A New Approach to Mixed Stock Analysis that Informs on the Management and Conservation of Hawksbill in the Wider Caribbean: the Case of the Legal Fishery in Jardines del Rey, Cuba

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Abstract Researchers have used mixed stock analysis (MSA) to infer the relevance of rookeries in sea turtle aggregations for conservation/management purposes. However, their approaches and assumptions are not always homogeneous or realistic. We assayed new MSAs using the annual haplotype frequencies of aggregations and rookeries of Eretmochelys imbricata in the Wider Caribbean (WC), and the population size was selected according to the sampler year most relevant on the maturity of the aggregation. The MSA results obtained using this approach were compared with MSAs executed with grouped haplotype frequency data as has been the most common practice in the literature. The relationship of Jardines del Rey (JR) legal fishing aggregation (Cuba) to other aggregations and rookeries in the region was analyzed with data collected in 2004 to 2006 and during the 1990s. The JR non-adult fishing ground presented high genetic diversity and Mexican rookery was identified as the primary contributor using haplotypes at the 384 bp length and each MSA approach that was used, congruent with the demographic growth reported for this rookery. Using haplotypes at the 740 bp length, the primary contributor to non-adult turtles at JR differed according to the MSA approach used, alternating between Mona Island and the Mexican rookery. Jardines del Rey is a route usually taken by non-adult hawksbills of diverse origin, reflecting the need to strengthen the sampling and conservation efforts on the WC rookeries with rare or orphan haplotypes, and to warn about the impact of the fishery occurring in similar areas. Likewise, adult turtles from JR were highly diverse and from multiple origins, with this area serving as a migratory corridor for first breeders (females) to many WC breeding grounds. Caution should be employed in any MSA approach due to the influence effect of sequence length, selection of the rookery size and haplotype frequencies, as well as other assumptions that may affect the estimated contributions.

Keywords Eretmochelys imbricata; Mixed stock analysis; Wider Caribbean; Jardines del Rey; Rookery size; Maturation category

Introduction Understanding the connectivity between breeding and feeding grounds is crucial for the management and conservation of migratory species (Harrison and Bjorndal, 2006). In marine species with high dispersion capability, it is challenging to obtain this information due to the absence of apparent physical barriers at wide scales of distribution (Shamblin et al., 2012). In particular, sea turtles have a complex life cycle characterized by a series of ecological transitions associated with continuous movement and habitat changes throughout their different life stages (Bjorndal and Bolten, 1988; Diez et al., 2003; Chaib et al., 2012). In these species, once sexual maturity is reached turtles begin periodic migrations between feeding and breeding/nesting areas, which are sometimes separated by thousands of kilometers (Miller, 1997), with females (Carr, 1967), and to a lesser extent males (Velez-Zuazo et al., 2008), exhibiting philopatric or “natal homing” behavior. This has been verified using flipper tags (Limpus et al., 1992; Horrocks et al., 2011), satellite tracking (Luschi et al., 2006; van Dam et al., 2008; Godley et al., 2010) and mtDNA markers (Bass et al., 1996; Bowen et al., 1996), in which has demonstrated significant differences in the mtDNA haplotype frequencies among nesting populations ( Bowen and...
Karl, 2007). This genetic structure is a necessary premise for inferring the connectivity between sea turtle aggregations and nesting populations (sources or rookeries) through the application of mixed stock analysis (MSA) (Pella and Masuda, 2001). For the purposes of conservation, identifying origins in aggregations is important because the sources, reproductively isolated, are concomitant in the mixed aggregations (Avise, 2007; Bowen et al., 2007). Therefore, a negative impact on these areas or the migratory routes that connect them with breeding/nesting areas may affect several sources as well as other foraging grounds (Proietti et al., 2012).

Of all sea turtle species reported for the Wider Caribbean (WC), *Eretmochelys imbricata* is one of the most suitable biological models to make inferences about regional management and conservation through the MSA. This species is circumtropical (Baillie and Groombridge, 1996) with little genetic flow between Brazilian and WC rookeries (Vilaça et al., 2013; Proietti et al., 2014), and limited transoceanic migrations (Marcovaldi and Filippini, 1991; Bellini et al., 2000; Grossman et al., 2007; Monzón-Argüello et al., 2011). On the other hand, the WC has the largest number of genetically characterized *E. imbricata* aggregations and rookeries (Bowen et al., 2007; Velez-Zuazo et al., 2008; Richardson et al., 2009; Blumenthal et al., 2009a; Leroux et al., 2012; Gorham et al., 2014). These sources temporarily exhibit genetic stability (Velez-Zuazo et al., 2008), and significant genetic structure between them and feeding aggregations (Bowen et al., 2007). In addition, most of these sources have historical demographic estimates (Richardson et al., 2006; Beggs et al., 2007; Mortimer and Donnelly, 2007).

Finally, the complex life cycle of the hawksbill (Bolten, 2003) along with solitary nesting (Witzell, 1983) and persistent consumptive use (Moncada et al., 2012), and further, the additional value of its shell (Mortimer and Donnelly, 2007), make this a Critically Endangered species (IUCN, 2016).

Currently, most MSAs are performed using the “many to many” method, where the rookery size *i.e.* number of nesting females or nests per year (Nr) is included as a constraint (Bolker et al., 2007) since Nr is an important determinant of the contributions from each rookery. In *E. imbricata* many studies use the Nr most recently reported (Blumenthal et al., 2009a; Wood et al., 2013; Gorham et al., 2014), which may be biased considering that this parameter has had a general increasing trend in WC (Mortimer and Donnelly, 2007). If the aggregation is a breeding area or composed of adult individuals, it is most appropriate to select the Nr that temporarily coincides with the aggregation sampling, because these individuals potentially belong to the effective size of these rookeries. Conversely, if the aggregation is composed of non-adult individuals then the selected Nr should coincide with the approximate moment at which these individuals hatched. This is because *E. imbricata* juveniles which have arrived at neritic habitats after their oceanic stage may take up to two or more decades to reach maturity (Boulon, 1994; Miller and Limpus, 2003), and the Nr can vary significantly over this period (Mortimer and Donnelly, 2007), thereby affecting the contributions.

On the other hand, many authors have used the cumulative frequencies from many years in each rookery to execute the MSA (Bowen et al., 2007), which increases the N but this assumption can overestimate some haplotypes. In other cases, the cumulative haplotype frequency in the rookeries may exceed the number of annual nesting females as in the *E. imbricata* rookery of Tortuguero (Costa Rica), which has 10 nesting females/year but 42 with assigned haplotypes between 2000 and 2003 (Tröeng et al., 2005). In addition, the use of maritime distance between rookeries and aggregations should be treated cautiously when inferring sea turtle dispersal/migration. There are two maritime distances to consider: the shortest distance between the rookery and the aggregation, and the distance representing the trajectory taken by the turtle depending on sea currents and other factors. With the first variant, correlations and regression models have been tested which generally do not show any significance or have relatively low coefficients (Luke et al., 2004; Bowen et al., 2007; Naro-Maciel et al., 2007; Prosdocimi et al., 2012). With the second variant, the results have indicated significant correlations between the contributions of rookeries to juvenile aggregations calculated with the haplotype frequencies and those calculated by passive dispersion of particles from rookeries to aggregations by means of ocean currents (Bowen et al., 2004; Blumenthal et al., 2009a; Proietti et al., 2012). However, turtle trajectory to a feeding/breeding ground does not always follow a logic of phylopatry, residence, or occur in accordance with sea currents (Cuevas et al., 2008; van Dam et al., 2008).
The Wider Caribbean has also been the scene of political conflict in the management of *E. imbricata*. The majority of WC nations had already abandoned the legal fishery for this species when Cuba permanently closed its legal fishery in January 2008. In fact, Cuba is the only country that has such a complete temporal series of morphometric, reproductive, genetic, flipper tags, and catch volume data recorded for decades in a fishery exclusively for chelonians (Carrillo et al., 1998a; 1999; Díaz-Fernández et al., 1999; Moncada et al., 1999; 2010; 2011; 2012). However, this fishery closed without determining the status of these fishing grounds by contrasting historical and recent data on morphometry, genetics and reproduction. Our study integrates for the first time these data belonging to hawksbill harvests during the periods of legal fishery between 2004 and 2006 in Jardines del Rey (JR), one of the two active fishery sites which continued in the Cuban archipelago after the significant reduction of this activity in 1994. The present study aims to test if the origins of the hawksbill fishing stock of Jardines del Rey are plausibly explained when annual haplotype frequencies are assumed, as well as the population size according to the maturation category. The study goals were 1) to calculate the contributions from sources to feeding/breeding grounds with emphasis on JR, and following several assumptions such as the selection of the Nr according to the maturation category of the individuals; 2) to compare these MSAs with those done following the criteria commonly used in the literature in order to discuss the validity of both approaches; and 3) to evaluate the relationship among contributions and the maritime distances between rookeries and aggregations.

