

EPA BRISTOL BAY SOCKEYE SALMON PORTFOLIO

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The proposed Pebble Mine would result in direct, secondary and cumulative impacts to fish and fish habitat within the watersheds of the North Fork Koktuli River, South Fork Koktuli River, and Upper Talarik Creek. This document includes 13 figures to describe the Sockeye Salmon portfolio as well as the habitat portfolio in the Project area. Four of the figures are from the Project's EIS or Project GIS data. Nine of the figures are from the scientific literature.

Sockeye salmon from Bristol Bay comprise one of the most valuable commercial fisheries in North America and produce relatively consistent returns due to the high degree of population diversity found within the species and region (Hilborn et al. 2003; Wood et al. 2008; Schindler et al. 2010). A major component of this population diversity is associated with the diversity of habitats used for spawning and has resulted in the formation of distinct spawning ecotypes (Quinn et al. 1995; Lin et al. 2008).

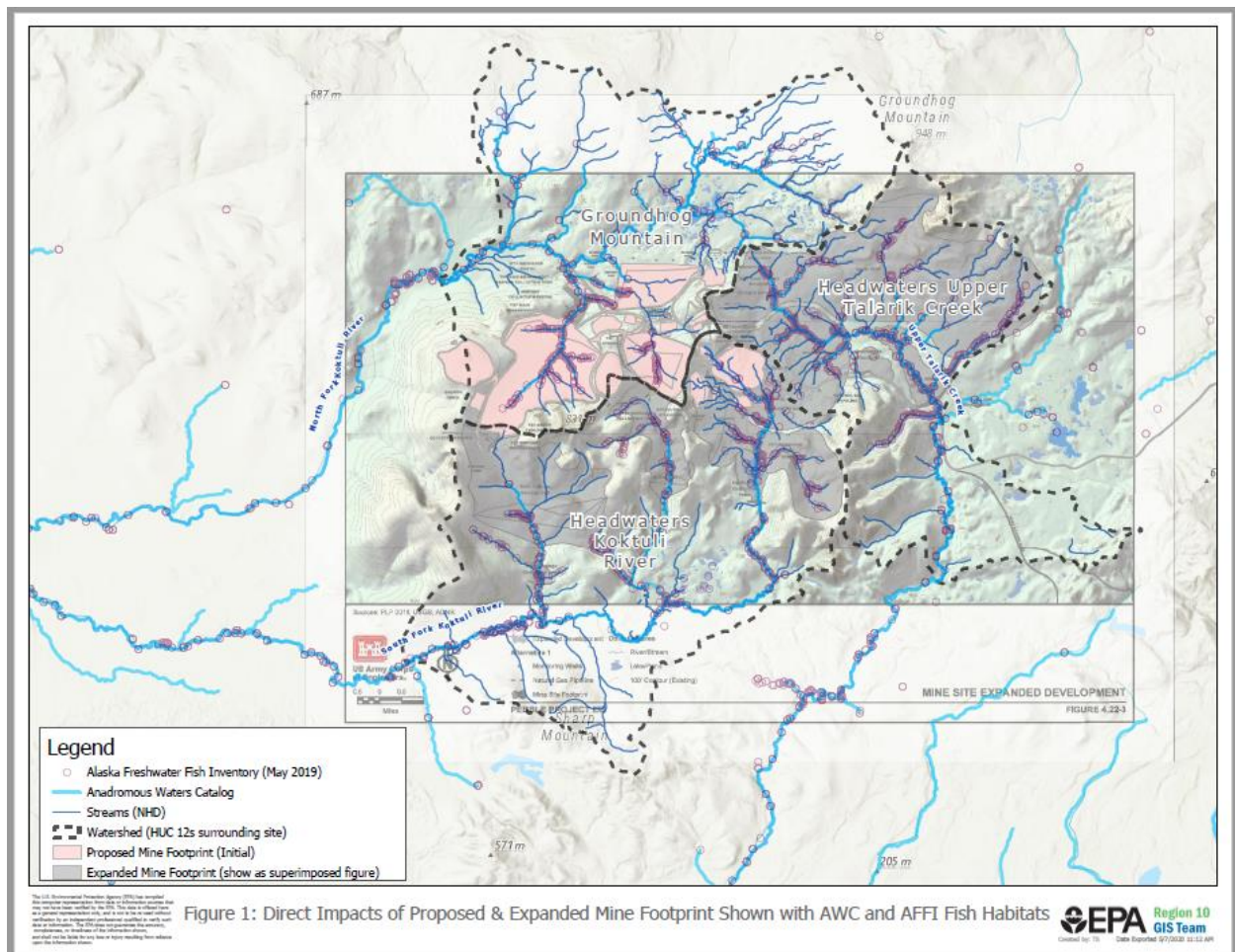


FIGURE 1: Figure 1 includes the USGS National Hydrography Dataset (NHD) stream network and 12-digit hydrologic unit Codes (HUCs). The State ADF&G Anadromous Waters Catalog (AWC) and Alaska Freshwater Fish Inventory (AFFI) data are also displayed. The figure also includes the initial and expanded (superimposed) project footprints.

