**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 Mckinnery 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

**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. Sub-basin structure
  3. Optimize tissue sampling
  4. Assess historical structure using archived scales
* 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
  + 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.