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Ontogenetic habitat shifts of green turtles (Chelonia mydas) suggested by the size modality in foraging aggregations along the coasts of the western Japanese main islands

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Abstract

To understand the life histories and ontogenetic habitat utilization of green turtles along the coasts of the western Japanese main islands, we collected size frequency and genetic data of green turtles captured by pound nets in three foraging grounds (FG): Nomaike (n = 38), Muroto (n = 93), and Kumano-nada (n = 31), and compared their natal origins among different size classes. Population genetic analyses based on an 820-bp fragment of mitochondrial DNA showed that the three FG were part of a single multiple-coast FG. Although turtles from all size classes originated mainly from rookeries in the Ogasawara Group, the size distributions clearly exhibited bimodality, with low occurrences of turtles in the 50–70-cm straight carapace length (SCL) range. The bimodal size distributions could not be attributed to demographic shifts in rookeries, because the number of female green turtles in Ogasawara has exhibited an increasing trend since 1979. We also examined whether factors such as seasonality and predation risk could have caused the size bimodality. There were, however, no strong relationships between sea-surface temperatures when turtles were captured and the sizes of the turtles ($r^2 < 0.2$), and it appeared that predation risk could not result in the size modality observed in the FG. Our results strongly suggest that after switching from a pelagic to a neritic lifestyle, the green turtles in the neritic FG along the western Japanese main islands undergo another ontogenetic habitat shift upon reaching ~50-cm SCL. Here, we explore the possibility that developmental growth might stimulate a
habitat shift, resulting in habitat differentiations by size and growth phase in the long-lived green turtle.

Keywords
Size distribution, Foraging ground, Ontogenetic habitat shift, Green turtle, Developmental change

Abbreviations
FG: Foraging ground
MSA: Mixed Stock Analysis
mtDNA: Mitochondrial DNA
SCL: Straight carapace length
SST: Sea surface temperature
RMU: Regional Management Unit

1. Introduction
The green turtle (Chelonia mydas) has a circumglobal distribution and is highly migratory and long-lived. It is believed that in its typical life cycle, after hatching on beaches the green turtle spends several years in the oceanic environment in its pelagic stage before moving back into the neritic zone (neritic stage), where its major food sources, seagrass and sea algal beds, are distributed (Bolten, 2003). Although this typical life cycle suits some populations, several studies have revealed that green turtles have non-homogenous
lifestyles, and may exhibit diversity or plasticity in behavior, food resources, and timing of ontogenetic dietary and habitat shifts among populations, regions, and individuals (e.g., Burkholder et al., 2011; Cardona et al., 2009; González Carman et al., 2012; Hatase et al., 2006; Hays et al., 2002; Parker et al., 2011). This lifestyle diversity suggests that the ecologies and life histories of green turtles may vary depending on their local environments, the availability of resources, and their biological requirements.

Foraging grounds (FG), where green turtles aggregate and spend the vast majority of their life spans, are some of the most important areas for understanding their ecology, migration, and life history. Previous studies have constructed hypothetical scenarios of the foraging aggregation processes of marine turtles by using mixed-stock analysis (MSA), estimating the contributions of various source rookeries to FG based on the haplotype compositions of mitochondrial DNA (mtDNA) in rookeries and FG (reviewed by Jensen et al., 2013). Many studies have focused on the early passive recruitment to neritic FG after the pelagic stage and proposed factors that might influence foraging aggregation, such as distance from rookeries (Bass and Witzell, 2000), relative sizes of rookeries (Lahanas et al., 1998), and oceanic currents (Bass et al., 2006). Yet in some FG, immature turtles were thought to have migrated from their initial FG to suitable FG closer to their natal rookeries (Luke et al., 2004).

