

Supplemental Information for:

Stepping up to genome scan allows stock differentiation in the worldwide distributed blue shark *Prionace glauca*

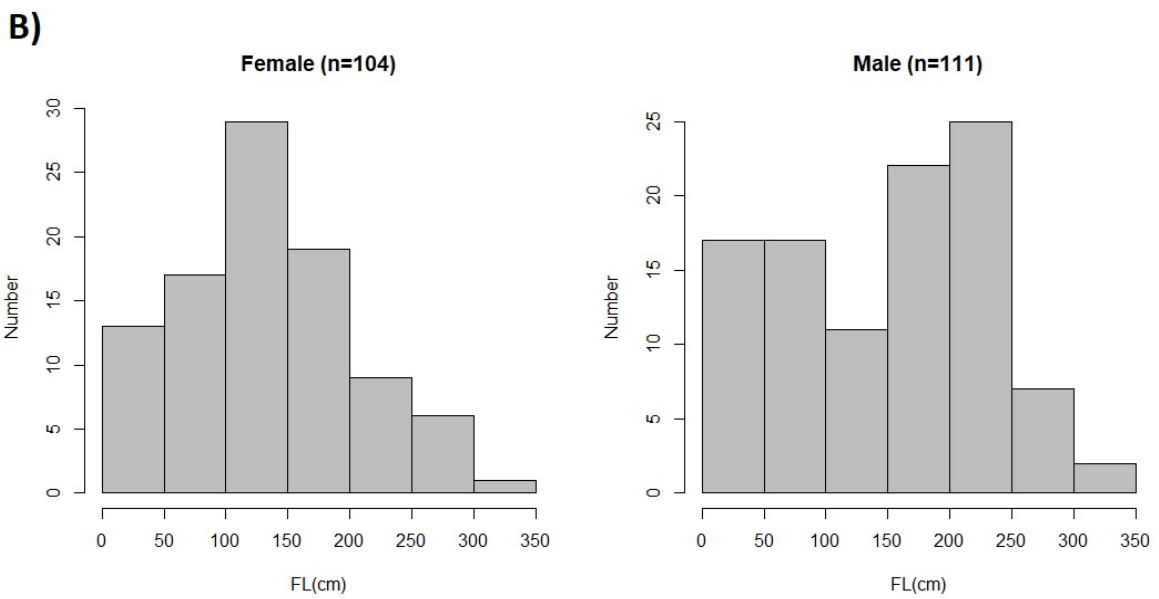
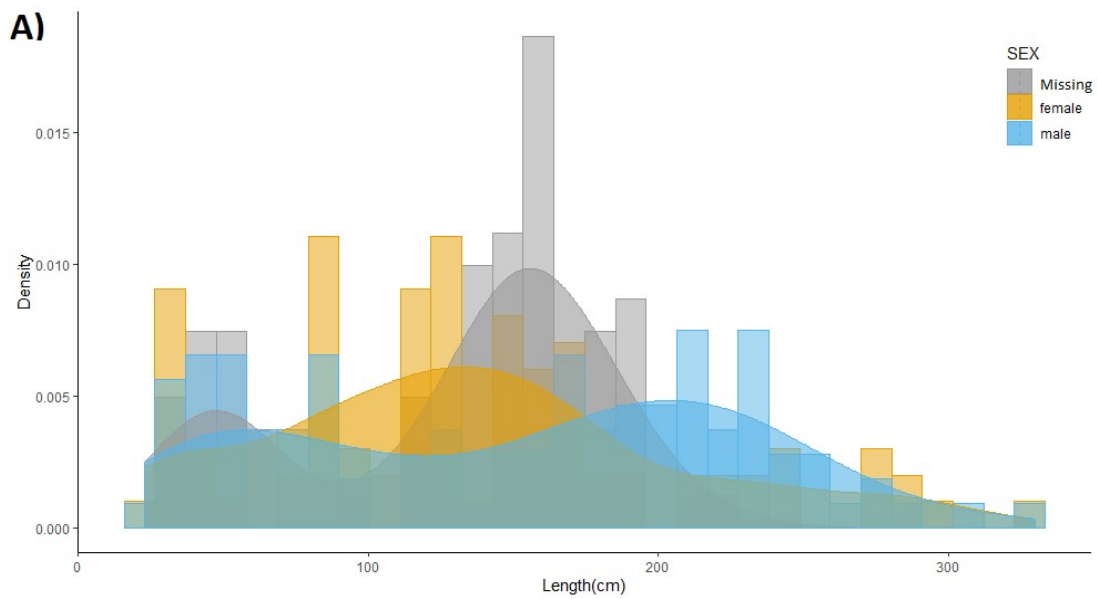
Natacha Nikolic, Floriaan Devloo-Delva, Diane Bailleul, Ekaterina Noskova, Clément Rougeux, Chrystelle Delord, Philippe Borsa, Cathy Liautard-Haag, Mohamad Hassan, Amandine D. Marie, Pierre Feutry, Peter Grewe, Campbell Davies, Jessica Farley, Daniel Fernando, Sebastian Biton-Porsmoguer, François Poisson, Denham Parker, Agostino Leone, Jordan Aulich, Matt Lansdell, Francis Marsac, Sophie Arnaud-Haond

