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Marine and Freshwater Research

Supplementary Material

Genomic population structure of great hammerhead sharks (*Sphyrna mokarran*) across the Indo-Pacific

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Table S1. Year of collection for catch location of samples from great hammerhead (*Sphyrna mokarran*)sharks used for genetic population structure analysis.

Location	Year collected	
Western Australia	2015–2021	
Northern Territory	2016–2019	
Gulf of Carpentaria	2016–2019	
North-east Queensland	2018–2020	
South-east Queensland	2003–2007 and 2019–2021	
New South Wales	2016–2018	
Red Sea	2011–2013	

Filtering step	Number of loci	Number of individuals
Initial import	83,579	233
Filter monomorphic loci	_	_
Filter repeatability and reproducibility (0.99)	74,170 (9409 removed)	-
Filter monomorphic loci	-	-
Filter loci call-rate (0.7)	71,387 (2783 removed)	-
Filter individual call-rate (0.55)	-	213 (20 removed)
Filter monomorphic loci	26,057 (45,330 removed)	-
Filter secondaries	23,866 (2191 removed)	-
Filter minor allele frequencies (0.01)	4358 (19,508 removed)	
Filter read depth (3–30)	4318 (40 removed)	-
Filter HWE		
Out any / Each population	4288 (30 removed)	-
Out across / All populations pooled	3915 (403 removed)	-
Sex linked loci (none detected)	-	-
Outflank outliers	3846 (69 removed)	
LEA / tess3r Admixture	3,846	211 (2 removed – outlier individuals)
DAPC	3,846	211
PCOA	3,846	211

Table S2. Filtering process of samples of great hammerhead (*Sphyrna mokarran*) for genetic population structure analysis.

	Gulf	Qld	NSW	NT	Red Sea
Qld	3.3619	*	*	*	*
NSW	2.8516	2.9071	*	*	*
NT	3.2815	3.2555	2.8151	*	*
Red Sea	4.5556	4.5719	4.1690	4.4124	*
WA	2.7669	2.9282	2.3401	2.7857	4.1104

Table S3. Genetic distance matrix for great hammerhead (*Sphyrna mokarran*) samples based on Euclidean distance.

Gulf, Queensland Guld of Carpentaria; Qld, Queensland; NSW, New South Wales; NT, Northern Territory; RS, Red Sea; WA, Western Australia.

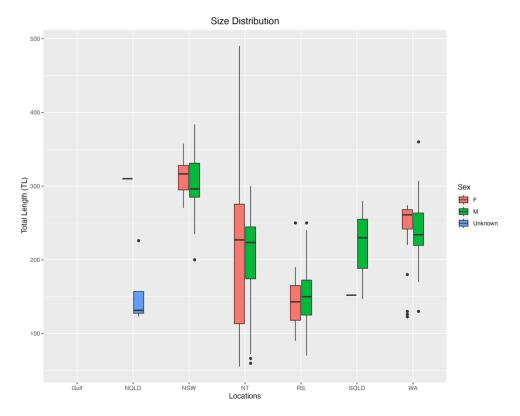


Fig. S1. Size distribution (total length, TL) for great hammerhead (*Sphyrna mokarran*) plotted from their catch location shown for each sex. Biological data for all Gulf and the majority of NQld individuals were unavailable. Gulf, Queensland Gulf of Carpentaria; NQld, northern Queensland; NSW, New South Wales; NT, Northern Territory; RS, Red Sea; SQld, southern Queensland; and WA, Western Australia.

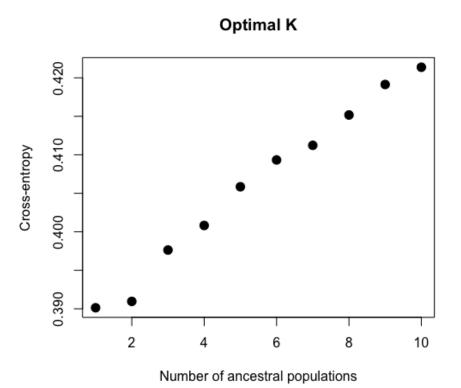


Fig. S2. The minimal cross-entropy in function of K for great hammerhead (*Sphyrna mokarran*) sampled across Australia and the Saudi Arabian Red Sea.

