

Close-kin mark-recapture (CKMR) design studies for Australian Spanish mackerel populations

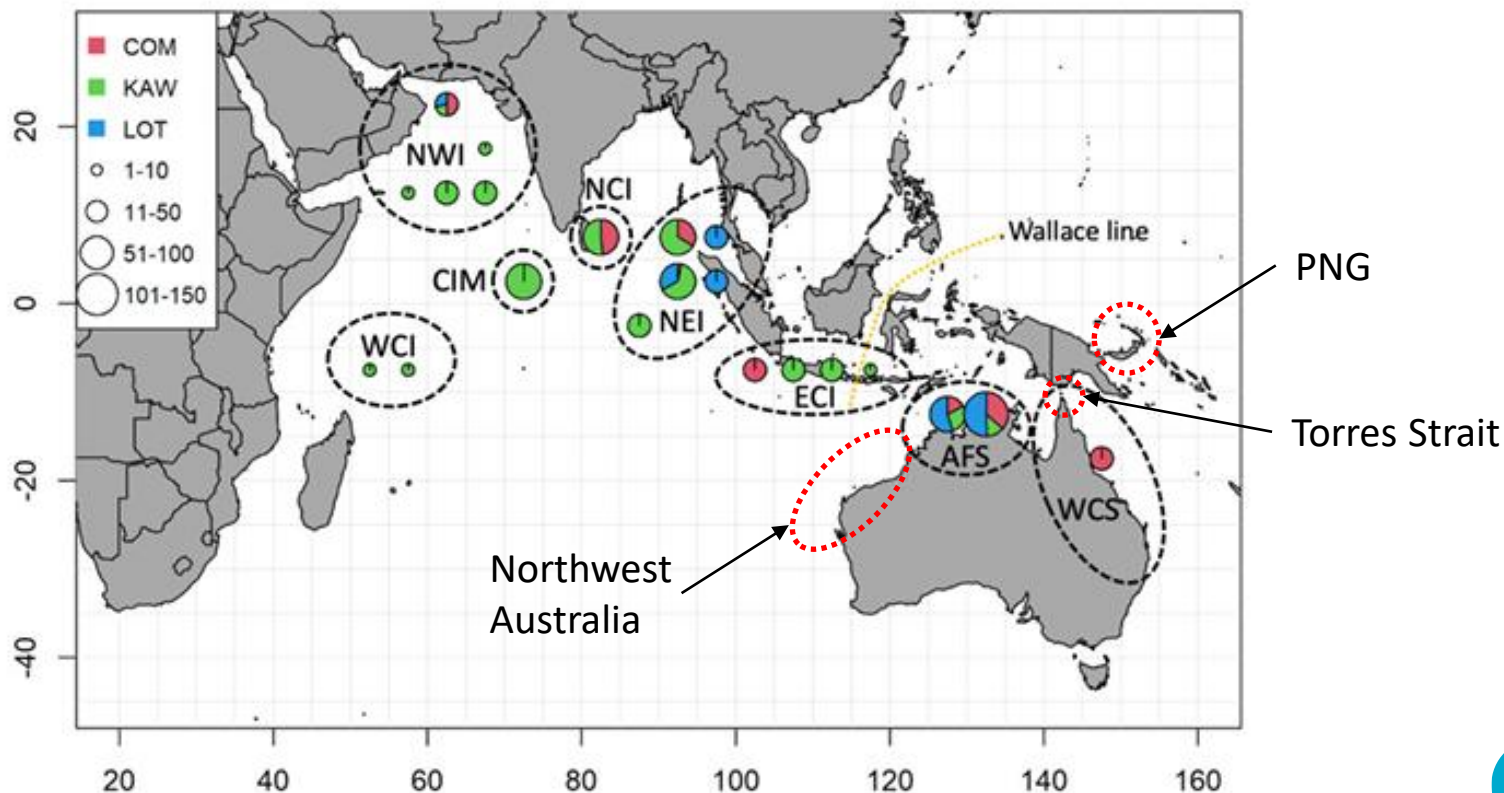
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Ashley Williams, Pierre Feutry, Laura Tremblay-Boyer, Rasanthi Gunasekera