Table of Contents:

S1	Page 1
S2	Page 2
S3, S4	Page 3
S5, S6	Page 4
S7	Page 5-6
S8	Page 7

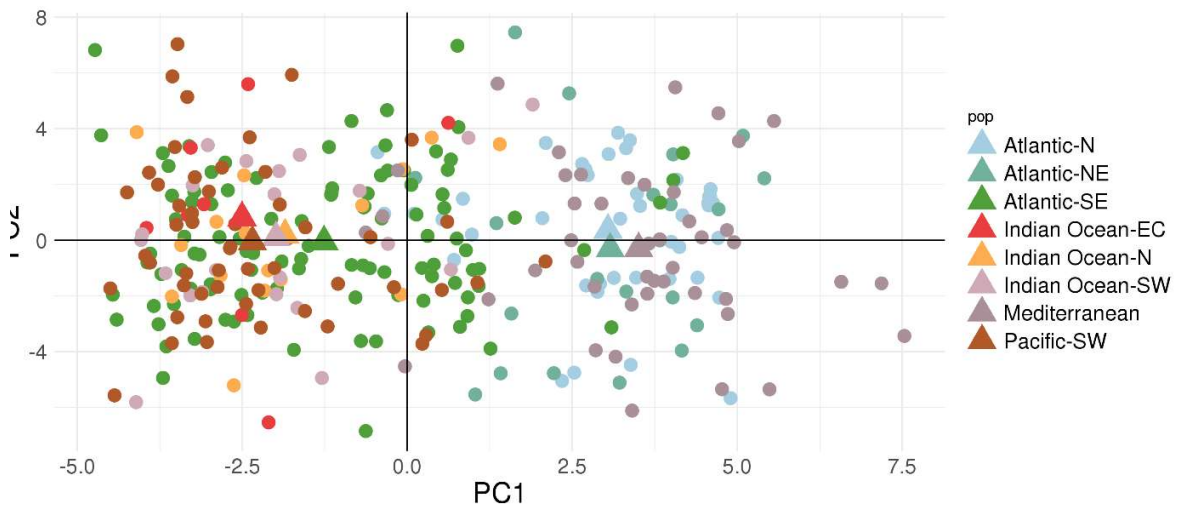
S1. R Markdown report of DarTseq data processing and population genetic analyses on R 4.1.0.
See the PDF file.

MOLECULAR ECOLOGY



MOLECULAR ECOLOGY

S2. Distribution of fork length (FL, in cm) per sex. Male (blue), female (yellow) and undetermined sex (missing, total of 149 individuals) (grey)) (A). Distribution of the total length (FL, in cm) for females and males (B).



S3. Principal Component Analysis on allelic frequencies on blue shark with 37,655 SNPs and 312 individuals on the eight geographic regions (DATA 4).

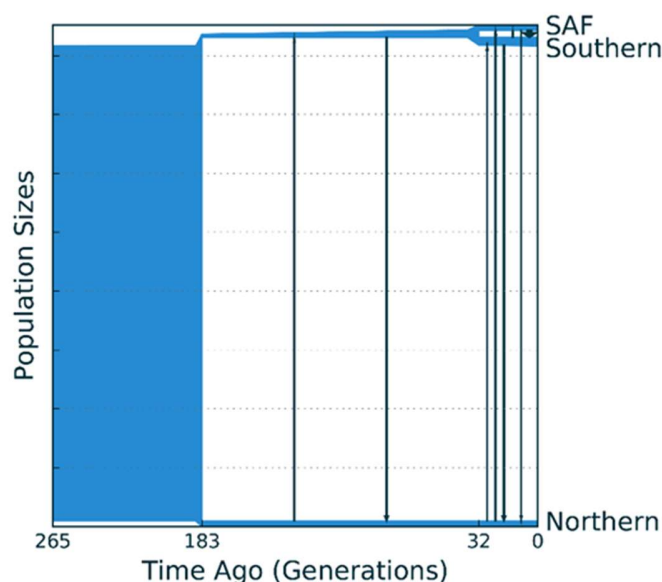
S4. Top three best demographic models from 50 independent demographic inference runs for the 2-population model (including northern and southern populations). Runs are sorted by the value of log-likelihood (logLL). See Table 4 for the variable names.

