USING GENETIC MARKERS TO ASSESS BYCATCH IMPACTS ON RIVER HERRING

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ARTICLE

Genetic stock composition of marine bycatch reveals disproportional impacts on depleted river herring genetic stocks

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- Aims of the study:
  - application of genetic stock identification to determine the regional stock composition of river herring bycatch
  - estimation of stock-specific bycatch mortality in the Atlantic herring fishery in 2012 and 2013

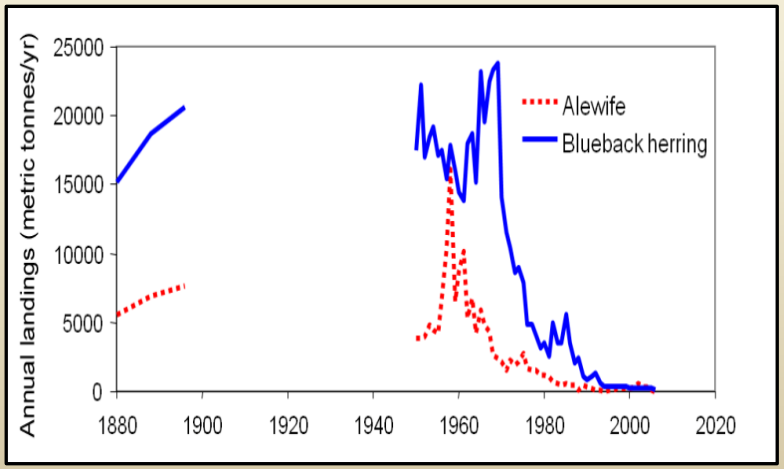
Outline

- Provide context
- Overview the study
- Clarify key findings
- Future directions

CONTEXT

- River herring have experienced dramatic declines since 1970s
  - anthropogenic factors (overharvest, dams, etc.)

- Palkovacs *et al*. (2014) - Recent declines in adult abundance and body size greatest for:
  - ALE: Mystic-Hudson (SNE)
  - BBH: Mystic-Neuse (SNE/MAT)



Data source: Limburg and Waldman (2009)

CONTEXT

- Freshwater focused remediation efforts
  - evidence for region-specific recovery (i.e., NNE, but not SNE or MAT)

- Could marine mortality be impeding conservation?

Incidental harm

- Bycatch in non-target marine fisheries
  - threat to recovery (Bethoney *et al*. 2013; Cournane *et al*. 2013)
  - high priority for fisheries management (ASMFC 2012)

- How is bycatch mortality partitioned among populations?
  - evenly distributed – minimal impacts for any particular population
  - concentrated – population-specific consequences

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OBJECTIVE

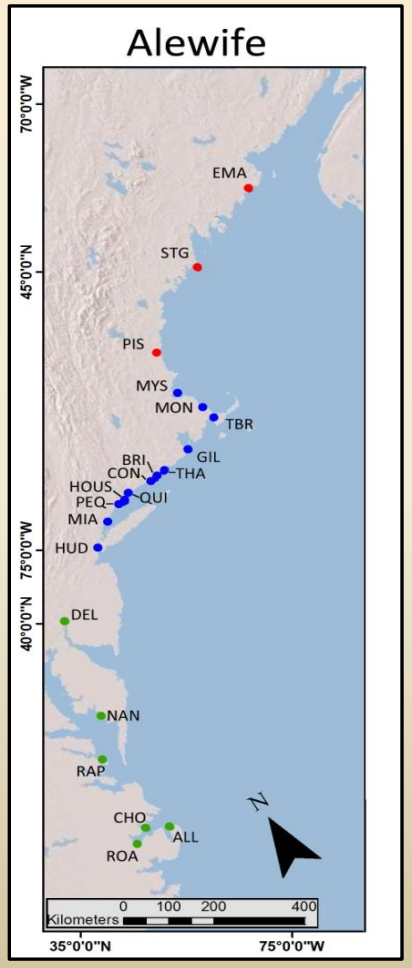
- Determine how river herring bycatch mortality in Northwest Atlantic commercial fisheries is partitioned among genetic stocks using Genetic Stock Identification (GSI):
  i. assign bycatch to genetic stock of origin
  ii. estimate genetic stock-specific mortality of ALE and BBH taken as bycatch in the 2012-2013 Atlantic herring fishery

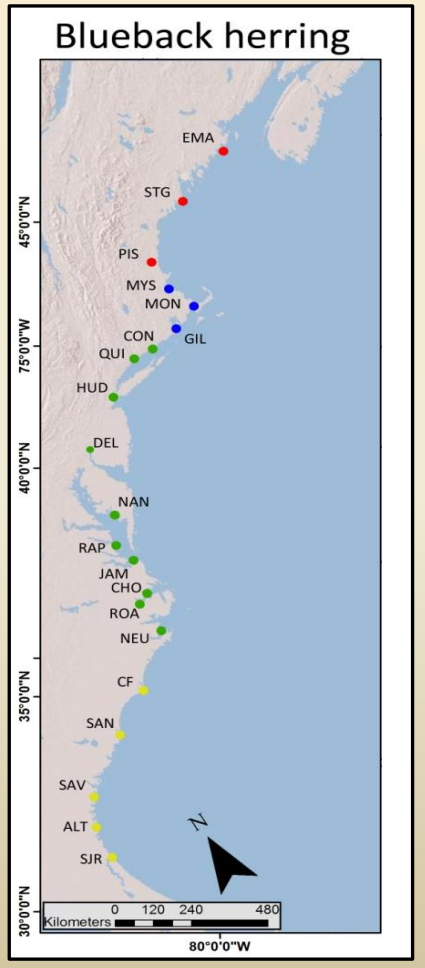
Genetic Stock Identification

- Two components:
  i. reference sample (baseline): spawning populations and stocks