As suggested by several mechanisms proposed above, green turtle size distribution
data in FG have also demonstrated that the timing of habitat shifts and patterns of habitat use
are varied and complex across regions, even after the shift from a pelagic to a neritic lifestyle. For example, in Atlantic sites many green turtle FG are dominated by immature turtles, and some FG are shared seasonally with migratory adults (Meylan et al., 2011). Also, evidence from the direct tracking of the developmental migrations of large immature green turtles in the Atlantic has shown that they can actively swim among different FG (Godley et al., 2003). In contrast, the FG in Pacific sites have well mixed compositions of adult and immature turtles year-round (Balazs, 1980; Limpus et al., 2005; Sterling et al., 2013). These mixed-size compositions were believed to be a result of their long-term strong fidelity to their foraging areas based on mark and recapture studies that showed limited movement between FG (Limpus et al., 1992). One study conducted MSA in the green turtle FG of the Torres Strait, in the southwestern Pacific, however, demonstrated that the contributions of source rookeries varied between the juveniles and the adults, suggesting either developmental migration by juveniles, or demographic shifts due to reduced hatching success at source rookeries (Jensen, 2010). Moreover, at Palmyra Atoll, in the central Pacific, discrepancies between the directions of oceanic currents and the distributions of haplotype data suggested that biological processes may be important factors driving green turtle foraging aggregation (Naro-Maciel et al., 2014). These results indicate that foraging aggregations were not always governed by the passive early recruitments. Thus, detailed
investigations of the composition and dynamics of each foraging aggregation, as well as information on the source rookeries, are critical for revealing the main influences on the lifestyle, ecology, and migration of this species.

Distributions of foraging green turtles on the coasts of the Japanese main islands in the northwestern Pacific, were determined based on incidental catch by coastal net fisheries, direct observation, and coastal stranding data (Kameda and Ishihara, 2009; Kamezaki et al., 2007; Okamoto et al., 2011; Shimada, 2009). Previous studies using MSA have revealed that green turtles in foraging aggregations along the Japanese main islands originate primarily from rookeries in the Ogasawara Group, the largest nesting site in Japan (Nishizawa et al., 2014, 2013). Foraging aggregations, however, have been described without regard to population dynamics, because available data on the size compositions of foraging green turtles around the Japanese main islands were limited (e.g., Okamoto et al., 2011). Here we describe the size compositions of green turtle foraging aggregations around the western Japanese main islands, discuss how these foraging aggregations were formed, and provide new insights into foraging aggregation dynamics and the factors affecting the ontogenetic habitat shifts of green turtles.

2. Materials and methods

2.1. Descriptions of the study sites and sample collection
The Japanese main islands are all situated beyond the northern limit of the female green
turtles’ nesting sites in the North Pacific, and green turtles distributed along these coasts are
therefore considered to be aggregated for the purpose of foraging. Our data set consists of
the aggregations from three FG located in the coastal areas of the western Japanese main
islands: Nomaike FG (31°25’N, 130°08’E), Muroto FG (33°15’N, 134°11’E), and
Kumano-nada FG (34°07’N, 136°27’E) (Fig. 1A). The Nomaike FG was located on the
southwestern coast of Kyushu Island. The pound net used at Nomaike was set at a depth of
27 m in the inner bay. The Muroto FG was located on the southeastern coast of Shikoku
Island. Our samples from the Muroto FG were taken from individuals captured in three
pound nets located within an 8-km area near the tip of the Cape. These pound nets were set
at depths ranging from 35–78 m, near the edge of the narrow continental shelf. The
Kumano-nada FG was located at the west side of the Kii Peninsula, in the central part of the
Pacific coast of the Japanese main island. These pound nets were set at depths of ~60 m in
the ria coasts.

Tissue samples were collected from green turtles captured from the three FG from
2004 to 2012 (Table 1, n = 162): 38 turtles from the Nomaike FG, 93 turtles from the Muroto
FG, and 31 turtles from the Kumano-nada FG. All turtles from the Nomaike FG and 59
turtles from the Muroto FG were previously examined by Hamabata et al. (2009). Twelve
turtles previously examined by Hamabata et al. (2009) that were listed as samples from
Owase were regarded as samples from the Kumano-nada FG in this study, as Owase is a part of Kumano-nada. Two turtles from the Muroto FG and two from the Kumano-nada FG were the same individuals as used in a morphological study by Okamoto and Kamezaki (2014); these four turtles correspond to ID nos. 8–11 in Okamoto and Kamezaki (2014; Appendix 1).

Living turtles were released after the attachment of plastic tags, Inconel tags, or both, and multiple samples from the same individual were avoided. Size frequency structures were constructed based on the straight carapace length (SCL). The relationship between water temperature and the sizes of turtles aggregating in FG were examined by regression analysis.

