seemed feasible, albeit at low incidence. Lagrangian drifter data have further shown this route to be possible with particle drift (Monzón-Argüello et al., 2010; Proietti et al., 2012). Finally, a similarly large-scale migration of post-hatchling green turtles from Suriname to Cape Verde was supported using mtDNA (Monzón-Argüello et al., 2010).

With this is mind we investigate two questions: 1) where do the post-hatchlings from Poilão disperse to?, and 2) do some of the juveniles found at Southwest Atlantic foraging grounds originate in Poilão? To answer these questions we greatly increased the available sample to characterize the genetic composition of Poilão’s nesting population, in an attempt to detect rare haplotypes. We then sought to improve our understanding of the migration patterns and connectivity among Atlantic green turtle populations by comparing our results with molecular data (n = 3,501 sequences) from 14 nesting populations and 17 foraging grounds, resulting in the most extensive analysis thus far for this species in the Atlantic.

Methods

Study site and sampling

Poilão Island (N10º52’, W15º43’) is part of the João Vieira and Poilão Marine National Park (PNMJVP), in the Bijagós Archipelago, Guinea-Bissau. It hosts one of the major green turtle nesting populations worldwide (Catry et al., 2002, 2009).This population has been monitored yearly around the peak of the nesting season (August -September) since 2004. In 2013 and 2014 we collected skin samples from 171 nesting females. Samples were taken from the shoulder area using a 6 mm sterile biopsy punch as the females laid their eggs and stored in

96 % ethanol at room temperature. All sampled individuals were identified with unique tags on both front flippers to avoid sample duplication. Furthermore, the loss of a metal tag leaves scar marks easily recognized within, so we were certain that no previously tagged individual was mistakenly identified as ‘new’. Sampling protocols were approved by the research ethics committee of the University of Exeter and the government of the Republic of Guinea-Bissau.

Sequencing and haplotype assignment

We extracted DNA using the QIAGEN® DNeasy blood & tissue kit, according to the manufacturer’s instructions. A fragment of ~860bp of the mtDNA control region was amplified in a polymerase chain reaction (PCR) with the primers LCM15382 (5’-GCTTAACCCTAAAGCATTGG-3’) and H950 (5’-TCTCGGATTTAGGGGTTT-3’) (Abreu-Grobois et al. 2006) which includes the short region (~486 bp) historically surveyed for green turtle genetic studies (Bjorndal et al., 2006; Encalada et al., 1996; Formia et al., 2007; Lahanas et al., 1998). Amplifications were performed in a total volume of 25 µl, containing 2.5 µl of Taq buffer, 3 µl of dNTPs, 1 µl of $MgCl_2$, 0.5 µM of each primer at 10 µM, and 0.2 µl of Taq DNA polymerase. Cycling conditions were 94º C for 5 min, followed 35 cycles at 94º C for 1 min, 55º C for 1 min and 72º C for 1 min with a final extension step at 72º C for 10 min. Desired PCR products were purified with a combined Exonuclease I and Shrimp Alkaline Phosphatase solution (ExoSAP®). The reaction was incubated for 15 min at 37°C, followed by 15 min incubation at 80°C to inactivate the two enzymes. Sequences of forward and reverse DNA strands were performed at Macrogen Inc. (Netherlands). Sequences were assembled and aligned manually using BioEdit 7.2.5 (Hall 1999). Unique haplotypes were identified using the Basic Local Alignment Search tool (BLAST) from the National Centre for Biotechnology information (http://www.ncbi.nlm.nih.gov/), following the nomenclature of the Archie Carr Center for Sea Turtle Research, ACCSTR; http://accstr.ufl.edu/ccmtdna.html.

Population structure

To assess the genetic diversity of the nesting population at Poilão compared with the other Atlantic nesting populations we truncated the mtDNA fragments to 490 bp length, the fragment historically explored and for which most genetic information of other locations is currently available. We used Arlequin 3.5.1.3 (Excoffier and Lischer 2010) to estimate the haplotype (*h*) and nucleotide (*π*) diversity of nesting populations, to estimate the genetic distances among population pairs (Φst) and to test the significance of differentiations with exact tests based on haplotype frequencies. A false discovery rate (FDR) correction (Narum, 2006) was applied to calculate the most fitting threshold for the P-value significance considering the number of comparisons involved in the analysis and under an expected original threshold of $P < 0.05$. To contextualize our sampling location within the Atlantic region, the genetic distances were used to perform a principal coordinate analysis (PCoA) using the package GenAlEX 6.5.0.1 (Peakall and Smouse, 2012). We tested the significance of the PCoA grouping with an AMOVA, using Arlequin 3.5.1.3 (Excoffier and Lischer 2010).

‘Many-to-many’ Mixed-stock analysis

We generated a dataset of 14 nesting populations (n=1,815) and 17 foraging grounds (n=1,686) when including our new mtDNA data for Poilão to the previously existing data for Atlantic nesting populations and foraging grounds (see figure 1 for sites included in this study and literature sources). We used only sequences generated by this study to characterize the genetic composition of Poilão in order to avoid potential pseudoreplication with datasets obtained in previous years. Relative contributions to foraging areas from nesting populations (mixed stock-centric approach), and probable use of foraging grounds from nesting populations (source-centric approach) were estimated with m2m MSA, using the R package mixstock (Bolker et al., 2007) and WinBUGS (Lunn et al., 2000). We conducted the MSA including the number of nesting females in each population (Seminoff et al., 2015) as a weighting factor (Prosdocimi et al., 2012). We used the Gelman-Rubin diagnostic to assess convergence of the chains to the posterior distribution, assuming that there was no evidence of non-convergence at values < 1.2 (Pella and Masuda, 2001). As it is reasonable to assume that other African juvenile aggregations remain to be identified we simulated a juvenile foraging ground fixed for haplotype CM-A8 (similar to Naro-Maciel et al 2012), with a sample size equal to the mean of the foraging grounds sample sizes (n=99), and added this sample to the dataset to conduct another m2m MSA, as described above.

Results

Genetic composition of Poilão

Genetic variability of the Poilão nesting population was the lowest of all Atlantic populations (h ± SD = 0.012 ± 0.011, π ± SD = 0.0001 ± 0.0003, table 1). The haplotype CM-A8 was dominant as suggested by previous studies (Formia et al., 2006). However the use of longer sequences (856bp sequences) distinguished two variants of this haplotype: CM-A8.1 (98.8 %) and CM-A8.3 (0.6 %). We also identified the haplotype CM-A42.1 (0.6 %), a previously orphan haplotype found to date only in juveniles from West Africa and South American foraging aggregations (see Table S1 for haplotype frequencies of nesting populations). Because this is a rare haplotype and not previously detected in the population we performed two independent PCRs, and sequenced the amplified fragment in two independent occasions, to confirm that this result was not a product of genotyping error.

