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Biomineralisation and Gene Expression in *Emiliania huxleyi*

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Biomineralisation in the marine phytoplankton *Emiliania huxleyi* is a stringently controlled intracellular process. The molecular basis of coccolith production is still relatively unknown although its importance in global biogeochemical cycles and sensitivity to increased pCO_2 levels has been well documented. Unravelling the cellular processes of biomineralisation including ion transport pathways and mineral nucleation will aid in our understanding of the effects of a changing ocean on this group of phytoplankton and could also shed light on isotope fractionation of elements used for proxies. This study uses three calcifying vs. non-calcifying comparisons to investigate the role of putative calcification genes in *E. huxleyi*. It analyses relative transcript levels using quantitative reverse transcription PCR. Calcification consistently induces the up-regulation of genes encoding a putative bicarbonate transporter belonging to the solute carrier 4 family, a calcium proton exchanger and a vacuolar H^+-ATPase in comparison to genetically identical non-calcifying cells. In contrast up to a 26 fold down-regulation of GPA, a calcium binding protein, is seen when cells are in their calcifying form. This data provides strong evidence that these genes play key roles in *E. huxleyi* biomineralisation.