Characterization and transcriptional analysis of hupSLW in Gloeothece sp. ATCC 27152: an uptake hydrogenase from a unicellular cyanobacterium

Paulo Oliveira, Elsa Leitão, Paula Tamagnini, Pedro Moradas-Ferreira and Fredrik Oxelfelt

Correspondence
Fredrik Oxelfelt
fredrik@ibmc.up.pt

1Department of Botany, Faculty of Sciences, University of Porto, Rua do Campo Alegre 1191, 4150-181 Porto, Portugal
2Institute for Molecular and Cell Biology – Cellular and Applied Microbiology Unit, University of Porto, Rua do Campo Alegre 823, 4150-180 Porto, Portugal
3Instituto de Ciências Biomédicas Abel Salazar, University of Porto, Largo Abel Salazar 2, 4099-003 Porto, Portugal

The structural genes (hupSL) encoding an uptake hydrogenase in the unicellular cyanobacterium Gloeothece sp. ATCC 27152, a strain capable of aerobic N₂ fixation, were identified and sequenced. 3'-RACE experiments uncovered the presence of an additional ORF 184 bp downstream of hupL, showing a high degree of sequence identity with a gene encoding an uptake-hydrogenase-specific endopeptidase (hupW) in other cyanobacteria. In addition, the transcription start point was identified 238 bp upstream of the hupS translational start. RT-PCR experiments revealed that hupW is co-transcribed with the uptake hydrogenase structural genes in Gloeothece sp. ATCC 27152. In addition, Northern hybridizations clearly showed that hupSLW are transcribed under nitrogen fixing conditions, but not in the presence of combined nitrogen. A putative NtcA binding site was identified in the promoter region upstream of hupS, centred at −41-5 bp with respect to the transcription start point. Electrophoretic retardation of a labelled DNA fragment (harbouring the putative NtcA-binding motif) was significantly affected by an Escherichia coli cell-free extract containing overexpressed NtcA, suggesting that NtcA is involved in the transcriptional regulation of hupSLW.

INTRODUCTION

Several species of bacteria and cyanobacteria are capable of N₂ fixation. During the N₂ fixation process H₂ is formed as a by-product. This nitrogenase-dependent H₂ production is often compromised by the presence of an uptake hydrogenase (encoded by hupSL) that rapidly consumes the H₂ generated. In addition, a bi-directional enzyme (encoded by hoxEFUYH) may be present which, depending on the growth conditions, may display the capacity of both producing and consuming H₂ (Lambert & Smith, 1981; Houchins, 1984; Schmitz et al., 2002; Tamagnini et al., 2002). All cyanobacteria examined so far contain an uptake, a bi-directional or both the hydrogenases (Schmitz et al., 1995, 2002; Boison et al., 1996; Tamagnini et al., 2000, 2002; Sheremetieva et al., 2002; Schütz et al., 2004). Moreover, the uptake-type enzyme has been found in all nitrogen fixing cyanobacterial strains studied to date (Carrasco & Golden, 1995; Oxelfelt et al., 1998; Happe et al., 2000; Tamagnini et al., 2000, 2002; Schütz et al., 2004).