- U.S. Stock structure (Palkovacs *et al*. 2014)
  - ALE: 3 genetic stocks (NNE, SNE, MAT)
  - BBH: 4 genetic stock (NNE, SNE, MAT, SAT)

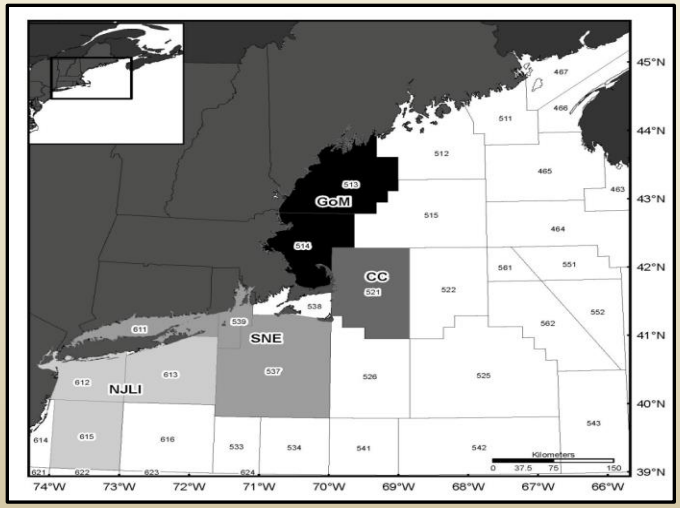
- Non-identical stock boundaries





Genetic Stock Identification

- Two components:
  ii. mixture sample (bycatch):
    - N=2928 (fisheries observers programs)
    - various fisheries (predominantly Atlantic herring)
    - time frame: 2012-2013 (fall/winter)
    - gear type: varied
    - various statistical areas comprising five nearshore regions:
      i. Gulf of Maine
      ii. Cape Cod
      iii. Southern New England
      iv. New Jersey-Long Island
      v. Delaware



Bethoney *et al*. (2014a)

Genetic Stock Identification

- Genotype baseline and mixture sample across same suite of 15 microsatellites

- *gsi_sim* (Anderson *et al*. 2008)
  - computationally efficient Bayesian approach to GSI
  - particularly useful for alewife and blueback herring – not all baselines are strongly differentiated

SIMULATIONS

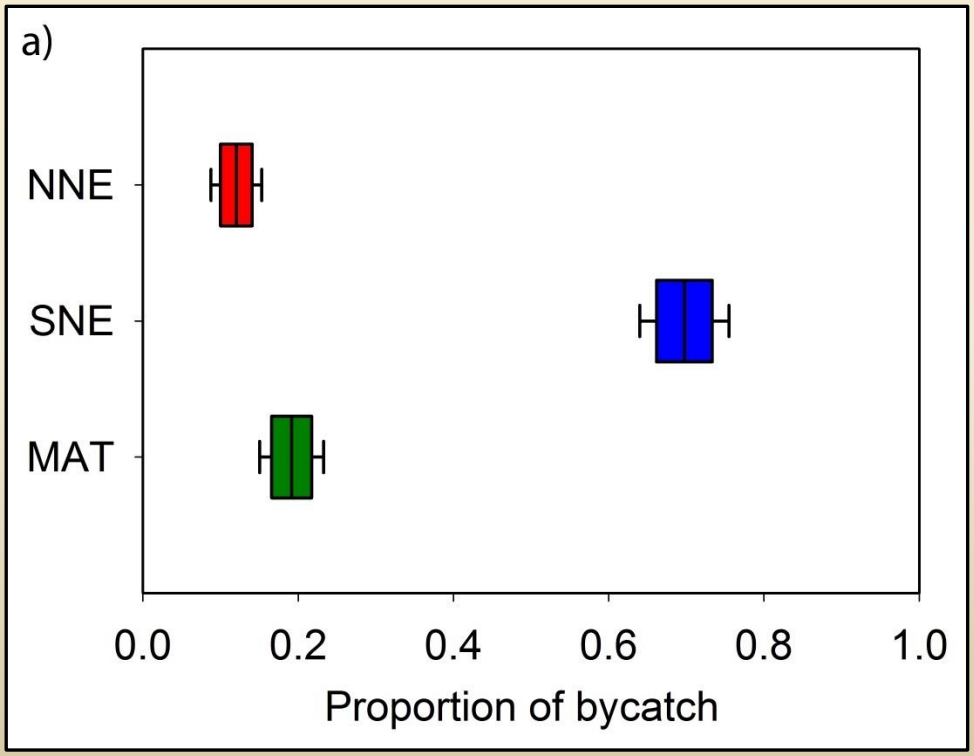
- Assess predicted bias and precision of genetic assignments
  - population-level assignment:
    - imprecise and evidence for bias
  - genetic-stock level assignment
    - concordance between distributions of estimated and simulated mixing proportions for ALE and BBH genetic stocks
    - high degree of reliability