1 Results

1.1 Genetic composition and diversity in the JR fishing aggregation

From the total number of *E. imbricata* individuals (N = 249) processed in the present study in JR, we obtained 119 sequences at the 740 bp length and identified 17 haplotypes among them (Table 1), some not recorded in the WC rookeries. The haplotype composition within the 2004-2006 period was independent of the maturation category ($X^2_{(df=32)}=19.32$, $p = 0.98$; Table 1). The EiA11 haplotype was the most abundant among non-adult individuals, followed by EiA01 and EiA24, EiA23 and EiA41. Among adult males, EiA01 was the most frequent haplotype, followed by EiA11. Among adult females (AF + BF), haplotypes EiA01 y EiA11 were equally frequent.

Haplotype composition was independent of the fishery year in non-adult individuals ($X^2_{(df=40)} = 35.74$, $p = 0.20$; Table 1). However, the ratio of EiA01 to EiA11 observed in 2004 was inverted in 2005. The most diverse year was 2005 with 11 haplotypes detected among non-adult individuals, 9 haplotypes in adult males and 6 haplotypes in adult females. Year 2006 was a low harvest year with EiA11 moderately represented.

The haplotype composition was also independent of the fishery year among adult males ($X^2_{(df=18)} = 15.35$, $p = 0.74$; Table 1). The EiA01 was equally frequent in 2004 and 2005, and EiA11 in 2004. In addition, year 2005 was the most diverse with most haplotypes poorly represented. Among the adult females (AF+BF) there was also no annual statistical dependence ($X^2_{(df=16)} = 23.97$, $p = 0.1$; Table 1). The EiA01 was similarly frequent in 2004 and 2005, whereas EiA11 was more frequent in 2004. Haplotypes EiA23 and EiA24+EiA41 were present only in 2005 and 2004 respectively. Breeding females were mainly distributed in classes IV and III, and in August and September. Similarly, when comparing the haplotype frequencies of 2004 and 2005 with those of the 1990s from Díaz-Fernández (1999) for the JR fishing aggregation there was no dependence on maturation categories (non-adults: $X^2_{(df=30)} = 32.33$, $p = 0.31$; adults: $X^2_{(df=26)} = 31.86$, $p = 0.11$).

In non-adult individuals from 2004 to 2006 the haplotype composition per fishery year was independent among SCL classes (2004: $X^2_{(df=7)} = 8.14$, $p = 0.27$; 2005: $X^2_{(df=9)} = 10.24$, $p = 0.36$) as well as by SCL class (class II: $X^2_{(df=9)} = 14.81$, $p = 0.06$; class III: $X^2_{(df=7)} = 6.67$, $p = 0.53$). In adult individuals from 2004 to 2006, genetic composition was independent among SCL classes by sexual class (males: $X^2_{(df=18)} = 14.56$, $p = 0.81$; females: $X^2_{(df=18)} = 15.27$, $p = 0.75$) or among fishery years per SCL class (class II: $X^2_{(df=4)} = 3.33$, $p = 1.0$; class III: $X^2= 7.14$, $p = 0.78$; class IV: $X^2_{(df=4)} = 3.55$, $p = 1.0$).

Genetic diversity was high in JR fishing aggregation (haplotypes at the 740 bp length) and similarly high within each maturation category, including adult sexual classes (Table 1). When these diversities were recalculated for non-adult individuals using haplotypes at the 384 bp length, the values of haplotype (h) and nucleotide (π) diversities decreased and increased respectively (Table 2). The non-adult individuals of the JR between 2004 and
2006 had a relatively similar value with respect to other WC non-adult aggregations, except for Río Lagartos, Cocodrilo, south of Dominican Republic, platform resident juveniles of Mona Island feeding aggregation, Cayman Islands, and those from Florida. On the other hand, only the \( \pi \) of Río Lagartos, south of Dominican Republic, Buck Island, and Florida aggregation were smaller than those of JR between 2004 and 2006. The \( h \) and \( \pi \) of adult males and females between 2004 and 2006 in JR were similar to the remaining WC adult aggregations, but were greater than those diversities existing in Doce Leguas and the \( \pi \) of the breeding males from the Mona Island aggregation.

Table 1 Haplotype composition and genetic diversities (740 bp) of *E. imbricata* fishing aggregations from Jardines del Rey (Cuba) during the 2004-2006 legal fishing period

| Haplotype (bp) | NA | AM | AF+BF |
|---------------|----|----|-------|
| 384 \(^1\) 480 \(^2\) 740 \(^3\) | 2004 | 2005 | 2006 | 2004 | 2005 | 2006 |
| A | CU1 | EiA01 | 5 | 11 | 1 | 4 | 4 | 2 | 1+2 \(^{III-}\)s,o | 2+2 \(^{III-}\)s | 1 |
| B | e | EiA03 | 1 | | | | | | | |
| c | EiA09 | 1 | | | | | | | |
| F | PR1 | EiA11 | 12 | 6 | 3 | 3 | 1 | | | |
| Y | CU2 | EiA13 | 1 | 1 | 1 | 1 | | | |
| N | PR2 | EiA20 | 2 | | | | | | |
| P | MX3 | EiA22 | 1 | | | | | | |
| | MX1 | EiA23 | 1 | 3 | 1 | | | | |
| | | EiA41 | 3 | 1 | 1 | | | | |
| Q | MX2 | EiA24 | 2 | 4 | 1 | 1 | 1 | | |
| | | EiA43 | 1 | | | | | | |
| a | EiA27 | 2 | 1 | 1 | 1 | | | |
| b | EiA28 | 1 | | | | | | |
| | CU3 | EiA29 | 1 | 1 | 1 | 1 | | |
| m | EiA35 | 1 | | | | | | |
| n | EiA36 | 1 | | | | | | |
| DR1 | EiA37 | 1 | | | | | | |

Total | 24 | 35 | 9 | 10 | 12 | 3 | 7+7 | 6+4 | 2 |

Note: AM: adult males, AF: non-breeding adult females, BF: breeding females, \(^1\)Bass et al. (1996), \(^2\)Díaz-Fernández et al. (1999), \(^3\)Abreu-Grobois et al. (2006), II: SCL class II (60.1-70.0 cm), III: SCL class III (70.1-80.0 cm), IV: SCL class IV (80.1-90.0 cm), a: April, g: August, s: September, o: October, n: November

Table 2 Haplotype (\( h \)) and nucleotide (\( \pi \)) diversities (384 bp) of *E. imbricata* aggregations in the Wider Caribbean. Values between square brackets represent adult individuals

| Aggregations | Genetic diversities | N |
|--------------|---------------------|---|
| JR90 | 0.800 ± 0.078 | 15 |
| | [0.857 ± 0.050] | |
| JRNA04 | 0.714 ± 0.081 | 24 |
| | [0.0662 ± 0.0335] | |
| JRNA05 | 0.733 ± 0.053 | 25 |
| | [0.0532 ± 0.0271] | |
| JRNA04-06 | 0.775 ± 0.029 | 54 |
| | [0.0529 ± 0.0262] | |
| JRAd90-04-06 | 0.790 ± 0.059 | 25 |
| | [0.0574 ± 0.0292] | |
| JRAd90-04-06 | 0.754 ± 0.042 | 26 |
| | [0.0510 ± 0.0260] | |
| JRAd90-04-06 | 0.768 ± 0.032 | 51 |
| | [0.0550 ± 0.0274] | |
| DL90 | 0.814 ± 0.062 | 21 |
| | [0.0604 ± 0.0309] | |
| IJ90 | 0.699 ± 0.033 | 83 |
| | [0.0584 ± 0.0288] | |
| IJ90 | 0.826 ± 0.040 | 31 |
| | [0.0575 ± 0.0290] | |
Continued Table 2

| Aggregations | Genetic diversities |
|--------------|---------------------|
|              | h ± SD  | π ± SD  | N  |
| RL90         | 0.605 ± 0.111 | 0.0123 ± 0.0070 | 21 |
| DO90         | 0.669 ± 0.034 | 0.0102 ± 0.0057 | 90 |
| BA90         | 0.740 ± 0.024 | 0.0093 ± 0.0053 | 78 |
| USVI90       | 0.750 ± 0.036 | 0.0108 ± 0.0060 | 68 |
| MI90         | 0.724 ± 0.033 | 0.0596 ± 0.0293 | 93 |
| MIRes00      | [0.833 ± 0.081] | [0.0725 ± 0.0382] | 13 |
| MI♀00        | 0.676 ± 0.050 | 0.0521 ± 0.0260 | 51 |
| CI00         | [0.677 ± 0.060] | [0.0346 ± 0.0175] | 54 |
| FKW00        | 0.584 ± 0.052 | 0.0424 ± 0.0213 | 47 |
| FPB00        | 0.490 ± 0.056 | 0.0268 ± 0.0137 | 91 |
| ToL00        | 0.7721 ± 0.057 | 0.0620 ± 0.0321 | 17 |
| ToW00        | 0.6003 ± 0.065 | 0.0479 ± 0.0240 | 49 |
| TnC00        | 0.733 ± 0.033 | 0.0541 ± 0.0272 | 36 |

