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Accuracy of species identification by fisheries observers in a north Australian shark fishery

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ABSTRACT

Despite the importance of observers to collect data for effective fisheries management worldwide, their species-identification abilities are rarely assessed. Misidentifications could compromise observer data particularly in diverse, multi-species fisheries such as those in the tropics where visual identification is challenging. Here, we provide the first estimates of the ability of scientific observers to identify five species of morphologically similar carcharhinid sharks (*Carcharhinus leucas*, *C. amboinensis*, *C. tilstoni*, *C. sorrah* and *C. brevipinna*) in a fishery in northern Australia. We compared observer field identifications of sharks with genetic validation (814 bp mtDNA NADH dehydrogenase subunit 4) to quantify species identification errors. We used binomial generalised linear models to determine the influences of species, gender, total length, and the observer's experience on identification error. We found that identification error (~20%) depended predominately on the species in question (highest error for *C. tilstoni*). Male sharks were misidentified less frequently than females, and error decreased marginally with increasing total length. Surprisingly, we found no statistical evidence that observer experience influenced identification error. Our results provide the first benchmark of identification accuracy of observers for carcharhinid sharks in northern Australia and show that estimates of error in species identifications need to be incorporated into management strategies to ensure successful recovery of the many recently over-fished shark populations.

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1. Introduction

Amid accelerating global declines of marine living resources over the past several decades (Dulvy et al., 2006; FAO, 2006; Hilborn et al., 2003; Hutchings, 2000; Jennings and Kaiser, 1998), there is growing pressure on fisheries to improve monitoring of catches (both harvests and discards) to determine whether current catches are sustainable. Correct species identification is fundamental to achieving these objectives. Without correct species identification, the likelihood of recognising ecosystem consequences, such as shifts in species abundances due to fishing, is greatly reduced or rendered impossible (Burgess et al., 2005a,b; Field et al., 2009b). Furthermore, the precision and accuracy of these data are crucial components for understanding the potential impact of current harvest rates on population viability (Dulvy et al., 2000; Field et al., 2009b; Nakano and Clarke, 2006).

One fish taxon in particular has experienced declines in many species globally: sharks and rays (chondrichthyans) (Burgess et al., 2005c; Dulvy et al., 2008; Field et al., 2009b; Robbins et al., 2006; Stevens et al., 2000; Walker, 1998). There has been much discussion regarding the causes of declines, with over-fishing identified as the greatest current threat (Coll et al., 2006; Field et al., 2009b; Jackson et al., 2001; Stevens et al., 2000; Ward and Myers, 2005; Worm et al., 2006). Historically, species-level identification of sharks in many fisheries has not been reported; rather, catch-records of similar-looking species were pooled. As such, determining whether current fishing pressures have already altered species abundances is often difficult to quantify (FAO, 2000). Changing current practices of record-keeping in commercial logbooks for species-level

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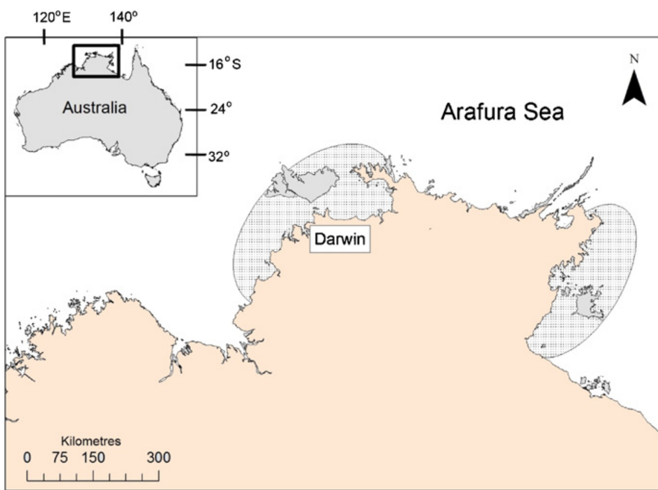

Fig. 1. Regions of northern Australian coastline sampled during Northern Territory Offshore Net and Line (NTONL) Fishery observer and shark tagging programmes. Total n (Observer species identification) = 632 (*Carcharhinus leucas*, n = 52; *C. tilstoni*, n = 201; *C. amboinensis*, n = 187; *C. brevipinna*, n = 40; *C. sorrah* n = 152).

reporting would improve regional estimates of species resilience, although correct species identification of many commercially valuable species such as the carcharhinids is confounded by their morphological similarity (Handley, 2010; Last and Stevens, 2009).

