





# **Initial Genetic Analysis**

- Pat Gaffney, U. Delaware
- Sequenced 8 large oysters (108-160 mm) from South SFBay
- 2 Mitochondrial genes (16S and COI) & 3 Nuclear genes

#### **Results:**

 Crassostrea gigas, with relatively high genetic diversity



# Impacts in Other Parts of the World

- Aggressive spread; exclusion/smothering of native organisms; alteration of habitats & food webs
- Native oyster populations harmed in Australia & NZ, leading to limits or bans on cultivation
- Mussels beds eliminated in areas in the Netherlands & Germany
- Power plant fouling; shore use impeded

### **Possible Impacts in SF Bay**

- Out-compete or overgrow native oysters, or impair their growth with metabolites, feces
- Out-compete or overgrow other epibenthic organisms
- Reduce phytoplankton biomass & productivity, limiting food resources for many pelagic & benthic species







# **Possible Vectors**

- Larval drift from commercial oyster farms (e.g. Drakes Estero, Tomales Bay)
- Larvae in ballast water
- Spawning adults on a boat or ship hull
- Illegally planted adults (e.g. San Rafael)
- CDFG experimental cultivation (1981 and earlier)
- Spawning adults in bioaccumulation studies (RMP, BCTCP & LEMP 1991-2002)

## Implications

- State of California / Exotic Species Management
- Oyster Farms
- Bioaccumulation Studies
  - use of exotic study organisms
  - transfer of genes
  - transfer of parasites or other associated organisms