

## DRAFT: Stock structure template for Bering Sea red king crab

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This stock structure template covers red king crab stocks in the Bering Sea which include - Bristol Bay red king crab (BBRKC), Pribilof Island red king crab (PIRKC), Norton Sound red king crab (NSRKC), Western Aleutian Island red king crab (WAIRKC), and northern district red king crab (Figures 1 and 2). The first four populations are managed as separate stocks under isolated federal and state co-management.

### Section 1: Genetic information

There have been a few studies focusing on red king crab genetics in Alaska water. Two of the most recent ones both examine evolutionary linkages for red crab in Alaskan waters - including the Bering Sea, Aleutians, Gulf of Alaska and Southeast Alaska (Vulstek et al. 2013, Grant and Cheng 2012, Figure 3a). Genetically red crab populations in the Western Aleutians and Norton Sound are isolated from the rest of the Bering Sea. Three genetic clusters resulted in both studies: Norton Sounds and western Aleutian Islands, southeast Bering Sea and Gulf of Alaska, and southeast Alaska (Figure 3b).

The Western Aleutian Island red king crab and Norton Sound red king crab populations are currently considered isolated populations and are fished as such. Genetic studies confirm this separation.

The Bristol Bay red king crab population clusters genetically with PIRKC and the western Gulf of Alaska populations (GOA) - specifically Kodiak. The Bristol Bay stock does show some indication that it may have undergone a recent bottleneck (reduction in genetic diversity due to low population size) using samples from 1989 and 2008, which would mean a loss of genetic diversity due to lower population size.

Overall, genetics indicates that there has been multi-generational (in genetics terms which could be 100s of years) geneflow between BBRKC, PIRKC, and other red crab in the Southeast Bering Sea and GOA. However, they cannot rule out demographically independent populations since the genetic connectivity may occur due to ice-age refuge ancestry and NOT current population gene flow. The tools in these studies are not useful in determining contemporary genetic structure, and ocean currents patterns and their interaction with larvae likely prevent large-scale mixing between populations within the Bering Sea area – specifically those in the western Bering Sea vs. southeastern Bering Sea.

The conclusions from genetic studies are that NSRKC and WARKCI are their own distinct populations due to genetic divergence and likely barriers in substantial geneflow, while the southern Bering Sea – BB, PI, and northern crab – are harder to determine current genetic linkage. More detailed genetic sampling and studies within the southern Bering Sea, paired with a seascape genetic study, may help understand the connectivity of these three stocks.

### Section 2: Non-genetic information

- Size compositions, growth, recruitment pulses (Figure 6)
- Physical barriers or oceanographic barriers
  - o Aleutian Islands Samalga Pass
  - o Norton Sound general current flow

### Section 3: History of spatial management units for Bering Sea red king crab

- History of these “stock” areas
  - o Established as historical fishing areas - BBRKC, PIRKC, WAIRKC, NSRKC
  - o Original boundaries drawn with help of historic fishery information and landmarks to help delineate fishing areas.

### Section 4: Summary and future work recommendations

The status of this document is in draft form, more work is needed to summarize current stock trends (biomass and recruitment) over the entire Bering Sea, specifically those 3 stocks in the southeastern Bering Sea. At this time the analysts believe it would be helpful for this stock structure template to focus on the southeastern Bering Sea stocks - BB, PI, and Northern district - since genetic and landscape data indicates separate stock structure for NSRKC and WAIRKC. Of these three stocks the Northern district is the one with the least known about it since it is not part of a current stock assessment. Figure 5 has size composition trends that include Northern district crab, but further analysis of the survey data is needed.

Future work to assist in understanding the connectivity of the BB, PI and Northern district crab should include:

- Bering Sea specific genetic studies with increased sampling locations and genetic tools, potentially utilizing seascape genetic analysis.
- Analysis of oceanographic information for the area - current flow, temperature, etc. - to determine potential linkages.
- Tagging data -specifically between BB and the Northern district. A summary of data currently available and future tagging needs.