Population Structure

The nesting population at Poilão was significantly different from all other Atlantic green turtle rookeries (Table S2). All other nesting populations were distinct from each other except when comparing Ascension Island with Bioko Island, Aves with Suriname, and Aves with Buck Island. The comparisons between Suriname and Buck Island, and between Sao Tome and Principe and Bioko became non-significant after FDR correction. Populations pairs where genetic differentiation was not detected were kept as discrete sources for the m2m MSA, based on their divergence in population size and geographic position (Monzón-Argüello et al., 2010; Putman and Naro-maciel, 2013). The PCoA separated rookeries by region and evidenced three major groups: South Atlantic, Southeast Caribbean and Northwest Caribbean (Fig. 2), each group defined by a major haplotype(s): CM-A8, CM-A5 and CM-A3/A1, respectively. An accumulated 85.5% of the genetic variability was explained by the two principal coordinates of the PCoA. Although located in the North Atlantic, Poilão clustered within the South Atlantic group. Using this *a-priori* grouping in the AMOVA, highly significant structure was observed among the three groups (F_{ST} = 0.691, P <0.001), with 55.9% of the variation found among groups.

'Many-to-many' Mixed-stock analysis

The source-centric m2m MSA indicated that most of Poilão's hatchlings recruit to African foraging grounds (51.4%), but 36.2% would reach juvenile aggregations in the Southwest Atlantic and 8.6% reached North Atlantic aggregations (Fig. 3). A small proportion of the Poilão rookery was attributed to an 'unknown' foraging area (3.7%). The foraging ground-centric m2m MSA estimated that at Sao Tome, Corisco Bay and 'West Africa' (Liberia to Benin) foraging grounds, over 60% of the juveniles originate at Poilão, as do 31% of the green turtles foraging at Cape Verde (Fig. 4). Notably, at the Southwest Atlantic foraging aggregations proportions ranging from 16 – 41% were attributed to Poilão (Fig. 4). Adding the simulated West African foraging ground did not change contributions at a regional scale, but the relative contributions to the Gulf of Guinea were significantly lower (8 to 14 % lower, Fig. S1), to accommodate a large contribution to this putative aggregation. Because CM-A42 is a rare haplotype and therefore difficult to detect when sampling a population, we decided to run two additional MSAs using simulated datasets, each of these including haplotype CM-A42 in one of the other two major green turtle rookeries in the Atlantic (i.e. Costa Rica and Ascension Island), and observed no significant changes (Fig. S1).

Discussion

One of the principal techniques that can offer insight into the migratory connectivity of species with complex life cycles is genetics. The robustness of subsequent inferences, however, are highly dependent on the amount of information available, including the number of populations and foraging grounds analysed, and the strength of the signal, including sample sizes at each site and length of the genetic sequence and number of genetic markers analysed. Here we substantially increased the sampling effort at one of the largest Atlantic green turtle rookeries, in Poilão, Guinea-Bissau, in order to resolve the uncertainties surrounding the connectivity between this nesting population and distant juvenile aggregations. We successfully found the origin of a previously orphan haplotype, present in West Africa but also in South American foraging grounds, giving strength to the hypothesis of east-to-west connectivity.

Post-hatchling dispersal to east and west

The contributions estimated by the m2m MSA confirm a strong connectivity within West Africa, as previously hypothesized (Godley et al., 2010), particularly with foraging grounds in the Gulf of Guinea (i.e. 'Sao Tome', 'West Africa' and 'Corisco'). This dispersal was also predicted under an ocean circulation model and through passive drifting associated with the Guinea current (Putman and Naro-Maciel, 2013). Due to the large size of the nesting population at Poilão, it is likely however that significant proportions of other African juvenile aggregations originate there. In Guinea-Bissau there are at least two known aggregations of immature green turtles; i) at Unhocomo and Unhocomozinho Islands, in the Bijagós Archipelago, *ca.* 100 km NE from Poilão Island, and ii) at Varela beach, *ca.* 200 km NE from Poilão, that have not been genetically described. The same is true for a foraging ground in Mauritania, mentioned in Godley et al (2010), and in Congo. We have shown that the estimated proportions of post-hatchlings distributed among West African foraging grounds depend on the inclusion of new juvenile aggregations. To fully understand the connectivity of the large nesting population at Poilão it is essential that investigation into identifying and genetically characterizing these aggregations is undertaken. The MSA also suggests the existence of a transatlantic developmental migration for the green turtle, from east to west, potentially associated with the Equatorial currents, and continuing south, reaching foraging grounds in the south of Brazil and in Argentina.

Studies using estimations of passive drift with major oceanic currents to predict the movements of post-hatchlings have suggested that dispersal from Guinea-Bissau to Southwest Atlantic is unlikely (Godley et al., 2010; Putman and Naro-Maciel, 2013). However, marine turtle hatchlings are capable of oriented swimming significantly impacting trajectories (Putman et al., 2012a, 2012b; Scott et al., 2012), and able to swim against currents (Booth, 2014). Indeed, recent research has shown that drifter tracks can diverge substantially from those of young turtles (Putman and Mansfield, 2015) and it is likely that this process is contributing to observed divergence between genetic- and drift-based predictions (Naro-Maciel et al., 2016). Because CM-A42 is a rare haplotype and therefore difficult to detect, we ran additional MSAs using simulated datasets, including this haplotype in each of the two other major green turtle rookeries in the Atlantic (i.e. Costa Rica and Ascension Island), and observed no significant changes (Fig. S1).

Expanded sample size and geographic coverage

Formia et al (2006) assessed the genetic composition of Poilão nesting females (n=51) and found it was fixed for the South Atlantic dominant mtDNA haplotype CM-A8. By extending this previous sample size, we were able to detect a rare haplotype, CM-A42, which to date had only been reported from juvenile green turtles foraging in South America, and in West Africa. This enabled the differentiation of Poilão from other Atlantic rookeries, agreeing with the high philopatry, characteristic of the green turtle, and the fine scale differentiation existent in other places. Increasing sample size has previously been shown to improve statistical power of detection of structure among populations, through the finding of rare haplotypes (Formia et al., 2007).

The existence of non-significant comparisons among certain population pairs could result from i) recent isolation, such that haplotype frequencies did not have time to differentiate, or ii) current gene flow, mediated by incidental deviations from natal homing. Lack of differentiation between Bioko and Ascension Island has been attributed to recent colonization of the former (Formia et al., 2006). Likewise, Aves and Buck Island may be more recent than the more diverse population in Suriname. Alternatively, the proximity between Aves and Buck Island (<300 km), and between Bioko and Sao Tome (<400 km), may be more likely to result in occasional migrants preventing substantial differentiation at an evolutionary timescale (Formia et al., 2006).

Our study further expands the geographic coverage of previous MSAs of the green turtle in the Atlantic, incorporating 14 nesting populations and 17 foraging grounds in our dataset. In particular the inclusion of African foraging grounds (i.e. Corisco Bay, Sao Tome and ‘West Africa’) improved the estimates for the distribution of hatchlings from Poilão, significantly reducing the estimate of the putative “unknown” foraging site (here 3.7%) compared to a recent MSA (14.3% in Putman and Naro-Maciel, 2013), as well as substantially reducing the confidence intervals. In a previous m2m MSA a high contribution of Ascension Island to Corisco Bay was estimated (ca. 40%, Bolker et al., 2007). Here that contribution drops to 9.2%, and we predict a much stronger connectivity between Poilão and Corisco. By including more foraging grounds in our analyses, we show that Ascension rookery contributes primarily to juvenile aggregations along the Southwest Atlantic (71.6%), also seen in Putman and Naro-Maciel (2013). Analogously, the foraging ground-centric MSA in Bolker et al (2007) attributes most of the Corisco Bay foraging ground to Ascension Island (>70%), while we estimate that 60.5% of the aggregation origins at Poilão, and only 27.7% would come from Ascension. Additionally, the contributions of Aves Island and NE Brazil to Corisco Bay estimated before (ca. 15% each, Bolker et al., 2007) were considerably lower in our study (2.7% and 4.8%, respectively), and these populations also seem to contribute more to the Southwest Atlantic. See tables S3 and S4 for m2m MSA summary results.

