

**Supplementary material**

**Life history of the common blacktip shark, *Carcharhinus limbatus*, from central eastern Australia and comparative demography of a cryptic shark complex**

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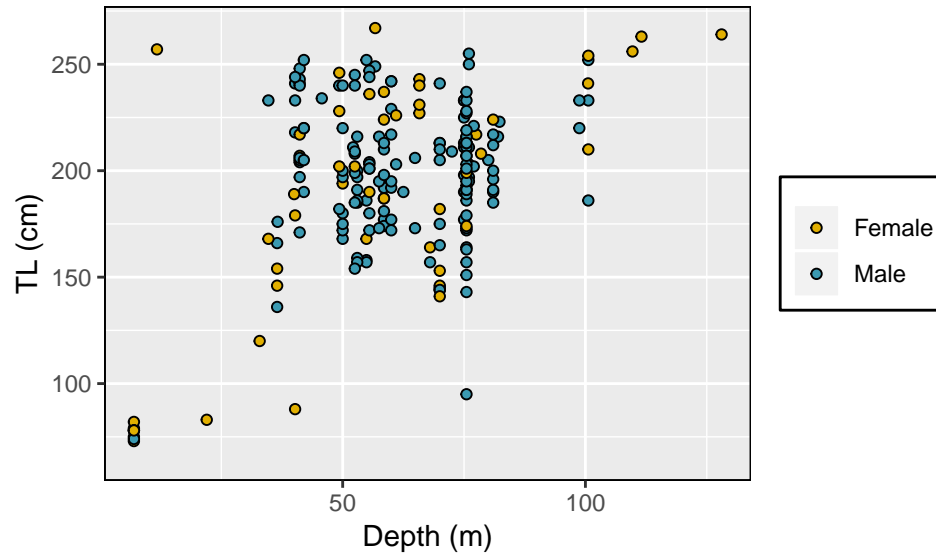
## Length-length relationships

The relationships among total length (TL), fork length (FL), and pre-caudal length (PCL) in *C. limbatus* for sexes combined were:

$$TL = 1.600 + 1.224 \cdot FL \quad (\text{ANOVA : } F = 138323, \text{d.f.} = 1, 469, P < 0.001)$$

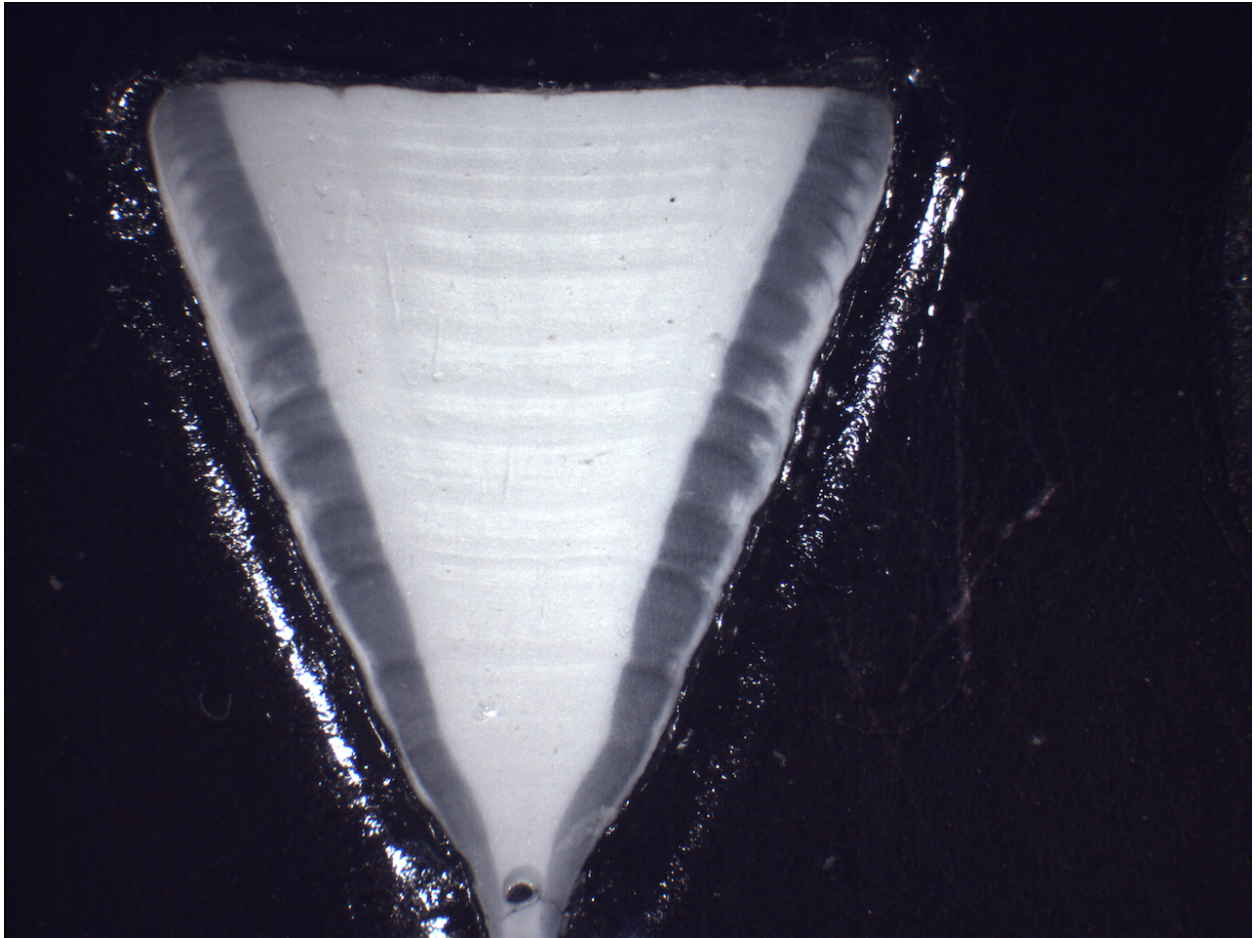
$$TL = 4.206 + 1.340 \cdot PCL \quad (\text{ANOVA : } F = 33643, \text{d.f.} = 1, 295, P < 0.001)$$

