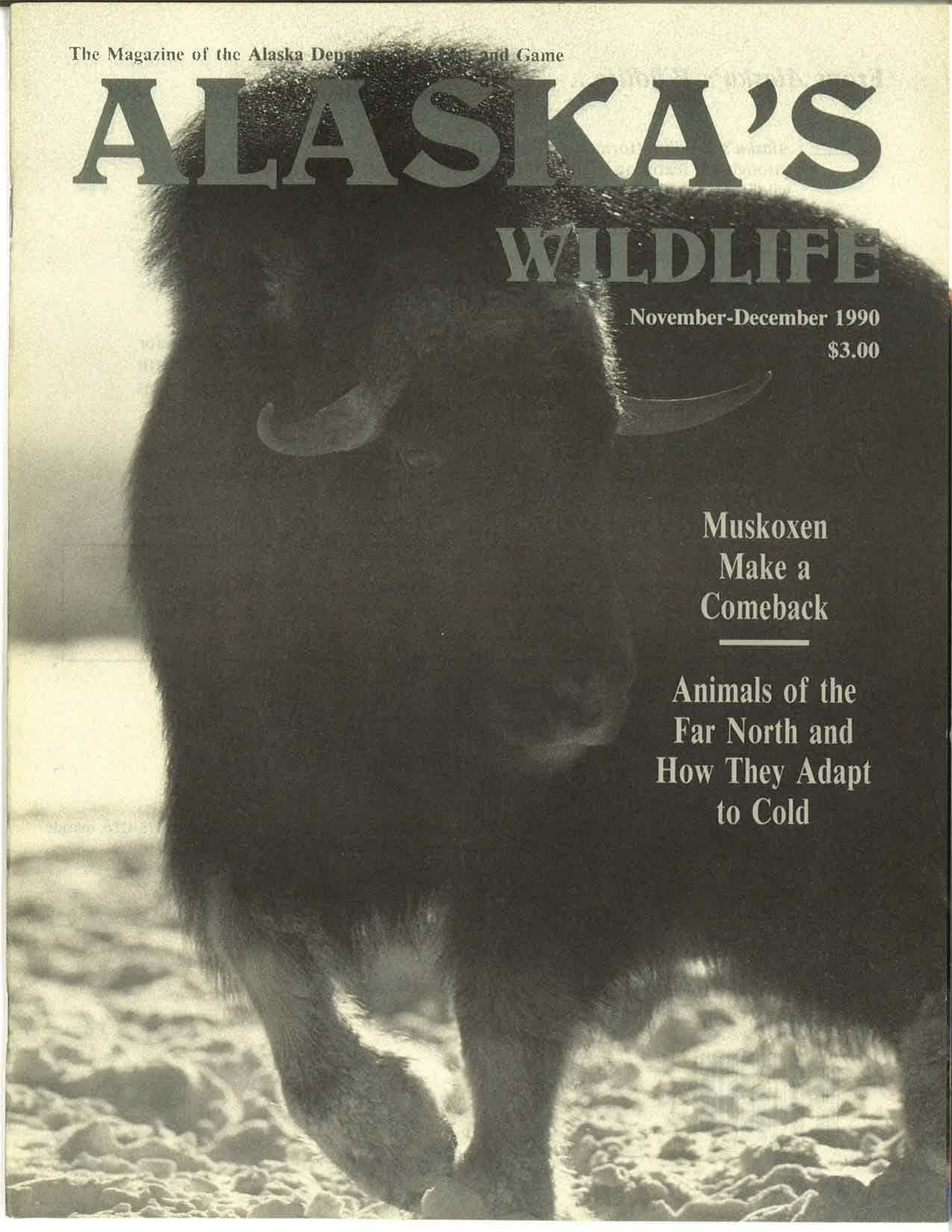
The Magazine of the Alaska Department of Fish and Game

ALASKA'S WILDLIFE

November-December 1990
$3.00



Muskoxen Make a Comeback

Animals of the Far North and How They Adapt to Cold

Red king crabs may grow to 24 pounds at about 15 years old.

