Editor's Comments

The two reviewers have made suggestions which we feel would improve your manuscript, and I encourage you to consider all these comments and make an appropriate revision of your manuscript.

Please carefully address the issues raised in the comments, such as:

1. Because PeerJ does not offer copyediting, please ensure that your revision meets the English language standards. Lines 12-16, 161-162, 258-264, 294-296, and the overall wordiness of the manuscript (e.g., in lines 258-259 “Based on these results, there seems to be no compelling reason to argue that the Mediterranean BS are fully panmictic with the BS inhabiting the adjacent North-eastern Atlantic” can be changed to “Our results suggest BS in the NE Atlantic and the Mediterranean are not panmictic.”

2. Complexity in structure between the Mediterranean and adjacent North-eastern Atlantic BS, by using other studies with similar distribution that will assist you in justifying the weak structure between the Med and the Atlantic. (ref#2)

3. Reshaping the intro following suggestions of ref#1

Dear Prof. Rita Castilho, Academic Editor, PeerJ

We are really grateful for the thorough review of our manuscript #2017:08:19869 “Genetic differentiation and phylogeography of Mediterranean-North Eastern Atlantic blue shark (*Prionace glauca*, L. 1758) using mitochondrial DNA: panmixia or complex stock structure?”.

The many helpful comments and suggested modifications have been integrated into the revised manuscript.

We revised and reorganised the manuscript following all suggestions. In particular,

1) Beside the compliance and suitability of the scientific content of revised manuscript, the writing language has been simplified and improved with the contribute of the native English speaker co-authors and of Professor Stefano Mariani, now co-author of this research work. Each section has been rephrased, simplified and shortened whenever possible to avoid excess of details, with the intention to improve the manuscript’s appeal to a wider reader audience.

2) As suggested by the reviewer 2, we added two references, on *Scyliorhinus canicula* and *Etmopterus spinax*, respectively, by Gubili, et al. (2014;2016), that present similar sampling distribution and results compared to those we obtained with the blue shark. The sentence is now: “Similar weak but significant genetic differences were observed in other shark species, more related to a benthic environment, such the small-spotted catshark, *Scyliorhinus canicula*, and the velvet belly lanternshark, *Etmopterus spinax* (Gubili, et al. 2014;2016)”.

Ref:

Gubili C, Macleod K, Perry W, Hanel P, Batzakas I, Farrell ED, Lynghammar A, Mancusi C, Mariani S, Menezes GM, Neat F, Scarcella G, Griffiths AM. 2016. Connectivity in the deep: Phylogeography of the velvet belly lanternshark. Deep Sea Research Part I Oceanographic Research Papers, 115: 233-239. https://doi.org/10.1016/j.dsr.2016.07.002

Gubili C, Sims DW, Veríssimo A, Domenici P, Ellis J, Grigoriou P, Johnson AF, McHugh M, Neat F, Satta A, Scarcella G, Serra-Pereira B, Soldo A, Genner MJ, Griffiths AM. 2014. A tale of two seas: contrasting patterns of population structure in the small-spotted catshark across Europe. Royal Society Open Science, 1: 140175. http://dx.doi.org/10.1098/rsos.140175.

3) We restructured the introduction in order to make it more linear and less verbose, following all suggestions from reviewer 1. As requested by the reviewer 1, we also moved few paragraphs from the discussion to the introduction.

As requested we are submitting the revised manuscript using Track Changes (MS Office Word), the clean revised manuscript (MS Office Word), as well as the detailed responses to each of the Reviewers' comments, provided in the Response to Reviewers file.

We are happy to provide you with any additional information you might need, and we thank you for your time and attention.

On behalf of the authors,

Best regards

Agostino Leone

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Reviewer 1 (Kevin Feldheim)

Comments for the Author

The authors use mtDNA sequencing to examine population structure between Mediterranean and Northeast Atlantic blue shark populations. The paper is interesting and will make a nice contribution to the literature. I have made comments and suggestions below.

