Different *gvpC* length variants are transcribed within single filaments of the cyanobacterium *Planktothrix rubescens*

Sven Becker, Paul K. Hayes and Anthony E. Walsby

School of Biological Sciences, University of Bristol, Woodland Road, Bristol BS8 1UG, UK

Transcripts of the gas vesicle genes *gvpA* and *gvpC* were detected in single filaments of the cyanobacterium *Planktothrix rubescens* using reverse transcription and quantitative real-time PCR. Primers were designed to amplify short sequences within *gvpA* and three length variants of *gvpC*. With genomic template DNA, and using Sybr Green to monitor product accumulation, similar amplification efficiencies were observed for each of these genes. The relative copy numbers of *gvpC* length variants in genomic DNA from five *Planktothrix* gas vesicle genotypes determined by real-time PCR were similar to those indicated by sequencing the gas vesicle gene clusters. The precipitation of *gvp* cDNA reverse-transcribed from cellular RNA from single filaments was required before amplification of the gene fragments; without this step it was not possible to detect the accumulation of the expected amplicons by dissociation analysis. Precipitation was also necessary to ensure the generation of product curves that allowed linear regression in an early stage of PCR, a prerequisite for the quantification of low-input cDNA amounts without the need for standard curves. This report shows that different *gvpC* length variants are transcribed within single *Planktothrix* filaments, both from laboratory cultures and from natural samples taken from Lake Zürich. This has implications for the efficiency of buoyancy provision by the possible production of gas vesicles of different strengths within individual cyanobacterial filaments. The hypothesis that post-transcriptional regulation may influence the type of protein (GvpC) present in gas vesicles is presented.

**INTRODUCTION**

In planktonic cyanobacteria, gas vesicles, which may account for about 10% of total cell protein, provide buoyancy and enable these organisms to control their depth on vertically decreasing light gradients in lakes. Gas vesicles are an important factor in cyanobacteria outcompeting other phytoplankton organisms (Oliver, 1994). Measurements of the rates at which cyanobacteria change their buoyant density when placed at different irradiances form the basis of understanding the vertical distribution of cyanobacteria in lakes and reservoirs (e.g. Kromkamp & Walsby, 1990); however, the observations that have been made on buoyancy change are several levels of understanding away from the molecular mechanisms that control buoyancy.

The buoyant density of a cell is determined by several classes of components which make the cell either more or less dense than water; of these, only the gas vesicle provides significant buoyancy. Gas vesicles are made entirely of proteins, which form a cylindrical shell enclosing a hollow space. There are two principal protein components, GvpA, which forms the ribs of the hollow cylindrical structure, and GvpC, which binds to the outer surface of the ribs, strengthening them against collapse by external pressure (for review see Walsby, 1994). Proteins encoded by other gas vesicle genes have been detected in gas vesicles of halobacteria (Shukla & DasSarma, 2004). GvpD and GvpE have been found to function as a repressor and activator, respectively, of the promoter for *gvpA* in *Halobacterium salinarum* (Pfeifer et al., 2002).

In cyanobacteria, changes in gas vesicle production have been studied in species of *Anabaena* and *Planktothrix* (*Oscillatoria*) (Oliver & Walsby, 1984; Utkilen et al., 1985), but what determines these changes at the molecular level is not known. However, it is assumed that a change in gas vesicle production must involve changes in the expression of relevant genes. The genes involved in gas vesicle production have been identified and sequenced in several cyanobacteria; the principal protein-encoding structural genes, *gvpA* and *gvpC*, occur in various arrangements in gene clusters containing additional ORFs. *Planktothrix* spp. possess *gvpA* genes that are nearly identical to those in *Anabaena* and *Calothrix* sp.; the *gvpC* genes, however, show only limited similarity to those in these two organisms.
(Griffiths et al., 1992; Albouy et al., 2001). In Anabaena there are multiple gvpA cistrons in tandem repeat followed by a single copy of gvpC (Hayes & Powell, 1995); in Planktothrix there are two or more copies of both gvpA and gvpC in an alternating arrangement (Beard et al., 1999).

