Is Close-Kin Mark Recapture feasible for IOTC Yellowfin Tuna Stock Assessment

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Contents

1 Summary

This paper provides (i) brief consideration of options to collect data for improving the IOTC yellowfin stock assessment, (ii) an introduction to the general concept of Close-Kin Mark Recapture (CKMR) - a reasonably new, but proven fisheries assessment tool (e.g. it has been successfully applied to southern bluefin tuna), and (iii) a rough evaluation of the logistical and economic feasibility of applying this tool to the IOTC yellowfin tuna (YFT) population.

CKMR is a form of mark-recapture experiment in which the spawning population size (and various other population parameters) can be estimated, based on the number of closely-related individuals identified (using modern DNA genotyping technologies) in a sample from the commercial catch. The population model estimator involves detailed demographic calculations (resembling typical age-structured assessment models, and with the potential to be integrated into such a model). However, the general concept is intuitively easy to understand, and illustrated with cartoon examples, e.g. given a random sample of individuals from a population, more closely-related pairs are expected to be observed in a smaller population.

CKMR avoids many of the problems that affected the IOTC RTTP tagging programme, including: i) there is no tag release phase that requires locating and handling live fish, ii) tagging mortality is irrelevant, because only the catch is sampled, iii) tag shedding is irrelevant because the “tag” is the DNA of the fish, and iv) tag recovery reporting rates are irrelevant because you know exactly which fish are “inspected for tags” (and there is effectively zero chance of missing the tag). CKMR also avoids many of the problems of commercial CPUE data, because the data are acquired from a systematic sampling design with the a priori intent of answering specific questions. In contrast, commercial fisheries are motivated to maximize profits and are expected to rapidly change fishing technology, species targeting, time and areas of operation, etc., without regard for the scientific requirements of proper experimental design (consistency, range coverage, orthogonal factor contrast, etc.). CKMR samples must be collected with forethought about spatial issues, but this should not be a problem for yellowfin tuna with IOTC member cooperation in commercial catch sampling.

Based on the population numbers estimated from the 2018 yellowfin assessment (and an alternative sensitivity case with numbers doubled), it appears that CKMR should be a viable assessment tool. A one-time application could provide information about absolute spawner abundance (and other population parameters) with a cost (of DNA extraction and genotyping) of 1-2 million Euro. This is around the cost of the current Indian Ocean stock structure project, or 10-20 % of the (inflation-adjusted) RTTP-IO tagging programme. An ongoing CKMR programme could be used to monitor population trends (for stock assessment and Management Procedures). This paper is only intended to introduce the CKMR concept to the IOTC WPM/WPTT and demonstrate that it is a viable option for raising the scientific rigour of IOTC yellowfin tuna stock assessments – it is not a full design study.

2 Do we need a new stock assessment tool for IOTC yellowfin?

> *There are risks and costs to a program of action. But they are far less than the long-range risks and costs of comfortable inaction.*
>
> *- John F. Kennedy*

As with most fisheries stock assessments, within the IOTC and elsewhere, there are concerns about data quality, and the assumptions that underpin fisheries models. The problems with yellowfin are a high priority now, because the biomass levels appear to be below target levels (e.g. Fu et al. 2018), and measures have been undertaken to reduce catches (IOTC Resolution 18/01 "*On an interim plan for rebuilding the Indian Ocean yellowfin tuna stock in the IOTC area of competence*"). Management Procedure evaluation results (based on Operating Models that resemble the recent stock assessment and the uncertainties recognized by the technical working parties), suggest that rebuilding to target biomass levels within a decade would require very disruptive catch reductions (Kolody and Jumppanen 2019).

There is strong evidence for an internal inconsistency in many recent YFT assessment models, that would not necessarily be evident for other IOTC species. In the stock assessment, and especially the conditioning of Operating Models for MP evaluation, multiple models are fit with different combinations of plausible assumptions. Many of these models have trouble removing the observed catch in recent years, and this may manifest as a numerical problem that justifies excluding an individual model from the ensemble (i.e. if we believe that the reported catch was taken, there must be something wrong somewhere else in the model). Many of the yellowfin models that do not have this obvious problem may be right on the edge of having it. Matsumoto et al. (2018) provide a good illustration of the general issue with their retrospective analysis of a recent stock assessment. If several years of recent data are removed, and the model refit, the model tends to estimate a population that is too small to sustain the catches that are observed in subsequent years. Adding more recent data makes the model progressively more optimistic in the recent past, while the most recent year is always very pessimistic. This dubious pattern has persisted for several years, and it seems reasonable to expect that the pattern will continue into the future. This is not a comprehensive review of data problems, but a reminder of the general issues that are frequently discussed in the IOTC WPTT:

1) **Catch**. It is difficult to quantify the errors in the yellowfin catch time series. Artisanal fisheries make up a large portion of yellowfin catches, and the catch data for many of these fleets are imputed by the Secretariat, with unknown bias and precision. Suggestions for the inclusion of alternative catch scenarios to represent this uncertainty have been put forward in the WPTT for around a decade (at least), but a satisfactory method for doing this has never been established.
2) **Longline CPUE**. Standardized longline CPUE time series provide the critical relative abundance index for the majority of industrial tuna fishery assessments around the world.

