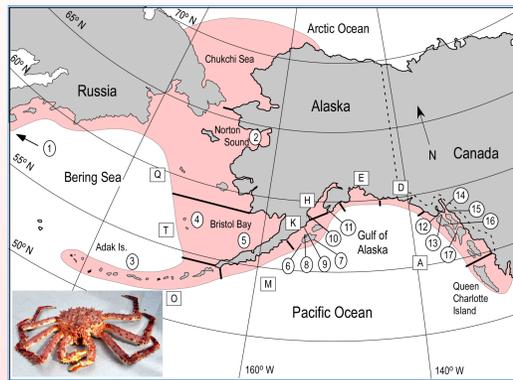


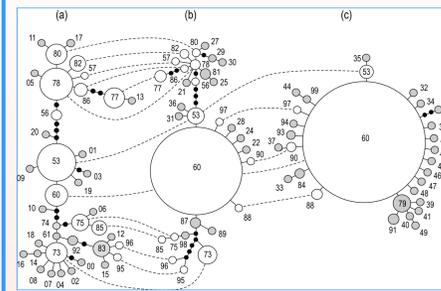
Deep and shallow genetic structure among red king crab populations in Alaska



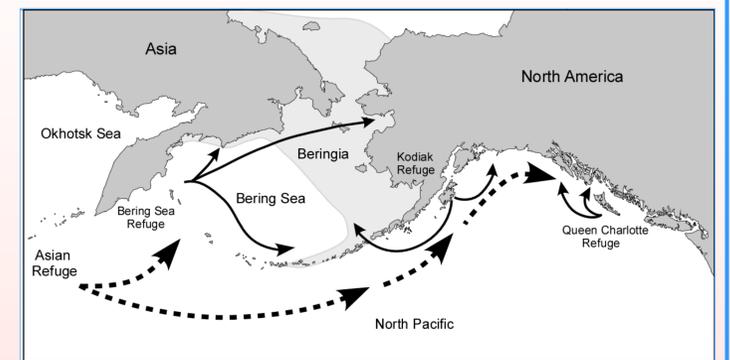
W. Stewart Grant and Wei Cheng, Alaska Department of Fish and Game, Anchorage



Distribution of red king crab samples (numbers) and Alaska harvest registration areas (letters).

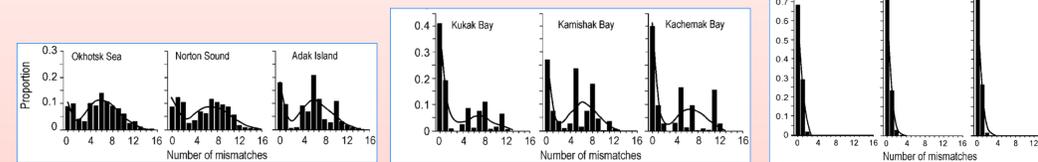


MtDNA haplotype networks of three major evolutionary groups of red king crab. Size is proportional to haplotype frequency. Open circles indicate observed haplotypes. Closed circles are hypothetical, but unobserved haplotypes. Grey haplotypes are unique to a particular group.



Phylogeography: On long time scales, Asian populations have contributed colonists to the NE Pacific. On short time scales, local refugia were the sources of colonists after the last glacial maximum.

MtDNA mismatch distributions



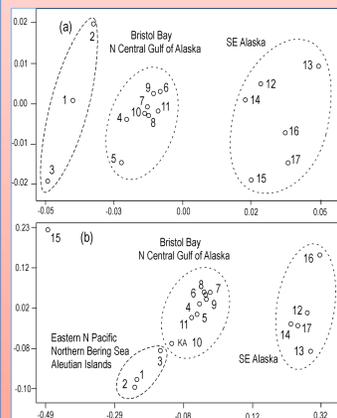
W. Pacific, N & W Bering

Kodiak Island

SE Alaska

Distributions are different among regions, indicating very different population histories.

