Title: Effective number of white shark (*Carcharodon carcharias,* Linnaeus) breeders is stable over four successive years in the population adjacent to eastern Australia and New Zealand

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Authors:

Danielle Davenportad, Paul Butcherb, Sara Andreottic, Dean C. Blowere, Conrad Mattheec, Andrew Jonesa, Jennifer Ovendena

Corresponding Author:

Danielle Davenport

Email: danidavenport.au@gmail.com

Paul Butcher <paul.butcher@dpi.nsw.gov.au>

Sara Andreotti <[andreottisara@gmail.com](mailto:andreottisara@gmail.com)

Conrad Matthee <cam@sun.ac.za>

Andrew Jones <andrewthomasjones@gmail.com>

Jennifer Ovenden < j.ovenden@uq.edu.au>

a Molecular Fisheries Laboratory and Schools of Biomedical Sciences, University of Queensland, St. Lucia 4072, Australia

b New South Wales Department of Primary Industries, PO Box 4321, Coffs Harbour, NSW 2450, Australia

c Evolutionary Genomics Group, Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Stellenbosch 7600, South Africa

d Ecosystem Science, Fisheries and Oceans Canada, 1 Challenger Drive, Bedford, NS, Canada

e Tern BioTec, Molecular Genetics, Computer modelling, & Bioinformatics, Emerald, Victoria, Australia

*Animal Ethics Permit Information*

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*Conflicts of Interest*

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*Contributions*

D.D performed sample preparation, data analysis, simulations and wrote the manuscript and prepared the correction. AJ calculated combined estimates and prepared the correction. J.O. & P.B coordinated and led the project. P.B collected NSW samples. S.A and C.M collected S.A samples and performed microsatellite genotyping. These authors contributed to the manuscript. D.B & P.B identified the error and provided analysis that assisted the correction. All authors approved the final corrected manuscript.

Abstract

Population size is a central parameter for conservation, however monitoring abundance is often problematic for threatened marine species. Despite substantial investment in research, many marine species remain data-poor presenting barriers to the evaluation of conservation management outcomes and the modelling of future solutions. Such is the case for the white shark (*Carcharodon carcharias*), a highly mobile apex predator for whom recent and substantial population declines have been recorded in many globally distributed populations. Here, we estimate the effective number of breeders that successfully contribute offspring in one reproductive cycle ( providing a snapshot of recent reproductive effort in an east-Australian New Zealand population of white shark. was estimated over four consecutive age cohorts (2010, 2011, 2012, 2013) using two genetic estimators (linkage-disequilibrium; LD and sibship assignment; SA) based on genetic data derived from two types of genetic markers (single-nucleotide-polymorphisms; SNPs and microsatellite loci). While estimates of using different marker types produced comparable estimates, microsatellite loci were the least precise. The LD and SA estimates of within cohorts using SNPs were comparable, for example the 2013 age-cohort was 96 (56, 198 95%CI) and ) was 247 (148, 567 95%CI). We show that over the time period studied was stable (showed no detectable trend), and ranged between74.6 (20.6 ±SD) and228.7 (57.8 ±SD) per year using a combined estimate of from SNP loci. In addition, a simulation approach showed that in this population the effective population size (Ne) per generation can be expected to be larger than Nb per reproductive cycle. This study demonstrates how breeding population size can be monitored over time to provide insight into the effectiveness of recovery and conservation measures for the white shark, where the methods described here may be applicable to other data-poor species of conservation concern.

*Introduction*

Assessing the size of natural populations is a key objective of monitoring programs which are vital for understanding the conservation status of species, the regulating effects of biotic and abiotic factors, and for the assessment of management efforts (Lindenmayer et al., 2020). However, for many marine populations, there is a lack of consistent monitoring programs at appropriate spatial and temporal scales for conservation and policy needs (Papa, Oosting, Valenza-Troubat, Wellenreuther, & Ritchie, 2020). This presents a significant problem for chondrichthyans (sharks, skates, rays and chimaeras), where more than half of known species are characterised by insufficient data and one-quarter are estimated to be at risk of extinction (Dulvy et al., 2014). Within the elasmobranchs (sharks, skates and rays), each contributes significantly to connect ecosystems and regulate marine food webs (Heupel, Knip, Simpfendorfer, & Dulvy, 2014). However, habitat loss and continued pressures on mortality though bycatch and targeted-fishing have resulted in many populations of elasmobranchs being depleted at a rate that exceeds their natural recovery potential (Worm et al., 2013). Given the significant challenges facing elasmobranchs and the importance of their role in regulating marine ecosystems, improvements for monitoring changes in natural populations is critical.