Specific promoter regions of gas vesicle gene operons have not been investigated in cyanobacteria; however, in Calothrix it has been demonstrated by Northern hybridization that gvpA and gvpC are co-transcribed (Damerval et al., 1987), while Anabaena produces single and multicistronic gvpA transcripts and also transcripts containing both gvpA and gvpC (Hayes & Powell, 1995). The gvp transcripts from Planktothrix sp. strain CYA18 are considerably longer than predicted for the single ORFs (J. Kromkamp & P. K. Hayes, 1995). There are multiple gvpC and gvpA in Anabaena and Planktothrix (Griffiths et al., 1992; Albouy et al., 2000). This allows a selection of different gas vesicle genotypes in lakes of different depths (Walsby & Bleything, 1988; Bright & Walsby, 1999).

For cyanobacterial genotypes with two gvpC length variants it is not known whether the genes are expressed differentially in response to environmental conditions. In order to perform culture-independent in situ studies on single filaments, a sensitive and specific methodology is needed to detect very low amounts of gvpC transcripts. This is possible with quantitative real-time PCR. The real-time monitoring of amplicon accumulation in PCR allows calibration by the threshold-cycle method (Heid et al., 1996), i.e. quantification is based on the number of cycles required to reach a certain concentration of amplicons rather than on the concentration reached after a fixed number of cycles in end-point analysis. The threshold cycle \( C_T \) is defined as the number of PCR cycles at which a fluorescence signal, developed by a dye–template complex or by TaqMan chemistry (Becker et al., 2000), exceeds a pre-set value. The \( C_T \) value is reached in few PCR cycles if a large number of templates is initially present, but requires many cycles if the reaction starts with few templates.

In this study we describe a protocol for the reverse-transcription of mRNA from a single cyanobacterial filament to cDNA, which is then used as a template in real-time PCR for the detection of different gas vesicle gene (gvp) transcripts. We demonstrate the potential of this methodology for the measurement of transcript abundance of individual genes in single filaments grown in laboratory culture or collected from their natural environment. Such studies will extend the knowledge of buoyancy regulation in cyanobacteria and their vertical movements in lakes.

**METHODS**

**Cyanobacterial cultures.** Planktothrix rubescens strains Pla 9303, Pla 9316 (Walsby et al., 1998) and Pla 9736 (Beard et al., 1999) from Lake Zürich and PCC 7821 from Lake Gjerseen in Norway (Skulberg & Skulberg, 1985) were grown at 20°C in 100 ml mineral medium (Bright & Walsby, 2000) in an incident photon irradiance of 3–10 \( \mu \)mol m\(^{-2}\) s\(^{-1}\).

**Sampling of Planktothrix filaments from Lake Zürich.** On August 12 and 13 2002, water samples from 8, 10-5 and 15 m depth were taken from Lake Zürich above the deepest point of the lake, immediately concentrated by filtration as described by Walsby et al. (1998) and stored on ice. Each single filament of Planktothrix rubescens was picked under a binocular microscope with a sterile syringe and washed successively in three drops of a sterile mineral medium (Bright & Walsby, 2000) containing all ingredients except FeNaEDTA and NaHCO\(_3\). Finally, a single filament was washed in one drop of sterile nuclelease-free water (Sigma), transferred to 30 \( \mu \)l nuclelease-free water and kept on ice before it was frozen at −20°C. The samples were shipped to Bristol on dry ice; through delay they arrived at room temperature, but were refrozen and then kept at −70°C until further processing.

**Nucleic acid extraction and synthesis of first strand cDNA from a single filament.** Genomic DNA from Planktothrix batch cultures was extracted as described by Beard et al. (1999). The concentration of DNA was calculated from the \( A_{260} \) measured with a diode-array S2000 UV/Vis spectrophotometer (WPA). For RNA extraction, a single filament was picked from a Planktothrix laboratory culture as described above and transferred to 20 \( \mu \)l nuclelease-free water (Sigma) with 20 units Rnasin ribonuclease inhibitor (Promega) and 2-2 mM Dithiothreitol (Sigma) before two cycles of freezing/thawing (−20°C/ice) were applied in order to fracture the cells, followed by freezing of the lysate at −20°C, storing at −70°C and thawing on ice prior to further processing.