## Depth at capture

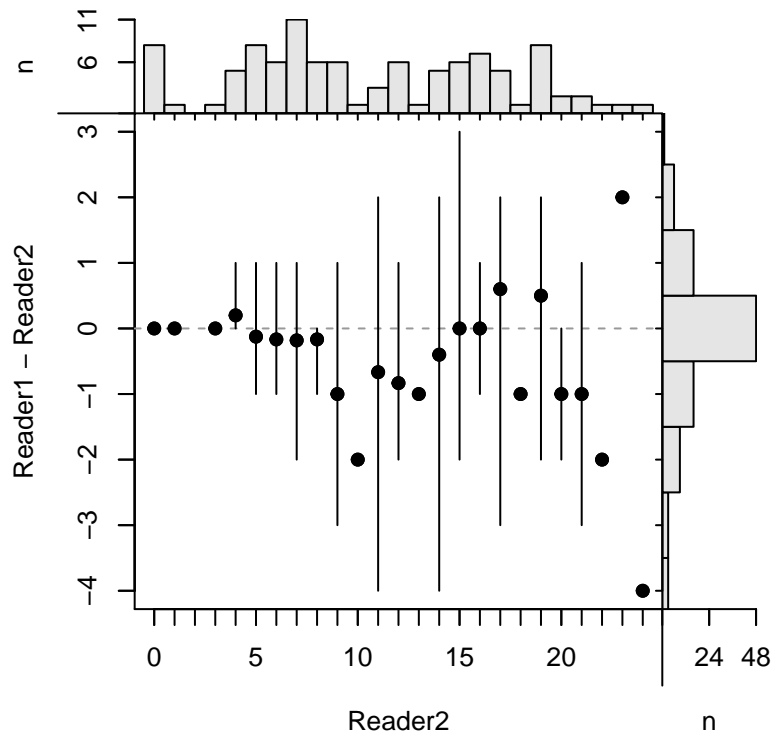


**Fig S1.** Depth at capture for male and female *C. limbatus* from New South Wales waters.

## Age and growth



**Fig. S2.** Vertebrae section from a 216-cm male *C. limbatus* with 15 growth zone pairs



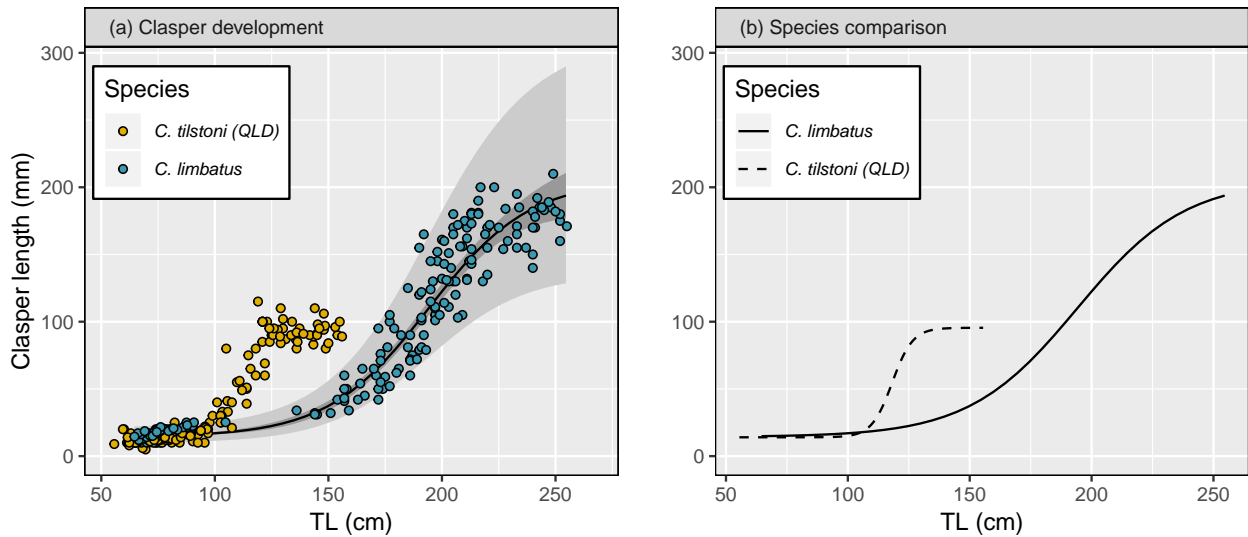
**Fig. S3.** Age bias plot showing mean age (plus and minus 95% confidence intervals) of Reader 1 relative to those of Reader 2. Sample size of each age class is denoted at the top of the graph.

## Clasper length

The male maturation process was investigated by modelling the development of clasper length, CL, as a function of length using a modified logistic regression equation

$$CL(l_i) = f + (g - f)[1 + e^{-\ln(19) \frac{l_i - CL_{50}}{CL_{95} - CL_{50}}}]^{-1} \cdot e^\epsilon \quad \epsilon \sim N(0, \sigma^2)$$

where  $f$  and  $g$  are parameters that determine the slope and intercept, and  $CL_{50}$  and  $CL_{95}$  are the lengths at which claspers are 50 and 95% of their maximum length. The relationship also has a practical purpose as CL is a useful characteristic for species identification (Stevens and Wiley 1986; Harry *et al.* 2012).



**Fig. S4.** Clasper length as a function of length for male *C. limbatus*. Panel (a) shows non-linear regression model with 95% confidence and prediction intervals for *C. limbatus*. Points are empirical clasper lengths for *C. limbatus* and Qld *C. tilstoni*. Panel (b) compares the mean relationship between the two species.

## Demographic analysis

This section describes aspects of the Monte Carlo simulation used to investigate sources of uncertainty in the demographic analysis, including areas where the approach for a specific species-stock deviates from the

general approach described in the methodology.

