Genetic Variation in Norton Sound Chum Salmon Populations

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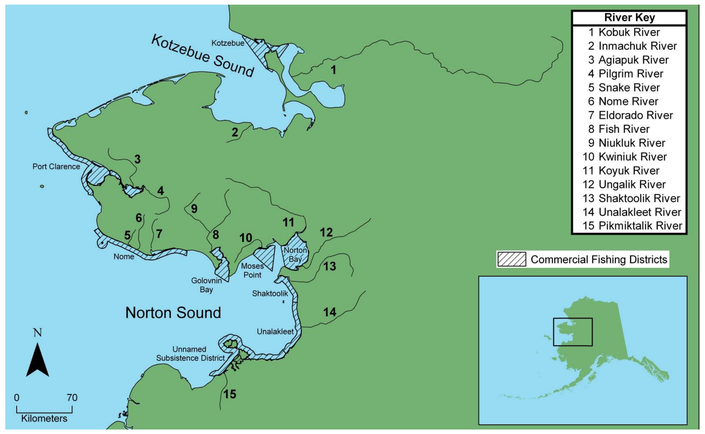
Introduction:

Norton Sound has suffered a progressive collapse in chum salmon populations since the mid 1960s that has greatly affected the lifestyle and culture of most residents. In this study, we used data from 15 populations from Norton and Kotzebue sounds at 20 microsatellite loci to evaluate factors influencing genetic diversity and determine if it has been impacted by the regional-level decline in abundance.

Objectives:

1) Evaluate spatial genetic structure and patterns of gene flow.

2) Estimate within-population variation and effective population size to evaluate genetic health.



Methods:

Sample Collection

- Chum salmon sampled from 15 locations in Norton and Kotzebue sounds. Mean sample size =146.
- Chum salmon from the Inmachuk and Agiapuk rivers are considered late run (returning late July-August); all others considered early run (returning late June through early August).

Data Analysis

Objective 1) Spatial structure and gene flow

- Phenetic clustering used to evaluate spatial genetic diversity.
- Correlation of genetic diversity with geographic proximity and run timing tested with isolation-by-distance modeling and Mantel and partial-Mantel tests.

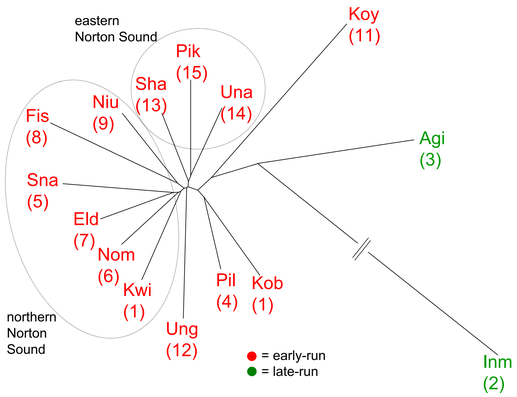
Objective 2) Genetic health

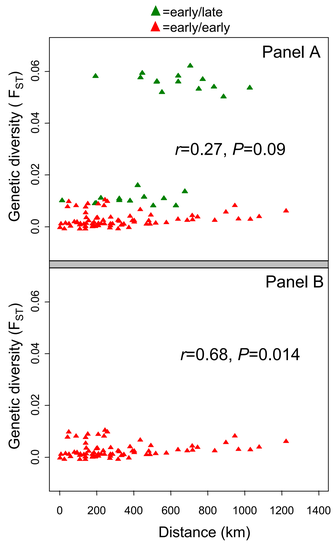
- Expected heterozygosity for Norton and Kotzebue sound populations compared to Yukon River to determine if reduced abundance has led to a regional loss of genetic variability.
- Effective population size (N_e, Wang and Whitlock method) calculated for four populations with age class data.

Results:

Objective 1) Spatial structure and gene flow

- Late-run Inmachuk and Agiapuk rivers, and the early-run Koyuk River are the most divergent. Two populations clusters correspond weakly to northern and eastern Norton Sound.



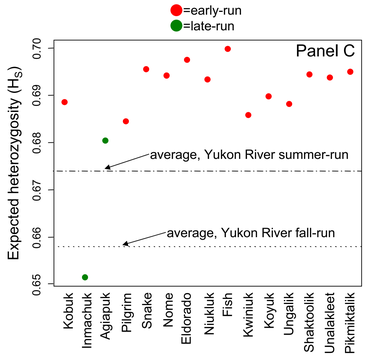


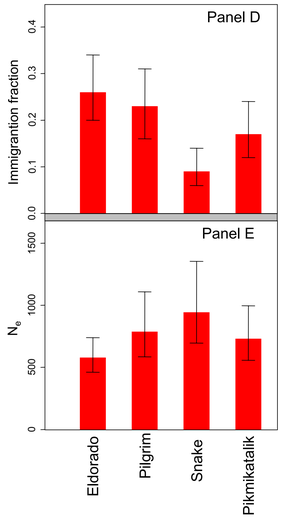
- Panel A: For all populations, correlation between pairwise genetic divergence and geographic distance measures is not significant.
- Late-run Inmachuk comparisons form a distinct cluster at F_{ST}=0.05 and Agiapuk at F_{ST}=0.015 (late-run, in green).
- Panel B: Correlation is significant when accounting for run timing (early-run populations only, in red).

Results:

Objective 2) Genetic health

- Panel C: Estimates of expected heterozygosity for Norton and Kotzebue sounds are larger (P=0.01) than 15 summer- and 14 fall-run Yukon River populations. Inmachuk River has lowest expected heterozygosity.





- Panel D: Estimates for the immigration fraction suggest that intra-population genetic diversity may be influenced substantially by gene flow.
- Panel E: N_e estimates for Eldorado, Snake, Pilgrim, and Pikmiktalik rivers are larger than values considered as general thresholds (N_e = 50 to 500) for isolated populations at risk of loss of genetic diversity.

Conclusions:

- Gene flow appears to be an important factor in maintaining genetic diversity. Maintenance of connectivity is important for long-term conservation of these populations.
- Genetic diversity could be monitored in these populations. Periodic examination could help identify trends in genetic diversity that may compromise genetic health or to evaluate conservation or management actions.

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