**Stray Thoughts:**

* Marc noted that because coastal chum spawn low in the system, IBD instead of the hierarchical structure more typical among salmon, may be appropriate. This insight is important and I’d like to expand on it a little
  + If IBD is the principal process structuring the genetic variation among chum population in Oregon, relatively limited sampling opportunity in minor systems is less of a problem than we think: spatially explicit analyses (e.g. spatial eigenanalysis) are potentially more powerful using a samples distributed across space than clustered into discrete sampling locations (Oyler-McCance *et al.* 2012). Increased spatial resolution of sampling should be prioritized, even if it comes from a small number of samples.
  + We can decompose spatial processes into those operating on different scales or with different barriers using methods beyond mantel and partial mantel tests. This will allow us to integrate results from sub-basin sampling with across-basin sampling, and can potentially inform us as to spatial scale at which IBD operates
  + Are GTseq panel markers appropriate to assess IBD?
    - FIND THE MP SMALL 2017 report on how GTseq markers were chosen among the RADseq markers
    - Stepped vs gradual IBD clines

**Current Regulatory Structure**

* Pacific Coast ESU – Southern Oregon border to Elwha River
* Other ESUs?

**Population Genetic Structure Studies**

* Johnson, O.W., W.S. Grant, R.G. Kope, K. Neely, F.W. Waknitz, and R.S. Waples. 1997. Status review of chum salmon from Washington, Oregon, and California. U.S. Dep. Commerce, NOAA Tech. Memo. NMFS-NWFSC No. 32.
* Small, M.P., B. Glaser, T. Hillson, and C. Bowman. 2011. Population genetic structure and recovery of chum salmon in the Lower Columbia River*.* Washington Department of Fish and Wildlife Molecular Genetics Laboratory, Olympia, WA. Available at: <https://pisces.bpa.gov/release/documents/documentviewer.aspx?doc=P122957>
* Johnson, O.W., A. Elz, J. Hard, and D.S. Stewart. 2012. Why did the chum cross the road? Genetics and life history of chum salmon in the southern portion of their range. North Pacific Anadromous Fish Commission Technical Report No. 8: 135-137.
* Rawson K, Candy J, Beacham T, Seeb L, Small M, Warheit K, Winans G. 2014. Chum Salmon Southern Area Genetic Baseline Enhancement. Final Report to Southern Fund Panel\_SNP 2014
* Seeb L, Seeb J, Warheit K. 2014. Development of high resolution DNA markers to manage fishery interactions of chum salmon in Western Washington, Final Report, NOAA Saltonstall-Kennedy Grant NA10NMF4270310, University of Washington, School of Aquatic and Fishery Sciences, Seattle.
* Waples RK, Seeb LW, Seeb JE. 2015. Linkage mapping with paralogs exposes regions of residual tetrasomic inheritance in chum salmon (Oncorhynchus keta). Molecular Ecology Resources.
* Small MP, Rogers Olive SD, Seeb LW, Seeb JE, Pascal CE, Warheit KI, Templin W. 2015. Chum Salmon Genetic Diversity in the Northeastern Pacific Ocean Assessed with Single Nucleotide Polymorphisms (SNPs): Applications to Fishery Management. North American Journal of Fisheries Management 35: 974-987.
* Mcphee and Mckinney 2017 Improved Resolution of Chum Salmon Genetic Stock Identification: Annual Progress Report to the Pollock Conservation Cooperative Research Center
* Small et al 2018: Report to Southern Panel-Chum GTseq development and SNP baseline
* A bunch of these reports at: https://www.psc.org/fund-project/chum-salmon-southern-area-genetic-baseline-enhancement-part-2-expanded-snp-collections-genotyping-and-amplicon-development/

**Oregon Populations**

* 3 basins with large, consistent returns
  + Tillamook
  + Nehalem
  + Yaquina
* 10 Others with small numbers or intermittent returns
  + Including: Necanicum, Nestucca, Salmon, Alsea, Siuslaw, Coos, Coquille, and Chetco
* Sample quality and limited efforts to elucidate the relationships among these population means that Oregon chum structure is still unknown
  + *2014 Coastal Multi-Species Conservation and Management Plan* identifies this as a critical uncertainty