Before DNase treatment, the thawed lysate was centrifuged for 5 min at 5000 r.p.m. at 4°C to pellet unlysed cells and cell debris. A 15 \( \mu \)l quantity of the supernatant was transferred to a fresh reaction tube and mixed with 2 units RQ1 RNase-free DNase (Promega), 2 \( \mu \)l RQ1 DNase 10× reaction buffer (Promega) and 40 units Rnasin ribonuclease inhibitor (Promega). After incubation at 37°C (45 min), 3 \( \mu \)l stop solution (20 mM EGTA, Promega) was added and the reaction mixtures were incubated for another 10 min at 65°C to inactivate the DNase.

Before thawing the Lake Zürich samples from −70°C, 40 units Rnasin ribonuclease inhibitor (Promega), 0.85 \( \mu \)M dithiothreitol (final concentration 2-3 mM; Sigma) and 5-25 \( \mu \)l nuclelease-free water (Sigma) were added to the 30 \( \mu \)l of water that contained a single filament. The samples then underwent two cycles of freezing/thawing (see above). For DNase treatment, a larger quantity (31-4 \( \mu \)l) of the lysate (supernatant after centrifugation, see above) was taken and the amounts of all other components of the reaction mixtures (see above) were adjusted accordingly.

For synthesis of first strand cDNA, 7.5 \( \mu \)l of DNase-treated lysate from a single filament was mixed with 7.5-10 \( \mu \)M reverse primer (Table 1), incubated at 70°C (4 min) and 60°C (1 min), and then kept on ice prior to the addition of 10 \( \mu \)l of a master mix containing the following: 200 units M-MLV Reverse Transcriptase (Promega), 5 \( \mu \)l 5× M-MLV Reverse Transcriptase reaction buffer (Promega), 1-25 mM dNTPs, 24 units Rnasin ribonuclease inhibitor (Promega) and 1-25 mM Dithiothreitol (Sigma). The reaction mixtures were incubated at 42°C for 1 h. Control reaction mixtures without reverse transcriptase were treated as above and contained the mixture...
Amperase UNG; 200 obtained by plotting the CT of reactions with various amounts of signals reach the threshold (at which the CT value is determined). In the similar lengths is the same in different assays when their fluorescence genotypes. This is possible because the number of amplicons with were used to calculate ratios of gas vesicle genes in same amount of genomic template DNA, but different primer pairs, other sequences from the GenBank/EMBL nucleotide sequence data-

of lysate and reverse primer, 5× M-MLV Reverse Transcriptase reaction buffer (Promega), dNTPs and water.

The cDNA (25 μl) was precipitated following a protocol modified from Liss (2002): 2.5 μg glycogen (Ambion) and 625 ng polydA DNA (Amersham Pharmacia) were added to the cDNA but no carrier RNA. The dried pellet was redissolved in nuclease-free water (Sigma) by incubating for 15 min at 45°C.

Quantitative real-time PCR. Oligonucleotide primers for gas vesicle genes gvpA and the three known gvpC length variants in Planktothrix rubescens (Table 1) were constructed using alignments of the gvp sequences published by Beard et al. (1999, 2000) and other sequences from the GenBank/EMBL nucleotide sequence data-

Q

The thermal programme for real-time PCR

Evaluation of real-time PCR with genomic DNA

RESULTS

Evaluation of real-time PCR with genomic DNA

To evaluate the performance of the real-time PCR assays used in this study, all gas vesicle gene primer pairs were used with genomic DNA from a Planktothrix culture known to carry the target genes. By plotting the CT values of the assays versus the dilution factor of DNA, log–linear standard curves were obtained over four to six orders of

