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Refining Marine Turtle Conservation: Introducing Marine Turtle Management Areas (MATMAs) as a Spatial Conservation Tool

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ABSTRACT

English Language Abstract: Marine turtle regional management units (RMUs) are region-wide population boundaries delineating marine turtle subpopulations. Analyses within RMUs can provide insights into their knowledge gaps and conservation status for those regions. However, their large spatial extent limits their effectiveness for localized conservation planning. This study introduces Marine Turtle Management Areas (MATMAs), a smaller, spatially defined conservation unit aimed at refining RMUs to improve conservation management in Southeast Asia into manageable units to make local and regional management more effective. To define meaningful MATMAs, we collated published and unpublished datasets on marine turtle movements, including satellite tracking, photo identification records and flipper tag recoveries. Nesting groups were also categorized and analyzed using a minimum convex polygon bootstrapping method to create MATMAs. Six green turtle MATMAs were identified for the Andaman Sea, Java Sea, Raja Ampat, South China Sea, northern Borneo/Kalimantan and the Sulu and Sulawesi Sea, while two hawksbill MATMAs were identified in the Melaka Straits and the Sulu Sea. We acknowledge that data availability influenced MATMA delineation, leading to potential gaps in the coverage for both turtle species in Southeast Asia. However, as a proof of concept, this study demonstrates that MATMAs offer a higher-resolution approach to marine turtle conservation, contextualizing jurisdictional boundaries and enhancing localized to seascape conservation strategies. MATMAs provide a valuable framework for conservation managers, informing targeted decision-making for immediate action.

Indonesian Language Abstract: *Regional Management Units (RMUs)* penyu laut merupakan batas populasi yang mendelineasi subpopulasi penyu laut dalam skala regional. Analisis-analisis dalam RMU dapat memberikan gambaran tentang kesenjangan pengetahuan dan status konservasinya di region tersebut. Meskipun demikian, besarnya cakupan spasial RMU membatasi efektivitas RMU dalam perencanaan pengelolaan konservasi pada skala lokal. Studi ini memperkenalkan konsep *Marine Turtle Management Areas (MATMAs)*, yaitu unit konservasi dengan cakupan spasial tertentu. Tujuannya adalah untuk meningkatkan pengelolaan konservasi di Asia Tenggara dengan cara membagi RMU menjadi unit—unit yang lebih kecil untuk meningkatkan efektivitas pengelolaan di tingkat lokal maupun regional. Dalam rangka mendefinisikan MATMA, kami mengumpulkan data tentang pergerakan penyu laut, baik yang sudah maupun belum dipublikasikan, termasuk pergerakan melalui pelacakan satelit, catatan-catatan identifikasi foto, dan penemuan-penemuan tag yang dipasang pada sirip penyu. Kami juga mengkategorikan dan menganalisis kelompok-kelompok peneluran dengan menggunakan metode minimum convex polygon bootstrapping untuk membuat MATMA. Kami berhasil mengidentifikasi enam MATMA untuk penyu hijau, yaitu di Laut Andaman, Laut Jawa,

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Raja Ampat, Laut Cina Selatan, sisi utara Kalimantan, serta Laut Sulu—Sulawesi. Selain itu, dua *MATMA* teridentifikasi untuk penyu sisik, yaitu di Selat Malaka dan Laut Sulu. Kami menyadari bahwa delineasi *MATMA* dalam studi ini dibatasi oleh ketersediaan data, sehingga ada kemungkinan bahwa *MATMA* yang kami hasilkan tidak mencakup semua lokasi penyu hijau dan penyu sisik di Asia Tenggara. Namun, sebagai konsep awal, studi ini menunjukkan bahwa *MATMA* menawarkan pendekatan resolusi yang lebih tinggi untuk konservasi penyu laut dengan mempertimbangkan batas-batas yurisdiksi serta memperkuat strategi konservasi dari skala lokal hingga bentang laut (*seascape*). *MATMA* menawarkan sebuah kerangka kerja yang penting bagi para pengelola konservasi melalui pengambilan keputusan yang lebih terarah dan tepat-sasaran secara cepat.

1 | Introduction

All but one species of marine turtles are listed on the International Union for Conservation of Nature (IUCN) Red List of Threatened Species (International Union for Conservation of Nature 2025), with most of them of global conservation concern. Positively, conservation efforts in many regions of the world have enabled populations of certain species to recover or begin to recover (Hays et al. 2025). For example, green turtle populations have globally been downgraded from endangered to least concern (Wallace and Broderick 2025). Many subpopulations around the world have demonstrated reduced human threats and are at reduced risk of population decline (Wallace et al. 2025). Initiatives such as altering fisheries practices or establishing marine protected areas are among the conservation efforts, which have paved the way for these conservation successes. Nonetheless, all marine turtle species continue to face several significant human threats across their range and are conservation dependent (Wallace et al. 2025).

One management response to threats requires demarcating or identifying areas for conservation (Naughton-Treves et al. 2005; Sullivan-Stack et al. 2024). Referred to as area-based conservation, this strategy has been used to minimize threats to marine turtles and has been developed at different scales. For example, regional management units (RMUs; Wallace et al. 2010, 2023) are global boundaries, which were developed for marine turtles to categorize populations into regions, below the species level but above the level of genetic stocks (Figure 1). These boundaries include overlapping life history stages from neighbouring genetic stocks (Wallace et al. 2023), thus spatially grouping these genetic stocks into subpopulations and regions. Beneath RMUs, management units are groups of nesting sites that can geographically identify genetic stocks, which can be used to develop management decisions for these distinct breeding stocks (Moritz et al. 2002). In Southeast Asia, three have been identified for green turtles across two different studies and which have stayed within national boundaries (Moritz et al. 2002; Nishizawa et al. 2016). Another area-based tool, which has recently been developed, is Important Marine Turtle Areas (IMTAs), which represent biologically and/or culturally significant areas for turtles (Bandimere et al. 2021). These can occur at national or transnational scales and at a much smaller scale than RMUs. IMTAs are an administrative response to RMUs used to highlight areas within the RMU that are important for the conservation of marine turtles. Unlike RMUs, which delineate population boundaries for each species across life history stages and genetic stocks, IMTAs are local-scale boundaries of biological or cultural significance and may not inherently reflect connectivity or genetic structure. While the IMTA framework

was recently developed, previous studies have identified seascape areas, which are important for marine turtle conservation, such as aggregations or nesting beaches (Pilcher et al. 2014; Pilcher 2021). However, identifying IMTAs based on the guidelines has not been developed yet. IMTAs can also be disconnected from broader conservation frameworks, which can make their integration into regional conservation policies challenging.

A critical gap exists between the RMU, management unit, and IMTA frameworks. RMUs are subpopulation boundaries of a species where several rookeries share the same seascape for overlapping life history stages; management units are geographic boundaries surrounding breeding and genetic stocks; and IMTAs are biologically and culturally important boundaries for turtles and the communities surrounding them. The drawback to these frameworks is their geographic scale; RMUs have large boundaries, which encompass coarse-resolution regions and can be akin to functional networks outlined by Poiani et al. (2000). Large boundaries such as these complicate pinpointing areas where smaller-scale conservation management is needed (Wallace et al. 2010, 2023). Management units, while identifying distinct breeding stocks, can be impacted if alleles have a large geographic distribution, which can result in very large confidence intervals that may overestimate geographic distributions (Moritz et al. 2002). IMTAs are more helpful in local or functional sites (Poiani et al. 2000), such as foraging grounds or rookeries within a nation's boundary, but using them to identify cross-jurisdiction networks or genetic stock-specific needs within which IMTAs lie (Poiani et al. 2000) is beyond the scale of IMTAs. An intermediate step between RMUs and IMTAs could help with local, regional, or transboundary management, particularly for genetic stocks in biodiverse RMUs where human threats are diverse in nature. This can facilitate linking specific threats to specific genetic stocks.

