

Population analysis of *Carcharodon carcharias* in localized areas surrounding South Africa
using semi-automated dorsal fin identification

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Abstract

The great white shark (*Carcharodon carcharias*) is a marine apex predator with a global distribution. In recent years, the number of white sharks has drastically declined as a consequence of anthropogenic activities such as illegal/targeted fishing, bycatch, and habitat disruption. Until recently, research on sharks has been lacking, resulting in an information gap on shark populations. This study aims to analyze the current population distribution of white sharks in the wild, to fill the research gap on white shark data, and to use this information to inform policies makers for improvements in white shark conservation measures. White shark population distribution between Gansbaai and Mossel Bay, South Africa, were estimated using semi-automated and manual dorsal fin identification techniques. Dorsal fin photos from Mossel Bay were organized into a both a coded database, and an edge pattern database, then matched to a pre-existing Gansbaai database to identify population dynamics between the two sites. The anticipated outcome of this study is an indication of the population dispersal along the South African coastline, to promote knowledge based improvement of existing marine conservation and fishing management strategies.

Keywords: Shark, photo identification, conservation, fisheries management, population

Introduction

The great white shark (*Carcharodon carcharias*) is a globally distributed apex predator, often negatively portrayed by the media and feared by the public. Despite this negative image, white sharks play a crucial role in marine ecosystems as ecological regulators (Cailliet et al. 1985, Bonfil et al. 2005, , Navia et al. 2010, Maduna et al. 2017, Bornatowski et al. 2018). White sharks maintain critical balance between predator and prey population sizes and distributions, which as a result has led to increased biodiversity in numerous marine ecosystems (Kuguru et al. 2019). This interaction highlights white sharks as keystone species, especially considering their strong environmental impact despite their population size being few in number (Cailliet et al. 1985, Bornatowski et al. 2018, Kuguru et al. 2019). Given their impact on lower trophic level organisms, loss of white sharks from ecosystems has the potential to trigger trophic cascades (Navia et al. 2010), implying devastating consequences for marine biomass as a whole (Navia et al. 2010, Gubili et al. 2015, Shiffman and Hammerschlag 2016, Maduna et al. 2017, Sutcliffe and Barnes 2018).

White sharks are a k-selected species, meaning they exhibit extended life history traits such as long lifespan, low fecundity, and slow rate of growth/maturation (Compagno 1984, Cailliet et al. 1985, Bonfil et al. 2005, , Kock et al. 2013). These traits make the species particularly vulnerable to exploitation, given that the rate of time for population recovery is slower than the rate at which populations are declining (Jackson et al. 2001, Kock et al. 2013). This is of particular concern considering many white shark populations are in decline due to pressure from increased anthropogenic activities such as by-catch, targeted fishing, habitat loss, and declining prey populations (Hall 1999, Jackson et al. 2001, Andreotti et al. 2016).

Overall, these pressures have led scientists and marine advocates to request enhanced protective measures for white sharks (Jackson et al. 2001). Unfortunately, due to the considerable knowledge gap on the biology, behaviour, and population dynamics of white sharks, arguing for increased conservation measures is challenging (Jackson et al. 2001, Andreotti et al. 2014, Veríssimo et al. 2017). The

International Union for the Conservation of Nature (IUCN) Red List reported that 39.0% of Chondrichthyes status is data deficient, creating a challenge for researchers when trying to implement conservation measures (The IUCN Red List of Endangered Species 2019). Before any effective conservation strategies and fishing management policies can be enforced, sufficient data outlining the population sizes, dynamics, and potential site fidelity need to be collected (Knip et al. 2012, Gubili et al. 2015, Merwe et al. 2017, Klein et al. 2019).

Sharks are difficult to study for extensive and continuous periods of time, partly because of their migratory range, but also due to their complex biology and long lifespans (Bonfil et al. 2005, Kock et al. 2013, Maduna et al. 2017). Previous studies have utilized genetic sampling, and/or acoustic telemetry to estimate population size, assess migratory patterns, and analyze biological traits of white sharks (Pardini et al. 2001, Gubili et al. 2015, Andreotti et al. 2016). These techniques are often costly and time consuming, which makes them less favorable for researching a species under time and budget constraints.