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Fig. 1. Standard curves for real-time PCR amplification of gas vesicle genes in serially diluted genomic DNA from various Planktothrix strains. gvpA, strain Pla 9401 (n = 6, r = 1:000); gvpC16, strain Pla 9736 (n = 4, r = 0:998); gvpC20, strain Pla 9303 (n = 8, r = 1:000); gvpC28, strain CYA 137 (n = 8, r = 1:000). Genomic DNA purified from Planktothrix batch cultures was used as a template in 10 µl real-time PCR assays with Sybr Green as a detector. DNA amount per reaction: DNA dilution (log_{20}). The ability of the primer pairs to discriminate between the three gvpC length variants was assessed by the amplification of genomic DNA from two Planktothrix strains of contrasting genotypes. For this analysis, the same DNA was used as in the assays shown in Fig. 1; therefore, an amplification efficiency (E) of 1 was assumed for the calculation of the degree of non-target amplification. With DNA from Planktothrix sp. Pla 9303, a strain with two copies of gvpA and gvpC20 (Beard et al., 2000), the lowest C_T value (28-17) was found with primers for gvpC20 (100 % signal), primers for gvpC28 produced no signal, and assays

with primers for gvpC16 gave a C_T value of 34-91. Assuming E = 1, the difference in the C_T values (ΔC_T = 6-74) shows that the signal with the primers for gvpC16 is 100/ 2^6.74 = 0.94 % of that with primers for gvpC20, indicating a small degree of mis-priming. With Planktothrix sp. CYA 137 (two copies of gvpA and gvpC28; Beard et al., 2000) the primer pairs for gvpC16 and gvpC20 led to mis-priming of 0-45 % and 0-008 %, respectively. Consequently, the copy number of specific gvpC variants may be overestimated by a maximum of 1 %.

To test the reliability of our new real-time PCR assays, we used them to determine the relative gvp gene copy numbers in genomic DNA from five Planktothrix strains of different gvp genotypes that had been characterized by sequencing (Beard et al., 1999, 2000). We used 10^3-fold diluted target DNA of strains Pla 9303, Pla 9316 and CYA 137 that had been used in the assays shown in Fig. 1; thus an amplification efficiency of 1 was assumed. By the construction of log-linear standard curves, the amplification efficiency with DNA from strains Pla 97112 and PCC 7821 was checked and also found to be close to 1 (data not shown). With the C_T values of the real-time PCR assays, the ratios of the gvp genes were calculated and compared with those revealed by sequencing the gene clusters (Beard et al., 1999, 2000). For genotypes 2a, 3b and 4a the calculated relative gene contents were similar to those found by sequence analysis, but in genotypes 1 and 6 the assays underestimated the copy number of gvpA relative to gvpC20 or gvpC28 copies (Table 2).

All assays from the experimental series shown in Table 2 were additionally analysed by gel electrophoresis in order to visualize the amplified fragments. As shown for genotypes 1, 2a and 3b (Fig. 2), the expected 185-190 bp amplicons were abundant in all assays (data for genotypes 4a and 6 not shown); no primer dimers were detected, but unidentified amplicons of 450 to 900 bp were present. In genotypes 2a, 3b (Fig. 2) and 4a (data not shown) an amplicon that may represent 769 bp could be explained by the amplification between two gvpA cistrons that occur in close proximity (Beard et al., 1999). Similar long and persistent side products that may stem from genes other than those in gvp clusters have also been detected in gas vesicle genotyping with genomic DNA from single Planktothrix filaments (Beard et al., 1999). We could not identify the side products by dissociation analysis (data not shown) because they may have a similar melting temperature to the desired amplicons. However, the side products contribute to the fluorescent signal and therefore cannot explain the relative underestimation of gvpA in genotypes 1 and 6 (Table 2).

Real-time RT-PCR with single Planktothrix filaments from cultures

A study by Liss (2002) on RT-PCR at the single-cell level had shown that the amplification of small amounts of cDNA can be inhibited by traces of reverse transcriptase, but this
Table 2. Ratio of gvp gene copy numbers in Planktothrix gas vesicle genotypes