Monitoring threatened elasmobranch species is particularly challenging for many reasons. In the case of the white shark, *Carcharodon carcharias* (Linnaeus, 1758) monitoring is a both a social and conservation priority, though efforts to establish long term population trends have been hampered by issues including detectability [misidentification in photo-ID surveys (Burgess et al., 2014), lack of re-sightings in mark-recapture studies (Gore, Frey, Ormond, Allan, & Gilkes, 2016), effects of environment on heterogeneity of behaviour (Jacoby, Croft, & Sims, 2012)] and a lack of catch statistics (Roff, Brown, Priest, & Mumby, 2018). The need for alternate methods to index shark populations has therefore led to the increasing use of molecular markers to evaluate change and inform management (Blower, Pandolfi, Bruce, Gomez-Cabrera, & Ovenden, 2012; Bruce et al., 2018; Hillary et al., 2018). In this study, we focus on the concept of genetic effective population size (herein effective population size −), which can be used to evaluate change in abundance from allele frequencies (Schwartz, Luikart, & Waples, 2007). When populations are small, genetic models predict that the evolutionary force of genetic drift (stochastic changes in allele frequencies) will predominate over other evolutionary forces such as natural selection, to reduce genetic diversity, population viability and evolutionary potential (Frankham, 1996; Franklin, 1980). The extent to which a population is vulnerable to such effects is inversely related to the magnitude of , where the effects of drift will occur more slowly in populations with larger effective sizes than those with smaller effective sizes (Wang, 2005). When a genetic sample contains only individuals from a single age-cohort (a group of individuals having the same age-class), then the estimate ofcorresponds to the effective number of breeders () which contributed offspring to that cohort (Wang, Santiago, & Caballero, 2016; Waples, Luikart, Faulkner, & Tallmon, 2013). For long-lived, iteroparous species, estimates of *Nb*are generally considered more useful for monitoring as they apply to a single breeding season and represent an accessible parameter for monitoring population trends at ecological timescales most relevant to conservation and management needs (Ovenden et al., 2016; Schwartz et al., 2007; Waples & Do, 2008). Past research has confirmed the power and usefulness of *Nb* as a tool to monitor population trends (Antao, Pérez-Figueroa, & Luikart, 2011; Nunziata & Weisrock, 2018). For instance, quantifying changes in over time provides high power to detect population declines (Luikart et al., 2020) and has helped to identify factors relevant to shaping populations (i.e., management interventions, demographic parameters) with successful outcomes reported for populations of commercially important bony fishes. Examples include salmon (Bacles et al., 2018; Perrier, April, Cote, Bernatchez, & Dionne, 2016), trout (Ruzzante et al., 2019; Whiteley et al., 2013; Wood, Belmar-Lucero, Hutchings, & Fraser, 2014), snapper (Jones et al., 2019) and tuna (Waples, Grewe, Bravington, Hillary, & Feutry, 2018). In these examples, both *Nb* and *Ne* were used to investigate demographic (i.e. variance in reproductive success under commercial harvest conditions) and environmental (i.e. stream productivity, competition, habitat quality, young-of-the-year development) effects on long-term population viability, with significant implications for management and conservation.

In this study, we trialled a sampling and genotyping protocol aimed at estimating *Nb* over time (four breeding seasons; 2010-2013) in a population of *C. carcharias* of conservation concern. We focus on the east Australia New-Zealand population (EAP) of *C. carcharias* which, due to patterns of coastal residency and site fidelity (Bruce, Harasti, Lee, Gallen, & Bradford, 2019; Spaet, Patterson, Bradford, & Butcher, 2020), is genetically distinct from other identified populations in the North-Pacific, South-West Australia, Atlantic, South Africa, and Mediterranean (Andreotti et al., 2016; Blower et al., 2012; Gubili et al., 2010; O’Leary et al., 2015; Tanaka, Kitamura, Mochizuki, & Kofuji, 2011). The EAP has experienced a large (> 90%) decline during the 20th century due to targeted fishing and mortalities associated with bather protection programs (Reid, Robbins, & Peddemors, 2011; Roff, et al., 2018), however recovery is now anticipated due to protection through international conventions and jurisdictional legislature [i.e. International Plan of Action for the Conservation and Management of Sharks (FAO, 2000) and the Environment Protection and Biodiversity Conservation (EPBC) Act of 1999 (EPBC, 1999)]. Previous efforts to detect population recovery using historical catch data (Roff et al., 2018) and genetic close-kin-mark-recapture (Bruce et al., 2018; Hillary et al., 2018) found a “stable” trend (Bruce et al., 2018). Updated bather-protection programs along parts of east coast Australia (i.e. 'Shark Management Alert in Real Time' (SMART) drumlines, see Tate et al., 2019), aimed at minimising unfavourable interactions with marine environment users, offer an opportunity for non-lethal tissue sampling and to determine the usefulness of this genetic monitoring method in the EAP. Our specific objectives were to: (i) use two genetic methodologies to estimate over time in the EAP [sibship assignment (SA) (Wang, 2009) and linkage-disequilibrium (LD) (Hill, 1974, p. 197; Waples, 2006)]; (ii) validate these results using two types of nuclear genetic markers (single-nucleotide polymorphisms and microsatellites); (iii) investigate ratios using published estimates of the adult population size (*Na*) and (iv) develop expectations for generational in the EAP using life-history information and simulations. Our results for the EAP of *C. carcharias* suggest that has not changed significantly year-to-year and provides insight into the effectiveness of recovery and conservation measures following historical declines.

*Methods*

*Tissue Sampling*

To obtain genetic data to estimate in the east coast Australia-New Zealand population of *C. carcharias* (EAP) tissue samples (*n* = 247) were non-lethally collected during 2015 to 2018 from juvenile and sub-adult *C. carcharias* between Buckley Beach, Narrawalle (-35.29873, 150.48331) and Seven Mile Beach, Lennox Head (-28.76130, 153.62020). Individuals were captured, restrained, tagged and released as part of the New South Wales (Australia) Shark Management Strategy. Fin-clips were collected for genetic purposes and fork length (FL) and total length (TL) measurements were taken from each individual. Since migration between populations can bias genetic estimates of both and (Macbeth, Broderick, Ovenden, & Buckworth, 2011),the population of origin of individuals was resolved through the inclusion of tissue samples of white sharks collected from other locations (Western Australia *n* = 3; South Australia *n* = 9; South Africa *n* = 20; total *n* including EAP samples = 279, see Table S1). All samples were used in the SNP discovery and genotyping pipeline.