General comments

Given the proximity of the populations, I was surprised the authors found genetic differentiation in their dataset. This is a very interesting result.

Authors: We thank the reviewer for the positive feedback. These results are unexpected and at the same time helpful to assess genetically the Mediterranean population and we hope they will give a valuable contribution for the next population assessments.

In some areas, the authors are a bit too verbose (examples: last sentence of Abstract; lines 76-80; lines 215-219; lines 237-242; lines 254-258; lines 316-330)

Authors: With the contribute of our native English speaker co-authors and of Professor Stefano Mariani, now co-author of this research work, we simplified and improved the whole manuscript, with a special focus on the abstract and the introduction.

I commend the authors for the interactive map of their sampling—this is very cool!

Authors: Thank you. We are glad that the interactive map was appreciated. With this research project, we also aim to bring readers, enthusiasts and students closer together by showing them the research process in real time, making the experience more interactive and transparent.

Why were the sequences not combined to a concatenated sequence and the same set of analyses run? Also, why the discrepancy between sample sizes for the two genes?

Authors: We could not combine the two markers to a concatenated dataset because, as noticed by the reviewers, we had relevant discrepancy between sample sizes for the two genes. Despite multiple attempts we weren’t able to amplify and sequence both markers for all specimens, especially for the individuals from the Celtic Sea (NNEATL). The molecular work was particularly challenging for the Control Region locus, despite the design of two species-specific primers, and several specimens lack the data for this marker. For this reason, a unique concatenated dataset would result in a reduced sample size dataset with an even more unbalanced sampling design**.**

Abstract:

I suggest changing “failed in finding evidences of constant migrations” to “failed to find evidence of migration”

I suggest changing “The network results revealed apparently no genetic structure through the Mediterranean-Atlantic seaway, quite the opposite, the Phist AMOVA and pairwise Phist analysis found a significant genetic structure among four geographical groups” to “Although no obvious genetic structure was apparent from the haplotype network, Phist analyses indicated significant genetic structure among four geographical groups.”

Authors: The abstract has been modified as suggested by the reviewer

Line 3: make “shark” plural and change “spreads” to “is found”

Authors: revised as requested by the reviewer

Lines 17-18: change to “on the western side” and “on the eastern side” (change “in” to “on” in each case).

Authors: changed as requested by the reviewer

Line 19: delete “and”

Authors: deleted as requested

Line 55: delete period after Mediterranean

Authors: deleted as suggested

Lines 65-66: authors cite a study stating that almost all BS caught in the Mediterranean were immature, yet in their dataset (Table S1), this is not the case. The authors do not speculate as to why this is. It would be interesting to touch on this in the Discussion if the authors have any insight.

Authors: we observed differences between the work of Megalofonou et al. (2009) and our work, when compared to the results of the tagging study of Kohler et al. (2002). Anyway, the specimens’ data from Kohler et al. (2002) came principally from volunteer recreational fishermen, while the individuals from Megalofonou et al. (2009) and from this work, originated principally as by-catch from commercial fisheries, such tuna and swordfish longline. This may explain the maturity/stage differences observed among the different works. Despite the inherent limit of our dataset, our observation for the Eastern Mediterranean is concordant with data reported in Megalofonou et al. (2009).

As suggested by the reviewer, we added a small paragraph in the Discussion section “The biological data reported in Megalofonou and colleagues (2009) describe a larger amount of big female in the easternmost Mediterranean (e.g. Aegean Sea) which is in agreement with the pattern inferred from our dataset. Conversely, using data on size and maturity stages, Kohler and colleagues (2002) observe that the majority of sharks from the Mediterranean Sea were juvenile and immature (99% of males and 98% of females; mean = 65 cm of fork length). The difference may be related to the different sampling design and fishing gear used in the studies. In fact, the majority of the data collected by Kohler and colleagues (2002) came from volunteer recreational fishermen, while the individuals from Megalofonou et al. (2009) and from this work, originated principally as by-catch from commercial fisheries, such tuna and swordfish longline”. See tracked changes document.