To combat this dilemma, our study will utilize manual dorsal fin identification techniques highlighted by Andreotti et al. (2014), and a recently developed semi-automated software (Andreotti et al. 2018) to analyze population dynamics of great white sharks in South Africa. Dorsal fin identification was originally designed for researching cetaceans, however it has since been adopted for use on shark population monitoring (Tienhoven et al. 2007, Chapple et al. 2011, Andreotti et al. 2018). This technique has become favorable for researching sharks because it is less invasive, cost-effective, and is reliable for identifying an individual over long periods of time (from either side of the animal) (Tienhoven et al. 2007, Chapple et al. 2011, Andreotti et al. 2014, 2016). Using a reference database of images identifying unique sharks spotted in Gansbaai, South Africa, this study aims to assess any movement of individuals across white shark aggregation sites. We hypothesize that using dorsal fin identification techniques will enable us to provide an insight of the population dispersal, for supporting existing genetic evidence of panmixia around the South African coastline (Andreotti et al. 2015). The results of this study will be used

to fill the knowledge gaps on shark life histories and population dynamics, ultimately being used as a steppingstone for future research in Elasmobranchs as a whole.

Materials & Methods

The project design consists of four key processes: 1) data collection, 2) dorsal fin database matching using Identifin© (as described by Andreotti et al. 2018), 3) dorsal fin database matching using a notch-coding system (as described by Andreotti et al. 2014), and 4) population dynamics analyses between the Mossel Bay database and the Gansbaai database.

Information for the databases was collected in Gansbaai and Mossel Bay (Figure 1) between 2009 and 2014, weather permitting, during white shark diving ecotourism activities provided by ‘Shark Diving Unlimited’. The Mossel Bay database was created during this project, while the Gansbaai database had been completed previously using both the manual and semi-automated dorsal fin identification techniques. A total of 427 unique sharks were identified in the Gansbaai database. 141 photos were collected during the Mossel Bay sampling period. Devices used were a Canon® EOS 300D (8.2 megapixel) or Canon® EOS 40D (10.1 Megapixel) SLR digital camera to take photos of white shark dorsal fins from the surface on a boat. Cameras were fitted with 55-200 mm zoom lenses (Tamron® Di-II) with polarizing filters to enhance contrast and reduce glare or reflection of light on the water’s surface. Using Adobe® Photoshop® 22.1.0 Desktop Release (@1990-2020), images were edited to all be 8.0cm x 7.9cm, while also enhancing contrast to emphasize the trailing edge of the dorsal fin. Only photos of sufficient quality were used for dorsal fin analysis.

Following image collection, the semi-automated dorsal fin ID software Identifin (Andreotti et al. 2018, © Dr. S Andreotti & Dr. P Holtzhausen 2016) employed the notch categorization method outlined in Andreotti et al. (2014) which identifies and organizes shark dorsal fin images into a reference database (Figure 2). The premise of this software is to first separate the dorsal fin from the background of the photo, and then to identify “principle notches” on the trailing edge of each individual shark’s dorsal fin

and compare this pattern to the image database. Principle notches are notches measuring 0.5cm-3.0cm deep (Andreotti et al. 2014, 2018). Both algorithms are of significance in order to accurately examine each individual fin and distinguish it from the image background (Andreotti et al. 2018). Due to occasional ambiguity between the base of the dorsal fin and the water surface, the software requires manual indication of the tip and base of the trailing edge (Figure 3a) for the dynamic time warp approach to accurately trace the fin edge (Figure 3b) (Andreotti et al. 2018). The path created must also be scaled first to the image size to gain an accurate measurement of the fin features, then scaled corresponding to the “maximum peak amplitude” of the fin to accentuate the identifying notches (Andreotti et al. 2018). Based on all of the above information, the software will produce a list of matches based on probability (highest to lowest match probability) that the analyzed fin may correspond to. A match is only considered perfect if the first image suggested by the software is the correct match (based on previous manual and genetic identification techniques).