*Cohort Assignment*

To group individuals into age-cohorts, a year-of-birth was assigned to each sample using the year the individual was sampled minus the age of the individual in that given year. To estimate the age of individuals, we used the von Bertalanffy growth function (VBGF) (Supplementary Appendix 2) to transform the relationship of TL to relationships at age using growth parameters specific to the EAP (O’Connor, 2011). We considered fork length (FL, defined here as the measurement from the tip of the rostrum to the fork in the tail over the body) the more accurate measurement at the time of sampling. Conversion of FL to TL was achieved by linear regression based on measurements of study samples using the *lm* function in R (O’Connor, 2011). Assumptions of linearity, normality, and heteroscedasticity were checked by means of residual and quantile plots and the following conversion was used to transform measurements:

TL (cm) = 6.80 + FL (cm) \* 1.07

Equation 1

*SNP and microsatellite loci datasets*

DNA was extracted from all samples (*n* = 279) using a standard salt precipitation procedure. The samples were genotyped by DArT P/L laboratory using DArTseqTM technology (Kilian et al., 2012). Sequencing steps followed Kilian et al., (2012) and were completed using an Illumina Hiseq2500. Resulting sequences were processed using the proprietary DArT analytical software, DArTsoft14. DArTsoft14 uses technical sample replicates to optimize its algorithm parameters and ensure scoring consistency (see Georges et al., 2018). Post-processing of SNPs was completed in R (R Core Team, 2018) using various R-packages (dartR, v.2 (Mijangos et al., 2022), hieferstat (Goudet & Jombart, 2022)) and custom R-scripts following current best practice (see O’Leary, Puritz, Willis, Hollenbeck, & Portnoy, 2018; Shafer et al., 2017). A two-stage post-processing approach was employed to the SNP dataset to identify and remove 1) migrants and 2) outlier (non-selectively neutral) loci. SNP data representing all samples (East Australia, South Africa, Western Australia, South Australia) were filtered following the steps outlined in Table S3.1 (Supplementary Materials 3), and subsequently used for sample population assignment and initial outlier loci discovery. Strongly divergent individuals create strong mixture LD which downwardly bias estimates of (Waples & England, 2011) and may contribute to upward bias in estimates using the SA method (Ackerman et al., 2017). To identify divergent individuals, we performed a Discriminant analysis of principal components (DAPC) (Jombart, Devillard, & Balloux, 2010) implemented in the R-package *adegenet* (Jombart et al., 2010). The optimal number of discriminant functions to retain was calculated using the function *xvalDAPC* using 80% of the data in the training set, and the number of PCs retained in the final DAPC were associated with the lowest Mean Squared Error. As indicated in Figure S3.1 (Supplementary Materials 3), two samples collected from east Australia appeared distinct from other EAP samples (subsequently confirmed using tracking data from acoustic tagging, Spaet et al., 2020). These samples were removed from subsequent analysis. We also performed tests for outlier loci which deviate from the assumptions necessary for estimating (Waples & England, 2011). We used *pcadapt* (Luu, Bazin, & Blum, 2017) which identifies outlier loci in a multidimensional space (we used *k* = 1 principal components). We removed loci when the q-value (test statistic) was smaller than the false-discovery rate (). In the second stage of SNP post-processing, we used a dataset (herein Dataset-2) containing all SNP loci except those identified as outliers and including samples representing genotypes of EAP origin only. We then filtered Dataset-2 using reproducibility greater than 98%, a minor-allele-count greater than three, coverage (minimum 5, maximum 25), retained only one SNP per locus and removed individuals missing (call rate) > 0.75 of SNP loci. Loci were further removed where Hardy-Weinberg disequilibrium mid-*p*  and if *FIS* was ± 0.5 (see Table S3.2, Supplementary Materials 3). Dataset-2 was then used to make estimates of *Nb*. We use the method of Luikart et al., (2020) (ordinary least squares regression), and Generalized least-squares (GLS regression) that incorporates an estimate of autocorrelation, to test the significance of a trend in Nb estimates across cohorts.

Extracted DNA from 192 EAP samples were further genotyped in another laboratory (Stellenbosch University) with nineteen species-specific microsatellite loci to provide alternate estimates of . Fourteen of the loci were derived from previous studies: Ccar1, Ccar13, Ccar6.27x, Ccar9, Iox10, Cca1419, Cca83, Cca1536, Cca1273, Cca711, Cca1072, Cca1466, Cca1276, Cca1226 (Gubili et al., 2010; O’Leary et al., 2015; Pardini et al., 2001). Five loci (CcSA1, CcSA2, CcSA3, CcSA4 and CcSA5) were developed using the methods described in Andreotti et al. (2016). Wet lab genotyping was performed as described by Andreotti et al. (2016) and genotype scoring was performed in *Geneious* v.5.6.5 (©2005 - 2012 Biomatters Ltd). Assessment of amplification errors, such as large allele drop-out, stuttering and null alleles was conducted in *Microchecker* v.2.2.3 (Van Oosterhout, Hutchinson, Wills, & Shipley, 2004). The program SHAZA (Macbeth et al., 2011) was used to detect duplicates in the dataset. Descriptive statistics, including observed heterozygosity (Ho) and expected heterozygosity (He) were calculated using the R-package *hierfstat* (Goudet, Jombart, & Goudet, 2015).