Southeast Asia is considered the centre of tropical biodiversity (Sodhi et al. 2004) and supports the nesting and foraging of six marine turtle species (Shanker and Pilcher 2003). Marine biodiversity in Southeast Asia faces substantial human threats, and marine turtles are no exception (Shanker and Pilcher 2003; Chan 2006). These threats include fisheries bycatch (Chan et al. 1988; Gautama et al. 2022), coastal development (Lai et al. 2015) leading to the loss of nesting and foraging habitat, pollution, and poaching (Senko et al. 2022) for tortoiseshell trade (Kirishnamoorthie et al. 2023) and meat (Joseph et al. 2019). In recent years, conservation efforts have been established within the region (Wallace et al. 2025), which have resulted in several populations stabilizing (Chaloupka 2001; Chan 2001, 2006, 2013). Considerable research has also been completed over the past few decades to identify distinct genetic stocks of green and hawksbill turtles (FitzSimmons and Limpus 2014;

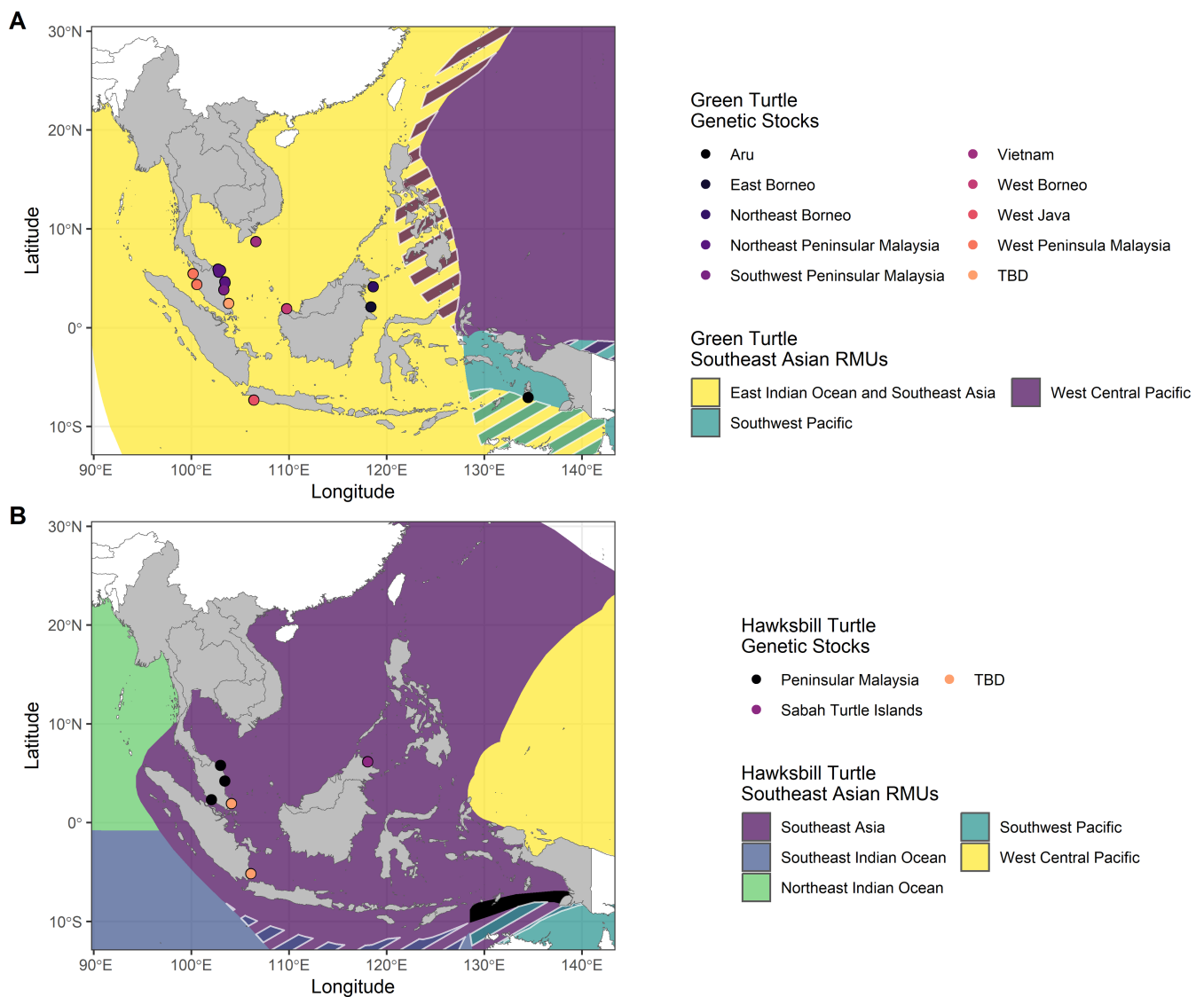


FIGURE 1 | The study region of Southeast Asia, with Southeast Asian countries shown in grey. Green turtle (A) and hawksbill (B) regional management units (coloured polygons) and genetic stocks (coloured points) are also displayed. Multicoloured spaces indicate areas where two RMUs overlap, whereas black polygon displayed in the hawksbill turtle RMU map indicates overlaps between the Southeast Asian, Southeast Indian Ocean and Southwest Pacific RMUs. RMU polygons are derived from Wallace et al. (2023).

Nishizawa et al. 2016, 2018) and advocate for their use in setting priorities for conservation. However, they generally represent aggregations of nesting sites and are made complex by mixed-stock foraging areas. The RMU and IMTA frameworks can be a boon to turtle conservation in the region as spatially explicit seascape areas can be identified for conservation. However, a spatial framework for management at a scale, which is smaller than RMUs but larger than IMTAs can be beneficial in identifying functional seascapes.

This study introduces Marine Turtle Management Areas (MATMAs), a spatial conservation framework that refines RMUs into smaller, biologically relevant management areas. Using published and unpublished location data (flipper tagging, photographic identification and satellite tracking) from Southeast Asian collaborators, we developed MATMAs using biologically important information to identify discrete management boundaries within RMUs. Dividing RMUs into biologically meaningful and smaller spatial areas that encapsulate

nesting-foraging networks can be beneficial to nesting sites or a set of nesting sites that may be linked to several distant foraging areas. Furthermore, because these are smaller geographical regions, they are more meaningful for conservation managers as they can quickly identify (1) what MATMAs are relevant to the national, regional or local interests, (2) if conservation action needs to be taken for their area and (3) what genetic stocks apply to different national jurisdictions based on MATMA's transnational nature. This intermediate-scale framework can also inform regional (e.g., the Coral Triangle Initiative) or national/local (marine protected areas) plans as it quickly identifies, which regions may have overlapping objectives. The overall objective of this study was to develop MATMAs for green and hawksbill turtles in Southeast Asia and to determine (i) how are MATMAs for green and hawksbills distributed across Southeast Asia and (ii) how does the availability of data impact the configuration and distribution of MATMAs within the region.

2 | Methods

2.1 | Study Area

Southeast Asia is a tropical geographic region of the world that sits between the Pacific and Indian Oceans spanning 88 ° E to 152 ° E and 12 ° S to 31 ° N. Countries defined to be Southeast Asia are part of the Association of Southeast Asian Nations: Myanmar, Cambodia, Laos, Vietnam, Thailand, Malaysia, Singapore, Indonesia, Brunei, the Philippines, and Timor Leste. Except for Laos, all ASEAN countries have coastal marine boundaries. Maritime Southeast Asia has more than 24,000 islands (Zhang et al. 2021) and is one of the world's most biologically diverse marine environments (Sodhi et al. 2004, 2010).