The manual notch coding format described by Andreotti et al. (2014) without utilizing the software was also performed to validate the accuracy of the software matches. This involved dividing dorsal fin images into a top, middle, and third section, then counting the number of principle notches within each section. The unique fin code created would begin with “M_” referring to the site ID (Mossel Bay), followed by the number of notches in each section in the order top, middle, bottom (Figure 4). Each Mossel Bay shark (and its corresponding notch-code) was compared to the Gansbaai notch-code database to check for potential matches.

Number of unique sharks identified in Mossel Bay were compared to the Gansbaai database to check for matches between the sites. Matches would indicate the shark has travelled from one site to the other, where broadscale movement between the populations would indicate that site fidelity is not occurring.

Results

Of the 141 photos captured in Mossel Bay, 32 were used to create the database. Throughout the sampling period there were 30 events involving sharks being lured to the boat for image capture (Table 1). After matching the photos within the Mossel Bay sample set using Identifin© and the manual notch-coding system, 27 unique sharks were identified. Of the 27, sex was identified for 16 sharks (3 male and 13 female). Total length (TL) was recorded (in metres) for 20 individuals, with sizes ranging from 1.5m to 4.3m. Juveniles were considered as sharks $\leq 3.0\text{m}$, while adults were considered sharks $>3.0\text{m}$ (as described by Kock et al. 2012). In the Mossel Bay dataset there were 9 juveniles and 11 adult white sharks.

After comparison to the Gansbaai database using Identifin©, only one shark was identified as having been recorded at both study sites (Figure 5). This shark (identified as “2011.08.11-07” in the software database and G_M_060801 in the notch-coding database) was a juvenile (2.8m) female. All other sharks identified in the Mossel Bay database (26 remaining) were not recorded in the Gansbaai database, suggesting potential evidence for site fidelity. This directly contradicts our hypothesis suggesting the shark populations in Gansbaai and Mossel Bay would be intermixed as one large population rather than subdivided into smaller populations.

Discussion

This project intended to use semi-automated (Andreotti et al. 2018) and manual notch-coding (Andreotti et al. 2014) dorsal fin identification techniques to evaluate population dynamics of white sharks between Mossel Bay and Gansbaai, South Africa. We hypothesized that the white sharks found in Mossel Bay would also be identified in Gansbaai to support existing genetic evidence of interbreeding between the two sites (Andreotti 2015). Evidence from the dorsal fin ID matching using both techniques revealed that only one shark was found migrating between the two sites, which directly contradicts our hypothesis.

To interpret our results, it's important to consider various behaviours that have been observed in sharks which directly impact population dynamics. One example is the seasonal migration patterns in South African white sharks (Kock et al. 2013). Shark populations in Gansbaai have been observed increasing in size from May to September (particularly in close proximity to Seal Island), and decreasing from October to April (Kock et al. 2013). Given that data collection for Mossel Bay took place from July-September, it is possible that sharks who are already prone to migratory behaviour had departed for Gansbaai, and those who remained were not yet in a migratory life stage (Pardini et al. 2001, Bonfil et al. 2005). To address this, additional samples from Mossel Bay would need to be taken between October-April to verify the presence (or absence) of migratory white sharks traversing between Mossel Bay and Gansbaai.

White sharks have been observed exhibiting four distinct migratory behaviours: rapid transoceanic return migrations, frequent long distance coastal return migrations, smaller-scale patrolling, and site fidelity (Bonfil et al. 2005). A constant across these behaviours is the act of returning to a specific location, possibly the site of birth or an ideal hunting space (Bonfil et al. 2005). It is possible that the sharks whose home range in Gansbaai have demonstrated coastal return migrations in which they frequent and interbreed with Mossel Bay sharks, while sharks whose home range is Mossel Bay are more prone to small-scale patrolling and site fidelity. This would account for the genetic panmixia observed in South African shark populations, but also permit the possibility of site fidelity in Mossel Bay sharks that this study has observed.

