



Bering Sea red king crab stock structure template

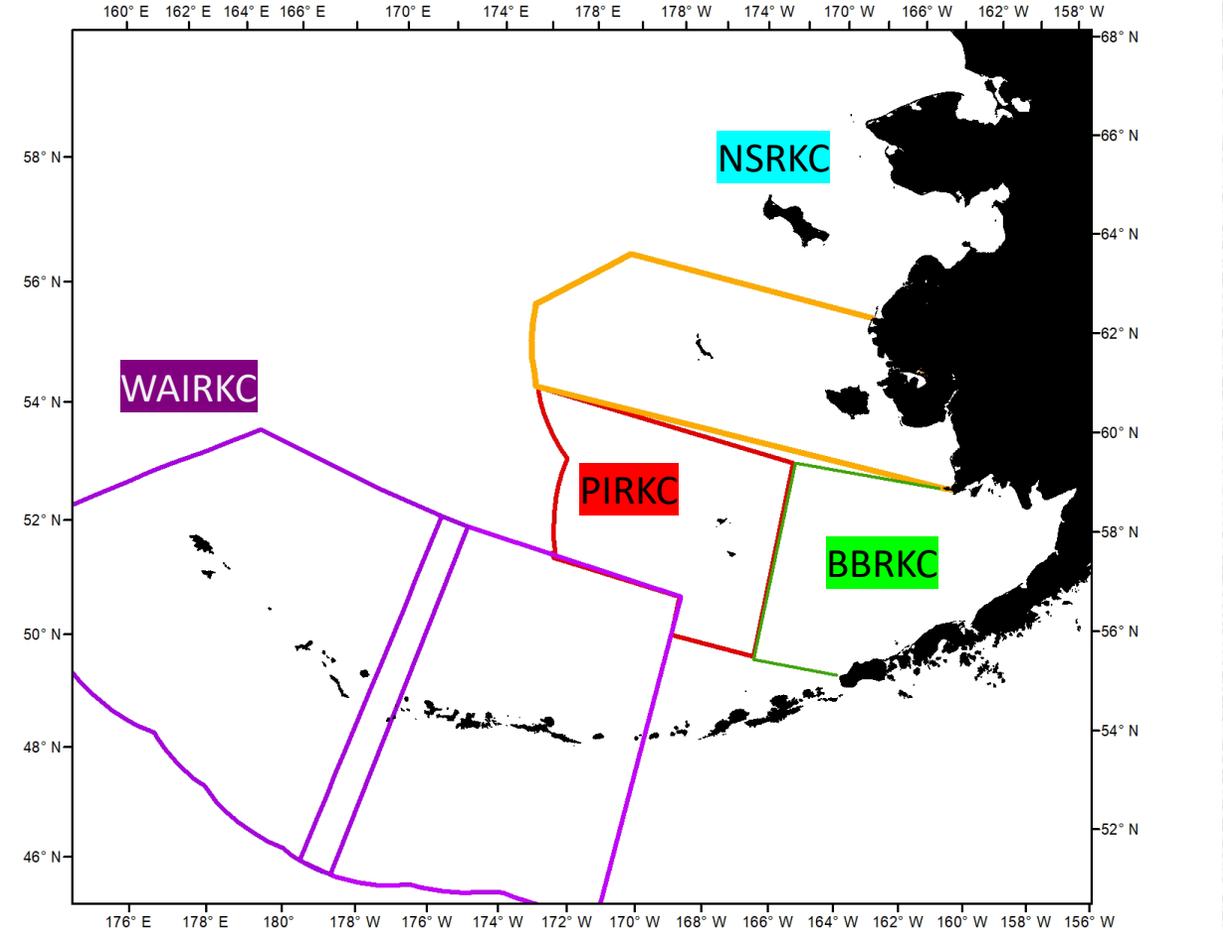
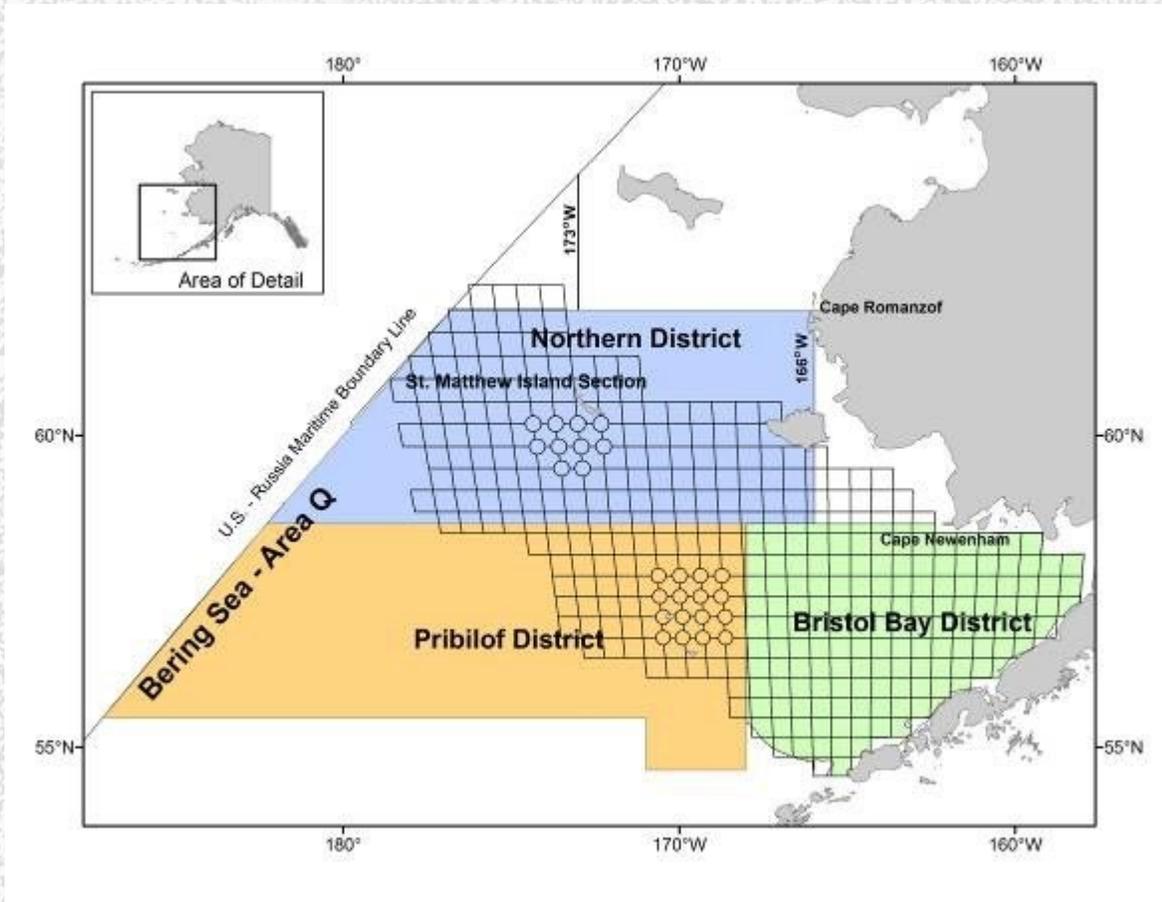
Katie Palof, Ben Daly, Cody Szuwalski, Hamachan Hamazaki

