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OF WILD FAUNA AND FLORA

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CSIRO BRIEFING TO DCCEEW ON INDIAN OCEAN WHALE SHARK ABUNDANCE ESTIMATES

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Australia's National
Science Agency

CSIRO briefing to DCCEEW on Indian Ocean whale shark abundance estimates

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Acknowledgement of Country

CSIRO acknowledges the Traditional Owners of the lands, seas and waters of the area that we live and work on across Australia and pays its respects to Elders past and present. CSIRO recognises that Aboriginal and Torres Strait Islander peoples have made, and will continue to make, extraordinary contributions to Australian life including in cultural, economic, and scientific domains.

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1 Purpose:

This document provides an overview of recent CSIRO estimates of abundance of breeding whale sharks (*Rhincodon typus*) in the Indian Ocean. The work has recently been completed and has not yet been submitted for peer review. This research was funded by Ningaloo Outlook (a strategic marine research partnership between CSIRO and Woodside Energy to better understand Ningaloo reef and its important ecological values). We acknowledge Baiyungu, Thalanyji, and Yinikurtura people, the traditional custodians of the land and sea country on which this study was conducted.

The work detailed here is supplied to support Australian Government processes and as general conservation advice. Although it has not yet been through external peer review, it has been through independent CSIRO internal review and CSIRO believe it is the most accurate estimate of whale shark abundance available for the Indian Ocean. CSIRO will seek to publish the study in the peer reviewed scientific literature as soon as possible, noting the importance of the results to various international conservation processes and regional fisheries management authorities.

2 Summary:

CSIRO has collected over 600 tissue samples from whale sharks at Ningaloo Reef in research conducted between 2016 and 2023. These were combined with samples collected by researchers in Madagascar and Tanzania and formed the basis of close-kin mark recapture (CKMR) modelling to estimate population size. From the resultant genetic data, 49 half sibling pairs were detected with clear evidence of shared parentage across the Indian Ocean basin. Population modelling estimated that the breeding size in 2000 was N = 3688 (95%CI: 2854–5889) individuals and that this has declined to just under N = 2065 (95% CI: 1469–3098) in 2019. The model estimated a declining population trend with a 43.47% decline (95% CI: 65%–3% decline) in the 19 years between 2000–2019. While this distribution is wide, there was a 97% probability from our model that the decline is negative and a 73% probability of the decline being greater than 2% per year.

As these are the first estimates of adult abundance based on CKMR there is limited abundance data to compare with our estimates. However, based on the number of kin pairs over a ~20-year period our data and estimates provide direct and strong evidence of a low and declining adult population size for whale sharks in the Indian Ocean. Further samples are required from other populations worldwide to obtain estimates of breeding population size on a global ocean basin scale, but these data indicate significant cause for concern for the species in the Indian Ocean.

3 Background:

The whale shark is the largest fish in the world, reportedly reaching sizes 18 m (McClain et al. 2015) and having the lowest biological productivity of any shark and species (Pierce et al. 2021). They are encountered at known aggregation sites around the globe in tropical waters, but animals that visit these sites are predominantly juveniles and subadults, and mostly males (see Rohner et al. 2021). Very little is known about adult whale sharks, including where pupping occurs. Only one gravid female has ever been examined by scientists (Joung et al. 1996, Schmidt et al. 2010), with this animal carrying 304 pups ranging in size from animals as small as 42 cm TL within in egg cases, to free living animals up to 64 cm in the uterus (Joung et al. 1996).

Due to the fact that they are rarely encountered and presumably travel large distances in remote open ocean waters, assessing adult whale sharks has been extremely challenging and estimates of their population size and status have been highly uncertain.

- Under the Ningaloo Outlook Project (NOP) (see https://research.csiro.au/ningaloo/outlook/), CSIRO collected over 608 tissue samples from whale sharks (see https://research.csiro.au/ningaloo/outlook/whale-sharks/) at Ningaloo Reef between 2016–2023.
- CSIRO also collaborated with researchers studying whale sharks in Madagascar and Tanzania to access tissue samples collected on the western side of the Indian Ocean.
- The aim of this component of the NOP was to estimate the number of breeding adult whale sharks in the Indian Ocean using CKMR.

