

Using High Throughput Genomic Sequencing to Predict Ecological Impacts on Sea Turtle Populations

Lesley Anderson^{1,2} and Lisa Komoroske²

¹California Polytechnic State University, San Luis Obispo ²Southwest Fisheries Science Center, National Marine Fisheries Service, NOAA

Sea Turtle Life History

 Unique life history makes sea turtles difficult to study



Threats to Sea Turtle Populations

- Threats include:
 - Habitat loss
 - Overexploitation

- Global warming
- Disease
- All marine turtles in U.S. waters are protected



Research Goals

Impacts of pollution on sea turtle health
 Identify SNPs to be used as biomarkers

- -Sex
- Size
- Migration
- Foraging



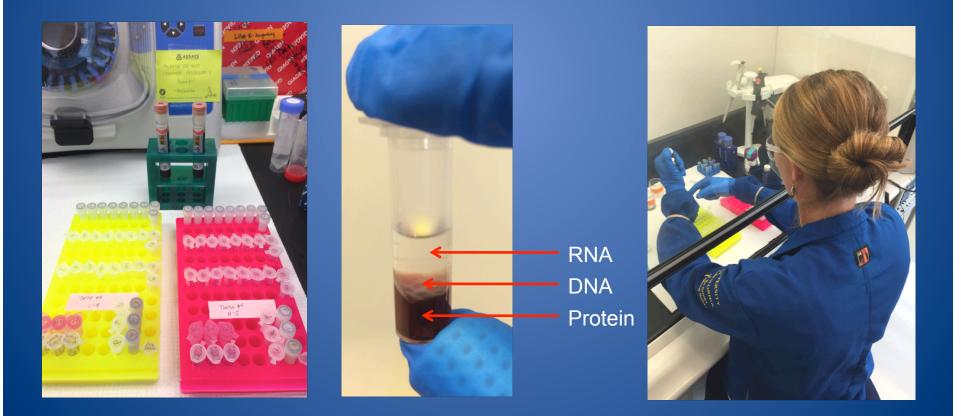
Field Sampling

Capture turtles in the fieldPaxgene whole blood samples



RNA Extraction

Optimization of SOPPhenol-chloroform extraction method

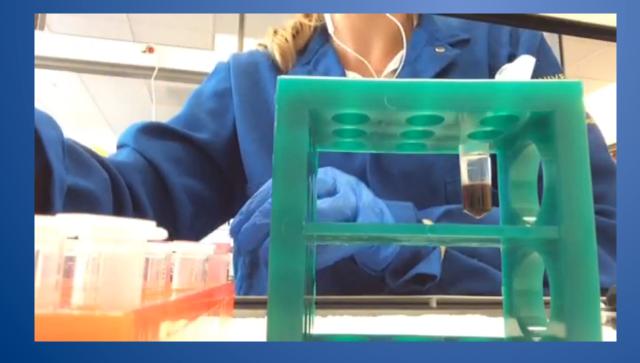


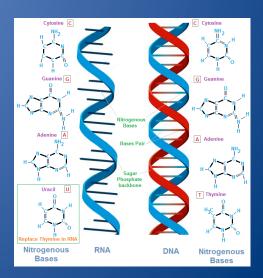
RNA Extraction

RNA is unstable

 Temperature sensitive
 Time sensitive



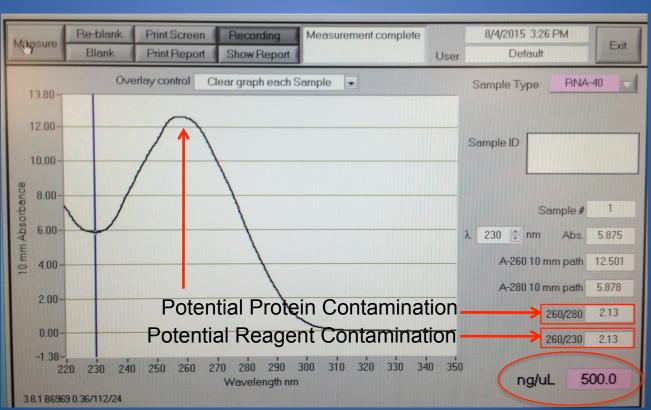




Quality Control

Nanodrop Spectrophotometry

 Assessment of nucleic acid purity

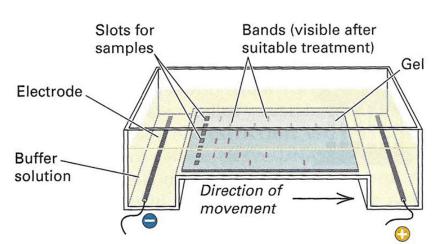




Quality Control

 Gel Electrophoresis

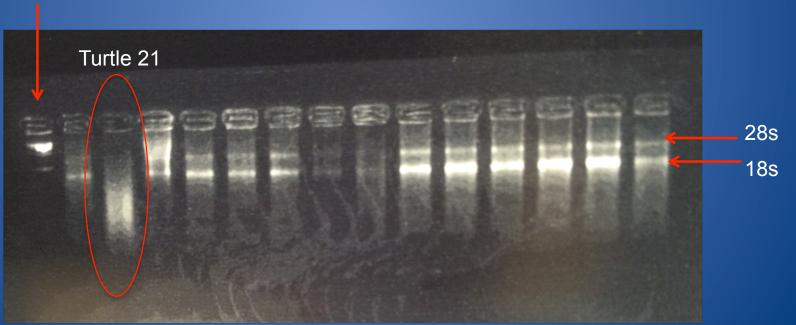
 Agarose gel
 Lighter fragments travel further
 Bands represent concentrations of base pairs



Quality Control

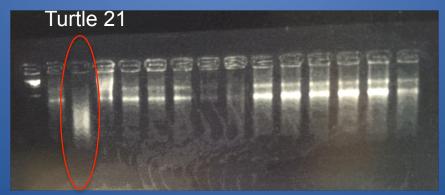
- Gel Electrophoresis
 - Causes of degradation?





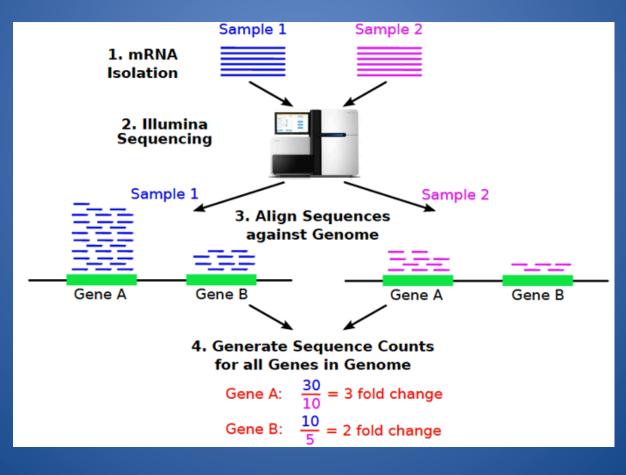
Hawaiian Sea Turtle Population

- Spring 2015: 11 turtles captured
