

Ilhan Dogan · Krishna R. Pagilla · Dale A. Webster  
Benjamin C. Stark

## Expression of *Vitreoscilla* hemoglobin in *Gordonia amarae* enhances biosurfactant production

Received: 22 June 2005 / Accepted: 29 January 2006 / Published online: 21 February 2006  
© Society for Industrial Microbiology 2006

**Abstract** The gene (*vgb*) encoding *Vitreoscilla* (bacterial) hemoglobin (VHb) was electroporated into *Gordonia amarae*, where it was stably maintained, and expressed at about 4 nmol VHb g<sup>-1</sup> of cells. The maximum cell mass (OD<sub>600</sub>) of *vgb*-bearing *G. amarae* was greater than that of untransformed *G. amarae* for a variety of media and aeration conditions (2.8-fold under normal aeration and 3.4-fold under limited aeration in rich medium, and 3.5-fold under normal aeration and 3.2-fold under limited aeration in mineral salts medium). The maximum level of trehalose lipid from cultures grown in rich medium plus hexadecane was also increased for the recombinant strain, by 4.0-fold in broth and 1.8-fold in cells under normal aeration and 2.1-fold in broth and 1.4-fold in cells under limited aeration. Maximum overall biosurfactant production was also increased in the engineered strain, by 1.4-fold and 2.4-fold for limited and normal aeration, respectively. The engineered strain may be an improved source for producing purified biosurfactant or an aid to microorganisms bioremediating sparingly soluble contaminants in situ.

**Keywords** Bioremediation · Biosurfactant production · *Gordonia amarae* · Trehalose lipid production · *Vitreoscilla* hemoglobin

I. Dogan · D. A. Webster · B. C. Stark (✉)  
Biology Division, Department of Biological, Chemical,  
and Physical Sciences, Illinois Institute of Technology,  
IIT Center, Chicago, IL 60616, USA  
E-mail: starkb@iit.edu  
Tel.: +1-312-5673488  
Fax: +1-312-5673494

K. R. Pagilla  
Department of Chemical and Environmental Engineering,  
Illinois Institute of Technology, Chicago, IL 60616, USA

*Present address:* I. Dogan  
Department of Molecular Biology and Genetics,  
Izmir Institute of Technology, Izmir, Turkey

### Introduction

Release of organic contaminants into the environment can be problematic because of their toxicity and their stability. Bioremediation by microorganisms, however, can often be an effective method to clean up contaminated sites [29].

Use of biologically produced surfactants as a tool in bioremediation has become a subject of increasing study, as they can dramatically increase the apparent solubility of insoluble and sparingly soluble compounds so that they can be taken up by cells and metabolized [19]. Biosurfactants are produced and released by microorganisms during growth on insoluble substrates in water [7]. They are currently used in several applications, including bioremediation, in which, unlike synthetic surfactants, they themselves are biodegradable and pose no additional pollution threat. Furthermore, most studies indicate that they are non-toxic to microorganisms and therefore are unlikely to inhibit biodegradation [2].

As with other microbial fermentations the goal in production of biosurfactants is to maximize productivity, and achieve high final concentrations [12]. In this way it is possible that solubilization and biodegradation rates of insoluble substrates can be increased by microorganisms. It has been reported that *Nocardia* species that are grown on hydrocarbons produce biosurfactants [23, 25]. In particular, the bacterium *Gordonia amarae* (previously known as *Nocardia amarae*) has been shown to produce biosurfactants that enhance removal of non-ionic organic contaminants from water [28, 36].

It has been demonstrated that expression of bacterial hemoglobin (VHb) in heterologous bacterial hosts engineered to contain the VHb gene (*vgb*) often results in enhancement of cell density, oxidative metabolism, protein and antibiotic production, and bioremediation, especially under oxygen-limiting conditions [17, 24, 35, 39, 40]. The beneficial effects of *vgb* have also been demonstrated in a variety of eukaryotes. These include

enhancement of antibiotic production in fungi [9], tissue plasminogen activator production in mammalian cells [31], and growth in plants and plant cell cultures [11, 14]. There is evidence that the beneficial effects in bacteria are the result of direct interaction of VHb with the terminal respiratory oxidase, delivering oxygen to it to enhance oxidative phosphorylation and thus the production of ATP [16, 30, 32]. In the case of bioremediation enhancement, a direct delivery of oxygen by VHb to oxygenases which degrade aromatics may occur [20, 21].

In the work reported here, *vgb* was electroporated into *G. amarae* and expressed in the resulting recombinant cells where it enhanced both growth and biosurfactant production. This is the first report in which engineering with *vgb* has been used in this way as a possible strategy to enhance biodegradation of sparingly soluble compounds. It suggests that engineering of biosurfactant-producing bacteria with *vgb* may be a useful way to extend the possible uses of *vgb* in strain improvement for bioremediation.

