Pacific oysters are exposed to a variety of stressors that occur on different time scales. These stressors elicit specific physiological responses from the oyster, triggering the up- and down-regulation of genes in stress-induced pathways. One of these pathways is ceramide metabolism, which has been proven to be instrumental in the vertebrate response to a variety of environmental stressors. I have identified four key genes in the ceramide pathway in the Pacific oyster, *Crassostrea gigas*. These genes correspond to enzymes that are responsible for the up- and down-regulation of ceramide *de novo* synthesis or catabolism. My preliminary work shows that these ceramide pathway genes are expressed differentially between adult tissues and that they may be important in the adult oyster immune response to a common pathogen. I have also found evidence that at least some of these genes are expressed in larval oysters. Since ceramide is a sphingolipid, one of the next logical steps in this research is to examine how this pathway is affected under differing nutritional regimes. The main hypothesis of my proposed research is that different nutritional qualities and quantities will affect how this particular sphingolipid is produced and used when *C. gigas* encounters environmental stresses.

 The four ceramide biosynthesis pathway genes that I have identified in *C. gigas* are serine palmitoyltransferase 1 (Sptlc1), 3-ketodihydrosphingosine reductase (3KDSR), acid ceramidase (AC), and ceramide glucosyltransferase (CMgst). Sptlc1 and 3KDSR are enzymes responsible for the *de novo* synthesis of ceramide from serine and palmitoyl CoA. CMgst catalyzes the reaction that creates glucosylceramide from ceramide. AC catalyzes the catabolism of sphingosine into ceramide. The similar end result of Sptlc1 and 3KDSR would preclude that these enzymes would have similar expression patterns. The other two, AC and CMgst, may differ in their expression patterns and how they respond to stress since they accomplish reactions downstream of ceramide *de novo* synthesis.

 The four enzymes show similar trends in tissue-specific expression levels in adult *C. gigas*. AC and Sptlc1 are expressed most highly in the gill, followed by the digestive gland, the mantle, and the adductor muscle. 3KDSR and CMgst follow similar patterns except the expression level of 3KDSR is similar in the mantle and digestive gland and the gene expression of CMgst is similar between the gill and digestive gland.

 In a study where we exposed adult *C. gigas* to the marine bacterium *Vibrio tubiashii* for three hours, three of the enzymes showed trends of up-regulation compared to non-diseased controls. The difference in expression between treatment and controls was not significant for Sptlc1 and 3KDSR, but it was significant for AC (p=0.045). CMgst did not show any evidence of differential expression between disease-exposed and control oysters.

 The research accomplished to date provides the groundwork for understanding how nutritional regimes that include different levels of lipids will affect ceramide synthesis and accumulation under stressful conditions. The ceramide pathway appears to be important in the oyster stress response and further study may uncover mechanisms of the *C. gigas* physiological response to environmental stressors.