 3 with known tumors (likely Fibropapillomatosis)
- Gel indicates one turtle with potential RNA degradation
 - Significance of degraded RNA in diseased turtles?



Library Sequencing

High throughput sequencing



Potential Implications

1. Impacts of pollution on sea turtle health

- Help conservationists and ecologists predict potential threats to habitat
- 2. Identify SNPs to be used as biomarkers
 - Provide useful genomic data to other researchers to support their studies





Acknowledgements



- Lisa Komoroske, SWFSC, NMFS-NOAA
- Special thanks to:
 - Camryn Allen
 - Gabriela Serra-Valente
 - Joel Schumacher
 - Billy Hilton



"This material is based upon work supported by the National Science Foundation through the Robert Noyce Teacher Scholarship Program under Grant No. (grantee must enter NSF grant number). Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation."

Literature Cited

- 1. National Wildlife Federation
- 2. Interpreting Nanodrop (Spectrophotometric) Results, University of Arizona
- 3. Interpretation of Nucleic Acid 260/208 Ratios, Thermo Scientific, 2012
- 4. Agarose Gel Electrophoresis of RNA and DNA, National Diagnostics
- Efficient Recovery of Whole Blood RNA A Comparison of Commercial RNA Extraction Protocols for High-Throughput Applications in Wildlife Species, D. Schwochow, L. Serieys, R. Wayne, O. Thalmann
- 6. Reference-free Transcriptome Assembly in Non-model Animals from Next Generation Sequencing Data, V. Cahais, et al, 2012
- 7. Next Generation Sequencing of Transcriptomes: a Guide to RNA Isolation in Nonmodel Animals, Y. Chiari, et al, 2011

Questions?