## Materials and methods

### Bacterial strains, plasmids, and media

*Gordonia amarae* (NRRL B-8176) was provided by the USDA National Center for Agriculture Utilization Research (Peoria, IL, USA). Plasmid pSC160 had been constructed [22] by inserting linearized pUC8:16 (which carries *vgb* on a 1.4 kb fragment from *Vitreoscilla* strain C1 [10] cloned into vector pUC8) into the *EcoRI* site of broad host range vector pKT230; pSC160 provides resistance to kanamycin and ampicillin. Routine plasmid maintenance and cloning utilized *Escherichia coli* DH5 $\alpha$ . Selection and routine strain maintenance used plates made from LB or LB with various antibiotics (LB<sub>Km</sub>+Amp, kanamycin, 40  $\mu\text{g ml}^{-1}$ , ampicillin, 100  $\mu\text{g ml}^{-1}$ ; LB<sub>Sm</sub>, streptomycin, 100  $\mu\text{g ml}^{-1}$ ), as appropriate.

### Construction of recombinant *G. amarae* strain

*Gordonia amarae* chromosomal DNA was isolated using Wizard Genomic DNA purification kits (Promega). Both this DNA and pSC160 were cleaved by *SacI*, and random *Gordonia* chromosomal DNA *SacI* fragments were ligated into the single *SacI* site in the plasmid. After transformation into *E. coli* DH5 $\alpha$ , recombinant strains were selected by resistance to the antibiotics ampicillin and kanamycin and sensitivity to sulphonamide and streptomycin (as the *SacI* site lies within the Sm<sup>r</sup> gene in pKT230/pSC160). For routine screening, recombinant plasmids were isolated from DH5 $\alpha$  using the method of Holmes and Quigley [15], but isolations for use for electroporation, used QIAprep Spin Miniprep Kits

(Qiagen). Recombinant plasmids were confirmed by restriction analysis.

*Gordonia amarae* cells were made competent and transformed with recombinant plasmids via electroporation (Gene Pulser; Bio-Rad Laboratories) according to the manufacturer's protocol. After electroporation, presumptive recombinant strains were selected by resistance to kanamycin and ampicillin and sensitivity to streptomycin-sulphonamide. Wild type *G. amarae* showed natural resistance to kanamycin to some degree; therefore, kanamycin and ampicillin were used together for selection. Control electroporations using *G. amarae* cells but no DNA yielded no colonies.

### Confirmation of *G. amarae* transformants

Total cell DNA was isolated from presumptive recombinant as well as untransformed *G. amarae* using Promega Wizard kits. PCR was run on these samples using primers which amplify a 0.3 kb internal portion of *vgb* [6]. Presence of VHb in presumptive *G. amarae* transformants was determined by running CO-difference spectra on whole cell extracts (late log-early stationary phase) according to the method of Dikshit and Webster [10]. Cell extracts were obtained (from presumptive transformants and untransformed cells) by suspending cells to 50 mg ml<sup>-1</sup> in potassium phosphate, pH 7.2 and sonicating for 10 min, followed by centrifugation to remove cell debris. VHb levels were calculated using the extinction coefficient  $E_{419-436\text{nm}} = 274 \text{ mM}^{-1} \text{ cm}^{-1}$ . BBL Columbia CNA SB agar and MacConkey agar, as well as Gram staining, were used for further characterization of the transformant.

### Growth measurements

For initial growth experiments the medium was either LB [27], or mineral salts medium [5] containing 0.5% (w/v) sodium acetate trihydrate. Single colonies of the untransformed and *vgb*-bearing *G. amarae* were inoculated into 5 ml of medium and grown overnight at 30°C and 200 rpm. For each experiment the two overnight cultures were diluted as necessary to contain an equal OD<sub>600</sub>. One hundred microliter of each diluted culture (containing 0.008 to 0.062 OD<sub>600</sub> units) was inoculated into the same medium (100 ml for normal aeration and 300 ml for limited aeration) in a 500 ml Erlenmeyer flask. In all cases this gave an OD<sub>600</sub> at time zero of 0.000. Incubation was at 30°C at either 200 rpm (normal aeration) or 50 rpm (limited aeration). Growth was monitored by OD<sub>600</sub> (samples were diluted as necessary with appropriate medium to maintain measured OD's below 0.5) and viable counts.

Although continuous oxygen monitoring was not practical for these shake flask cultures (and those described in the following section), rough adjustment of culture oxygen levels can be obtained by variation in

shaking speed and culture volume to vessel volume ratio [6, 16].