Note: JR: Jardines del Rey, Cuba; DL: Doce Leguas, Cuba; IJ: Isla de la Juventud, Cuba; RL: Rio Lagartos, Yucatan, Mexico; DO: south of Dominican Republic; BA: Bahamas; USVI: Buck Island, United States Virgin Islands; MI: Mona Island, Puerto Rico; CI: Bloody Bay and west of Grand Cayman, Cayman Islands; FKW: Key West National Wildlife Refuge, Florida, USA; FPB: Palm Beach County, Florida, USA; ToL: Tobago leeward; ToW: Tobago windward; TnC: Turks and Caicos; Ad: adult individuals, N: number of individuals with haplotypes, NA: non-adult individuals, Res: platform resident juveniles from Velez-Zuazo et al. (2008), SD: standard deviation. 00: decade of 2000, 04-06: total samples of the present study, 90: decade of 1990 from Díaz-Fernández (1999); *values extracted from Bowen et al. (2007); ♀: males; ♀: females

1.2 Mixed stock analysis

1.2.1 Non-adult aggregations

Contributions to the non-adult fishing aggregation of JR were heterogeneous in each MSA conducted (Figure 1). The Mexican (ME) and Tobago rookeries were the major contributors during the 1990s using the 384 bp length, while in 2004 and 2005 the ME rookery was the main contributor. For the MSAgr, ME maintained contributory supremacy followed by Mona Island (MI) and Barbados leeward coast (BaL). In 2004, using the 740 bp length, the major contributor to JR was the Barbados windward coast, followed by the MI and ME rookeries. In 2005 the ME rookery contributed highly to JR but in the MSAgr the MI rookery was the main contributor.

Many aggregations had contributions in the MSAoa congruent with those of the MSAgr. For Rio Lagartos the ME source was the primary contributor, while for the Tobago windward aggregation the BaL rookery was the major contributor with either 384 or 740 bp (Supplementary Material 1A). In Florida aggregations, the ME source was the highest contributor for any sequence length (Supplementary Material 1B).

Other aggregations presented different results given the MSA approach or the sequence length. The Turks and Caicos foraging aggregation had higher contributions from ME followed by the Tobago rookery in the MSAoa, but the second contributor was the BaL rookery in the MSAgr (Supplementary Material 1C). In Cayman Islands the Tobago rookery was the major contributor using the 384 bp length, while the BaL rookery was the major contributor when using the 740 bp length (Supplementary Material 1C). The Bahamas aggregation received a higher contribution from the ME rookery in the MSAoa but was a secondary contributor to the BaL rookery in the MSAgr (Supplementary Material 1D). In the feeding aggregation of the Dominican Republic the Tobago rookery presented the greatest contribution in the MSAoa but the BaL rookery was the major contributor in the MSAgr (Supplementary Material 1D). Similarly, the Doce Leguas fishing aggregation had a majority contribution from the homonymous rookery while for the MSAgr it was BaL (Supplementary Material 1E). In addition, the major contributor to the Tobago leeward coast aggregation was the Nicaragua rookery in both sequence lengths of the MSAoa, but in the MSAgr this rookery was substituted by the BaL rookery (Supplementary Material 1E). The remaining non-adult aggregations of the WC had not primary contributors but even contributions among different
rookeries and differed from MSAgr (Supplementary Material 1F; Supplementary Material 1G). From the rookery-centric perspective, the non-adult fishing aggregation of JR receives a low percentage of the total number of individuals hatched out in Las Coloradas, using each MSA approach (Figure 2).

Figure 1 Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ± 2.5–97.5% confidence intervals for the non-adult fishing aggregation of JR (black: 384 bp, gray: 740 bp)

Note: Circle, triangles and diamonds: MSAoa from Díaz-Fernández (1999), year 2004 and 2005 respectively; squares: MSAgr. ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize

Figure 2 Mixed stock analysis (rookery-centric) results showing mean proportional contribution ± 2.5–97.5% confidence intervals for the non-adult fishing aggregation of JR (black: 384 bp, gray: 740 bp)

Note: Circle, triangles and diamonds: MSAoa from Díaz-Fernández (1999), year 2004 and 2005 respectively; squares: MSAgr. ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize
1.2.2 Adult aggregations

The contributions using the 384 bp length to the adult fishing aggregation of JR were different over the decades and with respect to the MSAgr (Figure 3). In the 1990s, many rookeries contributed heterogeneously and with low percentages to this aggregation. In the 2000s, the main contributors were the ME and BaL rookeries followed by the Cuban rookery; while in MSAgr DL was the major contributor followed by the ME and BaL rookeries. In contrast, contributions with the 740 bp length haplotypes were similar to MSAgr: BaL as the primary contributor followed by the DL rookery.

Figure 3 Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ± 2.5–97.5% confidence intervals for the adult fishing aggregation of JR (black: 384 bp, gray: 740 bp)

Note: Circle and triangles: MSAoa from Díaz-Fernández (1999) and the 2004-2006 fishing period respectively, squares: MSAgr. ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize

In Mona Island aggregation of breeding males, the homonymous rookery was the major contributor in each decade and sequence length (Supplementary Material 1H). In the Doce Leguas fishing aggregation, BaL was the major contributor during the decade of 1990 followed by the Tobago rookery, while BaL was the dominant rookery in the MSAgr (Supplementary Material 1H). The Cocodrilo fishing aggregation had heterogeneous contributions during the 1990s and the MSAgr (Supplementary Material II).

The correlations among contributions calculated with both sequence lengths and maritime distances between rookeries and aggregations were not significant and these had very low coefficients (Table 3).

2 Discussion

When the Cuban Ministry of Fishery reduced the sea turtle harvest by Cuban fishing platforms in the 1990s, JR and Cocodrilo were the only sites that remained active for reasons of tradition (Carrillo et al., 1999). The sustainability of this fishery was supported on a supposed recruitment from Doce Leguas rookery to the Cuban fishing aggregations (Díaz-Fernández et al., 1999), and a fishery minimum size (SCL> 65 cm) based on the fact that *E. imbricata* individuals of the Cuban platform begin sexual maturation with SCL=60 cm (Moncada and Nodarse, 1994). Having the original data of Díaz-Fernández (1999) and Lee-González et al. (2015), we could detect non adult individuals within the harvested hawksbills in both sites. This demonstrates that the mature cohorts were non accurately managed in the fishery, being these ones well represented in the SCL classes III and IV and genetically heterogeneous. This places JR in the WC as the only genetically characterized *E. imbricata* fishery aggregation located in a confirmed migratory corridor. Although it is impossible to calculate or estimate
the true impact of the JR fishery in the WC, the results presented here indicate that this marine area is important for the hawksbill population dynamics, as well as its management and conservation.

Table 3 Correlation between maritime distances and the natural logarithm of the contribution for 384 and 740 bp regarding only Jardines del Rey or all aggregations

| Decade or year | Maritime distance | Non adult | Adult | Non adult | Adult |
|---------------|------------------|-----------|-------|-----------|-------|
| Jardines del Rey (384 bp) | SMD | -0.14_{11} / 0.64 | 0.27_{11} / 0.35 | | |
| 1990s | TMD | -0.21_{11} / 0.46 | 0.05_{11} / 0.86 | | |
| 2004 | SMD | -0.06_{11} / 0.84 | | | |
| TMD | -0.10_{11} / 0.74 | | | 0.01_{11} / 0.98 | 0.27_{11} / 0.35 |
| 2005 | SMD | -0.09_{11} / 0.76 | | | |
| TMD | -0.06_{11} / 0.82 | | | | |
| 2000s | SMD | | 0.22_{11} / 0.44 | | 0.17_{11} / 0.55 |
| Jardines del Rey (740 bp) | TMD | | | | |
| 2004 | SMD | -0.04_{11} / 0.90 | | | |
| TMD | 0.42_{11} / 0.15 | | | | |
| 2005 | SMD | -0.15_{11} / 0.62 | | | |
| TMD | 0.22_{11} / 0.47 | | | 0.36_{11} / 0.19 | 0.34_{11} / 0.25 |
| 2000s | SMD | | 0.27_{11} / 0.37 | | |
| TMD | | | | 0.37_{11} / 0.21 | |
| All aggregations (384 bp) | SMD | -0.09_{112} / 0.32 | 0.23_{112} / 0.09 | | |
| 1990s | TMD | -0.16_{112} / 0.09 | 0.11_{112} / 0.41 | -0.11_{112} / 0.13 | 0.17_{112} / 0.20 |
| 2000s | SMD | -0.13_{120} / 0.14 | 0.07_{120} / 0.71 | -0.11_{120} / 0.14 | 0.08_{120} / 0.54 |
| TMD | -0.10_{120} / 0.26 | 0.01_{120} / 0.98 | | | |
| All aggregations (740 bp) | SMD | -0.15_{104} / 0.14 | 0.11_{104} / 0.58 | | |
| 2000s | TMD | -0.06_{104} / 0.56 | 0.13_{104} / 0.52 | -0.11_{104} / 0.28 | 0.19_{104} / 0.40 |

Note: The correlations (Pearson coefficient \( r \) or probability) obtained from MSAgr are underlined. SMD: shortest maritime distance between rookeries and aggregations, TMD: maritime distance between rookeries and aggregate assuming a sea turtle trajectory similar to that of the passive dispersion of particles on regional ocean currents (Blumenthal et al., 2009a)

The independence between haplotype frequencies per SCL class and maturation category, the relatively high values of genetic diversity, and the absence of historical records of nesting in JR, enable the confirmation of this fishing aggregation as very diverse both phenotypically (Carrillo et al., 1998b) and genetically (Díaz-Fernández et al., 1999). Likewise, these elements corroborate the JR fishing ground as a suitable corridor for the reproductive migration of adult individuals and those at the height of the sexual maturity (Lee-González et al., 2015), or those that are migrating to other WC feeding aggregations. The temporal independence of the genetic composition as well as of the SCL class is yielded by the prevalence of the most distributed haplotypes in WC (EiA01 and EiA11, Leroux et al. (2012)), and the existence of other low frequency haplotypes.

