ABSTRACT

Light represents one of the key influencers of the biological world, and algae represent a versatile group to have exploited this resource. This thesisinvestigates two significant aspects of this response: (i) the ability to produce compounds for human interests, specifically fuels; and (ii) the process by which light can alter the metabolic response in photosynthetic organisms. While the first part of the thesis focuses on the ability of green algae to produce biofuel components, the second part looks at the generation of signaling molecule cAMP in the cyanobacterium *Spirulina platensis.*

Eight different algae were isolated from local environments (ponds, river, domestic reservoir and sea), identified as *Chlorella*sp. (MK01, MK06), *Neochloris* sp. (MK02), *Scenedesmus* sp. (MK03, MK08), *Coelastrella* sp. (MK04), *Desmodesmus* sp. (MK05) *and Dunaliella* sp. (MK07) based on morphological characteristicsand 18S rDNA sequence analysis. All algae comapratively grew well in modified BG11 medium among the different media evaluated. Among the isolates, *Chlorella* sp. (MK01), *Neochloris* sp. (MK02) and *Scenedesmus* sp. (MK03) attained much greater biomass concentrationof 0.78, 0.74 and 0.77 $gL^{-1}$and had good lipid content (34, 27 and 25% respectively) among the isolates evaluated. Thus these three isolates were taken for further studies. Requirement of carbonate, nitrate and phosphate for culturing these algae were evaluated as 0.18 mM, 1.5 gL^{-1} and 0.22 mM respectively and these conditions for obtaining high biomass 0.6, 0.6 and 0.7 gL^{-1} in *Chlorella* sp., 0.6, 0.5 and 0.6 gL^{-1} in *Neochloris* sp., and 0.6, 0.6 and 0.62 gL^{-1} in *Scenedesmus* sp.were identified.

Nitrate deprivation enhanced hydrocarbon and lipid content by 12 and 5 to 15%. Phosphate deprivation enhanced hydrocarbon and lipid content in *Scenedesmus* sp. by 6% and 8%. Carbonate deprivation resulted in 6% increase of hydrocarbon in *Chlorella* sp.

Under air-bubbled condition the isolates showed poor growth, lipid and hydrocarbon accumulation and cultivation under shaking condition did not significantly increase the biomass and lipid content. However, hydrocarbon content of *Chlorella* sp., and *Scenedesmus* sp. increased under continuous shaking (60 rpm) condition. Biomass and chlorophyll content of all the three isolates decreased with increasing salinity 25 to 200 mM, even though there was a significant increase in hydrocarbon and lipid accumulation under high salinity 200 mM. All the three isolates accumulated more hydrocarbons and lipid in nitrate limiting conditions compared to nitrate sufficient condition in a two stage cultivation processes. In addition, all three isolates *Chlorella* sp., *Neocholoris* sp., and *Scenedesmus* sp. produced more biomass 0.81, 0.88 and 0.73 gL^{-1} respectively under phototrophic compared to dark condition0.24, 0.45 and 0.24 gL^{-1}in the presence of glucose.The fatty acid profile of isolates *Chlorella* sp. and *Neochloris* sp. showed accumulation of saturated fatty acids, while *Scenedesmus* sp. accumulated more unsaturated fatty acids. In outdoor cultivation, in open tubshigh growth and lipid production in all three isolates was observed, as compared to photobioreactor cultivation under both direct and indirect exposure to sunlight. Also, similar to laboratory cultures cultivation *Chlorella* sp., and *Neochloris* sp. accumulated more saturated fatty acids and *Scenedesmus* sp. accumulated more unsaturated fatty acids under outdoor conditions as well.

In another series of investigations, intracellular signal response to light by algae was studied. Cyclic AMP level of all the eight green algaedid not

show any significant change during the day. However, in blue green alga *Spirulina platensis* the cyclic AMP level was related to the light phase of growth. Adenylate cyclase genes, *cyaA*, *cyaC* and *cyaG* of *Spirulina platensis* showed rhythmic expression. *CyaC* showed the highest flux in response to light compared to *cyaA* and *cyaG* genes. *CyaC* gene upstream region in the reverse orientation induced expression in a light dependent fashion in a bacterial host system which reveals a light responding transcription activator, that can be exploited in bacterial expression systems to express the specific genes or protein under light condition.