CSIRO Oceans and Atmosphere



Population Structure



Spanish mackerel fisheries - Australia

Total annual catch ~1100 t

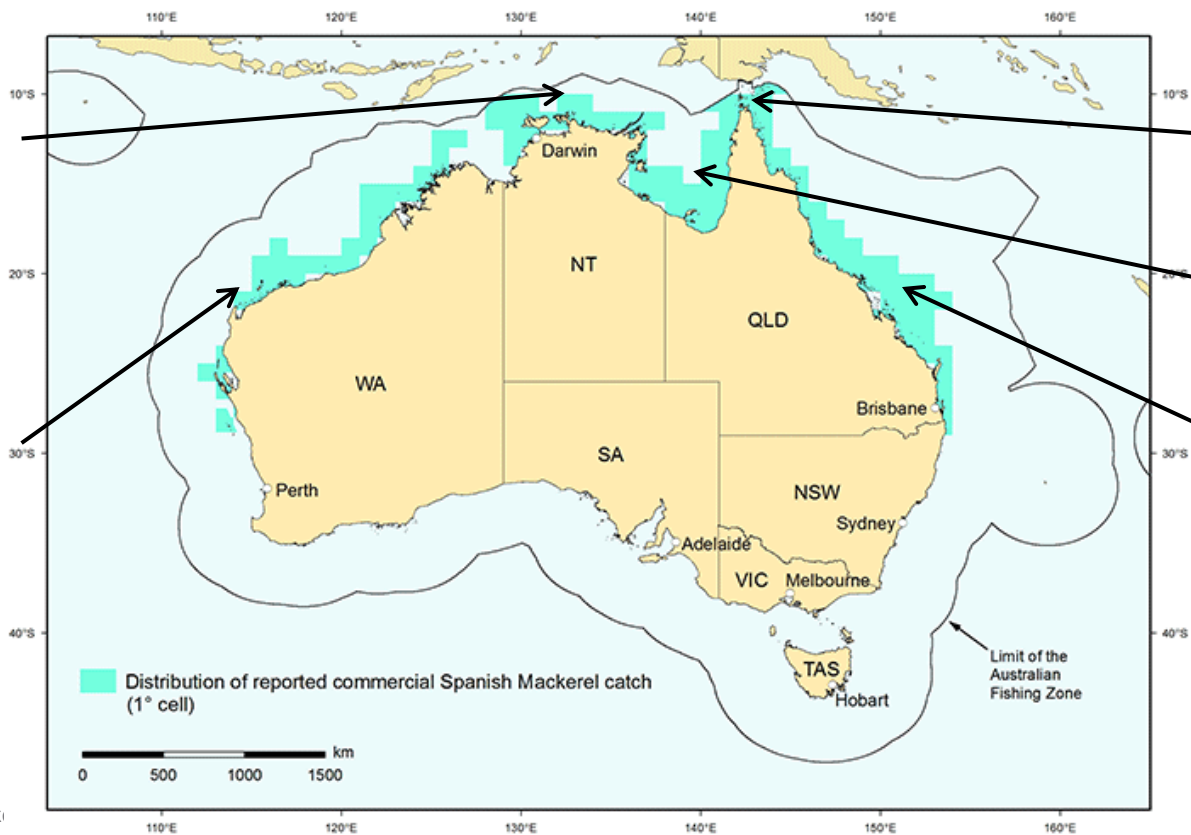
Northern Territory
~350 t

Western Australia
~250 t

Torres Strait
~50 t

Gulf of Carpentaria
~250 t

East coast
~250 t



Stock status

- Stock assessments indicate declining trend in abundance and some stocks close to overfished
- CPUE data provide index of abundance, but is a key uncertainty
- Close-Kin Mark-Recapture (CKMR) is an alternative approach to estimate abundance – *fishery independent, so no need for any fisheries data!*
- Applied successfully to southern bluefin tuna and other species

