

## **Towards the integrated biodiversity conservation of endemic catsharks**

Southern Africa has been identified as an area of conservation concern due to the threats to sharks. There is a high number of endemic elasmobranch (sharks, skates and rays) species in the area, particularly within the catshark family Scyliorhinidae. Catshark populations distributed in the southern Benguela ecosystem are thought to be declining as fewer individuals have been landed by the Department of Agriculture, Forestry and Fisheries (DAFF) research trawl surveys. This could be due to a direct effect of climate change or an indirect effect; such as, the redistribution of a food source (e.g. small pelagic fishes). Further exploration into the phylogenetic positions of catsharks, particularly those distributed in the Benguela ecosystem, is required as the family Scyliorhinidae has previously been suggested to be paraphyletic. Insight into the phylogenetic placement of southern African endemic catsharks is paramount for the understanding of their evolutionary histories as well as southern African elasmobranch biodiversity. Additionally, whole mitochondrial genome data for catsharks may provide insight into a region with a higher interspecific variability as standard barcoding (COI) for two southern African endemic catshark genera (*Haploblepharus* and *Poroderma*) has shown little to no interspecific sequence divergence. Whole mitochondrial genome data can shed light on possible reasons for low sequence divergence; whether the low divergence is due to interspecific hybridisation, recent species delineation or taxonomic oversplitting.