2.2 | Study Species

The study focused on green turtles, *Chelonia mydas*, and hawksbill turtles, *Eretmochelys imbricata*, due to their research and conservation interest in Southeast Asia. Green turtles are the most abundant species within the region (Chan 2006, 2013; Nishizawa et al. 2018) and one of the most well-studied in the world (Robinson et al. 2023). Several genetic stocks are found within the region (Nishizawa et al. 2018), with populations in the West Pacific RMU showing stable or increasing population trends (Chaloupka 2001; Chan 2001, 2006, 2013). However, threats to green turtles still persist throughout Southeast Asia (Shanker and Pilcher 2003; Chan 2006, 2013; Teh et al. 2018; Joseph et al. 2019; Liu et al. 2021).

Hawksbill turtles are critically endangered and have suffered sharp declines due to historical and ongoing poaching for the tortoiseshell trade (Miller et al. 2019; Senko et al. 2022; Kirishnamoorthi et al. 2023). Their increasing rarity within the region has resulted in the species being of conservation interest (Hamann et al. 2022). Studies in Southeast Asia have highlighted the lack of data to properly assess the state of hawksbill populations, both with regard to nesting numbers and genetic stocks (Nishizawa et al. 2016; Hamann et al. 2022). The combination of declining populations, continued threats faced by hawksbills, and data deficiency to substantiate the species' status within the region have contributed to their high conservation priority (Wallace et al. 2011, 2025).

2.3 | Data Collection and Processing

A desktop review of the peer-reviewed and grey literature (herein *literature*) was conducted to compile data on marine turtle movements (Supporting Information S1). Data sources included reports from transboundary or regional organizations, conference proceedings, or data provided from websites such as seaturtle.org. Literature was considered relevant if it contained information on linkages between nesting beaches and foraging sites within Southeast Asia. Such information could be (1) flipper tagging studies where females that were tagged at nesting beaches and were later recovered elsewhere in Southeast Asia, Australasia, or East Asia; (2) photographic identification of individual nesting turtles (herein *photo ID*);

and (3) satellite tracking data of nesting females returning to their foraging grounds.

Databases used for the desktop review were Web of Science, ProQuest, Scopus and Google Scholar. The search terms used for flipper tagging, photo ID or satellite tracking only differed in the final search term; flipper tagging used (*flipper tag OR flipper tagging*), satellite tracking used (*satellite tracking OR satellite track OR satellite telemetry*) and photo ID used (*photographic ID OR photo ID OR photographic identification OR photo identification*). The main search terms, which were the same for all methods, were (*green turtle OR hawksbill turtle*) AND (*Southeast Asia OR Myanmar OR Cambodia OR Vietnam OR Thailand OR Malaysia OR Singapore OR Indonesia OR Brunei OR Philippines OR Timor Leste*). Documents were limited to reports, review articles, research articles, and theses, with literature published up to 2023.

Unpublished data were also a key source of data for this study. Collaborator networks of researchers, conservationists, and government agencies provided substantial amounts of unpublished data. When precise coordinates for data points were unavailable for published or unpublished data, estimates based on beaches, towns, provinces or countries were used to an accuracy of 10 km. Where maps displaying satellite tracks were available but the actual tracking data were not, the tracks were georeferenced, digitized, and converted to points.

Details of each data point were collected and managed in a spreadsheet. Within the spreadsheet, a single marine turtle had two records: the first record indicated the *start*, which was where the satellite, flipper tag or photo ID sighting were deployed on the turtle or at the nesting beach; the second record indicated the *end*, which was where the transmission ended, where the flipper tag was recovered or where the photo ID of the same turtle was taken at a foraging site. Satellite tracking or KML/KMZ files would have data in between the start and the end, but as the start and end points were only needed for this study, all intermediate geolocations were removed. Hence, MATMAs were developed using the start and end points of satellite tracks, photo ID records and flipper tag recoveries.

2.4 | Developing MATMAs

To ensure MATMAs were biologically meaningful spatial areas that encapsulate nesting-foraging networks, all available tracking data were used. Given that some turtles from a nesting site could travel to foraging areas much further away than other turtles, it was important to ensure that a generated MATMA would represent an averaged home range rather than a range extent. Thus, a bootstrapping and averaging method was developed where satellite tracking points were resampled to create multiple minimum convex polygons (MCPs), which were then averaged. In early animal tracking studies, MCPs were used to determine the range extent for animals by creating bounding polygons that enveloped all (Mohr 1947) or a user-specified proportion of points (Worton 1987) in the smallest area possible. As MCPs were created around sighting or tracking points and are intended to capture the full range extent of an animal, population, or species, they tend to overestimate the area of use

(Burgman and Fox 2003; Laver and Kelly 2008). Quantitatively, an area such as a MATMA would represent an averaged boundary that would be smaller than the full range extent of an animal. Such a boundary can be developed by creating MCPs around bootstrapped points of the original data set at various proportions (Supporting Information S2).

Points were resampled 1000 times using a bootstrapping approach, generating multiple MCPs that were subsequently averaged to account for variation in movement patterns. 1000 iterations was chosen arbitrarily to obtain a stabilized averaged MCP, although 250–500 resamples appeared to be suitable enough to reach a stabilized and averaged MCP (more details in Supporting Information S2). Bootstrapping is a resampling method where limited data sets are treated as a population; the data set is sampled multiple times with or without replacement (resampled) to develop an estimate of population statistics (Efron 1979). This bootstrapping method has been shown to develop means, distributions (Efron 1979), and measures of accuracy (Efron and Tibshirani 1986; DiCiccio and Efron 1996) which are precise and more accurately reflect the mean and distribution of a population. Bootstrapping has been used in ecology and evolution as a superior method to estimate population statistics (Maitner et al. 2023), even when variances within samples are unequal (Johnston and Faulkner 2021). In spatial ecology, it has been used to develop accurate predictive spatial models (Valavi et al. 2022). Here, we provide an overview of how MATMAs were made, but technical details can be found in Supporting Information S2.

Data for each species were divided into *nesting groups*. These groups were based on marine turtles that nest in a specific nesting site and forage at different sites. For example, turtles, which nested on Turtle Islands in Sabah, Malaysia, and migrated to foraging sites in Indonesia or the Philippines were considered a single nesting group regardless of where they migrated. These nesting groups were further filtered to ensure there were at least 10 records within each data set as the MCP algorithm required a minimum of 5 points (Calenge 2006). This was important as the bootstrapping method we employed in this study used a random sample of 50% of the original data as one of the proportions; as the MCP algorithm required a minimum of 5 points to be used to generate an MCP, this means that nesting groups must have at least 10 records (more details in next paragraph). The end of the satellite track was assumed to be a foraging site if the satellite track ended in aggregations of shorter time-steps with more acute angles rather than longer time-steps with fewer turns (Dorfman et al. 2022).

To develop boundaries representing an average range (and hence a MATMA), we developed a bootstrapping method using random subsets of data from each nesting group to create multiple MCPs, which were then averaged. Subsets of nesting group data were taken in 10% increments from 50% to 90%; for example, 50% of the data from nesting group 1 was randomly sampled without replacement and used to develop the first MCP. The MCP utilized the IUCN definition of extent of occurrence, which was the minimum continuous boundary that encompasses all points within each subset (International Union for Conservation of Nature 2018). This was repeated for this nesting group at that subset (50%) 1000 times and then again for all increments (60%,

70%, 80% and 90%). All MCPs were converted to rasters with a cell value of one within the MCP and zero outside of it. These binary rasters were then overlaid and summed at each cell to produce a single raster layer where cells contained a value between 0 and 1000; cells with values of 1000 indicated spaces where all MCPs overlapped, while cells with 0 were spaces where no MCPs were found. This layer was normalized by dividing each cell number by 1000; normalized raster cells contained values between 0 and 1, where zero had no MCP and one was where all MCPs overlapped. We chose cells of values greater than or equal to 0.5 to be converted into polygons, which represented the final MATMA. The threshold of 0.5 was chosen as this would represent the median extent of areas used by the nesting group. In other words, a median extent included MCPs created using most foraging, nesting, and migration points available but excluding MCPs created from outlier points.