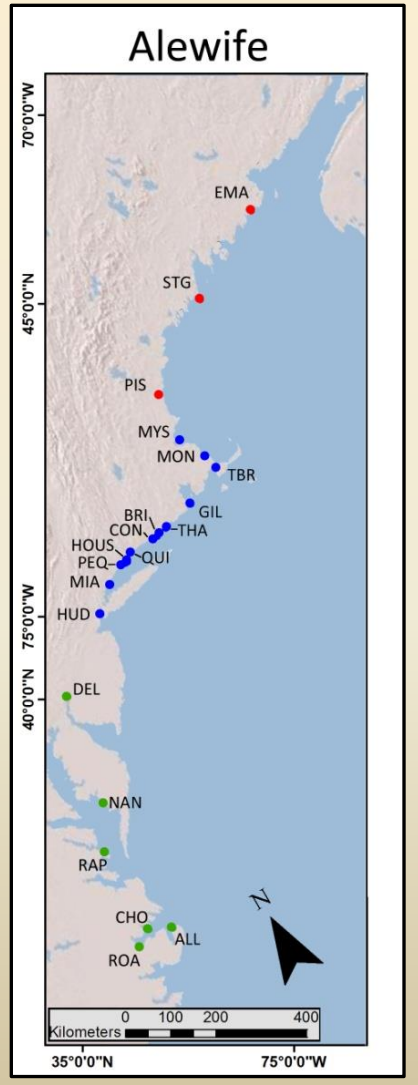
BYCATCH ASSIGNMENT

- Examined bycatch patterns in two complementary ways
  i. collectively - which genetic stocks were being encountered as bycatch across all fisheries
  ii. partitioned by 'strata' (i.e., year/season/region/target fishery/gear) to understand the effect of these factors on the genetic stock composition of bycatch
    - ALE (24 strata); BBH (16 strata)

OVERALL BYCATCH ASSIGNMENT (ALE)

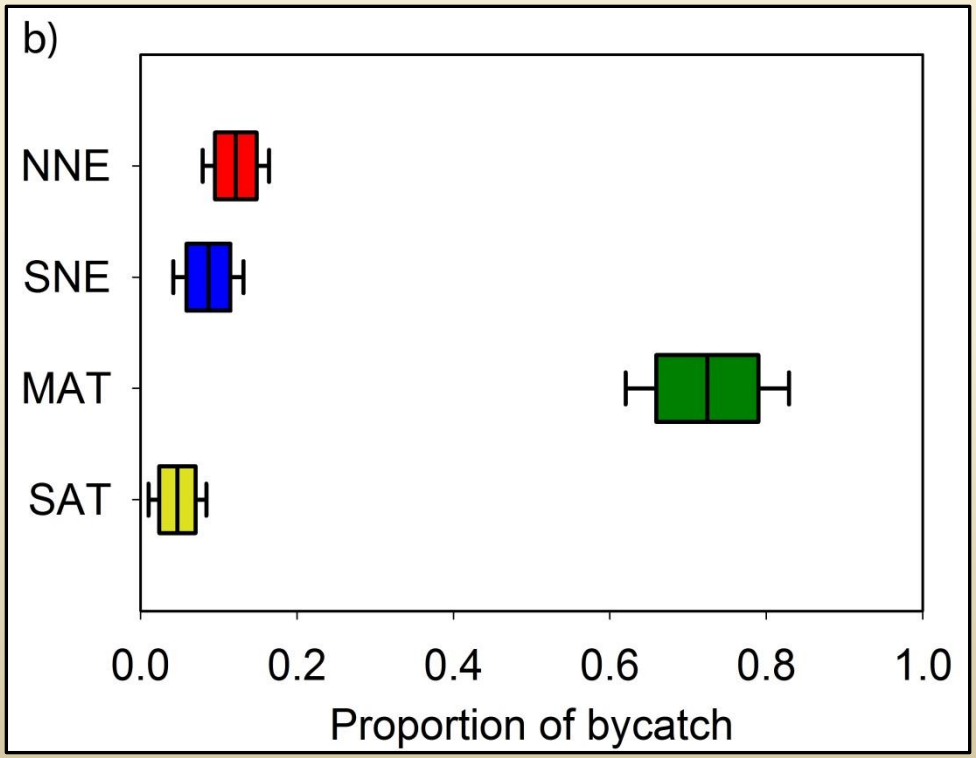
- Greatest proportion of bycatch across all fisheries assigned to Southern New England Stock ($\bar{x}$ = 0.70; 95% CI = 0.66-0.73)