Sept 2023

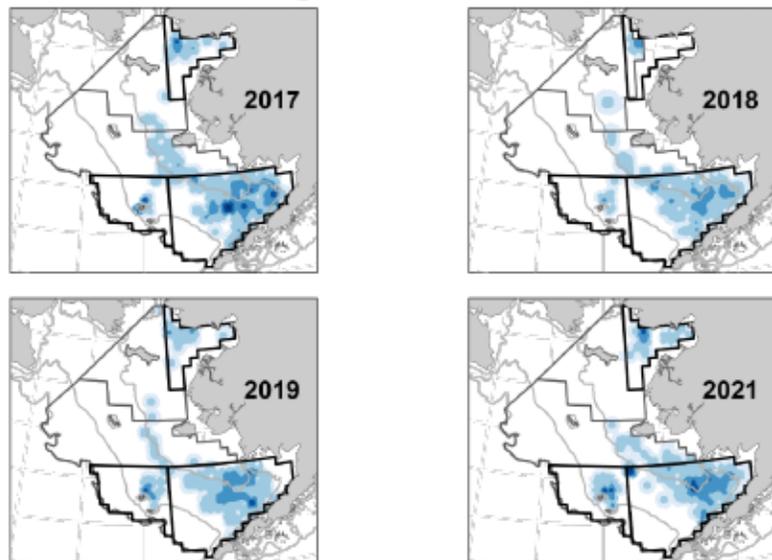
Stock structure template

- Request from SSC
- Draft in May
- Established to guide decisions on splitting or lumping populations/stocks for both stock assessment and management
- Bering Sea red king crab –
 - Bristol Bay, PIRKC, WAIRKC, Northern district, NSRKC
- Reference: Spencer, P. et al. 2010. Guidelines for determination of spatial management units for exploited populations in Alaskan groundfish fishery management plans. NPFMC Sept. 2010 plan team draft

Bering Sea stocks - Bristol Bay, PIRKC, WAIRKC, Northern district, NSRKC



Red King Crab Mature Male



2022 Tech Memo
NOAA trawl surveys

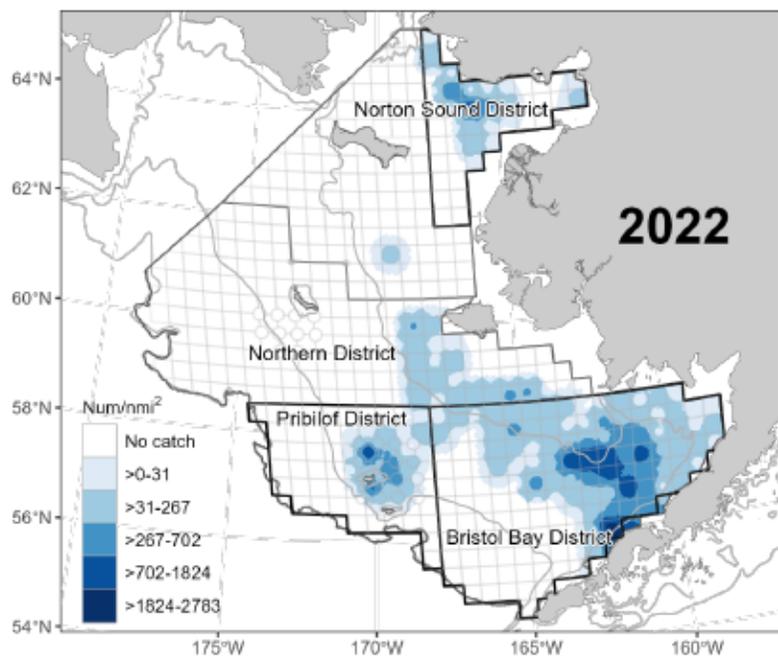


Figure 28. -- Estimated total density of mature-sized (≥ 120 mm carapace length in EBS and ≥ 94 mm in NBS) male red king crab (*Paralithodes camtschaticus*) for the past five survey years. Outlined areas depict management districts.