<table>
<thead>
<tr>
<th>Genotype (strain)</th>
<th>Ratio of gvp gene copies</th>
<th>Real-time PCR*</th>
<th>(C&lt;sub&gt;T&lt;/sub&gt; values†)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (Pla 9303)</td>
<td>1 A : 1 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>0·38 A : 1 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>(33:31 : 31:93)</td>
</tr>
<tr>
<td>2a (Pla 9316)</td>
<td>4 A : 3 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>4 A : 3·23 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>(27:23 : 27:54)</td>
</tr>
<tr>
<td>3b (Pla 97112)</td>
<td>6 A : 3 C&lt;sup&gt;16&lt;/sup&gt; : 1 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>6 A : 3·69 C&lt;sup&gt;16&lt;/sup&gt; : 0·84 C&lt;sup&gt;20&lt;/sup&gt;</td>
<td>(20:58 : 21:28 : 23:11)</td>
</tr>
<tr>
<td>4a (PCC 7821)</td>
<td>4 A : 3 C&lt;sup&gt;20&lt;/sup&gt; : 1 C&lt;sup&gt;28&lt;/sup&gt;</td>
<td>4 A : 2·68 C&lt;sup&gt;20&lt;/sup&gt; : 1·64 C&lt;sup&gt;28&lt;/sup&gt;</td>
<td>(23:01 : 23:59 : 24:46)</td>
</tr>
<tr>
<td>6 (CYA 137)</td>
<td>1 A : 1 C&lt;sup&gt;28&lt;/sup&gt;</td>
<td>0·41 A : 1 C&lt;sup&gt;28&lt;/sup&gt;</td>
<td>(23:42 : 22:14)</td>
</tr>
</tbody>
</table>

*See Methods for calculation based on C<sub>T</sub> values.
†Standard deviation of C<sub>T</sub> values not shown; coefficient of variation of all assays (n=4) ≤0·04.

Fig. 2. Separation of real-time PCR products from assays for the amplification of gas vesicle genes gvpA, gvpC<sup>16</sup> and gvpC<sup>20</sup> in Planktothrix gas vesicle genotypes 1, 2a and 3b (see Table 2). 10 μl PCR assays contained 4 μl 10<sup>3</sup>-fold diluted genomic DNA as a template. After completion of the thermal programme, 1 μl of the assays was loaded on a 10% acrylamide gel. Three no-template PCR assays contained primer pairs for genes gvpA, gvpC<sup>16</sup> or gvpC<sup>20</sup> (assays shown in this order). M, 100 bp DNA ladder (Promega).

Table 3. Effect of cDNA precipitation on gvp transcript detection in single filaments of Planktothrix strain Pla 9303

<table>
<thead>
<tr>
<th>Filament</th>
<th>Days after inoculation</th>
<th>Target gene</th>
<th>C&lt;sub&gt;T&lt;/sub&gt; value* (amplicon†)</th>
<th>–RT control*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Unprecipitated</td>
<td>Precipitated</td>
</tr>
<tr>
<td>1</td>
<td>20</td>
<td>gvpA</td>
<td>35·95 (−)</td>
<td>25·05 (+)</td>
</tr>
<tr>
<td>2</td>
<td>20</td>
<td>gvpC&lt;sup&gt;20&lt;/sup&gt;</td>
<td>33·38 (+)</td>
<td>23·21 (+)</td>
</tr>
<tr>
<td>3</td>
<td>27</td>
<td>gvpA</td>
<td>43·76 (−)</td>
<td>27·54 (+)</td>
</tr>
<tr>
<td>4</td>
<td>27</td>
<td>gvpC&lt;sup&gt;20&lt;/sup&gt;</td>
<td>31·47 (+)</td>
<td>24·16 (+)</td>
</tr>
<tr>
<td>5</td>
<td>33</td>
<td>gvpA</td>
<td>41·79 (−)</td>
<td>24·92 (+)</td>
</tr>
<tr>
<td>6</td>
<td>33</td>
<td>gvpC&lt;sup&gt;20&lt;/sup&gt;</td>
<td>29·83 (+)</td>
<td>24·14 (+)</td>
</tr>
<tr>
<td>7</td>
<td>57</td>
<td>gvpC&lt;sup&gt;20&lt;/sup&gt;</td>
<td>27·56 (+)</td>
<td>27·99 (+)</td>
</tr>
<tr>
<td>8</td>
<td>57</td>
<td>gvpC&lt;sup&gt;20&lt;/sup&gt;</td>
<td>27·34 (+)</td>
<td>27·07 (+)</td>
</tr>
</tbody>
</table>

ND, No signal detected.
*Mean of n=2.
†Confirmation (+) of the amplicon identity by dissociation analysis (see Methods).
inhibitors (most probably reverse transcriptase). In only one assay (Table 3, filament 7) did precipitation increase the CT value slightly, possibly because of the loss of a small amount of template. The carrier DNA that is used in the protocol usually prevents this, however. Dissociation analysis confirmed that gvpA amplicons were present only when precipitated cDNA was used as the template (Table 3). It appears, therefore, that purification of cDNA by precipitation is essential for real-time RT-PCR detection of certain gvp transcripts in a single cyanobacterial filament.