Another behaviour recorded among white sharks is sex-biased dispersal, in which males often migrate more frequently and longer distances than females (Pardini et al. 2001, Kock et al. 2013). One theory behind this behaviour is that males are more likely to travel between sites to mate, while females may exhibit reproductive philopatry (Pardini et al. 2001, Speed et al. 2016, Klein et al. 2019). This results in a possible nursery site, where females will gather for the purpose of giving birth, and where juveniles will reside until they mature enough to begin oceanic excursions (Pardini et al. 2001, Bonfil et al. 2005,

Kock et al. 2013, Klein et al. 2019). In our Mossel Bay database, the majority of sex-identified sharks are female (13/16) while only three were male. Of the males, two were juveniles, while the females were mostly adults (9/13). This suggests that there may be evidence supporting Mossel Bay as a nursery for mature females to deliver and juvenile sharks to grow. Females who have mated with males dispersed along the coasts of South Africa but returned to Mossel Bay could explain the genetic links between sites such as Mossel Bay and Gansbaai, while also supporting possible reproductive philopatry in female Mossel Bay sharks and the evidence for site fidelity. This hypothesis requires further exploration on the sex-specific dispersal patterns of sharks in Mossel Bay, and more in depth population analysis of juveniles in the area.

While the results of this project were not consistent with our hypothesis, the mechanisms behind our findings yield the opportunity for future exploration and understanding of white shark population dynamics in South Africa. Future studies should aim to identify sex-specific dispersal of mature sharks identified in Mossel Bay to evaluate possible reproductive philopatry in females. Comparison between male and female migration within and outside of Mossel Bay is needed to better evaluate site fidelity. Future research on population size and dispersal of juvenile sharks in the area may also clarify whether Mossel Bay is a site of interest as a nursery for young white sharks. Identification of areas important to shark populations is critical for ensuring effective conservation of the species (Knip et al. 2012, Veríssimo et al. 2017, Merwe et al. 2017, Klein et al. 2019), therefore more research is needed to evaluate the significance of Mossel Bay for white shark populations in South Africa.

References

- Andreotti, S. 2015, March. The conservation of South African white sharks : population number, genetic distinctiveness and global connections. Thesis, Stellenbosch : Stellenbosch University.
- Andreotti, S., S. von der Heyden, R. Henriques, M. Rutzen, M. Meÿer, H. Oosthuizen, and C. A. Matthee. 2016. New insights into the evolutionary history of white sharks, *Carcharodon carcharias*. *Journal of Biogeography* 43:328–339.
- Andreotti, S., P. Holtzhausen, M. Rutzen, M. Meÿer, S. van der Walt, B. Herbst, and C. A. Matthee. 2018. Semi-automated software for dorsal fin photographic identification of marine species: application to *Carcharodon carcharias*. *Marine Biodiversity* 48:1655–1660.
- Andreotti, S., M. Rutzen, P. L. Wesche, C. P. O’Connell, M. Meÿer, H. Oosthuizen, and C. A. Matthee. 2014. A novel categorisation system to organise a large photo identification database for white sharks *Carcharodon carcharias*. *African Journal of Marine Science* 36:59–67.
- Bonfil, R., M. Meÿer, M. C. Scholl, R. Johnson, S. O’Brien, H. Oosthuizen, S. Swanson, D. Kotze, and M. Paterson. 2005. Transoceanic Migration, Spatial Dynamics, and Population Linkages of White Sharks. *Science* 310:100–103.
- Bornatowski, H., R. Angelini, M. Coll, R. P. Barreto, and A. F. Amorim. 2018. Ecological role and historical trends of large pelagic predators in a subtropical marine ecosystem of the South Atlantic. *Reviews in Fish Biology and Fisheries* DOI 10.1007/s11160-017-9492-z.
- Cailliet, G., Natanson, L., Welden, B. & Ebert, D. (1985). Preliminary studies on the age and growth of the white shark, *Carcharodon carcharias*, using vertebral bands. *Memoirs of the Southern California Academy of Sciences* 9, 49–60.
- Chapple, T. K., S. J. Jorgensen, S. D. Anderson, P. E. Kanive, A. P. Klimley, L. W. Botsford, and B. A. Block. 2011. A first estimate of white shark, *Carcharodon carcharias*, abundance off Central California. *Biology Letters* 7:581–583.