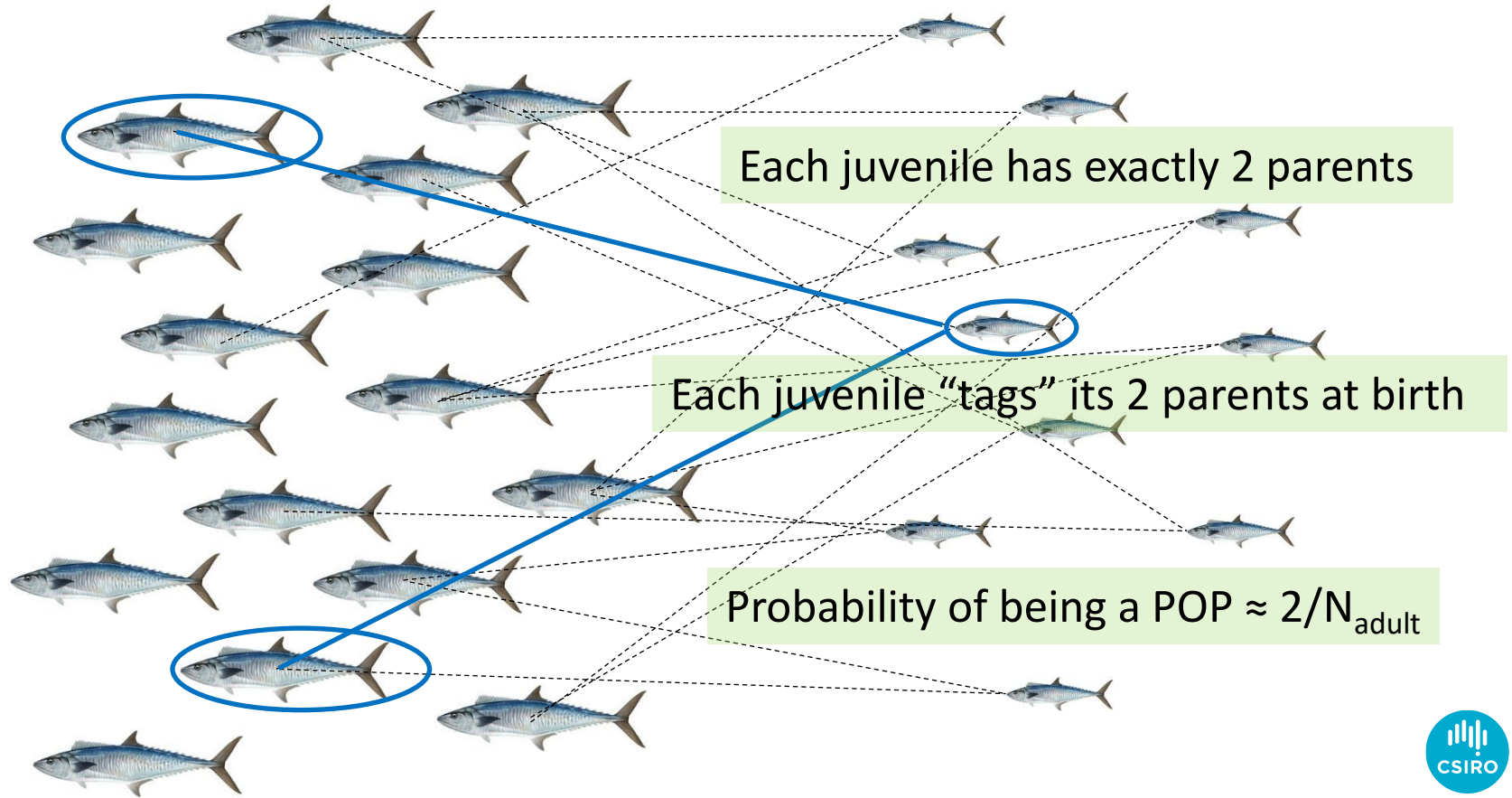
What is CKMR?

- Uses modern genetic techniques to identify closely related pairs
 - Parent-Offspring-Pairs (POPs) or Half-Sibling-Pairs (HSPs)
- Number of POPs and HSPs used to estimate absolute spawning biomass, mortality, connectivity