The problem is that one can never be sure that the standardization process results in a series that is consistently related to abundance over time. Commercial fisheries operate to maximize profit, frequently adopting new technologies, changing species targeting practices, changing gear configurations, fishing in different seasons and areas, etc. One can never be sure that the relevant operational changes are identified in the fisheries logbooks. However, even if the relevant data are recorded, changes are not implemented in a manner that necessarily allows the effects to be quantifiable (i.e. using experimental design principles of orthogonal contrast and replication). Creating relative abundance indices may also requires inferences about potentially large time/area strata that do not have any observations. Environmental variability is usually implicitly assumed to cause a lot of CPUE variability, but some of these effects could be introduced as long term trends in catchability. A recent problem afflicting Indian Ocean yellowfin is the large and sustained fleet movements associated with Somalian piracy. The usual assumption that abundance is proportional to standardized CPUE is also questionable, in that there is strong evidence for "hyperdepletion" early in the fishery history, with no agreed explanation of the mechanism, or when or why it should have suddenly stopped. Purse Seine (PS) CPUE has been suggested as an alternative to the longline CPUE. These series have similar or worse problems to the longline fisheries because of the rapid rate of technological uptake and are still considered a work in progress.

3) **Tags**. While the RTTP-IO tagging programme, combined with the smaller scale tagging programmes, were successful in releasing and recapturing many thousands of yellowfin in the 2000s, these data have not been as useful as anticipated in quantitative population models, because:

    - The only quantitative tag mortality estimates that are available provide a minimum estimate, but these values were still considered unacceptably high by some WPTT participants. This disagreement of views remains unresolved.
    - The tag release design was unbalanced, with the vast majority of tags released in the western Indian Ocean on very small fish.
    - With the notable exception of the EU and Seychelles PS fisheries (that participated in tag seeding experiments), reporting rates for recovered tags are unknown and probably very low (Maldives seems to represent an exception in that reporting rates may be high, but tag seeding experiments were not feasible).
    - Tag mixing rates (i.e. mixing of tagged and untagged fish) are poorly understood and probably lower than desired. This can introduce substantial biases to parameter estimates.

4) **Assessment model spatial assumptions** (e.g. Figure 1). The optimal model structure usually involves a trade-off between partitioning a population into more homogeneous sub-units (e.g. age, sex, region) without exceeding the number of parameters than can be effectively estimated from the data. Given the tagging problems above, movement parameters are difficult to estimate. Furthermore, given the estimated state of depletion, the numerical catch problems noted above may actually be concentrated in a small number of fishery-region-quarter strata, due to modelling artefacts. In the YFT operating

models, the constant movement assumptions may be flawed if unusual oceanographic events cause a temporary redistribution of the population among regions (in contrast, the assessment links movement to environmental indices, but these are also oversimplified assumptions that may be equally problematic). If there is stock structure (i.e. spawning ground fidelity), either approach will be oversimplified in assuming that all fish in a given strata have equal movement probabilities. However, spatial structure cannot be ignored if the tags are to be used, because the biases due to incomplete tag mixing are expected to increase with increasing region size.

While there is still scope for testing alternative yellowfin model formulations, it seems as though the same issues have been discussed repeatedly for many years. Eventually there will be a limit to what can be learned from the same data.

New paths for improving the yellowfin assessment data have been identified in the IOTC SC research plan for several years, including: i) commercial acoustic FAD-based surveys, and ii) Close-Kin Mark Recapture CKMR). We consider that the large-scale coverage provided by acoustic FADs offer some promise. However, several years will be required to investigate issues of data sharing, acoustic target strength standardization among transducers, species composition estimation, etc. In our view, the most promising technology for the short-term is CKMR, with a proven track record in tuna application.

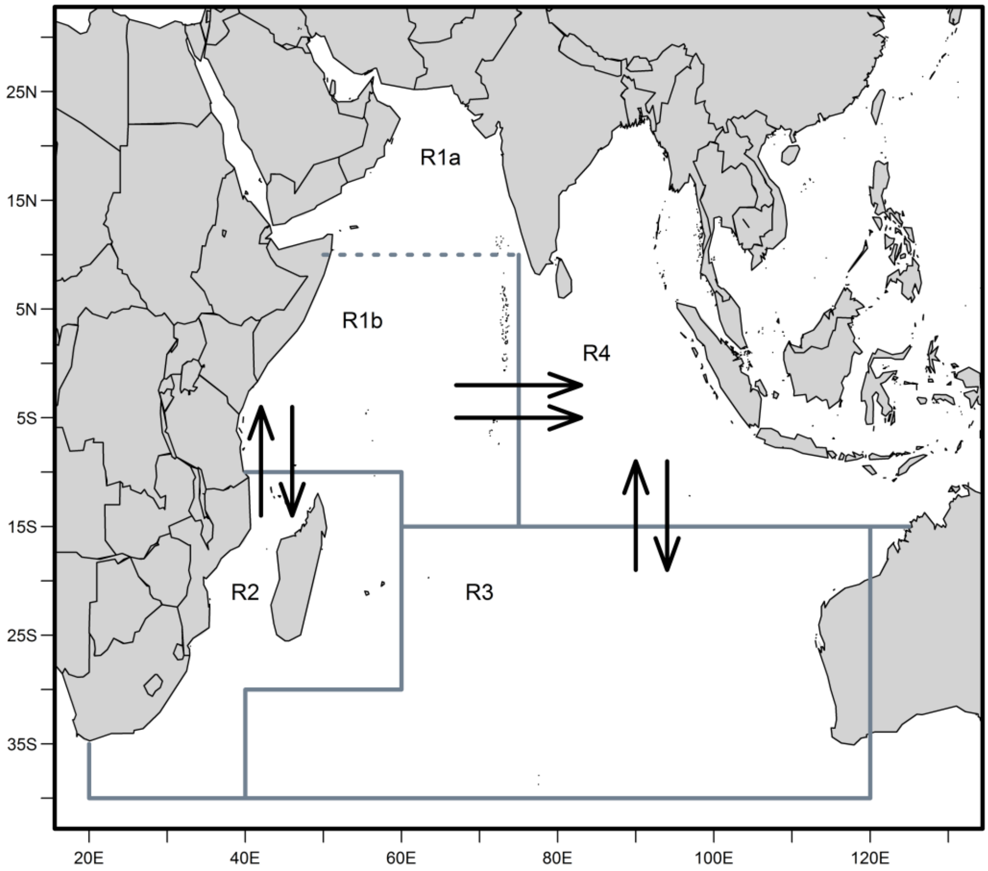


Figure 1. Spatial structure for recent yellowfin tuna assessments and operating models (from Fu et al. 2018).