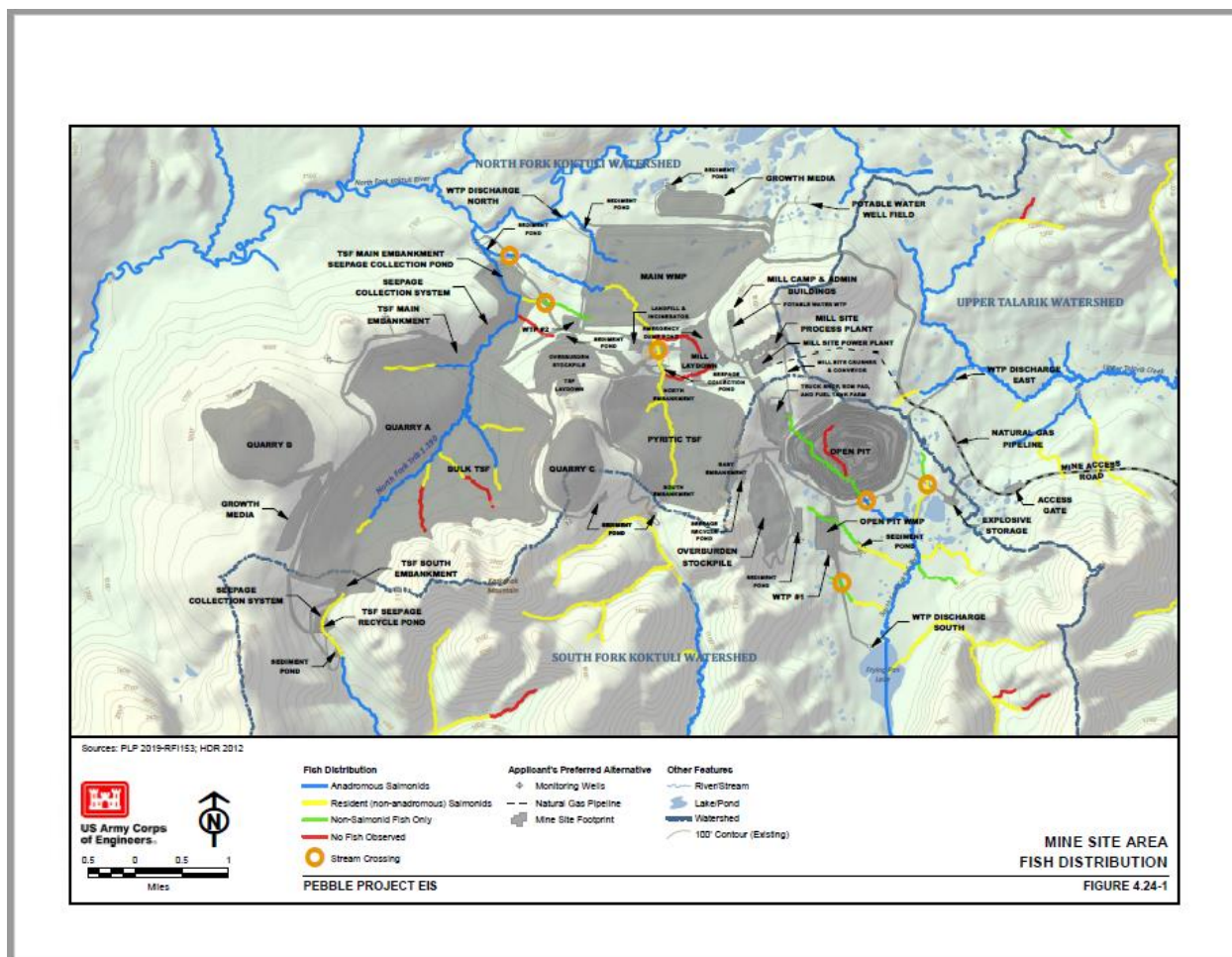


FIGURE 2: This figure is from the EIS (Figure 4.24-1) and depicts the results of baseline fish sampling in the project area. It does not depict the entire stream network from the NHD or the high-resolution stream channel network developed for the project, suggesting that not all project-area streams were sampled for fish presence. Development of the high-resolution stream network resulted in a 36 percent increase in the estimated stream miles within the initial project footprint from 73.2 in the DEIS to 99.7 in the PFEIS.

Figures 3 and 4 are taken from the PFEIS and show some of the Project's baseline data for salmon spawning downstream of the proposed mine site in the North Fork and the South Fork Koktuli rivers. Both figures also depict how salmon spawning activity is associated with groundwater inputs. Figures 1, 2, and 3 identify salmon spawning within the initial project footprint. The spawning habitat in downstream reaches in both the NFK and SFK would be altered by reductions in groundwater inflow, changes to the daily and seasonal discharge, increases in water temperature, alteration of the chemical signature of the water and the spawning substrate. For example, late winter discharges within the NFK Reach C will be dominated by treated effluent during a critical period for egg incubation and fry emergence.

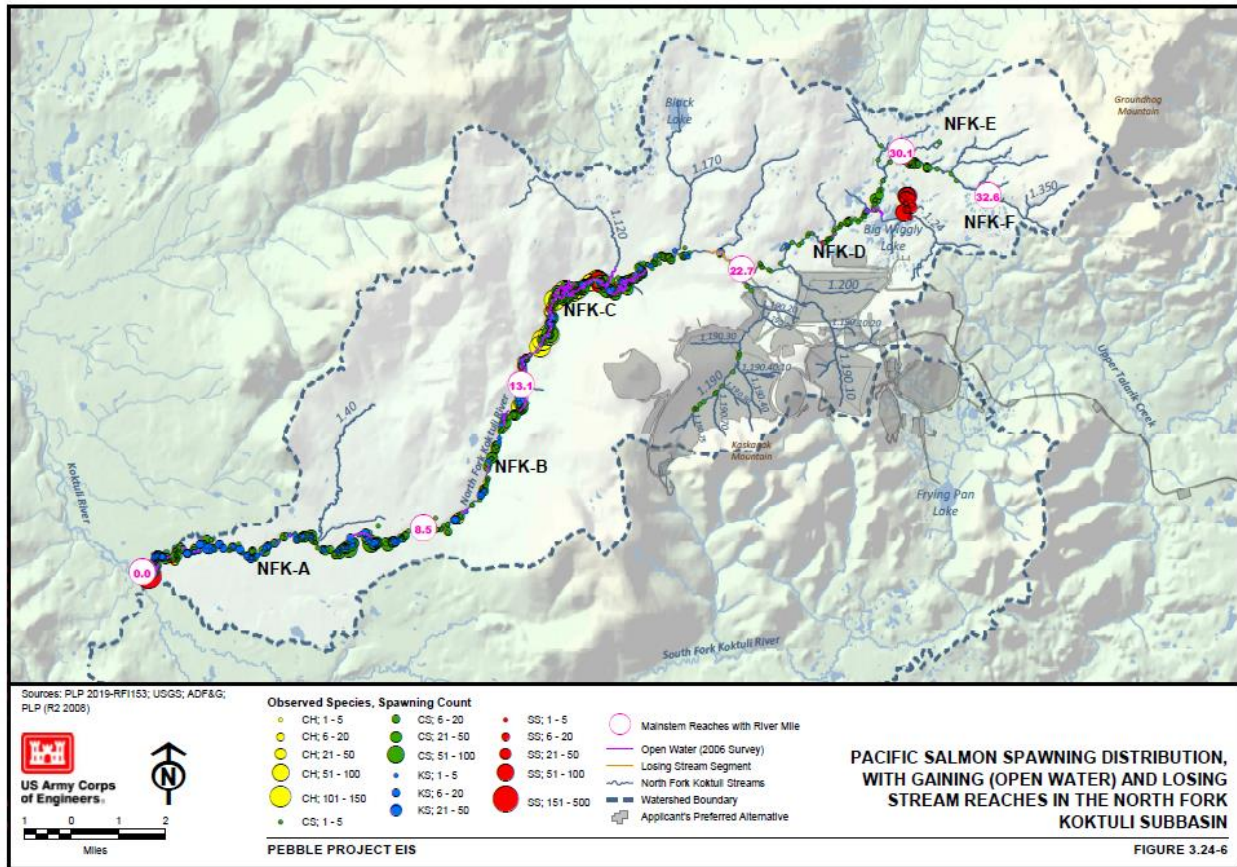


FIGURE 3: North Fork Kottuli Spawning (Source: PFEIS Figure 3.24-6)