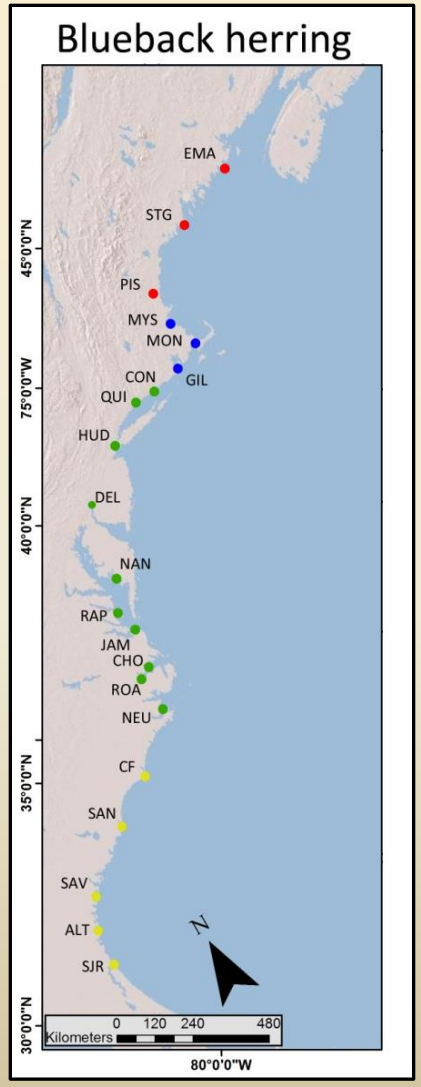




Overall bycatch assignment (BBH)

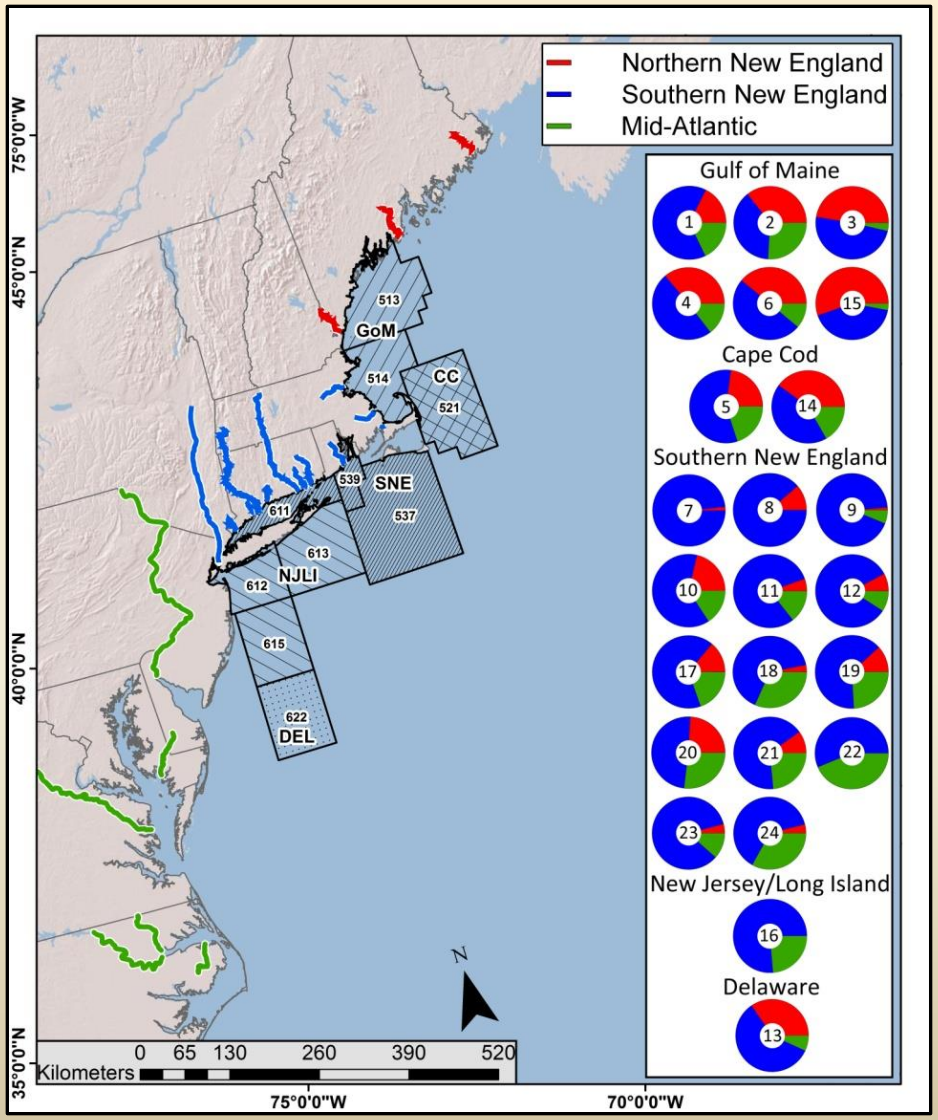
- Greatest proportion of bycatch across all fisheries assigned to Mid-Atlantic Stock ($\bar{x}$ = 0.78; 95% CI = 0.74-0.82)