4 Methods:

4.1 Size data collection/ tissue sampling:

- Under guidance of spotting aircraft, diver teams were guided to whale sharks in the Ningaloo aggregation.
- Divers took biopsies of tissue (Figure 1), collected video measurements using Diver Operated Video (DOV) and took photographs of the left and right flank of each shark to analyse spot patterns.
- The stereo pair of videos from the DOV were analysed using EventMeasure software (SeaGIS Pty Ltd) to record the size of each whale shark. This software utilises imagery from both the left and right cameras (which were previously calibrated using Cal (SeaGIS Pty Ltd) software) to make accurate measurements of fish length. The EventMeasure software also gives an estimate of the precision of each length measurement.
- Spot patterns and genetic samples were used to identify repeat sightings of individuals.

Figure 1. CSIRO dive team collecting a tissue sample from a whale shark along with DOV footage for growth estimation.

4.2 Kin finding:

- Next generation sequencing methods were applied to develop a large set of single nucleotide polymorphisms (SNPs). Each individual was sequenced for these SNPs and these data used to detect closely related individuals among the sampled sharks using CSIRO R package ("kinference") which implements methods used in Hillary et al (2018) and Patterson et al (2022) "
-
- Individuals were classified as either:
  - Self-recaptures
  - Full sibling pairs (FSP)
  - Half sibling pairs (HSP)
  - "Unrelated"—i.e. any relatedness was more distant than half sibling.
- Detected HSPs/FSPs were mapped in space using sampling location to examine potential for mixing or connectivity across the Indian Ocean. In other words, if juveniles sharing a parent are detected across the Indian Ocean, this indicates that a single parental stock is supplying juveniles into aggregations at an ocean basin scale.
- DOV was used to collect growth increments from animals resighted over subsequent years and were used to construct a Von Bertallanfy growth model for whale sharks. This was used to estimate age (with uncertainty) at length. Similar methods as detailed in Bradford et al. (2025) were used to model uncertainty in age-at-length associated with the predictions of age given length.

4.3 Population Modelling using CKMR data

A simple population model was applied to the CKMR data which is described by the following equation

$$N(t) = N(0)\ exp(r\ \Delta t) \qquad (1)$$

where

- $N(t)$ are numbers at time
- $N(0)$ is the numbers in the initial year
- The population growth rate r is estimated as $r = b - z$ where b is the per capita rate at which juveniles join the adult population and z is the total adult per capita mortality rate.
- Δt is the number of years elapsed in the model ($\Delta t = y(t) - y(0)$).

To account for uncertainty in age estimates, for a given set of cohort comparisons, ages a_i conditional on the observed length l_i were drawn from the uncertainty matrix of $a_i^* \sim \text{Prob}(a_i \mid l_i)$ and were resampled in a bootstrap procedure. For each iteration, a data set of CKMR data was formed with the resampled cohort years (based on sampled ages a_i^*) and the model (1) was fitted to the CKMR data. This was repeated 1000 times and the set of predicted abundances was summarised to give expected numbers (median of bootstrap samples) and confidence intervals. Distributions on the model parameters (r, b, and z) were also computed.

5 Results:

5.1 Samples Collected:

In total 608 samples were collected at Ningaloo Reef. Footage was processed to obtain length estimates. Repeat measurements for the same individuals are shown in Figure **2**(a). The resultant growth model is shown in Figure **2**(b). This model is likely underestimating the maximum length-at-age due to the samples coming from younger, smaller animals. However, any potential underestimate is not likely to be influential on our results as we only need to age the animals in our sample set which are all younger, and from ages where the model is likely to be accurate.

(a) (b)

