



Sequencing of the Quagga Mussel Genome

A Resource for Development of Genetic Biocontrols

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This project conducted DNA sequencing and assembly of the quagga mussel genome. A high-quality reference genome with chromosome-scale assembly was developed.

Mission Issue

Invasive quagga mussels pose a significant risk to Reclamation infrastructure and operations. The reference genome developed in the project will provide a resource for the development of novel controls.

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Problem

Invasive quagga mussels (*Dreissena rostriformis bugensis*) have become established in several reservoirs upstream of Reclamation dams. These mussels present a significant risk to infrastructure, threatening reliable power generation and water delivery. Quagga mussels also impact ecosystems and can limit recreational access to waters.

There are currently no available technologies that can be used to control or eradicate mussel populations in large waterbodies such as Lake Mead and Lake Powell.



"Having the quagga mussel genome sequenced and available to researchers is the key that will allow us to unlock potentially new biological control methods for this invasive organism."

Jacque Keele
Biologist
Technical Service Center

More Information

<https://www.usbr.gov/research/projects/detail.cfm?id=1866>

Solution

Genetic biocontrol, wherein the genome of an organism is edited to alter population dynamics, holds the potential to control or eradicate invasive populations of quagga mussels.

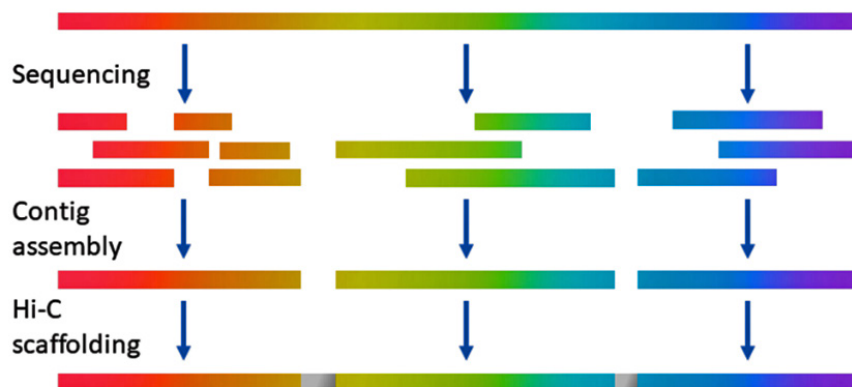
Development of genetic biocontrols requires detailed knowledge of the targeted organism's genome structure and composition. Such genomic DNA sequence data were not available for the quagga mussel.

Application and Results

This project conducted DNA sequencing and assembly of the quagga mussel genome using a variety of technologies and analytical approaches. The quagga mussel genome presented considerable challenges due to its large size and high degree of heterozygosity.

A high-quality assembly was developed for the quagga mussel with chromosome-scale scaffolding. The resultant reference sequence is one of the most complete and contiguous genomes developed to date for any bivalve mollusk.

Genomic DNA



Future Plans

The next step for analysis of the quagga mussel genome will be to conduct a detailed annotation to characterize the positions and organization of protein coding genes and other features of interest, such as repetitive elements.

An annotated reference genome will serve as an invaluable resource for the development of biocontrols, as well as providing new avenues for understanding the invasion biology of the mussels.