The final normalized polygons were merged with other normalized polygons if there was an overlap of 70% between them. The 70% overlap was chosen as the threshold to merge MCPs because it was a balance between quantitative rigour and ecological relevance. Setting a low threshold allowed more MCPs to be merged into larger MATMAs but had biologically irrelevant boundaries. A 70% threshold appeared to provide this balance. Once MCPs had been merged to MATMAs, concave boundaries were levelled; this was due to the fact that animals would move in a least-cost path, particularly within oceans (Sims et al. 2008; Freitas et al. 2018). Greater technical details on overlaps between MCPs can be found in Supporting Information S3.

2.5 | Software and Packages

All data processing and analyses were conducted in R v.4.2.2 (R Core Team 2022) and QGIS v.3.28.11 (QGIS Development Team 2022). Satellite tracks were digitized and georeferenced in QGIS while MCP bootstrapping was done in R. Shapefiles and rasters were processed with the *sf* (Pebesma 2018; Pebesma and Bivand 2023), *terra* (Hijmans 2022) and *raster* (Hijmans 2023) packages, while MATMAs were developed using the *mcp* function from the *adehabitatHR* (Calenge 2006) package.

3 | Results

3.1 | Data Summary

The desktop review on flipper tags, photo ID, and satellite tracking papers across the four search engines returned a total of 1566 papers (Table 1). Of these, seven papers were retained based on the criteria we required for the desktop review (DeSilva 1986; Charchinda et al. 2000; Sakamoto et al. 2000; Shiba et al. 2000; Basintal 2001; Sagun 2003; Adyana et al. 2008). Including unpublished data, the dataset consisted of 77 flipper tag recoveries, four photo ID recoveries, and 100 satellite tag points, representing 181 individual turtles which either originated or ended their migrations in Southeast Asia (Figures 2 and 3). Many data points were from Malaysia (*n* satellite tag = 49, *n* flipper tag = 65, *n* photo

TABLE 1 | The number of results (*N*) for flipper tags, photo ID, and satellite tracking from each of the four search engines used in the desktop review: Web of Science, ProQuest, Scopus and Google Scholar.

Search engine	N results (flipper tagging)	N results (photo ID)	N results (satellite tracking)
Web of Science	74	48	89
ProQuest	103	569	399
Scopus	1	7	7
Google Scholar	30	167	72
Total	208	791	567

ID=4), followed by Indonesia (*n* satellite tag=20, *n* flipper tag=7). Most data points originated from Southeast Asia with only a small proportion collected from outside the region (Supporting Information S4).

In total, the dataset was divided into 29 nesting groups for green turtles and two nesting groups for hawksbill turtles (Supporting Information S5). Green turtle nesting groups were predominantly distributed within the Sulu Sea and South China Sea (Figure 2), while hawksbill nesting groups were mainly found within the Melaka Straits and Sulu Sea (Figure 3). After filtering those nesting groups with 10 or more individual records, nine green turtle and two hawksbill nesting groups were used for developing MATMAs.

3.2 | Green and Hawksbill Turtle MATMAs of Southeast Asia

Six MATMAs were identified for green (Figure 4) and two for hawksbill (Figure 5) turtles (Supporting Information S5). Most MATMAs were north of the equator except for two green turtle MATMAs that spanned or were south of the equator. Green turtle MATMAs were located in the Andaman Sea, Java Sea, North Borneo/Kalimantan, Raja Ampat, South China Sea and the Sulu Sea, while hawksbill MATMAs were identified in the Melaka Straits and the Sulu Sea.

Green turtle MATMAs averaged at $822,196 \pm 1,022,454.0 \text{ km}^2$, which were about four times larger than those of hawksbill MATMAs ($148,181 \pm 181,421.0 \text{ km}^2$). Three green turtle MATMAs were found in the South China Sea and Sulu Sea: the South China Sea MATMA, the Sulu and Sulawesi Sea MATMA and the Northern Borneo/Kalimantan MATMA. Data were available for hawksbills in Indonesia and the Philippines, but there were too few individual records to develop nesting groups for MCP bootstrapping. Hence, no MATMAs were defined for hawksbills in Indonesia or the Philippines in this study.

Green turtle and hawksbill turtle MATMAs varied in their overlap with their respective RMUs (Figure 6, Supporting Information S6). Four of the six green turtle MATMAs were developed in a single RMU (East Indian and Southeast Asia). The Sulu and Sulawesi Sea MATMA overlapped with two RMUs:

the East Indian and Southeast Asian RMU and the West Central Pacific RMU. The Raja Ampat MATMA, on the other hand, overlaps with all three green turtle RMUs found in Southeast Asia: the East Indian and Southeast Asian RMU, Southwest Pacific RMU and West Central Pacific RMU. On the other hand, hawksbill turtle MATMAs were only developed within the Southeast Asian hawksbill turtle RMU.

4 | Discussion

4.1 | Distribution of Southeast Asian MATMAs

The objective of this study was to develop MATMAs for green and hawksbill turtles in Southeast Asia, which are discrete, quantitatively derived boundaries at a finer spatial resolution than RMUs. These MATMAs encapsulate nesting sites, foraging areas, and migratory corridors, which connect these two sites. While much of the data for green turtles were from studies that reported tagging or recoveries in Malaysia (*n* = 118), many of the MATMAs extended across the South China Sea to the Philippines. This can be attributed to migratory routes from Thailand (Pattaya), Malaysia (Terengganu), and Vietnam (Con Dao Island) leading to northern Borneo/Kalimantan and the Philippines, particularly Sabah and Palawan (Liew et al. 1995; Papi et al. 1995; van de Merwe et al. 2009; Liew et al. 2012; WWF IndoChina Vietnam and Marine Research Foundation 2009). This overlap explains the substantial connection between the South China Sea MATMA and the North Borneo/Kalimantan MATMA. Green turtles from Sarawak remained close to Borneo/Kalimantan's coastline, migrating to foraging grounds in Sabah within the Sulu Sea (Bali et al. 2002; Pilcher et al. 2019).

The green turtle MATMA distributions align with previous regional groupings from Nishizawa et al. (2018), developed for genetic stock differentiation via mixed-stock analysis. The Java Sea MATMA falls squarely within their East Indian Ocean regional grouping, while the Andaman Sea is in the eastern portion of the Malay Peninsula and South China Sea regional group. Furthermore, the Sulu-Celebes Sea MATMA is within the Sulu Sea and Celebes Sea regional group. However, the South China Sea and North Borneo/Kalimantan MATMAs spanned the South China Sea and Sulu and Sulawesi Sea regional groupings used by Nishizawa et al. (2018). In addition, the Raja Ampat MATMA crossed two different regional groups and was developed for where there was no regional grouping. This distribution does not necessarily mean these results are contradictory. First, Nishizawa et al. (2018) used these regional groups as an *a priori* basis for grouping management units and genetic stocks for their mixed-stock analysis, rather than boundaries or groupings that were quantitatively derived. Second, boundaries from our study use direct methods of locating turtle locations. Genetic studies may reveal orphaned haplotypes that are not linked to any particular foraging site or genetic stock (Bowen and Karl 2007), but even high sample numbers cannot determine the natal origin of a newly discovered haplotype due to the coarse resolution of the data (Shimada et al. 2021). However, a single satellite tag can identify the origin and location of where an animal moves (Hof et al. 2023).