The temporal independence of the genetic composition in each maturation category has also been reported in the Mona Island feeding ground, particularly for juveniles newly recruited to the platform and for breeding males (Velez-Zuazo et al., 2008). This apparently would indicate that the haplotype mixtures do not depend of the type of aggregation (i.e. breeding or feeding ground). However, the composition of maturation categories and size classes does vary depending on the structural characteristics of the marine area in question. In breeding aggregations, mating turtles have SCLs close to the average value in each sexual class (Miller, 1997) due to the reduced growth in this life stage (van Dam and Diez, 1998a). In feeding aggregations, the heterogeneity and abundances of SCL classes and life stages is a function of the available trophic resources and structural niches (León and Diez, 1999; Blumenthal et al., 2009b). Therefore, when the juveniles remain as residents for a long time (van Dam and Diez, 1998b; Meylan et al., 2011), the area should support a specific number of individuals with varying degrees of consumption according to their sizes (Diez and van Dam, 2002). In contrast, our study area is a corridor of *E. imbricata* which has experienced a temporary increase in the proportion of immature individuals in the smaller SCL classes (60.1-70.0 cm, Lee-González et al. (2015)). This is a reflection of the
demographic growth of nesting populations in the WC rookeries (Mortimer and Donnelly, 2007) whose juveniles use the JR corridor as a transitory route to other feeding grounds. In fact, the haplotype Q, best represented in the largest WC rookery (Las Coloradas), is more frequent in non-adult turtles from JR between 2004 and 2006 than the adult ones (Table 1), which was reflected in the increasing contributions from this source (Table 1; Figure 2).

Two immature individuals from JR with haplotypes EiA01 and EiA11 were identified as pubescent in a previous study on sexual maturation in the marine area of the present study (Pérez-Bermúdez et al., 2010). The presence of spermatozoa in these specimens indicated that they would reach the ability to copulate in ca. two months. In addition, these pubescent males had similar SCL classes to those of adult ones of the same fishing aggregation, which is relatively far from the WC breeding areas. Thus, these individuals would possibly complete their maturation during this migration reinforcing JR as a migratory corridor, in this case of first breeders taking this route to regional breeding grounds.

Although the present study incorporates in general E. imbricata rookeries and aggregations of the WC using 740 bp sequences, the MS Ao still results in wide confidence intervals due to the fact that haplotypes A/EiA01, F/EiA011 and Q are highly frequent and shared among WC rookeries (Leroux et al., 2012). Hence, the current MCMC model still has limitations that cannot process all the ecological complexity encrypted in the original data. Other factors that may contribute towards uncertainty are the moderate and sometimes limited sample sizes in some rookeries and aggregations; the quality and sampling frequency in both entities (Bowen et al., 2007); the genetic similarity of some rookeries, given that they are isolated reproductively-speaking (Browne et al., 2010; Leroux et al., 2012; Carreras et al., 2013); and the limited number of aggregations. This last one is present when adult aggregations are analyzed in our study whose number is a small fraction of the real number of adult aggregations in the WC. Consequently, these results could be biased and indicate the urgency to sample other adult aggregations to improve the inferences and to clarify of better way on the connectivity among these breeding, foraging and corridor grounds and the rookeries.

Furthermore, there are assumptions that can bias the results. For example, many studies have grouped the Cuban fishing aggregations (Cuba A, B and D) as a single entity, perhaps because these belong to the same political jurisdiction (Troëng et al., 2005; Blumenthal et al., 2009a; Browne et al., 2010). However, this is inappropriate since these Cuban aggregations are separated by hundreds of kilometers and differ structurally, as well as in the proportion of the maturation stages present (Carrillo et al., 1999). Consequently, we found marked differences between the MS A of both maturation categories in each fishing aggregation, probably reflecting a maturation category-specific dispersal behavior. In addition, the MS A of the present study using 740 bp still represent unrealistic scenarios since 1) there are few aggregations characterized with this sequence, 2) there are haplotypes that are frequent but orphaned (i.e. EiA24), and 3) the Belize rookery is only characterized for 384 bp. For example, the contribution of the ME rookery to non-adult and adult aggregations for JR between 2004 and 2006 with 384 bp is slightly higher than that with 740 bp (Figure 1; Figure 3). In the latter, individuals with the orphan haplotype EiA24 (N = 4) are excluded from the MSA with 740 bp, reinforcing the contributions of the BaL rookery. The importance of selecting the data in rookeries and aggregations as well as the assumptions to execute the MSA is more evident when our initial data are contrasted with these of other studies. For example, our approach excluded the cumulative haplotype frequencies in rookeries and aggregations as well as the Texas pelagic individuals from Bowen et al. (2007) and the Mona Island “new recruits of platform” individuals from Velez-Zuazo et al. (2008). These assumptions and data are used by subsequent authors to infer contributions (Blumenthal et al., 2009a; Monzón-Argüello et al., 2010; Vilaça et al., 2013; Proietti et al., 2014). Likewise, the Brazilian and Eastern Atlantic rookeries and aggregations used in Monzón-Argüello et al. (2010; 2011), Vilaça et al. (2013), Proietti et al. (2014), Putman et al. (2014) and the recent publication of Cazabon-Mannette et al. (2016) are excluded from our initial data. This partially explains that Doce Leguas rookery has been important for Tobago aggregations because Cazabon-Mannette et al. (2016) also took the corresponding population size from Mortimer and Donnelly (2007). This Nr is six times higher than that selected by us from Moncada et al. (2010), which is better estimated because came from the more systematic and recent surveys (nesting seasons from 1997/1998 to 2008-2009) in that archipelago.
Nevertheless, considering both approaches and haplotype lengths, we had some aggregations with the same primary contributors reported in the first publication where these ones appear (i.e. breeding males of Mona Island: Velez-Zuazo et al. (2008), Rio Lagartos: Bowen et al. (2007), Palm Beach County: Wood et al. (2013), Key West National Wildlife Refuge: Gorham et al. (2014)). This demonstrates that when the sampling or original data are robust the contributions will tend to the same result even if the a priori assumptions vary somewhat. These inferences coincide with the expected connectivity between these aggregations and their most represented rookeries, considering the effect of regional sea currents (Blumenthal et al., 2009a). Conversely, the lack of significance and the low coefficients in the correlations calculated between the TMD and the contributions of the 2000s (Table 3), make it impossible to establish a cause-effect relationship between these variables. If the haplotype distribution depends on sea currents then a high residence of the oceanic-stage juveniles newly recruited to the neritic habitats is expected. Nevertheless, an increase in their dispersal capability when oceanic-stage juveniles are growing could cause the lack of statistical dependence among these variables. Another possibility is that the TMDs calculated in the present study do not coincide with the true routes taken by the individuals to their residence sites. There are accurate studies on the swimming behavior of the small juveniles of hawksbill turtle but these studies are not in the Caribbean region. Nevertheless, the simulations have suggested that the swimming of the smaller juveniles can be very active on diverse ocean currents and sea temperatures (Putman et al., 2014). This phenomenon in the hot waters of the WC requires additional evidences to give a better explanation according to our results.