Tim Koeneman, ADF&G

Genetic Studies Track the Red King Crab in Alaskan Waters

by Lisa W. Seeb, James E. Seeb, Gordon H. Kruse

Everyone knows there are genetic races of humans and breeds of dogs, but what about genetic stocks of king crabs? For the past three years researchers at the Alaska Department of Fish and Game (ADF&G) and Southern Illinois University at Carbondale (SIUC) have been investigating this question. How are the Alaska red king crabs related to each other, and further, can we look at genetic markers from a collection of crab and determine where the crab were caught? Knowledge concerning the genetic stocks of crab can help managers better set harvest strategies and determine the level of fishing pressure that stocks can sustain.

Without knowledge of underlying population genetics, management strategies for crabs could lead to permanent loss of certain stocks and could forego future harvests.

The species of king crab under study was the red king crab, *Paralithodes camtschaticus*, which is distributed in Alaskan waters from southeast Alaska, around the Gulf of Alaska and Alaska Peninsula, and north through the Bering Sea. Red king crab, historically the most valuable of the Alaska king crab resources, have experienced an extreme decline in abundance in the last decade. Statewide landings of red king crab dropped precipitously from 146 million pounds in 1979 to only 12 million pounds in 1989. To conserve this dwindling resource, commercial fisheries for red king crab were open only in limited areas during recent years.

Several laboratory techniques have been widely used to genetically characterize stocks. We used one of these, protein electrophoresis, to identify genetic markers of red king crab.

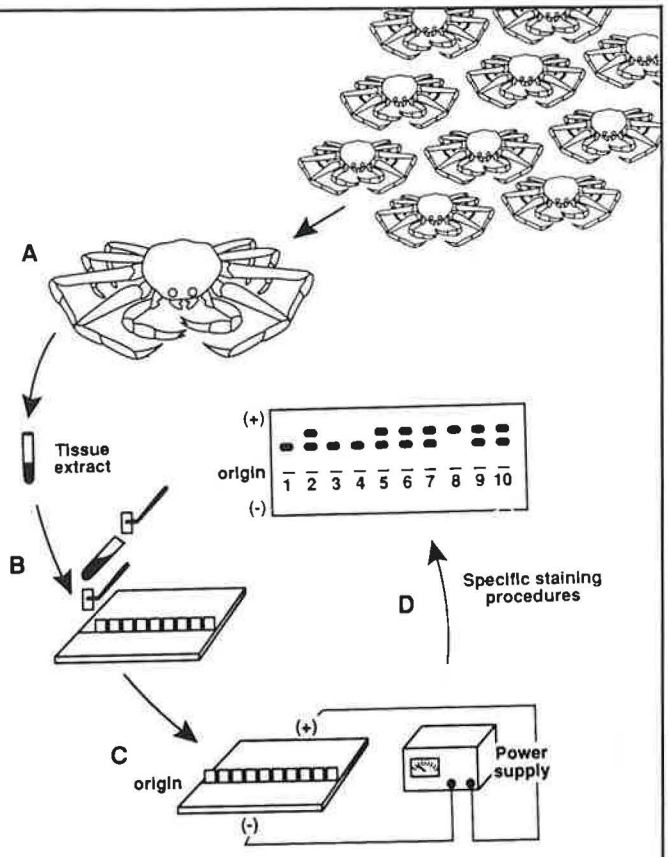


Figure 1. Standard steps in protein electrophoresis of crab tissues. (A) Enzymes are extracted from crab tissue. (B) Extracts are inserted into the starch gel with filter paper wicks. (C) The gel is connected to an electric current and enzymes move through the gel at a rate dependent on their molecular structure and charge. (D) Enzymes are visualized as bands on the gel. In the diagram the 10 crabs have three different patterns reflecting three genotypes. Adapted from Gharrett and Utter, 1982. Scientists detect genetic differences. Sea Grant Today 12(2):3-4.

This technique is similar to blood typing, but instead of determining the type or genotype of an individual for blood (grouped as A, B, AB, or O), we determine the genotype of an individual for many different enzymes.

This is the procedure we use. We obtain tissue samples of crabs in the field and bring these samples into the laboratory. First, a protein extract from each individual crab is made by homogenizing the tissue in water to release the enzymes into solution, and then this extract is absorbed onto a filter paper wick and inserted into a starch gel. An electrical current is applied to the gel for several hours, and each enzyme moves through the gel at a rate dependent on its molecular charge and structure. The positions of the enzymes in the gel appear as bands when treated with a chemical stain. Because enzymes that are specified by different genes may have different molecular properties (and hence migrate different distances in the gel), the genetic makeup for a particular enzyme can be established for each individual from the number and position of the bands on the gel (Figure 1).