### **Growth parameters**

Growth parameters for *C. tilstoni* populations based on vertebral ageing were similar (Davenport and Stevens 1988; Harry *et al.* 2013), although in both cases they were clearly biased as a result of uncorrected effects of gillnet selectivity. For Qld *C. tilstoni*, a logistic function was chosen to model length at age as the estimated  $L_{\infty}$  was closer to observed maximum length of the species. In the original analysis by Harry *et al.* (2013), this model was fit with a lognormal variance, and this led to unstable parameter estimates when attempting to resample random parameters from the variance-covariance matrix. To provide more reasonable values for the Monte Carlo simulation the model was refit with normal variance. For NT *C. tilstoni*, growth parameters estimated from size mode analysis were ultimately chosen in favor of those from vertebral ageing as, again, they were closer to observed maximum length of the species (Davenport and Stevens 1988). Because the original data were not available, growth parameters were randomly resampled from a normal distribution with a CV of 5%.

### **Weight at length**

No resampling was undertaken on the weight-length parameters for NT *C. tilstoni* due to the lack of raw data for this species.

### **Maturity at length**

For NT *C. tilstoni* uncertainty in reproductive output at age was incorporated by allowing the maternity ogive to shift horizontally over a range of values by adding a constant to  $A_{50}$  and  $A_{95}$ . Constants were drawn from a random normal distribution with a variance of 0.5 years (10% of  $A_{50}$ ). The 95% quantiles of random  $A_{50}$  values ultimately used in the Monte Carlo simulation were 4.03 to 5.98 years.