Lines 74-75: In the abstract, the authors state 8 populations—please clarify.

Authors: in the abstract we refer to the sampling site (8) while in the intro we mention the four geographical areas in which the sampling site were grouped. We detail this in the Methods section.

Line 80: change “Expected” to “These”

Authors: changed to “These” as suggested

Lines 116-119: Normally, final concentrations are reported (this is a minor point).

Authors: We added the reagents final concentrations, as requested. The text was modified in: PCR reactions were performed for both markers in a final volume of 50 μL containing 31.75 μL of distilled sterile H2O, 8 μL of Buffer 10x (Tris-HCl; final 1X), 3 μL of MgCl2 (25mM; final 1.5 mM), 2 μL of dNTPs (10mM; final 0.37 mM), 2.5 μL (10μM; final 0.46 μM) of each primer, 0.25 μL (5U/μL; final 1.5U) of *Taq* polymerase and 2 μL of template DNA (10-20ng).

Line 154: change “females outnumbered significantly males” to “females significantly outnumbered males”

Authors: changed as requested

Line 178: Which second one? It looks like only the haplotype with 61 individuals is shared by all populations except NNEATL (which is mentioned in lines 176-178).

Authors: We thank the reviewer for this, since this sentence was incorrect due to multiple editing. We corrected and clarify the sentence which is now: “In the Cytb network, the four main frequent haplotypes were shared by BS from all the four geographical areas, except for the most frequent haplotype which was shared by BS from the three geographical areas, SNEATL, WMED and EMED”.

Lines 231-236: which markers were used in these other studies and how do they relate to data here?

Authors: the markers used by these studies are both microsatellites and mtDNA loci. Specifically, for mtDNA loci, Sampaio Da Costa (2013) and Veríssimo et al. (2017) used the highly variable and neutral control region. Fitzpatrick (2012) used a 3107 bp concatenated sequences from the several mitochondrial coding genes (16s, COII, ATPase sub.8 & 6) and control region. These data are related to our data since we used both neutral (control region) and coding (Cytb) genes. The control region is the most used markers in all studies on phylogeography of sharks, while the Cytb was used to investigate the population structure of the Pacific blue shark population (Li, et al. 2016). Our dataset could be compared to the Pacific population, in the future. The choice of markers is due to the fact that both these loci have a good resolution power, which is fundamental for findings population structure in such a vagile species.

Ref: Li W, Dai X, Zhu J, Tian S, He S, Wu F. 2016. Genetic differentiation in blue shark, *Prionace glauca*, from the central Pacific Ocean, as inferred by mitochondrial cytochrome b region. Mitochondrial DNA Part A, 19:1-4. doi: 10.3109/19401736.2015.1137903.

Lines 242-245: Do you mean female philopatry when you say “reproductive movements?” The mtDNA structure found could very well indicate this, although it would help to have corresponding nuclear data to verify. Also, the authors don’t really stress whether or not these sampling locales were nurseries (although they do mention in passing)—I would suggest explicitly stating which sites are known (or suspected) nursery sites—the authors do this for the Mediterranean but not the Atlantic sites.

Authors: with “reproductive movements” here we mean behavioural patterns that can explain our results, and female philopatry could be one of them explain that. We avoided the specific assumption of female philopatry being the unique driver without having the nuclear data. Anyway, we rewrote the paragraph with “pattern of differentiation seems to suggest that reproductive movements, such as female philopatry, may occur between the Western Mediterranean and the Southern North-eastern Atlantic BS”. Furthermore, we revised the paragraphs as suggested, stating explicitly which sites are suspected to be nursery sites in the Eastern-Atlantic “Given that SNNEATL specimens are from a previously identified nursery site (Veríssimo, et al. 2017), the pairwise Φst values could suggest that specimens from WMED can be reproductively related to the SNNEATL, while EMED could represent a nursery site in itself (Megalofonou, et al. 2009)”.