The Indo-Pacific region, including northern Australia, is widely recognised as an area of high carcharhinid biodiversity and endemism, and supports several target and mixed fisheries that catch elasmobranches, including the endangered *Glyphis* spp. sharks and Pristidae sawfishes (Last and Stevens, 2009). In northern Australia, sharks are landed in the Offshore Net and Line Fishery that operates predominately within 12 nm of the Northern Territory coastline, although fishing occurs within an area of 522,000 km^2 up to the boundary of the Australian Fishing Zone (Handley, 2010; Field et al., 2012). The predominant fishing methods employed include longlines (15 nm total length and no more than 1000 snoods) or pelagic nets (1000–2000 m total length with 160–185 mm mesh size and 50–100 mesh drop). This fishery targets the Australian (*Carcharhinus tilstoni*) and common black-tip (*C. limbatus*) and spot-tail (*Carcharhinus sorrah*) sharks (Field et al., 2012). In 2009, the reported fishery landed 371 tonnes of *C. tilstoni* and *C. limbatus* combined, and 86 tonnes of *C. sorrah* (Handley, 2010). The reported dominant by-catch species were hammerhead (*Sphyrna* spp; 118 tonnes), bull (*Carcharhinus leucas*; 73 tonnes), pig-eye (*Carcharhinus amboinensis*, 41 tonnes), lemon (*Negraprion actidens*; 36 tonnes) and tiger (*Galeocerdo curvier*; 34 tonnes) sharks (Handley, 2010).

Despite the small size relative to other locations of commercial fisheries (12 operational licenses) across northern Australia, current and historic (i.e., back to the Taiwanese fishery of the 1970s) fishing rates in the region are associated with illegal, unregulated and unreported catches (Field et al., 2009a) and flag the importance of accurate species-level monitoring (Field et al., 2009a; Handley, 2010; Stevens and Davenport, 1991). The presence of scientific observers on commercial fishing boats in north Australia has improved the reliability of catch records (Northern Territory Government Department of Regional Development, 2008; Zeroni, 2006), although their accuracy in species identifications has yet to be assessed empirically.

Genetic analysis offers a simple tool to confirm species identity, since diversity in the nucleotide sequence of selected regions of DNA is greater among than within species (Holmes et al., 2009; Ward et al., 2008; Wong et al., 2009). Gene regions in mitochondrial DNA have successfully discriminated species of coastal sharks (Morgan et al., 2011; Ovenden et al., 2010) and thus can be used to assess the accuracy of fishery-observer identifications. Here, we use analysis of mitochondrial DNA sequence to quantify the probability with which fishery observers correctly identify five common species of carcharhinid sharks caught in the Northern Territory Offshore Net and Line Fishery in northern Australia. We also test the relative influence of species, gender, individual total length and observer experience on error. We hypothesise that observer errors should be similar between genders of the same species of shark, but should differ among species. We also hypothesise errors to decrease with increasing total length because smaller sharks often have different markings from adults that might contribute to difficulties in species identification. Finally, we expect that errors will decrease with observer experience, because veterans should be more adept at identifying subtle differences among similar-looking species than novice observers.