In a separate experiment we amplified gvpC20 cDNA from single filaments of two other Planktothrix strains (PCC 7821 and Pla 9316) and separated the PCR products by gel electrophoresis. With precipitated undiluted or 10-fold diluted cDNA from three filaments, the expected gvpC20 fragment (185 bp) was amplified; no products accumulated in the −RT controls (Fig. 3). In contrast to results with genomic DNA (Fig. 2), the production of unidentified amplicons was significantly reduced, particularly with the 10-fold diluted cDNA. The identity of the gvpC20 amplicon was confirmed by dissociation analysis in all assays (Fig. 4a for filament 1, other data not shown).

Detection of gvpC transcripts in single Planktothrix filaments from cultures and lake samples

With the new methodology described above (using 10-fold diluted precipitated cDNA in real-time PCR) we were able...
DISCUSSION

RT-PCR detection of gvpC length variant transcripts in a single cyanobacterial filament

The presence of different length variants of the gas vesicle gene gvpC in Planktothrix rubescens is associated with the occurrence of gas vesicles with different diameters and strengths (Bright & Walsby, 1999; Beard et al., 2000). In genotypes with two gvpC length variants it is not known whether the genes are transcribed differentially in response to environmental conditions. We therefore evaluated real-time RT-PCR to analyse transcript patterns in single cyanobacterial filaments.

Real-time PCR can be calibrated by the threshold-cycle (C_T) method (Heid et al., 1996), which is based on the number of amplification cycles required to reach a certain concentration of amplicons. To evaluate the overall performance and amplification efficiencies of the new PCR assays used in this study, we constructed log–linear standard curves with genomic Planktothrix DNA as a template (Fig. 1). The assays targeting gvpA and three gvpC length variants showed amplification efficiencies between 1·01 and 1·04, indicating a doubling of the amplicon concentration in each PCR cycle. The detection limits of the assays were similar, between 0·18 and 0·82 pg DNA. With a mean detection limit of 0·4 pg DNA per assay, a molecular mass of 650 Da of one base pair (bp) and an assumed Planktothrix genome size of 4·5 Mbp, the analytical sensitivity of the 10 µl assays can be calculated as 82 genomes (Becker et al., 2000).

If the amplification efficiency is known and genomic DNA is used as a template, differences in the C_T values between real-time PCR assays can be used to calculate the copy number ratio of different target genes. For three of the five Planktothrix gas vesicle genotypes investigated, the ratios of gvpC genes were similar to those determined by DNA sequencing (Table 2), although slight deviations from the expected ratios were observed in the genotypes 3b (gvpC16) and 4a (gvpC20). However in genotypes 1 and 6, the relative

Table 4. Transcripts of gvp in single filaments of two Planktothrix strains

<table>
<thead>
<tr>
<th>Filament</th>
<th>Strain</th>
<th>C_T value*</th>
<th>–RT control</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>gvpA</td>
<td>gvpC16</td>
<td>gvpC20</td>
</tr>
<tr>
<td>1</td>
<td>Pla 9736</td>
<td>36:14</td>
<td>34:5</td>
</tr>
<tr>
<td>2</td>
<td>Pla 9736</td>
<td>36:46</td>
<td>35:78</td>
</tr>
<tr>
<td>3</td>
<td>Pla 9736</td>
<td>37:18</td>
<td>34:94</td>
</tr>
<tr>
<td>4</td>
<td>PCC 7821</td>
<td>31:49</td>
<td>–</td>
</tr>
</tbody>
</table>

ND, No signal detected.
*With 10-fold diluted cDNA; results from undiluted cDNA are underlined.