Also, I would suggest analyzing sites without adults—if female philopatry could explain these results, I would expect an even stronger signal when solely analyzing juveniles/immatures from each site.

Authors:we thank the reviewer for this point. We performed analyses with only the data from the juveniles/immatures individuals from each site. Results from pairwise Φst and the AMOVA are now provided in the supporting information and mentioned in the main text as follow: “AMOVA and pairwise Φst analyses were performed on a reduced dataset, selecting only juvenile and immature specimens from each sampling site. Despite the reduced sample sizes and the complete absence of data from the site NNEATL, the results obtained are in agreement with the values observed with the complete dataset (**Tab. S3**; **S4**)”.

We avoided in the main text to split the dataset, since the NNEATL specimens are almost all large specimens with just two young specimens, which would have forced us to lose a very interesting study area, reducing the dataset to just three areas (SNNEATL, WMED, EMED). Furthermore, we would have excluded also a large portion of sharks from the Aegean Sea. Anyway, using only juveniles and immature we didn’t observe strong differences in the pairwise Φst values and AMOVA results. Additionally, we believe that analyzing only the large individuals of this dataset could lead to a bias due to really unbalanced samples size.

Lines 258-260: This isn’t necessarily true—they can be panmictic (with males mating across populations) with female philopatry. Based on other studies, I’d be surprised if nuclear data exhibited structure. Following, (lines 266-268)—nuclear data may not necessarily exhibit structure.

Authors: we agree with the reviewer and the sentence has been softened to “Such evidence of genetic structure was associated with geographical differences in sex-ratio and size. Based on these results, the Mediterranean BS seems to be not fully panmictic with the BS inhabiting the adjacent North-eastern Atlantic.”. And in the lines 266-268 (see tracked changes files for the exact lines after the revision), the sentence “for detecting subtle structure” has changed to “for investigating potential subtle structure”.

Lines 269-283: This paragraph seems out of place. Most of it belongs in the INTRO.

Authors: we agree with the reviewer and now the paragraph belongs to the Introduction. See tracked changes document.

Lines 316-330: Also seems a bit out of place, with a lot of this belonging in the INTRO. Ending with a comment on the fin trade doesn’t fit with this study. Instead, I would suggest stating the novelty of the Mediterranean population based on your results and how specific conservation measures should be implemented for the population (for example, leaving lines 321-325).

Authors: we followed the indication of the reviewer and modified the whole paragraph accordingly. We moved the sentences on fin trading to the Introduction section (See tracked changes document) and we emphasized the novelty of the Mediterranean population based on our data and how specific conservation measures should be implemented for the population (See tracked changes document).

Fig 1: This is minor, but I suggest changing “sampling design” to “sampling sites” as some of these sites weren’t designed but were instead from commercial fisheries.

Authors: we changed Figure 1 caption to “sampling sites” as suggested

Fig 1: In both the figure (either on the figure itself or in the legend) and also in the text, please include sample sizes of the four regions.

Authors: we added the sample size for each sampling location in figures, and in the the caption text for the 4 subdivided areas (NNEATL, SNEATL, WMED, EMED). In the text we included the samples sizes for each of the eight sampling sites, organized in the four areas (NNEATL, SNEATL, WMED, EMED). We thank the reviewer, since with this observation we noticed a minor text error, now corrected (THYR instead of TYRR).

Fig 2: I understand why the authors have multiple colors within certain haplotypes (for example, three green in haplotype 42), but without knowing the sample locales, these are meaningless. Since the authors break this down in the supplemental figure, I would suggest combining the colors for this figure.