Limitations of MSA and future directions

Although increasing the available sample size at Poilão and expanding the dataset for Atlantic green turtles has improved MSA estimates, this analysis is based on a single marker and on a short fragment of the mtDNA. To further unveil the green turtle connectivity puzzle in the Atlantic (and elsewhere) the strength of the genetic signal can be enhanced, at a lesser cost than substantially increasing sample sizes. Data from the longer mtDNA sequences should be obtained from existing samples and made available, to be incorporated in MSAs. Additionally, a new marker consisting of four AT short tandem repeats (STRs) in the 3' end of the mtDNA, the mtSTR, had been shown to add information on the genetic variability within unique mtDNA haplotype classes and to contribute to improve the knowledge on population connectivity and evolutionary relationships (Shamblin et al., 2015, Tikochinski et al., 2012). Recent research using nuclear markers have found significant structure among sea turtle rookeries, supportive of male phylopatry (Carreras et al., 2011; Naro-Maciel et al., 2012; Naro-Maciel et al., 2014; Roden et al., 2013). Finally, new genomic approaches are have the potential to greatly increase the signal resolution and detect fine-scale population structure (Benestan et al., 2015; Funk et al., 2012; Milano et al., 2014). Some of the above information is now becoming available at local scales. Hopefully future collaborations among research groups at wider scales will lead to significant advances in our understanding of the dispersal and distribution of marine turtles.

Adult linkage

Godley et al (2010) recorded the trajectories of eight post-nesting females from Poilão using satellite transmitters, finding that they foraged either locally, at the Bijagós Archipelago (n = 4) , or regionally (n = 4), at the Banc d'Arguin National Park, Mauritania (> 1000 km distant). This aspect of investigation would clearly benefit from enhanced sampling effort, preferably across multiple seasons, at different points of the season and across a range of size classes, to avoid inter-annual (Witt et al., 2011), seasonal (Rees et al., 2010) and phenotypic

(Hawkes et al., 2006) biases in dispersal. Future satellite tracking should be conducted in tandem with stable isotope analysis to facilitate the posterior assignment of turtles to these areas, facilitating the analyses of larger sample sizes, more relevant for population studies (Zbinden et al., 2011).

If nesting females from Poilão are limited to the East Atlantic it does not necessarily contradict our suggestion of transatlantic dispersal as post-hatchlings. Post-hatchling turtles forage during their developmental migration (Reich et al., 2007), which allows them to travel much longer distances than adults that typically fast during their reproductive migrations (Hays and Scott, 2013; Scott et al., 2014). According to Scott et al (2014), if the developmental foraging area is so far as to be too costly to be repeatable during the cyclic reproductive migrations, adults may forage locally, as observed at the Bijagós, instead of returning to the sites experienced when younger. This mechanism reduces the consumption of reproductive energy utilized, potentially increasing fecundity, however it is dependent on the availability of foraging areas.

Conservation implications

In this study we show the importance of Poilão rookery for the recruitment of juvenile green turtles in West Africa, and also that the link with the Southwest Atlantic is very likely. In Guinea-Bissau, despite marine turtles being fully protected by the national fisheries law, illegal take continues to occur without much law enforcement effort (Catry et al., 2009), particularly at the Bijagós Archipelago, where turtles are frequently harvested at the nesting beaches, mostly for local consumption (Catry et al., 2009). The nesting population at Poilão is one exception, thanks to the Bijagós traditional ‘law’ (reinforced by state authorities), restricting access to the island on very rare ceremonies of social and religious significance (Catry et al., 2009). Off Guinea-Bissau and along the coast of West Africa however, vast artisanal fleets and many industrial fishing fleets operate, using trawlers without turtle excluder devices (Catry et al., 2009; Zeeberg et al., 2006), and longlining (Moore et al., 2010). Unfortunately there is a scarcity of quantitative data in the region, either on bycatch or on targeted harvesting of marine turtles, particularly from artisanal fisheries (Moore et al., 2010). The foraging grounds in the Southwest Atlantic to which Poilão seems to contribute to, on the other hand, are mostly protected from illegal harvesting (Marcovaldi and dei Marcovaldi, 1999), although bycatch may be a problem (Wallace et al., 2010). Despite the existing threats, major green turtle populations are recovering globally following decades of conservation efforts (Bourjea et al., 2015, Broderick et al., 2006, Catry el at., 2009). It may be that the long term enhanced protection in South America and the efforts in Poilão itself are the principle factors involved in the recovery of this population.

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Table 1. Haplotypic and genetic diversity of Atlantic green turtle (*Chelonia mydas*) nesting populations (n = 14) included in a many-to-many mixed stock analysis (Bolker et al., 2007), using the control region of the mitochondrial DNA as a marker (490bp). The number of females refers to the total number of reproductive females in each population. The study population is represented in bold.

Nesting Population	**short name**	**sample size**	**no. of females***	**no. of haplotypes**	**haplotypic diversity (*h*)**	**nucleotide diversity (π)**
East central Florida	EcFL	311	4490	9	0.512 ± 0.020	0.0016 ± 0.0013
South Florida	SFL	174	3302	10	0.444 ± 0.043	0.0022 ± 0.0016
Southwest Cuba	CUB	28	2226	7	0.648 ± 0.089	0.0053 ± 0.0033
Quintana Roo, Mexico	MEX	20	18257	7	0.816 ± 0.058	0.0051 ± 0.0032
Tortuguero, Costa Rica	CR	433	131751	5	0.163 ± 0.023	0.0033 ± 0.0022
Matapica/Galibi, Suriname	SUR	73	13067	4	0.132 ± 0.053	0.0013 ± 0.0011
Buck Island	BUC	49	63	2	0.153 ± 0.065	0.0030 ± 0.0020
Aves Island	AV	67	2833	2	0.140 ± 0.055	0.0029 ± 0.0020
Rocas/Fernando Noronha	RC/FN	69	345	7	0.463 ± 0.071	0.0026 ± 0.0018
Trindade Island	TRI	99	2016	7	0.505 ± 0.052	0.0012 ± 0.0011
Ascension Island	ASC	245	1417	13	0.303 ± 0.038	0.0008 ± 0.0008
Poilão, Guinea-Bissau	**GB**	**171**	**29016**	**2**	**0.012 ± 0.011**	**0.0001 ± 0.0003**
Bioko Island, Eq. Guinea	BIO	50	850	2	0.184 ± 0.068	0.0004 ± 0.0006
Sao Tome and Principe	STP	26	376	7	0.569 ± 0.110	0.0026 ± 0.0019

* Seminoff et al., (2015)

