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Population genomics of the Small-Spotted Catshark (*Scyliorhinus canicula*) along the Western European Coast

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The small-spotted catshark *Scyliorhinus canicula* is a common small benthic shark inhabiting coastal waters along the eastern Atlantic and the Mediterranean Sea (Compagno et al. 2005). It is mostly taken as bycatch in demersal fisheries but its commercial importance is growing. As an Elasmobranch, it is characterized by slow growth rates, late maturity, low fecundity and production of few well-developed offsprings, with 29-62 eggs/year estimated for Northeast Atlantic populations (Ellis and Shackley 1997). Connectivity among populations of *S. canicula* is mainly dependent on actively swimming adults (Musick et al. 2004). Female philopatry, sexual segregation, and low dispersal ability suggest the potential for *S. canicula* to form localized populations (Gubili et al. 2014). Nonetheless, recent population genetic studies on this species have shown little to no evidence of genetic differentiation at nuclear microsatellite loci and at the mitochondrial control region (mtDNA CR) along its eastern North Atlantic range (Gubilli et al. 2014).

This study provides further insights into the population genomics of the small-spotted catshark along its eastern North Atlantic range, by using newly developed Single Nucleotide Polymorphism (SNP) markers with the potential to track both the neutral and the non-neutral genetic diversity. SNP markers were called and genotyped in a total of 96 samples of *S. canicula* collected from the North Sea (NS, n= 18), Irish Sea (IS, n=19), Celtic Sea (CS, n=19), Northern Portugal (NP, n=20) and Southern Portugal (SP, n=20), by applying the 2b-RAD protocol (Wang et al. 2012) with modifications. The dDocent pipeline (Puritz et al. 2014) was used for reference contig assembly, read mapping, and SNP genotyping. A total of 15,144 SNP loci were identified with 1,183 SNPs being genotyped in 71 individuals after quality filtering

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and trimming. Three independent neutrality tests detected 18 outlier SNP loci, with loci being considered as outlier only when detected by at least 2 of the 3 methods used. Accordingly, the original data set was split in a neutral subset (1,165 SNPs) and a putatively non-neutral subset (18 SNPs).

Discriminant Analysis of Principal Components (Jombart 2008; Jombart et al. 2010) consistently showed the presence of two distinct genetic clusters of individuals at both the putative non-neutral and neutral loci (Fig. 1): one cluster includes the 4 most northern collections, and another cluster includes only the SP collection. This finding indicates the presence of previously undetected population structure in the small-spotted catshark in the NE Atlantic, in contrast with the pattern of genetic homogeneity found in previous studies using microsatellite markers (Gubili et al. 2014, Cardoso 2015).

