Data Management Plan:

A. Types of Data:

Data generated from this project will include **(1)** fitness-related and physiological data from the common-garden and selection experiments, consisting of hatching rate, survival, development time, and fecundity **(2)** Gene expression data (Illumina RNA-Seq Reads) from the selection experiment, **(3)** DNA data (Illumina DNA HiSeq reads) from Evolve and Resequencing (E&R) during the selection experiment and also from the field population genomics surveys, **(4)** Metadata from the field population genomic surveys (salinity, temperature, latitude, longitude, etc. from sampling sites), and **(5)** processed and analyzed results from the RNA-Seq and DNA HiSeq raw sequence data above, such as gene expression patterns, SNP frequencies, allele frequencies, and signatures of selection.

B. Data Sharing and Dissemination:

All data will be made publicly available at the conclusion of this project. All fitness-related and physiological data, as well as metadata, will be shared Dryad Digital Data Repository (www.datadryad.org), which is a nonprofit repository that makes data freely available, and the Biological and Chemical Oceanography Data Management Office (BCO-DMO) (http://www.bco-dmo.org/data). RNA and DNA sequence data will be deposited at NCBI and also BCO-DMO.

(1) Fitness-related and Physiological Data from the Selection Experiment:

The fitness-related and physiological data obtained from the selection experiment will be submitted to the Dryad and BCO-DMO. Life history and quantitative genetic data from these experiments will include egg number, hatching rate, survival to metamorphosis, survival to adult, developmental time to metamorphosis, development time to adult, number males, number females, etc.

A matrix of the factors used in the linear model (for statistical analyses) will also be uploaded. Factors will include Population, Clutch, Selected Line, Time Point in Selection, Salinity, Temperature, and all the response variables listed in the previous paragraph.

(2) Gene Expression data (Illumina RNA-Seq Reads) from the Selection Experiment:

To provide ready access to data generated by this project and ensure its preservation, all Illumina sequence data will be deposited to NCBI, specifically to SRA (Sequence Read Archive, http://www.ncbi.nlm.nih.gov/sra). SRA stores raw sequencing data and alignment information from high-throughput sequencing platforms.

Data will be uploaded to BCO-DMO at the conclusion of the experiments (within 1 year of completion of the project).

(3) Illumina DNA HiSeq Reads from Evolve and Resequencing during the Selection Experiment and also from Field Population Genomics Surveys:

To provide ready access to data generated by this project and ensure its preservation, all Illumina sequence data will be deposited to NCBI, specifically to SRA (Sequence Read Archive, http://www.ncbi.nlm.nih.gov/sra). SRA stores raw sequencing data and alignment information from high-throughput sequencing platforms.

Data will be uploaded to BCO-DMO at the conclusion of the experiments (within 1 year of completion of the project).

(4) Metadata from the Field Population Genomics Surveys (salinity, temperature, latitude, longitude, etc. from sampling sites):

Metadata from the field population genomics surveys (salinity, temperature, latitude, longitude, etc. from sampling sites) will be deposited at Dryad (https://datadryad.org/) and BCO-DMO (http://www.bco-dmo.org/data).

(5) Processed and Analyzed Results from the RNA-Seq and DNA HiSeq Data:

These data will be the product of statistical analyses of the RNA and DNA sequence data. These results will include gene expression patterns, SNP frequencies, allele frequencies, and signatures of selection. These data will be deposited at Dryad (https://datadryad.org/) and BCO-DMO (http://www.bco-dmo.org/data).