The first data on cyanobacterial hupSL transcription appeared in 1995 (Carrasco & Golden, 1995). RT-PCR experiments on Anabaena/Nostoc sp. strain FCC 7120 demonstrated that hupL transcription coincides with the formation of heterocysts. Subsequent studies, in other filamentous strains, have confirmed the induction of an hupL transcript under nitrogen-fixing conditions only (Axelsson et al., 1999; Happe et al., 2000; Hansel et al., 2001). One exception is Anabaena variabilis ATCC 29413, where a low level of hupL expression has been detected in vegetative cells grown with the addition of ammonia (Boison et al., 2000). In all the cyanobacterial strains...
The maturation of hydrogenases is a complex process requiring a number of accessory proteins (Menon et al., 1993; Vignais & Toussaint, 1994; Maier & Triplett, 1996; Buhrke et al., 2001; Casalot & Rousset, 2001; Vignais et al., 2001; Blokesch et al., 2002; Paschos et al., 2002). One distinct feature in the NiFe-hydrogenases maturation process is the endoproteolytic cleavage of a C-terminal peptide of the large subunit precursor, carried out by a specific C-terminal endopeptidase (Casalot & Rousset, 2001; Paschos et al., 2002). Until now, the available data on the maturation of cyanobacterial NiFe-hydrogenases are scarce. Recently, the presence and expression of endopeptidases specific for cyanobacterial hydrogenases was reported (Wünschers et al., 2003). These authors screened three completed cyanobacterial genome sequences [Anabaena/Nostoc sp. strain PCC 7120 (www.kazusa.or.jp/cyano/Anabaena), Nostoc punctiforme ATCC 29133/PCC 73102 (http://genome.jgi-psf.org/draft_microbes/nospu/nospu.home.html), and Synechocystis PCC 6803 (www.kazusa.or.jp/cyano/Synechocystis)]] with the purpose of identifying genes putatively encoding C-terminal specific endopeptidases. In agreement with previous nomenclature they proposed the gene name hoxW (endopeptidase specific for the bi-directional hydrogenase) for the ORFs all0770 (Anabaena/Nostoc PCC 7120) and slr1876 (Synechocystis PCC 6803), whereas the ORFs slr1423 (Anabaena/Nostoc PCC 7120) and c509/tr320 (Nostoc PCC 73102) were named hupW (endopeptidase specific for the uptake hydrogenase). These ORFs are not clustered with any known hydrogenase-related gene(s).

A strong correlation between nitrogen fixation and uptake hydrogenase activity has been demonstrated in filamentous cyanobacteria (Lambert & Smith, 1981; Houchins, 1984; Wolk et al., 1994; Oxelfelt et al., 1995; Masukawa et al., 2002; Schütz et al., 2004). In cyanobacteria nitrogen control is mediated by a transcriptional regulator, NtcA, belonging to the CAP family (the catabolite gene activator or cAMP receptor protein) (Herrero et al., 2001). In response to ammonium withdrawal, NtcA binds to specific sites in the promoter region of regulated genes involved in nitrogen assimilation. The NtcA-activated promoter structure consists of a −10 box in the form TAN3T and an NtcA-binding site with the consensus sequence GTAN8TAC, usually located 20 to 23 nucleotides upstream of the −10 box, which appears to substitute for the −35 box (Luque et al., 1994; Muro-Pastor et al., 1999; Herrero et al., 2001). Other proposed consensus NtcA binding sites are TGN9/10ACA, and TGTTAN7TACA (Ramasubramanian et al., 1994; Jiang et al., 2000; Wisén, 2003).

Up to now, only limited amounts of biochemical/physiological data are available concerning uptake hydrogenases in unicellular cyanobacteria (Lambert & Smith, 1981; Houchins, 1984; Schütz et al., 2004). Recently, in the unicellular cyanobacterium Gloeothecae sp. strain ATCC 27152, the unequivocal presence of an uptake hydrogenase was reported, in contrast with the lack of hybridization signals when probes for hox genes were used (Schütz et al., 2004). However, a residual level of methyl-viologen-dependent H2 evolution could be detected, therefore the presence of a bi-directional hydrogenase in Gloeothecae sp. ATCC 27152 cannot be excluded.

This study presents the first comprehensive molecular data on an uptake hydrogenase being present in a unicellular cyanobacterium, and provides new information on how oxygen-evolving photosynthesis and an essentially anaerobic process like hydrogen uptake can occur within a single cell. The structural genes (hupSL) encoding this enzyme in Gloeothecae sp. ATCC 27152 were identified, sequenced and characterized. Moreover, a gene encoding a cyanobacterial hydrogenase specific endopeptidase – hoxW – was found immediately downstream of hupL, and was shown to be co-transcribed with hupSL. The three genes are transcribed under nitrogen fixing conditions, but not in the presence of combined nitrogen. Evidence for the involvement of NtcA in the transcriptional regulation of hupSLW is also presented.

**METHODS**

**Organism and growth conditions.** Gloeothecae sp. strain ATCC 27152 was cultured at 25°C in BG11 or BG11 for the Northern blot experiments (Rippka et al., 1979), under a 12 h light (10 μmol photons m−2 s−1)/12 h dark cycle regime.

**Hydrogen uptake activity.** In vivo hydrogen uptake was measured using a Hansatech DW1 O2/H2 electrode (Hansatech) according to the methods described previously (Oxelfelt et al., 1995).

