

Characterizing species assemblages and targeted screening for invasive species in ballast: DNA based species identification and enumeration

Objectives:

- Develop molecular techniques to characterize species assemblages in ballast samples
- Develop molecular techniques to detect nonindigenous species (NIS) in ballast
- Develop bioinformatic tools to mine molecular data sets to better characterize invasion events

Rationale:

Ballast (water and solid) exchange is one of the dominant avenues of introduction and spread of Non Indigenous Species (NIS) across the United States. Many ballast management programs currently mandate that ships execute open ocean ballast exchange to expel NIS carried in ballast taken up in coastal waters. Compliance with this requirement is difficult to assess from physical measurements such as salinity. An alternative approach now being considered is gauging compliance by characterizing species assemblages in ballast tanks- if tanks are completely purged during open ocean exchange, the species found in ballast tanks should be of oceanic, and not of coastal origin. However, the effectiveness of this compliance standard will be limited without accurate and efficient methods for characterizing species assemblages found in ballast.

Besides determining compliance, a goal of many ballast water management programs is to detect or screen ballast for NIS that are regularly transported by commercial shipping traffic. "Hit lists" of NIS have already been generated that identify species posing the greatest threat to estuarine ecosystems. These lists include NIS already established in domestic waters that may be secondarily introduced to other areas through regional transport. Screening species assemblages for NIS may also help determine the "NIS load" being carried in ballast. "NIS load" in part reflects the frequency of introductions, as well as what is known as "propagule pressure", or the effective population size of incoming cohorts of NIS. Both factors may determine whether a species will become established after being introduced into a novel environment. Measuring "NIS load" for species transported in ballast would help characterize invasion dynamics and may therefore lead to more effective management strategies.

Approach:

Development and application of DNA-based methods for identifying organisms in ballast samples can provide accurate and consistent species level identifications for all of the dominant taxonomic groups found in ballast (including species-level identification of organisms at all life stages). Unlike morphological data, molecular data sets developed for species inventories can also be mined for other purposes, such as determining the effective population sizes of incoming NIS cohorts and studying the temporal variability in NIS population demography. These data can also be mined to analyze the adaptive response of species to environmental change, and interspecific evolutionary relationships. By providing species level identifications and enumeration, DNA-based analyses can also be extended to assess ecological conditions and reference data on natural environmental variability.

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