–RT controls. In all assays the identity of the corresponding amplicon was confirmed by dissociation analysis (Fig. 4b for strain PCC 7821, other data not shown). However, in three assays this confirmation was possible only with undiluted cDNA; note that in Fig. 3 only undiluted cDNA from filament 3 resulted in an amplification product. In Fig. 4(b) we observed a shift between the fluorescence signals generated with the genomic template and gvpC20 cDNA; the major area of the latter peak was, however, within the peak of the control DNA.

We also applied the new real-time PCR assays to Planktothrix filaments from Lake Zürich (Table 5). In the summer of 2002, single filaments were picked from water samples that had been taken from various depths of the lake. Real-time PCR was performed with cDNA from single filaments and primer pairs for gas vesicle genes that have been identified in Planktothrix rubescens from this habitat (Beard et al., 2000). In all assays, an amplification signal (C_T value) was observed, no signal occurred in the –RT controls. The presence of the expected amplicons could only be confirmed (by dissociation analysis) for filaments 2 and 5 (Fig. 4c for filament 2, other data not shown). In both of these filaments, transcripts of gvpA, gvpC16 and gvpC20 were present.

Table 5. Transcripts of gvp in natural Planktothrix filaments from Lake Zürich

<table>
<thead>
<tr>
<th>Filament</th>
<th>Sampling date (dd/mm/yy)</th>
<th>Water depth (m)</th>
<th>C_T value* (amplicon identity†)</th>
<th>–RT control*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>gvpA</td>
<td>gvpC16</td>
</tr>
<tr>
<td>1</td>
<td>12/08/02</td>
<td>8</td>
<td>27:81 (+)</td>
<td>23:55 (-)</td>
</tr>
<tr>
<td>2</td>
<td>13/08/02</td>
<td>8</td>
<td>27:71 (+)</td>
<td>25:00 (+)</td>
</tr>
<tr>
<td>3</td>
<td>13/08/02</td>
<td>10:5</td>
<td>27:54 (-)</td>
<td>25:87 (-)</td>
</tr>
<tr>
<td>4</td>
<td>13/08/02</td>
<td>10:5</td>
<td>28:04 (-)</td>
<td>21:47 (+)</td>
</tr>
<tr>
<td>5</td>
<td>13/08/02</td>
<td>15</td>
<td>27:63 (+)</td>
<td>24:18 (+)</td>
</tr>
<tr>
<td>6</td>
<td>13/08/02</td>
<td>15</td>
<td>29:38 (-)</td>
<td>34:00 (+)</td>
</tr>
</tbody>
</table>

ND, No signal detected.
*Mean of n=2.
†Confirmation (+) of the amplicon identity by dissociation analysis (see Methods).
gvpA copy number was underestimated by a factor of about 2–5. We assume that the observed deviations are due to variation in the amplification efficiencies of single assays that can lead to shifts of CT values. Additionally, calculations based on the slopes of standard curves as shown in Fig. 1 may overestimate the amplification efficiency of single reactions (Ramakers et al., 2003). This can lead to amplification efficiencies slightly higher than 1 (compare Fig. 1). Therefore, for quantitative transcription analysis, and because it is impossible to construct standard curves with cDNA from single cyanobacterial filaments, it is essential to monitor the amplification efficiencies of single reactions (see below).

Real-time PCR not only provides a sensitive and specific detection method, but, when performing a dissociation analysis with Sybr Green as a detector, also allows the amplicon identity to be checked in the same assay, a prerequisite for reliable transcription studies. The dissociation analysis also circumvents the time-consuming electrophoretic separation of PCR products and makes it possible to identify the contribution of non-specific PCR products, such as primer dimers, to the fluorescence signal.

In this study we describe a protocol for the extraction of mRNA from a single cyanobacterial filament. After reverse transcription, small amounts of cDNA were detected in real-time PCR. By comparing the CT values of these assays with the results of gel-based amplicon separation (Fig. 3) and fluorescent dissociation analysis (Fig. 4), we showed that it is possible to detect transcripts of more than one type of gvpC variant in a single Planktothrix filament. Hence, transcripts of gvpC16 and gvpC20 or gvpC20 and gvpC28 were identified in laboratory cultures of Planktothrix strains Pla 9736 and PCC 7821, respectively (Table 4). These results indicate that both gvpC length variants are transcribed under our laboratory conditions.