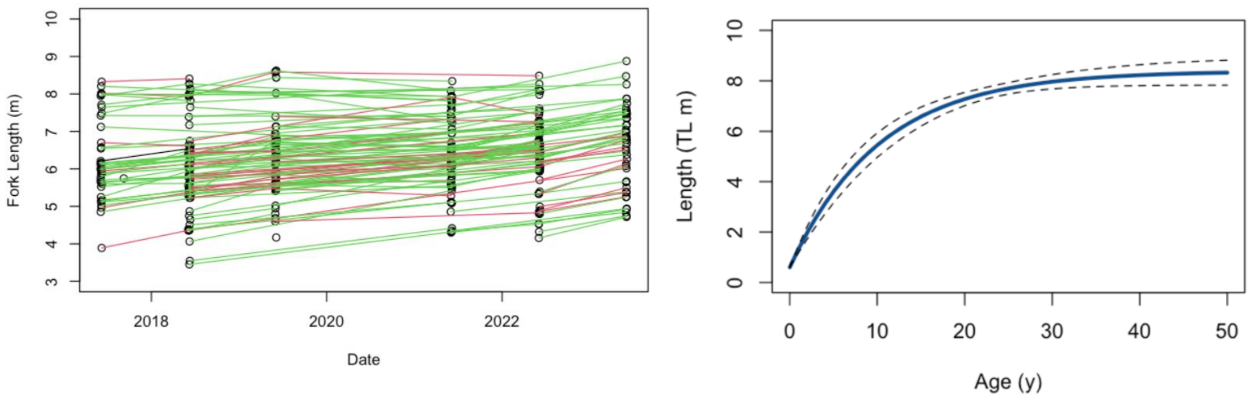
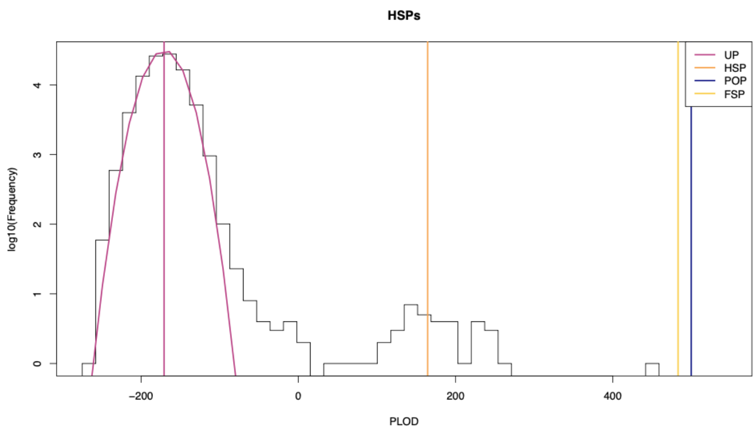


Figure 2. (a) Growth increment data (colours show males (green) and females (red)). (b) Estimated age-at length model used to age individuals and estimate a birth year for use in CKMR models (solid line is the model estimate and dashed lines are the -/+ 1 estimated standard error).

5.2 Kin finding results:

Application of “kinference” methods (CSIRO’s in house approaches for detecting kin-pairs) found N = 49 HSPs in the samples and N = 2 FSPs (Figure 3a). There was clear evidence of shared parentage across the Indian Ocean (Figure 3b) indicating a shared stock at some level. Additional samples from other aggregation sites within the Indian and Pacific oceans are required to confirm the extent of this.

(a)



(b)

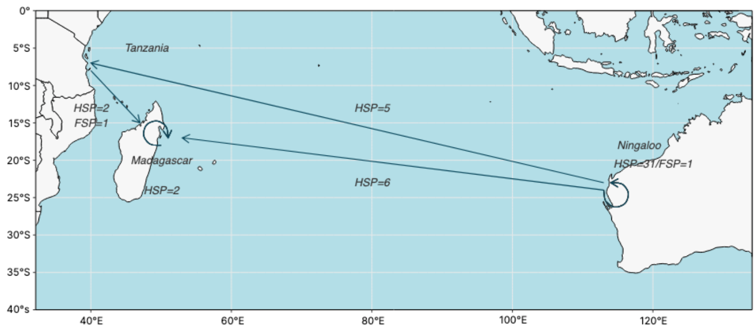


Figure 3. (a) Pseudo-log odds (PLOD) score statistic used to detect kin-pairs. The coloured lines show the theoretical expectation of distribution of unrelated, HSPs and FSPs (and parent offspring pairs—though none were found in this study). The histogram shows the distribution in the observed samples. (b) Evidence for spatial connectivity across the Indian Ocean boundary—HSPs and FSPs show the footprint of shared parentage between western African animals and Australian animals sampled at Ningaloo.

The distribution of detected kin per comparison (Figure 4) indicates evidence of an increasing hit rate through time, which is a signal of a declining population. This is because HSPs become more frequently detected as the population becomes smaller.

