

**CONTRIBUTIONS TO THE INTERNATIONAL
MARINE SHRIMP ENVIRONMENTAL GENOMICS
INITIATIVE (IMSEGI): MONITORING ECOSYSTEM,
ANIMALS AND PUBLIC HEALTH, 2000–2006**

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PREFACE

Worldwide, wild shrimp populations are seriously threatened by a variety of pressures, including habitat destruction, chemical and biological pollution, and gene depletion. These threats also jeopardize the continued success of global shrimp aquaculture and public health. In November 1996, with funding from the Rockefellers Brothers Fund, Inc., Tufts University scientists began collaborating with Dr. Jurgenne Primavera at the Southeast Asian Fishery Department (SEAFDEC), Philippines, to address some of these concerns with respect to the giant tiger prawn, *Penaeus monodon*. The researchers developed microsatellite genetic markers to assess genetic diversity of *P. monodon* in various locations in the Philippines and reported an estimate of the population structure using six microsatellite genetic markers. In addition, we discovered an association between genetic diversity and habitat status (i.e. presence of mangrove forests or intensity of shrimp aquaculture). In 1998, with support from Tufts University and anonymous private funding, we created the International Marine Shrimp Environmental Genomics Initiative (IMSEGI) to address similar issues representing the natural range of the species in other countries. (http://www.tufts.edu/vet/aquatics/ecg_research_shrimp_imsegi.html)

Individual researchers, academic institutions, and government agencies from Ecuador, Thailand, Guatemala, Mexico, China, and Peru, among others, have signed memoranda of understanding with Tufts University to join in and participate in field and basic research through this successful regional and international collaboration.

The long-term goals of IMSEGI are to support the conservation of penaeid shrimp species and develop a sustainable shrimp aquaculture industry. We are accomplishing these goals by collecting samples of wild shrimp on a regular basis and monitoring the following: (1) structure of the meta-population of wild penaeid shrimp species – began developing a database of species biodiversity based on taxonomy analysis, (2) levels of genetic differentiation of selected species – began with *Penaeus monodon* and *Litopenaeus vannamei*, (3) pollutant load – including pathogens, heavy metals, PCBs and PAHs in penaeid shrimp populations along their natural range.

Currently, we are compiling a database to track biological and environmental parameters such as shrimp length, weight, sex, prevalence of viral diseases, allele diversity, salinity, temperature, and the status of mangrove forests, among others. Using Geographic Information System (GIS), we also are collecting information on the biodiversity of accompanying species at different locations, and studying the association between genetic differentiation/pollutant load with ecosystem health (i.e. condition of mangrove forests and intensity of shrimp farming and other agro-industries).

Our discoveries could be valuable to both fishery managers and shrimp breeders in their efforts to conserve shrimp resources and develop a sustainable industry. We have disseminated our findings through both oral and poster presentations at various meetings of the World Aquaculture Society and Aquaculture America in past years. Specific papers report preliminary data about topics such as: conservation and population genetics of wild marine shrimp, ecosystem (mangrove forests) conservation and pollutants in wild marine shrimp, associations of disease prevalence with habitat status, and development of molecular markers for: population genetic studies, tracking pedigrees in shrimp breeding programs, differentiating among wild penaeid species, traceability of shrimp in international trade, assessing risk to natural shrimp populations caused by the potential release of cultured and transgenic shrimp, development of linkage maps and mapping quantitative trait loci (QTL) associated with fitness traits.

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