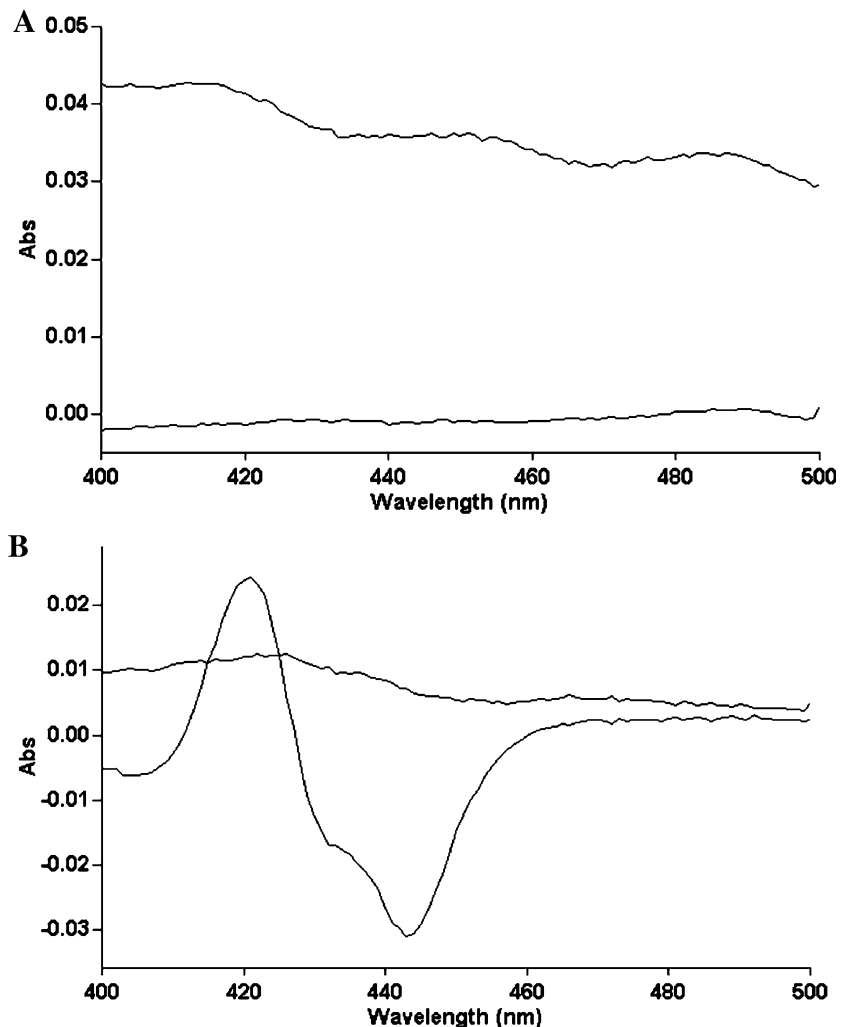
#### Trehalose lipid and biosurfactant measurements

For measurements of trehalose lipid and overall biosurfactant production, cells were cultured in a manner similar to that described above in LB plus 1% (v/v) hexadecane (which is known to induce biosurfactant production [8]). Inocula were prepared from overnight LB cultures as described in the previous section. For each experiment 0.8 ml containing an equal  $OD_{600}$  (0.31–0.35  $OD_{600}$  units) was inoculated into 800 ml medium in 4 or 1.5 l shake flasks for normal and limited aeration, respectively. In all cases this gave an  $OD_{600}$  at time zero of 0.000. Homogeneity of the cultures was maintained by using vigorous agitation with a magnetic stirrer; for both normal and limited aeration the stirrer speeds were the same. Cultures were incubated at room temperature. Samples were taken periodically to measure growth (by  $OD_{600}$  as described above) and trehalose lipid concentration by the anthrone method [13]. Trehalose lipid

determinations were made on both cells and cell free culture medium, which were separated from each other by centrifugation.

Samples from the cultures taken for trehalose lipid determinations were also used for measurements of surface tension. In these cases each sample was clarified by centrifugation and then filtered through a 0.45  $\mu\text{m}$  filter. Surface tension of these samples was measured by the upward pull method using a Du Nuoy tensiometer (Fisher Model 70535) equipped with a 6-cm circumference platinum–iridium ring. Before each experiment, the ring was rinsed with distilled water and flamed to destroy any organic matter on it. Data were collected as surface tension in dynes per centimeter. The critical micelle concentration (CMC) is the concentration of biosurfactant at which the surface tension reaches its lowest value and does not decrease any further with increased biosurfactant concentration. Each sample was serially diluted with distilled water until the surface tension increased from the lowest value. The dilution factor represents the XCMC (times CMC) of the biosurfactant concentration in the culture broth [28].

**Fig. 1** CO-difference spectra of untransformed (a) and recombinant (b) *G. amarae* cell extracts. The (approximately) horizontal line in each panel is the baseline



## Results and discussion

### Construction of recombinant plasmids and selection of *G. amarae* transformants

After the ligation of random *Gordonia* chromosomal DNA *SacI* fragments into the single *SacI* site in plasmid pSC160 and transformation of the ligation mixture into *E. coli* DH5 $\alpha$ , three recombinant plasmids were identified. Large amounts of these plasmids were produced and used for electroporation into *G. amarae*.

Homologous recombination between the *Gordonia* sequence within the plasmid and the corresponding sequences in the *Gordonia* chromosome presumably integrated the entire plasmid, including pSC160 and thus the *vgb* gene, into the *Gordonia* chromosome in each case (similar to what has been shown to occur in *Thermus* [18]). After 2 electroporation experiments, 11 recombinant strains were identified by resistance to kanamycin and ampicillin and sensitivity to streptomycin–sulphonamide. It is also possible that pSC160 can exist autonomously in *G. amarae*, although the likelihood for that event is unknown. Plasmid pSC160, however, is derived from plasmid RSF1010, which belongs to the Inc Q/P4 plasmid incompatibility group that can be propagated in a very extensive host range extending to Gram-positive bacteria and eukaryotes [26, 34, 37]. One of the recombinant strains (from electroporation using a recombinant plasmid with a 5.5 kb insert) was chosen for further studies.