Red King Crab Mature Female

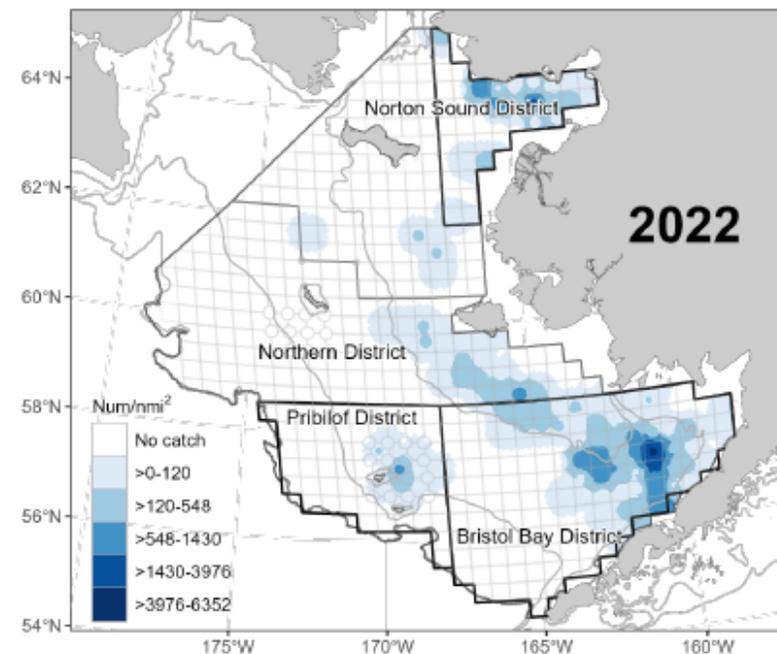
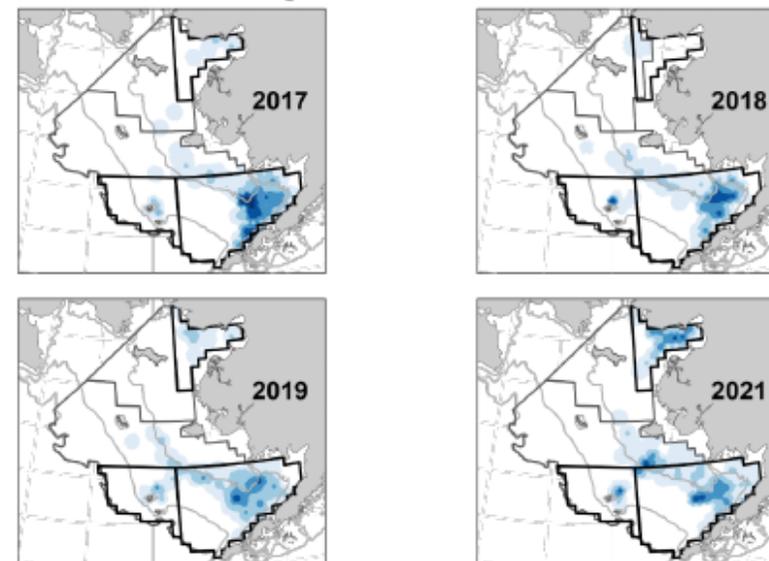
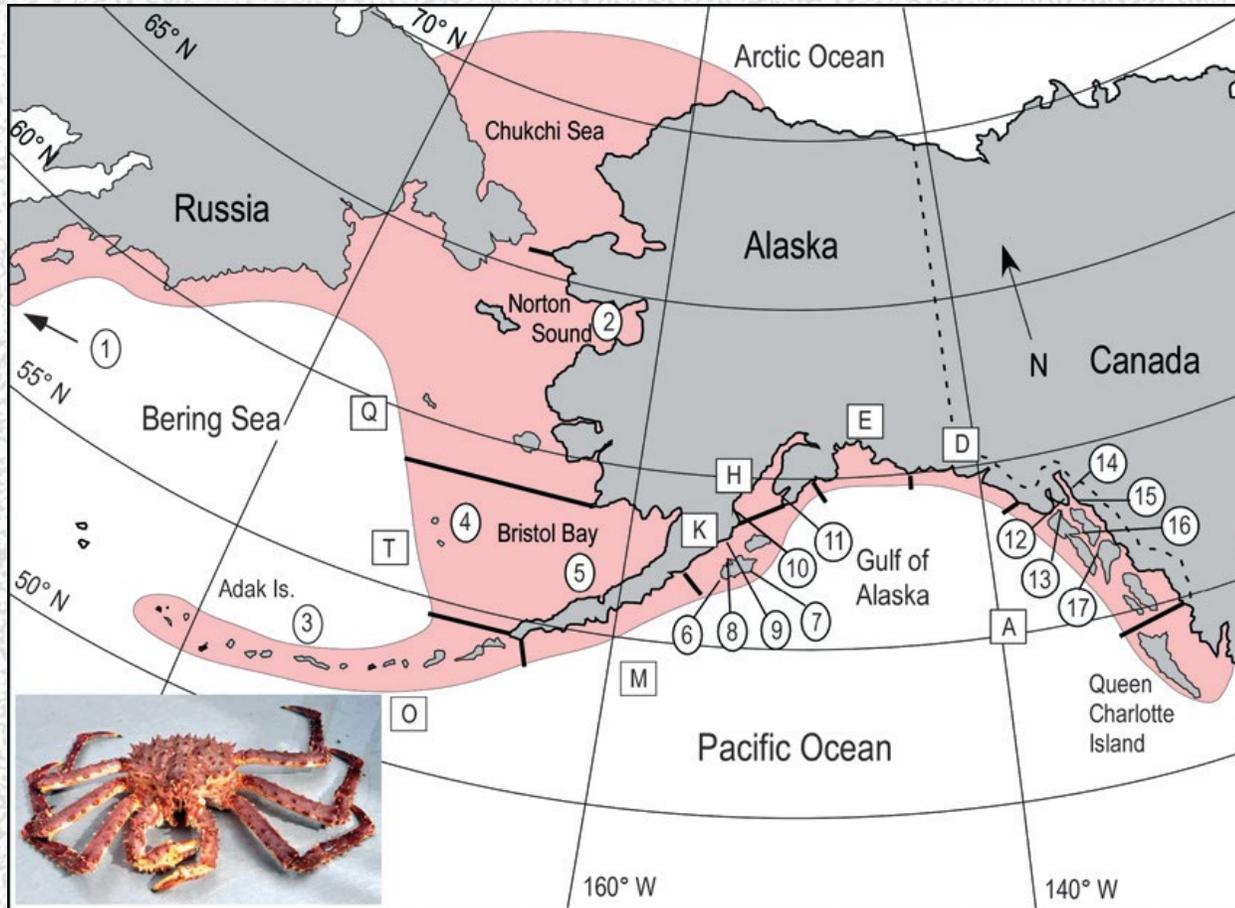


Figure 30. -- Estimated total density of mature female red king crab (*Paralithodes camtschaticus*) for the past five survey years. Outlined areas depict management districts. In years when a subset of stations were resampled, the resample stations replace data from the original stations.

Genetic studies



- Samples from Grant and Cheng 2012
- Note:
 - One sample from both PIRKC and BBRKC
 - No samples from Northern district crab