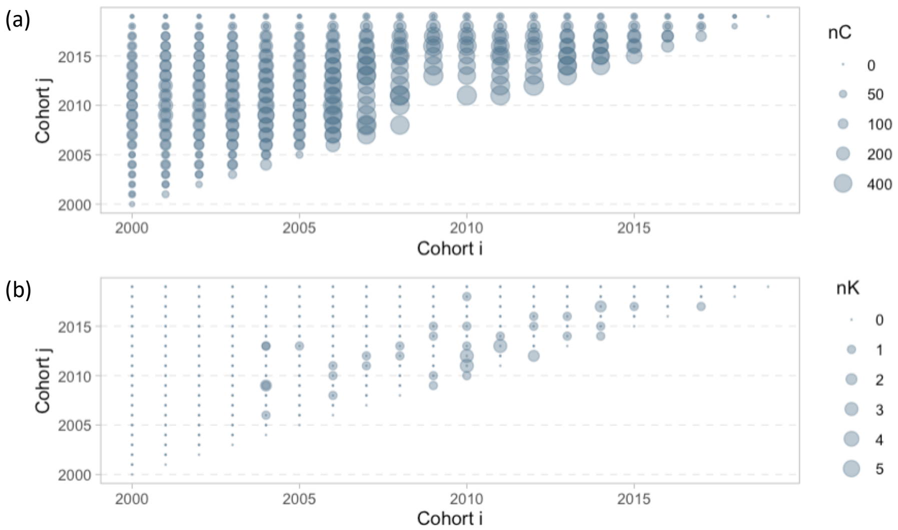


Figure 4. (a) Number of comparisons of individuals by cohort (birth year) against all other cohorts. (b) Number of kin pairs found in those comparisons. The hit rate (number of kin detected per comparison) is directly and inversely related to population size. The lower panel shows evidence of a higher hit rate in more recent years—which would indicate a declining population.

5.3 Population estimates

The population model fitted to the CKMR data indicated there was a low per capita rate of individuals estimated to transition from juvenile to adult (Figure 5a). Survival rates (Figure 5b) were estimated to be high (S = exp(-z): 0.82, 95% CI: 0.76–0.88). The model estimated a declining population trend at an annual rate of ~3.01% (95% CI: 5.7%–0.4% decline) per year (Figure 5c). The breeding size in the y(t) = 2000 was N = 3688 (95%CI: 2854–5889) individuals and that this has declined to just under N = 2065 (95% CI: 1469–3098) adults in y(t) = 2019. From this model, the population is predicted to have undergone a 43.47%

decline (95% CI: 65%–3% decline) in 19 years. While this distribution is wide there is a 97% probability from our model that the decline is negative and a 73% probability of being greater than 2% decline per year.