Sea surface temperature (SST) data were used for water temperature. We obtained the SST data from the Japan Oceanographic Data Center website (http://www.jodc.go.jp/index_j.html), the Kochi Prefectural Fisheries Experiment Station (http://www.suisan.tosa.pref.kochi.lg.jp/kaikyo_inf/show), and the Mie Prefectural Fisheries Research Institute (http://www.mpstpc.pref.mie.lg.jp/SUI/kaikyo/index.htm). For size analyses, the turtles from each FG were grouped into three size classes: i) SCL < 50 cm; ii) 50 cm ≤ SCL < 70 cm; and iii) SCL ≥ 70 cm. These size groupings were arbitrarily defined, with consideration of the shapes of the size distributions.

2.2. Molecular techniques and haplotype determination

Skin or muscle samples were preserved in 99% ethanol until laboratory analysis. We
isolated DNA from skin or muscle samples by phenol/chloroform extraction or DNeasy Blood and Tissue Kits (QIAGEN). Polymerase chain reaction (PCR) was performed using the primers LCM15382 and H950 (Abreu-Grobois et al., 2006), designed to target an 820-bp fragment containing partial sequence of the tRNAPro gene and the 5’ end of the control region of the mtDNA genome. For each PCR, 1–2 μl of template DNA was used in a 12.5- or 15.0-μl reaction volume under the following conditions: hot start at 94°C for 3 min; 35–40 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 60 s; a final extension at 72°C for 3 min; and then storage at 4°C. Sequences were obtained using an ABI model 3130xl (Applied Biosystems Inc.) sequencer, with all variable positions confirmed by comparing sequences from the forward and reverse strands. Sequences were assembled using DNA BASER (Heracle Biosoft S.R.L), and aligned with Muscle in MEGA 6 (Tamura et al., 2013). We sequenced all 162 samples, because short fragments of haplotypes (500-bp) were used in the previous study by Hamabata et al. (2009). Sequences were compared to previously described haplotypes based on 380-bp, 500-bp, and >700-bp fragments of the mtDNA control region reported by Chassin-Noria et al. (2004), Cheng et al. (2008), Dethmers et al. (2006, 2010), Dutton et al. (2008), Hamabata et al. (2009, 2014), Nishizawa et al. (2010, 2011, 2013, 2014), and Norman et al. (1994). The standardized haplotype names for the Indo-Pacific region were assigned to new sequences.
2.3. Population genetic analyses

Haplotype diversity \( (h) \) and nucleotide diversity \( (\pi) \) were estimated for each FG and each size class of the FG using ALREQUIN V.3.5. (Excoffier and Lischer, 2010) based on 380-bp sequences, to compare our results with FG from previous studies. Annual variations were examined in the Muroto and Kumano-nada FG (Muroto FG: \( n = 37 \) in 2005, \( n = 9 \) in 2006, \( n = 25 \) in 2007, and \( n = 17 \) in 2008; Kumano-nada FG, \( n = 14 \) in 2004, \( n = 3 \) in 2005, \( n = 6 \) in 2008, and \( n = 8 \) in 2009). Five turtles in the Muroto FG (\( n = 1 \) in 2004, \( n = 2 \) in 2009, and \( n = 2 \) in 2011) were excluded from this analysis due to the small sample sizes for annual comparisons. Annual variations were not examined in the Nomaike FG because all samples were collected in 2004. To examine seasonal variations within the FG, turtles were grouped based on two different SST as follows: i) SST < 20°C (\( n = 15 \) in the Muroto FG, \( n = 9 \) in the Kumano-nada FG) and SST ≥ 20°C (\( n = 78 \) in the Muroto FG, \( n = 22 \) in the Kumano-nada FG), and ii) SST < 25°C (\( n = 6 \) in Nomaike FG, \( n = 56 \) in Muroto FG, \( n = 16 \) in Kumano-nada FG) and SST ≥ 25°C (\( n = 32 \) in Nomaike FG, \( n = 37 \) in Muroto FG, \( n = 15 \) in Kumano-nada FG). In the Nomaike FG, only one turtle was captured at a SST < 20°C. Therefore, the Nomaike FG was excluded from the former analysis. Annual and seasonal variations were examined by exact tests of population differentiation (Raymond and Rousset, 1995) using a Markov chain length of 500,000 steps with 10,000 dememorization steps, implemented in ARLEQUIN.
Genetic data from the three FG examined in this study were also compared by exact tests with data from four other FG around Japan: Yaeyama and Ginoza in the Ryukyus, and Kanto and Sanriku in the eastern Japanese main islands (Nishizawa et al., 2013, 2014). The comparisons were conducted using shorter sequences, truncated to ~380 bp. The p-values of the multiple comparisons were corrected using the B-Y method (Benjamini and Yekutieli, 2001).

