



Insights into the carbonic anhydrases and autotrophic carbon dioxide fixation pathways of high CO₂ tolerant *Rhodovulum viride* JA756



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ABSTRACT

Biofixation of CO₂ is being extensively investigated to solve the global warming problem. Purple non-sulfur bacteria are fast growers that consume CO₂ and produce beneficial biomass. Better the growth at higher CO₂ levels, more efficient are the strains for biofixation. Nine among fifty strains that were analyzed at elevated CO₂ levels responded with better growth. Considering its enhanced growth at high CO₂ and metabolic versatility, *Rhodovulum viride* strain JA756 was chosen to make further studies. Strain JA756 tolerates up to 50% (v/v) CO₂ with its optimum between 20–40% (v/v), yielding a biomass of 3.4 g. L⁻¹. The pattern of specific enzyme activity of carbonic anhydrase corresponded well with that of its growth. To gain insights into the genomic composition and genes related to carbonic anhydrases and CO₂ fixation, draft genome sequencing of JA756 was carried out which revealed the presence of two non-homologous genes encoding for β and γ carbonic anhydrases, both of which are assumed to be implicated in maintaining intracellular inorganic carbon concentration at equilibrium. Most of the genes involved in the Calvin pathway, reductive tricarboxylic acid pathway, 3-hydroxypropionate bicycle and C₄ pathways were found in the draft genome. While the experimental determinations of active roles of two of these pathways are still underway, the expression of key genes of Calvin and C₄ pathway suggest their functional role in the organism. Owing to its metabolic versatility, JA756 can be advantageous for biological CO₂ assimilation facilities located by the coastline, inland and also at wide ranges of CO₂ concentrations.

1. Introduction

Global warming induced by increasing concentrations of CO₂, a chief greenhouse gas (Olah et al., 2009) is causing a great concern. While the upper safety limit for atmospheric CO₂ is 350 ppm (Hansen et al., 2008; Ramanathan and Feng, 2008), the present CO₂ levels have already surpassed 400 ppm (NASA Global climate change - https://climate.nasa.gov/climate_resources/24/graphic-the-relentless-rise-of-carbon-dioxide/; Earth's CO₂ home page - <https://www.co2.earth>). While there is no best method, several physical, chemical and biological

technologies are under investigation to mitigate CO₂ levels in atmosphere (Zheng et al., 2011). Photosynthetic organisms such as plants, algae and bacteria in addition to using atmospheric CO₂ for growth, also recycle it into potentially beneficial biomass; hence can be effectively employed as agents for biological CO₂ fixation. Though much of the work is focused on the plant systems, microorganisms are considered advantageous as they are capable of fixing several folds more CO₂ per unit area than plants (Salih, 2011). Moreover, since certain environments (such as power plants) emit high concentrations of CO₂ (15–20%) into the atmosphere, identification of high CO₂ tolerant

Abbreviations: 'C', carbon; 3-HP, 3-hydroxypropionate; 4-HB, 4-hydroxybutyrate; ACL, ATP-citrate lyase; ADP, adenosine diphosphate; CA, carbonic anhydrase; CBB, Calvin-Benson-bassham; CCL, citryl-CoA lyase; CCM, carbon concentrating mechanism; CCS, citryl-CoA synthetase; CHNS, carbon, hydrogen, nitrogen and sulfur; DC, dicarboxylate; DEAE/CM, diethylaminoethyl/carboxymethyl; kDa, kilodalton; Mb, mega base; OAA, oxaloacetic acid; OD, optical density; ORF, open reading frames; PDB, Protein Data Bank; PEP, phosphoenolpyruvate; PEPCK, phosphoenolpyruvate carboxylase; PEPCK, PEP carboxykinase; PNSB, purple non-sulfur anoxygenic phototrophic bacteria; PSI-BLAST, position-specific iterative basic local alignment search tool; RAST, rapid annotations using subsystems technology; rTCA, reductive tricarboxylic acid; RubisCO, ribulose-1,5-bisphosphate carboxylase/oxygenase

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species is equally important. Microalgae sit on the top of the choices for their small size, exceptionally high efficiency in energy conversion, CO₂ removal and usefulness of their byproducts (Salih, 2011; Zheng et al., 2011). There are several reports on CO₂ tolerant species of algae, such as *Chlorella*, *Scenedesmus* and *Cyanadium* which grow under 2–100% of CO₂ (Makarevičienė et al., 2011; Salih, 2011). At enriched CO₂ conditions, significant enhancement in algal growth rates as compared to ambient air were common and the rates declined only at much higher levels (Kodama et al., 1993; Nakano et al., 1995).

Purple non-sulfur anoxygenic phototrophic bacteria (PNSB) are a metabolically versatile group of bacteria which perform anoxygenic photosynthesis (Larimer et al., 2004; Pfennig, 1978). Most PNSBs are primary producers having the capability of photolithoautotrophic growth, in both aerobic as well as anaerobic illuminated environments, using inorganic compounds as electron donors and subsequently fixing CO₂ (Inui et al., 1999). They are known to use the Calvin pathway, mediated by RubisCO, for autotrophic CO₂ fixation. PNSB can prove highly beneficial for industrial applications similar to those for which microalgae are already being used in the field of biotechnology and microbiology (Becker, 1994), however their potentials are being recognized only recently (Merugu et al., 2012). Though PNSB are CO₂ fixers, equally environment friendly and share additional advantages over microalgae in having metabolic versatility, faster proliferation rates coupled to their harboring oxic as well as anoxic habitats (Sasikala and Ramana, 1995), the response of these bacteria to varying CO₂ concentrations has not been investigated. There is only a single report so far available which indicates a preliminary study on isolation of such bacteria from soils of elevated CO₂ chambers (Kumar et al., 2011). This study thus becomes an intriguing aspect considering the lack of research on growth of PNSB at varying CO₂ levels coupled to their CO₂ fixation pathways.