**Nucleic acid extraction and analysis.** Genomic DNA was isolated from Gloeothecae sp. ATCC 27152 cells by phenol/chloroform extraction as described elsewhere (Tamagnini et al., 1997). In order to obtain clean DNA (e.g. free from extracellular polysaccharides), additional washing steps were required: the cells were collected by centrifugation and resuspended in washing buffer [5 mM EDTA and 50 mM Tris/HCl pH 8] by centrifugation at 4°C, frozen in liquid nitrogen and left to thaw on ice. This freezing and thawing was repeated twice. Total RNA was then isolated following the protocol of Axelsson et al. (1999), with the exception that 20 μL DNase I FPLCpure (Amersham Biosciences) was added during the hot phenol treatment. RNA used for the Northern hybridizations was isolated using TRIZOL reagent (Invitrogen), following the manufacturer’s instructions. In the homogenization step, 0.5 g acid-washed 0.2 mm diameter glass beads were added to the samples, and the disruption of the cells was accomplished using a
Mini-Beadbeater (Biospec Products). DNA and RNA were analysed by agarose gel electrophoresis using 1× TAE or TBE buffer (Sambrook et al., 1989).

**PCR, DNA sequencing and sequence analysis.** All oligonucleotides used in this study are listed in Table 1 (see also Fig. 1a). PCR amplifications were carried out in a Gene Amp PCR System 2400 (Perkin-Elmer) thermal cycler with Taq DNA polymerase (Amersham Biosciences) as previously described (Tamagnini et al., 1997).

DNA fragments were isolated from agarose gels using the QIAEX II gel extraction kit (Qiagen) or the NucleoSpin Extract kit (Macherey-Nagel), following the manufacturer’s instructions. Sequencing reactions were performed with an ABI Prism BigDye terminator cycle sequencing ready reaction kit (Applied Biosystems), the thermal cycler mentioned above, and the ABI 377 DNA automated sequencer system (Applied Biosystems). Published sequences were retrieved from GenBank and computer-assisted sequence analyses were performed using CLUSTAL W (Thompson et al., 1994). Novel sequences associated with this study (Gloeothece sp. ATCC 27152 hupSLW) are available in GenBank under the accession number AY260103.

**Southern blot analysis.** The probe used for Southern hybridization was obtained by PCR using genomic DNA from Gloeothece sp. ATCC 27152 and the primer pair GloS1A/HS1B [probe GhupS (Fig. 1a) Schütz et al. (2004)]. The identity of the probe was confirmed by sequencing.

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**Table 1. Oligonucleotide primers used in the present study**

For the specific positions within the hupSLW sequence see Fig. 1(a).

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence 5’→3’</th>
<th>References</th>
</tr>
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<tr>
<td>NtcA1F (1)</td>
<td>TTCTTTGTCTCTCCTCAATTGACC</td>
<td>This study</td>
</tr>
<tr>
<td>S1 (2)</td>
<td>AAGCTACTCCTGCAAGGT</td>
<td>Tamagnini et al. (2000)</td>
</tr>
<tr>
<td>S1rev (3)</td>
<td>CACCTCGGCAGATGTC</td>
<td>This study</td>
</tr>
<tr>
<td>GloSIA (4)</td>
<td>GCTAGGAGACATCTTCAAC</td>
<td>Schütz et al. (2004)</td>
</tr>
<tr>
<td>GloSIB (5)</td>
<td>GTTGAAGATGTTCTCCATGC</td>
<td>This study</td>
</tr>
<tr>
<td>GloSRIB (6)</td>
<td>CTTGAGCATCTGGGGTTTA</td>
<td>This study</td>
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<tr>
<td>GloS3′A (7)</td>
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<td>This study</td>
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</tr>
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<td>GloHI′R (9)</td>
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<td>This study</td>
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<tr>
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<td>GloH6A (14)</td>
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**Fig. 1.** (a) Physical map of hupSLW in Gloeothece sp. ATCC 27152. The transcriptional start point is indicated by +1, and is located 238 bp upstream from the hupS start codon. The numbered grey arrowheads represent the oligonucleotide primers used in this study (see also Table 1). GhupS indicates the homologous probe used in Southern hybridization for the identification of the HindIII fragment (clone GhSL1, dashed line not to scale). Black vertical arrows indicate the restriction sites. The sequence harbouring the hupSLW (3891 kb) is available from GenBank under accession no. AY260103. (b) Nucleotide sequence of the promoter region upstream of hupS in Gloeothece sp. ATCC 27152. A putative NtcA binding site is boxed. The transcription start point is indicated by +1 and a putative −10 consensus sequence is underlined. The start codon of hupS is shown in bold and the deduced N-terminal amino acid sequence is given below.
Radioactive and non-radioactive Southern hybridizations were carried out at 57 °C, following previously described protocols (Tamagnini et al., 1997; Schütz et al., 2004).