- Compagno, L. J. V. (1984). FAO species catalogue. Vol. 4. Sharks of the world. An annotated and illustrated catalogue of shark species known to date. Part 1- Carcharhiniformes. *FAO Fish Synopsis*, 4, 250–655
- Gubili, C., C. E. C. Robinson, G. Cliff, S. P. Wintner, E. de Sabata, S. D. Innocentiis, S. Canese, D. W. Sims, A. P. Martin, L. R. Noble, and C. S. Jones. 2015. DNA from historical and trophy samples provides insights into white shark population origins and genetic diversity. *Endangered Species Research* 27:233–241.
- Hall SJ (1999) Fish biology and aquatic resources series 1. Blackwell, Oxford
- The IUCN Red List of Threatened Species. (n.d.). . <https://www.iucnredlist.org/en>.
- Jackson, J. B. C., M. X. Kirby, W. H. Berger, K. A. Bjorndal, L. W. Botsford, B. J. Bourque, R. H. Bradbury, R. Cooke, J. Erlandson, J. A. Estes, T. P. Hughes, S. Kidwell, C. B. Lange, H. S. Lenihan, J. M. Pandolfi, C. H. Peterson, R. S. Steneck, M. J. Tegner, and R. R. Warner. 2001. Historical Overfishing and the Recent Collapse of Coastal Ecosystems. *Science* 293:629–637.
- Klein, J. D., A. E. B. der Merwe, M. L. Dicken, K. L. Mmonwa, and P. R. Teske. 2019. Reproductive philopatry in a coastal shark drives age-related population structure. *Marine Biology* 166:1–12.
- Knip, D. M., M. R. Heupel, and C. A. Simpfendorfer. 2012. Evaluating marine protected areas for the conservation of tropical coastal sharks. *Biological Conservation* 148:200–209.
- Kock, A., M. J. O’Riain, and K. Mauff. 2013. Residency, Habitat Use and Sexual Segregation of White Sharks, *Carcharodon carcharias* in False Bay, South Africa. *PLOS ONE* 8:13.
- Kuguru, G., E. Gennari, S. Wintner, M. L. Dicken, J. D. Klein, C. Rhode, and A. E. B. der Merwe. 2019. Spatio-temporal genetic variation of juvenile smooth hammerhead sharks in South Africa. *Marine Biology Research* 15:568–579.
- Maduna, S. N., C. Rossouw, C. da Silva, M. Soekoe, and A. E. Bester-van der Merwe. 2017. Species identification and comparative population genetics of four coastal houndsharks based on novel NGS-mined microsatellites. *Ecology and Evolution* 7:1462–1486.

- Merwe, A. E. B. der, D. Bitalo, J. M. Cuevas, J. Ovenden, S. Hernández, C. da Silva, M. McCord, and R. Roodt-Wilding. 2017. Population genetics of Southern Hemisphere tope shark (*Galeorhinus galeus*): Intercontinental divergence and constrained gene flow at different geographical scales. *PLOS ONE* 12:e0184481.
- Navia, A. F., E. Cortés, and P. A. Mejía-Falla. 2010. Topological analysis of the ecological importance of elasmobranch fishes: A food web study on the Gulf of Tortugas, Colombia. *Ecological Modelling* 221:2918–2926.
- Pardini, A. T., C. S. Jones, L. R. Noble, B. Kreiser, H. Malcolm, B. D. Bruce, J. D. Stevens, G. Cliff, M. C. Scholl, M. Francis, C. A. J. Duffy, and A. P. Martin. 2001. Sex-biased dispersal of great white sharks. *Nature* 412:139–140.
- Shiffman, D. S., and N. Hammerschlag. 2016. Shark conservation and management policy: a review and primer for non-specialists. *Animal Conservation* 19:401–412.
- Speed, C. W., M. G. Meekan, I. C. Field, C. R. McMahon, R. G. Harcourt, J. D. Stevens, R. C. Babcock, R. D. Pillans, and C. J. A. Bradshaw. 2016. Reef shark movements relative to a coastal marine protected area. *Regional Studies in Marine Science* 3:58–66.
- Sutcliffe, S. R., and M. L. Barnes. 2018. The role of shark ecotourism in conservation behaviour: Evidence from Hawaii. *Marine Policy* 97:27–33.
- Tienhoven, A. M. V., J. E. D. Hartog, R. A. Reijns, and V. M. Peddemors. 2007. A Computer-Aided Program for Pattern-Matching of Natural Marks on the Spotted Raggedtooth Shark *Carcharias taurus*. *Journal of Applied Ecology* 44:273–280.
- Veríssimo, A., Í. Sampaio, J. R. McDowell, P. Alexandrino, G. Mucientes, N. Queiroz, C. da Silva, C. S. Jones, and L. R. Noble. 2017. World without borders—genetic population structure of a highly migratory marine predator, the blue shark (*Prionace glauca*). *Ecology and Evolution* 7:4768–4781.