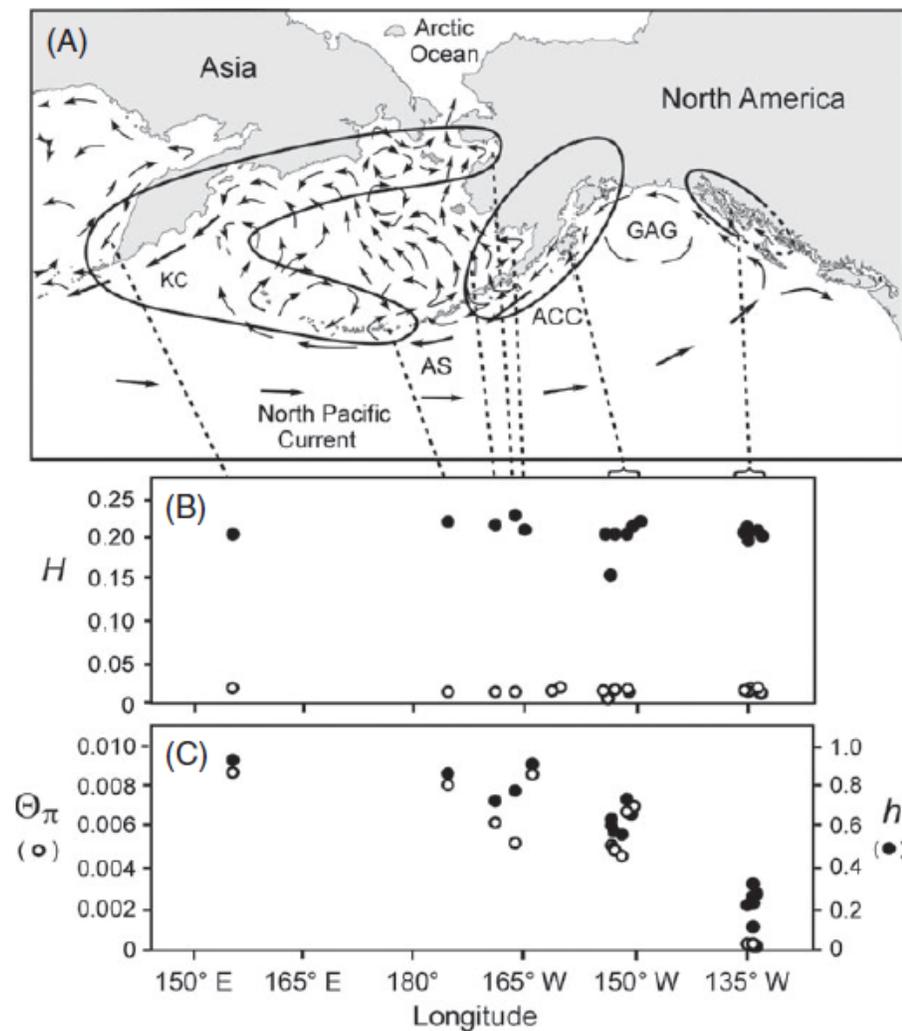


Figure 2 (a) Map of the North Pacific Ocean and Bering Sea showing generalized current patterns and three major population groups of red king crabs. (b) Average heterozygosity of 15 single nucleotide polymorphisms (closed circles) and average heterozygosity of 38 allozyme loci (open circles). (c) Mitochondrial DNA haplotype diversity (closed circles) and nucleotide diversity (open circles). KC, Kamchatka Current; AS, Alaska Stream; ACC, Alaska Coastal Current; and GAG, Gulf of Alaska Gyre.

Genetic results

- 3 main groupings
- NSRKC and WAIRKC – isolated genetically
- Bristol Bay
 - Groups with PIRKC and GOA
 - Reduction in genetic diversity? (samples 1989 and 2008)
- Could be isolated stocks, does not reflect contemporary genetic gene flow
- Greater detailed sampling needed
- Genomic sequencing prelim results suggest structure between PI and BB, potentially within BB (Carl St. John per comm.)

Non –genetic information

- Size compositions, growth, recruitment pulses
 - BB and Northern area similar but sample sizes for Northern are very low
- Physical barriers or oceanographic barriers
 - Aleutian Islands Samalga Pass
 - Norton Sound general current flow
 - Larval advection models suggest the ability of larvae to be carried outside of BB depends on timing of release and prevailing environmental conditions – which have likely changed over time (Daly et al. 2020)

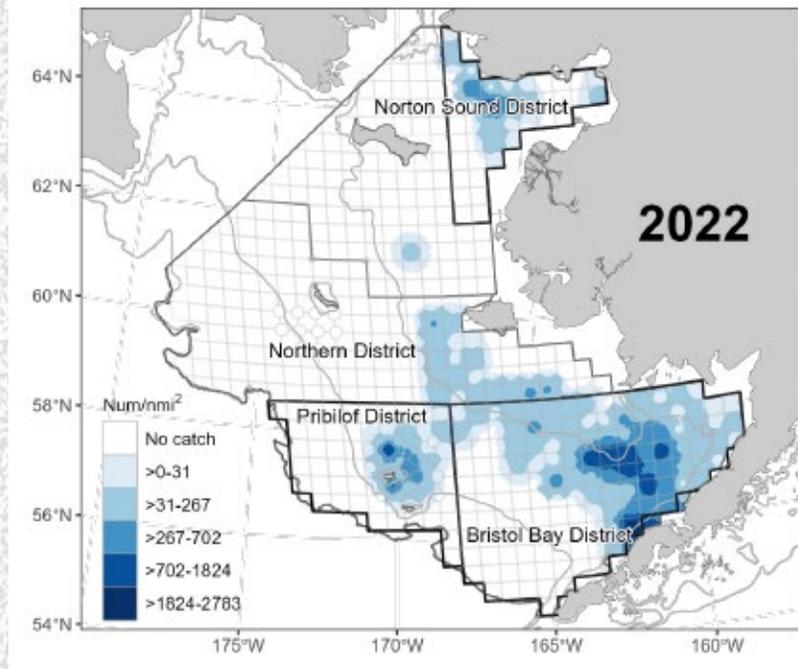
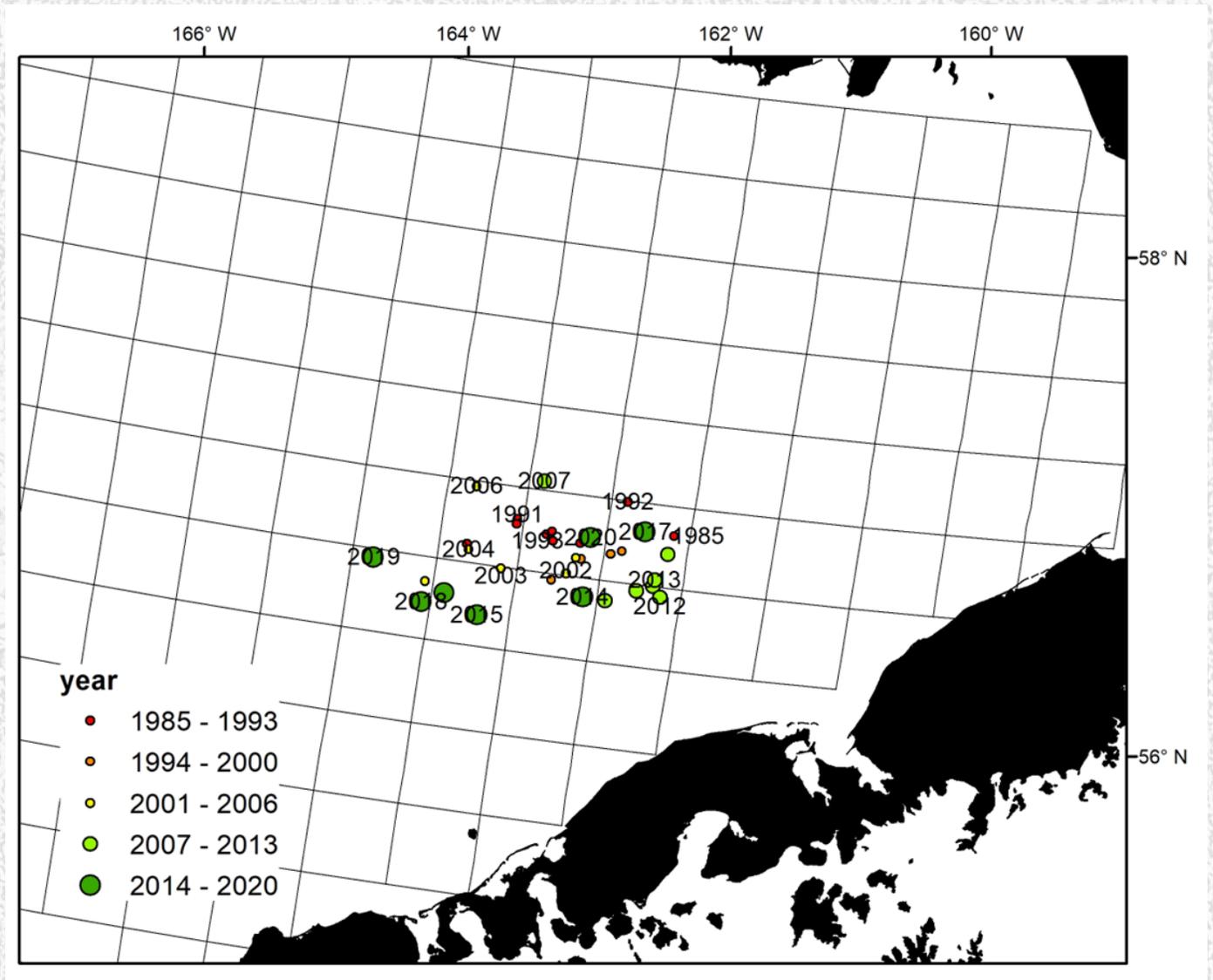
Historic management units