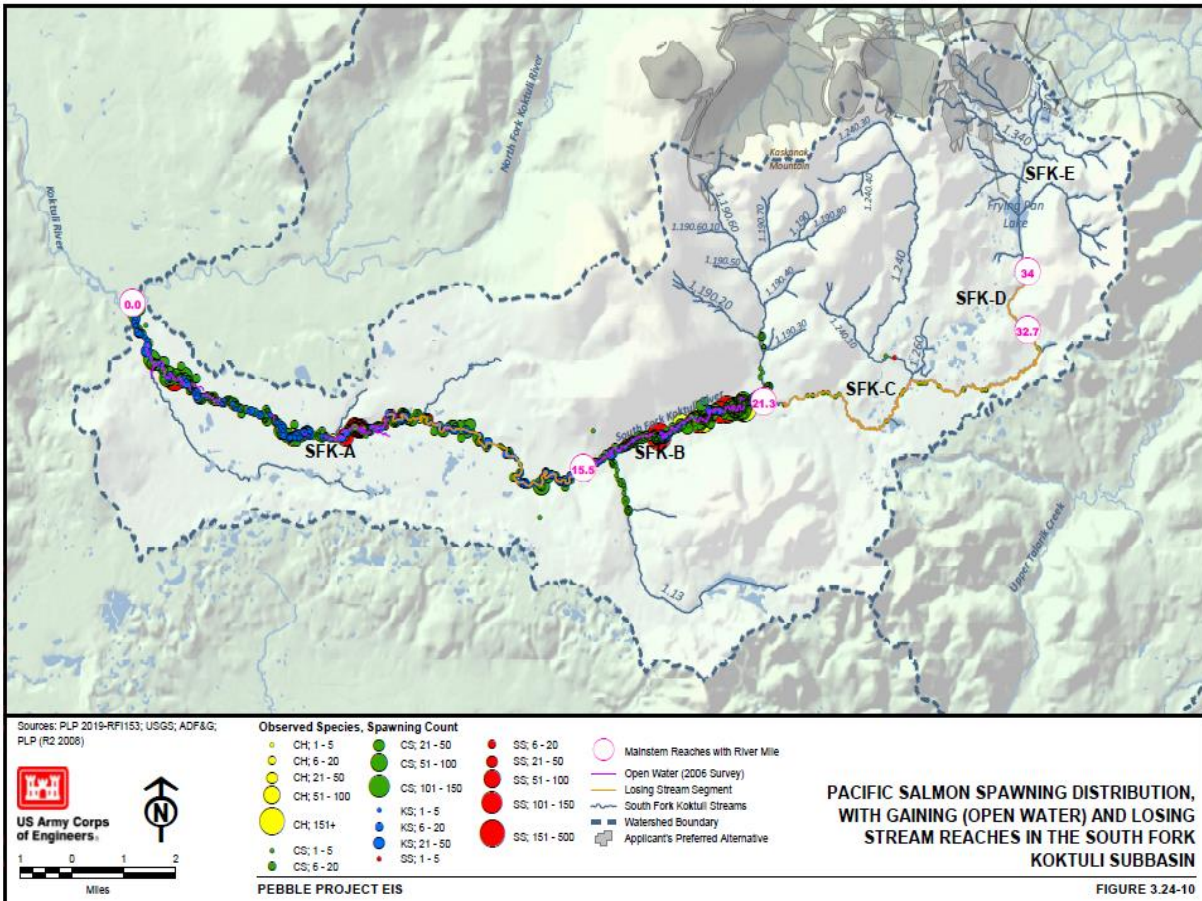


FIGURE 4: South Fork Kaktuli Spawning. (Source: PFEIS Figure 3.24-10)

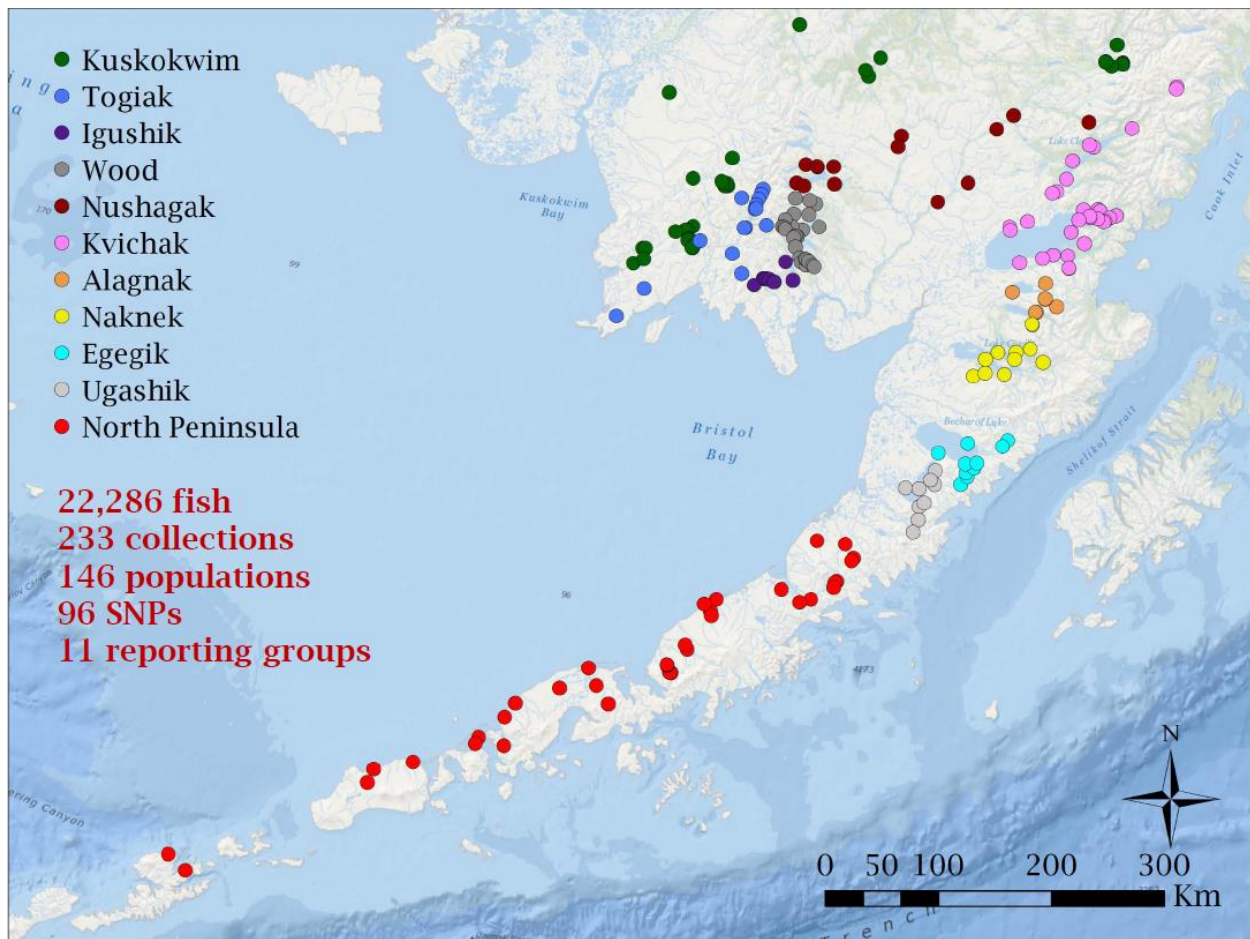


FIGURE 5: Bristol Bay Genetic Stocks. (Source: Dann et al., 2018)