*Estimation of Nb*

Two methods were used to estimate from data derived from SNP and microsatellite loci: (1) the linkage-disequilibrium method (LD) (Hill, 1974; Waples, 2006) and (2) the sibship assignment method (SA) (Wang, 2009). Estimates are referred to as and . Broadly, the LD method determines the size of the parental generation using a measure of the genetic association (or LD) in a given age-cohort. In finite populations, random genetic drift leads to associations of alleles at different loci. The LD method uses the extent of non-random association between alleles at different loci to estimate genetic *Ne* and reflects the inbreeding *Ne* when loci are unlinked (Hill, 1981; Waples & Do, 2010). The formulation of the LD method uses the observed average disequilibrium between pairs of independent (ie. non-linked), neutral loci in a sample of individuals taken from a single, isolated, randomly mating population. Estimates of *Nb(LD)* are based on the theoretical relationship between and as described in Hill (1981);

Equation 2a from (Waples & Do, 2010)

where r2 is the mean squared correlation of allele frequencies at different gene loci adjusted for sampling error (i.e. the observed average disequilibrium) and *S* is the number of individuals sampled. We implemented this method using the program *NeEstimator* v2.1 (Do et al., 2014). In contrast, the SA method uses the direct relationship between genetic relatedness and inbreeding *Ne*, such that any two individuals sampled randomly from a population with a small *Ne* will have a higher probability of sharing the same parent or parents (Wang, 2009). The SA method (Wang, 2009) determines the size of the parental generation by estimating the probability that dyad relationships are either full or half siblings in a sample from the same cohort, sharing two, one or zero parents, respectively;

Equation 10 from Wang (2009)

where Q1, Q2, Q3 are the paternal, maternal half-sibs and full-sibs respectively, N1 andN2 are the number of male and female parents, and is a measurement of the deviation from Hardy-Weinberg proportions in genotype frequencies (Wang, 2009). The SA method was implemented in the program COLONY (Wang, 2009).

Both and were estimated for the EAP across four year-of-birth-cohorts (2010, 2011, 2012, 2013) where sample size per cohort was greater than 25 individuals. Where the sample size of a cohort was less than 25, results are reported in Supplementary Materials Table S5.1. Estimates of and were made using either SNP or microsatellite marker data sets. To estimate with *NeEstimator v2.1* (Do et al., 2014) a random mating model was specified, rare alleles which upwardly bias estimates were excluded using the criterion = 0.05 as recommended in Waples and Do (2010), and jack-knife confidence intervals that accounts for pseudo-replication due to physical linkage and overlapping loci pairs were used (Jones, Ovenden, & Wang, 2016; Waples & Do, 2010). To estimate , relatedness coefficients were estimated for individuals within each year of birth cohort using COLONY v2.0.5.6 (Jones & Wang, 2010). COLONY estimates the likelihoods of full, maternal-half and paternal-half siblings depending on the mating system chosen in the programs settings, which may impact the final estimate of . We tested different COLONY parameters to determine any effects on the final estimates of (Supplementary Appendix 4). Results are presented for the maximum-likelihood with random mating model, with male polygamy/female monogamy, no update of allele frequencies, medium sibship prior (sibship size per parent , run for 5 replicate runs, error rate 0.001.

*Inference of Nb/Na ratios*

To calculate ratios we used as described in Bruce et al., (2018), where *Na* is the number of adults in the population. As the species has a low intrinsic capacity for population increase, low fecundity and low life-time variance in reproductive success (Bruce, 2008), the *Na* estimates from Bruce et al. (2018) apply to the time period corresponding to our study; =750 with an uncertainty range 470 to 1,030 (Bruce et al., 2018). Our estimates of and ) were combined (herein to provide a single-value of with which to infer ratios. and ) were combined by taking the harmonic mean of the two values, weighted by the inverse of their variances as suggested in previous studies (see Waples & Do, 2010); see Appendix A. In our study, the differences between the estimates from the LD and SA methods were not overly large, so using a combined estimate of to determine the ratio would not change the conclusions described herein.

*Expectations for Ne*

To develop expectations for generational *Ne* in the EAP of *C. carcharias*, we use a simulation-based approach. This route was taken as the assumptions of single-sample genetic estimators of , including LD and SA methods used herein, dictate that data used to make estimates represents a random sample of a population across an entire generation (Hare et al., 2011). Since the white shark is long-lived and samples in this study were mostly juvenile or sub-adults, we instead characterise the expected ratio using simulations based on published methods and parametrised using the life-history of white sharks, to permit a better understanding of inbreeding and implied fitness of the population. We use both deterministic and forward-time population simulations following methods described in Waples & Antao, (2014), to determine and . First, we implemented the discrete-time, deterministic hybrid Felsenstein–Hill method for calculating in iteroparous species (Waples, Do, & Chopelet, 2011). The model was implemented in the software *AgeNe* (Waples et al., 2011), herein , and parametrised using life-history information from white sharks in the EAP (Supplementary Appendix 6). Furthermore, since the Felsenstein-Hill method assumes the probability of reproduction is not affected by events in previous time periods, we also use forward-time population simulations implemented in simuPOP (Peng & Kimmel, 2005), to create a single, isolated, randomly mating population to further characterise the ratio under two intermittent-breeding scenarios as in Waples & Antao (2014). Each simulation was parametrised using outputs from AgeNe, including total population size and stable age distribution in the population, given the specified vital rates and a specified number of offspring produced per cycle that survived to age 1 (N1), here N1 = 1000. Each individual was represented by 100 microsatellite-like loci, each having 10 possible allelic states, no mutation, and data was tracked for 50 reproductive cycles after a burn-in period of 50 cycles. We forced a number of females to skip either zero, one or two cycles of breeding (a proportion of females) hypothesised in this species (Domeier & Nasby-Lucas, 2013; Mollet & Cailliet, 2002). Intermittent or skipped breeding occurs when sexually mature adults skip breeding opportunities (Last & Stevens, 2009; Shaw & Levin, 2011), in this case likely due to the costs of reproduction or prolonged gestation period in females (Bruce, 2008). We directly calculated mean () and variance () lifetime reproductive success, and and directly from simulation demographic data (not genetic data) for each reproductive cycle using Equation 1 and Equation 2 from Waples et al., (2014), where presented values represent the arithmetic mean of , and the harmonic means of and calculated across 10 population replicates, herein .