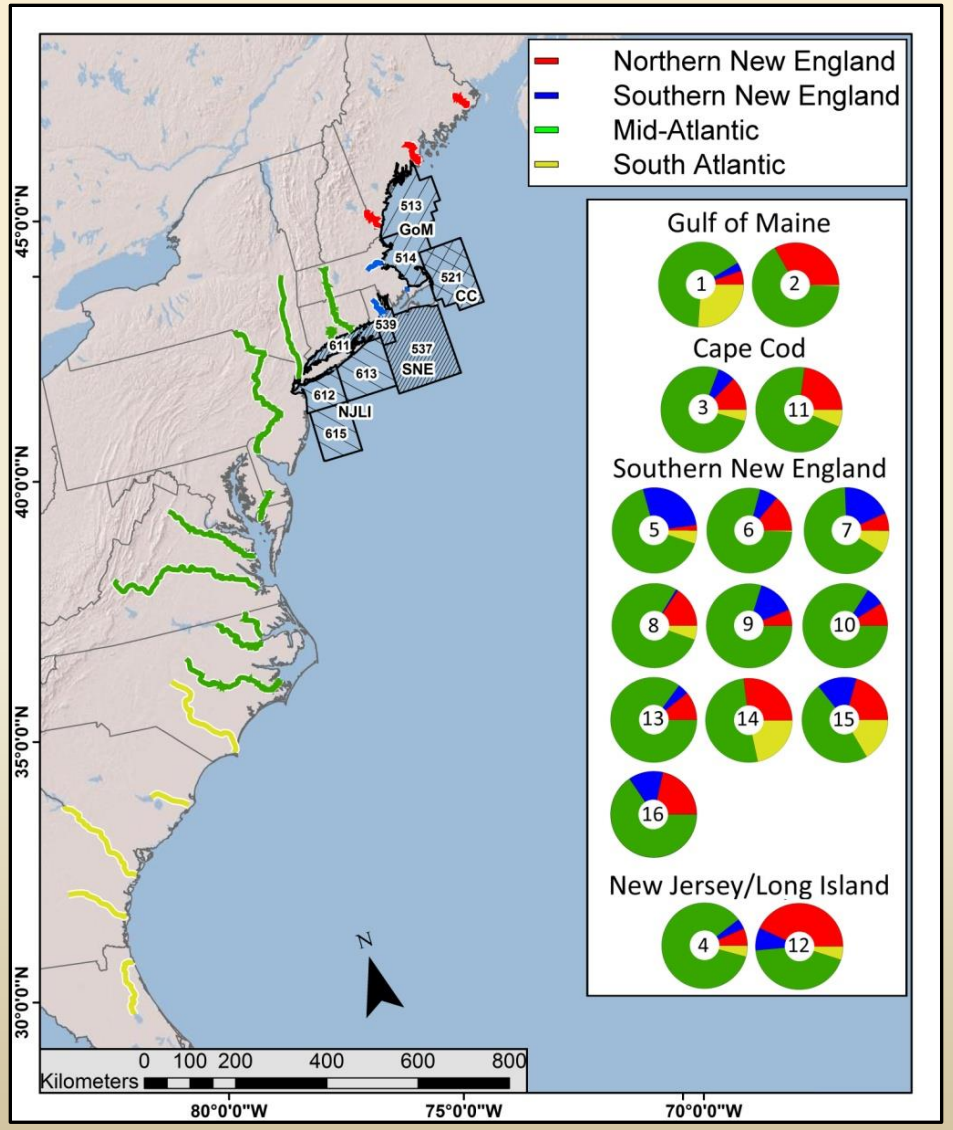
ALE BYCATCH STRATA

- Greatest proportion of ALE bycatch in various strata consistently assigned to SNE genetic stock
  - 0.38-0.98 ($\bar{x}$=0.66)
- 95% probability that SNE genetic stock comprises >67% of bycatch across strata
  - 20/24 strata are Atlantic herring fishery



BBH BYCATCH STRATA

- Greatest proportion of BBH bycatch in various strata consistently assigned to MAT genetic stock
  - 0.42-0.85 ($\bar{x}$=0.68)
- 95% probability that MAT genetic stock comprises >75% of bycatch across strata
  - all 16 strata are Atlantic herring fishery

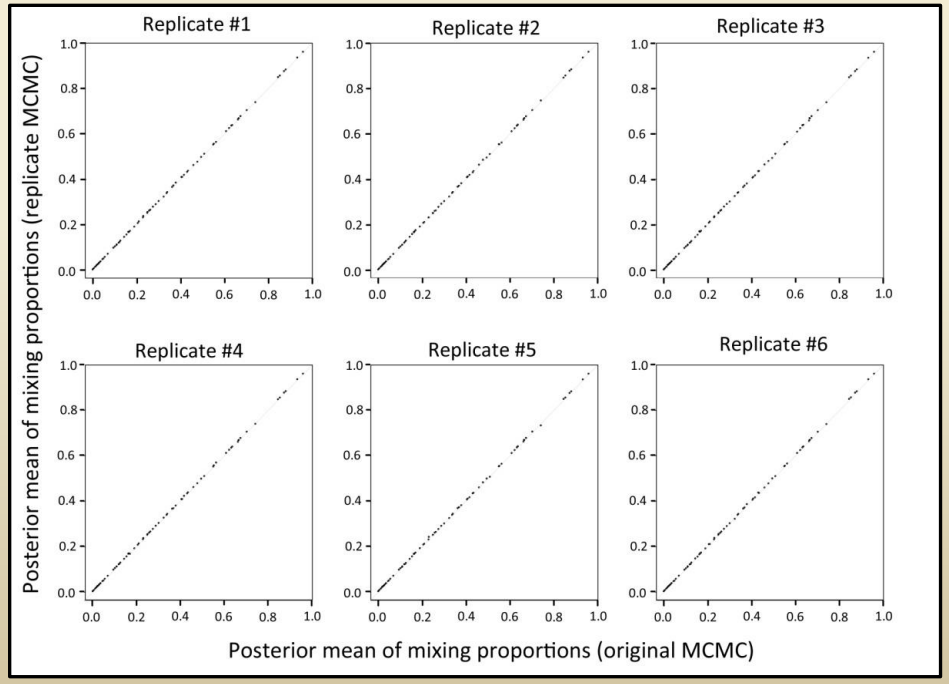


Repeatability of results

- Six additional runs of the model with different starting seeds to ensure proper mixing of the MCMC