To characterize a crab population, we examined between 50 and 100 individuals from each population and looked for enzymes with differences in mobility indicative of different genes. In red king crab, we detected genetic variation from eight enzymes (abbreviated as ALP, PGDH, GPI, MDH, EST, AH, LDH, and PEPLT). We then calculated the frequency of each gene observed for each of eight enzymes for all individuals in the sample. These enzyme gene frequencies are used to characterize the population, in essence creating a "genetic profile" of each crab population.

We are grateful to numerous ADF&G personnel who collected king crab tissue samples throughout Alaska during 1986-1989. Sampling sites ranged from southeast Alaska, around Kodiak Island, Adak Island, Norton Sound, where researchers cut through the ice to set and recover crab traps, and as far north as the Chukchi Sea. Crab tissues were frozen as soon as possible and sent by air freight to SIUC geneticists who had been awarded the contract to conduct the protein electrophoresis.

The laboratory analysis revealed distinctive regional stocks of red king crab with little interbreeding between stocks. For example, southeast Alaska, Adak Island, and Norton Sound populations have different gene frequencies and, thus, distinctive genetic profiles. The genetic differences indicate that little or no migration occurs between regions. These genetic profiles for different Alaska regions are shown in Figure 2. The pie diagrams depict the gene frequencies for each of the eight enzymes examined. For example, half of a pie of PGDH would indicate that the particular form of PGDH enzyme occurred at a 50 percent frequency.

The knowledge that there are regional differences should help managers more accurately define crab seasons and fishery management units. Fishing quotas can be set for local interbreeding populations rather than for vast geographic areas. Genetically unique stocks can be conserved as valuable, irreplaceable resources. Thus, regional populations will not be overfished, and management based on genetic information can help determine the maximum sustainable yield that the population of a species can provide.

As a bonus to the basic research for improving harvest strategies and understanding the stock structure, the genetic data have proved valuable for enforcement of fishing regulations. Charged with taking red king crab from a closed fishing area in the Bering Sea last fall, the owners and skipper of a commercial crabber, *Discovery*, claimed their catch had come from Adak Island in the Aleutian chain. These charges were based on circumstantial evidence including discrepancies in the ship's log, a marked crab pot bearing the ship's name, and

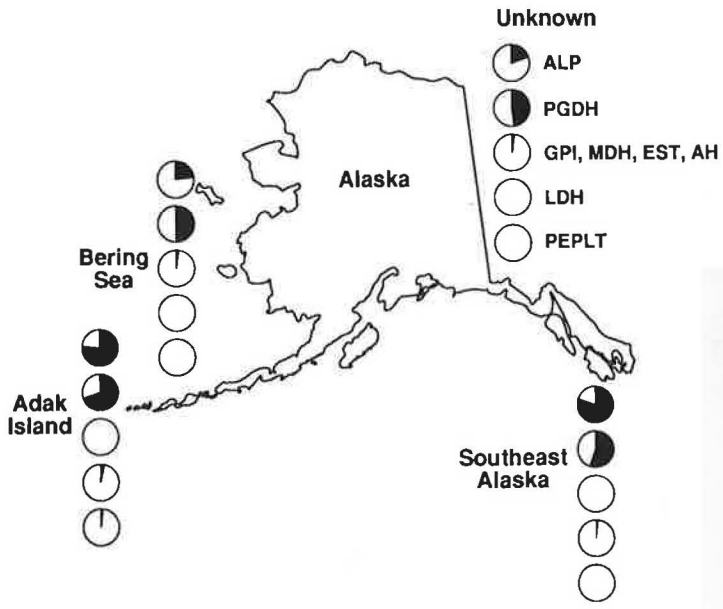
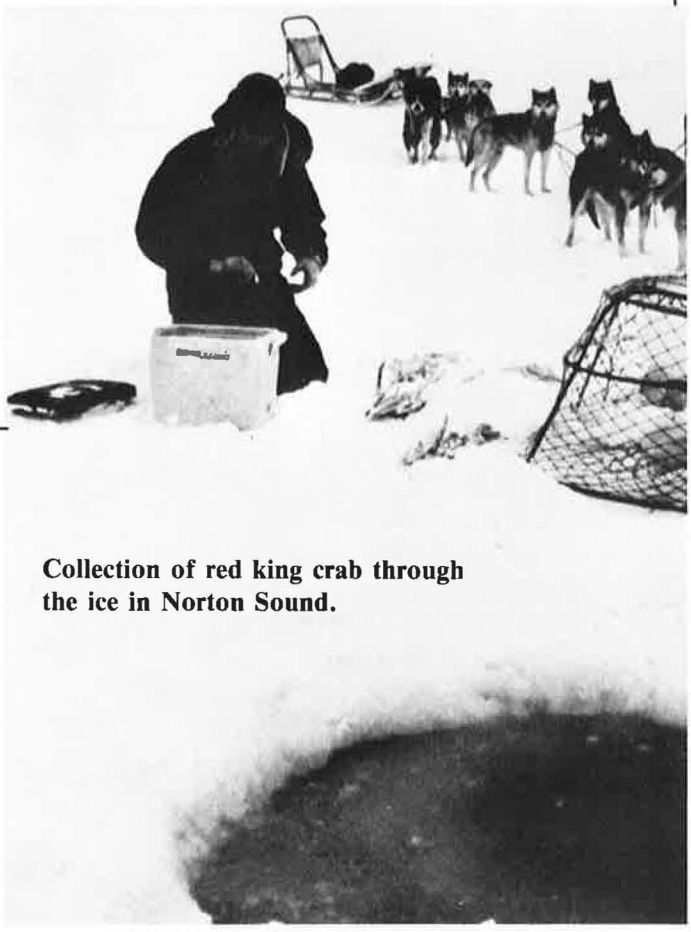


