Investigating the link between fermentative metabolism and hydrogen production in the green alga *Chlamydomonas reinhardtii*

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In *Chlamydomonas reinhardtii*, electrons required for hydrogen production come from a combination of biophotolysis and fermentation. Anoxia leads to the activation of several competing fermentative pathways, breaking down carbohydrate reserves into formic, lactic, malic and acetic acid along with ethanol, carbon dioxide and hydrogen. It has therefore been proposed that hydrogen yields can be increased by switching off competing fermentative pathways.

The aim of this study was to investigate the link between fermentative metabolism and H_2 production in *C. reinhardtii* with a view to aiding future efforts at metabolic engineering. A detailed bioinformatic analysis of the genome was used to identify potential fermentative enzymes and pathways. Polyclonal antibodies, raised against several of the putative fermentative enzymes following over-expression in *E. coli*, were used to determine the location of these enzymes in the cell and to determine changes in expression during anoxia.

Using artificial microRNAs (amiRNAs), knockdown mutants were created targeting key fermentative enzymes and the resulting impact upon hydrogen evolution and fermentation products was assessed.

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