*Data Availability*

Data for this study are available at zendoo: <https://doi.org/10.5281/zenodo.10172611>. All plots in this study were made using the *ggplot2* package in R (Wickham, 2016).

# *Results*

*Cohort Assignment*

Using the relationship between TL and age we found that one individual was born in 2005 with various years represented by the following number of individuals; 2007 (n = 3), 2008 (n = 6), 2009 (n = 10), 2010 (n = 30), 2011 (n = 43), 2012 (n = 53), 2013 (n = 67), 2014 (n = 23), 2015 (n = 9) and 2016 (n = 2). The physical size of individuals within age-cohorts increased with age (Figure S2.1). The range of FL between age-cohorts overlapped principally driven by heterogeneous year-of-capture sampling; 2010 (*n* = 30, 224 cm and 296 cm FL), 2011 (*n* = 43, 207 cm and 276 cm FL), 2012 (*n* = 52, 187 cm and 255 cm FL) and 2013 (*n* = 67, 174 cm and 268 cm FL) (Table S5). As low sample sizes can bias estimates of using the methods of this study, only age-cohorts containing greater than samples were used (2010, 2011, 2012 and 2013).

*SNP and microsatellite loci data*

The DArTsoft14 pipeline delivered 9841 SNPs across 9180 loci. The final SNP dataset after filtering consisted of 4256 diallelic SNPs consisting of 235 EAP individuals with high quality SNP genotypes (Dataset-2). Nineteen microsatellite loci were successfully genotyped across 181 EAP individuals. No evidence of null alleles or scoring errors were detected. The genotypic distribution of microsatellite genotypes per locus showed three loci did not conform to the expectations of Hardy-Weinberg equilibrium using (loci Cca1419, Cca1072, CcSA2). These markers were removed from further analysis (LD method only). One locus (CcSA5) was not polymorphic (see Table S6.1) and was also excluded. Per individual, 97% had no missing loci while the remaining 3% of samples had three or less missing loci.

*Estimates of Nb*

Using SNP data, estimates per year-of-birth cohort were similar between the LD and SA methods and had overlapping 95% confidence intervals (Table 1). Tests for a trend in Nb overtime using regression methods was not significant (OLS regression p-value = 0.345; GLS regression p-value = 0.861). Estimates of were not sensitive to changes in model parameters such as the sibship prior, inbreeding settings, error rate and polygamy settings (Table S4.1). This was consistent with the expectations of the SA estimator which becomes increasingly independent of the prior with increasing marker information and sample size.

Comparing between the SA and LD method using data from microsatellite loci, estimates of were higher than the equivalent estimate of . The number of estimated full and half sib-ships in each cohort sample was high and pairwise-probabilities were low (data not shown) compared to those sib-ships estimated using SNPs. This resulted in estimates being substantially lower than the equivalent SNP estimate, with the exception of 2011 (Table 1). The were the least precise estimates, where all but one cohort (2013) did not return an upper (95% CI) estimate.

The ratio was estimated using combined estimates of. For cohorts 2010 to 2013, ranged from the smallest estimated value in 2010, to the largest in 2011, (Table 1). The inferred ratio of ranged from = 0.10 to = 0.30, calculated using estimates of from Bruce et al., (2018).

The ratio of was evaluated using simulations. Using a standard model implemented in *AgeNe* yielded estimates of , of 372.7 and 857.2 respectively, and an ratio of 0.43. To account for variations in breeding biology, further forward-time population simulations in SimuPOP showed the equivalent no-skip breeding model closely reflected AgeNe results ( = 365.46, = 860.67), validating the model, while alternate breeding models decreased the ratio (see Table S6.2).

*Discussion*

Monitoringcan inform management decisions in populations of conservation concern, where is analogous to *Ne* except that it represents the effective number of breeders per year rather, rather than per generation. Using data from SNP and microsatellite loci and two single- sample genetic estimators of effective population size, our results show the effective breeding population () of the EAP has remained unchanged across four successive years (2010–2013), although we caution that these results may not be indicative of a broader temporal trend. Our study supports existing evidence (Hillary et al., 2018; Roff et al., 2018) that the white shark population has not changed significantly in size over the years studied herein, despite measures implemented to rebuild the population. The white shark recorded substantial declines through the 20th century in Australia and New Zealand and has since been the subject of legislated protection and management interventions targeted toward population recovery (i.e., National Plans of Action for the Conservation and Management of Sharks Commonwealth of Australia, 2013; EPBC, 1999; Shark Advisory Group, 2004). However, monitoring using the methods describe herein could assist management and conservation efforts. Indeed, as past studies have shown, monitoring for as few as five consecutive reproductive cycles could be used to detect change in (declines), even in species with long generation intervals (Antao et al.,2011; Wang, 2005; Luikart et al., 2020) such as the white shark, with implications for both and in some circumstances. For example, if were to decline significantly for multiple reproductive cycles, then both and may be affected (Luikart et al., 2020). Alternatively, if ratios are observed to be stable over many generations, then it has been suggested that (or ) may be inferred from , which would be of use to population monitoring and evaluation of conservation and management actions (Luikart et al., 2020). To this end, we recommend using to track year-to-year changes in the effective number of breeders as a timely assessment of population status over time to provide insights into the effects of current management actions and co-occurrences such as environmental changes. As in this study, future tissue samples for monitoring could be obtained as part of existing bather protection programs (i.e., SMART drumlines; see Tate et al., 2019).