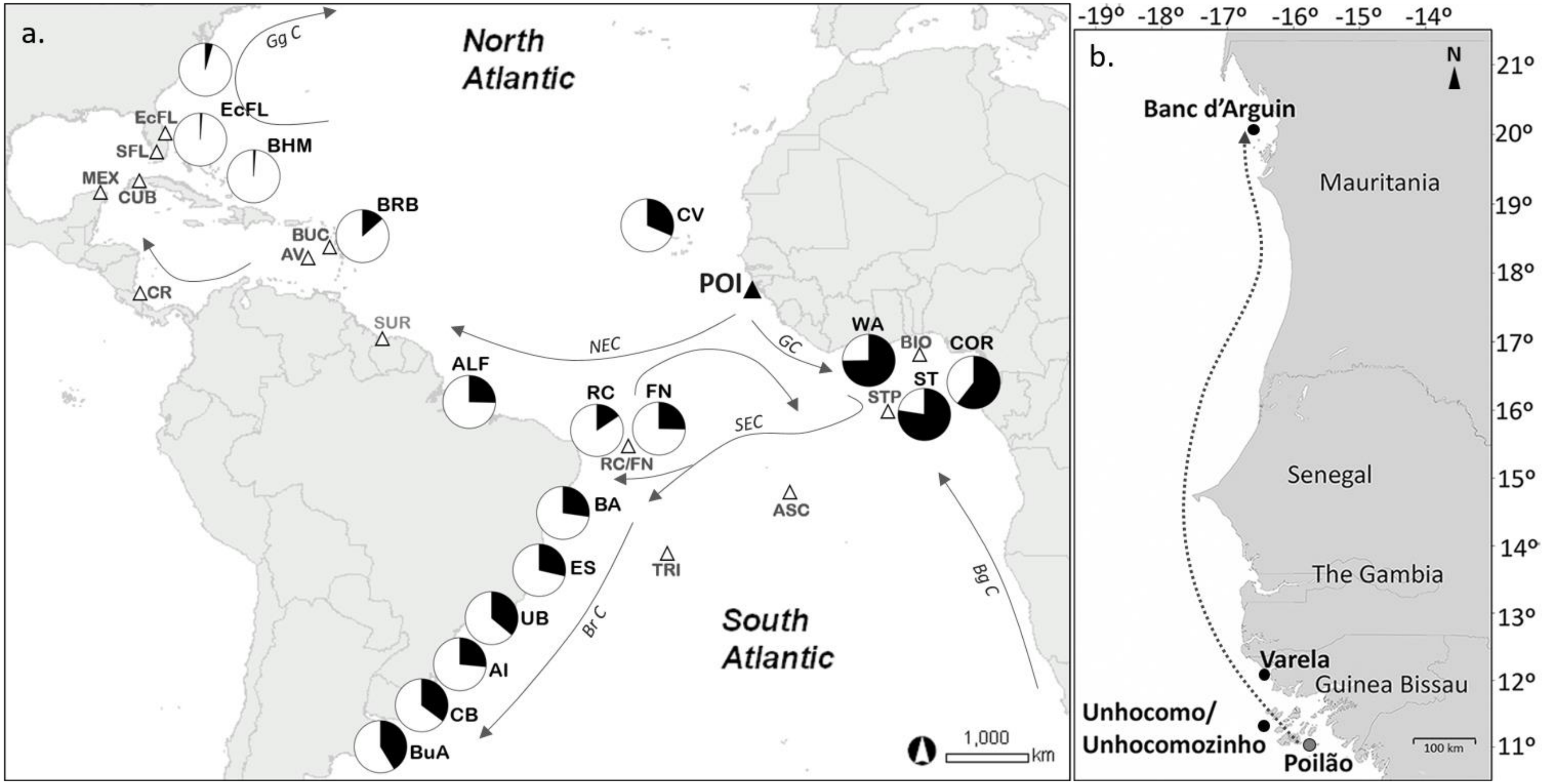

Figure 1. a) Atlantic green turtle (*Chelonia mydas*) nesting populations (n=14) and foraging grounds (n=17) used many-to-many mixed stock analysis (m2m MSA), and results of foraging ground-centric MSA (pie charts: proportion of each foraging site that origins from the study population in black). **Nesting populations:** EcFL, East central Florida, SFL, South Florida, USA (Shamblin et al., 2014); CUB: Southwest Cuba (Ruiz-Urquiola et al., 2010); MEX: Quintana Roo, Mexico (Encalada et al., 1996); CR: Tortuguero, Costa Rica (Bjorndal et al.,

2005; Encalada et al., 1996); SUR: Matapica and Galibi, Suriname (Encalada et al., 1996; Shamblin et al., 2012); AV: Aves Island (Lahanas et al., 1998, 1994; Shamblin et al., 2012), Venezuela; BUC: Buck Island (Shamblin et al., 2012); RC/FN: Rocas Atol and Fernando de Noronha (Bjorndal et al., 2006; Encalada et al., 1996), Brazil; ASC: Ascension Island (Encalada et al., 1996; Formia et al., 2007); TRI: Trindade Island, Brazil (Bjorndal et al., 2006); POI: Poilão, Guinea-Bissau (study population); BIO: Bioko Island, Equatorial Guinea (Formia et al., 2006); STP: Sao Tome and Principe (Formia et al., 2006). **Foraging grounds:** NC: North Carolina (Bass et al., 2006), EcFL: East central Florida (Bagley, 2003; Bass and Witzell, 2000), BHM: Bahamas (Lahanas et al., 1998), BRB: Barbados (Luke et al., 2004), ALF: Almofala, Brazil (Naro-Maciel et al., 2007), RC: Rocas Atoll, Brazil (Naro-Maciel et al., 2012), FN: Fernando de Noronha, Brazil (Naro-Maciel et al., 2012), BA: Bahia, Brazil (Naro-Maciel et al., 2012), ES: Espirito Santo, Brazil (Naro-Maciel et al., 2012), UB: Ubatuba, Brazil (Naro-Maciel et al., 2007), AI: Arvoredo Island, Brazil (Proietti et al., 2012), CB: Cassino Beach, Brazil (Proietti et al., 2012), BuA, Buenos Aires, Argentina (Prosdocimi et al., 2012), CV: Cape Verde (Monzón-Argüello et al., 2010), COR: Corisco Bay, Equatorial Guinea (Formia, 2002), WA: ‘West Africa’ (Liberia to Benin, Formia, 2006). *GfC*: Gulf Current, *NEC*: North Equatorial Current, *SEC*: South Equatorial Current, *BrC*: Brazil Current, *GC*: Guinea Current, *BgC*: Benguela Current; **b) Region map** with study site, Poilão, and three juvenile foraging grounds likely to partly originate at Poilão, to date genetically uncharacterized: Unhocomo/Unhocomozinho and Varela at Guinea Bissau, and Banc d’Arguin at Mauritania. Dashed arrow illustrates the direction of four green turtle females tracked from Poilão to Banc d’Arguin (Godley et al., 2010). (Maps created using www.seaturtle.org/maptool).