### Confirmation of *vgb*-bearing *G. amarae*

The presence of *vgb* in the recombinant *G. amarae* strain was verified by PCR using a set of primers that amplify a 0.3 kb portion of *vgb*. Untransformed *G. amarae* was used as a negative control. Only genomic DNA from the recombinant *G. amarae* produced a 0.3 kb fragment identical in size to that amplified using plasmid pSC160 as template.

VHb expression was checked using CO-difference spectra (in which VHb has a characteristic absorption maximum at 419 nm and minimum at 436 nm [10]). Cell free extracts from untransformed *G. amarae* showed neither peak nor trough, while the recombinant *G. amarae* cell free extracts showed a peak at approximately 420 nm, that was broader than that observed in *Vitreoscilla* or *E. coli* expressing VHb [10], and a trough at about 445 nm with a shoulder near 435 nm (Fig. 1). The reasons for these changes from the standard spectrum are unknown, but similar changes to the VHb CO-spectrum have also been observed in *Pseudomonas aeruginosa* [22] and *Burkholderia cepacia* [6].

The VHb level for the recombinant strain was about 4 nmole g<sup>-1</sup> wet weight of cells, which is about eightfold lower than that seen in *Vitreoscilla* and about 60-fold lower than *E. coli* bearing *vgb* on a high copy number

plasmid [10]. This is somewhat lower than levels which resulted in positive effects in *Pseudomonas* (8.8 nmol g<sup>-1</sup>) but higher than those that were not effective in *Burkholderia* (0.8 nmol g<sup>-1</sup>) [6]. It is, however, the lowest level we have found so far that is beneficial to any of the species we have transformed with the VHb gene.

### Characteristics of the recombinant strain

Both transformed and untransformed *G. amarae* grew on BBL Columbia CNA SB agar (supports growth for only Gram-positive bacteria) but not MacConkey agar (supports growth for only Gram-negative bacteria). Colonies of the transformant on LB plates were about twice the diameter of those of the untransformed strain. Gram staining showed that both the untransformed *G. amarae* (approximately 90% Gram-positive and 10% Gram-negative) and the recombinant *G. amarae* (approximately 10% Gram-positive and 90% Gram-negative) were Gram-variable. *Gordonia* are known to be Gram-variable [1], but the reason(s) for the difference

**Table 1** Growth of the untransformed (“wt”) and hemoglobin-bearing (“rec”) strains as measured by both OD<sub>600</sub> and viable cell counts as described in the text

Strain, medium, aeration	OD <sub>600</sub>	Time (h)
OD <sub>600</sub>		
wt, min, normal aeration	0.055 (0.001)	120
rec, min, normal aeration	0.19 (0)	72
wt, min, limited aeration	0.037 (0.003)	120
rec, min, limited aeration	0.12 (0.002)	120
wt, LB, normal aeration	1.13 (0.03)	72
rec, LB, normal aeration	3.15 (0.12)	96
wt, LB, limited aeration	0.16 (0.004)	120
rec, LB, limited aeration	0.54 (0.06)	96
wt, LB+hexadecane, normal aeration	1.08 (0.12)	96
rec, LB+hexadecane, normal aeration	2.50 (0.04)	120
wt, LB+hexadecane, limited aeration	0.80 (0.14)	144
rec, LB+hexadecane, limited aeration	1.45 (0.45)	144
Viable cell counts		
wt, min, normal aeration	2.63E+08 (2.30E+07)	72
rec, min, normal aeration	2.54E+09 (7.21E+07)	72
wt, min, limited aeration	8.00E+07 (2.07E+06)	72
rec, min, limited aeration	1.10E+09 (8.02E+07)	96
wt, LB, normal aeration	5.00E+09 (1.97E+07)	48
rec, LB, normal aeration	3.00E+10 (1.91E+09)	48
wt, LB, limited aeration	5.11E+08 (8.00E+05)	24
rec, LB, limited aeration	1.70E+09 (7.21E+07)	96

Data are maximum values for growth under both normal and limited aeration, and in LB, LB plus 1% v/v hexadecane, and mineral salts (“min”) media. Values are averages of three replicates (standard deviations in parentheses). Data were collected for 144 h for the experiments using LB plus hexadecane and 120 h for all other experiments; data points were taken at 0 h (inoculation) and at 4–24 h intervals thereafter; values in the rightmost column are times at which each maximum occurred. Experiments utilizing LB plus hexadecane measured only OD<sub>600</sub> (and not viable counts)