3 What is Close-Kin Mark-Recapture (CKMR)?

3.1 Qualitative description of CKMR

CKMR is a new form of mark-recapture experiment in which genes serve as the mark. The key innovative feature is that "recapture" does not consist of recapturing any individuals that were previously marked (tagged or otherwise identified). Rather, recaptures are the identification of close relatives. To intuitively conceptualize the idea, there is a simple analogy between a traditional (closed-population Petersen) mark-recapture experiment and CKMR (Figure 2 - Figure 3). If you tag a known number of fish, and subsequently take a random sample of the population, it is easy to appreciate that you would expect to recover a larger number of tagged fish from a smaller population. The CKMR experiment allows an analogous inference using only a single sample from the catch. For a given sample, you would expect more closely-related individuals to be observed from a smaller population (e.g. in a lot of small rural communities everybody seems to be related to everybody else, to the general amusement of visitors from the big city).

A simple population estimator can be applied to the cartoon in Figure 3, that is analogous to a closed population Petersen mark-recapture estimator (i.e. assuming that all adults are equally fecund, samples are truly random from the population, there is no mortality between spawning and capture, etc):

$$N_{adults} \approx \frac{2(m_{juveniles} m_{adults})}{k}$$

Where:

N_{Adults} is the total number of adults in the population,

m_{adults} is the number of adults sampled from the catch

$m_{juveniles}$ is the number of juveniles sampled from the catch, and

k is the number of observed parent-offspring pairs

This estimator is simply derived from the probability that any random adult-juvenile comparison is a parent-offspring pair:

$$Pr(\text{Parent-Offspring Pair}) = \frac{2}{N_{adults}}$$

The "2" above relates to the fact that there are 2 parents for every offspring. Thus the expected number of observed parent-offspring pairs, k, results from summing up the probability over all possible adult-juvenile comparisons (m_{adults} X $m_{juveniles}$) from the sample, i.e. $k = 2(m_{adults} \text{X } m_{juveniles}) / N_{Adults}$.

In the same way that a closed-population Petersen estimator is an oversimplification of how the conventional tagging data are used in the current yellowfin assessment, the CKMR cartoon application is also over-simplified. In a real application, one needs to consider additional complications, including the probability of surviving between spawning and capture, the proportion of fish of a particular age that spawn in a particular spawning event, the relative fecundity of fish of different ages/sizes, etc. One can also extract additional information on the basis of other types of kin relationships.

A CKMR application consists of several elements (the feasibility of which are discussed in section 4):

1) Tissue collection from an appropriately-stratified sample of the commercial catch (a design study should be undertaken to determine the size/age/sex structure and spatial locations that will yield the desired precision).
2) Genotyping of the samples, using a sufficient number of markers to identify closely-related pairs. Parent-offspring, and half-siblings have proved feasible and sufficient in applications to date (Bravington et al 2017; Hillary et al 2017). A parent-offspring pair is any combination of father or mother with daughter or son. A half-sibling pair refers to any two individuals that share either the same mother or the same father (full-siblings share a mother and father and are not useful for teleost CKMR applications).
3) CKMR requires some demographic co-variates from the population that are usually available for most data rich stock assessments (age of samples is preferable to length, but not essential, maturity schedule is useful for distinguishing half-sibling pairs from grandparent-grandchild pairs, etc.).
4) A population model is required that can calculate the expected number of closely-related pairs given the sampling design, to compare with the actual number of observed pairs (i.e. analogous to how the current yellowfin assessment model seeks to find the parameters that achieve the best fit between predicted and observed tag recoveries). Most of the demographic book-keeping is consistent with a standard age-structured population model. It is helpful to work with a sex-specific model, in recognition of sex-specific biology (e.g. fecundity-at-size) and to take advantage of additional genetic information (e.g. mitochondrial DNA provides information about whether the shared parent of a half-sibling pair was male or female).

Parent-offspring pairs and half-sibling pairs provide somewhat different information in CKMR population models, and the appropriate case-specific balance should be considered as part of a design study. Spawner abundance estimates are primarily informed by parent-offspring pairs, while total mortality is estimable from half-sibling pairs. Total mortality (Z) estimates can be further partitioned into natural mortality (M) and fishing mortality (F), when coupled with catch-at-age/size.

Depending on how CKMR is applied, and what auxiliary data are available, it can provide information about not only spawning population size, but also mortality and relative reproductive output by size/age. Major advantages of CKMR over a conventional tagging programme include:

- Live fish do not need to be located or handled in any way, which minimizes a major logistical problem and expense (and removes the problem of tag-induced mortality)
- DNA is a permanent marker, sampled as part of a scientific programme, thus avoiding the problems of tag shedding and unknown tag reporting rates
- The cost is potentially much lower as discussed in the next section.

Additionally, the mixing of tagged and untagged fish (which is required for traditional tag-based population estimators) is not relevant for CKMR. However, spatial processes cannot be ignored as discussed in the feasibility section.