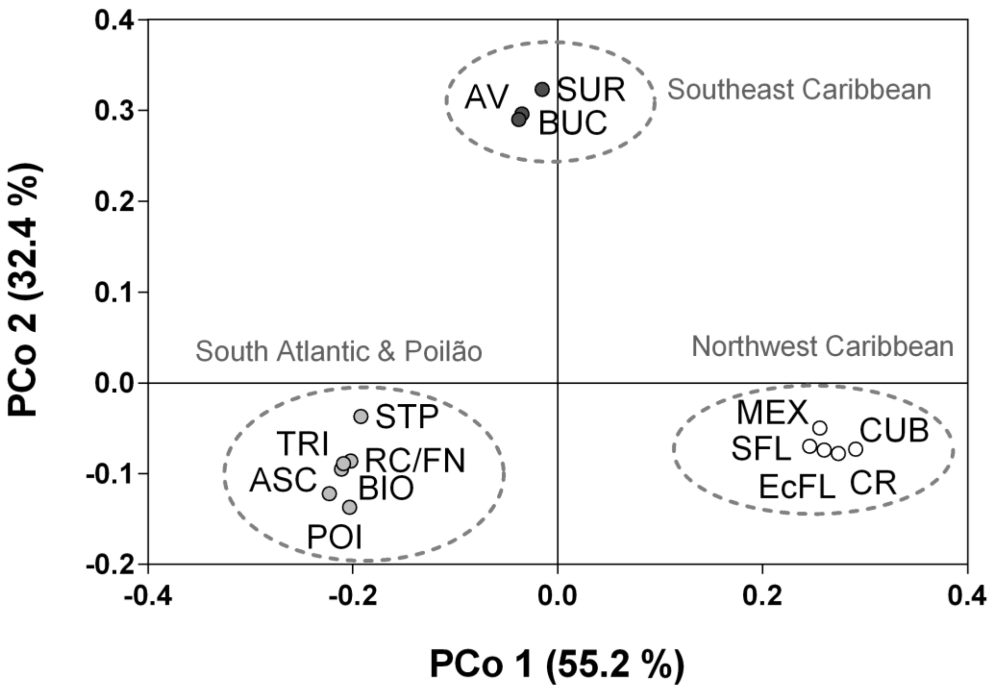

Figure 2. PCoA of the 14 Atlantic green turtle (*Chelonia mydas*) populations using ϕ_{st} and considering the 490bp fragment. The percentage of the variability explained by each coordinate is shown in brackets. ASC: Ascension Island; AV: Aves Island, Venezuela; BIO: Bioko Island, Equatorial Guinea; BUC: Buck Island; CR: Tortuguero, Costa Rica; CUB: Southwest Cuba; EcFL: East central Florida, MEX: Quintana Roo, Mexico; POI: Poilão, Guinea-Bissau (this study); RC/FN: Rocas Atol and Fernando Noronha, Brazil; SFL: South Florida, USA; STP: Sao Tome and Principe; SUR: Matapica and Galibi, Suriname; TRI: Trindade Island, Brazil.

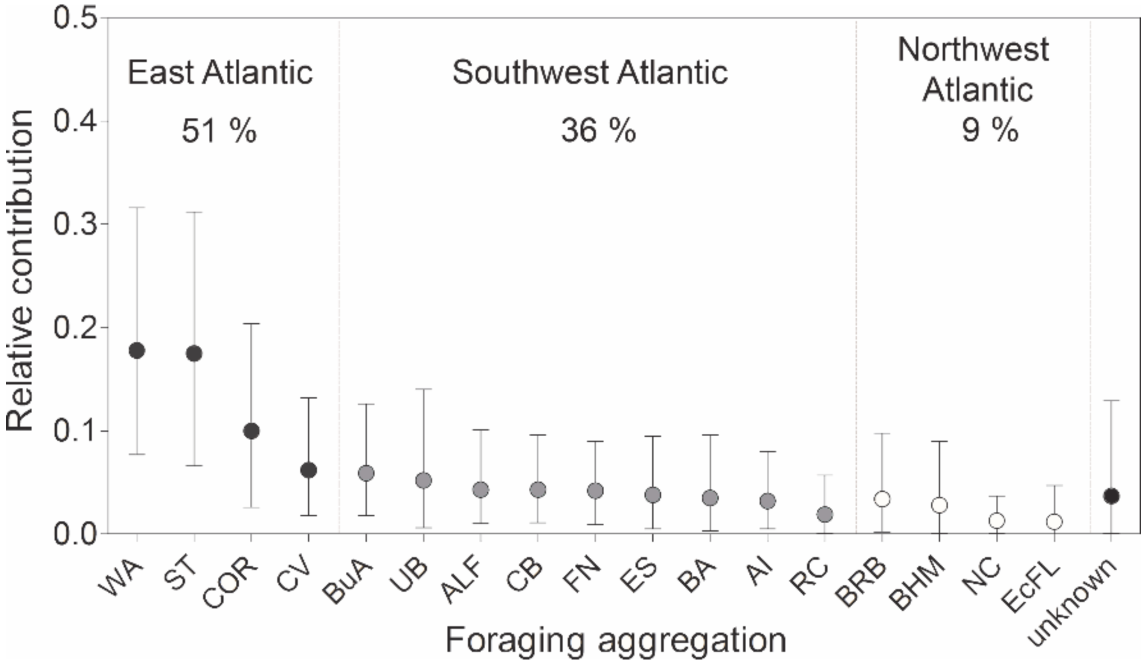

Figure 3. Mean relative contribution of Poilão (Guinea-Bissau) nesting population to 17 Atlantic green turtle (*Chelonia mydas*) foraging grounds, estimated by a many2many mixed stock analysis (Bolker et al 2007). Error bars show 95 % confidence intervals. WA: 'West Africa' – Liberia to Benin, ST: Sao Tome, COR: Corisco Bay, CV: Cape Verde, BuA: Buenos Aires, UB: Ubatuba, ALF: Almofala, CB: Cassino Beach, FN: Fernando de Noronha, ES: Espírito Santo, BA: Bahia, AI: Arvoredo Island, RC: Rocas Atol, BRB: Barbados, BHM: Bahamas, NC: North Carolina, EcFL: East central Florida. Dashed lines separate geographic regions.

Supplementary material:

Table S1. mtDNA control region haplotype frequencies (490 bp), at 14 Atlantic green turtle nesting populations with total no. of samples per area. See Fig. 1 for site abbreviations. Long haplotypes (856bp) for study area are shown in the table below.

Haplotype	**Nesting Populations**												
	EcFL[a,b]	**SFL**[b]	**MEX**[a]	**CR**[c,d]	**CUB**[e]	**BUC**[f]	**AV**[d,f,g]	**SUR**[a,f]	**RC/N**[a,h]	**TRI**[h]	**ASC**[a,i,j]	**POI**[k]	**BIO**[i]
CM-A1	197	27	7		3								
CM-A2	7	4											
CM-A3	92	127	5	395	16		5	1					
CM-A4				1		16							
CM-A5	2	4	1	32		45	62	68					
CM-A6								3			11		5
CM-A7								1					
CM-A8	1								50	67	204	170*	45
CM-A9									7	19	9		
CM-A10									2		5		
CM-A11									1	1			
CM-A12									5				
CM-A13	7	2											
CM-A15			1										
CM-A16	2	1	1										
CM-A17		2	2										
CM-A18	1	1	3										
CM-A20				2									
CM-A21				3									
CM-A23										6	1		
CM-A24										1	7		
CM-A25									3		1		
CM-A27					1								
CM-A28	2	3			1								
CM-A32									1	4	1		
CM-A33										1			
CM-A35													
CM-A36													
CM-A37													
CM-A38													
CM-A39											1		
CM-A42												1*	
CM-A44											1		
CM-A45											1		
CM-A46											2		
CM-A48					5								
CM-A50											1		
CM-A53		3											
CM-A56					1								
CM-A57					1								
n	311	174	20	433	28	61	67	73	69	99	245	171	50