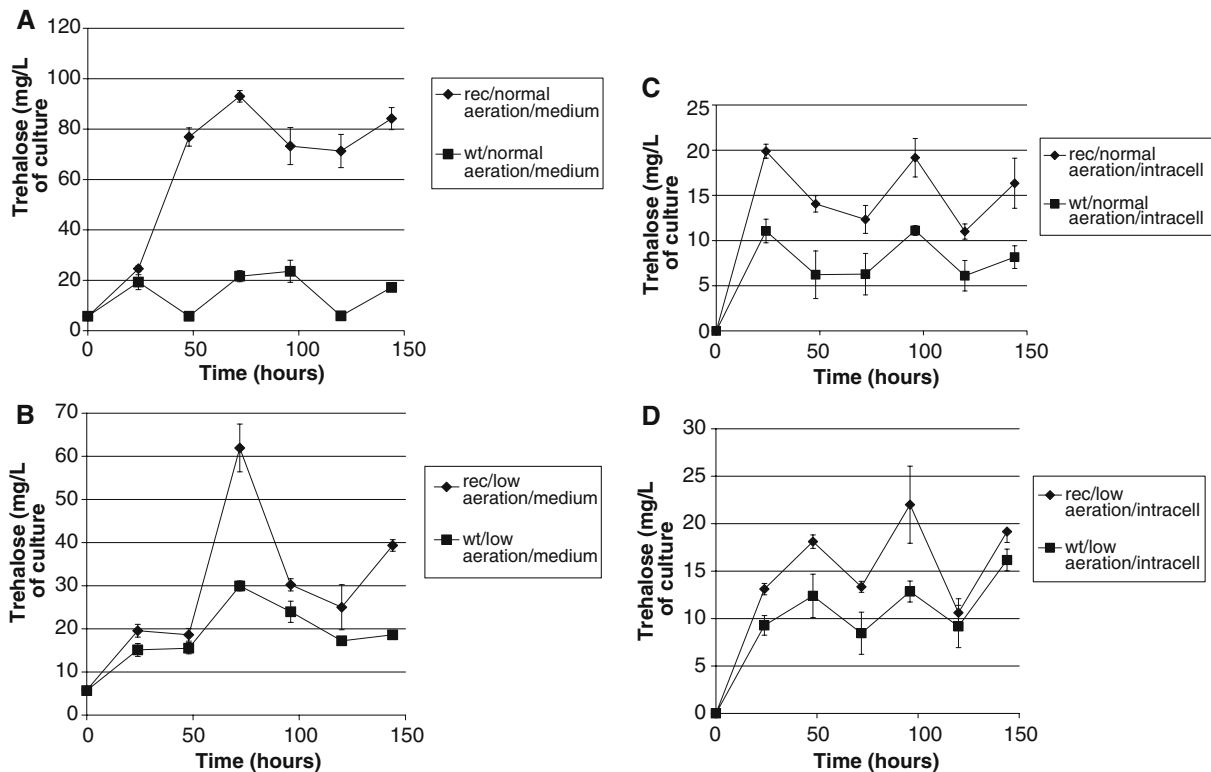
we see between transformed and untransformed strains in this property is not known. Gram variability has been shown to be related to the growth stage for a number of bacteria [3], which indicates that changes in the physiological state of cells could be its cause. The presence of *Vitreoscilla* hemoglobin (VHb) in *E. coli* cells has been shown to result in significant changes in the expression of hundreds of genes compared to cells which were not transformed with VHb [33]. If similar changes in gene expression occur in *Gordonia*, they might also lead to significant physiological changes which, in turn, affect Gram staining.

Despite its difference from the untransformed strain in Gram staining and colony characteristics, the identity of the transformed strain as *G. amarae* is supported by the following: (a) control electroporations using our *G. amarae* cultures and no DNA never gave any colonies, lessening the probability that some contaminant was present in the electroporated samples; (b) the transformants had precisely the drug resistance/sensitivity expected, which would be unlikely to occur from a random contaminant; (c) both transformant and untransformed cells grew on CNA SB agar, but neither grew on MacConkey agar; and (d) both transformant and untransformed cells produced extracellular biosurfactant and trehalose lipid.

The transformed strain was stable as indicated by its retention of both the antibiotic resistance provided by the vector pSC160 (which will remain with *vgb* whether on the plasmid or integrated into the host chromosome) and colony morphology upon repeated transfer of the recombinant strain over many months.

### Growth comparisons

Growth of untransformed and *vgb*-bearing *G. amarae* was compared in three different media for both normal and limited aeration (Table 1). In both LB and mineral salts medium plus sodium acetate and at both aerations the presence of *vgb*/VHb provided a substantial advantage regarding both maximum OD<sub>600</sub> and maximum viable cells. The advantages regarding OD<sub>600</sub> ranged from 2.8X to 3.5X and were similar at both aerations. The advantages regarding viable cells ranged from 3.3X to 14X and were greater in mineral salts medium. When cells were grown in LB plus hexadecane the advantages in maximum OD<sub>600</sub> were 1.8X and 2.3X for the VHb producing cells at limited and normal aerations, respectively. These figures are within the ranges seen in previous work. In some cases the presence of VHb in recombinant bacteria has resulted in no growth



**Fig. 2** Intra- and extracellular (*medium*) trehalose lipid concentrations (expressed as milligram trehalose per liter of culture) for the recombinant (*rec*) and the non-transformed (*wt*) strains grown under both normal and low aeration. **a** Medium concentrations for normal aeration; **b** medium concentrations for low aeration; **c** intracellular concentrations for normal aeration; **d** intracellular

concentrations for low aeration. Times indicate hours after inoculation that samples were taken. Growth data for the cultures are the last four entries in Table 1, OD<sub>600</sub>; late log phase was about 72 h for the recombinant strain under low aeration and about 48 h otherwise. Values are averages of three individual measurements. *Error bars* indicate standard deviations

advantage or even a slight growth disadvantage compared to VHB-free cells [4, 22], and sometimes to advantages as high as 2–3X on a dry cell mass basis [38] and as high as about 40X on a viable cell basis [39].

