

Genetic diversity in Alaska's red king crab may provide climate change resilience

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Red king crab on the deck of a research vessel. Credit: NOAA Fisheries / Erin Fedewa

New genetic research on the Alaska red king crab reveals previously undiscovered diversity among different regions, suggesting the species is

more resilient to climate change and changing ocean conditions.

Maintaining genetic diversity within and among populations is vital to ensure species are resilient to challenging conditions. Without it, a single disease or set of conditions—such as a prolonged change in ocean acidification—could drive a species to extinction.

Fortunately, new research has revealed more genetic diversity across Alaska's red king crab populations than originally documented. This suggests that the species will be more resilient in the face of changing conditions like ocean warming. However, any efforts to enhance red king crab populations need to be careful not to affect this genetic diversity.

King crab in Alaska

Historically, the red king crab fishery was Alaska's top shellfish fishery. It's embedded in the culture of Alaska's working waterfronts and king crabs have been the centerpiece of holiday feasts around the world. However, the red king crab fishery collapsed in the 1980s. Since 1983, most populations have been depressed statewide and the Gulf of Alaska fishery remains closed.

Wes Larson is co-author of the [research](#) published in *Evolutionary Applications* and the genetics program manager at the NOAA Alaska Fisheries Science Center. He reflects, "When it comes to understanding crab biomass declines and how to recover populations, we need to better understand [population structure](#) and local adaptation. There are a lot of concerned and invested fishermen, processors, and community members getting more engaged in these issues and it's propelling new and innovative research."

To dig into this need, Larson and a team of collaborators embarked on a

study to generate whole genome sequencing data on red king crab in different locations across Alaska. The benefit of whole genome sequencing over previous methods is that it's akin to reading the full story of an organism's makeup instead of just a chapter or two. This holistic approach offers more robust analysis in order to tease apart similarities and differences between locations.

New genetics research in Alaska

Traditionally, information about commercially important species comes from fisheries-dependent data (collected on commercial fishing vessels) or independent surveys (from scientific research vessels). From these, we gather data on abundance, size, sex, reproductive status, diet, etc.

Genetics tools help to fill in the information gaps from traditional surveys, and can be used to:

- Define [stock of origin](#)
- Assess local adaptation
- Document genetic diversity and inbreeding

Whole genome sequencing builds on past methods by enhancing our ability to detect important differences between populations at finer scales.

Red king crab live in diverse environments—from coastal bays in the north, to open sea shelves in the Bering Sea. They also live in small bays and fjords fed by glacial melt in Southeast Alaska and the Gulf of Alaska. King crab in Alaska generally inhabit the following five regions:

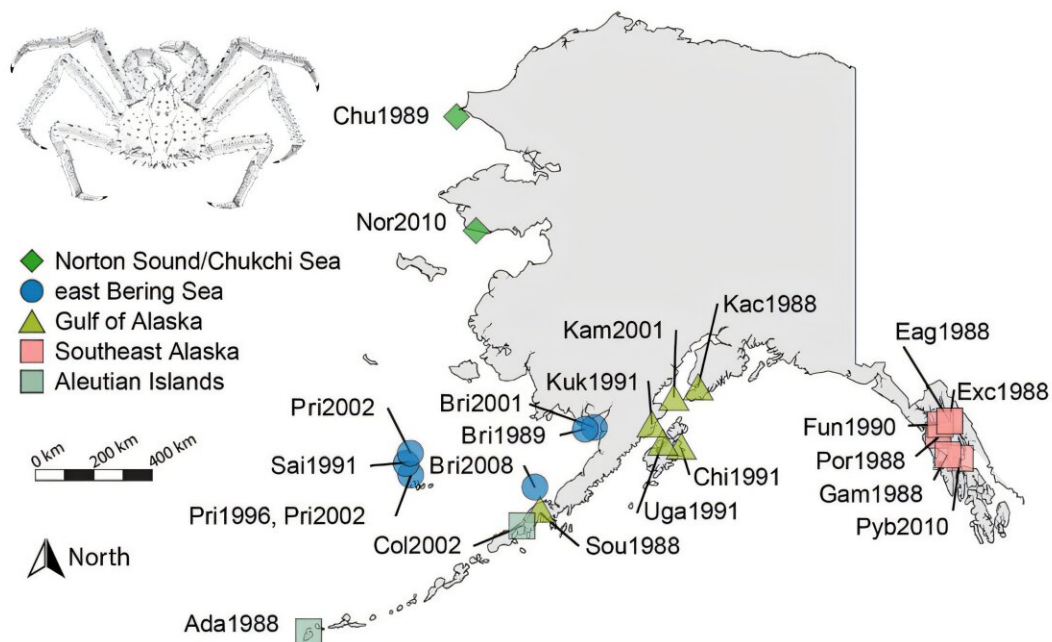
1. Southeast Alaska
2. Gulf of Alaska
3. Aleutian Islands