2.4. Mixed-stock analyses

We performed MSA on pooled size group data from the Nomaike, Muroto, and Kumano-nada FG, because no significant differences were observed between the same size classes among the three FG. Following Naro-Maciel et al. (2014), potential source rookeries outside of the northwestern Pacific were classified under the following regional management units (RMU) developed by Wallace et al. (2010): Hawaii, Eastern Pacific, Western and South Central Pacific, Southwestern Pacific, Eastern Indian, and Southeast Asia. The Northwestern Pacific RMU was divided into the following four regions for a more detailed investigation: the Taiwan and Hong Kong, Yaeyama, Central Ryukyu, and Ogasawara regional groups of rookeries (Fig. 1B). Haplotype data for the above rookeries were derived from Dethmers et al. (2006), Dutton et al. (2008), Chassin-Noria et al. (2004), Cheng et al. (2008), Hamabata et al. (2014), Nishizawa et al. (2011, 2013), Ng et al. (2014),
and Naro-Maciel et al. (2014). Additional data from four female turtles nested on the northwestern Amami Oshima Island, Central Ryukyus, in 2013, were also included for analysis (all four females possessed haplotype CmP39.1). The rookery size data for the MSA were obtained from Amorocho et al. (2012), Cheng et al. (2008), Dethmers et al. (2006), Maison et al. (2010), and Hamabata et al. (2014). Following Nishizawa et al. (2013, 2014), MSA estimations were conducted in two ways using Bayesian methods: many-to-one (M2O) analysis using the program BAYES, which examines each size class of the combined FG independently (Pella and Masuda, 2001), and many-to-many (M2M) analysis using the software package R which enables the estimation of multiple FG simultaneously (Bolker et al., 2007). In the M2M analyses we included the data from four other FG around Japan: the Yaeyama, Ginoza, Kanto, and Sanriku FG (Nishizawa et al., 2013, 2014). Both methods were carried out under two priors: (1) uninformative priors assumed that each rookery had the same likelihood of contributing individuals to the foraging aggregations (M2O_1 and M2M_1), and (2) informative priors incorporated the relative size of each rookery (M2O_2 and M2M_2). For the M2O analyses, six chains, corresponding to potentially contributing sources, were run with 20,000 Markov chain Monte Carlo (MCMC) steps and a burn-in of 10,000 runs to calculate the posterior distribution. For the M2M analyses, six chains were run with 50,000 MCMC steps and a burn-in of 25,000 runs. The Gelman and Rubin shrink factor diagnostic was calculated to
test that the posterior probability distribution of all chains had converged (shrink factor < 1.2). Orphan haplotypes, defined as haplotypes observed only in the foraging grounds and not in any of the nesting rookeries, were removed from the analyses.

3. Results

3.1. Size compositions

The sizes of turtles in the Nomaike, Muroto, and Kumano-nada FG ranged from 40.6 to 96.7, 37.2 to 105.2, and 37.3 to 95.4 cm SCL, respectively. All size distributions (three individual distributions and one pooled distribution), plotted in 5-cm increments, did not exhibit bell-shaped curves, but bimodal size distributions, with peaks in the 45–49.9-cm range, and either the 70–74.9- or 75–79.9-cm range (Fig. 2). There was no strong relationship between SST and SCL ($r^2 < 0.2$, Fig. 3).

3.2. Haplotype composition, genetic diversity, and differentiation

Twenty-seven 820-bp haplotypes were identified from a total of 162 samples from green turtle FG around the Japanese main islands (Table 1). Twenty-three haplotypes matched previously reported shorter haplotypes (380- or 500-bp), and 16 matched previously identified longer haplotypes (>700-bp). Two haplotypes did not match any previously identified sequences, and were assigned standardized haplotype designations. One new
haplotype, found in the Kumano-nada FG, differed from CmP50.1 by one base pair, and was assigned the name CmP210.1 (GenBank accession no. AB896707). The other new haplotype, found in the Muroto FG, was characterized by a 10-bp insertion difference from CmP39.1, and has been assigned the name CmP208.1 (GenBank accession no. AB896708).

