Exploring methane mitigation strategies in photosynthetic microorganisms through genome-scale metabolic models

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The problematic of greenhouse gas (GHG) emissions is a global environmental challenge that has raised concerns in the past few decades. Particularly, the increase in atmospheric concentrations of carbon dioxide, methane, and other damaging gases can lead to catastrophic repercussions to life as we know it. Therefore, reducing GHG emissions and fomenting strategies for their mitigation are crucial steps that need to be taken in order to meet the Paris Agreement and ultimately ensure a sustainable future for our planet and those that inhabit it.

Over the last 20 years, metabolic models have been widely used as a source of information for metabolic engineering, drug targeting, metabolic pathway analysis, and process optimization. Genome-scale metabolic (GSM) models allow the in silico simulation and prediction of metabolic fluxes on a large scale, providing a powerful tool for optimizing and designing metabolic engineering methods. By integrating high-throughput data with genome-scale models, a comprehensive understanding of cellular metabolism and identification of strategies to improve a certain objective function can be obtained. The importance of this emerging technology in industry stems from its ability to offer a faster and more cost-effective approach, surpassing the efficiency of traditional methods.

Taking this into account, as well as the urgent search for sustainable solutions addressing GHGs mitigation, our work aims at identifying the metabolic capabilities of photosynthetic microorganisms to reduce methane emissions. In this regard, we investigate the potential of these microorganisms, using genome-scale metabolic (GSM) models to understand their metabolic networks in detail. Therefore, herein we describe the reconstruction of GSM models for the microalga Chlorella vulgaris sp. – iGA1305, includes 2635 reactions and 1305 genes – and for the cyanobacterium Synechocystis sp. – iJG708, includes 2165 reactions and 708 genes –, which will be applied to understand their CH4-related metabolic networks in detail. Both GSM models provide a powerful tool for metabolic improvement, allowing predictions and simulations of CH4 metabolism in response to different culture conditions and genetic modifications.