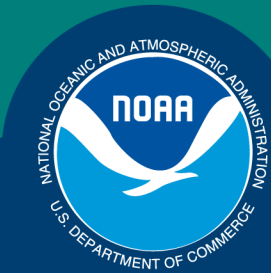


Science, Service, Stewardship



An overview of bycatch genetic analysis: leveraging new technology to improve deliverables

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**NOAA
FISHERIES
SERVICE**

Who am I?

- PhD at UW under Jim and Lisa Seeb
- Stock identification of Chinook bycatch
- Genomic analysis of western Alaska Chinook, Bristol Bay sockeye
- Spent 4 years in Wisconsin developing genomic methods to inform fisheries management



Updating bycatch genetics workflow

- New genotyping chemistry (GTseq)
- New analysis method (rubias)
- Ages for all samples
- Full integration with AKFIN database, collaboration with EMA quantitative ecologists, shiny app to facilitate data exploration
- Analyses conducted in R, automated workflow and report generation



What does this mean for you?

- Time saved will facilitate new analyses
 - More refined spatial/temporal analyses to understand long term trends, how environmental variables influence trends, and how to leverage this information to better facilitate avoidance of specific stocks
 - Cohort based analyses to parameterize AEQ models and track stock compositions by age class
- Begin conversation about faster turnaround
 - Streamlined reports available sooner
 - Potentially reduce lag time to one year if desired and logistically feasible with observer program (e.g., 2019 B season results available around start of 2020 B season)

Future of Auke Bay Genetics

- New research foci: marine genomics, environmental DNA
- New employees: 1 research geneticist, 2 laboratory technicians, 2 postdoctoral researchers
- Ongoing research:
 - Population structure of sablefish, pacific cod, rockfish
 - eDNA of nearshore and offshore environments



Pat Barry: PCCRC funded postdoc

- Funded by PCCRC and NOAA to update bycatch genetics workflow and analyze chum stock compositions across time
- Will give an update on new workflow, shiny app, and future analyses leveraging AKFIN database integration