In principle, a single synoptic CKMR sample can provide some information about recent spawning population trends (particularly for long-lived species), because a single sample provides information about a time series of spawning populations that produced multiple cohorts. However, information about spawning population trends can be substantially improved with repeated sampling over time.

Finally, we note that some people have proposed using CKMR spawning abundance estimates in generic stock assessment models as an independent abundance index series. This is possible in principle, but it would not be the most effective way to use all of the CKMR information.

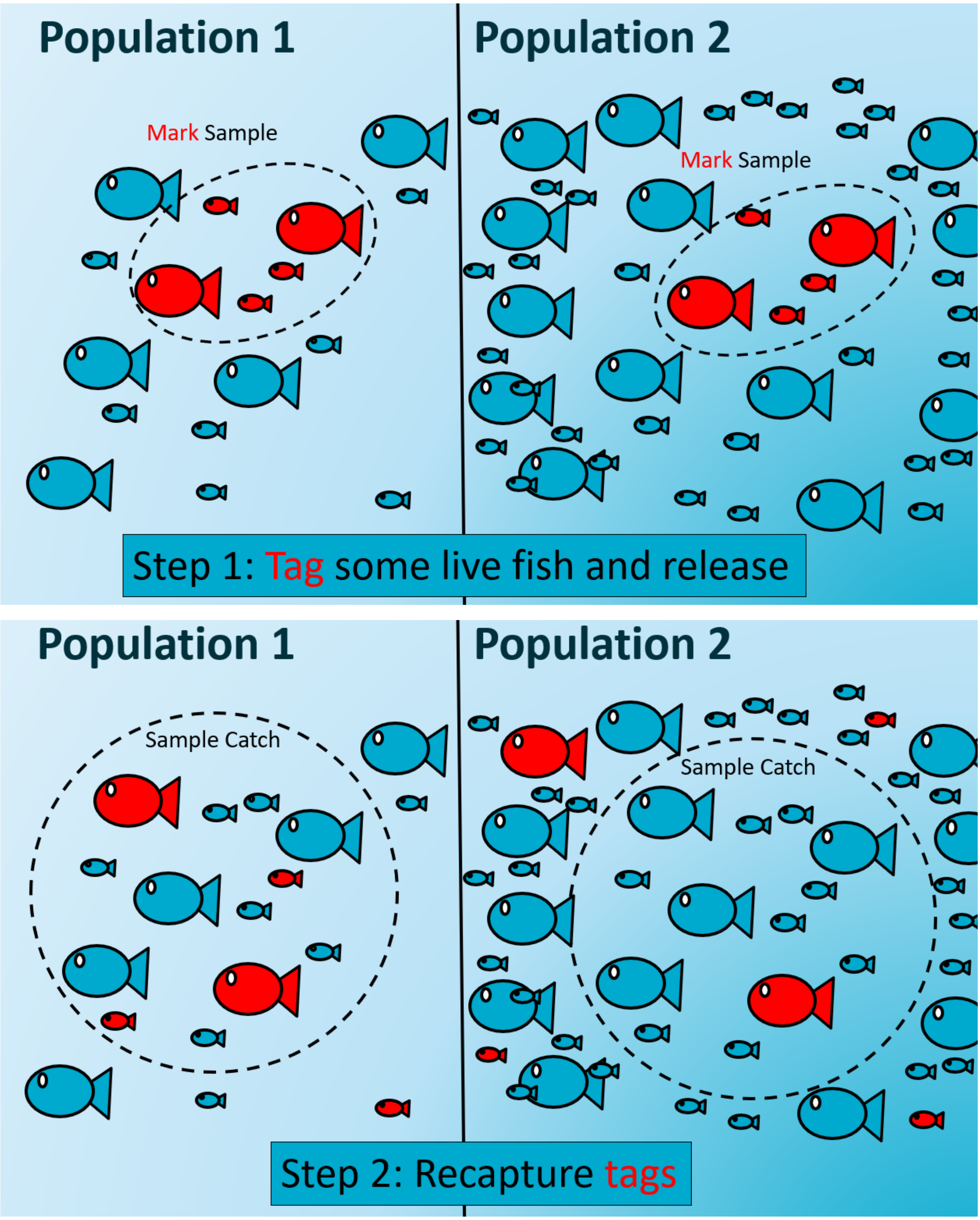


Figure 2. Cartoon of closed population Petersen tagging experiment. Red fish are captured, tagged and released in phase 1 (top), then randomly recaptured with untagged fish in the catch (bottom). Given the same number of tag releases and the same sample size from the catch, more recaptures are expected from the smaller population (left).

