Expression of biomineralisation genes in tissues and cultured cells of the abalone, *Haliotis tuberculata*

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Keywords: *Biomineralisation, gene expression, cell culture, gastropod, mollusc*

Mollusc shell biomineralisation involves a variety of organic macromolecules (matrix proteins and enzymes) that control $CaCO_3$ deposition, growth of crystals, the selection of polymorph, and the microstructure of the shell. Since the mantle and the hemocytes play an important role in the control of shell formation, primary cell cultures have been developed to study the expression of three biomineralisation genes recently identified in the abalone *Haliotis tuberculata*: a matrix protein, lustrin A, and two carbonic anhydrase enzymes.

This work aimed to semi-quantify the level of gene expression both in native tissues and cells derived from primary cultures. Metabolic assays (XTT) were performed to ensure cells remained viable over the time in culture. PCR and gel photograph analysis were used to semi-quantify the gene expression and compare the level of expression in native tissues and cultured cells. This work found that the genes of interest were being expressed in abalone tissues, with expression highest in the mantle and much lower in the hemocytes and gills. Lustrin A and carbonic anhydrase genes were also expressed significantly in primary cell cultures for up to fourteen days *in vitro*.

This study shows that primary cultures of target tissues are suitable models to study the cellular and molecular processes of biomineralisation. Further characterization of cells and cell typing would help specify the respective roles of epithelial and circulating cells in matrix components secretion and $CaCO_3$ deposition. Experiments are also underway to investigate the production of calcium carbonate deposits in primary cultures.