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

<u>Factor and criterion</u>	<u>Justification</u>
<b>Harvest &amp; Trends</b>	
Fishing mortality (5-year average percent of F <sub>abc</sub> or F <sub>ofl</sub> )	bbrkc - close to F <sub>ofl</sub> 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)	
<b>Barriers &amp; phenotypic characters</b>	
Generation time (e.g., >10 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)	??
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)	?
Meristics (Minimally overlapping differences in counts)	?
<b>Behavior &amp; movement</b>	
Spawning site fidelity (Spawning individuals occur in same location consistently)	??
Mark-recapture data (Tagging data may show limited movement)	Some tagging available for BBRKC stock (need a summary of this)
Natural tags (Acquired tags may show movement smaller than management areas)	??
<b>Genetics</b>	
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.

References:

Grant, W. S., and W. Cheng. 2012. Incorporating deep and shallow components of genetic structure into the management of Alaskan red king crab. *Evolutionary Applications* 5: 820-837.

Grant, W.S., et al. "Phylogeography of red king crab: implications for management and stock enhancement." *King Crabs of the World*, edited by Bradley Stevens, CRC Press, 2014, p.47-72.

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

Vulstek, S.C. et al. 2013. Spatio-Temporal population genetic structure and mating system of red king crab (*Paralithodes camtschaticus*) in Alaska. *Journal of Crustacean Biology* 33(5): 691-701.

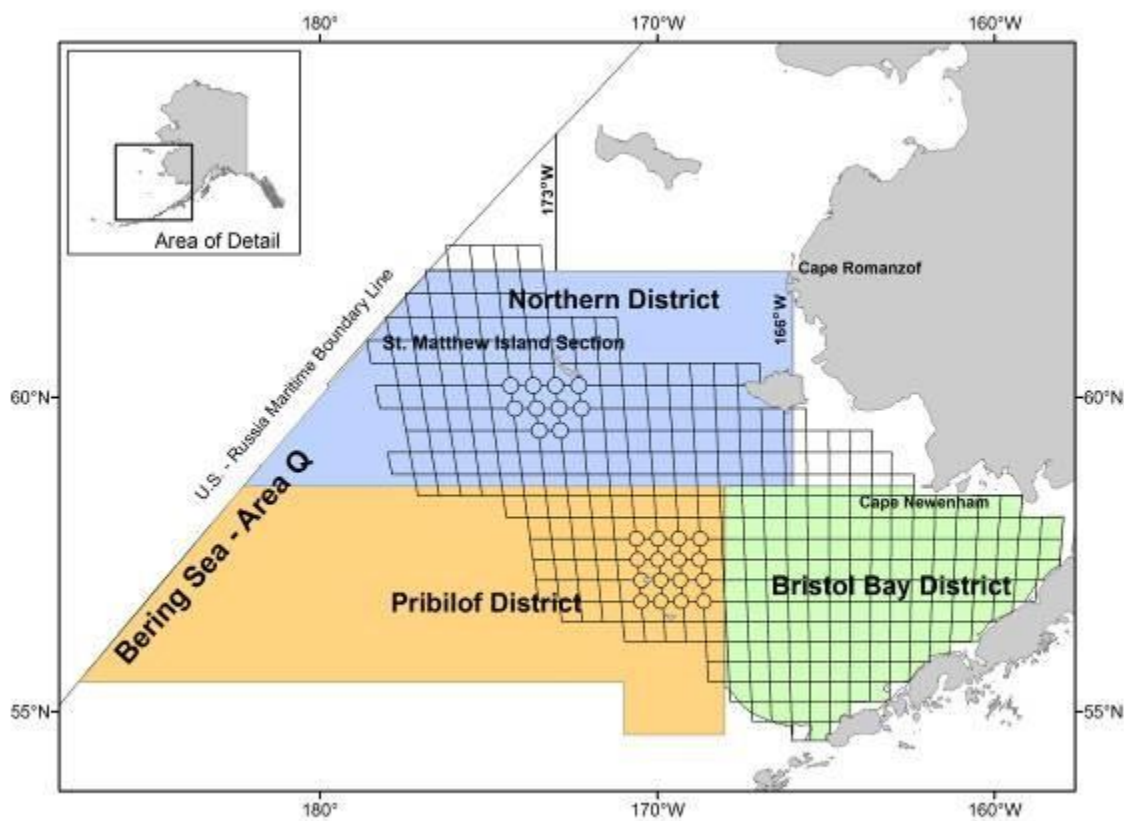


Figure 1. Bering Sea management areas (BBRKC, PIRKC, and Northern district), along with NMFS trawl survey stations. This figure does NOT include NSRKC or WAIRKC.