[a]Encalada et al. 1996, [b]Shamblin et al. 2014, [c]Bjorndal et al. 2005, [d]Lahanas et al. 1998, [e]Ruiz-Urquiola et al. 2010, [f]Shamblin et al. 2012, [g]Lahanas et al. 1994, [h]Bjorndal et al. 2006, [i]Formia et al. 2006,[j]Formia et al. 2007,[k]This study

* Long haplotypes (856bp): CMA8.1 (n=169), CMA8.3 (n=1), CMA42.1 (n=1)

Table S2. Pairwise exact test P-values (above diagonal) and pairwise F_{ST} values (below diagonal) among the 14 Atlantic green turtle (*Chelonia mydas*) nesting populations, based on ~490bp sequences of the control region of the mtDNA. The study site is in grey and in bold, and abbreviations follow those in Figure 1. Asterisks indicate statistically significant comparisons (*P < 0.05, **P < 0.01, ***P < 0.001) i) prior to corrections, in the low diagonal, ii) after false discovery rate (FDR) correction, in the above diagonal. Non-significant values, after FDR (Narum, 2006) correction, are marked in bold (for a P< 0.05 FDR = 0.0098, P< 0.01 FDR = 0.0020, P< 0.001 FDR = 0.0002).

	MEX	EcFL	SFL	CR	AV	BUC	CUB	SUR	TRI	RC/FN	ASC	**POI**	BIO	STP
MEX	-	0.009*	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
EcFL	0.082**	-	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
SFL	0.182***	0.197***	-	0.000***	0.000***	0.000***	0.009*	0.000***	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
CR	0.202***	0.254***	0.033***	-	0.000***	0.000***	0.009*	0.000***	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
AV	0.796***	0.895***	0.872***	0.820***	-	**0.342**	0.000***	**0.108**	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
BUC	0.783***	0.897***	0.873***	0.822***	0.000	-	0.000***	**0.045**	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
CUB	0.104***	0.243***	0.131**	0.154***	0.822***	0.811***	-	0.000***	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
SUR	0.880***	0.920***	0.905***	0.849***	0.021	0.031*	0.887***	-	0.000***	0.000***	0.000***	**0.000*** **	0.000***	0.000***
TRI	0.860***	0.899***	0.885***	0.820***	0.657***	0.659***	0.873***	0.759***	-	0.009*	0.000***	**0.000*** **	0.000***	0.000***
RC/FN	0.787***	0.886***	0.863***	0.810***	0.567***	0.554***	0.812***	0.666***	0.031**	-	0.000***	**0.000*** **	0.000***	0.009*
ASC	0.913***	0.918***	0.914***	0.852***	0.728***	0.735***	0.922***	0.795***	0.060***	0.037***	-	**0.000*** **	**0.243**	0.000***
POI	**0.953*** **	**0.931*** **	**0.929*** **	**0.855*** **	**0.805*** **	**0.823*** **	**0.950*** **	**0.895*** **	**0.146*** **	**0.070*** **	**0.016*** **	-	**0.000*** **	**0.000*** **
BIO	0.877***	0.909***	0.894***	0.824***	0.640***	0.646***	0.878***	0.789***	0.093***	0.037***	0.003	**0.106*** **	-	**0.036**
STP	0.766***	0.895***	0.870***	0.811***	0.522***	0.505***	0.792***	0.671***	0.083***	0.036*	0.067***	**0.201*** **	0.045*	-

Table S3. Summary of source-centric mixed stock analysis of Atlantic green turtle nesting populations (n=14) and juvenile foraging grounds (n=17).

Nesting Population	**Foraging grounds**																	
	NC	**EcFL**	**BHM**	**BRB**	**ALF**	**RC**	**FN**	**BA**	**ES**	**UB**	**AI**	**CB**	**BuA**	**CV**	**COR**	**ST**	**WA**	**X**
Poilão, Guinea Bissau																		
Mean	0.01	0.01	0.03	0.03	0.04	0.02	0.04	0.04	0.04	0.05	0.03	0.04	0.06	0.06	0.10	0.17	0.18	0.04
CI: 97.5%	0.04	0.05	0.09	0.10	0.10	0.06	0.09	0.10	0.09	0.14	0.08	0.10	0.13	0.13	0.20	0.31	0.32	0.13
CI: 2.5%	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.01	0.02	0.02	0.03	0.07	0.08	0.00
Bioko, Eq.Guinea																		
Mean	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.06	0.07	0.05	0.05	0.05	0.05	0.06	0.07	0.05	0.06	0.05
CI: 97.5%	0.17	0.17	0.19	0.19	0.18	0.20	0.19	0.20	0.22	0.19	0.19	0.18	0.19	0.20	0.22	0.19	0.21	0.18
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sao Tome and Principe																		
Mean	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.06	0.09	0.08	0.06	0.05
CI: 97.5%	0.17	0.18	0.18	0.19	0.17	0.17	0.17	0.17	0.17	0.18	0.17	0.22	0.16	0.19	0.31	0.27	0.19	0.20
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ascension Island, UK																		
Mean	0.01	0.01	0.02	0.05	0.09	0.09	0.05	0.05	0.08	0.11	0.09	0.08	0.07	0.02	0.09	0.03	0.04	0.02
CI: 97.5%	0.04	0.05	0.06	0.12	0.17	0.18	0.12	0.14	0.16	0.21	0.18	0.16	0.16	0.06	0.17	0.09	0.10	0.07
CI: 2.5%	0.00	0.00	0.00	0.00	0.03	0.03	0.01	0.00	0.02	0.04	0.03	0.02	0.02	0.00	0.03	0.00	0.00	0.00
Trindade, Brazil																		
Mean	0.03	0.03	0.04	0.04	0.04	0.08	0.04	0.12	0.08	0.05	0.10	0.09	0.08	0.03	0.03	0.04	0.03	0.04
CI: 97.5%	0.11	0.12	0.14	0.14	0.13	0.21	0.13	0.29	0.21	0.16	0.24	0.22	0.23	0.12	0.10	0.14	0.12	0.14
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Rocas/F.Noronha, Brazil																		
Mean	0.05	0.05	0.06	0.06	0.05	0.06	0.06	0.06	0.06	0.06	0.05	0.07	0.05	0.05	0.05	0.06	0.05	0.05
CI: 97.5%	0.20	0.19	0.19	0.20	0.19	0.22	0.19	0.19	0.20	0.20	0.19	0.23	0.18	0.19	0.16	0.19	0.18	0.19
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Suriname																		
Mean	0.01	0.03	0.05	0.07	0.07	0.05	0.14	0.07	0.08	0.03	0.04	0.04	0.05	0.17	0.01	0.02	0.03	0.04
low C.I.	0.04	0.09	0.15	0.16	0.15	0.11	0.25	0.15	0.15	0.07	0.09	0.09	0.12	0.31	0.03	0.06	0.09	0.12
upper C.I.	0.00	0.00	0.00	0.01	0.02	0.01	0.05	0.01	0.02	0.00	0.01	0.01	0.01	0.06	0.00	0.00	0.00	0.00