In single Planktothrix filaments from Lake Zürich (Table 5) transcripts of both gvpC16 and gvpC20 were found. These two length variants have been identified in Planktothrix isolates from this habitat (Beard et al., 2000). The presence of different gvpC transcripts in a single cyanobacterial filament has not previously been described. Currently no information is available to indicate whether the presence of two different gvpC transcripts reflects the expression (i.e. the translation to protein) of the two genes. Immunoblotting of proteins from pure Planktothrix gas vesicles has shown that only one GvpC protein species was present in gas vesicles isolated from strains carrying two gvpC length variants (S. J. Beard, unpublished results). It remains possible, however, that gas vesicles of different diameters and strengths may co-occur within a single filament under appropriate environmental conditions; this might contribute to the efficiency of buoyancy provision in Planktothrix. We hypothesize that post-transcriptional regulation may influence the type of protein (GvpC) present in gas vesicles. Information on gas vesicle gene promoters in cyanobacteria as well as insights into a possible translational regulation of gas vesicle formation and the structural assembly of the protein cylinders are necessary.

Quantification of transcripts in a single cyanobacterial filament

The level of transcription of a particular gene can be estimated by reverse transcription of mRNA to cDNA and measuring the number of cDNA copies by quantitative PCR. To achieve quantitative results, the preservation of mRNA in samples is crucial at the time of sampling. Since it might be difficult to maintain the required low temperature for working with RNA while processing samples, they could be treated directly with reagents that preserve the mRNA profile in the cells and allow storage at room temperature for a sufficient period of time. To achieve efficient reverse transcription of different mRNA species, it might be necessary, however, to purify extracted mRNA from single cyanobacterial filaments after preservation of the transcript profile with reagents such as RNPProtect Bacteria Reagent (Qiagen) or RNAlater (Ambion) (S. Becker, unpublished results).

In this study we confirmed results of Liss (2002), who had shown that it is essential to remove PCR inhibitors (e.g. carry-over of reverse transcriptase) from small amounts of cDNA that will be used as a template in real-time PCR. This can be done by the precipitation of cDNA. From the difference in the CT values between the assays with precipitated and unpurified cDNA it is calculated that the input template amount would have been underestimated by a factor of up to $10^3$ in the absence of the precipitation step (Table 3). It may be essential to use precipitated cDNA to confirm the presence of certain gvp amplicons by dissociation analysis (Table 3), a prerequisite for reliable transcription studies. Additionally, precipitation of cDNA appears to be essential for obtaining product curves that enable linear regression of the section before the plateau phase (data not shown), a prerequisite for quantitative analysis after Ramakers et al. (2003) (see below).

In real-time PCR, two quantification methods based on CT values are available: absolute quantification by the construction of log-linear standard curves as shown in Fig. 1 (Heid et al., 1996) and relative quantification by the comparative CT method (Livak & Schmittgen, 2001). However, standard curves with cDNA from single cyanobacterial filaments are not possible and both methods are prone to quantification errors if possible deviations in the amplification efficiencies between sample and standard assays are not taken into consideration (Ramakers et al., 2003). Therefore, as suggested for TaqMan chemistry (Becker et al., 2000), when using Sybr Green as a detector, the amplification efficiency in real-time PCR assays needs to be monitored in order to achieve reliable quantitative results. According to Ramakers et al. (2003), the input template copy number in a real-time PCR assay is reflected by the input fluorescence of the assay, which can be calculated by a regression of the linear section of an
exponential product curve in the early stage of PCR. This quantification method is independent from standard curves and can be used to monitor the amplification efficiencies between samples. The measurement of cDNA from single cyanobacterial filaments in which the mRNA has been preserved, and normalization of the PCR results to the filament biomass or number of cells (based on the filament length determined by image analysis, cf. Walsby & Avery, 1996), seem feasible for quantitative transcription studies in cultures and natural samples.

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