In this study, we used two genetic marker types (SNPs and microsatellites) and two single-sample genetic estimators of effective population size (LD and SA) to estimate . Both estimators showed more precision and power when SNPs were used to estimate compared to the few microsatellites used in this study. We therefore recommend the use of SNPs for the future monitoring of the EAP. Although estimated from both SNP and microsatellite were comparable and results reflected differences between genetic marker type similar to those reported in previous studies (e.g., Beebee, 2009), here the few microsatellite loci used were unable to estimate upper CIs for age cohorts without significant sampling effort (>50 samples). Of note, estimates of were consistently higher than the equivalent estimates of . This can be attributed to the overestimation of sibship dyads, which can be expected to decrease estimates of (Table 1). This has been noted in previous studies (Ackerman et al., 2017; Wang, 2009) which have demonstrated that false sibships (type I errors) occur with a higher frequency compared to false nonsibships (type II errors) when either genetic information or true sibship within a sample is insufficient (i.e., few loci, low polymorphism, small sample size relative to total population size, low inclusion of siblings).  estimated using SNPs differed between methods, although differences were not significant having overlapping CIs. estimated using SNPs showed those cohorts with larger numbers of samples (i.e., 2013) provided more precise estimates, a result expected given genetic methods for estimating contemporary effective size depend on signals that are proportional to (Waples et al., 2014, 2018).

Monitoring studies are often focused on the number of individuals in a population; however, the relationship between effective size and population size (i.e., , ) is important to understand since genetic drift results in the loss of neutral genetic variation at a rate inversely proportional to per generation, not (Wright, 1931) and can therefore be useful for examining how different ecological factors influence genetic variation (Nunney, 1996). In this study, the ratio of was approximately 1/3 of mature adults for a single reproductive cycle, where mature adults represent different adult age classes. This is somewhat comparable to ratios inferred for other Carcharhinidae, including *C. plumbeus* (sandbar shark) in Delaware Bay, North Atlantic, which ranges between 0.50 (95% CI 0.45) and 0.63(95% CI 0.57) (Portnoy et al., 2009). Since a ratio of applies to a single reproductive cycle; when ratios are close to 1, we can infer that the majority of the adult population contribute to the next generation and that the offspring number per adult approaches the standard scenario of binomial distribution (Hedgecock, 1994). In contrast, when ratios are < 1, we can infer there is some deviation from the ideal (Hare et al., 2011). A number of factors will affect this relationship (, ) including fluctuations in population size and several important life-history factors that change variance in reproductive success (e.g. mating system, generation time, sex difference including sex ratio, survival, recruitment age). In one case, may be expected to be reduced relative to Na if females with high fecundity skip reproductive cycles after giving birth, resulting in different females breeding in different cycles (Waples & Anato, 2014). This should decrease both lifetime and , while increasing . The ratio reported herein appears to be consistent with expectations for the breeding behavior of C. carcharias, suspected to undergo intermittent breeding (Bruce, 2008). Observations suggest the gestation period of *C. carcharias* females may approach 18 months from fertilization to parturition (Bruce, 2008; Mollet et al., 2000), resulting in the unavailability of a portion of adult females to produce offspring each cycle. However, we caveat that ratios determined in this study used estimates of from best available information from close-kin-mark-recapture estimates for the EAP in 2017 (see Bruce et al., 2018). Thus we assumed temporal stability of over time; an assumption which would be violated if has increased (or decreased) over the time period to which our estimates apply (2010-2013).