#### Trehalose lipid and overall biosurfactant determinations

Growth in LB plus hexadecane was also used to measure trehalose lipid production. This compound is a component of *G. amarae* produced biosurfactant, although its percentage of total biosurfactant is unknown. Biosurfactants include a variety of compounds, among which glycolipids are the major fraction [12]. As trehalose lipid is one of these glycolipids, its measurement is a useful indicator of biosurfactant production. Our measurement of overall biosurfactant levels (discussed below) supplemented the trehalose data to provide a more complete picture of biosurfactant levels. Hexadecane was included in the medium, as biosurfactant production is significantly greater when a hydrophobic carbon source is added to the growth medium [28]. The details of the genetics of this hexadecane effect, however, are not known.

The presence of VHB enhanced trehalose lipid production in the recombinant strain in both the broth and in cells (Fig. 2). Under normal aeration, the recombinant strain improved the maximum trehalose lipid level in the medium and cells by 4.0X and 1.8X, respectively. Under limited aeration, the same advantages of the recombinant strain were 2.1X and 1.4X, respectively. These differences in maximum biosurfactant levels are significant because biosurfactant would be harvested in batch experiments at these peaks. The levels of both intra- and extracellular (i.e., medium) trehalose lipid were determined for sake of completeness. The extracellular levels are perhaps most important, however, because of the relative ease of harvesting trehalose lipid from the medium.

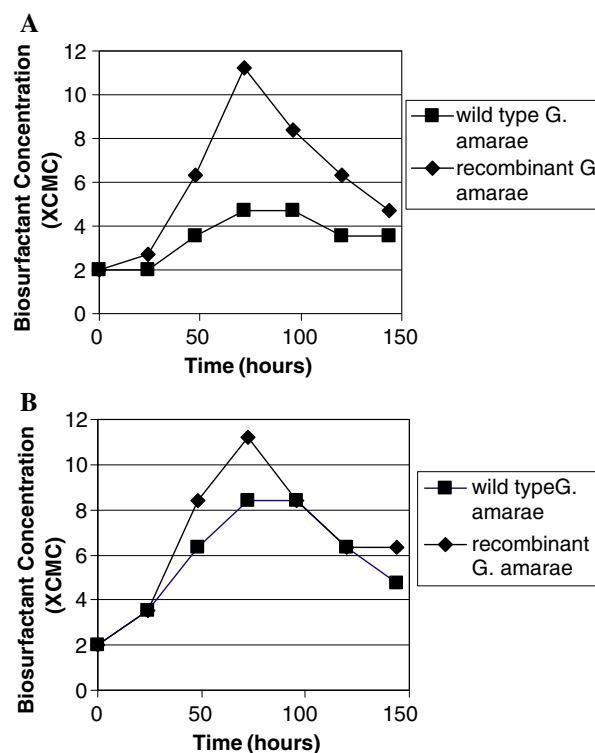
The levels of trehalose lipid measured for *G. amarae* by Pagilla et al. [28] were similar to those found in this study both in order of magnitude and in the cyclical nature of maxima and minima as a function of time in culture. This cyclical pattern is thought to be due to repeated periods of biosurfactant production, consequent solubilization of hexadecane, uptake of hexadecane and biosurfactant, and biodegradation of biosurfactant.

Another measure of biosurfactant production during growth is surface tension of the culture medium, which decreases with increased biosurfactant production, and after reaching a threshold, does not change further. As mentioned above, this threshold biosurfactant concentration is called the CMC. This technique is commonly used to measure the extent of biosurfactant production and is represented as XCMC [28]. For growth at both normal and limited aeration there was a greater production of biosurfactant (by this measurement) for the *vgb*-bearing strain as compared to its untransformed counterpart, and these differences paralleled roughly the

differences seen in trehalose lipid production between the two strains (Fig. 3). As was the case for trehalose lipid, the difference between *vgb*-bearing and untransformed strains was greater at normal than at limited aeration.

That the time courses of trehalose lipid measurements and biosurfactant levels determined by the surface tension assay are not identical is perhaps not surprising, since the surface tension data are a measure of total biosurfactant, of which trehalose lipid is only one component.