- Historic fishing areas
- Landmark boundaries
- Still represent the majority of RKC population centers in Bering Sea

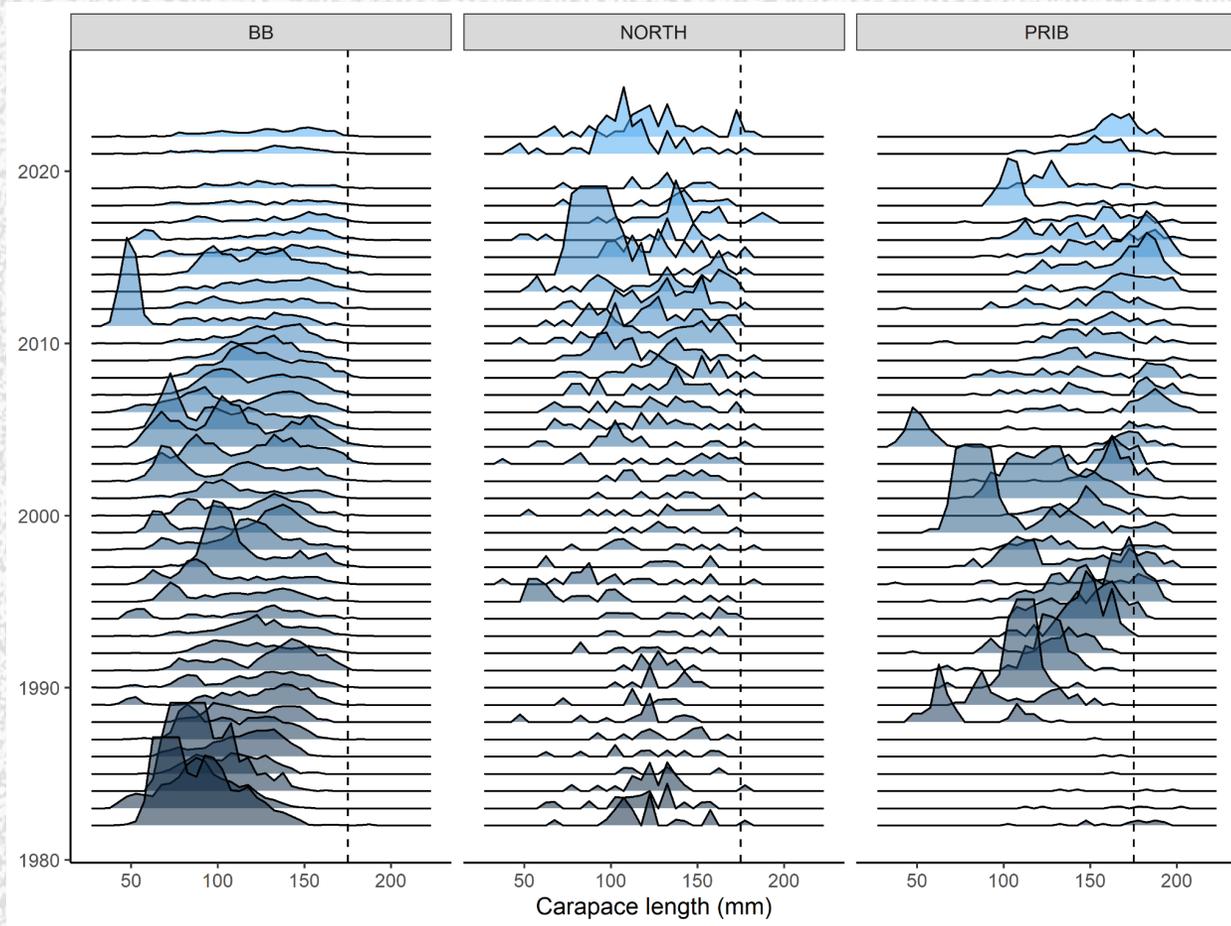
Fishery centroids

(right) BBRKC weighted centers of catch over time, fishery was closed in 2021/22 and 2022/23 seasons
(Source: September 2021 CPT presentation by B.Daly, ADF&G).

(bottom) mature males from NOAA tech memo



Survey size composition



- Not on the same scale
- Hard to determine potential linkages
- Provided by Cody Szuwalski

Table 1: Summary of available data on stock identification for Bering Sea red king crab

Factor and criterion	Justification
Harvest & Trends	
Fishing mortality (5-year average percent of F _{abc} or F _{o1})	bbrkc - close to F _{o1} last 3 years fisher was open, fishery closed in 21/22 & 22/23 waikc/pirkc - fishery closed.
Spatial concentration of fishery relative to abundance (Fishing is focused in areas << management areas)	Fishery in BBRKC typically occurs in the center of the stock boundaries (Figure 4)
Population trends (Different areas show different trend directions)	NS good, PI and BB low
Barriers & phenotypic characters	
Generation time (e.g., >10 years)	Unknown. Age to maturity estimated to be around 6 to 7 years
Physical limitations (Clear physical inhibitors to movement)	Norton Sound and Aleutian island chain. Biogeographical boundary at Samalga Pass attributes divergence between WAI population and southeastern Bering SEA (BB and PI)
Growth differences (Significantly different LAA, WAA, or LW parameters)	Growth differences exist in NS, not sure if we have information for other stocks
Age/size-structure (Significantly different size/age compositions)	Figure 5 shows comparison of size compositions for bbrkc, pirkc, and northern district crab.
Spawning time differences (Significantly different mean time of spawning)	Unknown.
Maturity-at-age/length differences (Significantly different mean maturity-at-age/ length)	BB and NS clear differences due to growth and size differences.
Morphometrics (Field identifiable characters)	Size at maturity between BB and NS
Meristics (Minimally overlapping differences in counts)	Unknown.