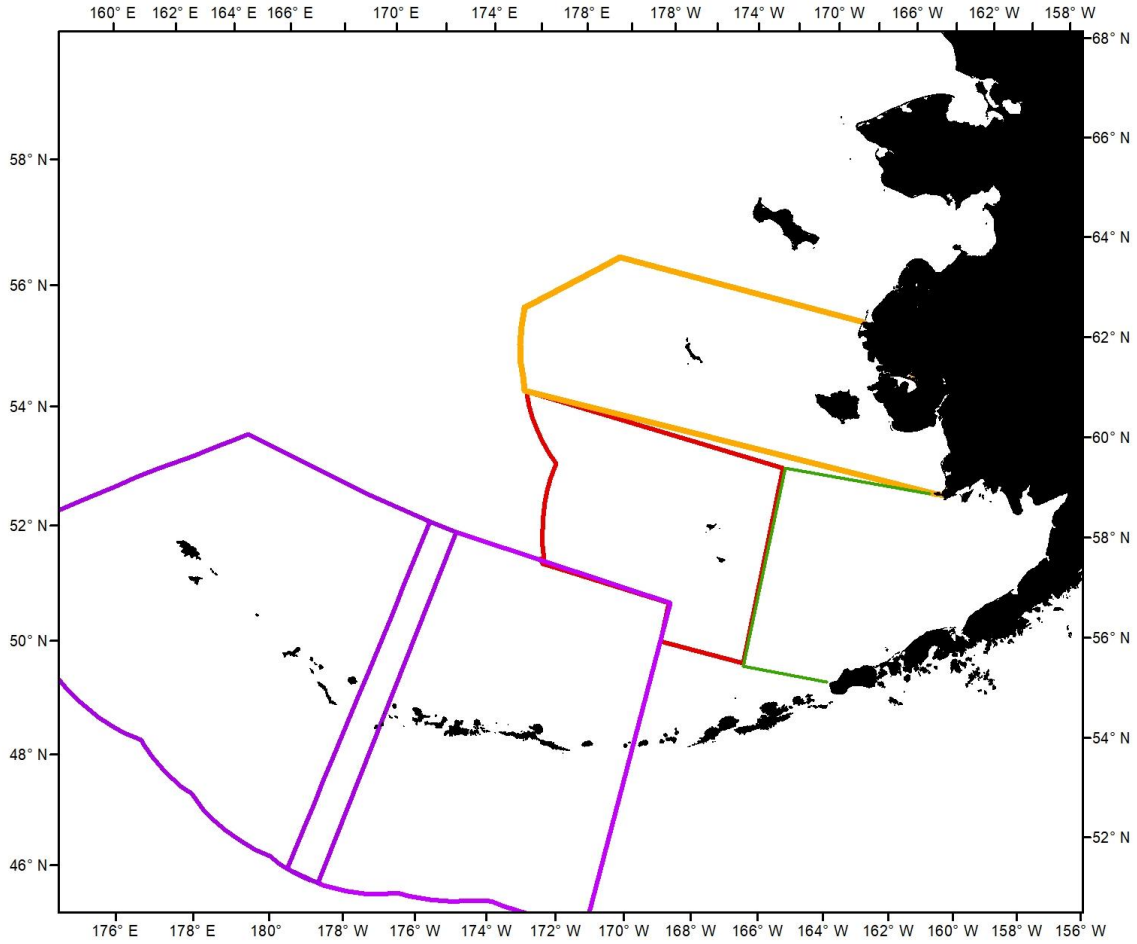


Figure 2. High level overview of some Bering Sea management areas (BBRKC - green, PIRKC - red, Northern district - yellow, WAIRKC - purple).