Figure 2. Pie diagrams showing gene frequencies for eight enzymes in representative collections from the eastern Bering Sea and Adak Island. Also shown are pooled frequencies from seven Southeast Alaska collections and the frequencies observed in the confiscated "unknown" sample.



Collection of red king crab through the ice in Norton Sound.

Bev LeMaster

witnesses who claimed to have seen the vessel traveling in a closed area.

Tissue samples of crabs confiscated from the *Discovery* were sent to SIUC for analysis. The genetic analysis placed the origin of the 10,600 confiscated crabs, worth $215,000, in the Eastern Bering Sea, most likely the closed waters of Bristol Bay, and not in Adak as claimed by the crabbers. The genetic profile of these unknown crabs was indistinguishable from that obtained from known Bering Sea crabs, clearly different from Adak Island stock (Figure 2). The overwhelming evidence was too much for the crabbers. They pleaded no contest in Unalaska District Court to charges of illegal crabbing. Criminal and civil penalties in the case totaled $565,000, the largest poaching settlement ever for Alaska's Division of Fish and Wildlife Protection.

Despite the interest in the *Discovery* case, the goal of the genetic analysis is to protect the resource, not to prosecute potential poachers. The knowledge by fishermen that unknown samples may be identified to population or region of origin should deter illegal fishing and improve the quality of catch statistics used to manage crab fisheries in the future.

During 1990, investigators at ADF&G and SIUC are continuing research to further genetically characterize red king crab populations within regions of Alaska. Ultimately, additional techniques including DNA-level analyses may further aid in finer stock discrimination. Staff from ADF&G have just begun to collect specimens of Tanner crab (*Chionoecetes opilio* and *C. bairdi*) and golden king crab (*Lithodes aequispina*) for analysis of the genetic structure of these commercially-important species, as well. We hope knowledge of the genetic relationships will allow managers to open fishing seasons on large resilient populations, while at the same time conserving smaller unique genetic stocks of crabs that are particularly vulnerable to depletion.

Lisa W. Seeb and James E. Seeb have worked with the Fisheries Research Laboratory and Department of Zoology at Southern Illinois University in Carbondale, Illinois. James E. Seeb was recently hired by the Fisheries Rehabilitation, Enhancement and Development (FRED) Division of ADF&G as Principal Geneticist. Gordon H. Kruse serves as Fishery Scientist with the Division of Commercial Fisheries, ADF&G, Juneau.

Contribution PP-023 of the Alaska Department of Fish and Game, Division of Commercial Fisheries, Juneau.