This figure depicts the eleven genetic reporting groups, also found at:

https://www.adfg.alaska.gov/index.cfm?adfg=fishinggeneconservationlab.bbaysockeye_baseline

These 11 reporting groups (stocks), are the nine major drainages of Bristol Bay and the two flanking regions (North Peninsula to the south and Kuskokwim to the north) believed to potentially contribute to the Bristol Bay fishery.

The genetic baseline is assembled by sampling of spawning populations contributing to the fisheries. In Bristol Bay, the baseline has recently increased from 96 populations to 146 distinct populations that range from the Kuskokwim River (to the north) to the Aleutian Islands (to the south). These baseline fish are genotyped with molecular markers called single nucleotide polymorphisms (SNPs).

The population information for the 2009 baseline report (Dann et al 2009) is included in Appendix 1, on page 94 (page 84 of report) of the pdf available here:

<http://www.adfg.alaska.gov/FedAidPDFs/FMS09-06.pdf>

ADF&G Genetic Stock Powerpoint:

http://www.adfg.alaska.gov/static/fishing/PDFs/research/bristolbay2006-2008harvest_stock_comp_print.pdf

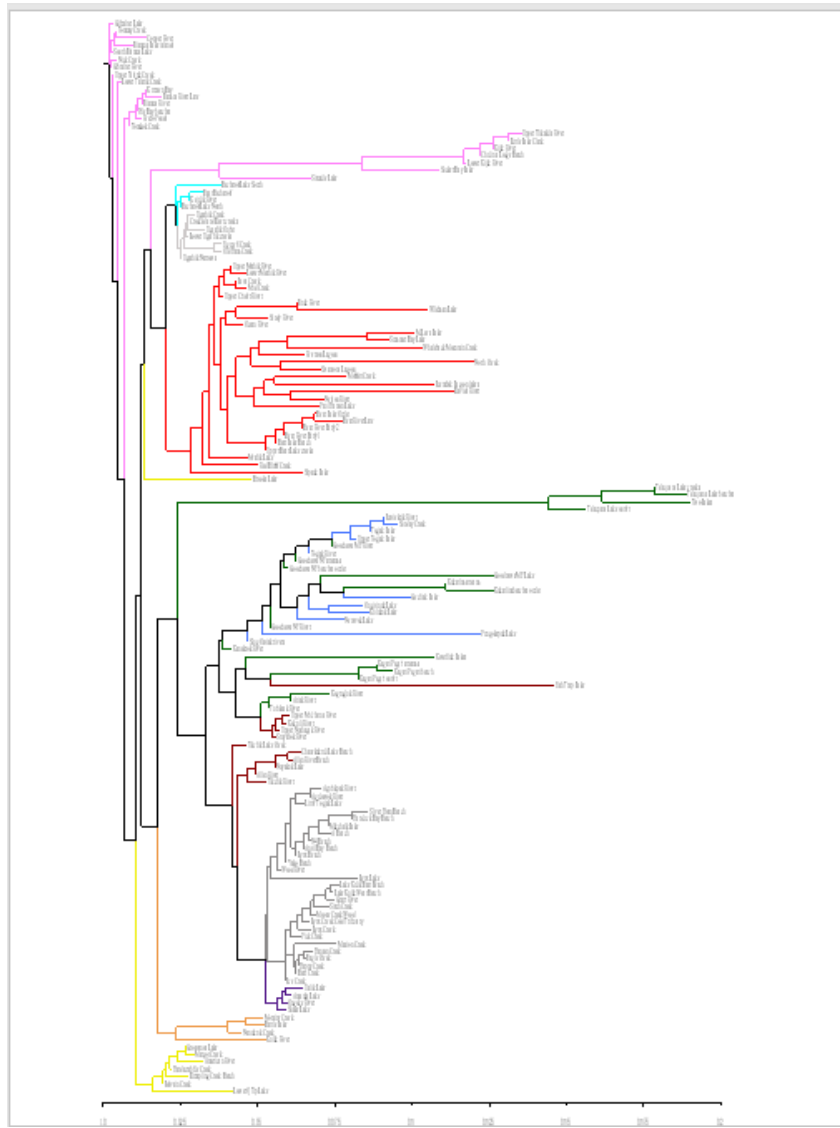


FIGURE 6: (Source: Source: Dann, T. H. *In prep.* An updated genetic baseline for Bristol Bay sockeye salmon. Alaska Department of Fish and Game, Fishery Manuscript Series No. XX-XX, Anchorage. Anticipated publication data fall/winter 2020). Population genetic structure of Bristol Bay sockeye salmon revealed by 96 SNPs. The tip of each bar on this Neighbor-Joining tree of genetic distances represents a population.

The length of horizontal bars represents genetic distances between populations: the shorter the bar, the more similar the populations. Populations generally cluster in groups based upon river system and a common nursery lake (Wood et al. 1994).

This figure shows that the upper Mulchatna River fish are distinct from the lower Mulchatna, and both are distinct from the upper Nushagak River fish. Sockeye Salmon spawning in the Koktuli River are part of the Lower Mulchatna River and have recently been determined to be genetically distinct (see below). The assessment of population-level effects to salmon from the Project should be at the scale of the Koktuli River population. The figure also shows that spills and releases from the mine site would have the potential to impacts all eight Nushagak River populations.

This NJ tree is also available at:

http://www.adfg.alaska.gov/index.cfm?adfg=fishinggeneconservationlab.bbaysockeye_baseline



Figure 7. Consensus neighbor-joining (NJ) tree based on pairwise F_{ST} between sockeye salmon populations sampled from spawning areas in drainages of Bristol Bay, Alaska.

(Source: Dann, T. H. *In prep.* An updated genetic baseline for Bristol Bay sockeye salmon. Alaska Department of Fish and Game, Fishery Manuscript Series No. XX-XX, Anchorage.)

This NJ tree shows that the Koktuli River Sockeye Salmon population is genetically distinct from the upper Mulchatna River Sockeye. Genetic diversity is driven by selective adaptive pressures from specific local habitat conditions.