Appendix



Figure 1: Map of South Africa's Western cape highlighting locations of Gansbaai and Mossel Bay. Mossel Bay (denoted by the blue circle) is located east of Gansbaai (denoted by the red circle). Original map designed featured by BBC <https://www.bbc.com/news/world-africa-56285651>.

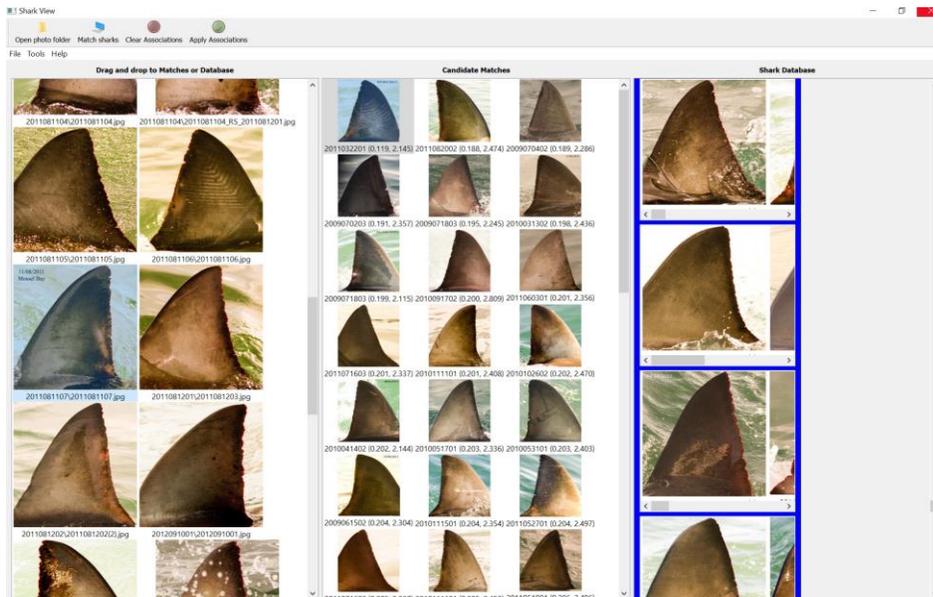


Figure 2: Screenshot from the main screen for Identifin (Andreotti et al. 2018, © Dr. S Andreotti & Dr. P Holtzhausen 2016). Images in the section on the left are uploaded to the software for analysis, and will be compared to the photos in the pre-existing database (shown in the section on the right). Images in the middle will be loaded when the user selects a traced fin to be matched. Potential matches are listed in order from most to least likely.



Figure 3: Screenshot from the notch tracing process performed in Identifin (Andreotti et al. 2018, © Dr. S Andreotti & Dr. P Holtzhausen 2016). To initiate a trace, the cursor will click on the tip of the dorsal fin and drag the line down to identify the location of the trailing edge for the software to analyze (3a). After releasing the cursor, the software will automatically identify the notch pattern and create a red line to highlight the edge (circled in blue) which contains the information to be extracted for the matching process (3b).

