

Prologue

This report was assembled following the review of an earlier version by Center of International Experts and regional reviewers. A workshop was held in Charleston, South Carolina in January 2026 during which study team members presented the rationale, methods, results, and conclusions from approaches employed by the South Atlantic Red Snapper Research Program (SARSRP) study team to estimate red snapper population size. Study approaches estimated Atlantic red snapper population size with a Bayesian integrated hierarchical model (BHIM) that utilized red snapper density estimates derived from camera sampling and hardbottom habitat distribution estimates, and a close-kin mark-recapture (CKMR) approach that utilized the occurrence of half-sibling pairs (HSPs) from DNA sequencing data derived from fin clip samples. Reviewers asked questions of the study team and subsequently submitted reports addressing the Terms of Reference for the workshop. The SARSRP study team sincerely thanks the CIE and regional reviewers for the time, attention, and effort they put into the review of the SARSRP study and report. The study team found reviewer questions to be thoughtful and well-considered, and feels the report has been improved based on responses to reviewer comments and in places where additional analyses were performed to address them. Team responses and statements about additional analyses or specific revisions are listed below, as well as addressed in the text of Chapters 2 and 3. Additionally, an additional appendix chapter was added to the report. *Appendix V* contains a paper by Kehoe et al. (2025a) that examines the sensitivity of CKMR population estimates for elasmobranchs and teleosts to uncertainty in fish life history parameters via simulation analysis. Reviewers commented that a more focused simulation study on Atlantic red snapper CKMR model sensitivities would be beneficial, which is now provided as *Appendix XI* (Kehoe et al. 2025c).

Response to CIE Comments on Chapter 2: BHIM Population Estimation

The review panel indicated bottom habitat information used in the BHIM was too uncertain to provide a sufficiently reliable estimate of age 2+ absolute abundance. Reviewers also questioned whether the effective sampling area (ESA) of camera-traps estimated based on data from one region is applicable to other sampling regions. Lastly, they suggested the BHIM population estimate is not entirely independent from stock assessment data. Responses to these concerns and more minor issues are addressed below.

1. Minor typos were fixed and wording clarifications were made throughout the chapter.
2. Text was added to clarify the statistical methods related to the conditional autoregressive model formulation and remotely operated vehicle offset parameter (Methods, Results, and a new Supplemental Figure S1).

3. Discussion text was revised to further clarify the challenges posed by limited hardbottom information, discrepancies in the published hardbottom maps, and assumptions of effective sampling areas.
 - a. Specific text on the limitations of hardbottom maps in the Discussion describes how a map known to be incorrect (i.e. The Nature Conservancy (TNC) alone map (Conley et al. 2017) that does not contain known Southeast Reef Fish Survey (SERFS) hardbottom sites) produced implausible (>99 million) and highly variable (<1 million vs >99 million) estimates of population size depending on model type. Additionally, maps that did contain the SERFS sampling areas (e.g., expert opinion (EO) map of Steward et al. 2022) gave less variable estimates of population size depending on map type used (e.g., combined TNC (all hardbottom confidence levels) plus EO map = ~7 million red snapper and combined TNC (high, very high hardbottom confidence levels) and EO map = ~5 million red snapper).
 - b. A statement was included to address CIE reviewer concern that ‘uncertainty in maps’ was not included in our uncertainty in the BHIM-derived red snapper population size estimate was. This text reads, “Finally, analyzing multiple data sources in a single integrated model allows population estimates to account for the uncertainty associated with each data source (e.g., ESA, ROV offsets, camera-trap, and ROV count data). However, population estimates remained conditional on the chosen hardbottom mapping approach (e.g., composite, EO, TNC) and did not incorporate uncertainty from the map selection itself. Future work that integrates uncertainty across mapping products could help address this additional layer of variation; however, a comprehensive, high-resolution hardbottom mapping effort would ultimately provide the most robust foundation for estimating reef-associated fish abundance in the SEUSA.”
 - c. Specific text relative to the “ESA being based only on one region” includes the fact that the posterior distribution on ESA differed from the prior distribution of ESA (that was based on that one region). The Discussion text reads: “For our analysis, we found that ESA posterior distributions for camera-trap video samples diverged from priors in ecologically consistent patterns, with bait attraction expanding the ESA when currents flowed away from camera-traps and reducing the ESA when currents directed bait plumes behind camera-traps, highlighting the critical role of current-mediated bait plume effects on camera-trap count.” However, we do acknowledge that although there was information in the count data that informed the posterior ESA estimates, those ESA estimates are fixed spatially and that this an area of future research: “Finally, we lacked information to allow the ROV offset and ESA parameters to vary across the study area. Instead, ROV offset and ESA parameters act as scaling factors affecting total population size. However, future research quantifying local, species-specific calibrations may identify processes important to unbiasedly estimating absolute abundance from underwater video surveys.”

4. The study team agrees with the reviewers that the BHIM used some of the same data as the stock assessment, specifically SERFS camera counts of red snapper, thus the two methods are not completely independent. However, the BHIM estimate of abundance and spatial distribution of abundances only shared that single dataset in 2021 and 2022, integrated several other data sources not used in the stock assessment (e.g., ROV counts, effective sampling areas, hardbottom maps), and developed an population size estimation procedure that was independent of the stock assessment methods and many of the assumptions therein. As such, population size estimates from BHIM and the stock assessment remained largely independent.