4. Eastern Bering Sea
5. Norton Sound / Chukchi Sea.

Previous genetic studies have hypothesized that king crab from these regions are split into three genetic groups:

1. Southeast Alaska
2. Gulf of Alaska / East Bering Sea
3. Aleutian Islands / Norton Sound.

However, these studies used older genetic techniques, which may not provide the resolution necessary to accurately define genetic structure. The current study reinvestigated the genetic structure of the red king crab in all five regions using high-resolution data derived from whole genome sequencing.



Map of collection sites and years of collections colored by regions. Credit: NOAA Headquarters

The results of this study were revealing and informative. Scientists found substantial [genetic structure](#) within populations and genetic diversity between regions. In some cases, scientists observed this diversity between populations separated by only a few hundred kilometers.

"Crabs have pelagic larvae, so this is very surprising given the potential for ocean currents to distribute these larvae long distances," said Larson. "However, these populations do not seem to be mixing and have become genetically isolated."

Ultimately, the previous hypothesis of three genetic groupings was revised by this whole genome sequencing study. This updated method provided more clarity of fine-scale genetic differences than previous methods. The data indicate that there are six, possibly seven, genetically distinct populations:

1. Southeast Alaska
2. Gulf of Alaska
3. Aleutian Islands
4. Bristol Bay
5. Pribilof Islands
6. Norton Sound / Chukchi Sea

Data showed previously unrecognized differences between the Gulf of Alaska and East Bering Sea regions. And the East Bering Sea region is split into separate Bristol Bay and Pribilof Islands populations.

Researchers also found that the Aleutian Islands and Norton Sound/Chukchi Sea regions are unique. Data suggests that Norton Sound and Chukchi Sea may be distinct as well. However, further research is required to determine if this is the case.

Scientists attribute this genetic diversity to a combination of factors including populations deriving from different glacial refugia. These are areas that remained ice-free during the Ice Age. And more recently, natural selection (genetic changes driven by adaptation) and genetic drift (genetic changes that are random) likely contributed to this diversity. The research documented evidence of local adaptation in most populations.

Fisheries management implications

The scientists' approach to sequence the [whole genome](#) of red king crabs was a more detailed method using orders of magnitude more data than previous studies.

It also confirmed that fisheries are being managed effectively by region in Alaska. For example, crab stocks in the Gulf of Alaska, Aleutian Islands, Bristol Bay, and Pribilof Islands regions are each managed separately. Prior to this new research, the Bristol Bay and Pribilof Islands were not found to be genetically distinct. This new understanding reinforces that we should continue to manage them separately.

Understanding population structure, and these newly discovered genetic signals of local adaptation, is also important for preventing overfishing on genetically unique populations. And it's critical to provide information on how local adaptations influence responses to different climatic conditions.

We may find that some populations have the potential to fare better in future climate conditions that are likely as [climate change](#) progresses. Genetics can also reveal shifts in population distribution. Some shifts may already be underway in the Bering Sea as the North Pacific warms.

Finally, with the Gulf of Alaska population being depressed, scientists

would expect a higher potential for inbreeding and lower genetic diversity. However, researchers found no evidence of reduced diversity, meaning genetic health did not suffer as the population declined. This foundation of genetic diversity means that genetic factors should not limit recovery.

This research also provides important data that can be used to inform broodstock selection for [red king crab enhancement programs](#). Enhancement programs raise young crabs in hatcheries and release them into the wild to enhance the population.

Given the genetic diversity of red king crab across Alaska, it's vital to prioritize local broodstock for enhancement before sourcing from elsewhere. This helps to keep [genetic diversity](#) intact and ensures that the genetic integrity of locally adapted populations is not jeopardized.

More information: Carl A. St. John et al, Whole Genome Sequencing Reveals Substantial Genetic Structure and Evidence of Local Adaptation in Alaskan Red King Crab, *Evolutionary Applications* (2024). DOI: [10.1111/eva.70049](https://doi.org/10.1111/eva.70049)

Provided by NOAA Headquarters

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