The incorporation in the MSAs of the present study of other WC rookeries and aggregations recently characterized (Carreras et al., 2013; Gorham et al., 2014; Cazabon-Mannette et al., 2016) reinforces the contributions from the largest rookeries (ME, BaL and MI). These populations have experienced the highest recovery rates in decades (ca. 6-8 times the Nr from the 1980s, Mortimer and Donnelly (2007)) and also have the highest frequencies of the most represented haplotypes in the region (A/EiA01, F/EiA11 and Q/EiA23). This is why rookeries with high or moderate frequency in these haplotypes but limited Nr (Dominican rookeries, Tortuguero, Barbados windward coast, etc.) generally had lower contributions and narrow confidence intervals. However, the use of the higher Nr, as occurs in the literature, does not always support the plausibility of the inferences made. For example, it is unlikely that BaL mainly contributes to the non-adult and adult fishing aggregation of Doce Leguas in the MSAg (Supplementary Material 1E; Supplementary Material 1I). This aggregation is in a foraging (Anderes and Uchida, 1994) and residence area of juveniles most probably born in the homonymous rookery, and some post-nesting females, also from this source (Moncada et al., 1998; 2012), with A/EiA01 being the most abundant haplotype (Díaz-Fernández et al., 1999). The contributions calculated in the MSAoa are more compatible with these evidences, and of the same way, the low values of genetic diversities in the adult individuals from this aggregation (Table 2). This does not imply that BaL rookery does not contribute individuals to this feeding aggregation, although only one adult female with a Barbados flipper tag has been reported in the period 1989-2009 (Moncada et al., 2012).

The analysis of the different MSAs presented here results in many interpretations of the role of JR in the dispersal/migration of *E. imbricata* in the WC. If only the MSAs with 384 bp (either MSAoa or MSAg) are considered in the non-adult fishing aggregations of 2004 and 2005 of JR, the explanation is more simple since this would mean that many non-adult individuals with Q most probably come from the Mexican source (Figure 1). The conclusion therefore is that JR is a corridor frequently used by the immature cohorts originating from the Mexican source to transit to regional foraging grounds. Thus, from a conservationist perspective, JR should also be a focus of attention for the protection of the Mexican source, consistent with the temporary demographic growth reported in the Mexican source (Garduño-Andrade et al., 1999; Pérez-Castañeda et al., 2007). In fact, this increase explains why the rookery-centric approach revealed that the ME rookery did not have a high percentage of its total number of hatched individuals represented in JR, indicating that the remainder are found in other WC aggregations. In contrast, in the MSAs with 740 bp the non-adult and adults individuals with EiA23 or EiA41 (Table 2) that migrated via JR are highly likely to have originated in Las Coloradas. However, with the haplotype EiA43 and EiA24 (N = 11) the derivation is different. The former is rare in the WC and this could mean that while
the Cuban fishery was active, there was a negative impact on the haplotype pool of the WC rookeries with smaller Nr, the haplotype EiA43, and other infrequent haplotypes. The negative impact of the Cuba fishery is even more marked if individuals from the same sources are also subject to consumptive use or affected by other anthropogenic causes as in the case of Pearl Cays rookery (Campbell et al., 2010). For the orphan haplotype EiA24, also frequent in the region (Velez-Zuazo et al. (2008): N=2, Blumenthal et al. (2009a): N=11), the interpretation is that JR is a migratory route of individuals born in WC rookeries although these individuals have not yet been characterized genetically or there is insufficient sampling. Consequently, by means of a different approach, the present work corroborates the study of Cazabon-Mannette et al. (2016): the need to prioritize sampling and conservation efforts of the "genetically unknown" rookeries or others with poor monitoring. In addition, the MSagr with both sequence lengths share the increased contributions of the MI and BaL rookeries in the non-adult aggregation of JR, indicating that the most inclusive criterion will favor the representativeness of those sources with higher Nr and common haplotypes and thus, the criteria of importance biased towards these sources. Finally, although Cuba permanently abandoned the legal chelonian fishery, other countries in the region continue to exploit these resources either legally (i.e. Turks and Caicos: Stringell et al. (2013)) or illicitly. Thus, it is necessary to apply these analyses in conservation and management, but researchers and managers should be cautious in their interpretation of the results, and they should use other approaches and complementary data. These results reveal new data that will strengthen the analysis of regional management units, a new approach that extensively examines published information to coordinate conservation and research strategies (Wallace et al., 2010; 2011). In addition, researchers could consider and evaluate if the MSAoa is applicable to the other sea turtles species, which has different migratory behavior, occupies regions that are more extensive and presents diverse management and conservation conflicts.

3 Materials and Methods
3.1 Study area and individual sampling
The individuals of E. imbricata sampled in this study were those harvested in the legal sea turtle fishery located in the offshore platform surrounding the fishing settlements "El Mangle"[22°00’12”N; 77°26’48”O] (Romano Key) and "Montañés”[21°56’06”N; 77°34’12”O] (Guajaba Key), which both belong to fishing zone D (JR) of the Cuban platform (Figure 4). Harvests were made during the last periods of active legal fishery (January-April and August-December) during 2004 (N = 95), 2005 (N = 106) and 2006 (N = 48). The place where sea turtle nets were located constitutes a migratory route of E. imbricata and the rest of the area serves as a foraging ground for Chelonia mydas and Caretta caretta (Lee-González et al., 2015).

Figure 4 Geographical representation of the sea turtle legal fishery in Jardines del Rey (Cuba) from 2004 to 2006
Note: Black circle: El Mangle, black square: “Montañés”, black dashed line: fishing aggregation
The methods of capture and data collection of the individuals as well as description of the variables are described in Lee-González et al. (2015). Of all the variables reported by these authors, we used the sexual class, the sexual maturity stage and the straight carapace length (SCL) divided in five SCL classes of 10 cm modified from Carrillo et al. (1998a). Individuals with SCL≥80 cm that were not directly examined by the authors and lacked secondary sexual characteristics according to the fishermen, were classified as adult females according to Moncada et al. (1999). All procedures practiced on the turtles were made according to the national regulations established by the Cuban Ministry of Fishery Industry. This institution provide us with the permissions to access to the fishery area and take the samples for the genetics, reproduction and morphometry studies.

3.2 Collection and processing of samples for genetic analysis

Biopsies of skeletal muscle or skin were taken from each individual and preserved in 96% ethanol saturated with EDTA and stored at room temperature. DNA extraction and purification were performed with FastDNA kit (MP Biomedicals). The mtDNA control region (ca. 800 bp) was amplified using the primers LTEi9 (GGGAATAATCAAAAGAGAAAGG-3') and H950 (GTCTCGGATTAGGGGT-3') from Abreu-Grobois et al. (2006). When DNA degradation hindered the PCR, we amplified the first half (ca. 400 bp) with LTEi9 and the primer REi397 (CAGAGCCGAAATAGATCG-3'), designed in this research; and the second half (ca. 500 bp) with Cont1a (ATTATCTCAACCATGAATATCG-3) (Diaz-Fernández et al., 1999) and H950. The PCR was developed in 25 μL of reaction volume for the 740 bp segment according to the PCR conditions of Velez-Zuazo et al. (2008), and Díaz-Fernández et al. (1999) for the second half. For the first half the same cycles were used but with an annealing temperature of 55°C for 45 seconds. The amplified products were purified using NucleoSpin Extract II columns (Macherey-Nagel) and sequenced in both directions with fluorochrome-labeled ddNTP (BidDye Terminator 3.1 Cycle Sequencing Kit, Applied Biosystems) in an ABI3100 genetic analyzer.

Sequences of 384 or 740 bp were aligned using Clustal X (Thompson et al., 1997) and matched against published WC hawksbill mtDNA haplotypes (Bass et al., 1996; Bass, 1999; Díaz-Fernández et al., 1999; Bowen et al., 2007; Velez-Zuazo et al., 2008; Leroux et al., 2012; Carreras et al., 2013). The haplotype (h) and nucleotide (π) diversity indices were calculated using the software Arlequin version 3.11 (Excoffier et al., 2005). For the genetic characterization of the JR fishing aggregation we compared the haplotype composition of non-adult individuals, adult males, and adult females annually and to the previous decade; and in turn these treatments distributed in the SCL classes through an X² test of pseudoprobability with 1000 Monte Carlo simulations (Roff and Bentzen, 1989), through CHIRXC software (Zaykin and Pudovkin, 1993).

3.3 Mixed stock analysis

The “mixstock” package in R version 2.15.1 (R Core Team, 2012) was used to compute a many to-many Bayesian MSA (Bolker et al., 2007) with rookery size (annual number of nesting females) as a constraint, for both 384 and 740 bp sequence lengths. The Markov chain Monte Carlo (MCMC) method was implemented by WINBUGS version 1.4 (Sturtz et al., 2005) executing 20000 iterations and a 10000 burning command. The Gelman-Rubin diagnostic was used to determine convergence in the MSA posterior distributions (Gelman and Rubin, 1992).

3.3.1 Aggregations

Genetic data from published feeding/breeding aggregations of the WC with neritic life-stages were used for the MSAs (Figure 5). The aggregations were segregated in two maturation categories: non-adult or adult individuals, declared as a “non-adult” or “adult aggregation” respectively. In each maturation category, the haplotype frequencies were separated by decade of sampling, i.e. non-adult (or adult) aggregations from the 1990s or 2000s (Supplementary Material 3A; Supplementary Material 3B). For the MSAs of non-adult aggregations the Nr of the decade previous to their sampling was used considering that (Supplementary Material 2): 1) in WC the individuals of E. imbricata have higher growth rates than in other regions (Moncada and Nodarse, 1994; van Dam and Diez, 1998a; Hawkes et al., 2014); 2) non-adult individuals of the present study had SCL classes similar to the adult ones (SCL classes II and III according to Lee-González et al. (2015)) and; 3) no demographic data exists for the rookeries during the 1970s. For the MSA of adult aggregations the Nr was selected from the same decade of
sampling. These MSAs were named “MSA according to our approach” (MSAoa). In addition, for each maturation category and sequence length, one MSA was executed in which the haplotype frequencies of each source and aggregation were temporarily grouped, using the most actualized Nr (decade of 2000) in consideration of the criteria most commonly used in the literature (Supplementary Material 4; Supplementary Material 5). This MSA, declared as "MSA grouped" (MSAgr), was compared with the MSAoa.