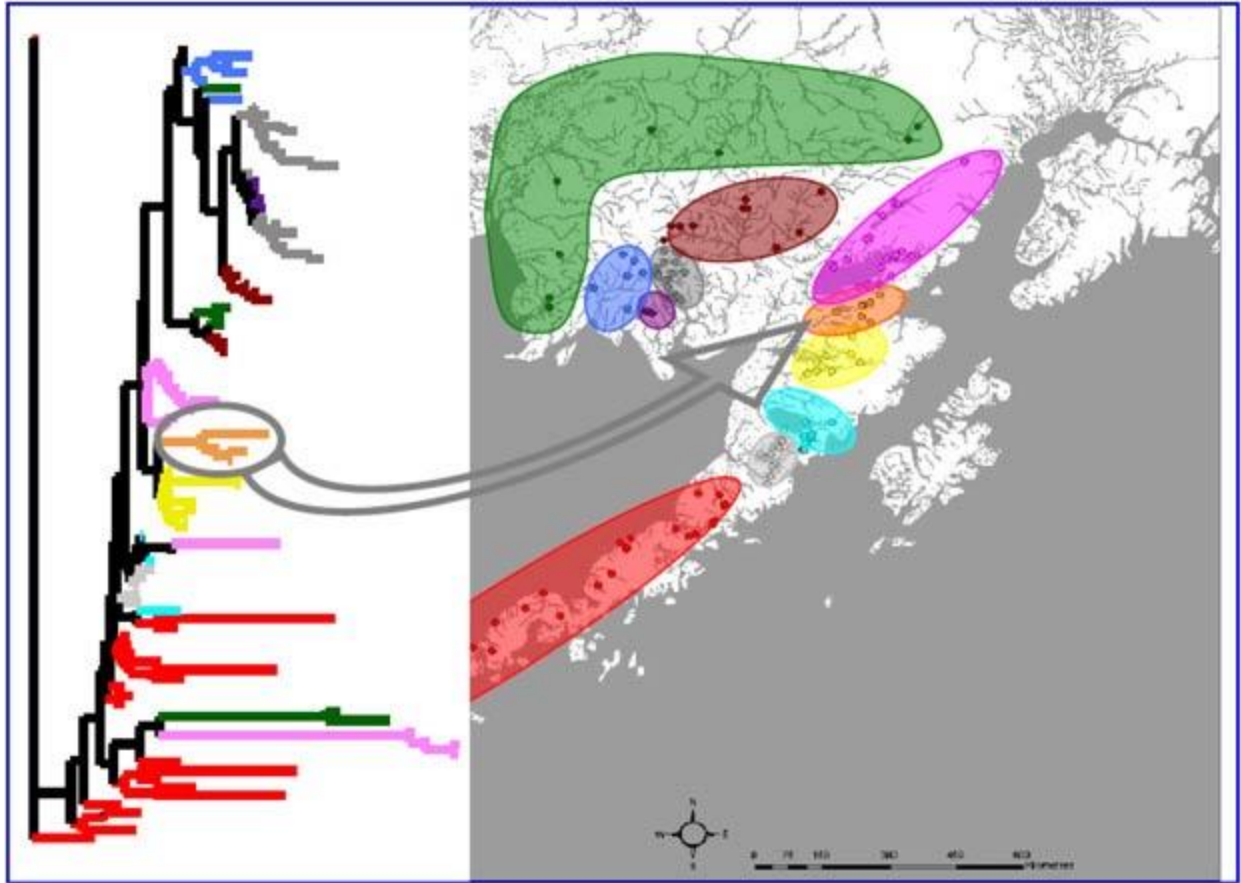


FIGURE 8: Bristol Bay Sockeye Salmon Lines of Genetic Divergence. (Source: Adapted from Dann et al., 2009). Eleven genetic reporting groups, color coded. In this figure, genetic relationships among baseline populations are shown schematically. The arrow is pointing to the Alagnak River reporting group, but one can see how the reporting groups are clustered across the landscape and how they link back to genetic lines of divergence; reflecting genetic differentiation between and among the groups (on the left side of the figure). As with the previous slide, the **PINK** represents the Kvichak River reporting groups. And the **DARK RED** represents the Nushagak River reporting group.

: <http://www.adfg.alaska.gov/FedAidpdfs/fms09-06.pdf>

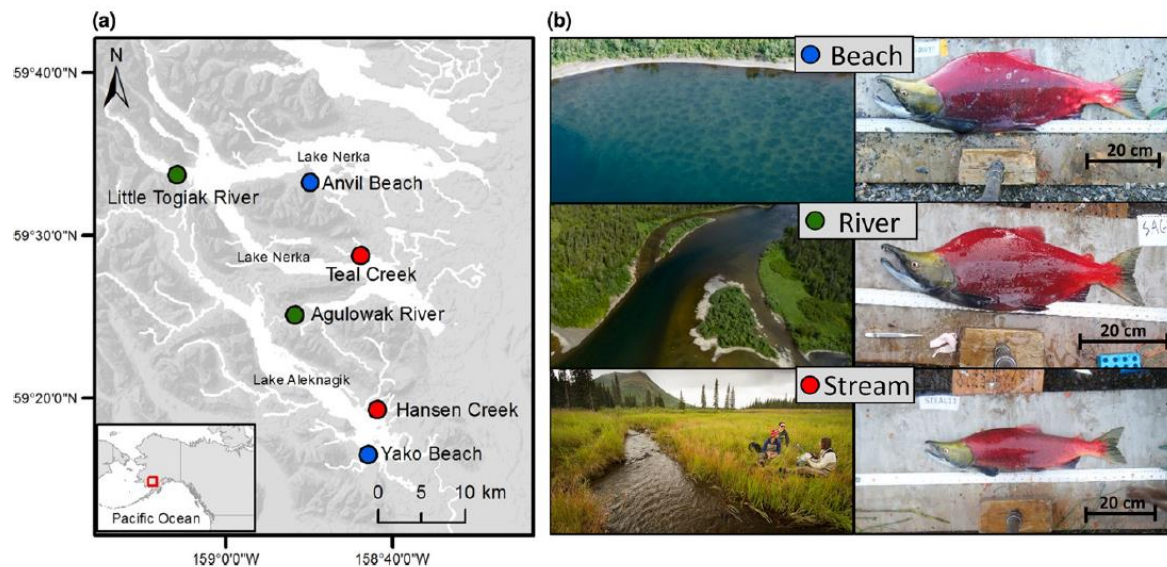


Fig. 1 (a) Map of Wood River basin. The six sample populations are colour coded by ecotype, and colours correspond to those in panel b. See Table 1 for more information on populations. (b) Photographs of representative males and typical spawning habitat from the three ecotypes found in Wood River lakes. Photographs of habitats courtesy of J. Armstrong (Oregon State University) and J. Ching (Alaska Salmon Program, University of Washington).