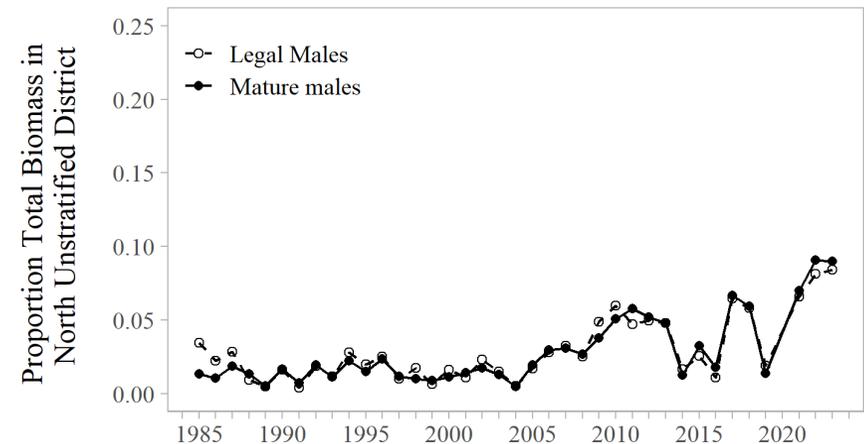
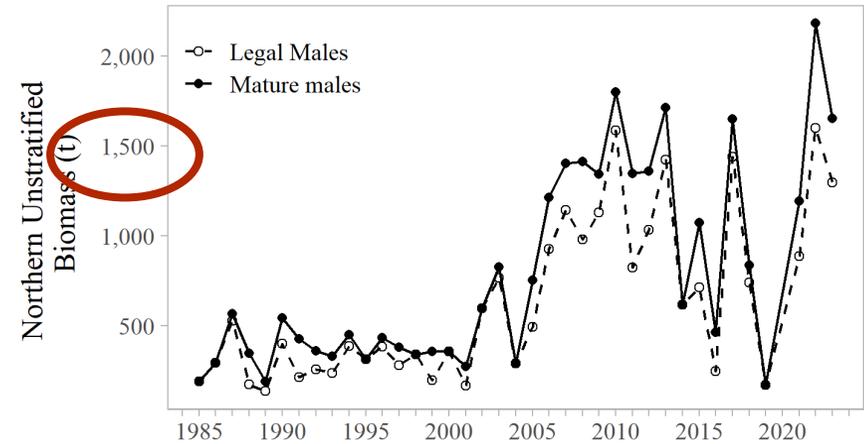
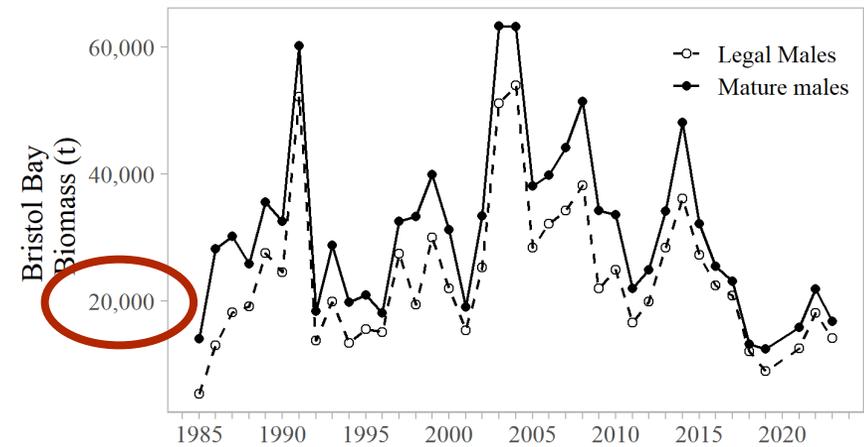
Factor and criterion	Justification
Behavior & movement	
Spawning site fidelity (Spawning individuals occur in same location consistently)	Unknown.
Mark-recapture data (Tagging data may show limited movement)	Recent and current tagging available for BBRKC stock, summary of this work is needed.
Natural tags (Acquired tags may show movement smaller than management areas)	Unknown.
Genetics	
Isolation by distance (Significant regression)	Present when compared to all Alaska samples (including SE Alaska, p <0.01). Just Bering Sea samples did not show significant IBD but there is some relationship (p=0.064).
Dispersal distance (<<Management areas)	Genetic data suggests gene flow between most of the Bering Sea – excluding NS and WAI red king crab which appear to be more genetically distinct.
Pairwise genetic differences (Significant differences between geographically distinct collections)	None significant within the southeastern Bering Sea.