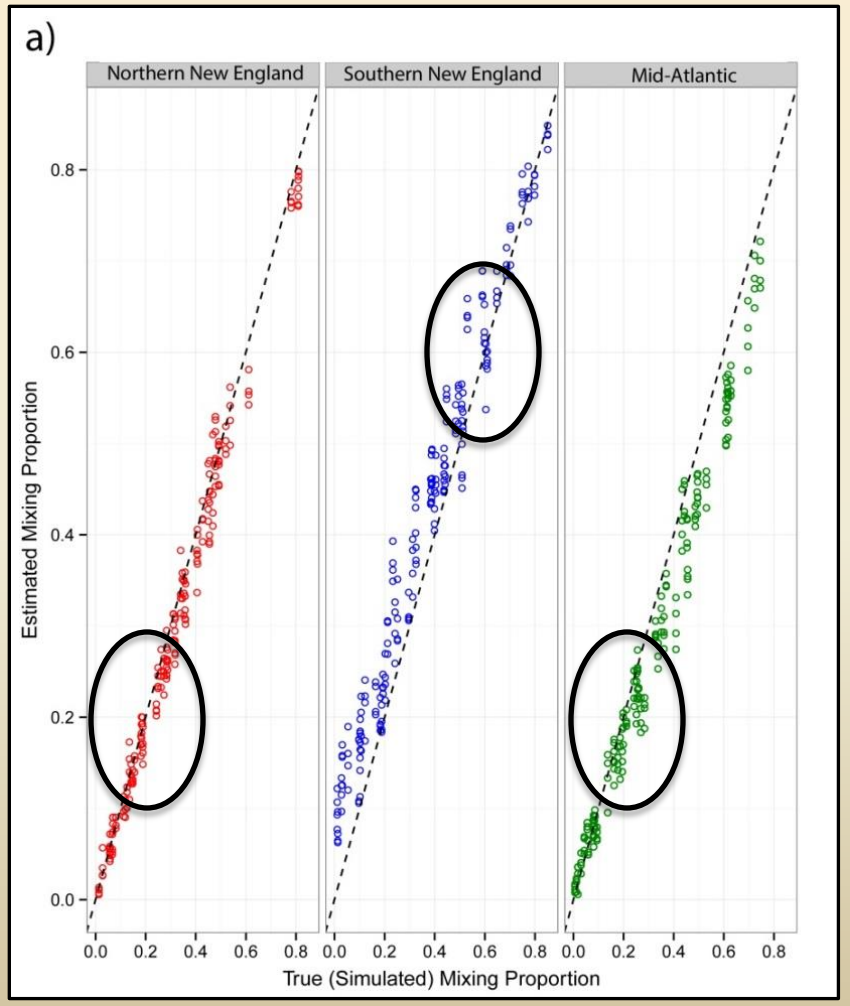
- Posterior mean estimates from all replicates were virtually identical to the initial run for both ALE and BBH

- Assignment probabilities of bycatch to genetic stock of origin are robust



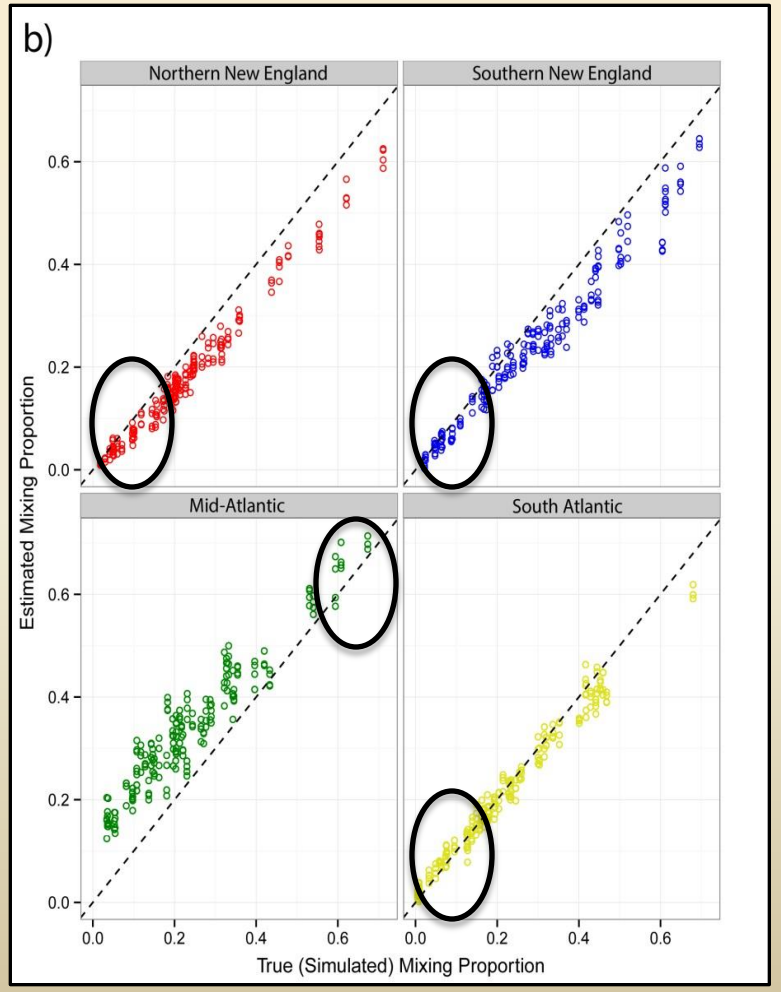
Evaluation of Assignment Bias (ALE)

