Bioresource Technology 124 (2012) 387–393

Contents lists available at SciVerse ScienceDirect

Bioresource Technology

journal homepage: www.elsevier.com/locate/biortech

Eukaryotic and prokaryotic microbial communities during microalgal biomass production

Aino-Maija Lakaniemi [a,*], Chris J. Hulatt [b,c], Kathryn D. Wakeman [a], David N. Thomas [b,c], Jaakko A. Puhakka [a]

[a] Department of Chemistry and Bioengineering, Tampere University of Technology, P.O. Box 541, FI-33101 Tampere, Finland
[b] School of Ocean Sciences, College of Natural Sciences, Bangor University, Menai Bridge, Anglesey LL59 5AB, UK
[c] Finnish Environment Institute, Marine Centre, P.O. Box 140, FI-00251 Helsinki, Finland

HIGHLIGHTS

- *Chlorella vulgaris* and *Dunaliella tertiolecta* grow well in the presence of diverse bacteria.
- *C. vulgaris* and *D. tertiolecta* have different associated bacterial communities.
- DGGE detects ciliates before they eradicate the microalgal cultures.
- qPCR shows relative microalgal and bacterial cell numbers from stable cultures.
- Raw culture samples serve as suitable templates for qPCR.

ARTICLE INFO

Article history:
Received 6 June 2012
Received in revised form 6 August 2012
Accepted 11 August 2012
Available online 19 August 2012

Keywords:
Microalgal cultivation
Photobioreactor
Associated bacteria
Quantitative PCR
DGGE

ABSTRACT

Eukaryotic and bacterial communities were characterized and quantified in microalgal photobioreactor cultures of freshwater *Chlorella vulgaris* and marine *Dunaliella tertiolecta*. The microalgae exhibited good growth, whilst both cultures contained diverse bacterial communities. Both cultures included Proteobacteria and Bacteroidetes, while *C. vulgaris* cultures also contained Actinobacteria. The bacterial genera present in the cultures were different due to different growth medium salinities and possibly different extracellular products. Bacterial community profiles were relatively stable in *D. tertiolecta* cultures but not in *C. vulgaris* cultures likely due to presence of ciliates (*Colpoda* sp.) in the latter. The presence of ciliates did not, however, cause decrease in total number of *C. vulgaris* or bacteria during 14 days of cultivation. Quantitative PCR (qPCR) reliably showed relative microalgal and bacterial cell numbers in the batch cultures with stable microbial communities, but was not effective when bacterial communities varied. Raw culture samples were successfully used as qPCR templates.

1. Introduction

Microalgae are potential feedstocks for fuels and energy due to their high growth rates and photosynthetic efficiencies (Brennan and Owende, 2010). Currently, microalgal biomass is produced commercially for high value products such as human food supplements, animal feed, cosmetics and pharmaceuticals (Gong et al., 2011). However, to date, the industrial-scale production of microalgal biomass for fuels and/or energy remains too costly and energy intensive (Amer et al., 2011; Beal et al., 2012; Hulatt et al., 2012).

In nature, microalgal growth is always associated with the growth of other organisms, notably bacteria (Reynolds, 2006). Microalgae provide organic and inorganic compounds for bacteria by excreting soluble material during normal growth, in response to environmental stress and/or via their lysis and decomposition after cell death (Cole, 1982; Reynolds, 2006; Hulatt and Thomas, 2010). Bacteria can supply vitamin B_{12} for the algae that are unable to synthesize it (Croft et al., 2005), provide CO_2 for algal growth, reduce oxygen tension (Mouget et al., 1995), recycle nitrogen compounds (Hulatt et al., 2012) and increase the solubility of nutrients and trace elements making them more bio-available for the microalgae (Keshtacher-Liebson et al., 1995). However, some microalgae also excrete compounds that limit bacterial growth (Stephens et al., 2010). Bacteria may also compete with microalgae for available nutrients, produce metabolites that are inhibitory to microalgal growth, infect microalgae or cause lysis of algal cells (Cole, 1982). Similarly, eukaryotic organisms, such as fungi, may promote microalgal growth by symbiotic associations (Watanabe et al., 2005) or compete with the microalgae for available nutrients.

* Corresponding author. Tel.: +358 40 198 1103; fax: +358 33 115 2869.
E-mail address: aino-maija.lakaniemi@tut.fi (A.-M. Lakaniemi).

0960-8524/$ - see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biortech.2012.08.048