Table S3. Continuation

Nesting Population	Foraging grounds																	
	NC	**EcFL**	**BHM**	**BRB**	**ALF**	**RC**	**FN**	**BA**	**ES**	**UB**	**AI**	**CB**	**BuA**	**CV**	**COR**	**ST**	**WA**	**X**
Aves Island, VNZ																		
Mean	0.04	0.05	0.06	0.07	0.07	0.06	0.07	0.06	0.05	0.06	0.06	0.05	0.06	0.07	0.03	0.04	0.05	0.05
CI: 97.5%	0.13	0.19	0.20	0.20	0.21	0.20	0.21	0.21	0.18	0.17	0.20	0.16	0.19	0.25	0.09	0.15	0.15	0.18
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Buck Island																		
Mean	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.06	0.05	0.05	0.06	0.06	0.05	0.05	0.06	0.06
CI: 97.5%	0.21	0.19	0.21	0.20	0.20	0.20	0.18	0.19	0.18	0.20	0.17	0.18	0.19	0.18	0.20	0.18	0.19	0.20
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Tortuguero, CR																		
Mean	0.01	0.15	0.53	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28
CI: 97.5%	0.04	0.33	0.84	0.04	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.64
CI: 2.5%	0.00	0.04	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Mexico																		
Mean	0.16	0.42	0.13	0.06	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.17
CI: 97.5%	0.42	0.72	0.38	0.18	0.02	0.01	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.04	0.00	0.02	0.03	0.49
CI: 2.5%	0.03	0.11	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Southeast Cuba																		
Mean	0.27	0.11	0.11	0.07	0.03	0.03	0.03	0.03	0.01	0.02	0.01	0.01	0.02	0.05	0.01	0.03	0.04	0.12
CI: 97.5%	0.53	0.34	0.34	0.24	0.14	0.10	0.10	0.11	0.05	0.07	0.05	0.06	0.06	0.18	0.03	0.12	0.13	0.37
CI: 2.5%	0.06	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Florida, USA																		
Mean	0.21	0.16	0.12	0.11	0.04	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.05	0.01	0.02	0.03	0.12
CI: 97.5%	0.51	0.48	0.39	0.36	0.14	0.10	0.10	0.09	0.04	0.05	0.04	0.04	0.05	0.17	0.02	0.09	0.10	0.40
CI: 2.5%	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
East central Florida, USA																		
Mean	0.30	0.20	0.12	0.09	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.04	0.00	0.02	0.02	0.11
CI: 97.5%	0.57	0.51	0.39	0.27	0.05	0.05	0.06	0.06	0.02	0.04	0.02	0.03	0.04	0.14	0.02	0.07	0.07	0.39
CI: 2.5%	0.04	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table S4. Summary of foraging ground-centric mixed stock analysis of Atlantic green turtle nesting populations (n=14) and juvenile foraging grounds (n=17).

Foraging grounds	Nesting populations													
	EcFL	**SFL**	**MX**	**CR**	**CUB**	**BUC**	**AV**	**SUR**	**RC/N**	**TRI**	**ASC**	**GB**	**Bio**	**STP**
North Carolina, USA														
Mean	0.19	0.10	0.35	0.16	0.08	0.00	0.01	0.02	0.00	0.01	0.02	0.05	0.01	0.00
CI: 2.5%	0.02	0.00	0.14	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CI: 97.5%	0.41	0.26	0.59	0.36	0.18	0.00	0.05	0.06	0.01	0.03	0.06	0.11	0.02	0.01
East central Florida, USA														
Mean	0.03	0.02	0.26	0.63	0.01	0.00	0.01	0.01	0.00	0.00	0.01	0.01	0.00	0.00
CI: 2.5%	0.00	0.00	0.12	0.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CI: 97.5%	0.11	0.08	0.43	0.78	0.03	0.00	0.02	0.04	0.00	0.01	0.03	0.04	0.01	0.00
Bahamas														
Mean	0.01	0.01	0.03	0.92	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00
CI: 2.5%	0.00	0.00	0.00	0.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CI: 97.5%	0.03	0.02	0.08	0.97	0.01	0.00	0.01	0.04	0.00	0.01	0.01	0.03	0.00	0.00
Barbados														
Mean	0.06	0.06	0.15	0.28	0.02	0.00	0.03	0.14	0.00	0.01	0.09	0.13	0.01	0.00
CI: 2.5%	0.00	0.00	0.02	0.08	0.00	0.00	0.00	0.03	0.00	0.00	0.01	0.01	0.00	0.00
CI: 97.5%	0.18	0.19	0.31	0.46	0.09	0.00	0.11	0.25	0.01	0.05	0.22	0.28	0.03	0.01
Almofala, Brazil														
Mean	0.01	0.03	0.02	0.14	0.02	0.00	0.04	0.19	0.00	0.02	0.26	0.25	0.01	0.00
CI: 2.5%	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.08	0.00	0.00	0.10	0.09	0.00	0.00
CI: 97.5%	0.04	0.09	0.07	0.23	0.06	0.00	0.15	0.29	0.02	0.07	0.43	0.41	0.04	0.02
Rocas Atol, Brazil														
Mean	0.02	0.03	0.02	0.05	0.02	0.00	0.06	0.21	0.01	0.05	0.37	0.16	0.02	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.15	0.01	0.00	0.00
CI: 97.5%	0.06	0.09	0.06	0.12	0.07	0.00	0.20	0.33	0.03	0.15	0.57	0.35	0.06	0.02

Table S4. Continuation

Foraging grounds	Nesting populations													
	EcFL	**SFL**	**MX**	**CR**	**CUB**	**BUC**	**AV**	**SUR**	**RC/N**	**TRI**	**ASC**	**GB**	**Bio**	**STP**
Fernando Noronha, Brazil														
Mean	0.02	0.02	0.03	0.02	0.01	0.00	0.04	0.40	0.00	0.02	0.16	0.26	0.01	0.00
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.00	0.02	0.09	0.00	0.00
CI: 97.5%	0.05	0.06	0.08	0.06	0.05	0.00	0.15	0.50	0.02	0.06	0.33	0.42	0.04	0.02
Bahia, Brazil														
Mean	0.02	0.02	0.02	0.03	0.02	0.00	0.06	0.25	0.01	0.08	0.21	0.27	0.02	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.01	0.02	0.03	0.00	0.00
CI: 97.5%	0.07	0.08	0.08	0.09	0.07	0.00	0.19	0.39	0.02	0.21	0.48	0.51	0.06	0.02
Espirito Santo, Brazil														
Mean	0.01	0.01	0.01	0.01	0.01	0.00	0.05	0.26	0.01	0.04	0.29	0.29	0.02	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.09	0.06	0.00	0.00
CI: 97.5%	0.03	0.03	0.03	0.04	0.03	0.00	0.16	0.36	0.02	0.12	0.52	0.47	0.07	0.02
Ubatuba, Brazil														
Mean	0.01	0.01	0.01	0.02	0.01	0.00	0.04	0.08	0.01	0.03	0.40	0.36	0.01	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.16	0.08	0.00	0.00
CI: 97.5%	0.04	0.04	0.04	0.05	0.04	0.00	0.13	0.17	0.02	0.10	0.68	0.60	0.05	0.02
Arvoredo Island, Brazil														
Mean	0.01	0.01	0.01	0.01	0.01	0.00	0.06	0.16	0.01	0.07	0.37	0.27	0.01	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.17	0.07	0.00	0.00
CI: 97.5%	0.03	0.03	0.04	0.04	0.03	0.00	0.18	0.27	0.02	0.16	0.59	0.47	0.06	0.02
Casino Beach, Brazil														
Mean	0.01	0.01	0.01	0.01	0.01	0.00	0.05	0.15	0.01	0.06	0.31	0.35	0.01	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.12	0.15	0.00	0.00
CI: 97.5%	0.03	0.04	0.04	0.04	0.03	0.00	0.16	0.26	0.03	0.15	0.53	0.55	0.06	0.03