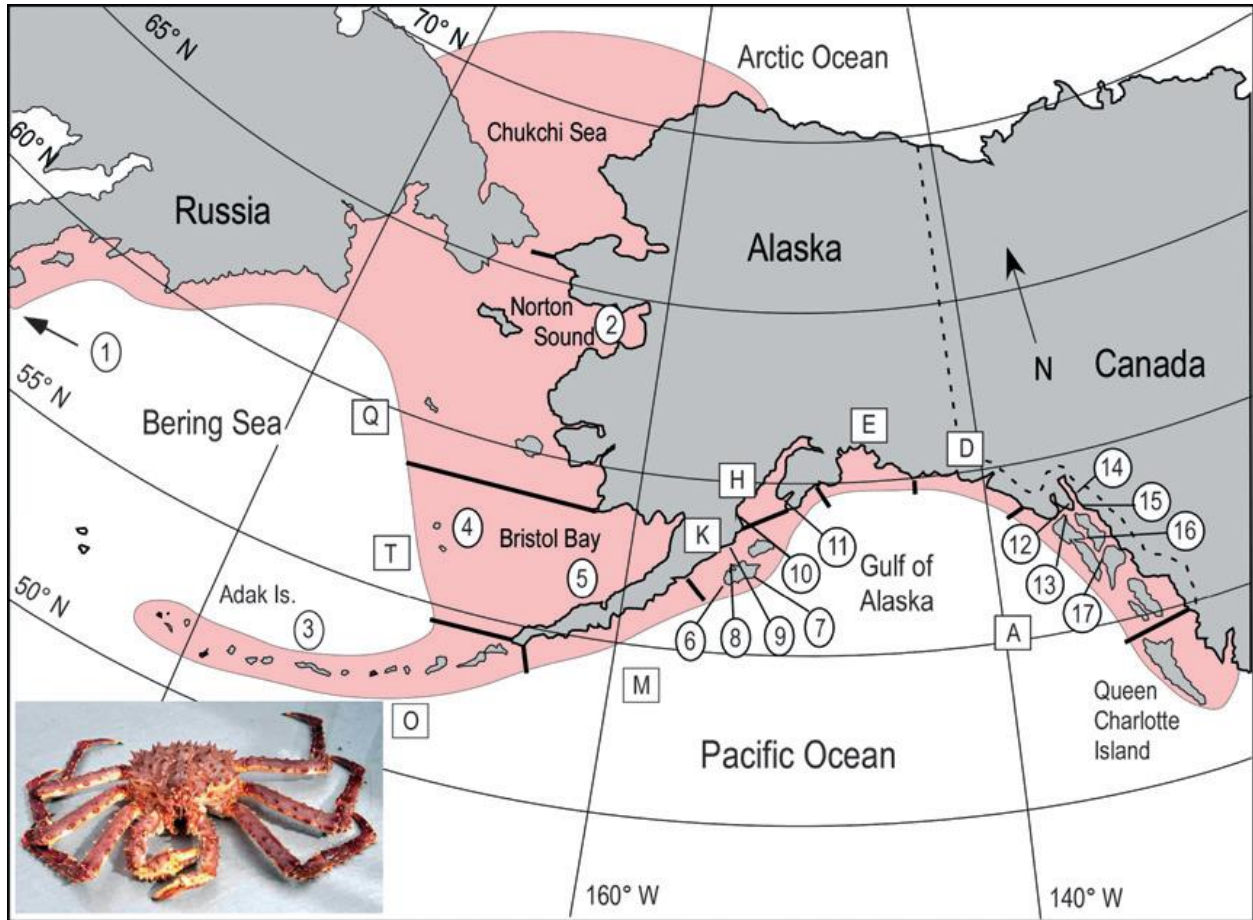