2. Materials and methods

2.1. Genetic sample collection and observer identification

Observers participated in the Northern Territory Offshore Net and Line Fishery and shark tagging programmes around the Northern Territory coastline between September 2006 and December 2008 (Fig. 1). Fishery observers employed at commencement of the study (n = 5) were trained to identify five commonly caught morphologically similar carcharhinids (*C. tilstoni, C. sorrah, C. brevipinna, C. leucas and C. amboinensis*) using keys in Last and Stevens (1994), from specimen collections at Northern Territory Fisheries and the Northern Territory Museum, as well as on-board training. When this study was initiated, the frequency of *C. limbatus* to *C. tilstoni* on the Northern Territory coast was thought to be <1%, so observers were not trained to identify that species (Lavery and Shaklee, 1991). Ovenden et al. (2010) subsequently suggested that their frequency was much higher, approximately equal (~50:50). Consequently, we present overall misidentification errors with and without the two cryptic species of blacktip sharks (*C. tilstoni* and *C. limbatus*). We did not record sharks that were not identified by observers as any of the five target species. We categorised observers as ">50 days experience" (n = 2) or "<50 days experience" (n = 3) at sea to implement their training in field-based identification. Observers recorded the species, total length, and gender of each shark. A small skin clip from the dorsal fin was also collected from each measured shark and stored in 10% NaCl saturated dimethyl sulfoxide (DMSO) solution for genetic sequencing.

2.2. Genetic identification

Sharks were identified by comparing mitochondrial DNA sequences from each specimen with DNA sequences obtained from individuals in reference collections. These individuals included museum voucher specimens where possible, or had been identified by experienced taxonomists. Reference individuals were obtained from the Northern Territory Museum, Commonwealth Scientific and Industrial Research Organisation and research studies (Ovenden et al., 2009, 2010). Reference sequences obtained were for the five target species: Australian blacktip (*C. tilstoni*), spot-tail (*C. sorrah*), spinner (*C. brevipinna*), bull (*C. leucas*) and pig-eye (*C. amboinensis*) sharks, and regional congenerics sandbar (*C. plumbeus*), whitecheek (*C. dussumieri*), bignose (*C. altimus*), common black-tip (*C. limbatus*) and graceful (*C. amblyrhychoides*) sharks.

2.3. Mitochondrial DNA extraction

Preserved tissue (50 mg) was placed in a 200-μl solution of 10% Chelex 100 in TE buffer (5 mM Tris CL pH 8.0 with 0.5 mM EDTA). Proteinase K (100 ng; 5 μl) was then added to the vial. Heating the vial at 55 °C for 3 h on a shaking platform digested the tissue. The mixture was subsequently boiled for 8 minutes and then centrifuged it at 13,000 × *g* for 5 min to precipitate the Chelex resin and bind polyvalent metal ions from the denatured DNA in solution. The supernatant containing the extracted DNA was then transferred to a clean vial for storage (Estoup et al., 1996; Walsh et al., 1991).

2.4. Amplification and sequencing

The applicability of the mitochondrial NADH dehydrogenase subunit 4 (ND4) gene to discriminate species of carcharhinid sharks has been demonstrated by Ovenden et al. (2010) and Morgan et al. (2011). Genes from 632 individuals (refer to Table 1 for species totals) were amplified and sequenced using polymerase chain reaction (PCR). We amplified and sequenced the 5′ end of the ND4 gene using the forward primer ND4 (CACCTATGACTACCAAAAGCTCATGTAGAAGC) (Arevalo et al., 1994) and the reverse primer H12293-LEU (TTGCACCAAGAGTTTTTGGTTCCTAAGACC) (Inoue et al., 2001). Amplification reactions using 20 μl PCR reaction mixtures contained 11.85 μl of demineralised water, 2 μl of 10x PCR reaction buffer containing 15 mM $MgCl_2$, 2 μl of 2.5 mM dNTP mix, 1 μl of each 10 μM primer, 0.75 units of *Taq* DNA polymerase (Sigma Aldrich, Missouri, USA) and 2 μl of DNA template. Thermocycling conditions included an initial denaturation step of 94 °C for one minute followed by 30 cycles of a denaturing step at 94 °C for 30 s, an annealing step at 50 °C for 30 s, and an extension step at 72 °C for 30 s. A final extension step of 5 min at 72 °C completed the thermocycling. PCR products were purified using commercial QIAquick PCR purification kits (Qiagen, Doncaster, Vic, Australia) and viewed them on a 1.5% agarose TAE (containing Tris base, acetic acid and EDTA) in a gel stained with ethidium bromide. Cycle sequencing reactions used ABI Big Dye Terminator v3.1®. We did fragment separation by capillary electrophoresis (Applied Biosystems 3130xl) under conditions recommended by the manufacturer, producing a total of 814 sequenced base pairs.