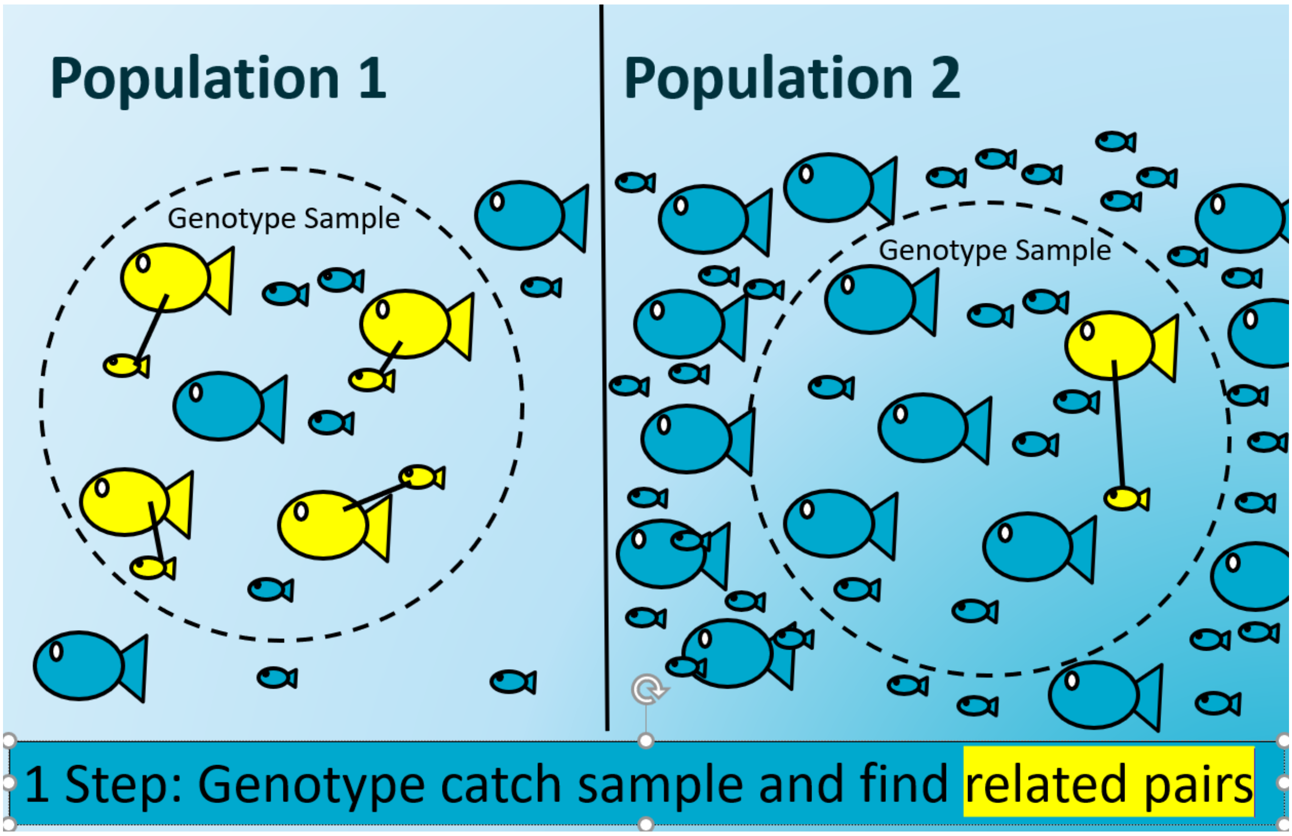


Figure 3. Cartoon of a simple closed population Close-Kin Mark-Recapture experiment. A sample of the catch is genotyped, and closely-related pairs (yellow, connected by lines) are identified. Given the same sample design, more closely-related pairs are expected from the smaller population (left).

3.1 Other CKMR case studies

Since the CKMR concept was first suggested (Skaug 2001), there have only been a handful of published applications. The number of case studies is now increasing rapidly, due to increased awareness and decreasing genotyping costs, but most are still in progress or in grey literature reports. We only cite a couple examples here.

The southern bluefin tuna CKMR project was the first commercial fishery example, and is most relevant to IOTC yellowfin. The technical CKMR situation is similar for both species, but there are also insightful historical fisheries management parallels. Since the 1980s, the southern bluefin tuna population has been recognized as being highly depleted (with an associated decline in recruitment). There was long-running uncertainty about how to interpret commercial longline CPUE as a relative abundance index, in part because the reduction in the time-area strata fished raised concern about a range contraction away from the strata that had been fished historically. The situation was further complicated when two decades of large, unreported, catches were revealed in 2006. It remains unknown whether these unreported catches affect the longline CPUE reported in logbooks. To reduce these uncertainties, CKMR was recognized as a potential method for providing fisheries-independent spawning biomass estimates. The initial application was based on the identification of Parent-Offspring Pairs (Bravington et al 2016a). The original analysis estimated that absolute spawning biomass was probably near the upper end of the uncertainty range calculated by the assessment before CKMR. CKMR is currently integrated into the stock assessment with all of the other data, and has been extended to include half-sibling pairs (Bravington et al 2017; Hillary et al 2017). Sampling is ongoing to provide a routine monitoring time series, and is under consideration for inclusion in the CCSBT Management Procedure (Hillary et al 2018, Anon 2018).

A number of other applications involve species of conservation interest, where CKMR has appeared to offer the only viable method of producing population estimates, e.g. Hillary et al. (2016) describe an example with white sharks. Jasper et al (2019) use CKMR to quantify dispersal rates of mosquito larvae. The latter is a fundamentally different sort of application from fisheries stock assessment, but of potential interest due to the spatial processes that might have some parallels with yellowfin tuna.

CKMR is not appropriate for all fisheries cases (e.g. long-lived, late-maturing species like orange roughy, that cannot be sampled as juveniles). But the problem cases should be recognizable in advance, and yellowfin is not one of those cases.

3.2 What CKMR is not

We briefly note the following genetics-based tools for studying populations, which are sometimes confused with CKMR in the IOTC scientific community. These are all fundamentally different from CKMR.

Stock structure studies look at the variability in gene frequencies among samples, and attempt to quantify the degree of population mixing among spawning regions and potentially the degree of population overlap in mixed-stock fisheries (e.g. ongoing IOTC project discussed in Davies et al 2018). These studies can be useful for identifying reproductively-isolated populations which might need to be managed independently (e.g. western and eastern Atlantic bluefin tuna). A potential shortcoming of these studies arises if the mixing rate among populations is large enough to create a genetically homogeneous population, but small enough that multiple populations might be effectively isolated at the relatively short time scales that are important for management. These studies do not provide information about population size (or mortality, fecundity etc.).