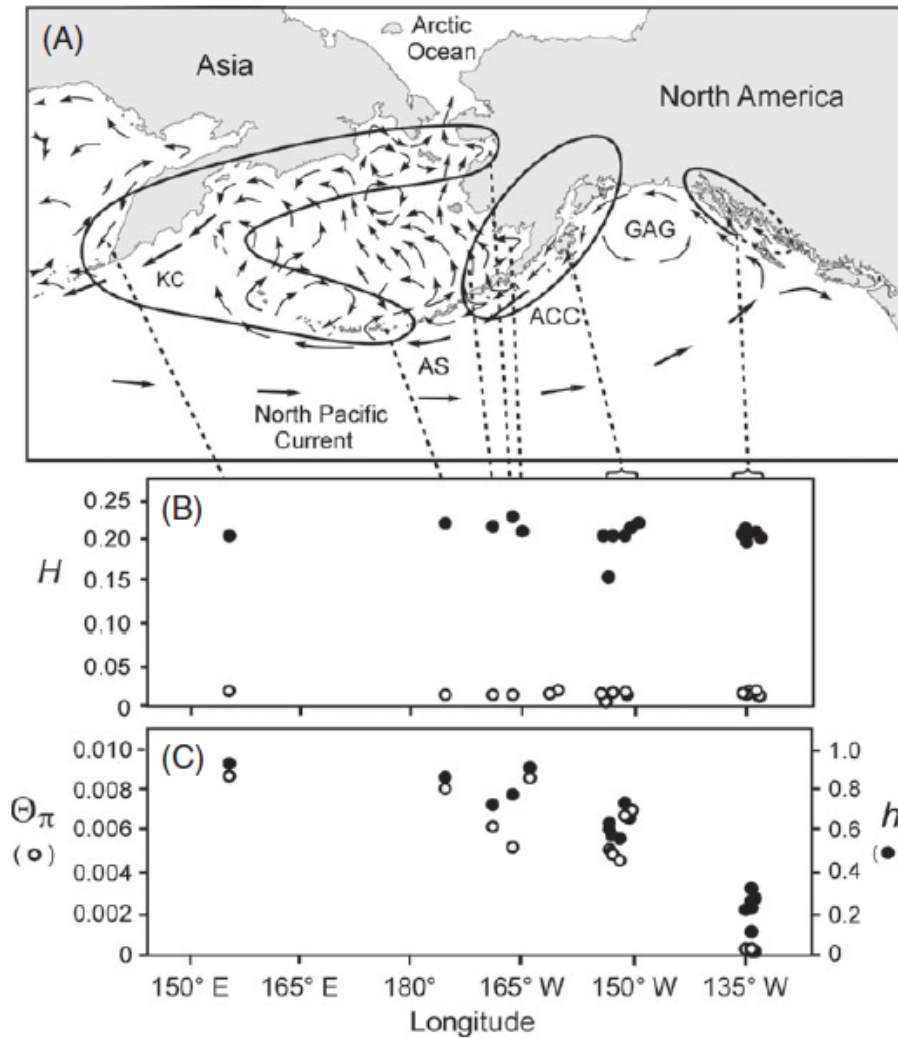