2.5. Analysis

ND4 sequences of the remaining individuals were aligned and edited using MEGA4 software (Kumar et al., 2008), and condensed them into haplotypes using Arlequin v 3.11 (Excoffier et al., 2005). Evolutionary distances between haplotypes and reference sequences were computed using the Kimura 2-parameter method (Kimura, 1980) that are in the units of the number of base substitutions per site. Phylogenetic analysis (neighbour-joining method) (Saitou and Nei, 1987) grouped both reference sequences and haplotypes identified from our samples into clades representing each species. Genetic species identities were assigned to haplotypes depending on clade membership (Fig. 2). The error variation among sites was modelled with a gamma distribution (shape parameter = 0.5), and eliminated missing data only in pairwise sequence comparisons (pairwise deletion option). Confidence limits on phylogenies were generated with bootstrapping (Felsenstein, 1987). Fisheries observer identification error was calculated as the proportion of individuals that were not correctly assigned to their genetically identified species.

Binomial generalised linear models (log link function) was applied to test for the effects of species, sex, total length and observer experience on identification error (correct = 1; incorrect = 0). To equalise variance in length among species (as some species reach greater total length than others), we removed large individuals (greater than 1500 mm total length) of two species (*C. leucas* and *C. amboinensis*) from the sample, leaving a remaining sample of 521 individuals. Akaike's information criterion corrected for small sample size (AIC_c) was applied to estimate Kullback Leibler (K–L) information loss to rank models according to their bias-corrected distance from the 'true' model (Burnham and Anderson, 2002; Link and Barker, 2006). Here, the relative weight of evidence for each model was its AIC_c weight ($wAIC_c$). The strength of evidence ($wAIC_c$) for any particular model varies from 0 (no support) to 1 (complete support) relative to the entire model set (Burnham and Anderson, 2002). Each model's goodness of fit was also estimated using the percentage of deviance explained (% DE) relative to the null (intercept-only) model.

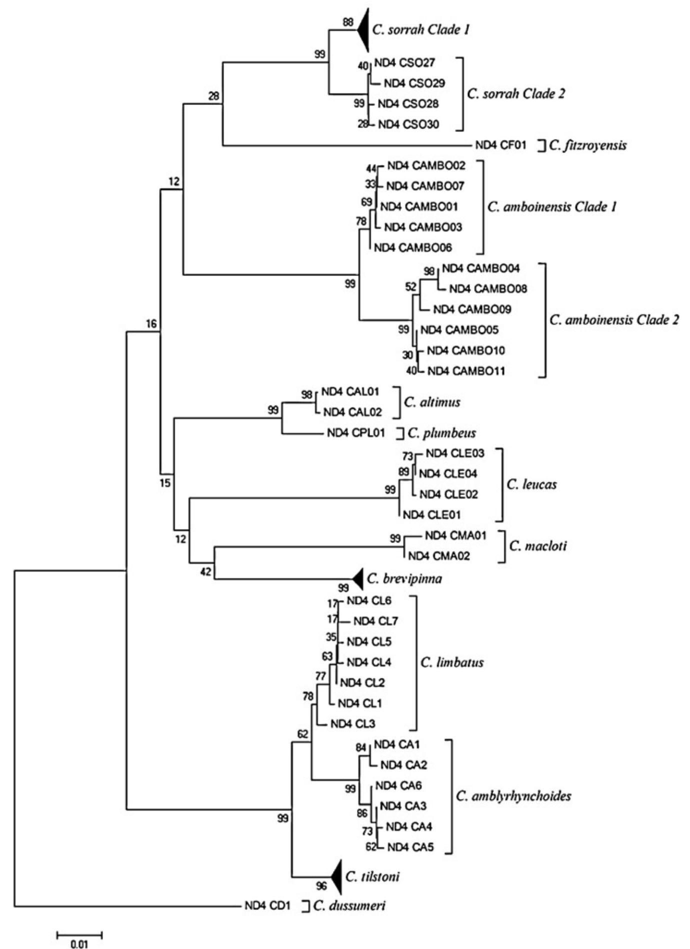

Fig. 2. Inferred phylogeny of 99 mitochondrial DNA ND4 haplotypes from 11 *Carcharhinus spp.* reconstructed using the neighbour-joining method and rooted with sequences from *C. dussumieri*. Some clades are condensed (◀). Bootstrap values (500 replicates) are shown next to the branches.