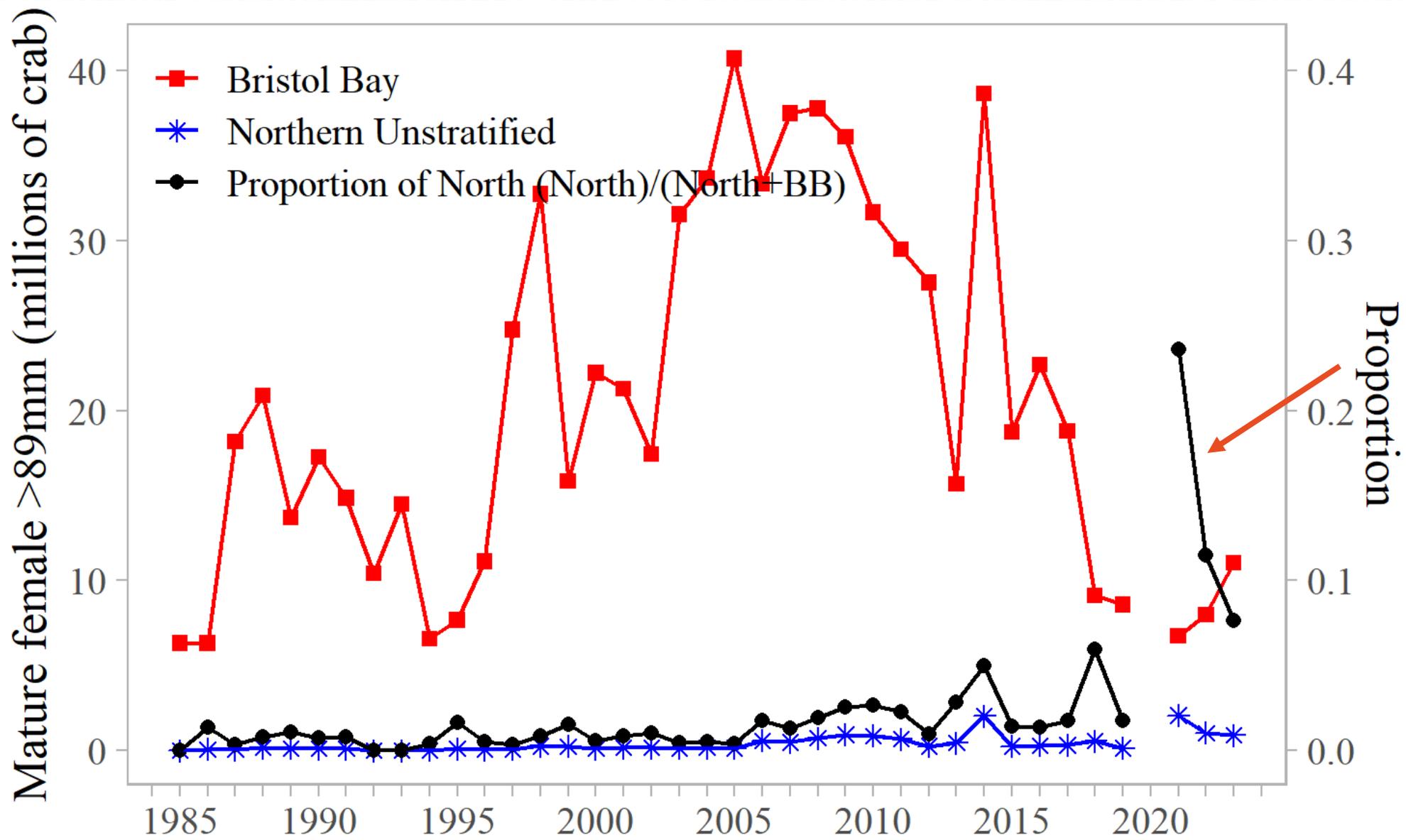
Future work / next steps

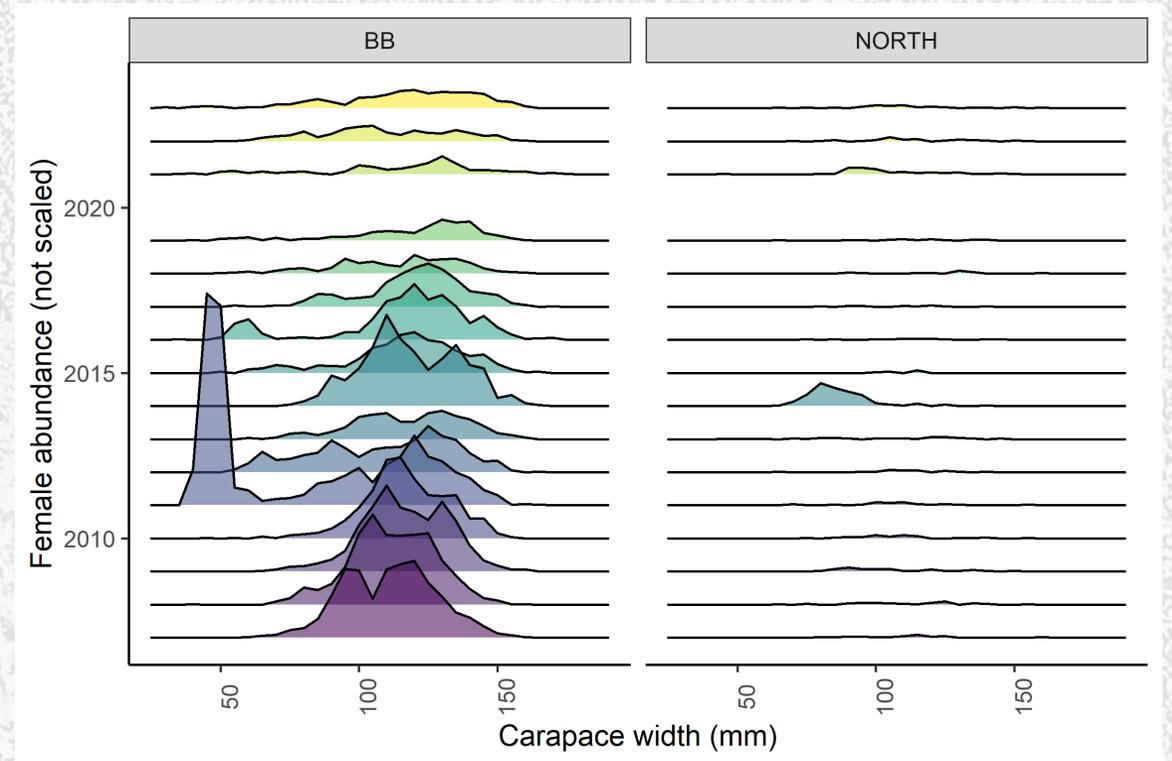
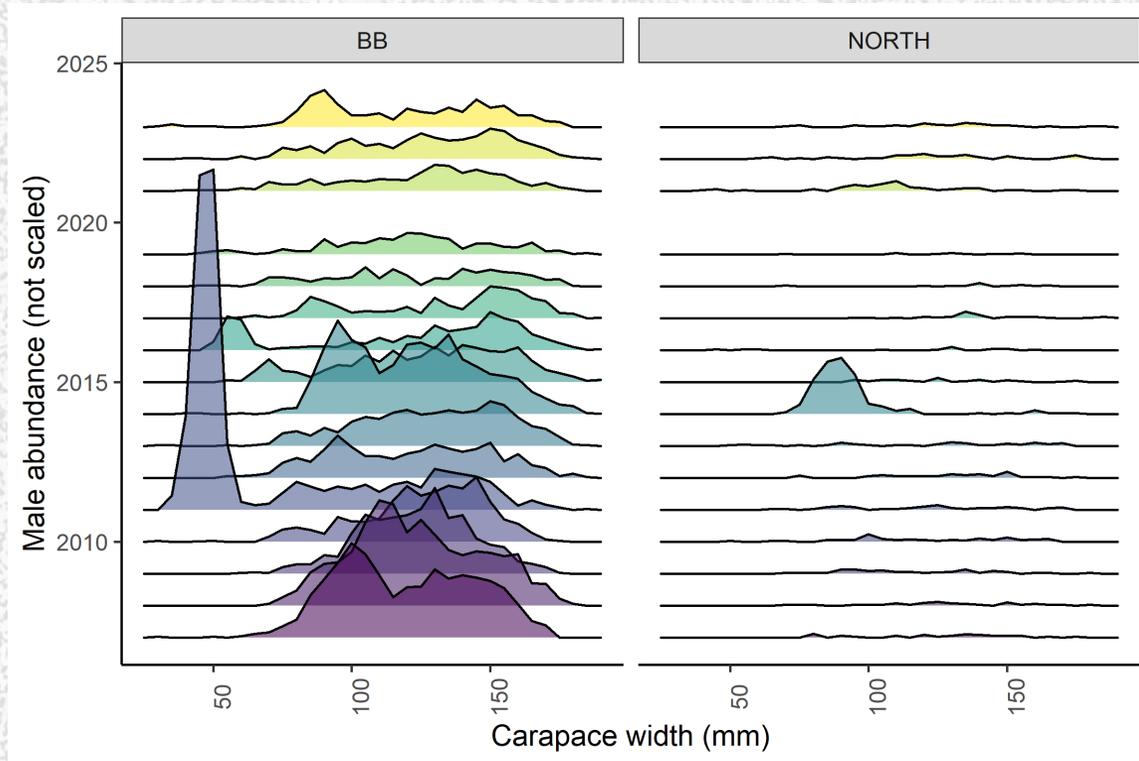
- Conclusions thus far:
 - Focus on Southeastern Bering Sea stocks
 - NS and WAI distinct stocks based on genetics and growth, size, etc.
 - Summary of tagging data that exists around Bristol Bay important for further stock structure analyses
 - Objective of determining if Northern district red crab are part of the functional BBRKC stock?
- Future work
 - Increased genetic sampling around Bristol Bay / Northern area
 - Update on genetic work at Jan meeting? (Carl St. John, PhD candidate)
 - Additional oceanographic information and potential larval flow? (follow up to Daly et al. 2020)

Northern area crab relative to Bristol Bay

- Northern area biomass 10x smaller than Bristol Bay in large years
- Last 15 years some changes in Northern vs BB proportion (panel 3)
 - Trend of increase with some fluctuation to low levels in the North
 - Highest level still only 10% of mature males in Northern area







- Last ~15 years on the same scale.
- Note the inability to see trends in the Northern area

Tagging information – only near the boundary?