Authors: we agree with the reviewer and we have revised the haplotype networks displayed in Figure 2, to convey more linear and clear information. According to comment of the Reviewer 2, we removed the small figure displaying the size (number of individuals) per haplotype, since we have the exact same data (number of individual in each haplotype) written on the network itself.

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**Reviewer 2 (Anonymous)**

Basic reporting

The paper is nicely presented, has an adequate number of references and has a sufficient number of tables and figures. I have added minor suggestions for the authors.

Background

“but genetic structure has not been confirmed even at interoceanic distances.” Remove the word “even”. There are plenty of recent papers on BS describing genetic structure on an intraoceanic level.

Authors: the word “even” was deleted as requested by the reviewer and the entire abstract was revised and simplified as requested by the reviewer 1 and the editor

Results

Remove “apparently” and replace “quite the opposite” with whereas.

Authors: we changed the entire sentence as requested by reviewer 1, the new simplified sentence is “although no obvious pattern of geographical differentiation was apparent from the haplotype network, Φst analysis indicated significant genetic structure among four geographical groups”.

Introduction

Line 3: Please use a reference for the previous statement.

Authors: We thank the reviewer for this observation. We added the missing reference which is Compagno, 1984.

Line 40: The authors use the term mating clubs. It might be better to include them into quotation marks.

Authors: The part was revised and simplified as requested by the reviewers and the editor. See the tracked changes document for details

Line 55: remove the first “.”

Authors: removed as requested.

Line 71: Add a space before “On the other hand”

Authors: space added as requested.

Material and Methods

Lines 87-90: Please add the number of individuals per sampling area in case readers will not have to check supplementary material.

Authors: we number of individuals per sampling area as requested by the reviewer and in congruence with the same request by reviewer 1.

Lines 110-111: Why did the authors required to design new primers for the species, since they could follow previous attempts? See Verissimo et al., 2017 for CR primers. Can they justify their decision?

Authors: We thank the reviewer for the question, that gave us the possibility to highlight another novelty of this work. Since not all samples we processed were stored adequately, we wondered if the use of a primer designed for a different species was a suitable strategy. In fact, for the amplification of the CR, Verissimo, et al. 2017, used a couple of primers designed by Pardini, et al. (2001) for the white sharks, *Carcharodon carcharias*. Here we designed 2 pairs of species specific primer for the blue shark, which minimize the risk of unsuccessful PCR amplification, that represent a useful resource for future studies.

Ref: Pardini, et al. (2001) Sex-biased dispersal of great white sharks. Nature, 412: 139-140

Line 120: replace “annealing at 60ᵒC for 30s” with “annealing at 60ᵒC for 30 s”.

Authors: changed to “annealing at 60°C for 30 s” as requested.

Line 139: Describe the four groupings for the AMOVA analysis.

Authors: the AMOVA groupings are now described as requested, following the scheme reported in Table2

Results

Line 179: What does the N≥10 mean? Number of individuals? Number of haplotypes? Please clarify.

Authors: We thank the reviewer for the point. It means number of individual. We changed N to N° individuals to clarify.

Discussion and Conclusion

Line 244: Replace “Φsts” with “Φst values”.

Authors: changed to Φst values as requested

Lines 252-253: I am wondering about the role of the Adriatic as a nursery for BS. The authors claim to confirm Megalofonou et al., 2009 suggestions about the matter. I also assume that the authors have probably used samples provided from the same dataset used in that manuscript.

Authors: the great abundance of juveniles observed in the Adriatic Sea strongly suggest that this area could represent a nursery for the species. Furthermore, multiple previous works observed the same pattern: 1) Bianchi I., Clo` S. and Costantini M. (1997) Med-Tag and Baby shark: two projects for tagging sharks. First results, considerations and prospects. Quaderni della Civica Stazione Idrobiologica di Milano. 22, 137–146; 2) Tudela S. (2004). Ecosystem Effects Of Fishing In The Mediterranean: An Analysis Of The Major Threats Of Fishing Gear And Practices To Biodiversity And Marine Habitats (Gfcm Studies and Reviews). In: General Fisheries Commission for the Mediterranean Studies and Reviews No. 74. Food & Agriculture Organization (FAO).