Effective Population Size ($N_{effective}$)

CKMR uses genetics for estimating actual numbers of living animals (e.g. a census-based population size - N_{census}), and is useful for evaluating sustainable catches, even for large populations. In contrast the purely genetic concept of $N_{effective}$ (e.g. Waples et al 2014) relates to the genetic diversity of a population, and is most useful in the conservation of rare species. While there are deep connections between N_{census} and $N_{effective}$, there are also fundamental differences, notably:

- The equations of CKMR are explicitly linked to time (year-of-birth etc), and there is no requirement to assume steady-state population dynamics (which are rarely appropriate for fisheries). In contrast, $N_{effective}$ is almost invariably built around steady-state assumptions and the role of time is obscured, even if $N_{effective}$ is calculated repeatedly in a time-series.

- For $N_{effective}$, one very important parameter is the "lucky litter effect"- i.e. extent of within-year random-reproductive-variability – the majority of progeny may result from relatively few spawning events. For CKMR, the lucky litter effect is just an annoyance which is dealt with, either by introducing extra parameters into the model, or by restricting the analysis to exclude within-cohort half-sibling comparisons.

The lucky-litter issue means that N_{census} and $N_{effective}$ can sometimes differ by several orders of magnitude, especially for species like teleost fish that have large litters. Thus, $N_{effective}$ is not useful as a measure of absolute abundance. Also, the lack of a clear time-dependence in $N_{effective}$ makes it difficult to interpret trends, even in a relative sense.

In fact, many of the demographic parameters required to calculate $N_{effective}$ can be obtained as a by-product of CKMR analysis (including the magnitude of lucky-litter effects). Further, although it is sometimes suggested that estimates of $N_{effective}$ can be made "cheaply" (i.e. from many fewer samples than CKMR), that claim does not bear close scrutiny: forming a reliable estimate of recent-historical $N_{effective}$ actually requires comparable sample sizes to CKMR-based census N_{census}.

Gene-tagging is analogous to conventional tagging, with the main difference that “tagging” consists of a biopsy that is genotyped. Preece et al (2013) describe the southern bluefin context. Recapture consists of genotyping a sample of the catch to identify the previously biopsied fish. Gene tagging avoids the critical problems of tag shedding and unknown tag recovery reporting rates. However, live fish must still be handled and released (with associated mortality), unlike CKMR. Gene-tagging (and conventional tagging) can be used in the context of recuitment monitoring, while CKMR is most useful for spawning population size and cannot be used to monitor recruitment. The CCSBT uses both gene-tagging and CKMR for southern bluefin as complementary approaches, (e.g. Hillary et al 2018, Anon 2018, Preece et al 2018).

4 Is CKMR a viable tool for IOTC yellowfin?

4.1 Logistical feasibility

In this section, we consider possible technical impediments to the success of a yellowfin CKMR project, while costs are considered in the following section.

It is necessary to obtain appropriately-stratified catch samples from across the Indian Ocean, in terms of spatial locations (see below) and age/size. Fisheries with diverse gear types operate in many parts of the Indian Ocean. Assuming that IOTC members recognize the value of a CKMR programme and actively contribute to catch sampling, we do not expect that obtaining samples would be a problem. Genetic sampling should not affect the marketability of the product, and the sampling gear is easy to use and very portable. The CKMR sampling does not need to be proportional to the catch distribution, but does need to ensure that key locations and age classes are adequately sampled.

The genetic analysis methods for identifying closely-related pairs are now well-established for tunas, at least to the level of parent-offspring and half-sibling pairs (e.g. Bravington et al 2017, Davies et al 2018a). Cost is the main limiting factor, as discussed in the next section. But costs are continuously dropping, and methods are continuously evolving such that more distant relations (i.e. cousins) might be included in the future.

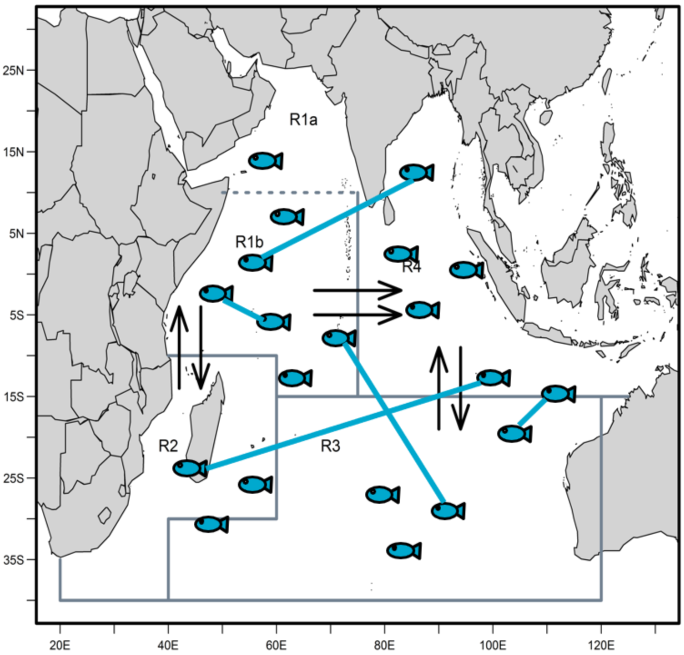
The population dynamics modelling techniques for CKMR are also well-established, at least in the spatially-aggregated context (e.g. Bravington et al. 2016b). We would anticipate that spatial considerations are important for yellowfin as discussed in the next section.