3. Results

The species phylogeny based on DNA sequences conformed to expectations (Fig. 2). MtDNA ND4 sequences discriminated all species as predicted by Morgan et al. (2011). Tree topology was similar to the phylogeny based on allozyme characters by Lavery and Shaklee (1991) and cytochrome c oxidase subunit I (COI) sequences by Ward et al. (2008). Clades within species (*C. sorrah, C. amboinensis*) were as previously identified (Ovenden et al., 2009; Tillett et al., 2012).

Observers incorrectly identified 30% of landed *C. tilstoni* (predominately mis-identified as *C. limbatus* or *C. brevipinna*), 14.8% of

Table 1
Percentage (individual counts in parentheses) of genetically identified sharks of each of five observer identified species. Total $n = 521$.

Genetic species identification	Observer species identification				
	C. leucas ($n = 27$)	*C. tilstoni* ($n = 200$)	*C. amboinensis* ($n = 104$)	*C. brevipinna* ($n = 39$)	*C. sorrah* ($n = 151$)
C. leucas	85.2 (23)		1.0 (1)		
C. tilstoni		70.0 (140)		7.7 (3)	1.3 (2)
C. limbatus		19.0 (38)			1.3 (2)
C. amblyrhynchoides		1.0 (2)	12.5 (13)		0.7 (1)
C. ambionensis	14.8 (4)	0.5 (1)	86.5 (90)		0.7 (1)
C. brevipinna		7.5 (15)		87.2 (34)	2.0 (3)
C. sorrah		1.5 (3)			92.7 (140)
Unknown		0.5 (1)		5.1 (2)	1.3 (2)
Total	100.0 (27)	100.0 (200)	100.0 (104)	100.0 (39)	100.0 (152)

Table 2
Information-theoretic ranking of models testing the effects of species (*id*), sex (*sex*), total length (*tl*), and observer experience (*obex*) on species identification error as confirmed by mitochondrial DNA•. Models with < 0.003 $w\mathrm{AIC}_c$ were omitted.

Model	k	AIC_c	$\Delta\mathrm{AIC}_c$	$w\mathrm{AIC}_c$	%DE
~*sex* + *tl* + *id*	7	459.403	0	0.3315	9.49
~*sex* + *id*	6	461.185	1.782	0.1360	8.71
~*sex* + *tl* + *id* + *obex* + *obex***id*	12	461.272	1.869	0.1302	10.8
~*sex* + *tl* + *id* + *obex*	8	461.385	1.982	0.1230	9.51
~*sex* + *id* + obex + *obex***id*	11	462.715	3.312	0.0633	10.08
~*sex* + *tl* + *id* + *sex***id*	11	463.01	3.608	0.0546	10.44
~*sex* + *id* + *obex*	7	463.237	3.834	0.0487	8.71
~*sex* + *tl* + *id* + *obex* + *tl***sex*	9	463.34	3.937	0.0463	9.53
~*sex* + *id* + *sex***id*	10	464.738	5.336	0.0230	9.67
~*sex* + *id* + *obex* + *sex***id* + *obex***id*	15	466.225	6.823	0.0109	11.07
~*tl* + *id*	6	466.734	7.331	0.0085	7.58
~*sex* + *id*+ *obex* + *sex***id*	11	466.825	7.422	0.0081	9.67
~*id*	5	467.964	8.561	0.0046	6.91
~*tl* + *id* + *obex* + *obex***id*	11	468.284	8.881	0.0039	8.95
~*tl* + *id* + *obex*	7	468.789	9.386	0.003	7.58

LL (maximum log-likelihood); k (number of model parameters); AIC_c (Akaike's information criterion corrected for small samples); $\Delta\mathrm{AIC}_c$ (differences between the current and top-ranked model AIC_c); $w\mathrm{AIC}_c$ (AIC_c weights); %DE (percent deviance explained).