Since neutral genetic variation is lost at a rate of per generation (Wright, 1931), even numerically large populations can be at genetic risk if is small (Waples et al., 2018). Although important, due to sampling restriction (i.e., difficulty sampling across a generation as required by estimators) and uncertainty of breeding histories, we could not estimate directly nor did we consider the linear relationship between and which requires either true or estimated to be quantified (Waples et al., 2013). Blower et al., (2012) provided the first genetic estimate of for the EAP using 6 SSR markers. Finite point-estimates showed effective population size was = 380, Pcrit = 0.18 (95% CI = 31 − ∞, n = 62), however, as the authors used both juvenile (n = 55) samples and adult samples (n = 7), this value likely represents something between and . Instead in this study, using simulations, we show that maybe expected to be less than using life-history information for white shark (, and that can be expected to be much less than if intermittent breeding were occurring. This aligns with expectations of where a small number of offspring, delayed maturation, intermittent breeding, and low lifetime variance in fecundity act to increase relative to or (Waples & Antao, 2014). This result is important as it suggests the study population in the EAP at least exceeds the inbreeding avoidance goal ( > 100) (Frankham et al., 2014) (previously the -50 rule), which describes the short term goal required to avoid inbreeding, which results in excess homozygosity for deleterious and recessive alleles, leading to inbreeding depression and reduced fitness (Frankham et al., 2014). However, in relation to the long-term viable population benchmark, 1,000 (previously > 5 00) (Frankham e t al., 2014) our results are less certain, and we caveat that this rule ( > 1000) refers to the loss of additive genetic variation that may negatively affect adaptation in response to changes in selective regimes, not inbreeding effective size as estimated herein. We suggest any genetic effects of a recently and significantly reduced population size in the EAP, such as a decline in or loss of heterozygosity, may not be fully realized until adequate benchmark studies can be completed (i.e., historical or ancient DNA). However, genetic bottlenecks in white sharks have been recorded elsewhere (O’Leary et al., 2015). Given this, together with the lack of evidence from other studies to date of an expected recovery (except see Department of Primary Industries, 2019), our results emphasize the importance of continued monitoring, improved protections, and interventions to reduce mortality. Indeed, the vulnerability of chondrichthyan fishes to exploitation has been comprehensively documented (Hutchings et al., 2012) and relative to other marine fish, the intrinsic capacity for population increase and rebound potential in white shark is low (Cortés, 2002) (i.e., long-lived, late age to maturity, high juvenile survival). In addition, shark species often travel large distances and use different habitats throughout their lives (Fujioka & Halpin, 2014), where they may be vulnerable to environmental changes (density, food availability, climate, illegal fishing). Regrettably, mortalities continue to occur in the EAP driven by action taken to mitigate human–shark interactions. During the years 2018–2019, 51 bather protection nets were distributed across seven regions of NSW (Australia). Catches of white shark and other shark species are only recently increasing year-on-year (Department of Primary Industries, 2019) following long term declines over 80 years of the bather-protection program along the east coast of Australia, which has been lethal for sharks despite catch-and-release programs (Roff et al., 2018). The recent modeling of the recovery of the North West Atlantic white shark population provides a useful principal in this regard; “every fish counts” (Bowlby & Gibson, 2020, p.9).

*Conclusion* We

We have used genetic data to estimate the size of the effective breeding population () over four consecutive years (2010 to 2013) for white sharks in an east Australian–New Zealand population, representing an indirect measure of reproductive effort over a relatively short temporal period. Our results suggest has remained stable over four years and agrees with previous studies that report stability of population size in the EAP, where estimates were more precise using data from SNP rather than microsatellite loci and estimates from two single-sample genetic estimators were similar. However, longer time series of data are needed to determine the efficacy of past and present management and conservation actions on the genetic constitution of the population. We suggest future monitoring using should continue given the availability of nonlethal tissue samples from bather protection programs, the ease of genomic data collection and analyses, and the complementary nature of and estimates.

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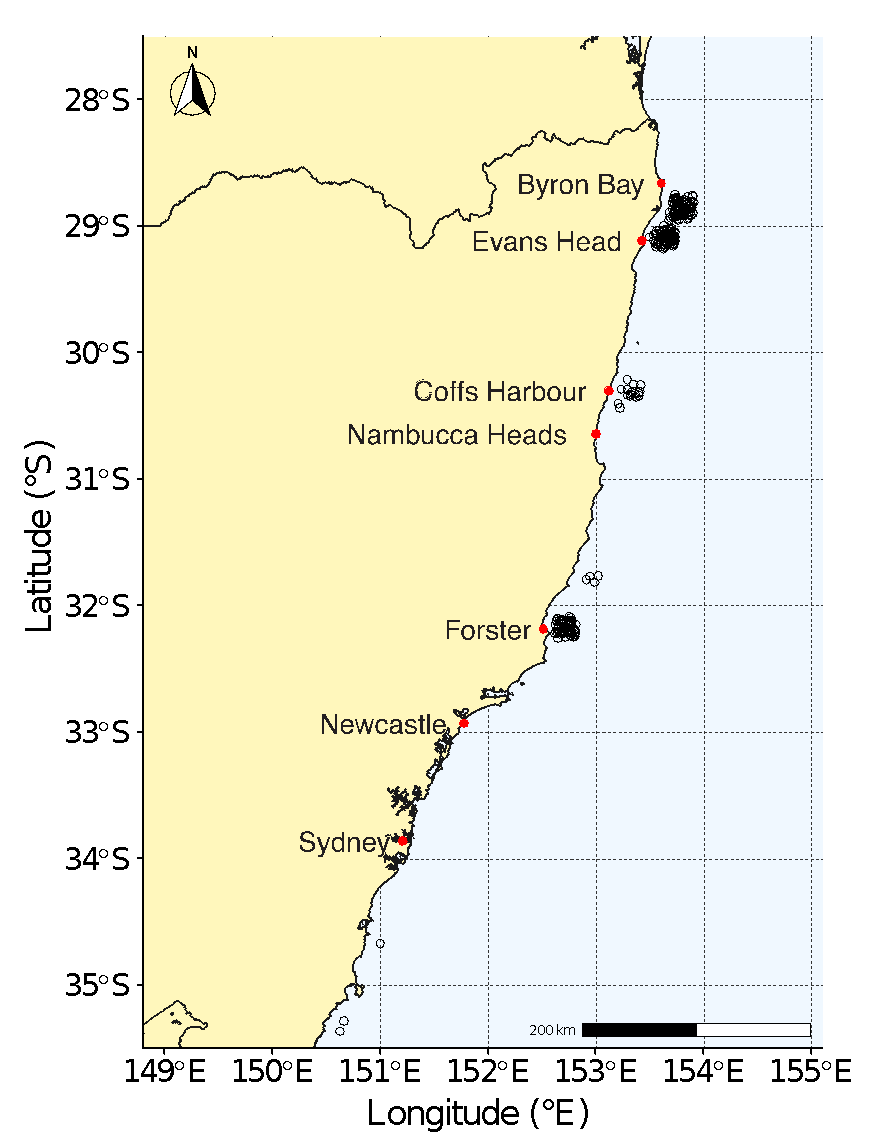
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*Figures*



**Figure 1.** Map of sampling locations, where 247 EAP samples (open circles) were collected along the NSW coast and used to determine Nb.