The shortage of global CKMR expertise, and growing demand for applications, means that it may be difficult to secure the required personnel to conduct the analyses (both in terms of the statistical expertise to identify the degree of relatedness among individuals, and the population modelling skills). The large volume of genetic samples and data might require specialized facilities, and such a project might best be managed through an international collaboration.

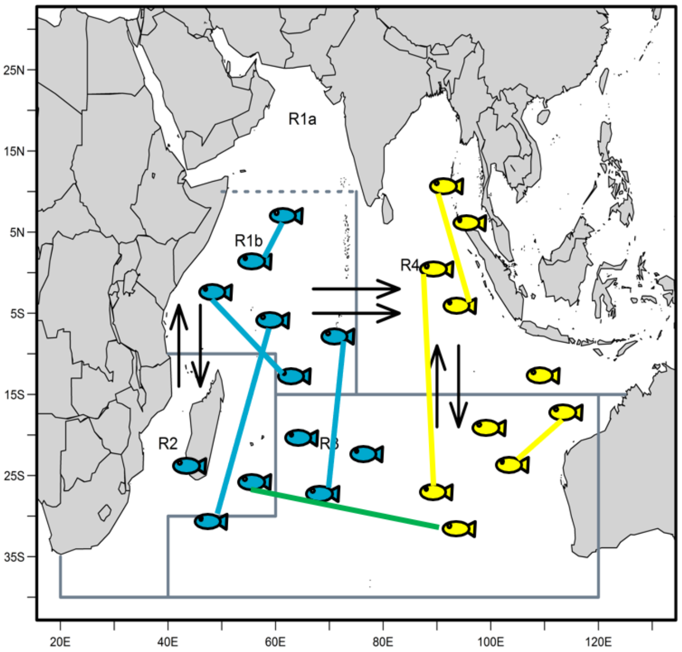
Spatial Complications

Stock structure and low mixing rates could be problematic if the sampling is not appropriately-stratified spatially, but we note that CKMR can actually provide considerable useful information about population structure. For example, Figure 4 illustrates two possible stock structure scenarios. If there is a single, well-mixed population, the sample locations do not matter. If there are western and eastern sub-populations, then CKMR sampling in only the west would estimate a population that is smaller than the total. If catch sampling covers the whole ocean, the locations of the related pairs are identified and provide useful information about how to appropriately structure the population models. This can potentially be used to quantify the degree of movement in a manner that is more informative than stock structure studies. CKMR observations of closely-related pairs provide a direct measure of population connectivity (e.g. like fragments of human genealogical records). As noted previously, stock structure studies might not be able to recognize two populations that are effectively isolated for management purposes, if there is low level gene-flow below the populations.

Davies et al. (2017) provide some considerations of population structure in the context of an Atlantic bluefin scoping study, and Jasper et al (2019) demonstrate how the degree of relatedness within mosquito populations decreases with distance, in a manner analogous to what we might expect in analysing the populations from Figure 4. We are not aware of anyone publishing a CKMR estimator that includes movement among regions, but this represents a natural extension of CKMR theory. The extension requires additional calculations (life history integration) related to the probability that individuals would be in the particular times and locations caught, conditional on the times and locations of the spawning event(s) that established their relatedness.



A) One well-mixed population



B) Two weakly-mixed sub-populations

Figure 4. Cartoons contrasting possible CKMR outcomes, A) single well-mixed population, and B) two weakly-mixed sub-populations. Closely-related pairs are connected by lines. Spatial sampling biases would not be a problem in case A, but could be a problem in case B. Representative spatial sampling would provide direct information to distinguish between situations A and B (or other possibilities), even if the alternatives were not recognized in advance.

4.2 Economic feasibility

It is only within the past decade or so that genotyping technologies have become inexpensive enough to allow large-scale applications. The proven southern bluefin tuna application has two apparent advantages over yellowfin: 1) the population is much smaller (e.g. recent annual catches of IOTC yellowfin are around 25X larger than southern bluefin) and 2) southern bluefin is much more valuable per individual caught. Thus it seems intuitively reasonable to expect that a smaller, more profitable fishery would be more amenable to a relatively expensive research programme. However, this is not strictly true because of some economies of scale discussed below.

We conducted a quick feasibility study which suggests that the cost for a yellowfin CKMR project is favourably in line with other recent IOTC research programmes. This study involved calculating the number of closely-related pairs (parent-offspring and half-siblings) that would be expected from a population, assuming that:

- The current yellowfin population numbers and other biological characteristics, are identical to the 2017 population numbers from the (Fu et al 2018) reference case yellowfin assessment.
- Age estimation from length is “sufficiently” accurate (for younger fish)
- The population is currently in equilibrium
- Male and female numbers and reproductive characteristics are identical
- Fecundity and selectivity are purely age-based
- It is possible to appropriately sample the catch from across the Indian Ocean, with a total of 64 – 128K fish, equally distributed from quarterly age-classes (4-8 and 13-17), over a 12 month period.
- Results exclude potential grandparent-grandchild pairs, and same-cohort half-sibling pairs

We refer to this feasibility test as case A, and contrast it with a small number of alternative sampling designs and population assumptions in Table 1. Note that doubling the sample size quadruples the number of pairwise comparisons and the number of expected close-kin pairs identified. This leads to a quadratic increase in estimator efficiency as population size increases. E.g. If the IO YFT population was exactly 25 X larger than southern bluefin (but otherwise biologically identical and subject to the same general sampling design), we would expect the same level of precision in the population estimates for a yellowfin sample of $\sqrt{25} = 5$ X larger than southern bluefin. Bravington et al. (2016b) noted that, under simplified (ideal) conditions, a CV on a population estimate should approach 15% with ~50 parent-offspring pairs identified (CV($\widehat{N}$) ~ 1/√(expected number of parent-offspring pairs in sample)). They suggested that a target of 50-100 matches should be achievable for a particular application to be considered feasible (and worthy of a follow-up design study). The designs tested in Table 1 predict 27-219 parent-offspring pairs, most of which are comfortably in line with this rule of thumb. Considering the difference in perceived population sizes, this compares favourably with the initial southern bluefin application, which identified 45 parent-offspring pairs from a sample size of 14 000 (roughly half adults and half juveniles).