The Hawaiian and Eastern Pacific haplotypes (CmP4.1, CmP6.1, and CmP15.1) were observed in the Muroto and Kumano-nada FG (Table 1). Orphan haplotypes (CmP51.1, CmP79.1, CmP93.1, CmP122.1, CmP131.1, CmP208.1.1, CmP210.1.1, CmP213.1) made up 6.8% (n = 11) of the total sample population. Both the haplotype and nucleotide diversity in the Muroto FG and the haplotype diversity in the Kumano-nada FG were highest in the 50–70-cm SCL class despite the smaller sample sizes than the other size classes; however, the nucleotide diversities of the 50–70 cm SCL classes in the Nomaike and Kumano-nada FG were lower than those of the other size classes, showing no consistent pattern in diversity indices (Table 2). The diversity of the total sample population was similar to that of the Sanriku FG, and lower than the other FG in the Ryukyus and Kanto (Table 2).

Neither annual nor seasonal variations were observed in any of the FG (annual: p > 0.055, and seasonal p > 0.482). Exact tests revealed that significant population differentiation occurred between the FG in the Ryukyus (Yaeyama and Ginoza) and the Muroto and Kumano-nada FG, but no significant differences were observed among the Nomaike, Muroto, and Kumano-nada FG (Table 3). In addition, significant population
differentiations were supported between the Kumano-nada and Kanto FG by the exact tests, even after the correction for multiple comparisons (Table 3), but no significance was observed among the three FG of the present study and the Sanriku FG, which was more distant than the Kanto FG. Although a significant difference was observed between the 50–70-cm SCL class of the Muroto FG and the >70-cm SCL class of the Kumano-nada FG, the difference was absent after correction for multiple comparisons (Table 4).

3.3. Mixed-stock analyses

All estimations by MSA indicated that in the FG of the western Japanese main islands, many turtles in all size classes originated from rookeries in the Ogasawara Group, although the proportion decreased in M2M analyses, especially in M2M of the 50–70-cm SCL classes (Fig. 4). While the contributions from the Northwestern Pacific rookeries (the Taiwan, Hong Kong, Yaeyama, and central Ryukyu rookeries) were very small in the M2O analyses (the lower limits of 95% probability intervals included zero), in M2M the 95% probability intervals of these rookeries were larger (Fig. 4). The probability intervals were broader in the M2M of the 50–70-cm SCL classes (Fig. 4).

4. Discussion

4.1. Genetic structure of the foraging aggregations along the Japanese coasts
The non-differentiation of genetic compositions among the three FG examined in the present study suggests that turtles migrate among the coasts of the western Japanese main islands as if they constitute a single foraging site. This is supported by a report that one turtle tagged at the Kumano-nada FG on 3 November 2005 was recaptured at the Muroto FG eleven days later (Okamoto and Kamezaki, 2014). Our additional population genetic analyses highlighted significant differences between the Yaeyama FG and all FG along the Japanese main islands. Yet, the extent of the multiple-coast foraging site was unclear, because the significant differences did not show a clear pattern. For example, the Kumano-nada FG was not significantly differentiated from the Sanriku FG, but was significantly differentiated from the closer Kanto FG. These results suggested that the boundaries among the FG were complex or that more samples are needed to reveal the boundaries conclusively.

4.2. Size compositions in the FG and population trends in the natal region

The range of SCL in the present study indicated that green turtles in various growing stages aggregate around the Japanese main islands. The mixed-size compositions of all three FG in the present study were consistent with size ranges from other FG in the Pacific. The smallest turtles in the three FG were ~40 cm SCL. This size is similar to that at which pelagic juveniles in the Pacific appear to switch to a neritic lifestyle (e.g., Balazs, 1980; Limpus et
The size distributions of the three FG, however, clearly demonstrated a characteristic bimodality with a low frequency of turtles of 50–70 cm SCL, similar to reports from FG in Shoalwater Bay in eastern Australia (Limpus et al., 2005), and in eastern Taiwan (Cheng and Chen, 1997). Bresette et al. (2010) also reported a bimodal size distribution of pooled green turtles from Mooney Harbor and the eastern Quicksands, west of Key West, Florida, USA, although the bimodality was not noted in their study. Interestingly, the peak sizes of the present size distributions were consistent among all three FG. Some FG in the Atlantic are seasonally shared by immature and adult green turtles, and their size compositions could change temporarily to be similar to a bimodal distribution (Meylan et al., 2011). The bimodality of the present study, however, was not a result of seasonal sharing among turtles in different life stages, as both smaller and larger turtles were captured in various sea surface temperatures.