![Figure 5 Aggregations (triangle) and rookeries (square) used in the MSAs of the present study](image)

Note: 1: Rio Lagartos (RL), Yucatan, Mexico; 2: Las Coloradas (ME), Yucatan, Mexico; 3: Key West National Wildlife Refuge (FKW), Florida, USA; 4: Palm Beach County (FPB), Florida, USA; 5: Bahamas (BA); 6: Jardines del Rey (JR), Cuba; 7: Turks and Caicos (TnC); 8: south of Dominican Republic (Do); 9: Jaragua National Park (DoJ), Dominican Republic; 10: Saona Island (DoS), Dominican Republic; 11: Mona Island (MI), Puerto Rico; 12: Buck Island (USVI), United States Virgin Islands; 13: Jumby Bay (ANT), Antigua; 14: Trois Ilets (GU), Guadeloupe; 15: Barbados leeward (BaL) and windward (BaW) coasts; 16: Tobago leeward (ToL) and windward (ToW) coasts; 17: Tortuguerio (CR), Costa Rica; 18: Pearl Cays (NI), Nicaragua; 19: Gales Point (BE), Belize; 20: Bloody Bay and west of Grand Cayman (CI), Cayman Islands; 21: Doce Leguas (DL), Cuba; 22: Cocodrilo (IJ), Isla de la Juventud, Cuba

Although the monthly frequency of harvested *E. imbricata* individuals in the JR fishing ground did not vary significantly between the years according to sexual and SCL classes (Lee-González et al., 2015), we found an inversion of the frequency of the haplotypes EiA01 and EiA11 for non-adult individuals between 2004 and 2005. Thus, we consider it appropriate to analyze each year as an independent non-adult fishing aggregation. As JR did not have a representative sample in 2006 for any maturation category, this year was grouped with 2004 and 2005 in the JR adult aggregation.

We could segregate all Cuban fishing aggregations from the 1990s in both maturation categories because we had access to the original data of Díaz-Fernández (1999). All individuals from the aggregations of that study having CU1 and PR1 were regarded EiA01 and EiA11 respectively. We use the original name for Cuba A (Doce Leguas) and Cuba B (Cocodrilo) fishing aggregations. For non-adult aggregations from Mona Island of the 1990s we only selected the sample of Díaz-Fernández (1999) because of its larger sample size as compared to other 1990s studies (Bowen et al., 1996; Bass, 1999) and its haplotype frequency did not present significant statistical differences. The haplotypes absent in the selected samples of JR and Mona Island aggregations but belonging to other temporal samplings were also included. The foraging aggregation of new recruits from the Mona Island platform from Velez-Zuazo et al. (2008) was excluded from the MSAs because we considered this is a very premature non-adult stage having smaller SCLs than the remaining WC non-adult foraging aggregations.

3.3.2 Rookeries

Genetic data from WC rookeries were used to calculate WC source contributions to the JR fishing ground (foraging ground-centric), or the proportions of individuals in each rookery in JR (rookery-centric).
As there was not a significant genetic structure over time for most WC rookeries (Leroux et al., 2012), the Nr in the present study is annual, and the cumulative haplotype frequencies of the rookeries can exceed the Nr biasing the true number of annual nesting females; for all MSAoa we selected the same haplotype frequencies in each rookery but these being equivalent to the corresponding value of the one year of genetic sampling, keeping the haplotype proportions of the original publications and always taking the larger annual sample (Supplementary Material 2). In addition, the haplotypes reported in other nesting seasons but absent in the chosen sample by us, were also included. Under this criterion, the haplotype frequencies of many rookeries were divided by the number of nesting seasons. Thus, the haplotype frequencies of Jumby Bay, Pearl Cays and Buck Island according to Leroux et al. (2012) were divided by two, eight and six respectively (see the number of nesting seasons in the Supplementary Material of these authors). In Tortuguero the frequencies were divided by four due to the original values came from 2000-2003 nesting seasons (Troëng et al., 2005) and the population size (Nr=10) is under the number of reported haplotypes (N=42). For both, Mexican y Barbados leeward beaches rookeries, we took the original Genetic data because they are the greater regional populations. In Doce Leguas the haplotype composition was completed with data from final report in 2004 of the project WWF-Canada: Population genetics of hawksbill Eretmochelys imbricata: new data for its conservation in Cuba and the Caribbean region.

3.3.3 Rookery sizes

Rookery sizes were generally taken from the tables for nesting sites of continental or insular Caribbean by Mortimer and Donnelly (2007) and other studies (Supplementary Material 2). In the case where Nr intervals appeared, the larger value was selected. In the Mexican source Nr was taken from Campeche data because they reflected the temporal growth of this source (Garduño-Andrade et al., 1999) and the larger Nr is maintained with respect to the other WC rookeries. The Nr1990s in Doce Leguas was selected from Moncada et al. (1999) given this was the only nesting season where 100% of the nesting beaches were sampled (1997/1998). Thus, if there were 198 nests in total, and nest number/female in Doce Leguas ranged from 1 to 5 (Moncada et al., 2010) being 3 the median value, the Nr1990s and Nr1980s were estimated in 66 nesting females/year. For this rookery Moncada et al. (2010) determined that there were 150 nests/year between 1997/1998 and 2008/2009 nesting seasons, representing the 50% of the total nesting in Doce Leguas (300 nests/year), the Nr2000s was 100 nesting females/year. The Nr1980s and Nr1990s from both Dominican rookeries were assumed higher and similar values than the Nr2000s, respectively, based on the reported decline during these two decades. Nrs were recalculated for the Barbadian rookeries assuming that: 1) according to Browne et al. (2010) the nesting on the leeward coast is 87.5% of the value informed in Beggs et al. (2007), and 2) this proportion has been temporally maintained. As the Nr1990s is not reported for Gales Point (Belize), we assumed the same value for the 1990s, and similarly the Nr1980s and Nr1990s of the Tobago rookery corresponded with the Nr2000s. The Nr1990s of Cayos Perla (Nicaragua) was the average of the other decades as well, as in Tortuguero (Costa Rica).

3.4 Contribution versus maritime distance

To determine if the contributions were affected by the distance between sources and aggregation we calculated the shortest maritime distance between these entities (SMD), and the distance from the source to the aggregation in accordance with the trajectory of passive dispersion of particles (TMD) reported in Blumenthal et al. (2009a). These distances were obtained in Google Earth version 5.1 (Google, 2009). Contribution, SMD and TMD were tested with a Pearson correlation analysis using the software Statistica version 8.0 (StatSoft, 2007).

Authors’ contributions

EPB worked in sample processing, genetic analysis, mixed stock analysis and drafted the manuscript. In fact, this study is part of the PhD thesis of EPB. ARU conceived, designed and directed the study, drafted the manuscript and took fishery data. LRG and GEL participated in genetic analysis, critical revision of manuscript and contributed to the study design. ILG actively participated taking the fishery data and conducing many statistical analysis. BP drafted the manuscript and critically analyzed the grammatical and spelling in it. All authors read and approved the final manuscript. All authors read and approved the final manuscript and do not have conflict of interest in any aspect.
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Supplementary Material 1 Mixed stock analysis of the foraging or breeding aggregations (not in Jardines del Rey) assayed in the present study.

Supplementary Material 1A Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult feeding aggregations in Rio Lagartos (striped: 384 bp) and Tobago windward coast (black: 384 bp, gray: 740 bp).

Note: Circles: MSAoa for decade of 1990, triangles: MSAoa of the decade of 2000, squares: MSAg. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; Ni: Pearl Cays, Nicaragua; BE: Gales Point, Belize.

Supplementary Material 1B Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult feeding aggregations in Key West National Wildlife Refuge (vertically striped: 384 bp, horizontally striped: 740 bp) and Palm Beach County (black: 384 bp, gray: 740 bp), Florida.