Construction of a partial genomic library of Gloeothece sp. ATCC 27152 and identification of hupSL. Genomic DNA was digested by the restriction endonuclease HindIII and separated on a 1% (w/v) agarose gel. A region between 3.5 and 4.5 kb was cut out and the DNA was extracted from the gel as described above. Ligation into the vector pGEM 3Zf+(+) (Promega), transformation and screening (using the probe GhpSp; see also Fig. 1a) were performed as described previously (Oxelfelt et al., 1998). Positive clones were detected using a Typhoon 8600 Variable Mode imager (Amersham Biosciences).

Transcription start point identification and the use of 3'-RACE to obtain the 3' end of hupL. To locate the transcription start point, 3'-RACE experiments were carried out, using a commercially available kit (FirstChoice RLM-RACE kit; Ambion). The instructions of the manufacturer were followed, except that a double volume (2 μl) of the reverse transcription (RT) reaction was used in the outer PCR and that the extension was prolonged to 1 min in both the outer and inner PCR amplifications. The gene-specific antisense primers from the 5' end of hupS of Gloeothece sp. ATCC 27152 used were: S1rev, GloS1B and GloSR1B.

To identify the 3' end of hupL in Gloeothece sp. ATCC 27152, 3'-RACE was performed essentially following the manufacturer’s protocol (FirstChoice RLM-RACE kit; Ambion). As in the 5'-RACE, 2 μl of the RT reaction was used for the outer PCR. For both the outer and inner PCR amplification a touch-down PCR was carried out with the following profile: 95 °C for 3 min, followed by eight cycles of 30 s denaturation at 95 °C, 45 s annealing at 62–56 °C (decreasing 2 °C every second cycle), and 1 min elongation at 72 °C, then 32 identical cycles with the exception that the annealing temperature was set to 55 °C, and concluding with 7 min at 72 °C. The gene-specific sense primers for the 3' end of hupL of Gloeothece sp. ATCC 27152 used were: GloH4A and GloH4A2.

PCR products were cloned, using the pGEM-T Easy vector system (Promega), into XL-1 Blue supercompetent cells (Stratagene). Plasmid DNA was isolated from Escherichia coli using the GenElute plasmid miniprep kit (Sigma-Aldrich). Sequencing was performed as detailed above.

Transcriptional studies. RT reactions (with 0.5–1 μg total RNA) were performed essentially following the protocol of the Thermoscript RT-PCR system (Invitrogen), using the antisense primer GhpW1R. A double volume of the RT reaction (compared to the manufacturer’s protocol) was used in PCR amplifications with the primer pairs GloS3A/GloH1R (hupS-hupL detection) and GloH6A/GhpW1R (hupL-hupW detection). Negative controls included the omission of reverse transcriptase in the RT reaction prior to the PCR, and a PCR to which no template was added. Genomic DNA from Gloeothece sp. ATCC 27152 was used as a positive control. The PCR program profile was: 95 °C for 2 min followed by 35 cycles of 45 s denaturation at 95 °C, 45 s annealing at 55 °C and 1 min elongation at 72 °C, concluding with 7 min at 72 °C. Generated PCR products were analysed on a 1% agarose gel.

Northern hybridizations were performed at 65 °C following the protocol of Ausubel et al. (1993). The probes used were obtained by PCR using genomic DNA from Gloeothece sp. ATCC 27152, and the primer pairs GloS1A/GloSR1B (hupS-specific probe) and 106F/781R [165 RNA gene-specific probe; Nübel et al. (1997)]. Stripping of the membranes was performed following the protocol provided with the Hybond-N+ nylon membrane (Amersham Biosciences).