Three major groups



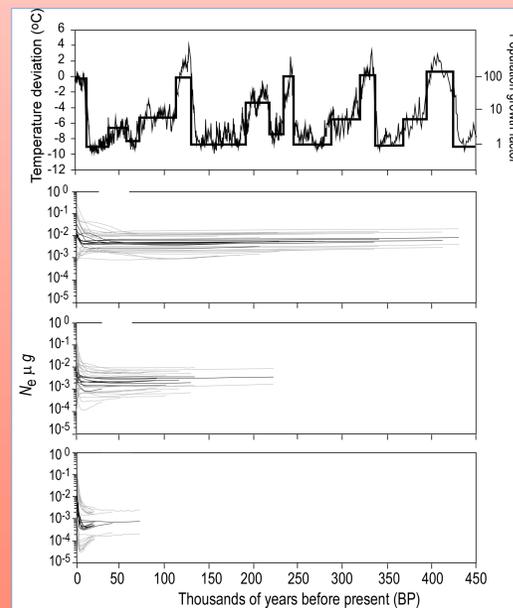
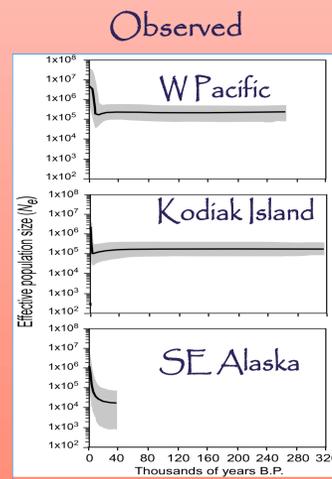
Principal coordinate plots:

SNPs (a) and mtDNA (b) show three major lineages that are significantly different from one another (AMOVA).

Northern Bering Sea and SE Alaska populations are genetically heterogeneous, but populations in the center of the range are homogeneous. The general lack of differentiation may be due to gene flow or to a post-glacial expansion.

MtDNA Bayesian Skyline Plots

Simulations



Left: Bayesian skyline plots of demographic history of three major groups of red king crab.

Right: Simulations using Pleistocene temperature model based on oxygen isotopes in Antarctic ice cores (Joucel et al 2007).

Inference: Any genetic signal of past population swings is lost after one last glacial cycle.

Conclusions:

Three major evolutionary groups of red king crab, each with different levels of mtDNA diversity and phylogeographic histories.

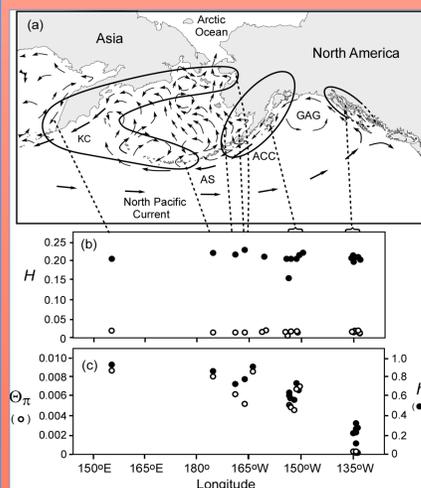
Genetic signals of population swings are lost in one glacial cycle, but genetic diversities are not affected.

Marginal populations in Bering Sea and SE Alaska are more heterogeneous than are central populations.

Harvests should be managed on a small geographical scale, as is presently implemented. Conservation goals should focus on regional groups of populations.

Thanks to Jeff Guyon & Zac Grauvogel for marker development, and to the many biologists who have collected samples over the years and extracted DNA from tissues. We also appreciate technical advice from Mike Canino and Carita Pascal.

MtDNA diversity gradient



(a) Geographical boundaries of three major evolutionary red king crab lineages.

(b) Allozymes (○) and SNP (●) do not show diversity gradients

(c) Diversity gradient in haplotype and nucleotide diversities.