Note: Triangles and diamonds: MSAoa, squares: MSAg. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; Ni: Pearl Cays, Nicaragua; BE: Gales Point, Belize.
Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult feeding aggregations in Turks and Caicos (striped: 384 bp) and Cayman Islands (black: 384 bp, gray: 740 bp)

Note: Circles and triangles: MSAoa, squares: MSAgr. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize

Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult feeding aggregations in Bahamas (striped: 384 bp) and Dominican Republican (black: 384 bp)

Note: Circles: MSAoa, squares: MSAgr; ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize
Supplementary Material 1E Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult fishing aggregations in Doce Leguas (striped: 384 bp) and Tobago leeward coast feeding aggregation (black: 384 bp, gray: 740 bp)

Note: Circles and triangles: MSAoa, squares: MSAgr. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize

Supplementary Material 1F Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult aggregations of Buck Island (striped: 384 bp) and Cocodrilo (black: 384 bp)

Note: Circles: MSAoa, squares: MSAgr. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize
Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the non-adult feeding aggregations of Mona Island (black: 384 bp, gray: 740 bp)

Note: Circles: Díaz-Fernández (1999), triangles: platform resident individuals from Velez-Zuazo et al. (2008), squares: MS Agr. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize

Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the adult aggregations of Mona Island (black: 384 bp, gray: 740 bp)

Note: Circles: Díaz-Fernández (1999), triangles: breeding males aggregation from Velez-Zuazo et al. 2008, squares: MS Agr. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize
Supplementary Material 1: Mixed stock analysis (foraging ground-centric) results showing mean proportional contribution ±2.5–97.5% confidence intervals for the adult fishing aggregations of Doce Leguas (striped: 384 bp) and Cocodrilo (black: 384 bp). Circles: MSAoa, squares: MSAg. ME: Las Coloradas, ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize.

Supplementary Material 2: Annual haplotype frequencies of source populations (rookeries) of *E. imbricata* in the Wider Caribbean employed in the MSAs according to our approach, and rookery sizes (Nr, number of nesting females/ year) used in the present study.

| Haplotypes (bp) | Rookeries |
|-----------------|-----------|
| 384^1           | ME^{3,4}  |
| 740^2           | DL^{3,4}  |
| 741^3           | DoJ^6     |
| 742^4           | DoS^6     |
| 743^5           | MI^{1,2,3}|
| 744^6           | USVI^{1,8}|
| 745^7           | ANT^{1,4} |
| 746^8           | GU^9      |
| 747^9           | BaL^10    |
| 748^10          | BaW^10    |
| 749^11          | To^11     |
| 750^12          | CR^{4,12} |
| 751^13          | NI^4      |
| 752^14          | BE^1      |

| A | EiA01 | 33 | 1 | 3 | 1 | 3 | 16 | 2 | 41 | 1 | 24^A |
|---|-------|----|---|---|---|---|----|---|----|---|-----|
| α| EiA02 |     |   |   |   |   |    |   |    |   | 2   |
| | EiA52 |     |   |   |   |   |    |   |    |   | 1   |
| B| EiA03 | 2  | 1 | 12|    |    |    |    |    |    |     |
| F| EiA09 | 2  | 1 | 1 | 55 | 3  | 2  | 1  | 11 |    |     |
| | EiA11 | 3  | 22| 28| 27 | 1  | 9  | 9  | 7  | 7  | 11   |
| F+10| EiA84 |     |   |   |   |    |    |    |    |    | 1    |
| G| EiA12 |     |   |   |   |    |    |    |    |    | 1    |
| Y| EiA13 |     |   |   |   |    |    |    |    |    | 1    |
| H| EiA14 |     |   |   |   |    |    |    |    |    | 1    |
| I| EiA15 |     |   |   |   |    |    |    |    |    | 1    |
| L| EiA18 |     |   |   |   |    |    |    |    |    | 1    |
| | EiA47 |     |   |   |   |    |    |    |    |    | 1    |
| N| EiA20 |     |   |   |   |    |    |    |    |    | 1    |
| O| EiA21 |     |   |   |   |    |    |    |    |    | 1    |
| P| EiA22 |     |   |   |   |    |    |    |    |    | 1    |
| Q+10| EiA43 |     |   |   |   |    |    |    |    |    | 1    |

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Continued Supplementary Material 2

| Haplotypes (bp) | Rookeries | ME | DL | Doj | DoS | Mt | USV | ANT | GU | Bal | BaW | To | CR | Ni | BE |
|-----------------|-----------|----|----|-----|-----|----|-----|-----|----|-----|-----|----|----|----|----|
| 384^1 740^2     |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 3  |
| EiA28           |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 1  |
| EiA29           |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 1  |
| EiA30           |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 1  |
| EiA65           |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 1  |
| EiA72           |           |    |    |     |     |    |     |     |    |     |     |    |    |    | 1  |
| Total           | 36        | 38 | 15 | 50  | 35  | 31 | 58  | 41  | 13 | 40  | 14  | 13 | 14 |    |
| Nr1980x         | 12913      | 6614 | 6  | 46^*| 3913 | 2313 | 2913 | 4013 | 5210,18 | 810,18 | 112^* | 1413 | 2519 | 63^* |
| Nr1990x         | 58313      | 6614 | 3^*| 23^*| 9913 | 2613 | 3313 | 6613 | 9010,18 | 1310,18 | 112^* | 1212 | 43^* | 6313 |
| Nr2000x         | 74513      | 101,15 | 316 | 2316 | 247,15 | 5613 | 5213 | 8817 | 422,10,18 | 6110,18 | 11211 | 1011 | 6120 | 5615 |

Note: ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaW: Barbados windward coast; BaW: Barbados leeward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize. ^1Bass et al. (1996), ^2Abreu-Grobois et al. (2006), ^3Díaz-Fernández et al. (1999), ^4Leroux et al. (2012), ^5Project WWF-Canada ^6Population genetics of hawksbill Eretmochelys imbricata: new data for its conservation in Cuba and the Caribbean region” (2004 nesting season), ^7Carreras et al. (2013), ^8Velez-Zuazo et al. (2008), ^9Bass (1999), ^10Peter Dutton (personal communication), ^11Browne et al. (2010), ^12Cazabon-Mannette et al. (2016), ^13Tröeng et al. (2005), ^14Mortimer and Donnelly (2007), ^15Moncada et al. (1999) ^16Moncada et al. (2010), ^17Revela et al. (2012), ^18Kamel and Delcroix (2009), ^19Beggs et al. (2007), ^20Incer (1984), ^21Lagueux et al. (2003), ^A with 384 bp exist an additional haplotype A, ^Bnesting season of 1997, ^Cnesting season of 2003, ^Dassumed in this study.

Supplementary Material 3A Haplotype frequencies of the decade of 1990 of non-adult and adult (square bracket) aggregations of E. imbricata in the Wider Caribbean used in the MSAs according to our approach. For MSA of non-adult and adult aggregations were used the Nr1980x and Nr1990x, respectively (see the values in Supplementary Material 2).

| Haplotypes (bp) | Aggregations |
|-----------------|--------------|
| 384^1 740^2     |              |
| A               |              |
| EiA01           | 6 [7]        |
| EiA61           | 8 [20]       |
| EiA68           | 34 [10]      |
| BAL             | 28           |
| DoS             | 42           |
| USV             | 28           |
| Mt              | 29 [2]       |
| B               | 1 [1]        |
| C               | 1 [1]        |
| F               | 1 [1]        |
| EiA09           | 1 [1]        |
| EiA11           | 9 [1]        |
| EiA45           | 20           |
| 1 [3]           |
| 3 [2]           |
| 18 [6]          |
| 30              |
| 17              |
| 31 [5]          |
| F+10            | 1 [1]        |
| G               | 2 [1]        |
| 1 [1]           |
| 1 [1]           |
| 1 [1]           |
| N               | 1 [1]        |
| EiA02           | 1 [1]        |
| EiA12           | 2 [1]        |
| EiA13           | 2 [4]        |
| EiA14           | 1 [1]        |
| EiA15           | 1 [1]        |
| O               | 1 [1]        |
| EiA20           | 7 [3]        |
| EiA21           | 2 [6]        |
| EiA22           | 3 [2]        |
| Q+10            | 1 [1]        |
| P               | 2 [1]        |
| EiA25           | 1 [1]        |
Continued Supplementary Material 3A

| Haplotype (bp) | Aggregations |
|---------------|--------------|
| 384^1 740^2   | RL^1 JR^1 DL^3 IJ^1 BA^1 Do^1 USVI^1 MI^1 |
| Q            | EiA23 12    | 3 [1] 2 [2] |
|              | EiA41 6    | 9 6 |
|              | EiA24 1    |
|              | EiA43 5 [2] |
|              | EiA28 3    |
|              | EiA29 2 [1] 3 |
|              | EiA30 1 [2] |
|              | EiA65 5    |
|              | EiA72      |
| Total        | 18 16 [21] | 21 [22] 78 [30] | 77 87 66 87 [10] |

Note: RL: Río Lagartos, Yucatan, Mexico; JR: Jardines del Rey, Cuba; DL: Doce Leguas, Cuba; IJ: Cocodrilo, Isla de la Juventud, Cuba; BA: Bahamas; Do: south of Dominican Republic; USVI: Buck Island, United States Virgin Islands; MI: Mona Island, Puerto Rico. [#]: adult individuals, \(^1\)Bass et al. (1996), \(^2\)Abreu-Grobois et al. (2006), \(^3\)Díaz-Fernández (1999), \(^4\)Bowen et al. (2007)