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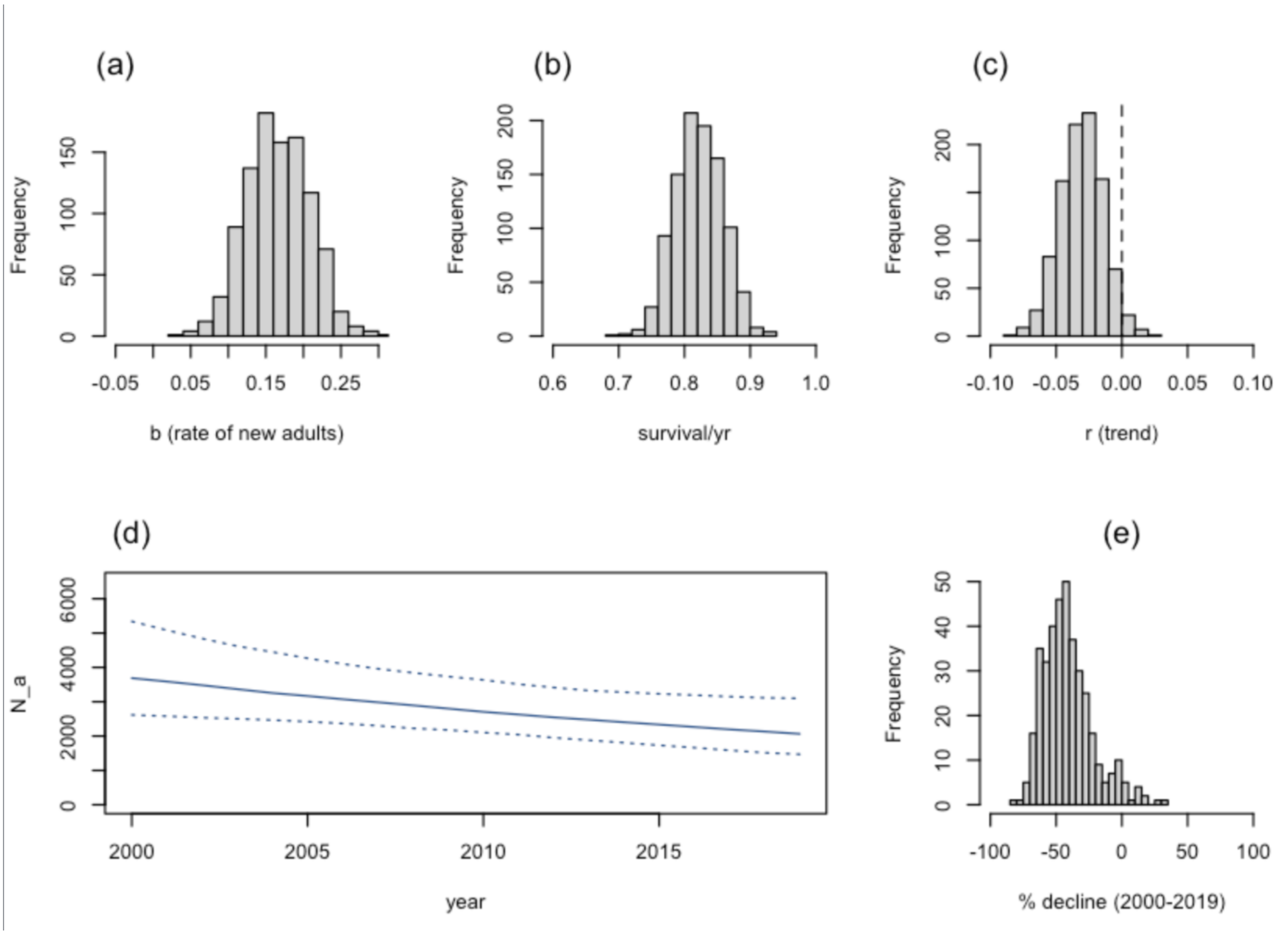

Figure 5. Parameter estimates: (a) The rate of juveniles transitioning to the adult population (per year). (b) Annual survival estimates. (c) Inferred rate of change in the population—the distribution shows very little chance that the population trend is >0. (d) Estimated numbers through time with bootstrap uncertainty intervals (accounting for ageing uncertainty). (e) Distribution of % decline over the years 2000–2019 predicted by the population model.

6 Conclusions

This study presents new data which provide an updated view of the population status of the world's largest fish species. It also provides updated information on growth and population structure.

The detection of shared HSPs between Australia and western African aggregation sites on opposite sides of the Indian Ocean indicates that the two regions share a common parental population. CSIRO is seeking to obtain samples from other sites around the Indian and Pacific oceans to confirm that there is one population of adults in the Indo-Pacific region. This is thought to be the most likely scenario and previous population genetics supports this (Vignaud et al. 2014).

The population estimates produced in this study indicate a small and rapidly declining adult population. While there are gaps in the sampling here, as not all Indian Ocean aggregation sites contributed samples, these data represent the most intensive study of whale shark adult abundance globally. The numbers here are much lower than existing estimates of global effective population size (~103,000–238,000; Castro et al. 2007; Schmidt et al. 2009). However, estimates from CKMR are absolute numbers and do not represent historical abundance.

The data presented herein support previous inferred estimates of whale shark population trend that were the basis for listing the species as Endangered under The IUCN Red List of Threatened Species (Pierce and Norman 2016). Using a number of data sources in the Indo-Pacific, whale shark population declines of 40–92% over the 75 y were inferred (Pierce and Norman 2016).

The results obtained through CKMR are consistent with a regional decline and therefore a substantial cause for concern for the species' ongoing viability. While whale sharks have not been targeted by industrial fisheries since 1990–2000, current sources of mortality include bycatch, ship strike and some targeted artisanal/subsistence fisheries in some regions (Speed et al. 2008; Li et al. 2012; Rowat and Brooks 2012; Capietto et al. 2014). Climate change and ingestion of plastic are also thought to be an emerging threat to the species (Rowat et al. 2021). Due to the long-lived nature of whale sharks, it is uncertain whether the observed decline is due to historical mortality or whether there is ongoing mortality resulting in declining adult abundance. Ongoing monitoring is required to determine this.

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