Marine Non-indigenous Species Monitoring

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https://www.wildlife.ca.gov/OSPR/Science/Marine-Invasive-Species-Program

The Marine Invasive Species Program (MISP) is responsible for biological sampling and analysis of non-indigenous species (NIS) in California's coastal waters

ABSTRACT

The MISP is responsible for analysis of shipping vectors responsible for the introduction of non-indigenous species (NIS) into California's coastal waters. MISP collaborates with the Smithsonian Environmental Research Center (SERC) and Molecular Ecology Laboratory at Moss Landing Marine Labs (MLML) on an extensive program to analyze spatial and temporal patterns of NIS invasions in marine and estuarine waters of California.

The monitoring program includes statistically robust field sampling, DNA-assisted taxonomic analyses, and data analysis. Sampling primarily focuses on 10 estuaries or bays and high-salinity water along the California open coast. Three communities are surveyed: hard substrate, soft-sediment, and plankton.

Sampling Timeline (2012-19)

We intensively sampled 10 estuaries plus outer coast transects from 2012-2018. We are beginning re-sampling of the 10 estuaries in 2019.

BAYS & ESTUARIES	Hard Substrate (Subtidal/Sessile)								Plankton								Soft Sediment (Subtidal)							
YEAR	12	13	14	15	16	17	18	19	12	13	14	15	16	17	18	19	12	13	14	15	16	17	18	19
Humboldt Bay			x			x					x			x					x					
Bodega Bay/Tomales Bay	x				x						x			x										
Morro Bay		x								x														
Port Hueneme				x								x											x	
Marina del Rey Harbor			x								x													
Los Angeles Harbor / San Pedro				x	x						x			x						x				
Newport Bay				x							x			x										
Mission Bay		x								x			x						x					
San Diego Bay		x								x			x					x						
San Francisco Bay	x	x	x	x	x	x	x		x	x	x	x	x	x			x	x	x	x	x	x	x	
OUTER COAST	Intertidal								Subtidal															
Marin		x			x				x															
Monterey		x							x			x												

SERC-Methods

- Smithsonian Environmental Research Center samples epifauna using PVC settlement plates deployed for three-month periods, set at ten sites per estuary.
- Paired samples are collected quarterly for morphological analysis by taxonomists, as well as, molecular genetic analysis by MLML.

MLML-Methods

- MLML provides genetic analysis, including species identification of whole samples (metagenetics) collected from planktonic, hard- and soft-substrate communities.
- Genetic analysis is used to corroborate morphological identifications and screen for possible cryptic species.
- This project was the first to use next-generation sequencing for routine, high volume DNA barcoding of marine NIS.

Statewide Results
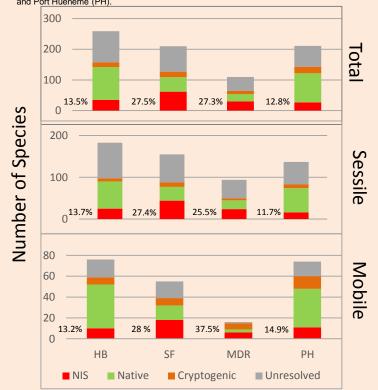
Phase 1 Results (2012-2014) 2 New NIS Found

- Only 2 NIS were found that were not previously reported in CA in our extensive sampling, over multiple years and habitats including both sessile and mobile species
- The 2 NIS are Fredericella indica and Watersipora subovoidea

Fredericella indica

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Watersipora subovoidea

Photo by J. Winston, courtesy of the American Museum of Natural History.

Phase 2 Results (2015-2016) - Statewide Species Richness

- NIS contributed 12-28% of total observed species richness per estuary for sessile invertebrates.
- The percent contribution was highest in San Francisco Bay (SF) and Marina del Rey (MDR).
- The same pattern in percent contribution by NIS is observed for mobile invertebrates and all species combined, ranging from 13-38% and 13-28% of species richness.
- The relative dominance of NIS in San Francisco Bay and Marina del Rey was driven by both relatively high NIS richness and low native species richness compared to Humboldt Bay (HB) and Port Hueneme (PH).

Total: 13.5% (HB), 27.5% (SF), 27.3% (MDR), 12.8% (PH)

Sessile: 13.7% (HB), 27.4% (SF), 25.5% (MDR), 11.7% (PH)

Mobile: 13.2% (HB), 28% (SF), 37.5% (MDR), 14.9% (PH)

Legend: ■ NIS ■ Native ■ Cryptogenic ■ Unresolved

Conclusion

- In Phase 1, we found a relatively low number of species that were new to California, implying a possible decline in the rate of new invasions in recent years. Ongoing sampling and analysis will test if the slowing rate of new invasions is real and if it is caused by ballast water management. Results will be published in peer-reviewed journals.
- The efficiency of metagenetic analyses will allow us to sample more estuaries and will be the basis of a future broad scale monitoring and detection program.
- In phase 2, we found that San Francisco Bay has the highest percentage of NIS richness, followed by Marina del Rey. Further analysis will be reported later this year.