We used samples provided by the colleagues participating in this study. In details, for Adriatic Sea Megalofonou, et al. (2009) collected specimens from south Adriatic, while here we use specimens from central Adriatic provided by University of Bologna colleagues. Regarding the Aegean Sea, a portion of the samples provided within the project MedBluesGen, <https://fishreg.jrc.ec.europa.eu/web/medbluesgen/sampling-data>, only partially used here, are from the dataset of Megalofonou, et al. (2009).

Considering the lack of information on sampling dates (I do not remember seeing a table with the actual dates that the samples were caught), have the authors compared the sizes or sex ratios based on time of capture? Do they have other individuals caught in the same period for direct comparison and subsequently prove their argument?

Authors: we thank the reviewer for the question. We are aware of the limits of our dataset. Basically, we have sparse specimens from different time period. The majority of the specimens were caught in the time span 2013-2016, while few specimens (N = 5) from the AEGE are from 2003-2005, and few specimens from the LIGU site (N ~ 10) are from 2005-2009. Unfortunately, our dataset is not homogeneous per years, season, size of the specimens. Given the different time ranges represented in our dataset and the fact that this time span is max 13 years, which is 1 generation (Generation time for North Atlantic BS stock = 9.8 years (Mejuto, J., & García-Cortés, B.2005). we avoided any temporal comparisons, due to not sufficient data that could lead to non-significant and biased results. As stated also in a comment of the reviewer 1, we think that a proper analysis of differences in size and sex ratio needs for a bigger and homogeneous dataset, since observed differences can be the results of the different sampling strategy (e.g. different gear: commercial vs. recreational).

Ref: Mejuto, J., & García-Cortés, B. (2005). Reproductive and distribution parameters of the blue shark *Prionace glauca*, on the basis of on-board observations at sea in the Atlantic, Indian and Pacific oceans. Collective Volume of Scientific Papers, ICCAT, 58(3), 951–973.

Figures and Tables

Figure 2: What is the point of the additional small figure displaying the size+number of individuals per haplotype, when you have the number of individual in each haplotype? Please remove it, as it does not add anything to the Figure.

Authors: We agree with the reviewer and the size legend figure was deleted as requested.

Figure 3: You need to add the details for the sampling locations. NNEATL: North North-eastern Atlantic; SNEATL: South North-eastern Atlantic; WMED: Western Mediterranean; EMED: Eastern Mediterranean.

Authors: As suggested by the reviewer we added the details for the sampling locations in the caption of Figure 3.

Experimental design

The importance of the sampling area is highlighted throughout the manuscript. The Mediterranean is a very important mating and nursery ground for chondricthyans. The methods are sufficiently described.

However, I was wondering about the sampling dates. Sampling took place from 2003 to 2016. Have the authors checked for temporal differences?

Authors: We are aware of the limits of our dataset that prevent us to do a proper assessment of temporal differences. Basically, we have sparse specimens from different time period. The majority of the specimens were caught in the time span 2013-2016, while few specimens (N = 5) from the AEGE are from 2003-2005, and few specimens from the LIGU site (N ~ 10) are from 2005-2009. Unfortunately, our dataset is not homogeneous per years, season, size of the specimens. Given the different time ranges represented in our dataset and the fact that this time span is max 13 years, which is 1 generation (Generation time for North Atlantic BS stock = 9.8 years, Mejuto, J., & García-Cortés, B.2005), we avoided any temporal comparisons, due to not sufficient data that could lead to non-significant and biased results.

Ref: Mejuto, J., & García-Cortés, B. (2005). Reproductive and distribution parameters of the blue shark Prionace glauca, on the basis of on-board observations at sea in the Atlantic, Indian and Pacific oceans. Collective Volume of Scientific Papers, ICCAT, 58(3), 951–973.