RESULTS AND DISCUSSION

Identification and characterization of hupSL. The presence of an uptake hydrogenase in Gloeothece sp. ATCC 27152 was recently demonstrated by Schütz et al., 2004. These authors showed that Gloeothece sp. ATCC 27152 is able to fix nitrogen both under aerobic and anaerobic conditions, yet no nitrogenase-mediated H2 evolution was observed, most likely due to consumption by an active-uptake hydrogenase. Subsequently, these results were confirmed using additional homologous probes (generated using oligonucleotide primers designed against conserved regions within other cyanobacteria) in Southern hybridizations, and by measuring hydrogen uptake activity using a H2 electrode (this work, data not shown). Moreover, to obtain a contiguous sequence Gloeothece sp. ATCC 27152-specific primers were designed, and the respective PCR products sequenced. This revealed the majority of the hupSL sequence, disclosing the presence of a 259 bp intergenic region. Concomitantly, a partial genomic library was constructed, and a 4 kb HindIII fragment (clone GhSL1) was isolated and sequenced (see Fig. 1a). To obtain the remaining 3’-end of hupL, 3’-RACE reactions were carried out, and a number of cDNA clones of different lengths were obtained (most likely due to the fact that the mRNA polyadenylation in prokaryotes appears to be a relatively indiscriminate process, able to occur at all mRNAs’ 3’-ends, and does not require a specific consensus sequence as in eukaryotes; see Sarkar, 1997; Rauhut & Klug, 1999; Wagner, 2000). Sequencing revealed that all these clones consisted of the 3’-end of hupL. Multiple sequence alignments were carried out to obtain the sequence
encompassing the region upstream of \( hupS \), \( hupL \) and the intergenic region. The \( hupS \) and \( hupL \) of \textit{Gloeothece} sp. ATCC 27152 are the first structural genes encoding an uptake hydrogenase to be cloned and sequenced for a unicellular cyanobacterium, and they show a high degree of identity (ranging from 75 to 79 % and 74 to 76 %, respectively) with the corresponding genes from \textit{Trichodesmium erythraeum}, \textit{Lyngbya majuscula}, \textit{Anabaena/Nostoc} PCC 7120, \textit{A. variabilis} and Nostoc PCC 73102. Although \textit{Gloeothece} sp. ATCC 27152 HupSL cluster together with non-heterocystous cyanobacteria, HupL is exactly the same length as in heterocystous strains, lacking the extra amino acids found in the filamentous non-heterocystous \textit{T. erythraeum} and \textit{L. majuscula} (Leitão, E., Oxelfelt, F., Oliveira, P., Ferreira, D. & Tamagnini, P., unpublished results). Overall, the \textit{Gloeothece} sp. ATCC 27152 HupSL share the distinctive characteristics of cyanobacterial uptake hydrogenases (Tamagnini et al., 2002), including all the conserved cysteine residues involved in the formation of the [FeS] clusters and Ni-binding sites. Since no transmembrane domains were found in \textit{Gloeothece} sp. ATCC 27152 HupSL, it is probable that a membrane anchoring protein/subunit exists, as was previously predicted for other cyanobacterial strains (Leitão et al., unpublished results; Lindberg, 2003).