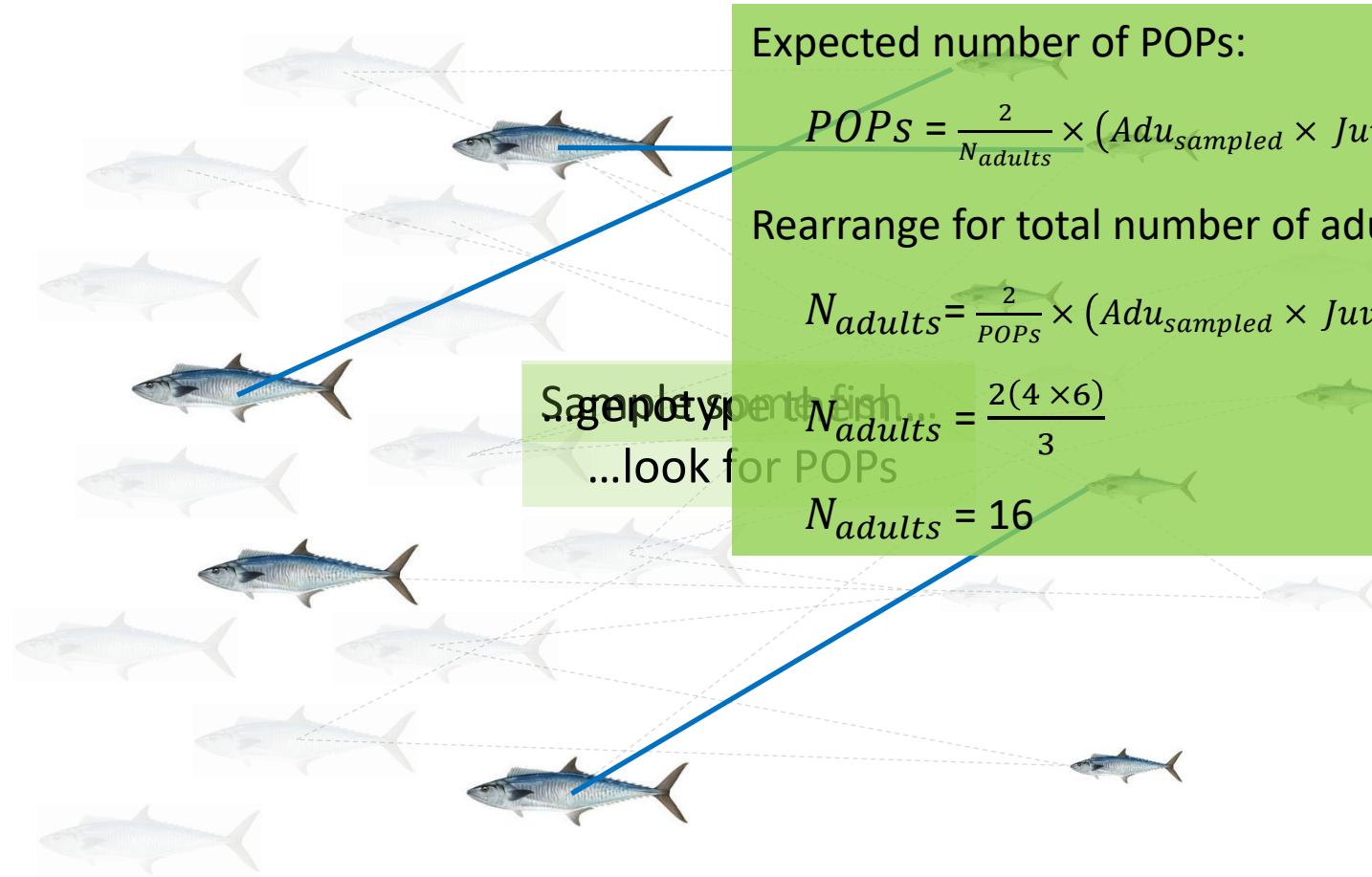
What do we need for CKMR?

- Small tissue sample from juveniles & adults – for genotyping
- Information on the age and/or size (plus other biology)

