Oysters are broadcast spawners, producing a huge amount of larvae per spawning event, allowing for the phenomenon of sweepstakes selection. In sweepstakes selection, numerous offspring are produced from a wide range of adults, but overall spawning effective population size (Ne) is small since only the genotypes well suited to current environmental conditions survive. In *C. gigas*, there is evidence of one of the largest genetic loads (*L*) in nature (Launey & Hedgecock 2001). The impacts of climate change could increase the effects of deleterious alleles and thus increase *L* (Launey & Hedgecock 2001). Increasing *L* could result in a greater reduction in Ne over time, decreasing a population’s ability to respond to future environmental phenomena. It is therefore imperative to understand how environmental change could affect the population genetics and viability of broadcast spawners.

The phenotypic expression of a genotype can be affected by environmental cues. Under certain environmental regimes, a particular genotype may be benign, but a shift in regimes could render its expression lethal (Launey & Hedgecock 2001). This environmentally induced lethality would increase the overall genetic load of a population by increasing the distance between mean fitness and optimum population fitness. Oysters already have a very high genetic load (Launey & Hedgecock 2001) and the added effects on load of sustained climate change could have long-term effects on genetic diversity. The amount of *L* in a population can be easily measured by calculating distortions in Mendelian ratios in polymorphic markers, such as SNPs or microsatellites. This analysis, performed in conjunction with gene expression, will uncover the impact climate change will have on future genetic diversity in populations of oysters.