C. leucas (predominately mis-identified as *C. amboinensis*), 12.8% of *C. brevipinna* (predominately mis-identified as *C. tilstoni*), 13.5% of *C. amboinensis* (predominately mis-identified as *C. amblyrhychoides*) and 7.3% of *C. sorrah* (equally mis-identified as other species) (Table 1; Fig. 3). The overall species identification error was 19.8%.

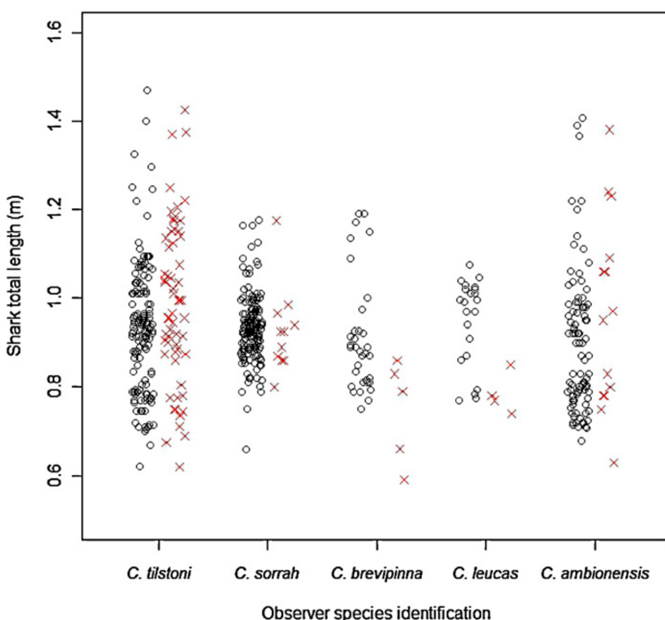

Fig. 3. Influence of total length on species identification error. Correct (○) and erroneous (×) observer species identifications are shown.

Combined influences of shark species, gender and total length best explained overall species identification error. Of these factors, *species* had the greatest influence (%DE = 6.9%; Table 2) and this was highest for *C. tilstoni* recording above-average species identification error (Fig. 4; Table 3). Unexpectedly, species identification error increased with increasing size, and males were less likely to be misidentified than females (Table 3). We found little influence of observer experience on identification error, nor was there any evidence for interactions between variables tested (Table 2).

After removing *C. tilstoni*, the most commonly mis-identified species (subsequent total $n = 431$), overall species identification error was halved to 9.75% (42 individuals). For this reduced dataset, weight of evidence suggested gender had the greatest influence on identification error (Table 4). The influence of *species* was greatly reduced (%DE = 1.58%) and was consistent across the remaining target species. Also, as hypothesised, identification error decreased, albeit weakly, with increasing total length (%DE = 0.4%), and there was no detectable effect of observer experience.

Table 3
Binomial Generalised Linear Model (GLM) results summary for the most appropriate model given the model selection (*identification error* ~*sex* + *tl* + *id*) as determined by information-theoretic ranking of models. *Carcharhinus leucas* is not presented due to limited sample size.

	Estimate	St. error
(Intercept)	−0.741	1.256
sex-M	−0.446	0.327
tl	−0.001	0.001
id – *C. amboinensis*	−0.181	0.510
id – *C. brevipinna*	−0.224	0.606
id – *C. sorrah*	−0.686	0.532