A proper design study (e.g. next section) should be undertaken to refine the sample requirements. The base case is probably near the lower end of what one would want (particularly if the true population is considerably larger than the recent assessment), while doubling the samples (cases B and F) would appear to provide an adequate number of close kin matches in either case (with a modest buffer). If the spawning population turns out to be substantially larger than assumed in the design study, this will inflate the CV, but the confidence intervals would be valid and would provide strong evidence that the population is larger than originally assumed. Conversely, it the population is smaller than assumed in the design study, the precision should be higher than the original target.

Based on other recent CSIRO projects, we would expect DNA extraction and genotyping costs of around USD 17.5 per individual sample for a total cost of approximately USD 1-2 million. Economies of scale and continuously improving technology could result in lower costs per sample. Sample processing is the largest expense, but there would be additional analytical costs for conducting the CKMR analysis, and potentially in-country tissue sampling.

This would not be a small research project. But it would be expected to deliver key information to greatly improve IOTC yellowfin stock assessments, for a price that compares favourably to other recent IOTC initiatives. For comparison, the IOTC stock structure project (e.g. Davies et al. 2018b) cost USD 1.7 million (assuming current exchange rates), while the RTTP-IO programme (Murua et al 2015) cost 14M euros, or about USD 23 million in 2019 currency (assuming 2006 exchange rates and 2% annual inflation from 2006).

Table 1. Preliminary feasibility study for 5 possible yellowfin CKMR situations. As a simple rule of thumb, a minimum target of 50 close-kin pairs should be attainable for the approach to be considered worth further investment to a proper design study.

Case	*Assumed N	Sample period (months)	Adult samples (1000s)	Juvenile samples (1000s)	Expected Parent-Offspring Pairs	Expected Half-Sibling Pairs	Genetics Cost (thousands) USD	
A	SA	12	32	32	55	96	970	1070
B	SA	12	64	64	219	382	1940	2140
C	SA	24	32	32	52	87	970	1070
D	SA	12	16	48	50	161	970	1070
E	2 X SA	12	32	32	27	47	970	1070
F	2 X SA	12	64	64	109	191	1940	2140

*Assumed population size for the analysis: SA = the terminal numbers-at-age from the (Fu et al. 2018) reference case stock assessment (2 X SA is twice as big).

5 Design study

The economic feasibility study above is not a substitute for a proper design study. Such a study should be undertaken before sampling collection begins and include elements of:

- Attempt to represent the biology more accurately with respect to:
    - Non-equilibrium population dynamics
    - Male/female differences
    - Age estimation error
    - Sampling options relative to fishery selectivity and likely CPC cooperation
- Quantify expected precision of different population parameter estimates (e.g. recent spawning population, spawning population trends, reproductive output at age, total mortality by time and age) with respect to sampling design:
    - Ages/sizes sampled (gear type)
    - Sampling duration (how many years)
    - Spatial sampling (fishery locations)
- Combined costs of catch sampling, DNA extraction, genotyping, close-kin analysis, and population modelling.

These elements should be summarized in a table of options with costs and benefits for the broader IOTC community to consider before proceeding. We would expect such a design study to cost around USD 100K.

6 Conclusions

1) CKMR is a reasonably new fisheries assessment tool, which has been successfully applied to another tuna species (as well as several non-teleost species). The method is independent of the data quality problems and systematic biases of commercial fisheries operations (that are motivated by economic returns rather than scientific design principles). However, CKMR does take advantage of commercial catch to inexpensively obtain samples. CKMR also avoids several problems of conventional tagging, including: the need to handle large numbers of live fish, tag shedding, tag-induced mortality and unknown tag return rates from most fleets.

2) Close-Kin Mark Recapture appears to be logistically-feasible for Indian Ocean yellowfin, provided that catch samples can be obtained from appropriate locations and fisheries across the Indian Ocean through the cooperation of the IOTC members. Given that this is a new technique, there could be difficulties assembling a team with the appropriate

expertise to handle the statistical modelling and the large volume of genetic samples. This might be best handled through an international collaboration.

3) CKMR appears to be economically feasible for reducing yellowfin stock assessment uncertainty. Sample processing and genotyping is predicted to have a cost similar to the recent IOTC international stock structure project, or around 10-20% of the mid-2000s RTTP-IO tagging programme. If the spawning population turns out to be substantially smaller than the design study assumptions, this should result in greater precision of population estimates than targeted. In contrast, if the spawning population turns out to be much larger than assumed, the estimator precision will be lower than targeted. However, the latter case would presumably also reveal that the stock status represents much less of a management risk than currently assumed.

4) We are not aware of any other methods that have the capacity to reduce the stock assessment uncertainty by a similar degree in the near future, for a competitive cost. If the IOTC recognizes that yellowfin CKMR is worth pursuing, the first priority would be to commission a proper design study to identify i) the specific assessment questions to be addressed, and ii) the best sampling programme(s) to achieve these outcomes (i.e. in terms of age composition and spatial distribution). We would expect such a design study to cost around USD 100K.

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