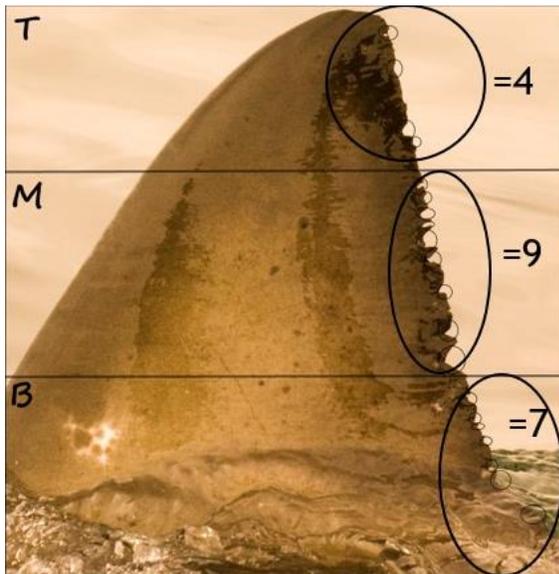


Figure 4: Example of a notch-coding schematic on a Mossel Bay shark used for generating a unique notch code as a means of identification. The top section (T) contains a portion of the dorsal fin with 4 distinct principal notches. The middle section (M) contains 9 principal notches, and the bottom section (B) contains 7 principal notches. Since the shark was identified in Mossel Bay, the unique notch code ID for this shark would be “M_040907”. Schematic produced using Adobe® Photoshop® 22.1.0 Desktop Release (@1990-2020)

Table 1: Summary of sharks identified in Mossel Bay, South Africa, from September 22, 2011 to September 14, 2011. In total 27 individual sharks were identified, with only one matched to a shark in the Gansbaai database. Shark names represent the date the shark was capture (yr.m.d) followed by the order in which the sharks were spotted on that day (...-01, -02, etc.). Fin codes assigned according to Andreotti et al. (2014). Site code is written in order from site of “First ID” to most recent. Site codes are Gansbaai (G), Mossel Bay (M), and Struisbaai. Fin codes followed by a letter (e.g. A or B) denote different sharks with the same fin code. Fin codes with (2) denote re-captured sharks. Sex denoted as female (F) or male (M). Juveniles are considered sharks $\leq 3\text{m}$, while adults are considered $>3\text{m}$ (Kock et al. 2012).

Name	Fin (code)	Sex	LengthTL (m)	First ID
2011.07.22-01	M_111202	F	3.3	M
2011.07.22-02	M_040907	F	4.3	M
2011.07.22-03	M_050705	M	3.0	M
2011.07.22-04	M_060704	F	3.0	M
2011.07.22-05	M_051009	F	4.2	M
2011.07.22-06	M_030805	F	4.2	M
2011.07.23-01	M_060703 A	F	3.6	M
2011.08.11-01	M_080705	M	3.2	M
2011.08.11-02	M_050702	F	2.3	M
2011.08.11-03	M_040803	F	3.2	M
2011.08.11-04	S_M_050704	M	2.5	S
2011.08.11-05	M_050504		2.0	M
2011.08.11-06	M_060004	F	3.2	M
2011.08.11-07	G_M_060801	F	2.8	G
2011.08.12-01	M_071008	F	2.8	M
2011.08.12-02	M_040403	F	3.2	M
2012.09.10-01	M_040603		1.5	M
2012.09.10-02	M_060703 B		3.3	M
2012.09.10-03	M_050301		2.0	M
2012.09.10-04	M_040704	F	3.4	M
2012.09.11-01	M_040703			M
2012.09.11-02	M_080908			M
2012.09.11-03	M_111202 (2)			M
2012.09.11-04	M_030402			M
2012.09.12-01	M_050102			M
2012.09.12-02	M_060703 B (2)			M-2011.09.10-02
2012.09.12-03	M_030603			M
2012.09.12-04	M_040503			M
2012.09.12-05	M_040703 (2)			M-2011.09.10.04
2012.14.12-01	M_060302			M