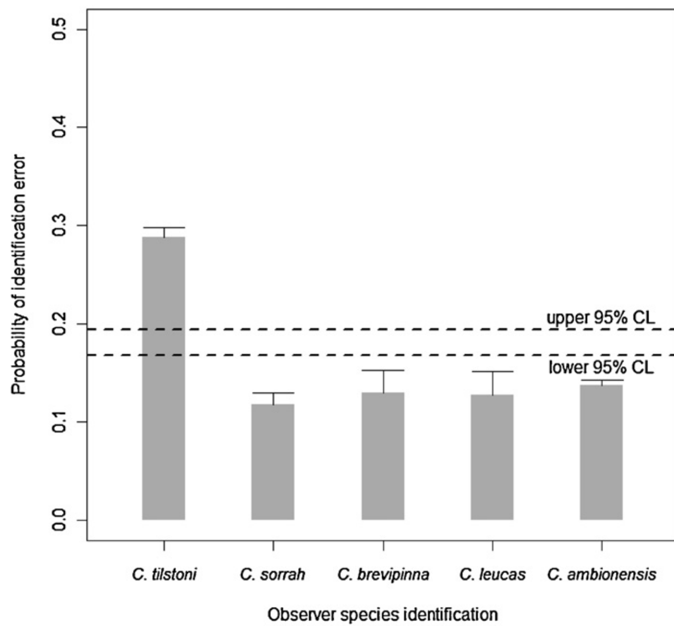

Fig. 4. Comparison of species-specific probabilities of identification error. Species-specific variation is represented by error bars. Upper and lower 95% confidence limits for the average species identification across all species is represented by the dashed lines.

4. Discussion

Our results provide the first baseline estimates of identification error for sharks in observer data, reiterating the importance of not assuming correct identification from other datasets. The high identification error for *C. tilstoni* was not unexpected because there are few external morphological features, other than its relatively smaller average size, that can be used for field-based discrimination from *C. limbatus*. A total of 19% of sharks identified by observers as *C. tilstoni* were genetically identified as *C. limbatus*, which was similar to the proportions reported for these species in the Northern Territory (Ovenden et al., 2010). The discrimination of these two species is further confounded by the recent discovery of inter-species hybridisation (Morgan et al., 2012), indicating that mtDNA will not always provide accurate identification of these two species.

We did not expect that the misidentification error of *C. amboinensis* would be the same as that for other species. This species is classified as *Data Deficient* in the IUCN Red List (www.iucnredlist.org), specifically because of confusion in the field between *C. amboinensis* and *C. leucas* is thought to preclude accurate collection of biological data. However, results suggest mis-identifications of *C. amboinensis* are no more frequent than other morphologically similar carcharhinids. Furthermore, the true identities of most (93%) mis-identified *C. amboinensis* were *C. amblyrhynchoides*, rather than the predicted *C. leucas*, reiterating morphological similarities between these three species. Broad patterns of mis-identificaion supported similar traits defined in species keys. *C. leucas* and *C. amboinensis* were never mis-identified as *C. tilstoni*, *C. sorrah* or *C. brevipinna*, suggesting grouping these species in commercial log books could improve species resolution of reported catch data, if individual species abundance in landed catch cannot be recorded.

The larger influence of gender than total length on species identification error was also unexpected. Although sexual dimorphism is common in vertebrates, there are only a few examples in sharks other than females obtaining greater total length than males (Allen and Wintner, 2002; Branstetter and Musick, 1994; Castro, 1996; Simpfendorfer et al., 2002). For example, male bonnet-head sharks *Sphyrna tiburo* develop a distinct bulge on their cephalofoil at the onset of maturity (Kajiura et al., 2005). Similarly, dentition (a common distinguishing character in shark keys) differs between male and female Atlantic stingrays *Dasyatis sabina* (Kajiura and Tricas, 1996). More female mis-identifications that we found might reflect the easier identification of maturity in males due to the presence of claspers increasing the likelihood of successfully discriminating 'large' mature sharks as *C. tilstoni*. Removing black-tip sharks from analyses suggests that sexual dimorphism, other than total length, might be more widespread among the target carcharhinid sharks than previously recognised, which could have confounded their identification.

We hypothesised that as an individual grows their defining attributes and colour markings should become more prominent (Last and Stevens, 1994), making identification more accurate. However, we found a subtle increase in identification error with body size, a finding driven mainly by the data on *C. tilstoni*. As mentioned above, size is the principal morphological feature used to discriminate the two sympatric northern Australia species of black-tip sharks (*C. tilstoni* and *C. limbatus*), which might explain why 'large' immature *C. tilstoni* tended to be identified as *C. limbatus*. However, this simplistic association did not apply to all individuals, because error increased as total length increased. Field characters for the identification of these species are needed, but are unlikely to overcome issues of morphological similarity created by inter-species hybridisation (Morgan et al., 2012). Removing black-tip sharks from analyses reversed this trend as hypothesised, suggesting that the remaining three species could be more accurately identified if they were large. For example, small *C. brevipinna* were consistently misidentified (Fig. 3).