	logLL	Nanc	Nanc2	Dyn(Nanc->Nanc2)	Nsou0	Nsou	Dyn(Nsou0->Nsou)	Nnor0	Nnor	Dyn(Nnor0->Nnor)	Msou->nor	Msou->nor	Tanc	Tsplit
Units		ind	ind	Dynamic	ind	ind	Dynamic	ind	ind	Dynamic	frac per gen	frac per gen	years	years
Model #1	-2054.75	30422	176072	Linear	4220	6356	Linear	NA	5255	Constant size	0.0168	0.0004	1171152	5004
Model #2	-3239.55	76659	767	Exponential	NA	4	Constant size	1	31	Exponential	31.5	0.00003	653	0.2
Model #3	-3241.37	76651	767	Sudden change	7	18396	Exponential	767	1534	Exponential	0.0001	0.65	168	9

MOLECULAR ECOLOGY

S5. Detailed comments on the 3-population demographic inference:

The best model with three populations was obtained with the First tree model (i.e., with SAF population originating from the Southern cluster). Estimates from the 3-population model with 50x50x50 JAFS displayed similar demographic qualitative trends than 2-population scenario (i.e., including only northern and southern populations), in spite of showing slightly more contrasted estimated values when compared to the 2-population 50x50 JAFS model (and also showing a much lower likelihood, in which it could be considered as less efficient or representative than the 2-population model). Overall, the 3-population model using 50x50x50 JAFS suggested the following. First, the ancestral population growth in its size linearly began in the same period than with the 2-population model (Figure 4). The split of the ancestral population from this model is later (ab. 183 generations ago, S7 and S8) forming the two new northern and southern subpopulation (S7). The northern population had a constant size and the southern population experienced linear growth after the split (S8), as in the previous 2-population scenario (Table 4). About 32 generations ago (corresponding to ab. 288 years ago [259-314 years ago]) Southern African (SAF) subpopulation would have split from the Southern population (S8). Two migration rates (SAF → northern; northern → southern) are very small and close to zero (S8). Otherwise, migration rate from SAF to Southern population was estimated the strongest (S7).



S6. Schematic plot of the best demographic history for the 3-population model (northern,

southern and South Africa (SAF)) from now to the past time split in term of number of generations (inferred from the 50x50x50 JAFS and the First tree model). The vertical arrows represent asymmetric migration after the split.

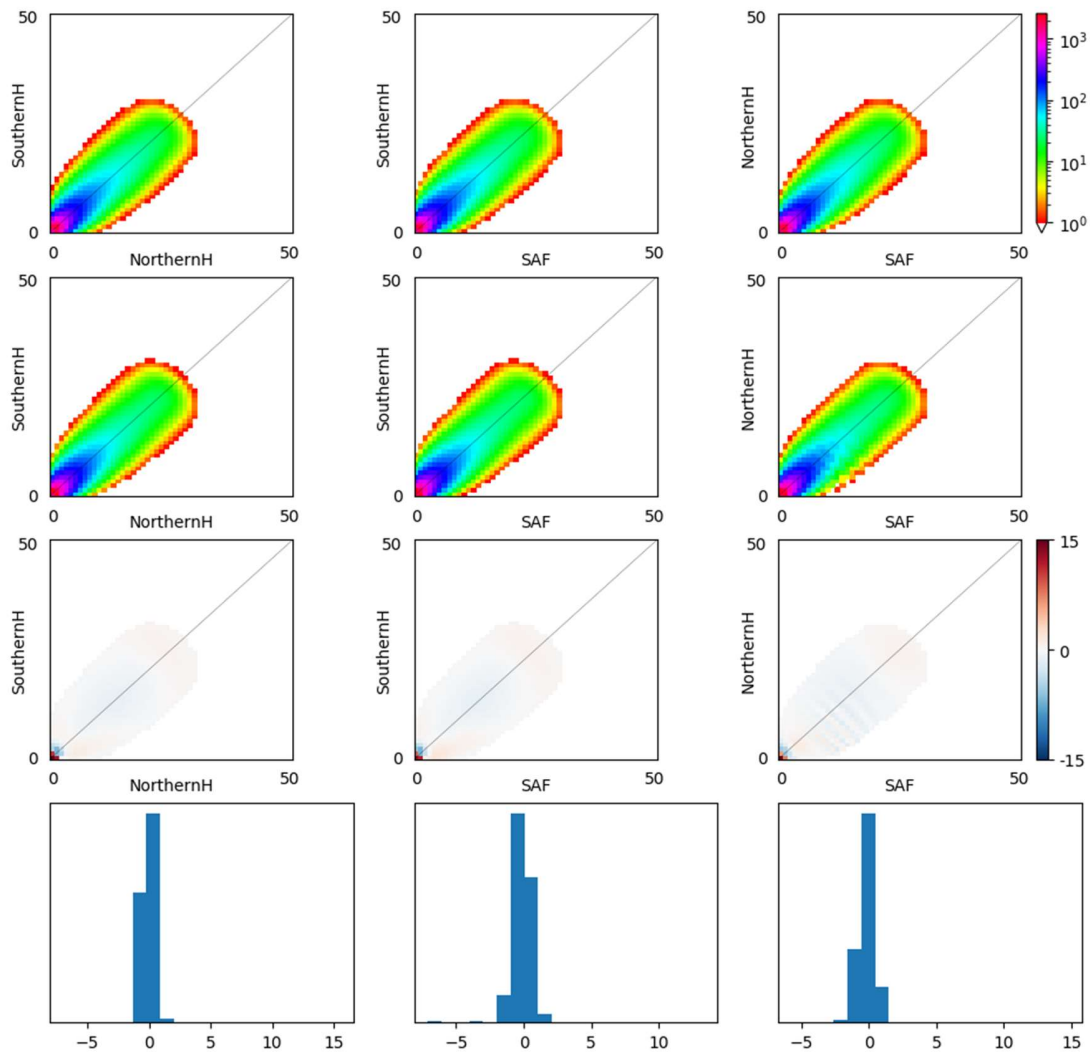
S7. Demographic parameters with 3-population models (including northern, southern, and South Africa (SAF) populations) inferred by *GADMA* from 50x50x50 JAFS. Demographic history for the 2-population model was used for inference: SAF (South Africa) population was added to the model according to one of two different trees (i.e., First and Second tree*), and its additional parameters were inferred by *GADMA*. All other parameters were extracted from the 2-population model and fixed during demography reconstruction. Log-likelihood is presented for 50x50x50 JAFS and both tree models, with best values marked in bold. *(First tree – Figure 3 picture a) the ancestral population is splitted into northern population and common population of SAF and southern that is splitted later. (Second tree – Figure 3 picture b) the ancestral population is splitted into southern population and common population of SAF and northern that is splitted later. CI below the values of first tree model (Confidence intervals).

