Introduction

Line 51-54: You started the paragraph mentioning the high level of gene flow in large marine organisms and then the given example is talking about inbreeding – which is very unlikely to happen when there is high gene flow occurring. I suggest modifying this paragraph by potentially including the first two sentences of paragraph two together with the last sentence of paragraph one and having it as a separate paragraph.

Line 57: "*fantastic opportunity to explore these problems"* – What problems? You need to make it clear to your reader.

Methods

Line 136 – Explain in more details how and why those enzymes were chosen for the digestion.

Line 185-197 "We determined geographic distances based on a least-cost path analysis using the R package *marmap* (Pante & Simon-Bouhet, 2013)" – Since the sampling description of your samples say that they were obtained from fisheries, I would like to know what type of geographic information was used to calculate the "geographic distance". Opportunistic sampling usually does not offer geographic information. Please, explain this in your methods a little bit more.

Results

Table 1 – Interesting to see that the COI presented a lot more number of haplotypes and diversity than the CR region. Line 239-241 "For the CR, our sample size of 65 individuals was sufficient to recover both 95% and 99% of the haplotype diversity in the species (Figure S2C–D)".

Would you have an idea why that might be considering that the CR is usually the most polymorphic region in the mDNA? Perhaps the CR region where the primer was designed do not cover the polymorphic region of this gene? This should definitely be considered when designing a primer.

Line 247-250 – For better visualization, I suggest adding the pairwise Fst figure for the CR region in Figure 2. CR is the most used mtDNA marker in population genetic studies, so I think displaying it as the main result is necessary.

Line 265-267 – I do not think is necessary to display the figures referring to K>2. I would suggest displaying only the K=2 as it is the optimal value for your samples.

Table 4 – UAE and Oman seem to have low genetic diversity considering the number of samples analyzed for these locations compared to Bangladesh and Saudi Arabia.

Discussion

Line 312-325 – What was taken into consideration when targeting the CR region during primer design? The CR region has approximately >1000bp and most of the population genetic studies targeting elasmobranchs cover at least 750bp. I suggest modifying the discussion on this topic to account for the technical limitation of this study. You brought up several reasons of why this might be happening but did not provide references to support your statement (Lines 319-321).

Line 333-337 – Very good observation.

Line 372 – 375 - It is not ideal to make this type of affirmations or suggestions when the study do not present a standardized sample size. For the SNPs, Saudi Arabia is only represented by two samples. I suggest exploring more this reference Domingues et al. 2018 for this paragraph.