Validity of the findings

Despite the complexity of the results, the authors do a very good job describing and justifying their results. Their findings are robust. and statistically sound. There are a couple of things that need to be clarified.

There is a lack of discussion regarding the sex ratio differences found between the two seas despite the results they reported in Lines 154-164. Do the authors have any suggestions? Moreover, can you justify the differences in male/female sex ration found in the Mediterranean between your results and the ones reported by Megalofonou et al., 2009?

Authors: we think that a proper analysis of differences in size and sex ratio needs for a bigger and homogeneous dataset, since observed differences can be the results of the different sampling strategy (e.g. different gear: commercial vs. recreational). However, in the work of Megalofonou, et al. (2009), the authors used specimens from the Eastern Mediterranean, specifically Aegean Sea, Ionian Sea, Levantine Sea and South Adriatic, while we here we used a dataset that cover most of the Mediterranean basin, including the Central Adriatic.

Lines 254-268: You are trying to justify the complexity in structure between the Mediterranean and adjacent North-eastern Atlantic BS. You are doing an excellent job by justifying your data with the results from tagging data (previous studies). Considering the lack of nuclear data, I believe that you can also use studies with similar distribution might partially help you justify this weak structure between the Med and the Atlantic. There are at least three papers (2 on Scyliorhinus canicula and one on Etmopterus spinax) that might be able to help the authors add to their discussion, particularly in the absence of nuclear data.

Authors: we thank the reviewer for the references suggested. We added the suggested reference about *Scyliorhinus canicula* and *Etmopterus spinax* by Gubili, et al. (2014;2016) and Kousteni, et al. (2015).

The sentence is now: “Similar findings of genetic differences were observed in other shark species, more related to a benthic environment, such the small-spotted catshark, *Scyliorhinus canicula*, and the velvet belly lanternshark, *Etmopterus spinax* (Gubili, et al. 2014;2016; Kousteni, et al. 2015)”.

Ref: Gubili C, Macleod K, Perry W, Hanel P, Batzakas I, Farrell ED, Lynghammar A, Mancusi C, Mariani S, Menezes GM, Neat F, Scarcella G, Griffiths AM. 2016. Connectivity in the deep: Phylogeography of the velvet belly lanternshark. Deep Sea Research Part I Oceanographic Research Papers, 115: 233-239. https://doi.org/10.1016/j.dsr.2016.07.002

Gubili C, Sims DW, Veríssimo A, Domenici P, Ellis J, Grigoriou P, Johnson AF, McHugh M, Neat F, Satta A, Scarcella G, Serra-Pereira B, Soldo A, Genner MJ, Griffiths AM. 2014. A tale of two seas: contrasting patterns of population structure in the small-spotted catshark across Europe. Royal Society Open Science, 1: 140175. http://dx.doi.org/10.1098/rsos.140175

Kousteni V, Kasapidis P, Kotoulas G, Megalofonou P. 2015. Strong population genetic structure and contrasting demographic histories for the small-spotted catshark (Scyliorhinus canicula) in the Mediterranean Sea. Heredity,114: 333–343. doi:10.1038/hdy.2014.107

Comments for the Author

This is a nice study with sufficient mtDNA data that is well analyzed and well presented. The figures are clear. I feel that the study will be of broad interest to readers of the journal because of the interesting region being sampled. Our understanding of elasmobranch genetic structure is greatly improved by studies such as this. This is especially true in light of recent papers that have presented genetic structure in the Mediterranean.

I think there is the basis for a nice publication on the population structure of Prionace glauca, and I believe that the manuscript could be improved as few things are not presented adequately.

Authors: We thank the reviewer and we are glad that the manuscript was appreciated. We followed all the precious suggestions by the reviewers and the editor, which have considerably improved the manuscript.