**Table 1.** A comparison of empirical annual effective size determined from genetic data (microsatellites - MSAT and single-nucleotide polymorphisms - SNP) using either the linkage-disequilibrium or sibship assignment method per year-of-birth-cohort for the EAP of *C.carcharias*. Lower and upper confidence intervals in braces (lower CI-upper CI) and the number of samples used to make the estimate (*n*) is reported. The standard deviation (±*SD*) is reported for the combined estimate of and the number of full and half-sibling pairs are reported in square braces [full-sib, half-sib in square brackets].

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | **2010** | **2011** | **2012** | **2013** |
| **MSAT** | ***n*** | **21** | **33** | **39** | **54** |
|  |  | ∞  (82.5-∞) | 263.9  (51.4-∞) | 128.7  (43.1-∞) | 122.6  (49.3, 12934.9) |
|  |  | 33  (18,74)[7,56] | 49  (30,84)[3,95] | 51  (36,88)[5,97] | 62  (41,96)[17,137] |
| **SNP** | ***n*** | **29** | **39** | **52** | **63** |
|  |  | 62.1(32.7, 249.5 | 208.1 (110.1, 1135.9) | 201.9 (126.7, 449.0) | 179.8 (121.9, 320.8) |
|  |  | 96(56,198)  [7,3] | 247(148,567)[4,5] | 196(132,332)[8,15] | 174(123,252)[16,22] |
|  |  | 74.6 (20.6) | 228.7 (57.8) | 197.21 (39.08) | 174.85 (29.3) |
|  | † | 0.10 | 0.30 | 0.26 | 0.23 |

† The ratio *Nb/Na* determined using combined estimate, where *Na* represents the adult population size, estimated for the year 2017 (Bruce et al., 2018)

*Appendix A*

**Inverse-variance weighted mean method and worked example**

This is a worked example using data from a fictious sample. This weighted mean will give the lowest variance of any weighted mean of the values. As with nearly all Ne calculations the harmonic mean must be used as the real quantities of interest is proportional to 1/Ne.

**Values**

**LDNe: 208.5**

**COLONY: 289**

**Sample Size: 63**

## **The Variances**

Unfortunately, neither COLONY or NeEstimator (Do et al., 2014; Jones & Wang, 2010) provides the raw variance figures required, however these can be approximated by working backwards from the provided confidence intervals.

### **COLONY**

Colony generates 95% confidence intervals using the following formula:

where V\* is the variance of the estimate of 1/. Knowing the upper and lower bounds of this confidence interval, we can estimate V\* as,

or,

Where L\* and L are the lower confidence bounds in terms of 1/ and respectively. An identical argument follows for the upper bounds. However, we desire the variance of , which we can approximate using a first order Taylor expansion. That is,

. Substituting in our particular case,

We also have

via the upper bound. These are now in terms of known values and we can estimate .

|  |  |  |  |
| --- | --- | --- | --- |
| Ne | U | L | . |
| 289 | - | 200 | 4134.811506 |
| 289 | 461 | - | 2906.636596 |
| Mean | | | 3520.724051 |

### **Ne Estimator**

Similar to COLONY Ne Estimator does not provide raw variances, and we need to work in terms of the confidence intervals for which we will call here r\*. The drift term is approximately , where S is the sample size. The 95% confidence interval for r\* is explicitly normal in the case of the jackknife confidence interval (Jones, Ovenden, & Wang, 2016). Thus, V\*, the variance of r\* is approximated by

where U and L are the upper and lower bounds provided for r\*. However, again, we wish to have the variance in terms of . Using the same approach as for COLONY, we will approximate this using The true function used to calculate Ne using r\* can be found in Table 1 in Waples & Do (2008), here we use the simpler original form (Equation 1 in Jones et al 2016 and others) as our for this estimate, that is

Working as before,

However, we still need to obtain and the upper and lower confidence bounds for r\*. This can be achieved by inverting the function of r\* and S from Table 1 in Waples & Do (2008). In this particular case we cannot use the simple approximation. In our case the inverted function is

|  |  |  |  |
| --- | --- | --- | --- |
| Ne | CI Bound (Ne) | CI Bound () |  |
| 208.5 | 116.4 | 0.000368638 | 6523.337897 |
| 208.5 | 712.7 | 6.05919E-05 | 10252.64749 |
| Mean | | | 8387.992693 |

**Weighted Mean and Final Variance**

Now we follow the formula the weighted harmonic mean,

where the weights, , sum to 1. In this case we need to normalise the inverse-variances to sum to 1.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Ne** | **Method** | **Variance** | **Inverse Variance** | **Normalised Inverse Variance Weight** |  |
| 289 | COLONY | 3520.724051 | 0.000284032 | 0.704357394 | 0.003460208 |
| 208.5 | LD | 8387.992693 | 0.000119218 | 0.295642606 | 0.004796163 |

The final mean estimate is:

259.3917339

The COLONY estimate has a lower variance and thus contributes around 2/3 of the final estimate (70.4%).