Supplementary Material 3B Haplotype frequencies of the decade of 2000 of non-adult and adult (square bracket) aggregations of *E. imbricata* in the Wider Caribbean used in the MSAs according to our approach. For MSA of non-adult and adult aggregations were used the Nr\(_{1990}\) and Nr\(_{2000}\), respectively (see the values in Supplementary Material 2)

| Haplotype (bp) | Aggregations |
|---------------|--------------|
| 384^1 740^2   | JR04 JR05 JR04-06 FKW^3 FPB^4 MI^5 ToL^6 ToW^6 CI^7 TnC^8 |
| A            | EiA01 5 11 [18] 13 2 15 [5] 5 29 44 |
|              | EiA61 1 |
|              | EiA68 1 |
|              | EiA02 1 1 4 2 2 1 |
|              | EiA52 1 |
|              | EiA03 1 |
|              | EiA05 1 |
|              | EiA09 2 [2] 2 4 6 1 2 8 |
|              | EiA11 12 6 [12] 5 12 17 [29] 4 9 17 12 |
|              | EiA45 2 1 |
|              | EiA84 1 |
|              | EiA12 1 |
|              | EiA13 1 [3] |
|              | EiA14 1 |
|              | EiA15 1 |
|              | EiA18 1 |
|              | EiA47 1 |
|              | EiA20 2 1 2 [9] 1 1 |
|              | EiA21 6 [1] |
|              | EiA22 1 |
|              | EiA25 1 |
|              | EiA23 1 3 [3] 23 48 1 [1] |
|              | EiA41 3 [2] 3 12 2 |
|              | EiA24 2 [4] |
|              | EiA43 1 1 3 1 [2] 2 |
|              | EiA28 1 |
|              | EiA29 2 1 |
|              | EiA30 1 |
|              | EiA65 1 |
|              | EiA72 2 |
| Total        | 23 28 [48] 47 91 53 [55] 15 44 86 36 |

\(^{3}\) Bass et al. (1996), \(^{2}\)Abreu-Grobois et al. (2006), \(^{3}\)Díaz-Fernández (1999), \(^{4}\)Bowen et al. (2007)
Supplementary Material 4 Cumulative haplotype frequencies (384 bp) of rookeries and non-adult and adult (square brackets) aggregations of *E. imbricata* in the Wider Caribbean used in the different MSAs grouped

| Haplotypes<sup>1</sup> | Rookeries | Aggregations |
|------------------------|-----------|--------------|
|                        | ME<sup>2,3</sup> | DL<sup>2,4</sup> | Do<sup>5</sup> | Do<sup>5</sup> | MI<sup>2,6,7</sup> | USVI<sup>1,6,7</sup> | ANT<sup>1,3</sup> | GU<sup>1</sup> | Bal<sup>8</sup> BaW<sup>8</sup> To<sup>9</sup> | CR<sup>1,7</sup> Ni<sup>1</sup> | BE<sup>1</sup> | RL<sup>10</sup> FKW<sup>11</sup> FPB<sup>12</sup> BA<sup>7</sup> JR<sup>10,11</sup> | DL<sup>10</sup> | IJ<sup>10</sup> | Do<sup>7</sup> USVI<sup>7</sup> | MI<sup>2,7,14</sup> Tol<sup>5</sup> ToW<sup>9</sup> Cl<sup>15</sup> TnC<sup>16</sup> |
| A                      | 69 | 1 | 3 | 3 | 13 | 42 | 2 | 54 | 3 | 25 | 13 | 2 | 28 | 23 [25] | 8 | 20 | 34 | 10 | 42 | 28 | 53 | 7 | 5 | 29 | 44 | 12 |
| α                      | 15 | 19 | 1 | 1 | 1 [1] | 2 | 1 | 6 | 3 | 6 | 4 | 2 | 2 | 1 |
| B                      | 2 | 3 | 29 | 1 | 1 | 1 | 1 [1] | 2 | 3 | 1 | 1 | 1 |
| C                      | 2 |
| F                      | 1 | 5 | 22 | 74 | 95 | 1 | 71 | 27 | 11 | 42 | 54 | 11 | 2 | 7 | 16 | 20 | 24 | 4 [2] | 27 | 7 | 30 | 17 | 80 | 34 | 6 | 11 | 25 | 12 |
| F+10                   | 5 |
| G                      | 6 | 18 | 1 | 1 | 1 | 1 [1] | 2 | 1 |
| V                      | 6 | 1 |
| H                      | 1 |
| I                      | 1 |
| L                      | 1 | 2 | 2 | 6 | 1 [1] | 1 | 1 | 3 | 7 | 1 |
| N                      | 6 | 40 | 4 | 1 | 2 | 3 | 7 [3] | 6 | 6 [1] | 1 |
| O                      | 7 | 6 |
| P                      | 3 |
| Q+10                   | 1 |
| Q                      | 69 | 8 | 3 | 1 | 1 | 16 | 13 | 27 | 63 | 21 | 19 [11] | 2 | 5 | 4 | 6 | 9 | 16 [4] | 2 | 11 | 9 |
| CU3                    | 1 | 4 | 1 [3] | 3 | 2 | 1 |
| CU4                    | 1 | 1 | 3 [2] | 1 | 2 [1] | 5 |
| EiA28                  | 3 |
| EiA65                  | 1 |
| EiA72                  | 1 |

**Note:** ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; Bal: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; Ni: Pearl Cays, Nicaragua; BE: Gales Point, Belize. [#]: adult individuals, Bass et al. (1996), Diaz-Fernández et al. (1999), Leroux et al. (2012), Project WWF-Canada “Population genetics of hawksbill *Eretmochelys imbricata*: new data for its conservation in Cuba and the Caribbean region” (2004 nesting season), Carreras et al. (2013), Bass (1999), Bowen et al. (2007), Browne et al. (2010), Cazabon-Mannette et al. (2016), Diaz-Fernández (1999), Gorham et al. (2014), Wood et al. (2013), this study, Velez-Zuazo et al. (2008), Blumenthal et al. (2009a), Richardson et al. (2009)
Cumulative haplotype frequencies (740 bp) of rookeries and non-adult and adult (square brackets) aggregations of *E. imbricata* in the Wider Caribbean used in the different MSAs grouped

| Haplotypes | Rookeries |
|------------|-----------|
| EiA01      | ME1,2 DL1,3 DoJ4 DoS4 MI1,2 USVI1,2,5,6 ANT2,7 GL1 BaL8 BaW8 To9 CR2,6 NI2 |
| EiA02      | 2 2 1 1 1 4 2 2 |
| EiA03      | 2 1 12 |
| EiA05      | 2 |
| EiA09      | 2 1 1 55 3 2 1 2 4 [2] 6 1 2 8 |
| EiA11      | 3 22 28 27 1 9 9 7 7 5 12 21 [12] 17 [29] 4 9 17 |
| EiA84      | 1 |
| EiA12      | 1 1 |
| EiA13      | 1 2 [3] |
| EiA18      | 2 1 |
| EiA47      | 1 |
| EiA20      | 6 16 2 1 2 2 [9] 1 |
| EiA21      | 2 6 [1] |
| EiA22      | 1 |
| EiA25      | 1 |
| EiA23      | 30 4 1 23 48 4 [3] 1 [1] |
| EiA41      | 1 |
| EiA43      | 3 4 1 1 2 1 3 1 [1] 1 [2] 2 |
| EiA28      | 3 4 |
| EiA29      | 1 |
| EiA30      | 1 |
| EiA65      | 1 |
| EiA72      | 1 |
| Total      | 36 38 15 33 50 35 31 58 41 13 39 14 13 47 91 54 [44] 49 [54] 14 44 81 |

Note: ME: Las Coloradas, Yucatan, Mexico; DL: Doce Leguas, Cuba; DoJ: Jaragua National Park, Dominican Republic; DoS: Saona Island, Dominican Republic; MI: Mona Island, Puerto Rico; USVI: Buck Island, United States Virgin Islands; ANT: Jumby Bay, Antigua; GU: Trois Ilets, Guadeloupe; BaL: Barbados leeward coast; BaW: Barbados windward coast; To: Tobago; CR: Tortuguero, Costa Rica; NI: Pearl Cays, Nicaragua; BE: Gales Point, Belize. [#]: adult individuals, 1Díaz-Fernández et al. (1999), 2Leroux et al. (2012), 3Project WWF-Canada “Population genetics of hawksbill *Eretmochelys imbricata*: new data for its conservation in Cuba and the Caribbean region” (2004 nesting season), 4Carreras et al. (2013), 5Bass (1999), 6Bowen et al. (2007), 7Bass et al. (1996), 8Browne et al. (2010), 9Cazabon-Mannette et al. (2016), 10Gorham et al. (2014), 11Wood et al. (2013), 12this study, 13Velez-Zuazo et al. (2008), 14Cazabon-Mannette et al. (2016), 15Blumenthal et al. (2009a), 16platform resident juveniles and [breeding males]