One of the most important factors affecting the population demographics was the number of births in the rookeries. The estimations by MSA indicated that in the three FG of the present study, the main natal origin of turtles of all size groups was the Ogasawara Group, although some turtles from the central Ryukyu and Yaeyama rookeries were also observed in the FG. Therefore, variations in the numbers of births in Japan, especially Ogasawara, the largest nesting site in Japan and the predominant source for the present FG, would substantially affect the demographics of these foraging aggregations. The number of
nests in the Ogasawara Group has been monitored since 1979 and demonstrated an increasing trend up to 2005 (Chaloupka et al., 2008; Yamaguchi et al., 2005). The precise age to reach ~50 cm SCL has not been estimated for wild green turtles born in the Ogasawara Group; however, based on estimates from other Pacific regions that females reach sexual maturity at around 20–40 years (Zug et al., 2002), an increasing number of nests over the past 25 years would not result in such SCL bimodality. In addition, although mortality during the pelagic life stage or in the FG could influence the size compositions of foraging aggregations, in the past decades no specific factors that could have increased the mortality of green turtles in the pelagic stage or in the FG are known. Therefore, there is no reason to believe that the bimodal size compositions of the three FG reflects skewed population demographics in which green turtles of 50–70 cm SCL were less abundant in the wild. Presumably, the size modality is attributable to location shifts by turtles of ~50-cm SCL into habitats that were not sampled, as indicated by data from the Shoalwater Bay, where over 18 years of sampling adults were captured at a higher frequency than late-stage juveniles (Limpus et al., 2005).

4.3. Possible factors contributing to the bimodal size distributions

What factors could cause green turtles to choose their habitat locations according to their sizes? In several FG, green turtles were known to demonstrate size-partitioning of habitats
as a result juveniles inhabiting shallower waters, and larger turtles inhabiting deeper water
(Balazs, 1980; Bresette et al., 2010; Koch et al., 2007; Limpus et al., 2005; López-Mendilaharsu et al., 2005). Such size-partitioning of habitats has been explained by
the minimization of predation risk. Yet, all pound nets in our study sites were set at depths
deep enough (> 27 m) for large predators such as sharks to approach turtles of all sizes. Thus,
the differences in predation risk among sizes probably did not cause the bimodality.

We speculate that a developmental change, which commonly occurs in green
turtles, could have stimulated habitat shifts in some FG based on the evidence that low
occurrences of turtles in the 50–70-cm SCL range were common in all of the FG exhibiting
bimodal size distributions. The size range of 50–70 cm SCL corresponds to an accelerated
somatic growth phase that occurs before the sub-adult stage (Chaloupka et al., 2004). The
requirement for food resources at this stage is probably increased compared to younger
stages, resulting in increased competition within the habitat. Meylan et al. (2011) surmised
that in the Atlantic, FG dominated by immature turtles formed because immature green
turtles were avoiding intraspecific competition with adults, as green turtles showed
density-dependent growth, indicating that intraspecific competition can limit the growth
rate (Bjorndal et al., 2000). Similarly, in some FG, the developmental change that is
characteristically observed in green turtles upon reaching ~50-cm SCL may drive them to
depart to other FG, where they can maintain their growth rate by avoiding intraspecific
competition with turtles of other size classes. The possibility of habitat shifts corresponding to developmental growth has been reported in Kemp’s ridley turtles, *Lepidochelys kempii* (Schmid et al. 2003). At present, there is no evidence to support this hypothesis or data showing conditional differences, such as higher intraspecific competition in the three FG from the present study than in other FG with unimodal size distributions. Future studies examining to which location the 50–70-cm SCL turtles move and evaluating differences in the growth rates between unimodal and bimodal FG are needed to verify size-specific habitat preferences and ontogenetic habitat shifts. Nevertheless, our results strongly suggest that developmental growth in green turtles can cause shifts in habitat selection. It is likely that the green turtle foraging aggregations along the coasts of the western Japanese main islands are not maintained by long-term residents, but by periodic and continually dynamic populations resulting from ontogenetic habitat shifts.

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Table 1. Frequencies of 820-bp mtDNA haplotypes for each size class in the FG. The size classes are denoted as follows: i, SCL < 50 cm; ii, 50 cm ≤ SCL < 70 cm; and iii, SCL ≥ 70 cm.

