Advancing global monitoring of ship borne invasive species through streamlined metabarcoding

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Abstract

The unintentional transport of invasive species through the global shipping network causes substantial losses to social and economic welfare. Addressing this global challenge requires identification of potentially harmful species, and confirmation of their movement along highly frequented shipping routes.

As we have previously shown, properly calibrated network models are able to describe passive movement of invasive species around the world. These models can be substantially improved when suitable *in-situ* biological data is becoming available, now possible by sequencing of environmental DNA (eDNA) from port waters.

Here we report a simple and scalable approach to generate metabarcoding data of 18S ribosomal and other eDNA collected in four major US ports. Between Long Beach, Houston, Miami, Baltimore and a multitude of Chinese ports, ships travel both frequently or infrequently while linking to different ecosystems of East Asia.

By controlling for ecoregions and ship traffic, we will shortly be able to estimate ship-borne invasive species spread between the two largest global economies, USA and China. With further port DNA sampling and network model refinements, we will also soon be able to provide global assessments of ship-borne invasive species spread to inform management and policy decision makers.

Keywords (10):

eDNA, invasive species, shipping, metabarcoding, networks, management

Short Description (120 characters): Port water metabarcoding in the USA and China to understand transport of ship borne invasive species.

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