Carbonic anhydrases (CAs) are Zn containing metalloenzymes which catalyse the inter conversion between CO₂ and HCO₃⁻. This enzymatic conversion is a vital process which not only helps the cells to concentrate CO₂ for fixation by cellular enzymes but also helps the cells to maintain an equilibrium between CO₂ and HCO₃⁻ to carry out cellular process (Smith and Ferry, 2000). CAs can be found located in cytoplasm or/and periplasm and their localization in the cell helps in understanding physiology (Smith et al., 1999). Prokaryotic CA's belong to 3 different classes- α , β and γ and there are no significant sequence homologies between representatives of different classes, implying their convergent evolution (Smith and Ferry, 2000). While genes encoding for one/two or all of the three classes of CAs can be present in a given organism, why three classes have evolved and what advantage each class provides over the other is still unknown (Smith and Ferry, 2000)! The ubiquitous occurrence of CAs in photosynthetic organisms has shown that there is a direct correlation between these enzymes and CO₂ metabolism (Bundy, 1976). Later a primary role of CAs in efficient autotrophic CO₂ fixation pathways was understood (Smith et al., 1999) and CAs are now considered as efficient biochemical markers for carbon sequestration (Warriner and Jayaraj, 2015). In oxygenic phototrophs, CA and RubisCO are associated in the carboxysomes and pyrenoids, respectively (Price et al., 1992; Puskas et al., 2000), where the former accumulate CO₂ at the active site of RubisCO, thus increasing the availability of CO₂ per minute for efficient fixation of CO₂. When CAs catalyse the reversible reaction, HCO₃⁻ accumulates in the cell aiding in the progress of C₄ pathway (Berg, 2011).

The present study aims in understanding the CO₂ tolerance and thereby CO₂ fixation capabilities of a PNSB, *Rhodovulum viride* JA756 with further establishing a correlation between CO₂ concentration and its CA activity. Purification, characterization and protein chemistry of CA is also described. Genome sequence analysis further helped in gaining insights into the possible CO₂ fixation pathways operating in this organism.

2. Materials & methods

2.1. Cultivation conditions

Pure cultures of purple bacteria were obtained from the stock cultures available in our laboratory (Supplementary Table S1 online). For initial screening of these bacteria for photolithoautotrophy, cultures were cultivated anaerobically (28 ± 2 °C; light 2,400 lx) for 2–4 days on agar slants in a selective mineral medium (Lakshmi et al., 2009) supplemented with sodium bicarbonate (0.1%, v/v) as the sole carbon source and Na₂S (1 mM) as electron donor. For further experiments, a buffered liquid medium provided with CO₂ as the sole carbon source was employed. For comparisons at different CO₂ concentrations, buffered medium without CO₂ was maintained as a control (unless otherwise mentioned) while the test samples contained varying concentrations of CO₂ (0.1–100%, v/v of gas phase unless mentioned). Growth was monitored by measuring an increase in optical density (OD_{660nm}), dry weight or bacteriochlorophyll content. For the adaptation studies of potent strains, the cultures were acclimatized to CO₂ by maintaining them for few subcultures in a medium supplemented with desired CO₂.

2.2. Biomass, carbon content and CO₂ fixation rate of *Rhodovulum viride* JA756

Triplicate samples of strain JA756 at each of the CO₂ concentration was checked for biomass concentration (g.L⁻¹) at regular time intervals by measuring the bacteriochlorophyll content (Blankenship et al., 1995; Clayton, 1966), optical density (OD_{660nm}) spectrophotometrically and a calibration curve of OD_{660nm} versus dry biomass was obtained. Productivity (g.L⁻¹.day⁻¹) was obtained according to Schmidell et al. (2001). Biomass carbon content was determined using a Thermo Finnigan Flash EA 1112 series CHNS (carbon, hydrogen, nitrogen and sulfur) element analyzer calibrated to 100% value using a cystine standard (de Moraes and Costa, 2007a). CO₂ fixation rate (g.L⁻¹.day⁻¹) at the respective CO₂ concentration was calculated from the CHNS biomass carbon content values (Zheng et al., 2011).

2.3. Genome sequencing and annotations

Genomic DNA was isolated from strain JA756 and sequencing was carried out using Illumina HiSeq 2500 by paired end chemistry which was outsourced from SciGenom Labs. The sequence data were *de novo* assembled using the SPAdes assembly software. The raw reads were checked for the quality and trimmed by using fastQC and fastx tools, respectively. tRNA and rRNA were predicted using RNAMmer. Annotations were performed using the Rapid Annotations using Subsystems Technology (RAST) server (Aziz et al., 2008).

2.4. RNA isolation and real time analysis

For transcription analysis of β -, γ - CA, small-, large subunits-RubisCO and PEPCK, JA756 was grown photolithoautotrophically at ambient CO₂ condition. The cells maintained as five replicates each were then treated with selective CO₂ concentrations of 0.1%, 5%, 10% and 20% during their mid-log phase. After a definite time of exposure to CO₂, the replicates from individual experiment were pooled together, to minimize biological variation and the cells were harvested by centrifugation (5000 rpm for 5 min, 4 °C), snap frozen in liquid nitrogen and stored at -80 °C until further process. Cells grown photo-organoheterotrophically (with pyruvate [22 mM] as carbon source and electron donor) were maintained as untreated control calibrators. The total RNA was isolated by the Trizol method (Rio et al., 2010) and cDNA synthesis was carried out for 2 μ g RNA. Real-time PCR using gene-specific primers (Supplementary table S3 online) was carried out in triplicates for each of the above genes along with *rpoZ* as a

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