FIGURE 9: Bristol Bay salmon genetic lines of divergence are linked to ecotones. (Source: Larsen et al., 2017). This slide depicts Sockeye Salmon from the Wood River system, linking genotypic diversity to phenotypic diversity. This figure provides examples of phenotypic variation as a result of selective adaptive pressures from the heterogeneity of habitats across the landscape.

For example, Sockeye Salmon that spawn in small streams are much smaller than those that spawn on beaches or in rivers because sexual selection for large body size is overwhelmed by size-selective predation from bears and physical constraints of stream depth (Fig. 1, Quinn et al. 2001). The spawning environments of these ecotypes also vary in other characteristics including temperature, gravel size, and spawning density, leading to differences in egg morphology (Quinn et al. 1995; Hendry et al. 2000), spawn timing (Schindler et al. 2010) and pathogen susceptibility (hypothesized in Larson et al. 2014a; c.f. Miller et al. 2001). Maintaining habitat diversity is key to maintaining salmon genetic diversity. Genetic diversity is key to sustaining salmon populations over time.

Specific to populations in the Mulchatna River, including the Koktuli River, these Sockeye Salmon are river-type sockeye. According to the Alaska Department of Fish and Game (ADF&G) the river-type form/ecotype of Sockeye Salmon is relatively rare in Bristol Bay. There are self-sustaining populations in the Kuskokwim, Togiak, and Nushagak rivers, and then not really any others until the Susitna River, then in the Taku/Stikine in southeast Alaska. The river-type is an important form of genetic diversity, as these populations typically exhibit greater diversity within populations and less diversity among populations than the more abundant lake-type sockeye salmon. They are the colonizers of the species (Wood 1995). Additional

information can be found at: <https://onlinelibrary.wiley.com/doi/full/10.1111/j.1752-4571.2008.00028.x>

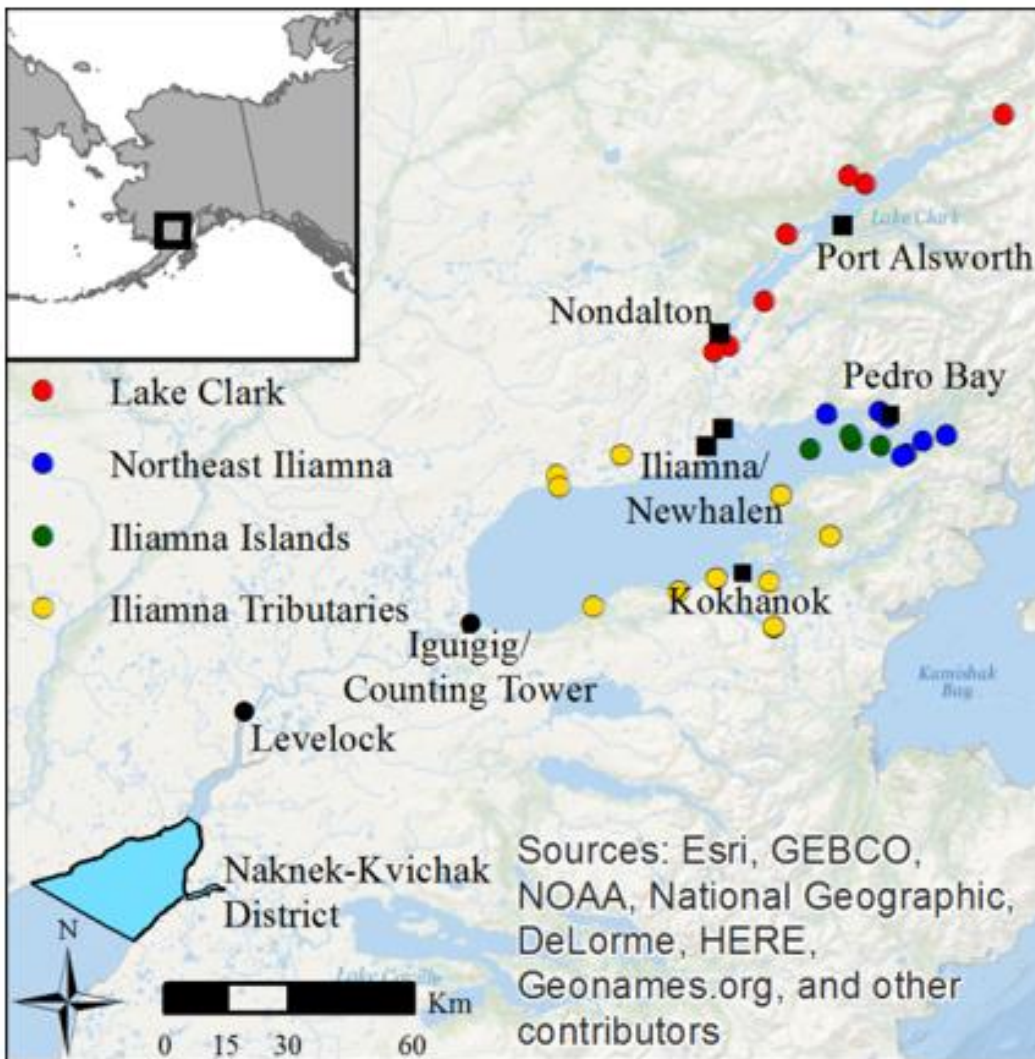


Figure 1: Locations of the 22 populations of sockeye salmon from the Kvichak River included in the baseline, color-coded by reporting group.

FIGURE 10: Kvichak River Sockeye Salmon (Source: Dann. T., 2016). This is another example of how the selective pressures from the diversity of habitats result in genetically unique populations. You can see that Lake Iliamna itself supports genetically unique populations within

tributary, island and lake shoreline ecotones, as identified by research conducted by the ADF&G Gene Conservation Lab. Upper Talarik Creek is identified as one of the 22 populations.

This phenotypic and genetic diversity within the sockeye salmon portfolio is distributed hierarchically: between ecotypes, among drainages within ecotypes, and among populations within drainages. Research has demonstrated the strong role that habitat diversity plays in generating and maintaining genetic diversity.