The presence of VHB is usually, although not always, most effective regarding its positive effects when cells are grown in limited aeration conditions [35]. In the case of *G. amarae*, the positive effects (growth, trehalose lipid production, overall biosurfactant production) are similar or greater at normal versus limited aeration. The reasons for this are not known, but in *Vitreoscilla*, *E. coli*, and perhaps other bacteria, VHB levels increase under hypoxic conditions (thus, presumably leading to a greater relative advantage of VHB-producing cells when aeration is limited), and this may not occur in



**Fig. 3** Biosurfactant concentration [at normal (a) and limited (b) aeration] in cell free culture medium (measured in terms of XCMC) versus growth time. For each time point, data from identical dilution series of medium from three replicate cultures were averaged and used to construct a surface tension versus dilution plot. From each plot, one of the data points in **a** and **b** was calculated, using the method referenced in the text. Times indicate hours after inoculation that samples were taken. Growth data for the cultures are the last four entries in Table 1,  $OD_{600}$ ; late log phase was about 72 h for the recombinant strain under low aeration and about 48 h otherwise

*G. amarae*. It is also possible that the uptake of dissolved oxygen (DO) may be very high when hexadecane is present in the growth medium as an additional carbon source, and limited aeration conditions may not be sufficient to provide sufficient DO, even with VHb. In fact, Pagilla et al. [28] used pure oxygen instead of air to supply DO when 1% hexadecane was used for biosurfactant production with this species.

In summary, then, genetic engineering of biosurfactant producing strains with *vgb* may be an effective method to increase biosurfactant production. This approach may be useful in both in situ applications, where inoculation of an engineered bacterial strain into a site contaminated with a sparingly soluble chemical can continuously produce biosurfactant to enhance metabolism of this compound by itself or another species, or for enhanced production of biosurfactant for purification and utilization in that form to replace synthetic surfactants.

**Acknowledgements** This work was supported by NSF grant number MCB-9910356. We thank Dr. John Kilbane for helpful discussions, Dr. Kevin Kayser for help with electroporation, and Dr. Sangeeta Patel for help with the Gram staining.

