



# Genetic diversity across the mitochondrial genome of eastern oysters (*Crassostrea virginica*) in the northern Gulf of Mexico

Chani R. Rue<sup>1,\*</sup>, Jason D. Selwyn<sup>1,\*</sup>, Patricia M. Cockett<sup>2</sup>, Bryan Gillis<sup>3</sup>, Lauren Gurski<sup>1</sup>, Philip Jose<sup>1</sup>, Brandi L. Kutil<sup>4</sup>, Sharon F. Magnuson<sup>1</sup>, Luz Ángela López de Mesa<sup>1</sup>, R Deborah Overath<sup>5</sup>, Delbert Lee Smee<sup>6,7</sup> and Christopher E. Bird<sup>1,8</sup>

<sup>1</sup> Department of Life Sciences, Texas A&M University—Corpus Christi, Corpus Christi, TX, United States of America

<sup>2</sup> Harte Research Institute, Texas A&M University—Corpus Christi, Corpus Christi, TX, United States of America

<sup>3</sup> Conrad Blucher Institute, Texas A&M University—Corpus Christi, Corpus Christi, TX, United States of America

<sup>4</sup> Department of Undergraduate Studies, Texas A&M University—Corpus Christi, Corpus Christi, TX, United States of America

<sup>5</sup> Department of Mathematics and Sciences, Texas Southmost College, Brownsville, TX, United States of America

<sup>6</sup> Dauphin Island Sea Lab, Dauphin Island, AL, United States of America

<sup>7</sup> Marine Sciences, University of South Alabama, Mobile, AL, United States of America

<sup>8</sup> Hawai'i Institute of Marine Biology, University of Hawaii at Mānoa, Kāne'ohe, Hawai'i, United States of America

\* These authors contributed equally to this work.

## ABSTRACT

The eastern oyster, *Crassostrea virginica*, is divided into four populations along the western North Atlantic, however, the only published mitochondrial genome sequence was assembled using one individual in Delaware. This study aimed to (1) assemble *C. virginica* mitochondrial genomes from Texas with pooled restriction-site-associated DNA sequencing (ezRAD), (2) evaluate the validity of the mitochondrial genome assemblies including comparison with Sanger sequencing data, and (3) evaluate genetic differentiation both between the Delaware and Texas genomes, as well as among three bays in Texas. The pooled-genome-assembled-genomes (PAGs) from Texas exhibited several characteristics indicating that they were valid, including elevated nucleotide diversity in non-coding and the third position of codons, placement as the sister haplotype of the genome from Delaware in a phylogenetic reconstruction of *Crassostrea* mitochondrial genomes, and a lack of genetic structure in the ND4 gene among the three Texas bays as was found with Sanger amplicons in samples from the same bays several years prior. In the comparison between the Delaware and Texas genome, 27 of 38 coding regions exhibited variability between the two populations, which were differentiated by 273 mutations, versus 1–13 mutations among the Texas samples. Using the full PAGs, there was no additional evidence for population structure among the three Texas bays. While population genetics is rapidly moving towards larger high-density datasets, studies of mitochondrial DNA (and genomes) can be particularly useful for comparing

Submitted 7 June 2021  
Accepted 3 September 2021  
Published 28 September 2021

Corresponding author  
Jason D. Selwyn,  
jdselwyn@gmail.com,  
jason.selwyn@tamucc.edu

Academic editor  
Khor Waiho

Additional Information and  
Declarations can be found on  
page 15

DOI 10.7717/peerj.12205

© Copyright  
2021 Rue et al.

Distributed under  
Creative Commons CC-BY 4.0

## OPEN ACCESS