Parent-offspring pair (POP) cartoon

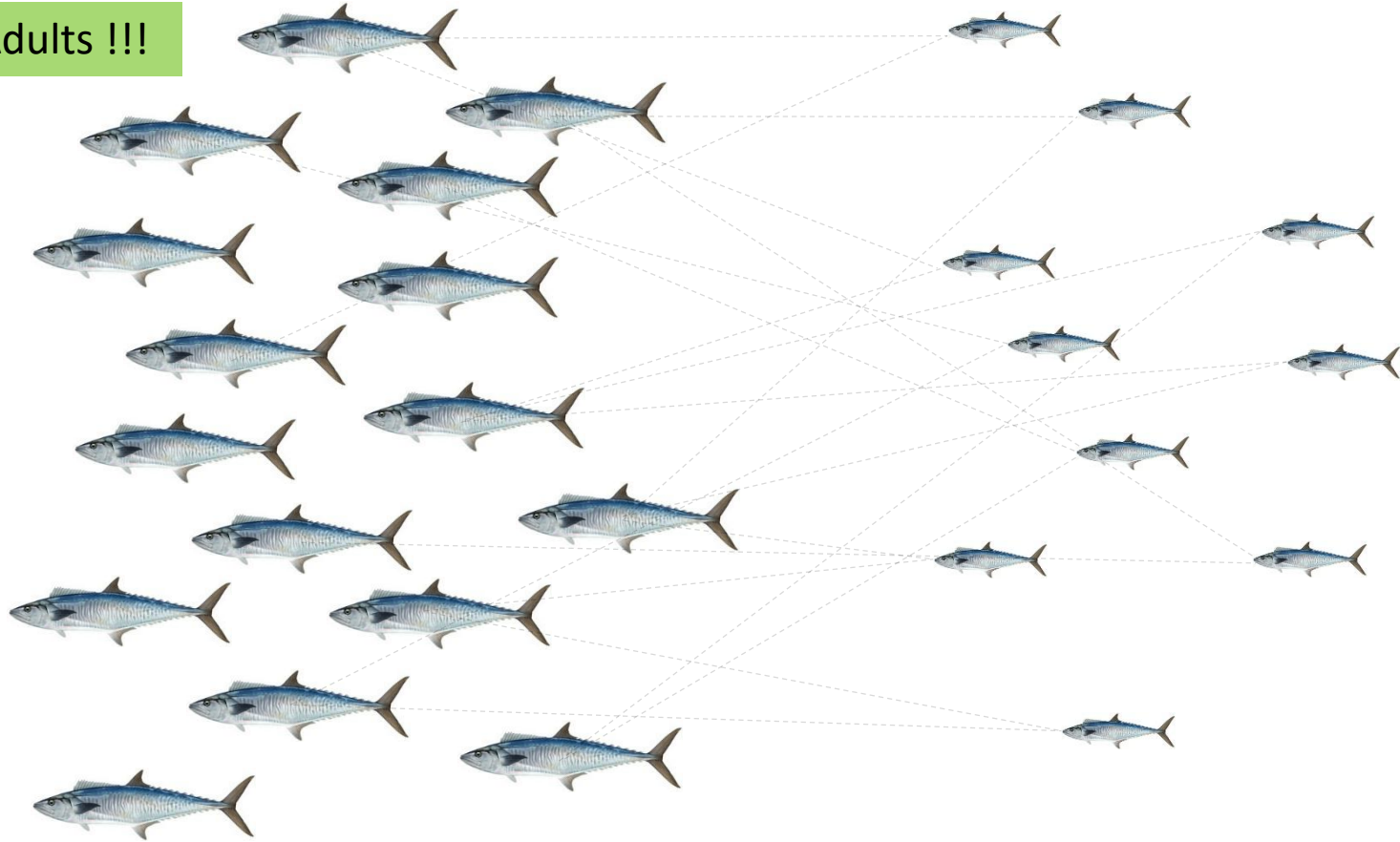


Parent-offspring pair (POP) cartoon

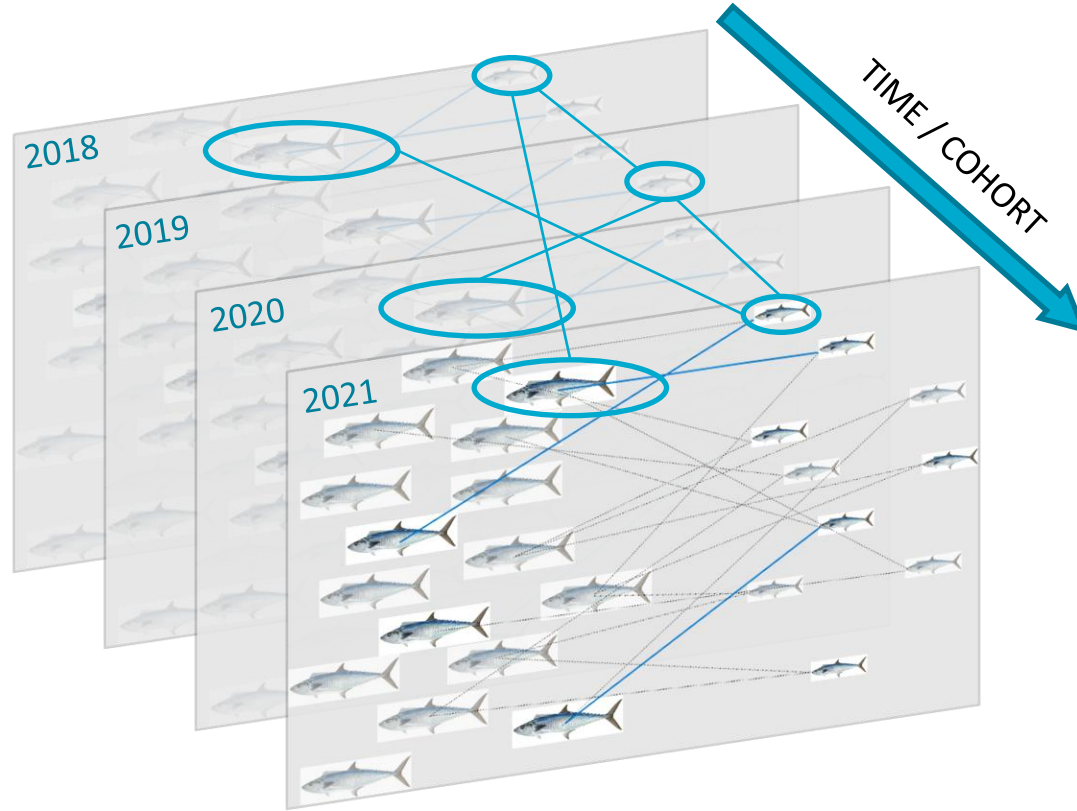


Parent-offspring pair (POP) cartoon

16 Adults !!!



CKMR in practice



- Sample many different cohorts, years, ages
- Compare each sample to every other sample -> many comparisons
- Fit population dynamics model (similar to stock assessment)
- POPs -> estimate of adult abundance
- HSPs -> estimate of mortality
- Distribution of POPs & HSPs -> connectivity

What do we want from CKMR?

- CKMR can provide absolute abundance, mortality, connectivity
- Best sampling program differs depending on what questions are most important e.g.
 - One-off estimate of abundance to “ground-truth” assessment – short period intensive sampling
 - Trend in abundance for ongoing assessment – ongoing but less-intensive sampling
 - Estimate of mortality – More half-sibling pairs
 - Connectivity – spatially structured sampling