### hupW is localized directly downstream of hupL

Sequencing the longer clones obtained in the 3’-RACE experiments (see above) revealed the presence of an additional ORF located 184 bp downstream of \( hupL \). Comparative analysis suggested that this ORF encodes a hydrogenase maturation protease (endopeptidase), involved in the C-terminal cleavage of the hydrogenase large subunit precursor protein (Casalot & Rouset, 2001; Vignais et al., 2001; Paschos et al., 2002). In a recent study, a gene encoding an uptake-hydrogenase-specific endopeptidase (named \( hupW \) in the referred work) was identified while screening the available genome sequences of \textit{Anabaena/Nostoc} PCC 7120 and \textit{N. punctiforme} ATCC 29133/PCC 73102 (Wünschers et al., 2003). However, the identified gene was not part of any known hydrogenase-related gene cluster. Therefore, the location of \( hupW \) immediately downstream of \( hupL \) in \textit{Gloeothece} sp. ATCC 27152, and in the same direction, contrasts with the position of the corresponding gene in the two heterocystous cyanobacteria. A putative \( hupW \) is also present in the draft genome of the heterocystous cyanobacterium \textit{A. variabilis} (contig 249), while \( hupL \) are located on contig 240 (http://genome.jgi-psf.org/draft_microbes/anava/anava.home.html). Screening the genome sequence of the marine filamentous non-heterocystous \textit{T. erythraeum} (http://genome.jgi-psf.org/draft_microbes/trier/trier.home.html) also revealed the presence of an ORF showing a high degree of identity with \( hupW \), and located 614 bp downstream of \( hupL \). Deduced amino acid sequence alignments of the putative endopeptidase from \textit{Gloeothece} sp. ATCC 27152 and the HupW from \textit{Anabaena/Nostoc} PCC 7120, Nostoc PCC 73102 and \textit{T. erythraeum} revealed an overall high identity (Fig. 2). The HupW protein of \textit{Gloeothece} sp. ATCC 27152 contains the two conserved aspartic acid residues and the conserved histidine residue which, in HyPD of \textit{E. coli}, form a nickel-binding site (Fritsche et al., 1999). In \textit{Gloeothece} sp. ATCC 27152, the C-terminal end of HupW, harbours six to ten additional amino acid residues in comparison to the corresponding protein in the other cyanobacterial strains.

### The hupSLW genes in \textit{Gloeothece} sp. ATCC 27152 are co-transcribed

RT-PCR experiments, using total RNA extracted from \textit{Gloeothece} sp. ATCC 27152 cells grown under nitrogen fixing conditions, were performed for the transcriptional analysis of the \( hupS \), \( hupL \) and \( hupW \) genes. The culture was harvested 5 h into the dark phase, hydrogen uptake activity was confirmed using a hydrogen electrode (data not shown), and RNA was extracted. An RT reaction using GhpWIR as the \( hupW \)-specific antisense primer was performed, and the resulting cDNA was used as template in PCR amplifications for the detection of \( hupS-hupL \) and \( hupL-hupW \) co-transcription. The results showed that the three genes (\( hupSLW \)) are indeed transcribed together (Fig. 3). The 3’-RACE results described above already indicated that \( hupW \) could be transcribed along with \( hupL \). In the cyanobacterial strains studied so far, the \( hupSL \) genes constitute a single transcript with no additional ORFs (Happe et al., 2000; Lindberg et al., 2000). Moreover, the transcription of \( hupW \) in \textit{Anabaena/Nostoc} PCC 7120 and \textit{N. punctiforme} ATCC 29133/PCC 73102 has been shown in the referred work). Conserved nickel-coordinating amino acid residues are indicated by grey bars.

Fig. 2. Deduced amino acid sequence alignment of the putative hydrogenase-specific protease of \textit{Gloeothece} sp. ATCC 27152 (\( hupW \) G27152) and the corresponding protein in \textit{Anabaena/Nostoc} sp. PCC 7120 (\( hupW \) AT29132), \textit{N. punctiforme} PCC 73102 (\( hupW \) N73102) and \textit{T. erythraeum} IMS 101 (\( hupW \) Te). Conserved nickel-coordinating amino acid residues are indicated by grey bars.
to occur independently of that of hupSL (Wünschiers et al., 2003). Thus, this is the first time that the gene (hupW) encoding an uptake-hydrogenase-specific endopeptidase has been reported to be co-transcribed with the uptake hydrogenase structural genes (hupSL) in cyanobacteria.

Transcription start point identification and characterization of the hupS promoter region

5’-RACE permitted the identification of the transcription start point (tsp), 238 bp upstream from the hupS start codon (Fig. 1). In Gloeohce sp. ATCC 27152, a putative -10 box (TAATGT) is located six nucleotides upstream of the tsp, matching well with the consensus σ70-like -10 box sequence (TAN3T) found in other cyanobacteria (Luque et al., 1994; Herrero et al., 2001). A putative NtcA binding site (GTAAACCATGATAC) was also identified 22 nucleotides further upstream of the -10 region. This sequence contains the highly conserved palindromic NtcA-binding region signature GTAN8TAC (Luque et al., 1994; Herrero et al., 2001), and is flanked by T-rich sequences both upstream and downstream.