Response to CIE Comments on Chapter 2: CKMR Population Estimation

The review panel stated the CKMR estimate is not independent of the stock assessment and concern was raised whether it can be used as an input to the next stock assessment. The panel also suggested uncertainty in age estimation via the age-length key, estimated stock age composition, and demographic parameters meant the estimated CV on the population estimate could be too low. The panel also questioned the assumption of equal sex-specific fecundity-at-age or fecundity-at-size and indicated this was not tested by the study team. Lastly, the panel suggested proving chromosome-level genome sequencing to assess the degree of linkage among the approximately 1,755 multiallelic haplotypic loci used to obtain the CKMR-derived population estimate. Study team responses are provided below, along with an indication of where changes were made in Chapter 3.

5. Some of the inputs to CKMR are data inputs that are also used in the stock assessment but are not products of the stock assessment. In all cases, life history parameters utilized were those evaluated to be the best scientific information available during the recent Southeastern Data, Assessment, and Review Data Workshop for Atlantic red snapper. An exception to this general statement are the data used to generate red snapper relative age composition for years 2104-2023, which were informed by SEDAR (2024) assessment output. To test how sensitive the CKMR model was to these relative (i.e. proportions not numbers at age) composition data, we also ran the CKMR under an equilibrium age composition, young-biased age composition, and old-biased age composition to produce estimates of population size (Methods, pages 75–76). (Results, pages 85–86) indicate changes to the age composition input had only mild effect with point estimates ranging from 1.29 million (biased old) to 1.91 million (biased young) among all scenarios examined, and 90% credible intervals overlapping for all scenarios. Lastly, CIE reviewer, Joe Powers, indicated a strength of the CKMR approach is it could be incorporated directly into the stock assessment model and the model’s objective function, whereby the issue of independence would be moot.

6. Uncertainty in age estimation via the age-length key was in fact incorporated into the coefficient of variation on estimated population size (see page 71 for a description). The study team tested assumptions of stock age composition and aspects of demography which show fairly consistent results but did not include them in the estimate of uncertainty. One area which was not addressed in the previous draft of the report was what effect persistent differences in fecundity among individuals across years, if they existed, would have on estimated population size. An examination of this potential effect was added to the current study (Methods, pages 75–76) and results indicate persistent differences in fecundity among individuals across years, if they existed, would have only a minor effect on the population estimate (Results, 85–87). Additionally, the new simulation study focused solely on Atlantic red snapper CKMR (*Appendix XI*) clearly demonstrates error caused by even moderate levels of bias or imprecision in demographic inputs would be relatively minor.
7. The study team sequenced the entire mtDNA genome for 40 putative half-sibling pairs (HSPs) following the review workshop to examine the question about potential differences in realized fecundity between sexes (Methods, page 70). The mtDNA molecule is maternally inherited, such that maternal half-siblings inherit the same mtDNA (and hence the same mtDNA sequence), while paternal half-siblings carry mtDNA sequences that are not identical by descent, and therefore are expected to be different. This latter point, Atlantic red snapper mtDNA was highly variable with only 0.2% of unrelated pairs having matching mtDNA sequences, while 40% of related individuals did (Results, page 81). Results from mtDNA of HSPs indicated haplotype sharing among siblings was not significantly different from the expectation of 1:1. This demonstrates HSPs had an equal probability of sharing a mother or a father, thus suggesting realized fecundity was not significantly different for male versus female Atlantic red snapper. This inference is also consistent with the recent finding from the SEDAR 90 Data Workshop that red snapper display a sex ratio that is not significantly different than 1:1 across ages.
8. Simulation analyses examining the effect of bias or imprecision in life history parameters on CKMR-derived population estimates were streamlined, with changes being made to make the results and interpretation of the simulation study more directly applicable to the red snapper CKMR model utilized in Chapter 3. This revised simulation study now appears as report *Appendix XI*.
9. At the time of report submission, the red snapper epigenetic clock was still being optimized, thus could not be utilized to estimate the age composition of putative HSPs. The study team anticipates the optimization process will be completed in the first half of this 2026, making the clock available for a wide range of assessment applications, including estimating age composition for subsequent CKMR analyses. At that stage, age estimation for HSPs included

in Chapter 3 could be revisited, along with examination whether potential parent-offspring kin pairs exist among the study data.

10. The current red snapper genome is not a chromosome level assembly ($L_{50} = 15,544$), thus the team was unable to use it to directly assess physical linkage among haplotype loci. Red snapper heart tissue samples were collected by the study team in winter 2026 and are now undergoing genetic sequencing to assemble a chromosome-level genome for red snapper. Once completed, it could be utilized to examine genetic linkage as suggested by CIE reviewer, Daniel Ruzzante. This level of genome mapping will serve as a resource that can be used to refine myriad red snapper genetic and genomic studies. In the current study, potential issues in estimating the false negative rate caused by physical linkage were examined via simulation with results indicating very little potential effect on population estimation results (Discussion, page 90–92).

References

- Conley, M.F., M.G. Anderson, N. Steinberg, and A. Barnett. 2017. The South Atlantic Bight Marine assessment: species, habitats and ecosystems. The Nature Conservancy, Eastern Conservation Science.
- SEDAR. 2024. Stock Assessment of Red Snapper off the Southeastern United States – Update of SEDAR 73 Assessment. Technical report, SEFSC, Beaufort, NC. URL <http://sedarweb.org/sedar-73>.
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