Hawksbill MATMAs were identified only in the Melaka Straits and the Sulu Sea. However, this does not suggest the absence

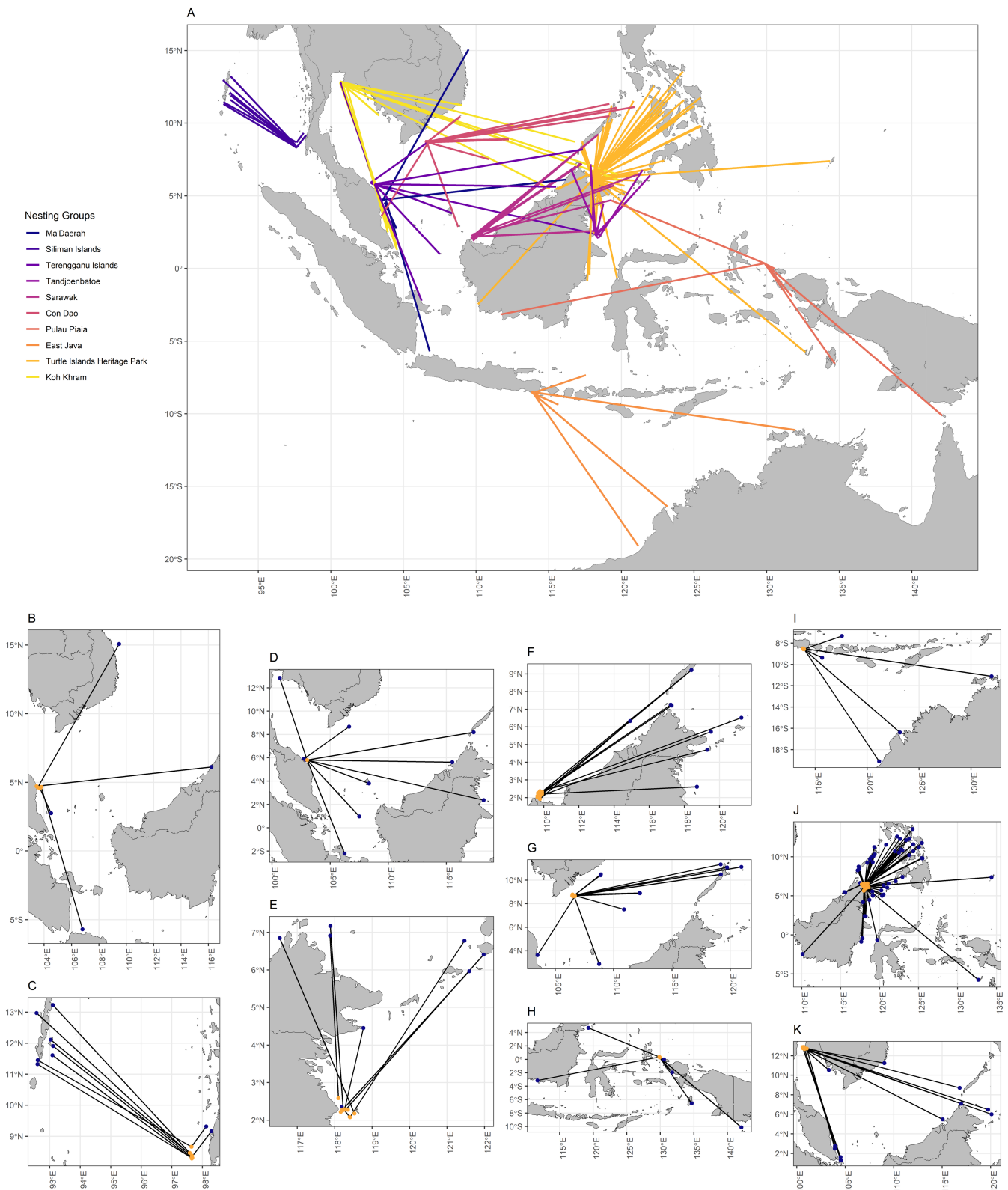


FIGURE 2 | Overview of nesting groups for green turtles (A). The nesting and foraging sites extracted from each satellite track, flipper tag record and photo ID incidents are shown, with linkages between nesting and foraging sites indicated with black lines. Each panel indicates a separate nesting group, with nesting (orange/light) and foraging (purple/dark) sites for green marine turtles in Southeast Asia: B = Ma'Daerah, C = Siliman Islands, D = Terengganu Islands, E = Tandjoenbatoe, F = Sarawak, G = Con Dao, H = Pulau Piaia, I = East Java, H = Turtle Islands Heritage Park, J = Koh Khrum. Nesting groups depicted here are only those with 10 or more records. Data used for these nesting groups came from original works by Adyana et al. (2008), Basintal (2001), Charchinda et al. (2000), DeSilva (1986), Sagun (2003), Sakamoto et al. (2000), Shiba et al. (2000) and Pilcher et al. (2019) as well as unpublished data by co-authors of this study.