<table>
<thead>
<tr>
<th>Haplotype name</th>
<th>Nomaike FG</th>
<th>Muroto FG</th>
<th>Kumano-nada FG</th>
<th>GenBank Accession no.</th>
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<td>i  ii  iii</td>
<td>i  ii  iii</td>
<td></td>
</tr>
<tr>
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<td>1</td>
<td></td>
<td>KC306666</td>
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<td><strong>Total</strong></td>
<td>6 9 23 32 9 52 13 6 12</td>
<td>69</td>
<td>23</td>
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Table 2. Haplotype (h) and nucleotide (π) diversities of green turtles in FG along the Japanese coasts. Values were calculated for both the total samples from each FG and the three size groups from each FG and regional FG based on 380-bp haplotypes. Data for the Yaeyama, Ginoza, and Kanto FG were from Nishizawa et al. (2013), and data for the Sanriku FG were from Nishizawa et al. (2014).

<table>
<thead>
<tr>
<th>Foraging ground</th>
<th>N</th>
<th>h (±SE)</th>
<th>π (±SE)</th>
</tr>
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<tbody>
<tr>
<td><strong>Nomaike</strong></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>total</td>
<td>38</td>
<td>0.6913 ± 0.0823</td>
<td>0.02363 ± 0.01236</td>
</tr>
<tr>
<td>&lt; 50 cm</td>
<td>6</td>
<td>0.8000 ± 0.1721</td>
<td>0.02721 ± 0.01672</td>
</tr>
<tr>
<td>50–70 cm</td>
<td>9</td>
<td>0.5833 ± 0.1833</td>
<td>0.01073 ± 0.00668</td>
</tr>
<tr>
<td>&gt; 70 cm</td>
<td>23</td>
<td>0.7273 ± 0.0971</td>
<td>0.02717 ± 0.01434</td>
</tr>
<tr>
<td><strong>Muroto</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>total</td>
<td>93</td>
<td>0.6746 ± 0.0477</td>
<td>0.02320 ± 0.01193</td>
</tr>
<tr>
<td>&lt; 50 cm</td>
<td>32</td>
<td>0.6351 ± 0.0915</td>
<td>0.02106 ± 0.01116</td>
</tr>
<tr>
<td>50–70 cm</td>
<td>9</td>
<td>0.7500 ± 0.1121</td>
<td>0.03248 ± 0.01838</td>
</tr>
<tr>
<td>&gt; 70 cm</td>
<td>52</td>
<td>0.6825 ± 0.0642</td>
<td>0.02189 ± 0.01140</td>
</tr>
<tr>
<td><strong>Kumano-nada</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>total</td>
<td>31</td>
<td>0.6946 ± 0.0888</td>
<td>0.02450 ± 0.01284</td>
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<tr>
<td>&lt; 50 cm</td>
<td>13</td>
<td>0.6923 ± 0.1187</td>
<td>0.02747 ± 0.01505</td>
</tr>
<tr>
<td>50–70 cm</td>
<td>6</td>
<td>0.8000 ± 0.1721</td>
<td>0.01839 ± 0.01160</td>
</tr>
<tr>
<td>&gt; 70 cm</td>
<td>12</td>
<td>0.6818 ± 0.1482</td>
<td>0.02722 ± 0.01504</td>
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<tr>
<td><strong>Combined</strong></td>
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<tr>
<td>total</td>
<td>162</td>
<td>0.6785 ± 0.0385</td>
<td>0.02324 ± 0.01189</td>
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<tr>
<td>&lt; 50 cm</td>
<td>51</td>
<td>0.6525 ± 0.0691</td>
<td>0.02257 ± 0.01175</td>
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<tr>
<td>50–70 cm</td>
<td>24</td>
<td>0.7391 ± 0.0891</td>
<td>0.02391 ± 0.01268</td>
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<tr>
<td>&gt; 70 cm</td>
<td>87</td>
<td>0.6855 ± 0.0528</td>
<td>0.02352 ± 0.01209</td>
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<tr>
<td>Yaeyama</td>
<td>-</td>
<td>142</td>
<td>0.8355 ± 0.0215</td>
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<tr>
<td>Ginoza</td>
<td>-</td>
<td>20</td>
<td>0.8789 ± 0.0432</td>
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<td>Kanto</td>
<td>-</td>
<td>47</td>
<td>0.7438 ± 0.0448</td>
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<tr>
<td>Sanriku</td>
<td>-</td>
<td>39</td>
<td>0.6478 ± 0.0745</td>
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</table>
Table 3. P-values from exact tests based on the 380-bp haplotypes identified in FGs around Japan. Data for the Yaeyama, Ginoza, and Kanto FGs were from Nishizawa et al. (2013), and data for the Sanriku FG were from Nishizawa et al. (2014).