## References

- Arenskotter M, Broker D, Steinbuchel A (2004) Biology of the metabolically diverse genus *Gordonia*. *Appl Environ Microbiol* 70:3195–3204
- Banat IM, Makkar RS, Cameotra SS (2000) Potential commercial applications of microbial surfactants. *Appl Microbiol Biotechnol* 53:495–508
- Beveridge TJ (1990) Mechanism of gram variability in select bacteria. *J Bacteriol* 172:1609–1620
- Buddenhagen RE, Webster DA, Stark BC (1996) Enhancement by bacterial hemoglobin of amylase production in recombinant *E. coli* occurs under conditions of low O<sub>2</sub>. *Biotechnol Lett* 18:695–700
- Cha DK (1990) Process control factors influencing *Nocardia* populations in activated sludge. PhD Dissertation, University of California, Berkeley
- Chung JW, Webster DA, Pagilla KR, Stark BC (2001) Chromosomal integration of the *Vitreoscilla* hemoglobin gene in *Burkholderia* and *Pseudomonas* for the purpose of producing stable engineered strains with enhanced bioremediating ability. *J Ind Microbiol Biotechnol* 27:27–33
- Cooper DG, Zajic JE (1980) Surface active compounds from microorganisms. *Adv Appl Microbiol* 26:229–253
- Davis JB (1964) Cellular lipids of a *Nocardia* grown on propane and n-butane. *Appl Microbiol* 12:301–304
- De Modena JA, Gutierrez S, Velasco J, Fernandez FJ, Fachini RA, Galazzo JL, Hughes DE, Martin JF (1993) The production of cephalosporin C by *Acremonium chrysogenum* is improved by the intracellular expression of a bacterial hemoglobin. *Biotechnology* 11:926–929
- Dikshit KL, Webster DA (1988) Cloning, characterization and expression of the bacterial globin gene from *Vitreoscilla* in *E. coli*. *Gene* 70:377–386
- Farres J, Kallio PT (2002) Improved cell growth in tobacco suspension cultures expressing *Vitreoscilla* hemoglobin. *Biotechnol Prog* 18:229–233
- Georgiou G, Lin S-C, Sharma MM (1992) Review of surface-active compounds from microorganisms. *Biotechnology* 10:60–65
- Hodge JE, Hofreiter BT (1962) Determination of reducing sugars and carbohydrates. *Methods Carbohydr Chem* 1:389–390
- Holmberg N, Lilius G, Bailey JE, Bulow L (1997) Transgenic tobacco expressing *Vitreoscilla* hemoglobin exhibits enhanced growth and altered metabolite production. *Nat Biotechnol* 15:244–247
- Holmes DS, Quigley M (1981) A rapid boiling method for the preparation of bacterial plasmids. *Anal Biochem* 114:193–197
- Kallio PT, Kim DJ, Tsai PS, Bailey JE (1994) Intracellular expression of *Vitreoscilla* hemoglobin alters *Escherichia coli* energy metabolism under oxygen-limited conditions. *Eur J Biochem* 219:201–208
- Kang DG, Kim JYH, Cha HJ (2002) Enhanced detoxification of organophosphates using recombinant *Escherichia coli* with coexpression of organophosphorus hydrolase and bacterial hemoglobin. *Biotechnol Lett* 24:879–883
- Kayser KJ, Kilbane JJ (2001) New host-vector system for *Thermus* spp. based on the malate dehydrogenase gene. *J Bacteriol* 183:1792–1795
- Lang S, Wagner F (1987) Structure and properties of biosurfactants. In: Kosaric N, Cairns WL (eds) *Biosurfactants and biotechnology*. Marcel Dekker, New York, pp 21–46
- Lee SY, Stark BC, Webster DA (2004) Structure-function studies of the *Vitreoscilla* hemoglobin D-region. *Biochem Biophys Res Commun* 316:1101–1106
- Lin JM, Stark BC, Webster DA (2003) Effects of *Vitreoscilla* hemoglobin on the 2,4-dinitrotoluene (DNT) dioxygenase activity of *Burkholderia* and on DNT degradation in two-phase bioreactors. *J Ind Microbiol Biotechnol* 30:362–368
- Liu SC, Webster DA, Stark BC (1995) Cloning and expression of the *Vitreoscilla* hemoglobin gene in *Pseudomonas*: effects on cell growth. *Appl Microbiol Biotechnol* 44:419–424
- MacDonald CR, Cooper DG, Zajic JE (1981) Surface-active lipids from *Nocardia erythropolis* grown on hydrocarbons. *Appl Environ Microbiol* 41:117–123
- Magnolo SK, Leenutaphong DL, De Modena JA, Curtis JE, Bailey JE, Galazzo JL, Hughes DE (1991) Actinorhodin production by *Streptomyces coelicolor* and growth of *Streptomyces lividans* are improved by the expression of a bacterial hemoglobin. *Biotechnology* 9:473–476
- Margaritis A, Kennedy K, Zajic JE, Gerson DF (1979) Biosurfactant production by *Nocardia erythropolis*. *Dev Ind Microbiol* 20:623–630
- Mazodier P, Petter R, Thompson C (1989) Intergeneric conjugation between *E. coli* and *Streptomyces* species. *J Bacteriol* 171:3583–3585
- Miller JH (1972) *Experiments in molecular genetics*. Cold Spring Harbor Laboratory, Cold Spring Harbor
- Pagilla KR, Kim H, Sood A (2002) *Gordonia amarae* foaming due to biosurfactant production. *Water Sci Technol* 46:519–524
- Parales RE, Bruce NC, Schmid A, Wackett LP (2002) Biodegradation, biotransformation, and biocatalysis (B3). *Appl Environ Microbiol* 68:4699–4709
- Park KW, Kim KJ, Howard AJ, Stark BC, Webster DA (2002) *Vitreoscilla* hemoglobin binds to subunit I of cytochrome *bo* ubiquinol oxidases. *J Biol Chem* 277:33334–33337
- Pendse GJ, Bailey JE (1994) Effect of *Vitreoscilla* hemoglobin expression on growth and specific tissue plasminogen activator productivity in recombinant Chinese hamster ovary cells. *Biotechnol Bioeng* 44:1367–1370
- Ramendep, Hwang KW, Rajee M, Kim KJ, Stark BC, Dikshit KL, Webster DA (2001) *Vitreoscilla* hemoglobin: intracellular localization and binding to membranes. *J Biol Chem* 276:24781–24789
- Roos V, Andersson CIJ, Bulow L (2004) Gene expression profiling of *Escherichia coli* expressing double *Vitreoscilla* haemoglobin. *J Biotechnol* 114:107–120
- Schafer A, Kalinowski J, Simon R, Seep-Feldhaus A-H, Puhler A (1990) High-frequency conjugal plasmid transfer from Gram-negative *E. coli* to various Gram-positive coryneform bacteria. *J Bacteriol* 172:1663–1666

35. Stark BC, Webster DA, Dikshit KL (1999) *Vitreoscilla* hemoglobin: molecular biology, biochemistry, and practical applications. *Recent Res Dev Biotech Bioeng* 2:155–174
36. Sutton R (1992) Removal of sparingly soluble organic chemicals from aqueous solutions by biosurfactants produced by *Nocardia amarae*. MS Thesis, Illinois Institute of Technology, Chicago
37. Trieu-Cuot P, Carlier C, Martin P, Courvalin P (1987) Plasmid transfer by conjugation from *E. coli* to Gram-positive bacteria. *FEMS Microbiol Lett* 48:289–294
38. Tsai PS, Hatzimanikatis V, Bailey JE (1996) Effect of *Vitreoscilla* hemoglobin dosage on microaerobic *Escherichia coli* carbon and energy metabolism. *Biotechnol Bioeng* 49:139–150
39. Urgan-Demirtas M, Pagilla KR, Stark BC, Webster DA (2003) Biodegradation of 2-chlorobenzoate by recombinant *Burkholderia cepacia* expressing *Vitreoscilla* hemoglobin under variable levels of oxygen availability. *Biodegradation* 14:357–365
40. Urgan-Demirtas M, Pagilla KR, Stark BC (2004) Enhanced kinetics of genetically engineered *Burkholderia cepacia*: role of *vgb* in the hypoxic metabolism of 2-CBA. *Biotechnol Bioeng* 87:110–118