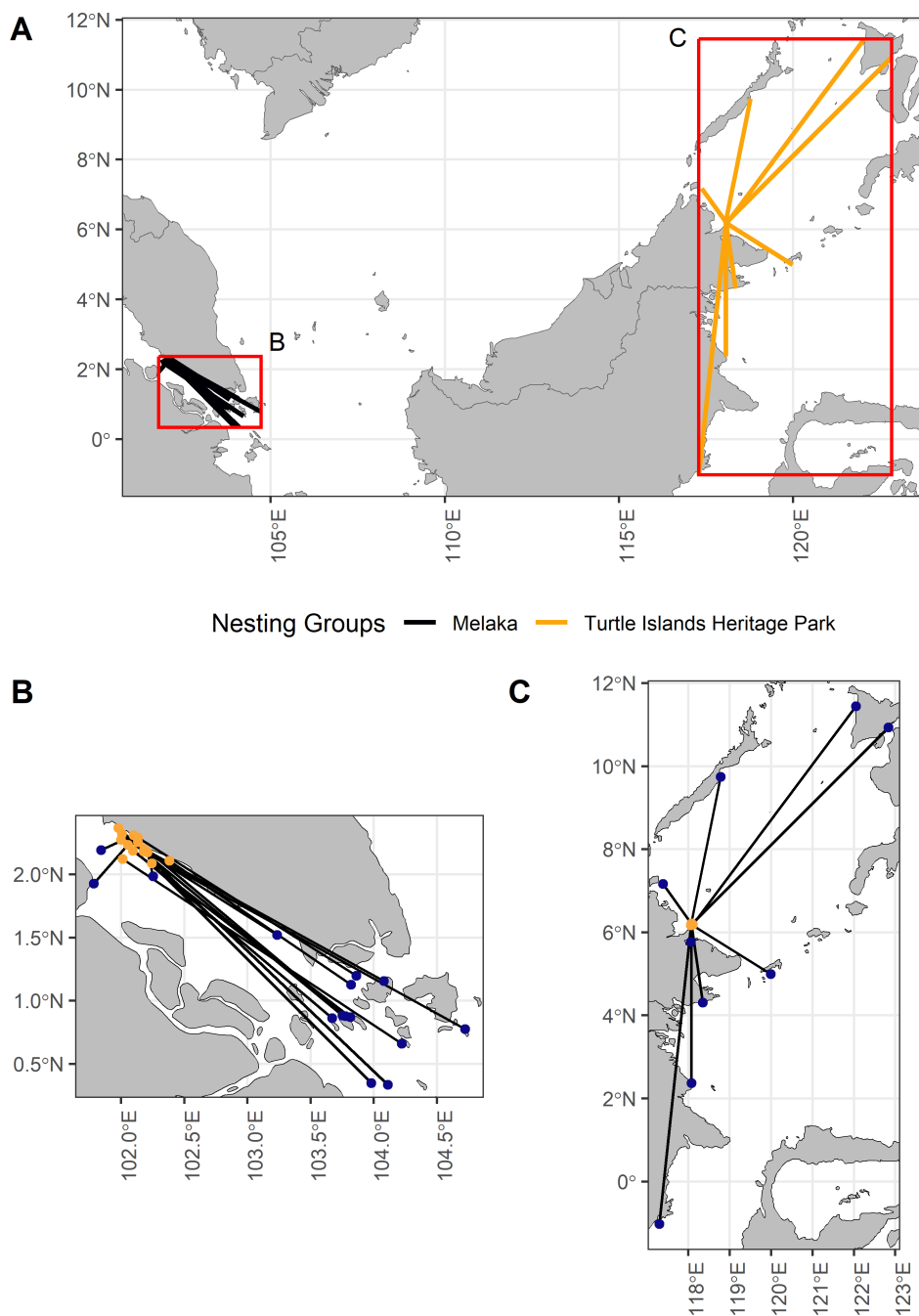


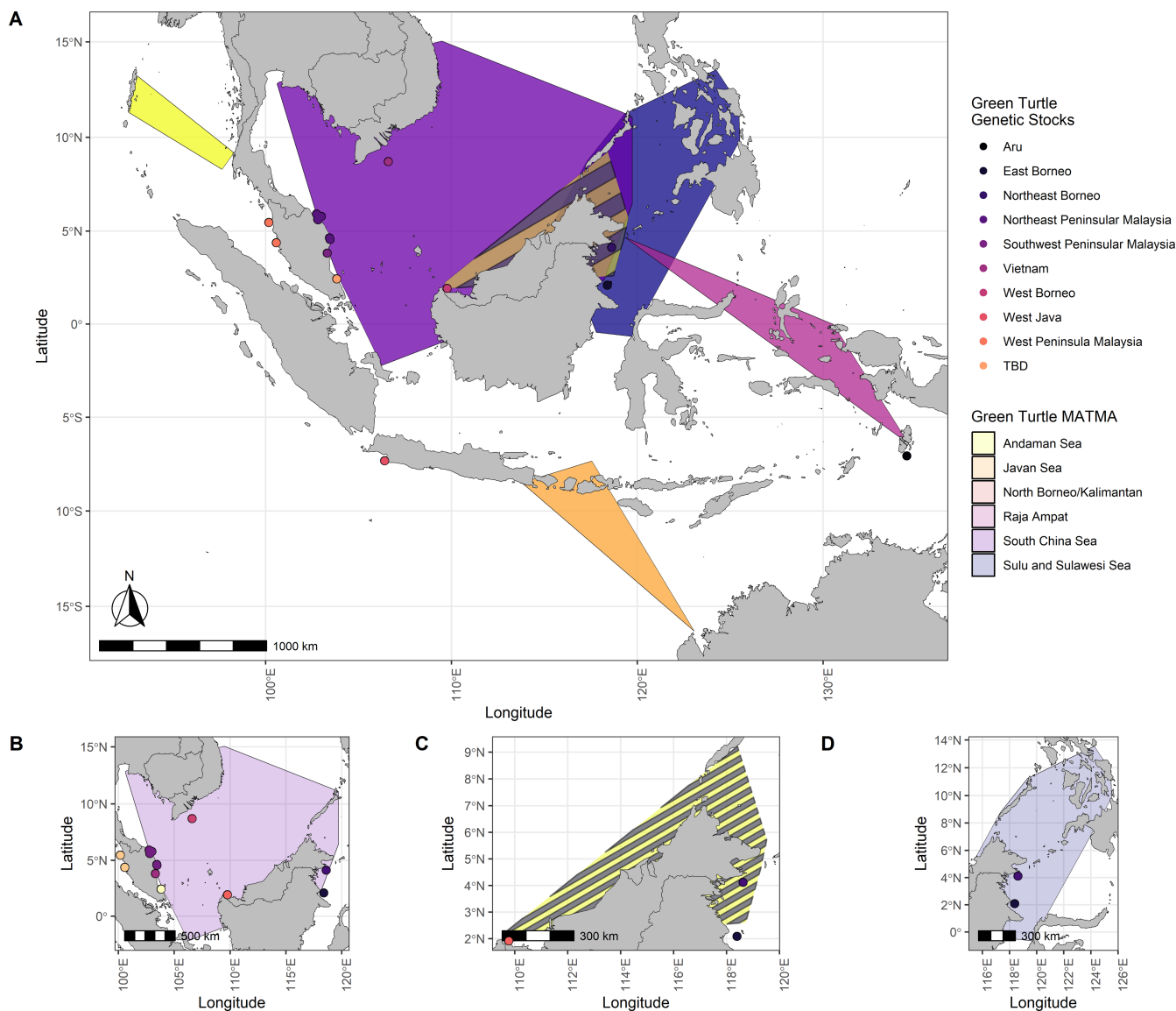
FIGURE 3 | Overview of nesting groups for hawksbill turtles (A). The nesting and foraging sites extracted from each satellite track, flipper tag record and photo ID incidents are shown, with linkages between nesting and foraging sites indicated with black lines. Each panel indicates a separate nesting group, with nesting (orange/light) and foraging (purple/dark) sites for hawksbill turtles in Southeast Asia: B = Melaka (Malaysia), C = Turtle Islands (Malaysia/Philippines). Data used for these nesting groups came from original works by Adyana et al. (2008), Basintal (2001), Charchinda et al. (2000), DeSilva (1986), Sagun (2003), Sakamoto et al. (2000), Shiba et al. (2000) and Pilcher et al. (2019) as well as unpublished data by co-authors of this study.

of hawksbills elsewhere in Southeast Asia. Studies reviewed by FitzSimmons and Limpus (2014) and data collated by Hamann et al. (2022) indicated additional rookeries in Indonesia, and genetic data suggest that hawksbills occupy a broader range, including Peninsular Malaysia and Singapore (Nishizawa et al. 2016; Tiong et al. 2023). Satellite tracking data of nesting hawksbill turtles in Singapore (National Parks Board, unpublished) indicate movements of individuals along the western coastline of Peninsular Malaysia into Thailand. Thus, the current MATMAs

represent an incomplete distribution of hawksbill turtles in the region.

4.2 | Data Availability and MATMA Distribution

The limited coverage of hawksbill MATMAs can be attributed to data scarcity. For example, the Sulu Sea MATMA was developed using satellite tracking and flipper tagging of 11 hawksbills from



the Turtle Islands Protected Area. One hawksbill turtle from the Turtle Islands Protected Area travelled south to Sungairaden, Indonesia, a region much further south than Tanjung Batu. The methods used in this study ensured that only a majority of the points were used to develop MATMAs in order to reduce the inclusion of outlier satellite locations during bootstrapping and MCP averaging. Hence, the foraging site in Sungairaden was not included in the hawksbill Sulu Sea MATMA. It is likely that this noninclusion is a result of the small sample size of hawksbills and that other individual hawksbills may travel further south in Indonesia but have yet to be tracked. Nondetection of biodiversity can result in underestimated distribution models (Chambert et al. 2018; Gu and Swihart 2004; MacKenzie and Bailey 2004), and it is likely that the hawksbill Sulu Sea MATMA is similarly impacted.

