Subject: Thesis Defense: Piper Thacher, MS in Biology
Date: Wednesday, April 8, 2026 at 10:20:07 AM Eastern Daylight Time
From: SSB Faculty List on behalf of Diane St. Germain
To: SSB-FACULTY-LIST-L@LISTSERV.GMU.EDU

Thesis Defense Announcement
To: The George Mason University Community

Candidate: Piper Thacher

Program: M.S. in Biology

Date: April 22, 2026

Time: 12:00 pm

Location: via Zoom
Join Zoom Meeting:
https://gmu.zoom.us/j/95859606177?pwd=iF6XsR1nwpIzP7q8qEdeXkNZIwgDRE.1

Meeting ID: 958 5960 6177
Passcode: 181430
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Committee Chair: Dr. Ancha Baranova

Committee members: Dr. Sally Bornbusch, Dr. David Luther

Title: Non-invasive health monitoring in eastern north pacific gray whales (*Eschrichtius robustus*): Integrating hormonal and microbial indicators of stress and physiology

Abstract:

Environmental pressures can elicit physiological stress responses in wildlife, potentially leading to systemic health effects. Monitoring the consequences of rapid environmental change on an animal's physiology is therefore critical for species management and conservation. Fecal samples offer a noninvasive way to track health biomarkers such as stress-related hormones and the gut microbiome. Gut microbiomes play fundamental roles in host metabolism, immune regulation, and stress physiology, yet remain poorly characterized in many mysticetes, including gray whales (*Eschrictius robustus*). The Pacific Coast Feeding Group (PCFG) is a subgroup of Eastern North Pacific (ENP) gray whales with a distinctively short migration. PCFG whales, compared to ENP whales, have poorer body condition and shorter body length, and additionally experience annual variation in prey availability, body condition, stress hormones, and possibly suffer from an epidermal disease. The goal of this thesis was to investigate how (1) hormone concentrations and gut microbiomes vary across gray whale individuals, over time, and with stressors like nutritional stress, and (2) whether hormones and gut microbiomes co-vary significantly. Fecal samples (n=135) from 16 whales were collected from 2016-2023. I measured cortisol and prostaglandin E2 (PGE2) concentrations using ELISA assays and used 16S rRNA sequencing to assess gut microbiome diversity, composition, and taxonomic membership. I found that cortisol varied significantly between years and with food availability, whereas I found no significant patterns in PGE2. In regard to microbiomes, microbial diversity also varied by year, with whales in 2019 showing markedly decreased microbial richness and phylogenetic diversity. We further found that whales in 2019 had distinct microbial community composition, reflecting changes in abundant and rare microbial taxa. Specifically, whales in 2019 had enriched abundances of *Turicibacter* and *Eubacterium brachy group*, associated with pathogenicity and host inflammation, as well as a lower abundance of *Oscillibacter,* a producer of anti-inflammatory metabolites associated with cholesterol metabolism. Additionally, the taxa *RF39*, *Veillonellales-Selenomonadales*, and *Anaeroplasma* were associated with cortisol concentrations, indicating that certain gut taxa were sensitive to cortisol concentrations. This study provided the first characterization of gray whale gut microbiomes and their relationships to environmental stressors and hormone fluctuations, which is vital for understanding the effects of environmental change on the gray whale populations.

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