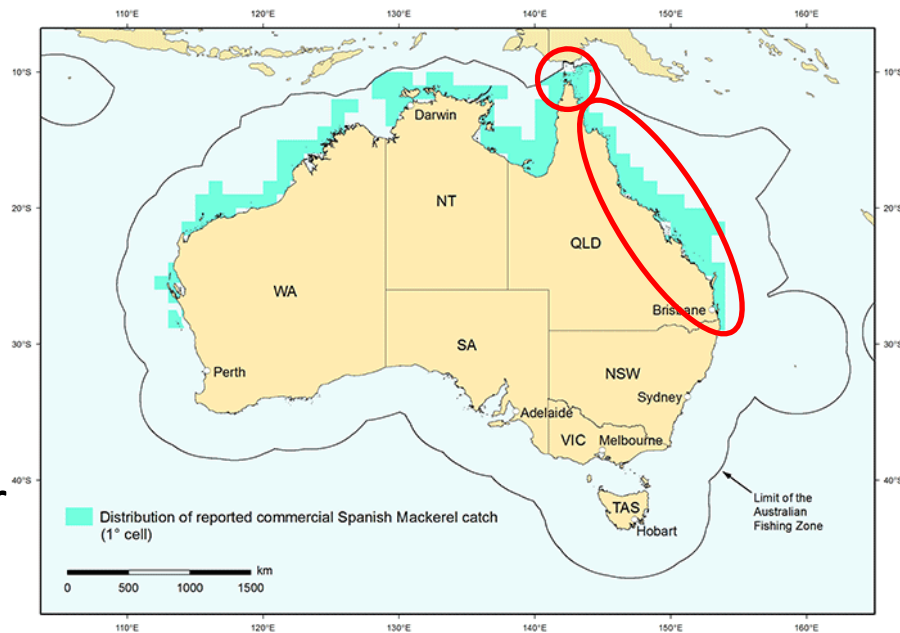
Need for a design study

- Imprecise population estimates are not very useful
 - Estimate of 90,000-110,000 fish more useful than 50,000-150,000 fish, even if midpoint the same
- More kin pairs detected = higher precision in estimates from CKMR
 - (rule of thumb: 100 kin pairs gives ok precision)
- Need more samples to detect same number of kin pairs in large vs. small populations
- Design study (simulation) can tell us how many samples are needed, over how many years, to achieve objective with target precision

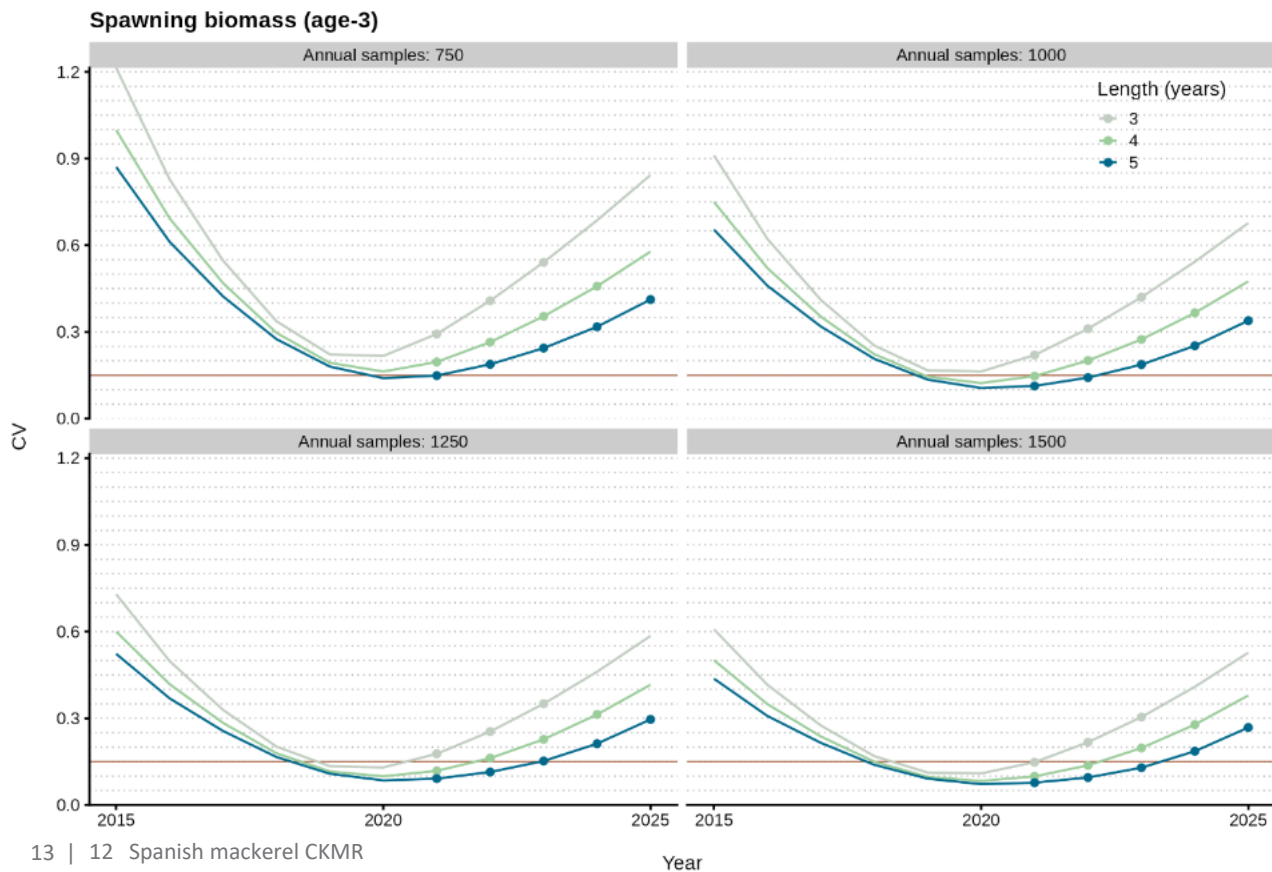
CKMR designs for Torres Strait & East Coast