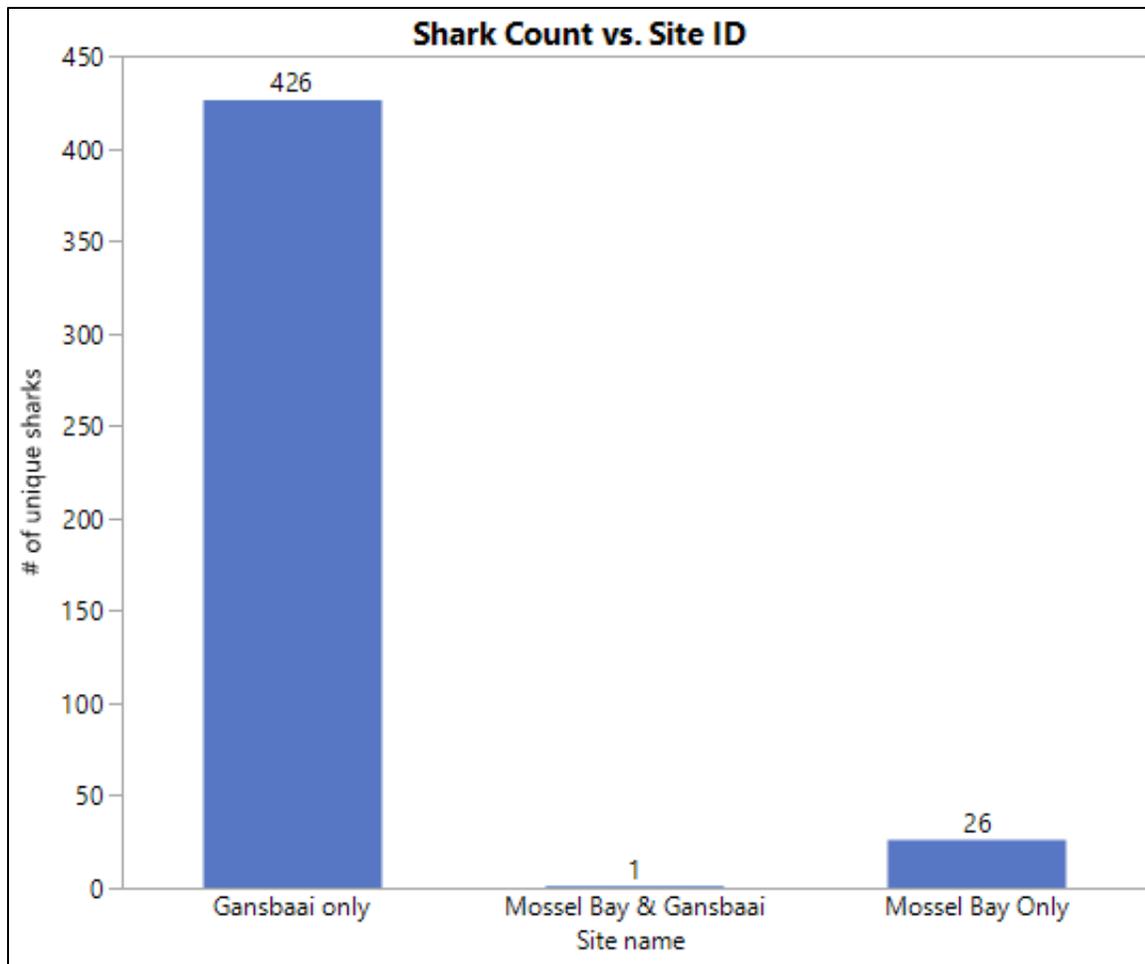


Figure 5: Number of unique sharks identified in Gansbaai only, Mossel Bay only, or both Mossel Bay & Gansbaai. Out of a total (n=) 453 sharks, 426 unique sharks were identified in Gansbaai alone, while Mossel Bay only had 26 unique sharks. Only one shark was identified in Mossel Bay and Gansbaai. Compared to our hypothesis stating the sharks in Mossel Bay would also be identified Gansbaai, using a binomial proportions hypothesis test we can see there is a significant difference in the proportion of sharks identified between both sites