**Data Sharing Plan**

The data collected by the work described in this proposal will consist of 1) nucleotide sequence data derived from Illumina resequencing of gDNA and mRNA collected from experimental and wild populations of *D. melanogaster* and *D. pulex* and 2) phenotypic measurements of the life history, physiological measurements and stress response measurements from *D. pulex*. As such, they will be of interest to the evolutionary genomics and quantitative genetics communities, as well as the broader Drosophila and Daphnia communities.

Nucleotide sequence data will be stored and disseminated as raw data in original FASTQ format and as annotated SNP tables in VCF format. Both formats are considered the community standards and are employed by other large population based resequencing efforts (e.g., 1000Genomes). Unix shell script files that perform all steps necessary to convert FASTQ to VCF files will be generated to reconstruct of VCF tables in a reproducible way. These script files will include all parameters (e.g., quality score thresholds) used in the final analysis. Metadata, including but not limited to, time and date of collection and the number of flies in each pool will be stored in .txt files.

Nucleotide data (raw, processed and metadata) will be securely backed up in redundant hard drives at two locations. We will store nucleotide data locally in the Bergland lab on a RAID-5 enabled Direct Storage Device as well as independent JOBD arrays. All raw data will also be uploaded to NCBI’s SRA. This multilayered data backup and retrieval system will ensure the long term storage of all nucleotide data collected. In the case that any one backup drive fails, it will be replaced in a timely fashion. **All hard-drives will be maintained for at least three years after the completion of this grant.**

Phenotypic measurements will consist of life history, behavioral, physiological and stress response measurements of the a newly formed panel of Daphnia that we will resequence. Data will be stored in original form as hand-records on paper, scanned .pdf copies of originals, and in digital format as Excel workbooks. For long term storage and for universal accessibility, data will be backed up as CSV files and uploaded to Data Dryad. Genotype-phenotype association statistics will be performed using R or plink. All scripts necessary to perform such analysis will be stored alongside phenotype data. **All paper copies and hard drives storing phenotype data will be maintained for at least three years after the completion of this grant.**

**Genotype and phenotype data will be disseminated in a timely and open format.** Upon publication of any papers using our pooled genome resequencing data, we will post processed VCF files and raw FASTQ files on our website. **In the case that we have not published papers using these data within one year after the completion of this grant, we will post data on the websites listed above.**

**Sharing model Organisms**

All Drosophila and Daphnia stocks used in this study will be available to the scientific community upon request.