Figure 3a. Map of the Bering Sea and Gulf of Alaska showing the geographic distribution of red king crab (red) and locations of samples. Numbers in ovals represent sample locations, and letters in squares represent State of Alaska harvest management areas (registration areas). Thick lines indicate management area boundaries (Source: Grant and Cheng 2012).



**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.

Figure 3b. Genetic groupings and generalized current patterns (Source: Figure 2 from Grant and Cheng 2012).

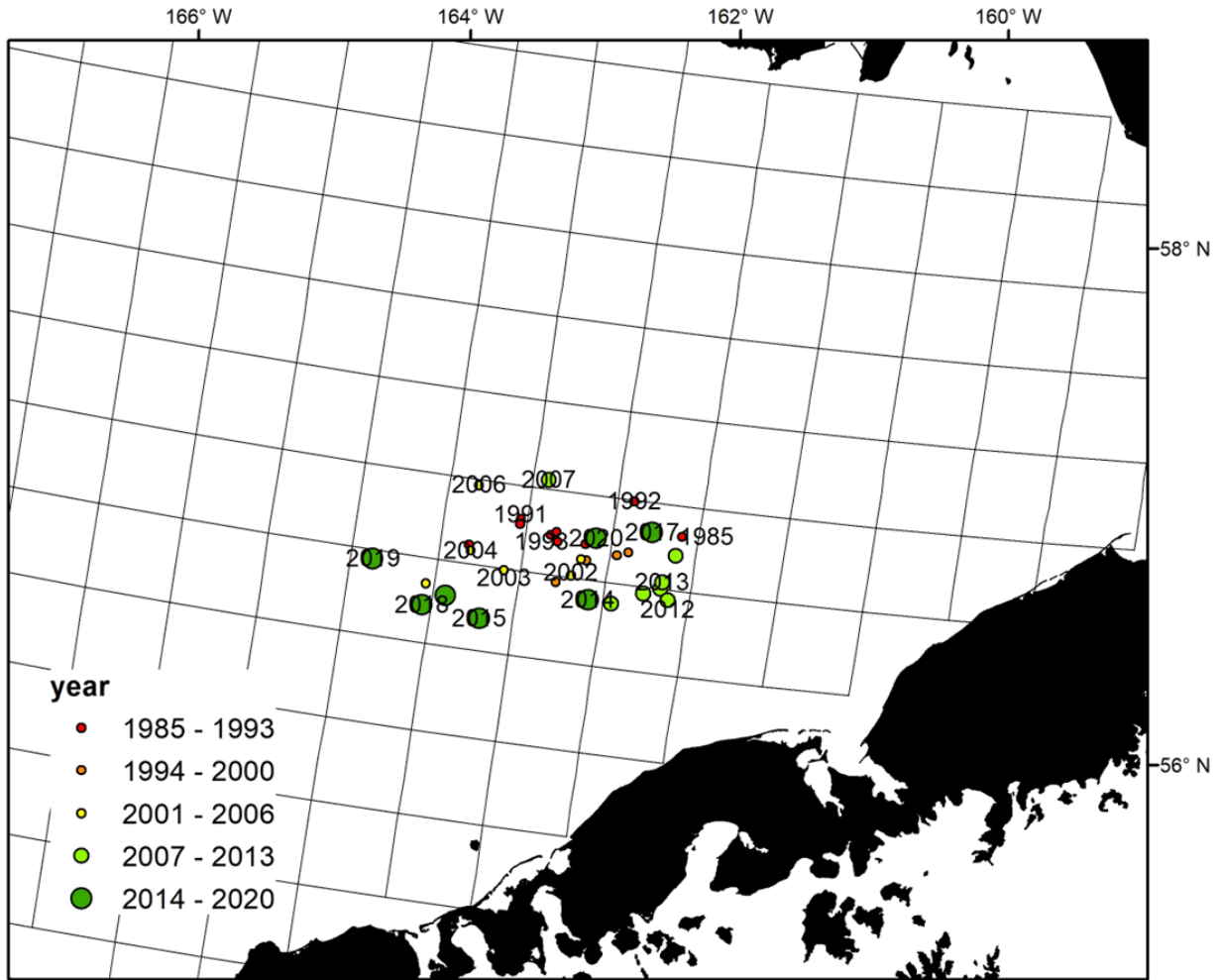


Figure 4. BBRKC weighted centers of catch over time, fishery was closed in 2021/22 and 2022/23 seasons (Source: September 2021 CPT presentation by B.Daly, ADF&G).