Table S4. Continuation

Foraging grounds	Nesting populations													
	EcFL	**SFL**	**MX**	**CR**	**CUB**	**BUC**	**AV**	**SUR**	**RC/N**	**TRI**	**ASC**	**GB**	**Bio**	**STP**
Buenos Aires, Argentina														
Mean	0.01	0.01	0.01	0.01	0.01	0.00	0.04	0.17	0.00	0.05	0.25	0.41	0.01	0.00
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.08	0.20	0.00	0.00
CI: 97.5%	0.04	0.04	0.04	0.04	0.03	0.00	0.16	0.27	0.02	0.14	0.48	0.58	0.05	0.02
Cape Verde														
Mean	0.03	0.03	0.04	0.04	0.02	0.00	0.04	0.40	0.00	0.01	0.04	0.31	0.01	0.00
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.14	0.00	0.00
CI: 97.5%	0.10	0.09	0.13	0.14	0.07	0.00	0.16	0.54	0.02	0.05	0.16	0.47	0.04	0.02
Corisco Bay, Eq. Guinea														
Mean	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.04	0.00	0.01	0.28	0.60	0.01	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.37	0.00	0.00
CI: 97.5%	0.02	0.01	0.02	0.02	0.01	0.00	0.05	0.08	0.02	0.04	0.47	0.77	0.07	0.04
Sao Tome, Sao Tome and Principe														
Mean	0.01	0.01	0.01	0.01	0.01	0.00	0.02	0.04	0.00	0.01	0.07	0.77	0.01	0.01
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.62	0.00	0.00
CI: 97.5%	0.04	0.04	0.05	0.05	0.04	0.00	0.07	0.10	0.01	0.05	0.19	0.87	0.04	0.03
West Africa: Liberia to Benin														
Mean	0.01	0.01	0.02	0.02	0.01	0.00	0.02	0.06	0.00	0.01	0.08	0.75	0.01	0.00
CI: 2.5%	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.58	0.00	0.00
CI: 97.5%	0.05	0.05	0.06	0.07	0.04	0.00	0.07	0.13	0.01	0.04	0.22	0.86	0.03	0.01

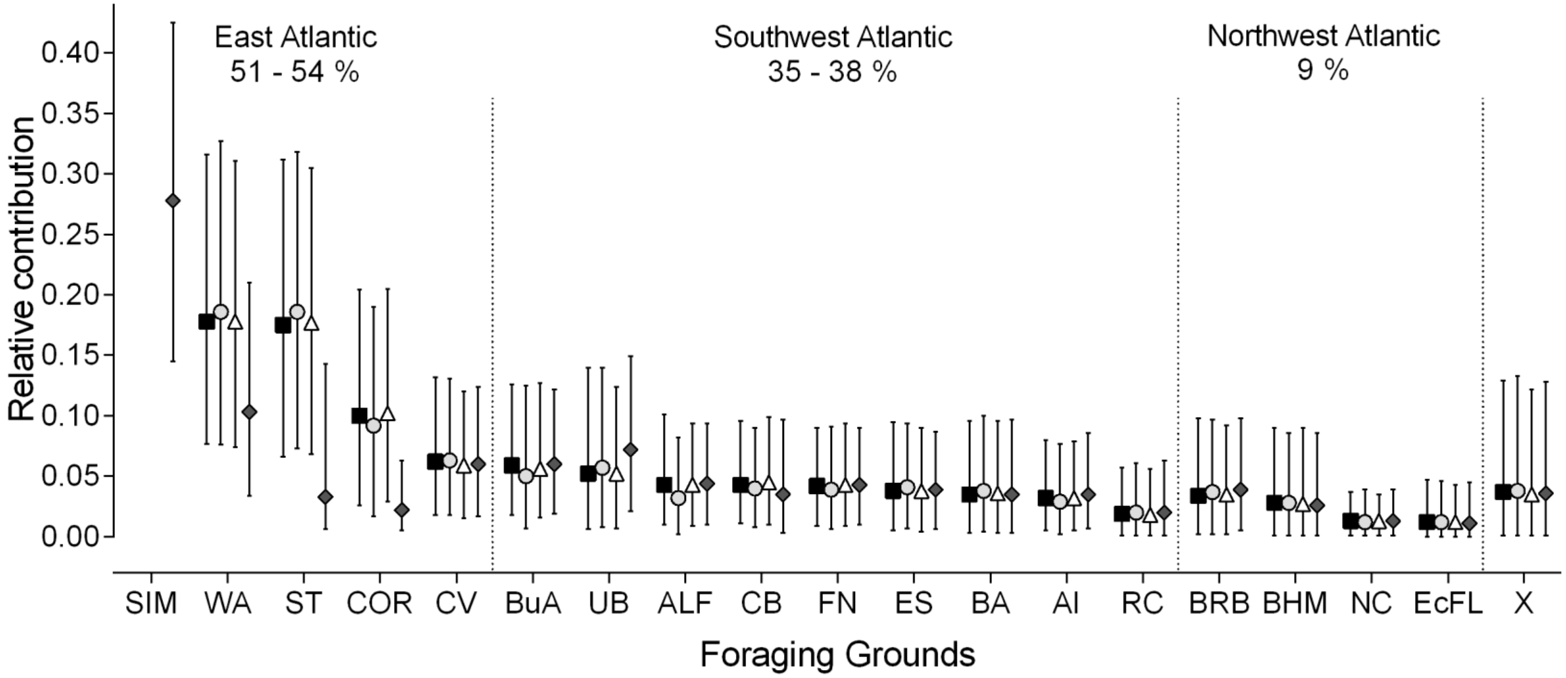

Figure S1. Comparison of mean contributions and 95% confidence intervals from Poilão rookery (West Africa) to 17 green turtle Atlantic foraging aggregations, estimated through a many-to-many mixed stock analysis, using different simulated datasets against the actual dataset - black squares. Grey circle – including a rare haplotype (Cm-A42) found at Poilão in Ascension Island sample, white triangle – including CM-A42 in Costa Rica sample, and grey diamond – adding a putative foraging ground fixed for haplotype CM-A8 (n = 99). SIM: simulated foraging ground, WA: ‘Western Africa’ – Liberia to Benin, ST: Sao Tome, COR: Corisco Bay, CV: Cape Verde, BuA: Buenos Aires, UB: Ubatuba, ALF: Almofala, CB: Cassino Beach, FN: Fernando de Noronha, ES: Espírito Santo, BA: Bahia, AI: Arvoredo Island, RC: Rocas Atol, BRB: Barbados, BHM: Bahamas, NC: North Carolina, EcFL: East central Florida. Dashed lines separate geographic regions.