	First tree model	Second tree model		
Log-likelihood for 50x50x50 JAFS	-10714.8	-10890.8		
Parameters	Values first tree	Values second tree	Units	Parameters' definition
N _A	20,448 [15,976 - 21,733]	28,064	Individuals	Size of the ancestral population.
N _{A_split}	165,077 [158,382 - 169,528]	153,743	Individuals	Size of the ancestral population after linear growth.
N _{Nor0}	1,920 [1,366 - 2,131]	2,669	Individuals	Size of northern population after split of ancestral population.
N _{Nor}	1,920 [1,366 - 2,131]	2,669	Individuals	Size of northern population now.
N _{Sou0}	1,120 [937 - 1,239]	3,835	Individuals	Size of southern population after split of ancestral population.
N _{Sou}	2,917 [2,054 - 3,258]	1,044	Individuals	Size of southern population now (after linear growth).
N _{SAFO}	1,708 [938 - 2,232]	479	Individuals	Size of SAF population after split from either northern or southern population.
N _{SAF}	1,593 [888 - 1,821]	570	Individuals	Size of SAF population now (after exponential growth).
T _A	163,057 [157,567 - 176,887]	135,519	Number of generations	Time of the beginning of ancestral population linear growth

MOLECULAR ECOLOGY

T_{split}	183 [136 - 201]	679	Number of generations	Split of ancestral population into northern and southern populations.
T_{SAFsplit}	32 [24 - 35]	449	Number of generations	Split of SAF population either from northern or southern population.
$M_{\text{Sou-Nor}}$	0.0588 [0.0396 - 0.1054]	0.1027	Proportion per generation	Migration rate from southern population to northern
$M_{\text{Nor-Sou}}$	~0 [0 - 0]	~0	Proportion per generation	Migration rate from northern population to southern
$M_{\text{Sou-SAF}}$	0.0019 [0.0016 - 0.0026]	0.1178	Proportion per generation	Migration rate from southern population to SAF
$M_{\text{SAF-Sou}}$	0.2245 [0.0342 - 0.5090]	0.1781	Proportion per generation	Migration rate from SAF population to southern
$M_{\text{Nor-SAF}}$	0.0290 [0 - 0.0784]	0.1317	Proportion per generation	Migration rate from northern population to SAF
$M_{\text{SAF-Nor}}$	~0 [0 - 0]	0.1781	Proportion per generation	Migration rate from SAF population to northern

MOLECULAR ECOLOGY



S8. Comparison of the joint allele frequency spectrum used for demographic analysis and simulated JAFS for best demographic history. (Top, line 1) Pairwise projection of 50x50x50 JAFS for northern, southern and SAF populations. Demographic history was inferred for this spectrum. (Line 2) Pairwise projection of simulated under best demographic model (log-likelihood -10754.7) JAFS. (Line 3) Anscombe residuals of the projections on first line and second. (Bottom, line 4) The histogram of the Anscombe residuals.