Estimate precision in biomass that could be achieved from alternative sampling designs considering:

- Stock assessment biomass estimates
- Age structure of sampled population
- Ageing error
- Length of sampling program
- Number of samples collected per year

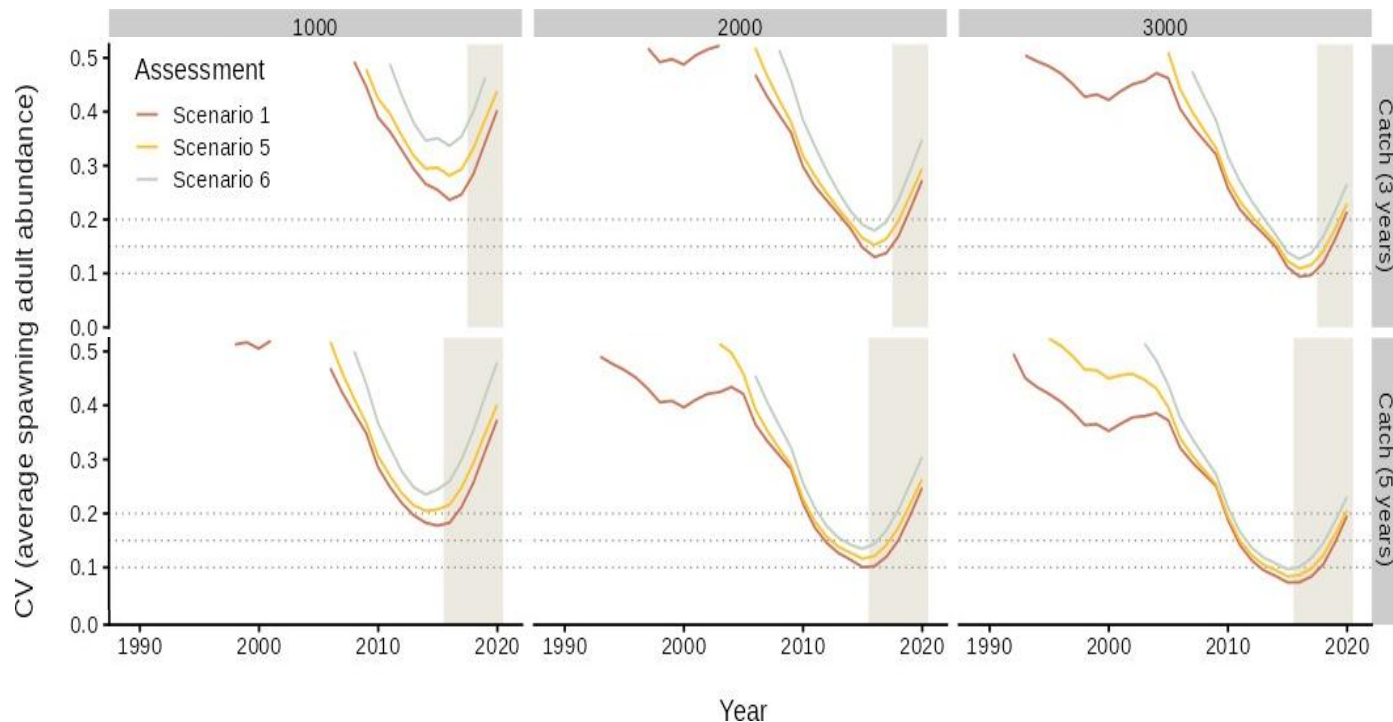


Precision in biomass estimates – Torres Strait



1000 samples/year
for 5 years

Precision in biomass estimates – East Coast



2000 samples/year
for 3 years

Now what?

- Sufficient samples collected from Torres Strait (~5000) and east coast (~6600) to commence sequencing & estimate abundance
- Developing proposal for joint project for Torres Strait and east coast – estimate abundance and examine connectivity
- Exploring options for the application of CKMR in Indian Ocean coastal state fisheries
- Number of samples required for some Indian Ocean populations may be larger than for Australian populations

Thank you

Environment

Ashley Williams

ashley.williams@csiro.au

Australia's National Science Agency