The absence of any detectable effect of observer experience on identification error reiterates the strength of morphological similarities between carcharhinid sharks. Although classification of observer experience in the current study seems arbitrary, these preliminary findings suggest an error that was apparently not corrected through improved training, which is particularly concerning for fisheries management. Instead, this inherent error might need to be incorporated as a constant in all future species resilience

Table 4
Information-theoretic ranking of models (black-tip sharks, *C. tilstoni*, removed) testing the effects of species (*id*), sex (*sex*), total length (*tl*), and observer experience (*obex*) on species identification error (*err*) as confirmed by mitochondrial DNA•. Models with < 0.01 $wAIC_c$ were omitted.

Model	k	AIC_c	ΔAIC_c	$wAIC_c$	%DE
~*sex*	2	218.369	0.000	0.1706	1.20
~*sex* + *tl*	3	219.487	1.118	0.0976	1.62
~*tl*	2	220.102	1.733	0.0717	0.40
~*sex* + *obex*	3	220.405	2.036	0.0616	1.20
~*id* + *obex* + *id***ob*	8	220.941	2.572	0.0471	4.77
~*obex*	2	220.958	2.588	0.0468	0.00
~*sex* + *id* + *obex* + *obex***id*	9	221.153	2.784	0.0424	5.64
~*sex* + *tl* + *sa***tl*	4	221.408	3.038	0.0373	1.68
~*sa* + *tl* + *obex*	4	221.52	3.151	0.0353	1.63
~*id*	4	221.628	3.259	0.0334	1.58
~*sex* + *id*	5	221.686	3.317	0.0325	2.51
~*tl* + *obex*	3	222.138	3.768	0.0259	0.40
~*tl* + *id* + *obex* + *ob***id*	9	222.358	3.989	0.0232	5.09
~*sex* + *tl* + *id* + *obex* + *obex***id*	10	222.481	4.112	0.0218	6.01
~*sex* + *id* + *obex* + *sa***id* + *obex***id*	12	222.838	4.469	0.0183	7.81
~*tl* + *id*	5	223.164	4.795	0.0155	1.82
~*sex* + *tl* + *id*	6	223.21	4.841	0.0152	2.76
~*sex* + *id* + *sex***id*	8	223.354	4.985	0.0141	4.63
~*sex* + *tl* + *obex* + *sex***tl*	5	223.449	5.080	0.0135	1.69
~*id* + *obex*	5	223.689	5.320	0.0119	1.58
~*sex* + *id* + *obex*	6	223.761	5.392	0.0115	2.51

LL (maximum log-likelihood); k (number of model parameters); AIC_c (Akaike's information criterion corrected for small samples); ΔAIC_c (differences between the current and top-ranked model AIC_c); $wAIC_c$ (AIC_c weights); %DE (per cent deviance explained).

predictions. Current results may be skewed by the absence of any formal training or feedback programmes for observers, which would allow them to rectify errors improving accuracy of species identification over time. Despite this, current results provide a valuable and necessary baseline for continual monitoring of observer species identification error which would also confirm suggested trends.

Overall species identification error described here suggests bycatch of non-target species within this species complex in the Northern Territory Offshore Net and Line Fishery is underestimated by 10% due to the routine misidentification of target species as *C. amboinensis*, *C. amblyrhynchoides* or *C. brevipinna*. This is unlikely to impact on consumer demand directly because the quality of the product does not differ between species. As consumer awareness for shark conservation grows, any statements of uncertainty around harvest methods for sharks are likely to erode consumer confidence in sustainable fisheries (Roheim et al., 2011), leading to the enforcement of legislation requiring species-level identification of seafood products sold. Importantly, fishery mortality estimates used for modelling stock resilience for these species are likely to be inaccurate. Although the initial estimate of species identification error (20%) was high, the removal of *C. tilstoni*, which are notoriously difficult to discriminate in the field and which hybridise, reduced identification error (9.75%). The occurrence of such error and questionable effect of observer experience on species identification reiterates problems distinguishing morphologically similar carcharhinids and calls for species identification error to be quantified and monitored in other geographical regions that have similar fisheries for shark. Incorporation of this error into models estimating species' resilience will be necessary for the sustainable harvest and successful recovery of over-fished shark populations.

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