- ALE:
  - minimal bias around key mixing proportions



Evaluation of Assignment Bias (BBH)

- BBH
  - slight downward bias for NNE
  - slight upward bias for MAT
- Why? Unequal number of populations among genetic stocks
- modest impact on precision of assignment to genetic stock of origin



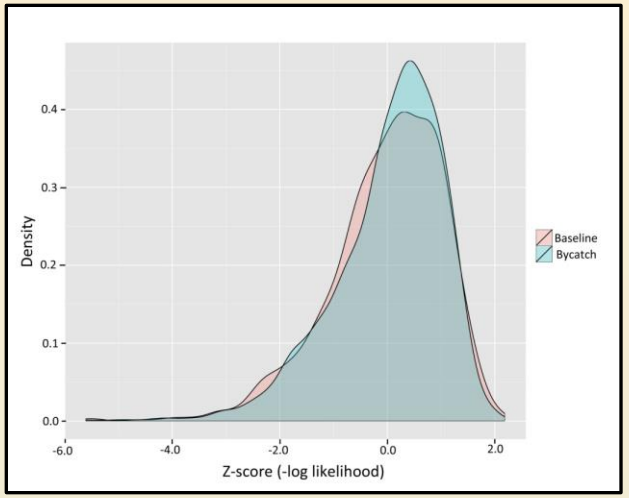
Missing baselines?

- *gsi_sim* yields unbiased estimates of GSI accuracy assuming that all populations in the bycatch are represented in the baselines

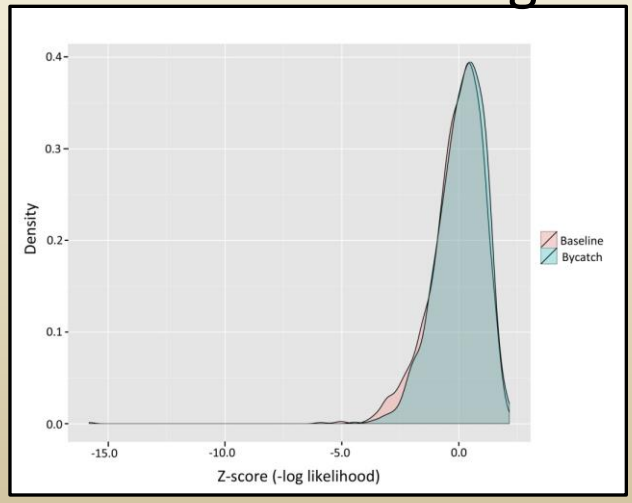
- examined distribution of Z-scores from *gsi_sim* to ensure that bycatch did not originate from reference populations not included in baseline (K-S test)

- NS difference ($p>0.05$) for either species; bycatch did not originate from non-sampled baselines

Alewife



Blueback herring



GENETIC STOCK-SPECIFIC MORTALITY

- Atlantic herring fishery in southern New England (2012-2013)
  - expansion factor (Bethoney *et al*. 2014a) used to convert mass of bycatch to numbers of individuals:

$$X_{s,i} = \frac{W_{s,i}}{w_{s,i}},$$

  - total number of individuals caught for each year and gear type estimated by:

$$\frac{\sum_i X_{s,i} * n_{s,l,i}}{\left[\frac{N-n}{N}\right]}$$

  - applied genetic stock proportions and 95% CI from GSI to estimate genetic stock-specific mortality for ALE and BBH
    - KS test to assess differences between years and gear types

BYCATCH MORTALITY (2012-2013)

- 4.95 million river herring taken as bycatch in Southern New England Atlantic herring fishery
  - 2012: 1.3 million (MW trawl: 82.3%; Bottom trawl: 17.7%)
  - 2013: 3.65 million (MW trawl: 48.5%; Bottom trawl: 51.5%)

	ALE	BBH
2012	410,000	890,000
2013	3,210,000	450,000

GENETIC ASSIGNMENT (2012-2013)

- Bycatch mortality not evenly distributed among genetic stocks (Table 2)
  - proportional genetic stock composition of bycatch did not differ between gear types or between years for ALE or BBH
  - b/c different species dominated bycatch in 2012 vs. 2013, we detected different genetic-stock specific mortality
    - 2012 BBH: MAT genetic stock – 54.7% of river herring mortality
    - 2013 ALE: SNE genetic stock – 64% of river herring mortality