hupSLW transcription under different growth conditions

Northern blot experiments were performed with total RNA extracted from Gloeohce sp. ATCC 27152 cells grown under nitrogen-fixing or non-nitrogen fixing conditions, and 12 h light/12 h dark cycles. Samples were collected at four different time-points from both growth conditions (Fig. 4). The hybridizations were carried out using a hupS-specific probe. The results clearly show that the transcript(s) is present when Gloeohce sp. ATCC 27152 cells are grown under nitrogen-fixing conditions, but totally absent under non-nitrogen fixing conditions (NaNO3, Fig. 4). In addition, there is an evident light/dark regulation, with the highest transcript levels detected during the light cycle. This is interesting since Gloeohce sp. ATCC 27152 has been shown to fix nitrogen mainly in the dark (Reade et al., 1999), and consequently displays a higher hydrogen-uptake activity during the dark cycle (confirmed in this study using a hydrogen electrode, data not shown). The appearance of the transcript(s) prior to a detectable hydrogen uptake activity may be due to the fact that the uptake hydrogenase requires a complex maturation process. In contrast to heterocystous strains (Anabaena Nostoc PCC 7120 and Nostoc PCC 73102), in which hupW is transcribed independently from hupSL (Wünschiers et al., 2003), hupSLW in Gloeohce sp. ATCC 27152 appear to be co-transcribed. This difference, together with the fact that there is a temporal separation between photosynthesis and nitrogen fixation/hydrogen-uptake activity in Gloeohce sp. ATCC.
27152, may result in an extended period between transcription and activity. Furthermore, the Northern hybridizations revealed the presence of at least three different transcripts [or possibly a combination of transcript(s) and degradation products]. The largest transcript being approximately 3800 nt, and therefore probably corresponding to $hupSLW$, a smaller transcript of about 2000 nt (possibly a degradation product), and a third transcript of about 1200 nt possibly corresponding to $hupS$ alone. These results corroborate the RT-PCR data (co-transcription of $hupSLW$), but also suggest the possibility of multiple transcripts.

**Binding of NtcA to the promoter region of the $hupS$ gene**

The potential NtcA binding site, identified in the *Gloeothece* sp. ATCC 27152 $hupS$ promoter region, is centred at $-41\pm5$ bp with respect to the transcription start point. In order to confirm binding of NtcA to the promoter region, gel mobility shift DNA-binding assays were performed. Cell-free extracts were prepared from *E. coli* BL21(DE3) (pREP4, pCSAM70), where the overexpression of NtcA had been induced by 1 mM IPTG (Muro-Pastor et al., 1999). The mobility shift assays were carried out with a 366 bp, $^{32}$P-labelled DNA fragment covering the promoter region of $hupS$ ($-101$ to $+265$). Fig. 5 shows that electrophoretic retardation of the labelled DNA fragment was significantly affected by the *E. coli* cell-free extract containing the overexpressed NtcA, whereas no retardation could be detected when a non-related *E. coli* cell-free extract (not carrying a cloned ntcA gene) was used. Band retardation of the $^{32}$P-labelled fragment was successfully outcompeted by the identical unlabelled DNA fragment (Fig. 5, lane 6). These results suggest that NtcA binds specifically to the identified putative site (GTAACCAAGATTAC).

![Fig. 5. Gel mobility shift analysis of NtcA binding to the target sequence in the promoter region upstream of $hupS$ in *Gloeothece* sp. ATCC 27152. Five nanograms of the 366 bp labelled DNA fragment ($-101$ to $+265$) was used throughout the experiment. Lanes: 1, labelled DNA fragment only; 2–4, assays carried out with 500 ng, 1 µg and 10 µg total protein of *E. coli* cell-free extracts expressing NtcA, respectively; 5 and 6, assays carried out with 1 µg total protein, and in the presence of fivefold (lane 5) or 50-fold (lane 6) molar excess of the corresponding unlabelled fragment as competitor DNA; 7 and 8, 1 µg total protein and the presence of fivefold (lane 7) or 50-fold (lane 8) molar excess of an unrelated, unlabelled fragment; 9 and 10, assays carried out with 1 or 10 µg total protein of a *E. coli* cell-free extract not expressing NtcA, respectively.](http://mic.sgmjournals.org/3653)