<table>
<thead>
<tr>
<th></th>
<th>Yaeyama</th>
<th>Ginoza</th>
<th>Nomaike</th>
<th>Muroto</th>
<th>Kumano-nada</th>
<th>Kanto</th>
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</thead>
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<tr>
<td>Ginoza</td>
<td>0.3725</td>
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<td></td>
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<tr>
<td>Nomaike</td>
<td>&lt; 0.001**</td>
<td>0.0469*</td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>Muroto</td>
<td>&lt; 0.001**</td>
<td>0.0110**</td>
<td>0.2683</td>
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<tr>
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<td>0.0063**</td>
<td>0.3074</td>
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<tr>
<td>Kanto</td>
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<td>0.1433</td>
<td>0.0166*</td>
<td>0.1981</td>
<td>0.0090**</td>
<td>0.0547</td>
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<tr>
<td>Sanriku</td>
<td>&lt; 0.001**</td>
<td>0.0059**</td>
<td>0.0869</td>
<td>0.3910</td>
<td>0.1623</td>
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*P < 0.05, **P < 0.0137 in B-Y method for 21 simultaneous tests
Table 4. P-values from exact tests of comparisons of FG size classes based on the 380-bp haplotypes.

<table>
<thead>
<tr>
<th>Size class</th>
<th>Nomaike FG</th>
<th>Muroto FG</th>
<th>Kumano-nada FG</th>
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<tr>
<td></td>
<td>&lt; 50 cm</td>
<td>50–70 cm</td>
<td>&gt; 70 cm</td>
</tr>
<tr>
<td>Nomaike</td>
<td>0.474</td>
<td>0.716</td>
<td>0.702</td>
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<tr>
<td>Muroto</td>
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<tr>
<td>Kumano-nada</td>
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</tbody>
</table>

Significant differences were absent after correction for multiple comparisons (P < 0.01198 in B-Y method for 36 simultaneous tests).

*P < 0.05
**Figure Legends**

**Fig. 1.** Locations of the FG (A), and rookeries (black dots) and regional groups of rookeries (dashed circles) used in this study (B). Stars indicate the FG analyzed in this study. Circles indicate the referenced Sanriku, Kanto, Ginoza, and Yaeyama FG. Rookery location data were from Chassin-Noria et al. (2004), Dethmers et al. (2006), Cheng et al. (2008), Dutton et al. (2008), Naro-Maciel et al. (2014), Nishizawa et al. (2011 and 2013), and Hamabata et al. (2014).

**Fig. 2.** Size frequency distributions of straight carapace lengths (SCL) in the FG: Nomaike (A, n = 38), Muroto (B, n = 93), Kumano-nada (C, n = 31), and the combined data of the three FG (D, n = 162). The minimum sizes considered to be adults in male and female of the Ogasawara Group are 79.4 and 82.1 cm SCL, respectively (Tachikawa, 1991).

**Fig. 3.** Sea surface temperatures (SST) and sizes (SCL) of green turtles captured at each FG: Nomaike (A), Muroto (B), and Kumano-nada (C). Each point represents an individual.

**Fig. 4.** Estimated mixed-stock analysis (MSA) of green turtle foraging aggregations along the coasts of the western Japanese main islands. Circles and triangles represent M2O and M2M analyses, respectively. Bars indicate 95% probability intervals. Uninformative prior
estimations (M2O₁, M2M₁) are indicated in black, and informative prior estimations (M2O₂, M2M₂) are indicated in white. Abbreviations of location and RMU are as follows: HK = Hong Kong, SW Pacific = Southwestern Pacific, W & SC Pacific = Western and South Central Pacific, and SE Asia = Southeast Asia. Size classes are as follows: A, SCL < 50 cm; B, 50 cm ≤ SCL < 70; C, SCL ≥ 70 cm.
Fig. 1. A Self-archived copy in Kyoto University Research Information Repository https://repository.kulib.kyoto-u.ac.jp
Fig. 2

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Kyoto University Research Information Repository
https://repository.kulib.kyoto-u.ac.jp