	ALE	BBH
NNE	7.5%	9%
SNE	72.5%	10%
MAT	20%	80%
SAT	-	1%

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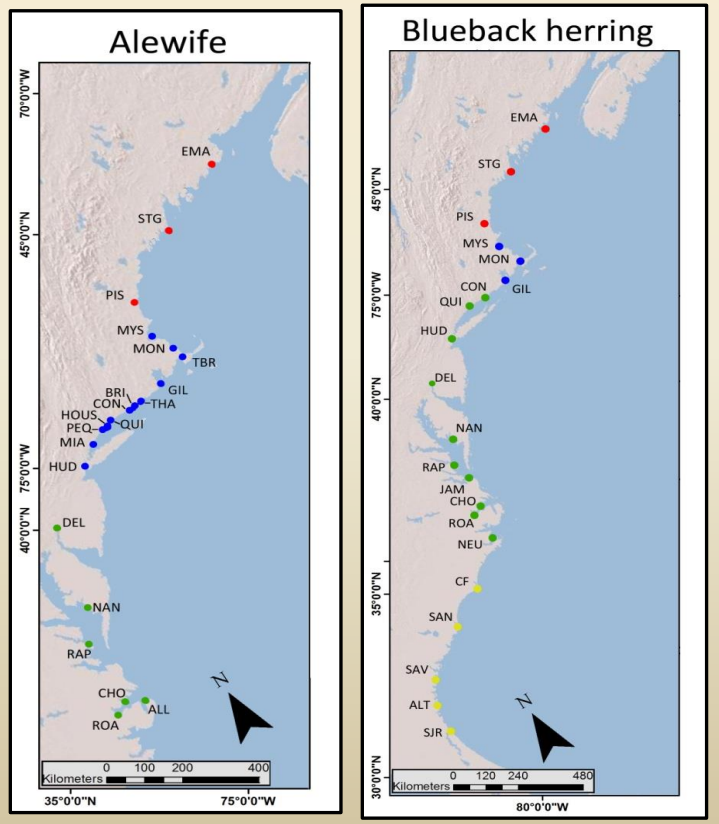
KEY FINDINGS

1. Bycatch mortality is not evenly distributed among genetic stocks
   - disproportionately assigned to the genetic stocks that have experienced the greatest declines
     - could be hindering recovery efforts in rivers that comprise those genetic stocks
   - ALE: SNE genetic stock dominated bycatch overall and across strata
   - BBH: MAT genetic stock dominated bycatch overall and across strata

KEY FINDINGS

2. Hypothesis: populations from rivers that drain into Long Island Sound (LIS) are disproportionately impacted by bycatch in the SNE Atlantic herring fishery

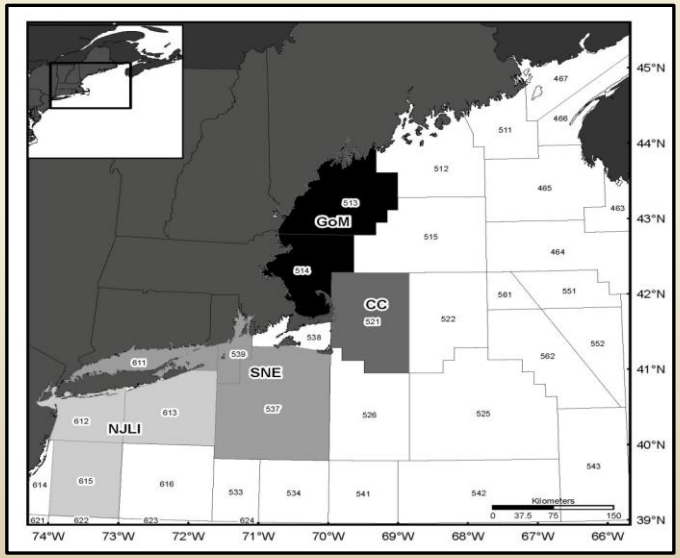
- genetic stock boundaries overlap



KEY FINDINGS

2. Hypothesis: populations from rivers that drain into Long Island Sound (LIS) are disproportionately impacted by bycatch in the SNE Atlantic herring fishery

- genetic stock boundaries overlap
- >55% of bycatch strata came from SNE Atlantic herring fishery adjacent to LIS
- RH bycatch is greatest just offshore where populations have declined the most (Bethoney et al. 2013, 2014b)
- *CAUTION: genetic stock boundaries extend beyond LIS



Bethoney *et al*. (2014a)

LIMITS TO INTERPRETATION

- Bycatch may be an important contributing factor in lack of recovery for LIS populations, but other factors need to be considered in conjunction with bycatch

- Potential for biased or incomplete sampling of bycatch across trips made by the fleet as a whole? (needs to be addressed)

- “Linking the magnitude of bycatch mortality to declines in [abundance] and evaluating the impacts of bycatch on [recovery] is complicated by the absence of reliable spawning run count data for many populations.”

- “…our results present a temporal snapshot of a highly variable fisheries management problem.”

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Moving forward

- Increase spatial resolution of genetic assignments
  - new markers (SNPs), expand baselines
  - implement new version of *gsi_sim* to account for unequal number of populations per genetic stock

- Maintain bycatch monitoring to establish longer time series
  - implement standardized sampling regime

- Implement (rangewide) standardized methods of enumerating spawning run counts to assess the *impacts* of bycatch

*Open questions

- How representative is bycatch sampling among trips within the years sampled?
- How much do patterns in bycatch (and bycatch assignment) vary across years?
- What rivers within genetic stocks are most affected by bycatch?
- *Future bycatch paper can help address these issues

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