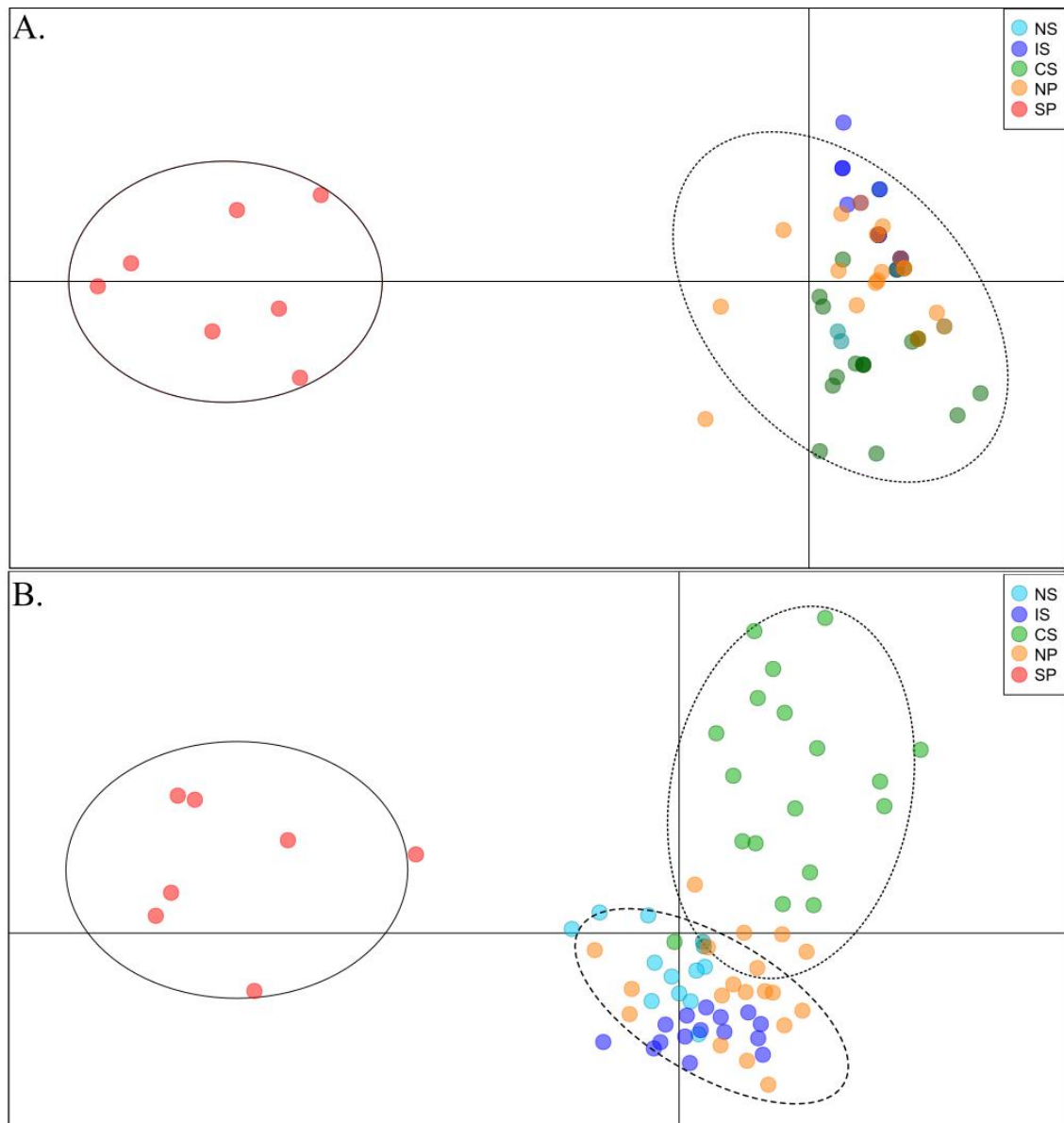


FIGURE 1. Population genomics of the small spotted catshark *Scyliorhinus canicula* among different locations in the eastern North Atlantic: North Sea (NS), Irish Sea (IS), Celtic Sea (CS), Northern Portugal (NP) and Southern Portugal (SP). Discriminant Analysis of Principal Components performed on a) putatively non-neutral loci (n=18 loci), and b) neutral loci (n=1165 loci).

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The presence of a genetic break around southern Iberia found at neutral and non-neutral loci suggests restricted genetic connectivity between South Portugal and northern areas. Restricted gene flow may also lead to increased genetic drift if the effective size of populations on either side of the break is low. However, it is also plausible that the distinct environmental conditions found in South Portugal (e.g. higher water temperatures compared to northern areas) may act as a selective force driving local adaptation of *S. canicula* in this region. In addition to the above genetic break, we found the CS collection to be different from other northern areas at both neutral loci and non-neutral loci. This result was unexpected and suggests further structuring of *S. canicula* along the western European range. However, this signal deserves to be explored further to test for the robustness of the differences found here.

We also tested the hypothesis of Isolation-By-Distance (IBD) along the sampled range to compare pairwise genetic relatedness among individuals at neutral loci with geographic distances. We found a significant correlation between genetic and geographic distances ($p < 0.000$), in line with the expectations based on the limited dispersal along the continuous distribution of the species in the study area. Follow-up studies are being conducted to explore the association between genetic diversity and environmental conditions, by testing also the contribution of the different environmental variables to the spatial variance in genetic diversity distribution.

In conclusion, we show the presence of population structure in *S. canicula* along the eastern North Atlantic, which supports the current management strategy for the species in considering the presence of multiple local populations along the western European coast. Also, we confirm the potential of population genomics as a powerful tool for fisheries management, providing increased resolution to unveil the patterns of species' population structure.

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