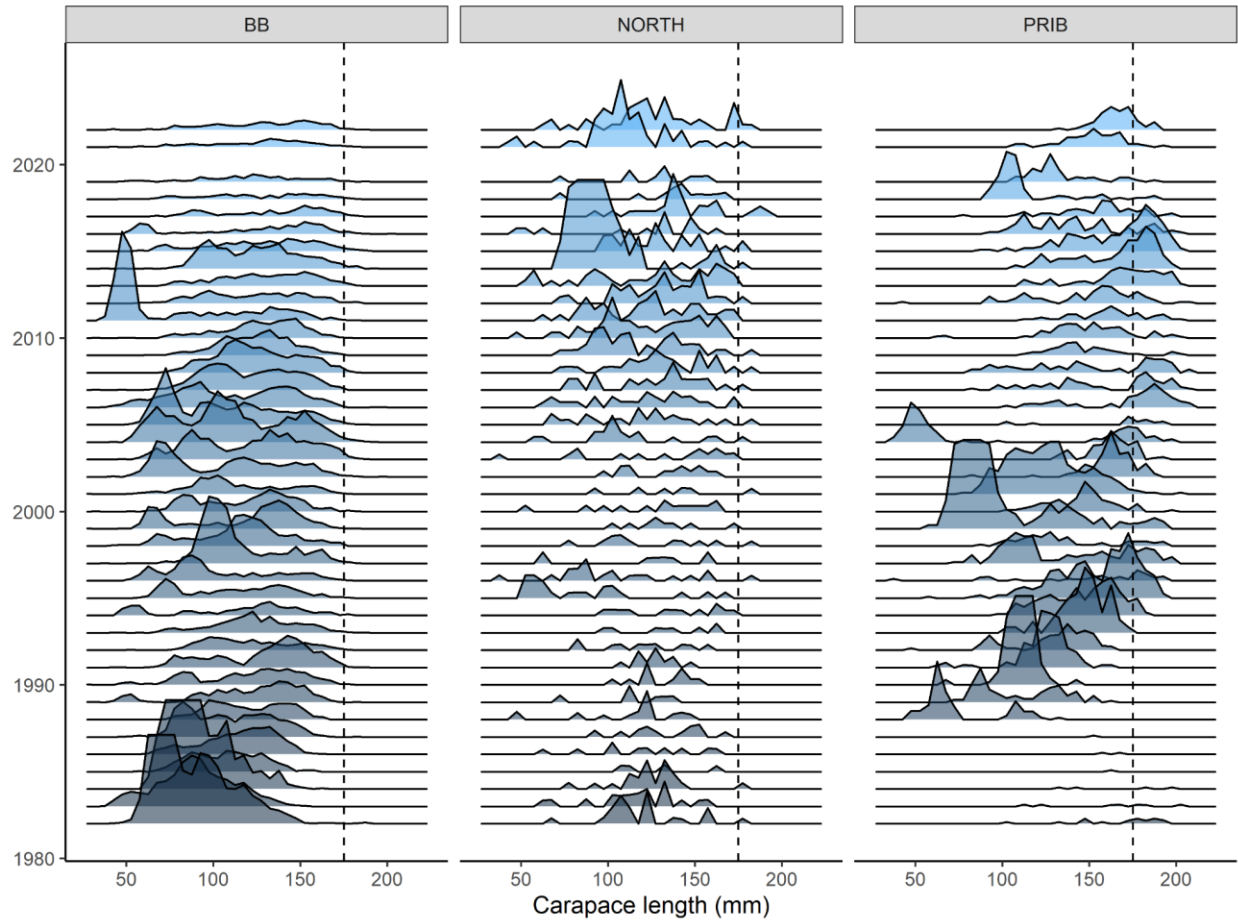


Figure 5. Six composition comparisons over time for BBRKC, Northern district, and PIRKC (Source: provided by Cody Szuwalski).

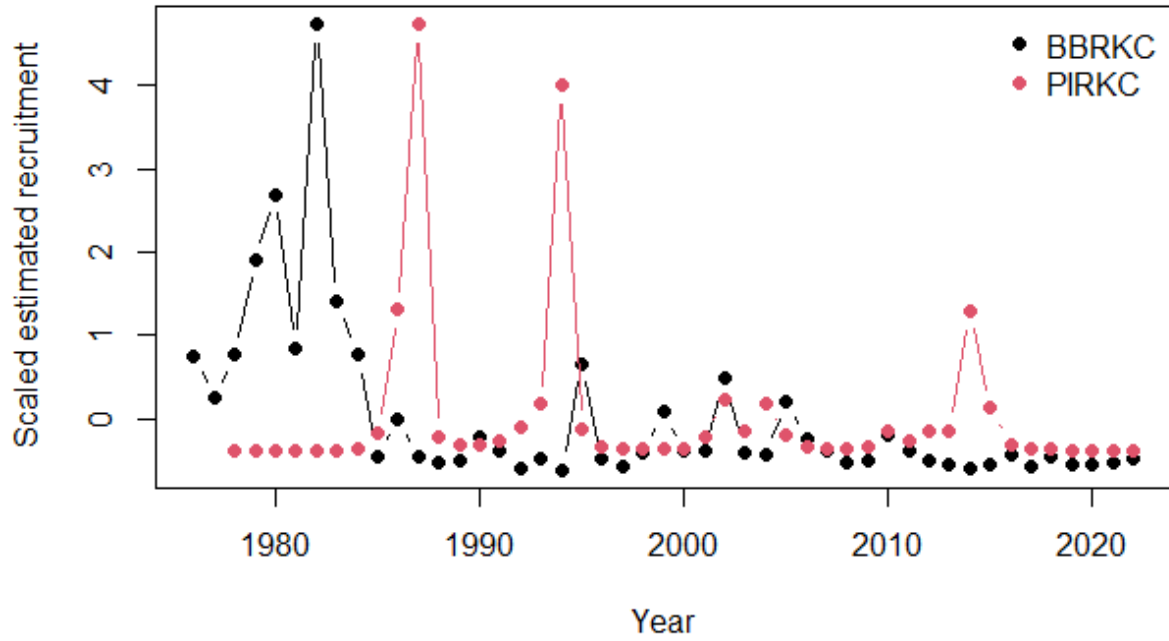


Figure 6. Scaled estimated recruitment from the stock assessments for BBRKC and PIRKC. PIRKC is advanced 2 years to account for the difference in size ranges modeled in each assessment. BBRKC starts at 67.5 mm carapace length; PIRKC starts at 37.5 mm carapace length.