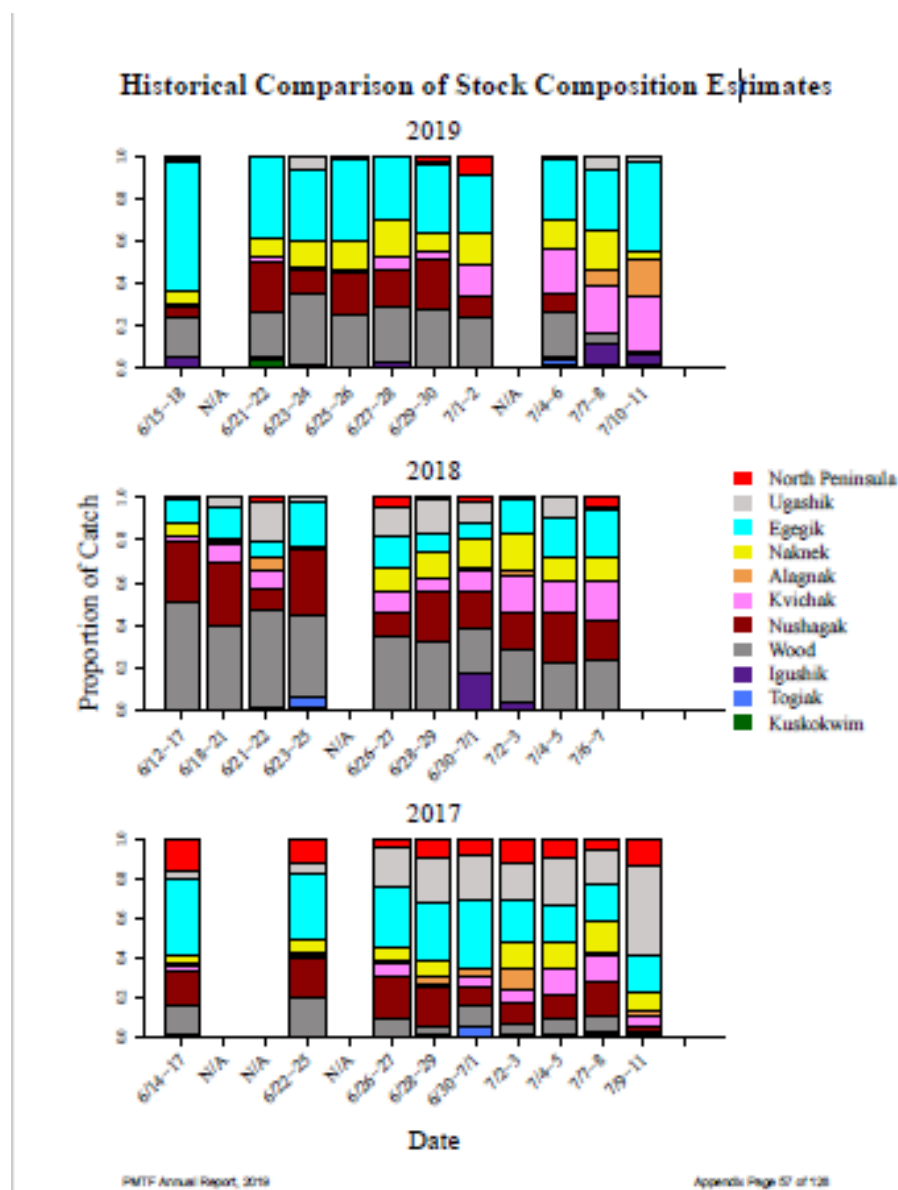


FIGURE 11: Bristol Bay Portfolio (Source: Link et al., 2019)

This figure again uses the 11 genetically distinct baseline reporting groups to highlight the synchrony of each stock contribution to the annual commercial catch composition, on a weekly basis. This figure highlights the Portfolio Effect and the Sockeye Salmon assets that strengthen the Bristol Bay portfolio. The representation of stocks across the temporal scale (sampling events) varies across years. Some years, for example, the Nushagak Sockeye show up stronger early in the season, tapering off later in the season (2017 and 2019), and Kvichak River Sockeye Salmon show an increasing strength during those same timeframes. The diversity within stocks strengthens the overall portfolio. The populations supplement and complement each other. The contributing productivity of the populations/reporting groups depends upon the viability and suitability of availability spawning habitats-the riverine, stream/tributary, lake ecotone habitats shown earlier.

Table 5.–Preliminary 2019 Central Region commercial salmon harvests, by fishing area and species, in **thousands of fish**.

<u>Fishing area</u>	<u>Species</u>					
	<u>Chinook</u>	<u>Sockeye</u>	<u>Coho</u>	<u>Pink</u>	<u>Chum</u>	<u>Total</u>
Naknek-Kvichak District	3	11,528	1	1	135	11,667
Nushagak District	22 (66%)	14,762 (34%)	33 (41%)	2 (29%)	856 (61%)	15,675 (35%)
Egegik District	3	14,686	18	0	156	14,864
Ugashik District	2	1,038	1	0	20	1,061
Togiak District	4	1,019	28	4	228	1,282
Bristol Bay Total	33	43,033	81	7	1,395	44,549

FIGURE 12: Bristol Bay Salmon Harvests (Source: Brenner et al., 2020)

The highlighted data from 2019 reflect the importance of the Nushagak District in supporting the overall Bristol Bay harvest, but also the degree to which the District dominates the production and harvest of Chinook, Chum, and Coho salmon in the region. In particular, the Nushagak produces five times more Chinook Salmon than any other district. Many of these fish come from the Mulchatna River system which is renowned as a Chinook Salmon producer.