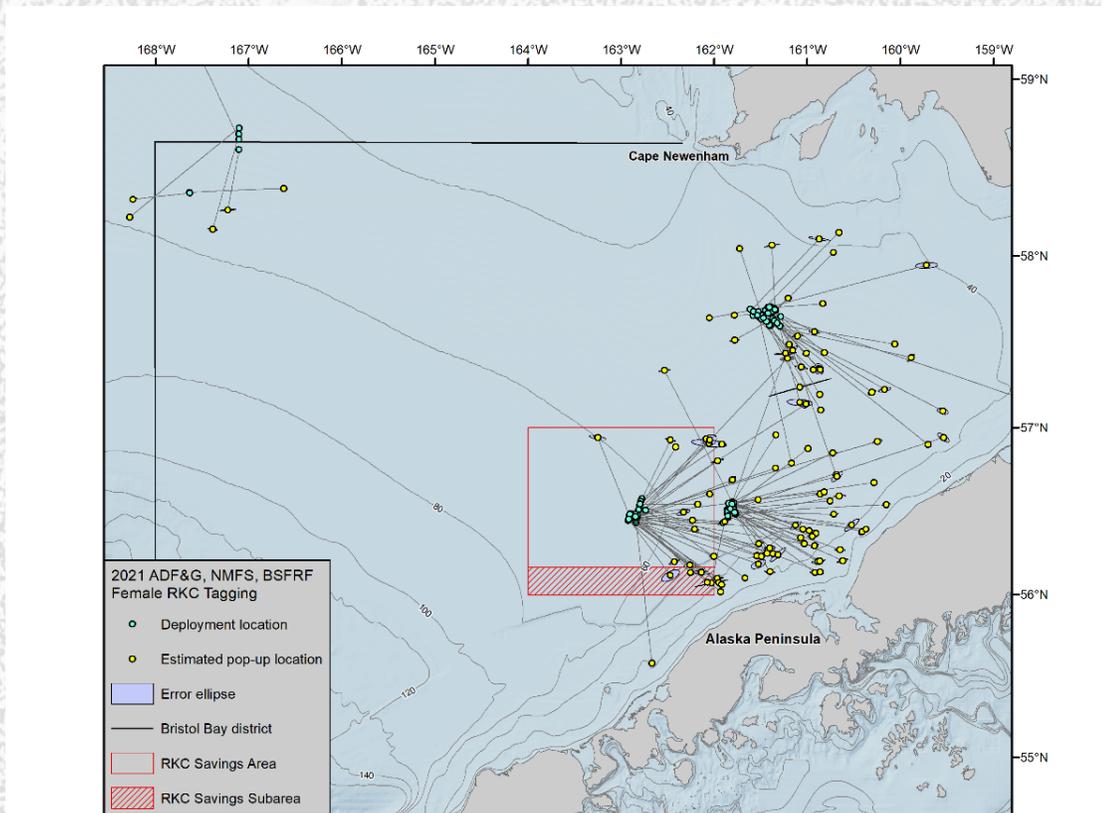


Figure 3-1 Movement of female crab from fall (November 2021) to spring (late-April/early-May 2022) based on pop-up satellite tag results from the ADFG/NMFS/BSFRF study

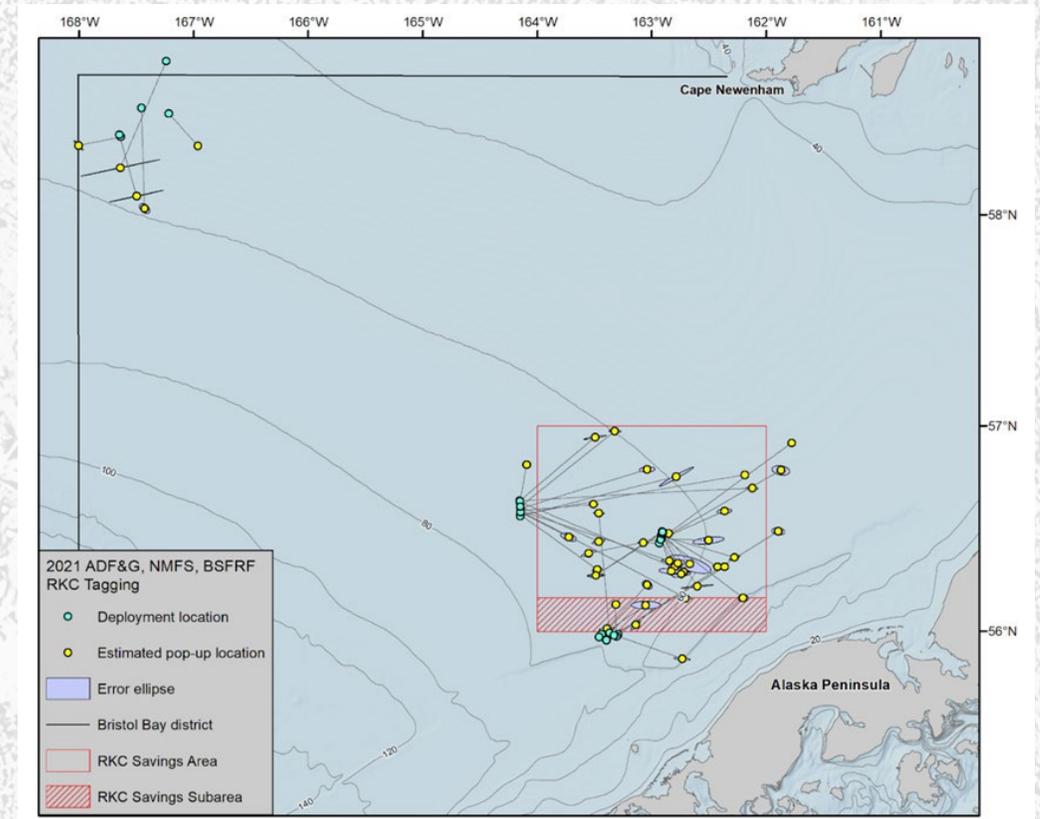


Figure 3-2 Movement of male crab from fall (November 2021) into winter (January 2022) based on pop-up satellite tag results from the ADFG/NMFS/BSFRF study

Northern area and Bristol Bay future work

- Are Northern crab part of the same mating population?
 - For a yes, evidence for genetic linkage needed AND movement data to suggest these crab are part of mating aggregations OR indication of larvae exchange
 - For a no, evidence of genetic differences AND movement data to suggest they do NOT move into Bristol Bay
- Genetic samples from Northern area
- Tagging for Northern crab further north of the boundary