

A new look at growth and movement of the white shark *Carcharodon carcharias* in Australian waters

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Documenting growth in white sharks has been hampered by a lack of samples despite this being one of the most important demographic parameters for understanding population dynamics. This study used vertebral centra amassed from 98 Australian white sharks ranging in size from 127 to 520cm TL, the most comprehensive data series so far used in ageing studies of this species. Microtomographic (MicroCT) technology was used to enhance visibility in growth structures of the vertebrae giving unprecedented options for manipulation of images to generate growth models. The sample size and techniques used allowed for more robust estimates of growth parameters for white sharks in Australia. The best fitting growth model gave a theoretical maximum length and age of 7.47m and 65.4 years respectively. Growth rate was slow ($k = 0.053$), but similar to other lamnid species, with males growing slower than females. Microchemical analysis of vertebrae was applied to examine signatures of movement between different water masses as predicted from previous satellite tracking-based research. Microchemistry of vertebral cartilage was sampled in a transect from the focus to the outer edge of the corpus calcareum using laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS). By transposing pre-determined age data for each centra onto the corresponding microchemical profile, elemental signatures were allocated to each shark. 72% of vertebrae analysed indicated a trend in declining concentrations of Mn and Zn over time, indicating a potential shift of juvenile sharks from nutrient-rich coastal waters to deeper offshore habitats. 18% of samples showed synchronised patterns of spikes in As, Sn and Hg during particular years coinciding with drops in the Sr:Ba ratio. This pattern supports previously reported age-related movement patterns of juvenile white sharks showing temporary seasonal residency in onshore areas as indicated by changes in salinity and influence of water bodies contaminated with heavy metals.

Limited by blue blood? Genetic, structural and functional traits driving haemocyanin evolution and thermal adaptation in octopods.

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The octopods worldwide colonisation of diverse thermal habitats from -1.8°C to more than 30°C relied on the capacity of their circulatory and ventilatory system to supply sufficient oxygen for aerobic metabolism at a given environmental temperature. The blood pigment haemocyanin transports oxygen in octopods, which however, suffices oxygen supply only within a defined thermal range and thus may limit octopod radiation and distribution. This study aims to determine and link genetic, structural and functional properties of haemocyanin to understand mechanisms of protein evolution relevant to thermal adaptation in octopods. A combination of oxygen binding experiments, native gel electrophoresis and gene sequencing was used to compare properties of haemocyanin between cold and warm adapted octopods. Morphological and COI barcode identification of octopods collected during cruise ANT XXVII/3 of RV "Polarstern" confirmed high species diversity in sub and high Antarctic waters. Physiological and structural analysis of haemocyanin revealed differential oxygen binding properties and a heterogeneous abundance of two distinct isoforms of the functional unit G (FU-G) among polar species. The haemocyanin of Antarctic *Pareledone charcoti* displayed fewer acidic amino acids than of the temperate *Enteroctopus dofleini*. However, comparisons across multiple species from warm and cold habitats showed highly variable isoelectric properties of haemocyanin FU-G. We conclude that differential haemocyanin isoform patterns among polar species likely explain differences in oxygen binding. The lack of a universal "cool" haemocyanin among Antarctic octopods may reflect independent colonisation and adaptation events to sub-zero temperatures. Further analysis will focus on warm adapted octopods and the search for amino acid residues that account for adaptive changes of haemocyanin.