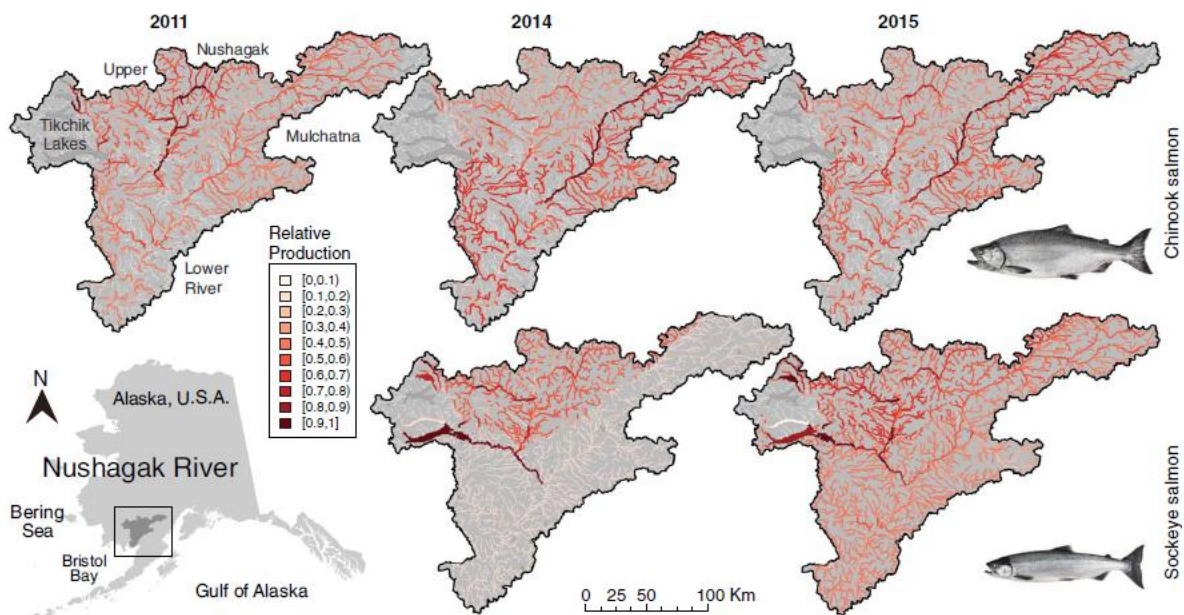


Fig. 1. Productive habitats for salmon shift across river basins. Areas of high Chinook salmon production in 2011 shifted from the upper Nushagak River to the Mulchatna River in 2014 and 2015. Sockeye salmon production was concentrated in Tikchik lakes in 2014 but was more evenly distributed in 2015 including across riverine habitats.

FIGURE 13: Habitat Portfolio (Source: Brennan et al., 2019)

This research further augments the AK Department of Fish and Game’s studies about the diversity and portfolio of salmon in the Project area. This figure depicts how productivity for Sockeye and Chinook Salmon shifts within the Nushagak watershed from year to year. As the productivity of individual habitats and within sub-watersheds changes from year to year depending on conditions, maintaining habitat diversity across the landscape is key to the sustainability and productivity of salmon populations. The phenotypic, genotypic and behavioral diversity of these salmon populations is dependent on the habitat diversity.

References cited

Brenner, R. E., S. J. Larsen, A. R. Munro, and A. M. Carroll, editors. 2020. Run forecasts and harvest projections for 2020 Alaska salmon fisheries and review of the 2019 season. Alaska Department of Fish and Game, Special Publication No. 20-06, Anchorage.

Brennan, S. R., D. E. Schindler, T. J. Cline, T. E. Walsworth, G. Buck and D. P. Fernandez. 2019. Shifting habitat mosaics and fish production across river basins
DOI: 10.1126/science.aav4313

- Dann, T. H. *In prep.* An updated genetic baseline for Bristol Bay sockeye salmon. Alaska Department of Fish and Game, Fishery Manuscript Series No. XX-XX, Anchorage.
- Dann, T. H., G. Buck, C. Cunningham. 2018. AFS Powerpoint presentation: Genetic tools inform management and run reconstruction of sockeye salmon from Bristol Bay, Alaska. August 2018. Atlantic City, NJ.
- Dann, T. H. Alaska Sustainable Salmon Fund 2016 Call for Proposals Project Proposal. 2016. Stock composition of subsistence harvests and total return of sockeye salmon from the Kvichak River. Alaska Department of Fish and Game.
- Dann, T. H., C. Habicht, T. T. Baker, and J. E. Seeb. 2013. Exploiting genetic diversity to balance conservation and harvest of migratory salmon. *Can. J. Fish. Aquat. Sci.* 70: 785–793 (2013) [dx.doi.org/10.1139/cjfas-2012-0449](https://doi.org/10.1139/cjfas-2012-0449).
- Dann, T. H., C. Habicht, J. R. Jasper, H. A. Hoyt, A. W. Barclay, W. D. Templin, T. T. Baker, F.W. West, and L. F. Fair. 2009. Genetic Stock Composition of the Commercial Harvest of Sockeye Salmon in Bristol Bay, Alaska, 2006–2008. FMR Series 09-06, Anchorage, Alaska. <http://www.adfg.alaska.gov/FedAidpdfs/fms09-06.pdf>
- Hendry A.P., J. K. Wenburg, P. Bentzen, E. C. Volk, T. P. Quinn. 2000. Rapid evolution of reproductive isolation in the wild: evidence from introduced salmon. *Science*, 290, 516–518.
- Hilborn R, T. P. Quinn, D.E. Schindler, D. E. Rogers. 2003. Biocomplexity and fisheries sustainability. *Proceedings of the National Academy of Sciences*, 100, 6564–6568.
- Larson W.A., J. E. Seeb, T. H. Dann, D. E. Schindler, L.W. Seeb. 2014a. Signals of heterogeneous selection at an MHC locus in geographically proximate ecotypes of sockeye salmon. *Molecular Ecology*, 23, 5448–5461.
- Larson, W. A., M.T. Limborg, and J. Garrett. 2017. Genomic islands of divergence linked to ecotypic variation in sockeye salmon. *Molecular Ecology* (2017) 26, 554–570 doi: 10.1111/mec.13933
- Lin J, T. P. Quinn T.P., R. Hilborn, L. Hauser. 2008. Fine-scale differentiation between sockeye salmon ecotypes and the effect of phenotype on straying. *Heredity*, 101, 341–350.
- Link, M.R., S.W. Raborn, and T.H. Dann. 2019. Annual Report for the 2019 Port Moller Test Fishery. Report prepared for the Bristol Bay Science and Research Institute, the Bristol Bay Fisheries Collaborative, and the Bristol Bay Regional Seafood Development Association. 38 pp. + 128 pp. appendices. Available online: www.bbsri.org/port-moller-test-fishery
- Miller K.M., K. H. Kaukinen, T. D. Beacham, R. E. Withler. 2001. Geographic heterogeneity in natural selection on an MHC locus in sockeye salmon. *Genetica*, 111, 237–257.
- Schindler D. E., R. Hilborn, B. Chasco et al. 2010. Population diversity and the portfolio effect in an exploited species. *Nature*, 465, 609–612.

Quinn T.P., A. P. Hendry, L. A. Wetzel. 1995. The influence of life history trade-offs and the size of incubation gravels on egg size variation in sockeye salmon (*Oncorhynchus nerka*). *Oikos*, 74, 425–438.

Quinn T. P., L. Wetzel, S. Bishop, K. Overberg, D. E. Rogers. 2001. Influence of breeding habitat on bear predation and age at maturity and sexual dimorphism of sockeye salmon populations. *Canadian Journal of Zoology*, 79, 1782–1793.

Wood, C. C. 1995. Life history variation and population structure in sockeye salmon. Pages 195-216 [In] Jennifer L. Nielsen and Dennis A. Powers, editors. *Evolution and the Aquatic Ecosystem: Defining Unique Units in Population Conservation*, Proceedings of the American Fisheries Society Symposium 17, 23-25 May 1994, Monterey, California. American Fisheries Society, Bethesda, Maryland.

Wood, C.C., B.E. Riddell, D.T. Rutherford and R.E. Withler. 1994. Biochemical genetic survey of sockeye salmon (*Oncorhynchus nerka*) in Canada. *Can. J. Fish. Aquat. Sci.* 51(sup. 1):114–131.