The lack of data from other regions in Southeast Asia also highlights that the distribution of MATMAs is biased to areas

where studies have been conducted and where data is available. Several studies have indicated large sample sizes (>100) are needed to develop accurate ocean-basin species distribution models, especially when they are made of animal movement data (Fossette et al. 2014; Queiroz et al. 2016; Sequeira et al. 2019). The sample size in this study was from 181 animals and made up of satellite tracking data, photo-ID data, and flipper tagging records. A majority of this data were primarily from nesting beaches in Peninsular Malaysia and ended in northern Borneo/Kalimantan (Sarawak and Sabah) and Palawan, Philippines, which resulted in many MATMAs developed in and around the South China Sea. Thus, while sample size is an important criterion for sufficiently developing animal distribution models (Sequeira et al. 2019; Shimada et al. 2021), the origins of the data are just as critical (O'Toole et al. 2021). However, despite the data limitation, the coverage of MATMA boundaries across Southeast Asia is significant. The inclusion of additional data could improve the coverage

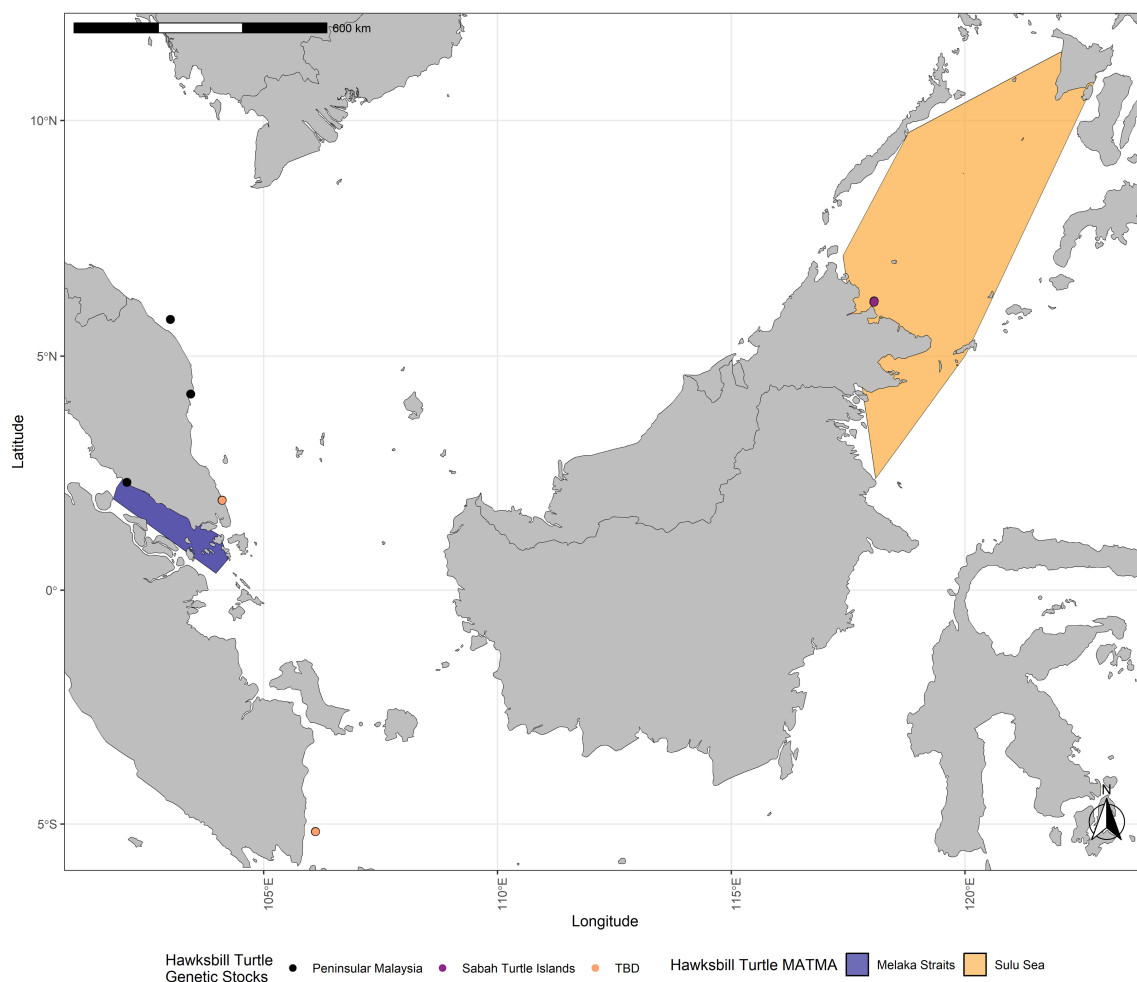


FIGURE 5 | Marine turtle management areas (MATMAs) for hawksbills in Southeast Asia.

of MATMAs across this region, which can have better implications for conservation. For example, several genetic stocks were not included in some MATMAs within this study, such as the Penang and Perak green turtle genetic stock on the west coast of Peninsular Malaysia (Nishizawa et al. 2018). Indeed, additional data from across the region could improve the coverage of other MATMAs within Southeast Asia as well. Hence, it would be beneficial to responsibly collect photo-ID, satellite tracking, and flipper tag data throughout the region to enhance MATMA coverage.

4.3 | Value of MATMAs

MATMAs provide a novel and valuable tool at an appropriate scale for area-based conservation. Conservation strategies have historically been structured around the following three spatial scales (Poiani et al. 2000): functional sites, such as breeding grounds, which are spaces that provide a specific function for a species in a localized area; functional landscapes, such as coastal areas with several habitats (seagrass, coral, sandy bottoms, etc.), which are seascapes that contain a habitat mosaic that is important for a species; and functional networks, which are coarse-resolution, regional scale areas that consider the connectivity of species to different functional landscapes and sites. RMUs are analogous to functional networks as they form large,

regional boundaries, while IMTAs are analogous to functional sites. MATMAs fill a gap of functional landscapes by linking nesting beaches to specific foraging areas and migratory pathways. We recognize a caveat of MATMAs is that they do not consider other life history stages such as the oceanic stage for neonate turtles. However, MATMAs are still useful as they represent boundaries for fewer genetic stocks and their specific foraging grounds, as well as the migratory corridors that connect these two functional, local sites.

As an intermediate area-based conservation tool, MATMAs can facilitate targeted conservation management approaches by bridging the gap between local-scale conservation (such as MPAs) and RMU strategies. Conservation approaches should be tailored to spatial scales that demonstrate conservation outcomes. For example, seabirds have more localized aggregations for breeding but cover a wider range for foraging; MPAs are a better conservation approach for local scales at breeding sites as the size of the area to enforce is easier and simpler to manage. Conversely, managing fisheries bycatch through fishing gear would be more appropriate for scales where foraging areas are larger and where enforcement of boundaries may be difficult (Oppel et al. 2018). Similarly, MATMAs can refine conservation planning within RMUs by developing strategies that are more appropriate at the scale of seascapes, particularly when multiple jurisdictions and stakeholders are involved (Treml et al. 2015).

