

Executive Summary of Spatial and temporal analysis of marine invasions in California, Part II: Humboldt Bay, Marina del Rey, Port Hueneme, and San Francisco Bay

The Smithsonian Environmental Research Center (SERC) and Moss Landing Marine Laboratories (MLML) have undertaken an extensive program with the California Department of Fish and Wildlife (CDFW) to analyze spatial and temporal patterns of nonindigenous species (NIS) invasions in marine and estuarine waters of California, as requested by SB497. This is a summary of Phase II of the initial phase. In Phase II of the program, the geographic scope has expanded to include Humboldt Bay, Marina del Rey, and Port Hueneme. In addition, San Francisco Bay is surveyed each year.

The surveys found that NIS contributed 16-40% of total observed species richness per estuary for sessile invertebrates. The percent contribution was the highest in San Francisco Bay at 40%. NIS occupied a mean of >50% per sampling plate for sessile invertebrates in both San Francisco Bay and Marina del Rey. San Francisco Bay differed from the other three bays in relative abundance of both native species and NIS. The results of repeated surveys among three years shows a high degree of consistency both in the number of NIS detected each year and in reaching an asymptote. This suggests that the surveys are sampling a high percentage of the total species pool for this focal habitat in San Francisco Bay.

Using the repeated survey method across years 2014-2016 in San Francisco Bay hard substrate communities, we detected several NIS for the first time. Four species were tunicates (*Microcosmus squamiger*, *Molgula ficus*, *Perophora japonica*, and *Styela canopus*) and six polychaetes. Several of the new tunicate records appear to be northward range expansions from southern California that coincide with unusually warm water. This suggests a change of environmental conditions that may have contributed to colonization.

Using the repeated survey method across years 2014-2016 in San Francisco Bay soft sediment communities, we detected that 71% of the community were NIS in 2014, 88% in 2015, and 66% in 2016. In Humboldt Bay in 2015, 13% of the community were detected as NIS. The accumulation curves suggest that we have detected >90% of the estimated total NIS in Humboldt Bay and 84-100% of the estimated total NIS in San Francisco Bay across each of the three years.

The percent contribution of NIS to total species richness in San Francisco Bay and Humboldt Bay shows that San Francisco Bay has a much higher average proportion of NIS relative to Humboldt Bay. In 2015, NIS made up a disproportionately larger percentage of overall richness, with greater variation among sites and change that may have been related to a marine heat wave that occurred that year. NIS made up a much larger percentage of individuals in our grab samples than native species reaching a maximum abundance of 93% of all individuals. In San Francisco Bay, there was a significant variation among sites and years in relative abundance of NIS ranging from 29% to 93%. In Humboldt Bay, the NIS abundance was very low at the sites closer to the mouth of the Bay.

Using morphological taxonomy during 2014-2016 of soft sediment surveys in Humboldt Bay, we detected two new NIS records of Asian cephalaspidean gastropods, *Philine auriformis* and *P. orientalis*, both of which were known previously from the U.S. Pacific coast. It seems unlikely

that either record represents a significant range expansion along the coast. No new taxa were detected in San Francisco Bay surveys of the shallow subtidal zone in 2014-2016.

The relative lack of new records is surprising given the spatial and temporal scale of these sampling efforts and detailed morphological analyses. The results suggest that the rate of invasion or detection may be quite variable over time or that a shift in invasion rates has occurred since previous analysis in the late 1990s. Repeated sampling over time in each bay will help determine whether this is a lasting or ephemeral pattern.

The MLML DNA barcode database version used herein contains 269 species and is continuing to grow as we add additional voucher analyses. However, a fully genetic approach to voucher analysis is premature, at least by the next-generation sequencing approach used in this study.