

Comparison of kinship-identification methods for robust stock assessment using close-kin mark-recapture data for Pacific bluefin tuna

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Abstract

There have been many attempts to understand population dynamics in fishery resources such as tuna species using an integrated-analysis model with multiple data sources. However, estimating the absolute abundance level in practical stock assessments remains challenging. The close-kin mark-recapture (CKMR) method provides information about the number of adults in a population utilizing close-kinship pairs (i.e., parent-offspring, full-sibling, or half-sibling pairs) identified based on statistical methods that employ genetic markers. To introduce the CKMR method into the stock assessment by integrated analysis, it is necessary to clarify the potential errors obtained from the uncertainties in the CKMR method and other data sources. In this paper, we applied three methods of kinship identification for samples from the wild Pacific bluefin tuna population using genome-wide DNA markers to determine the potential errors in statistical kinship estimates. Herein, one method used a random-forest classification algorithm called fraRF that employed pairwise identity-by-descent values. The other two methods were CKMRsim and COLONY. Comparisons among these three methods revealed differences in the numbers of inferred kinship pairs, especially for sibling relationships. The differences among the three methods seem to occur mainly from uncertainty of the kinship identification in the CKMR method. Therefore, this result provides an understanding of ways to incorporate the CKMR method into the integrated analysis model with the possible CKMR errors.

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