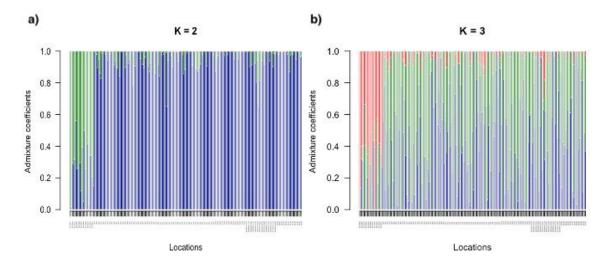


Fig. S3. The ancestry admixture proportion for each individual great hammerhead (*Sphyrna mokarran*) plotted against their catch location for scenario (a) K = 2 and (b) K = 3. Colours represent the different admixture defined by K. Locations are ordered left to right from west to east: Red Sea, Western Australia (WA), Northern Territory (NT), Queensland Gulf of Carpentaria (Gulf), northern Queensland (Qld), southern Qld and New South Wales (NSW).

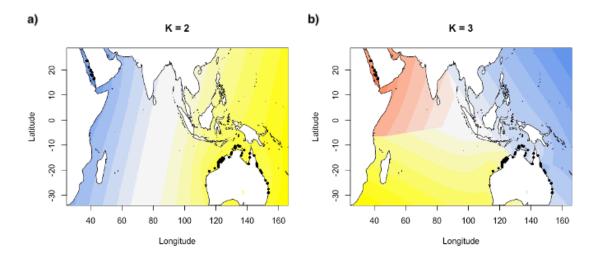


Fig. S4. The ancestry admixture proportion for each individual great hammerhead (*Sphyrna mokarran*) plotted from their catch location shown for scenario (a) K = 2 and (b) K = 3. Colours represent the different admixture clusters defined by K.

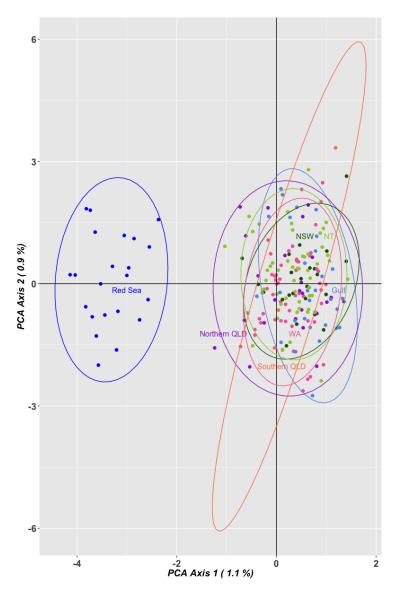


Fig. S5. Scatterplot of great hammerhead (*Sphyrna mokarran*) Indo-Pacific structuring using PCoA modelling. The first two principal coordinate axes are shown with the amount of variance explained by each axis in parentheses.

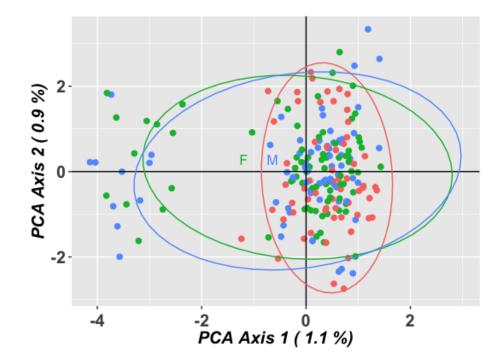


Fig. S6. Sex distribution for great hammerhead (*Sphyrna mokarran*). Biological data for all Gulf and the majority of NQld individuals were unavailable. F (green), females; M (blue), males; orange, unknown sex.

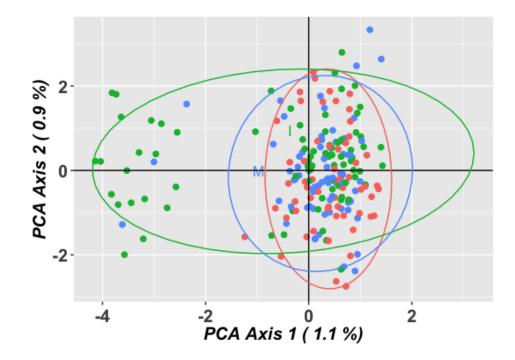


Fig. S7. Maturity distribution for great hammerhead (*Sphyrna mokarran*). Biological data for all Gulf and the majority of NQld individuals were unavailable. I (green), immature; M (blue), mature; orange, unknown size.