**Oregon Coastal Chum Salmon Genetics Pilot Study 2019-2021**

* Objectives
  1. Investigate structure among major OR coastal chum spawning locations
  2. Investigate sub-basin structure
  3. Optimize tissue sampling
  4. Assess if examining
* Sampling
  + spawning reaches of the Nehalem, Tillamook, Netarts, Siletz, and Yaquina basins in November-December 2019
  + sub-basin sampling in Tillamook: Kilchis and Miami

**Reading Notes**

*(Johnson 2012)*

Microsatellites and life-history from WA, ColR and OR chum

* Intro has a lot of older citations pointing to historically large and geographically wide-ranging chum populations from Sacremento River northwards
* Contemporary relic populations more to Southern OR (Elk and Sixes) as the lower extent of range
* Samples: Miami, Kilchis, Yaquina, Siletz, Kilchis, Tillamook, Nehalem, Necanicum, ColR + Hood Canal and WA coastal rivers
* Results
  + Homozygote excess -> small Ne/inbreeding
  + “little heterogeneity among samples of chum collected in different Oregon and Washington coastal rivers”
  + “few private alleles in the coastal populations, and this suggests there are not “unique populations” from further south migrating into northern regions, but that these coastal fish are natural, indigenous populations”
  + “heterogeneity among regional groups (e.g., Puget Sound and Oregon Coast) and some spatial structure among Washington and Oregon coastal samples. However, poor sample quality preludes more detailed conclusions at this time. Columbia River chum salmon samples also showed genetic differences from coastal chum salmon, but at a lower level than from other areas”
  + No sig differences in life-history

*Mcphee and Mckinney 2017*

RADseq to resolve W Alaska summer run chum and contribute to GTseq panel

* Results summary: found structure using ~30k SNPs, sufficient Fst for accurate GSI
* Pulled 500 highest ranked SNPs according to Fst and random forest classification then used them for GSI

*(Small et al. 2015)*

SNPs for BC and WA chum

* Intro Notes
  + Population genetic structure:
    - IBD
    - metapopulation structure in which spawning aggregates are connected genetically through straying
    - strays choose tributaries with similar ecological conditions as their home tributary
  + demographic history
    - standard coastal species story: expansion from coastal refugia during glacial retreat
  + run timing
    - fall run more common in south, summer run in north
    - in some regions, summer runs are derived from fall runs, in others summer and fall runs in the same systems do not share each others’ most recent ancestors
* Methods
  + ~5k samples from 55 collections ranging from Haida Gwaii/North BC to Columbia River (no WA coastal collections though), winter summer and fall run timing
  + Fluidigm genotyping at 89 SNPs
* Results
  + No loci out of HWE, 8 out of 55 collection were overall out of HWE
  + Diversity cline: both He and allelic diversity (why for SNPs?) decline towards the south
  + Six loci candidates for selection
  + Fst, clustered into 11 groups
    - Nearly all pairwise comparisons significant
    - 0.009 - 0.12
  + AMOVA, nearly all loci have sig Fst both among pops and region/run-group clusters
  + PCoA
    - Three clusters: (Hood Canal summer run), (north and central British Columbia coast and Queen Charlotte Islands collections), and (all the remaining regions and run-groups), first two aces: 50% and 22% of variation
    - Split the last group off and ran a second PCoA (? Why not just look at subordinate PCs?), split into regional clusters
  + GSI simulations
* Discussion notes
  + High within-region Fst attributed to population declines: large drift resulting from small population size and extirpation in some tributaries leading to a loss of genetic connectivity
  + Hood Canal summer are distinct
    - “Different run timings appear to have evolved multiple times and may play an important role in structuring and maintaining genetic diversity in Hood Canal and greater Puget Sound”

*Small 2018 Report to the Southern Fund*

Development of SNPs for GTseq panel, attempt to improve over Rawson 2014/Seeb 2014 SNPs particularly to resolve close populations that span CA-US border

This is the Oke350 panel we’re using

* Combined

Johnson OE, Anna; Hard, Jeffrey; Stewart, David (2012) Why did the chum cross the road? Genetics and life history of chum salmon in the southern portion of their range. *North Pacific Anadromous Fish Commission Technical Report* **8**, 135-137.

Oyler-McCance SJ, Fedy BC, Landguth EL (2012) Sample design effects in landscape genetics. *Conservation Genetics* **14**, 275-285.

Small MP, Rogers Olive SD, Seeb LW*, et al.* (2015) Chum salmon genetic diversity in the northeastern pacific ocean assessed with single nucleotide polymorphisms (snps): Applications to fishery management. *North American Journal of Fisheries Management* **35**, 974-987.