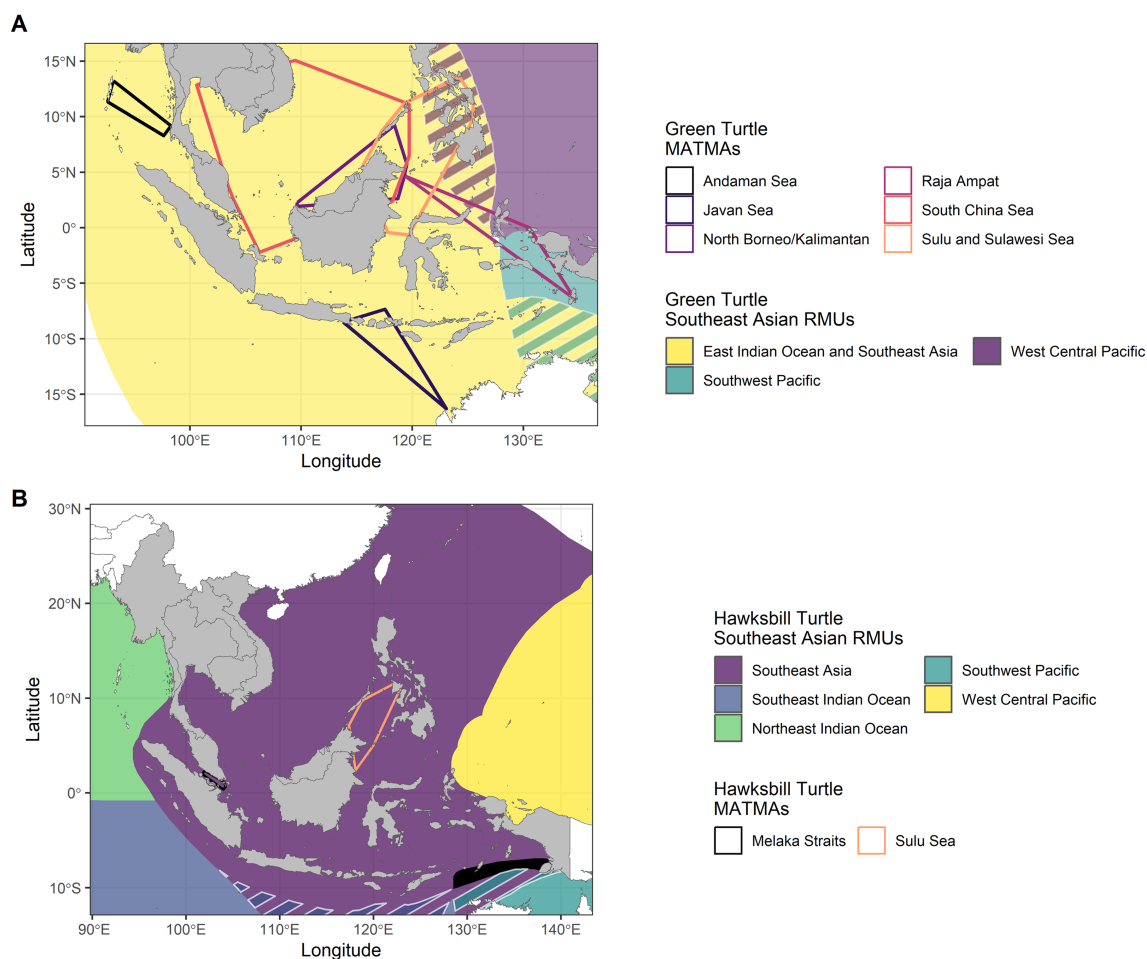


FIGURE 6 | Green (A) and hawksbill (B) turtle MATMAs overlayed with RMUs. Multicoloured spaces indicate areas where two RMUs overlap, whereas black polygon displayed in the hawksbill turtle RMU map indicates overlaps between the Southeast Asian, Southeast Indian Ocean and Southwest Pacific RMUs. RMU polygons derived from Wallace et al. (2023).

MATMAs as an intermediate spatial framework can fulfil the role below RMUs to identify areas that would require subregional conservation action.

MATMAs are also beneficial as they can identify which genetic stocks are at risk of impact from specific threats within an RMU. Genetic stocks are important units of conservation for turtles as they represent genetically unique populations that do not mix with other populations, and hence maintain genetic heterogeneity within an RMU at a regional scale and for the species at a global scale (FitzSimmons and Limpus 2014; Komoroske et al. 2017). While a benefit of the RMU framework is the ability to link threats to genetic stocks (Wallace et al. 2011), RMUs are large, and threats in one corner of an RMU could be linked to any number of genetic stocks. In other words, the link between a threat in a specific area and a specific genetic stock may not be immediately clear. MATMAs are small enough that specific threats in one location can be linked to specific genetic stocks, which benefit the genetic diversity within that MATMA and within the RMU. These threats can then be mitigated with regulations that can benefit those MATMAs. For instance, bycatch in the South China Sea MATMA can be mitigated with turtle excluder devices installed onto trawler vessels, benefiting four green turtle genetic stocks within it.

Additionally, MATMAs can help prioritize conservation and management action within RMUs. Conservation priorities assigned to RMUs are valuable as regions which require urgent conservation action have been identified (Wallace et al. 2011; Wallace et al. 2025). However, just as the RMUs themselves are coarse (Wallace et al. 2023), so too are the conservation priorities assigned to the RMUs. Just as RMUs have been assigned a conservation priority to identify regions of the world that need urgent attention (Wallace et al. 2011; Wallace et al. 2025), once MATMAs are identified, they can be used to identify seascapes within an RMU where focused action can be carried out. Conservation priorities within an RMU are not likely homogeneous, so assigning conservation priorities to different areas of an RMU with MATMAs can narrow down where actions are more urgently needed, such as where IMTAs should be developed or integrated into marine spatial planning first.

While MATMAs are not the same as protected areas, they can inform spatial planning efforts, similar to how Key Biodiversity Areas influence policy without direct legal enforcement (Eken et al. 2004). We do not encourage MATMAs to be used as a way to identify spaces to be gazetted as protected areas, as large areas such as these can be difficult to manage (Rassweiler et al. 2012). This is especially true when boundaries are transnational and

where legislative protections differ between nations (Ezekiel et al. 2018). These are meant to be informative boundaries, which pave the way for legal protections within respective countries, such as the MPA networks that were developed within the Sulu-Sulawesi Marine Ecoregion between Malaysia, Indonesia and the Philippines (Mclat et al. 2006; Murphy et al. 2021). Continued learning networks between nations within cross-boundaries MATMAs (Pietri et al. 2015) can further identify shortcomings in management that need to be addressed (Ellett 2021).

5 | Conclusions

This study identified six green turtle MATMAs and two hawksbill turtle MATMAs in Southeast Asia in the first attempt to establish finer resolution boundaries beneath RMUs, which can be useful for the conservation of turtles in the region. While the current MATMAs do not capture the full extent of turtle habitats in the region, future refinements will be possible as additional data becomes available. The methods used here can be applied to other RMUs, and we advocate for researchers and conservationists to begin the work to divide RMUs into smaller subboundaries to identify smaller areas for management. Given the high biodiversity and conservation challenges in equatorial regions, MATMAs offer a valuable framework for prioritizing conservation actions and allocating limited resources effectively. By refining and expanding the MATMA framework, conservationists can better address the urgent needs of marine turtles in Southeast Asia.

Author Contributions

Rushan Abdul Rahman: conceptualization, investigation, funding acquisition, writing – original draft, methodology, visualization, writing – review and editing, formal analysis, resources. **Juanita Joseph:** supervision, writing – review and editing, conceptualization. **Putu Liza Mustika:** supervision, writing – review and editing, conceptualization. **Windia Adnyana:** data curation, resources. **Stephanie Duce:** methodology, writing – review and editing. **Nicolas J. Pilcher:** data curation, writing – review and editing, resources. **Jaya Ratha:** data curation, resources. **Thi Dieu Thuy Nguyen:** data curation, resources. **Mark Hamann:** supervision, project administration, writing – review and editing, conceptualization.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data used for the development of MATMAs is made available in Supporting Information S1.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Data S1:** Data Source Used to Develop MATMAs. **Data S2:** Technical Details of MATMA Development. **Data S3:** Proportion of Overlap Between Nesting Group MCPs. **Data S4:** Origins and End Points of Data Points. **Data S5:** MATMA Composition and Size. **Data S6:** MATMA RMU Overlap.