## **Fecundity**

For NT *C. tilstoni* values of fecundity were drawn from a normal distribution with a mean of 3 (Stevens and Wiley 1986) and a CV of 10%. For *C. limbatus* values of fecundity were randomly resampled with replacement from a vector of mean fecundity values including this and four other studies (Bass *et al.* 1973; Dudley and Cliff 1993; Capape *et al.* 2004 ; White 2007).

## **Natural mortality**

$M$  was calculated using a constant, size-based method (Then *et al.* 2015) that required growth parameters  $L_\infty$  and  $K$  from the von Bertalanffy equation. This presented a problem for Qld *C. tilstoni* where a logistic growth model was used to model growth. Using the values of  $L_\infty$  and  $K$  from the von Bertalanffy model in Harry *et al.* (2013) was also deemed unsuitable because they were strongly biased, and led to unrealistically small values of  $M$ . To address this problem, a von Bertalanffy growth function was re-fit to the length at age data in Harry *et al.* (2013), constraining  $L_\infty$  to the value in the logistic growth curve. As per *C. limbatus* and *C. tilstoni*, values of  $L_\infty$  and  $K$  used to derive  $M$  for the Monte Carlo simulation were then resampled from a multivariate normal distribution with a mean and covariance matrix obtained from this constrained model. Noting the high level of uncertainty in  $M$ , for each simulation additional variability was added to the calculated value of  $M$ , drawn from a random normal distribution with a CV of 20% of  $M$ .

## **Additional discussion points on the ecology of central eastern Australia *C. limbatus***

The ecology of *C. limbatus*, like its life history, has historically been confounded by its co-occurrence and hybridisation with *C. tilstoni*. Large, adult *C. limbatus*, which are clearly separable from *C. tilstoni* have been reported in small numbers throughout northern Australia (Stevens and Wiley 1986; Salini *et al.* 2007; Johnson *et al.* 2017). Neonate *C. limbatus*, also easily separable (Harry *et al.* 2012), have been reported from communal shark nursery areas on both the east and west coasts of Australia (Simpfendorfer and Milward 1993; White and Potter 2004; Gutteridge 2011; Taylor and Bennett 2013; Yates *et al.* 2015).

Although the species occurs throughout northern Australia, data from this study indicate that the central east coast of Australia might be an area of higher relative abundance for *C. limbatus*. Taylor *et al.*'s (2013) study of the shark fauna of Moreton Bay showed *C. limbatus* to be one of the most commonly caught sharks, suggesting the area would likely meet the formal criteria needed to be classified as a nursery *sensu* Heupel *et al.* (2007). In this study we assumed the neonates in Moreton Bay were part of the same population as those larger sharks sampled off northern NSW. This is not known definitively, but is a reasonable assumption given the absence of any other reported parturition areas for *C. limbatus* to the south and the absence of adults from within Moreton Bay itself (Taylor and Bennett 2013). Nine small (73–83 cm) sharks were also captured during January and February in 2008 and 2009 from 7m depth off Woody Head (29°20'S, 153°21'E). Although they were not examined for the presence of an umbilical scar, all were aged as 0+ and were therefore likely to have been no more than a few months old. These individuals provide possible evidence that *C. limbatus* parturition might also occur in NSW waters.

Little is known about the spatial ecology of *C. limbatus* or potential linkages between individuals from the central east coast of Australia in the present study, and those individuals found in tropical waters further north. Welch *et al.* (2010) investigated the stock structure of *C. limbatus* off the east coast and identified two management units separated by the Tropic of Capricorn. Macbeth *et al.* (2009) also found potential evidence of a seasonal migration in *C. limbatus*, with the species predominantly caught between January and June.



This suggests a potential northward seasonal migration during part of the year. Such behaviour would be consistent with that of some other large carcharhinid sharks (Braccini *et al.*, in press) including populations of *C. limbatus* in the northwest Atlantic and southwest Indian Ocean (Dudley and Cliff 1993; Kajiura and Tellman 2016).

In keeping with previous studies on hybridisation, no evidence of intermediate types was found in this study among hybrid sharks (Harry *et al.* 2012; Johnson *et al.* 2017). All hybrid individuals showed biological characteristics that were macroscopically similar to that of purebred *C. limbatus*. The single purebred *C. tilstoni* identified from NSW using nDNA was a 145-cm female captured from a depth of ~42 m near the mouth of the Clarence River, NSW (29°32.99'S, 153°25.48'E). This is the southernmost record confirmed for this species (excluding individuals with hybrid ancestry identified solely using mtDNA). The previous southernmost record was a juvenile *C. tilstoni* from Moreton Bay identified using a pre-caudal vertebral count (Harry *et al.* 2012).

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