The \textit{pknH} gene restrictively expressed in heterocysts is required for diazotrophic growth in the cyanobacterium \textit{Anabaena} sp. strain PCC 7120

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\textit{Anabaena} sp. strain PCC 7120 is a filamentous cyanobacterium in which certain vegetative cells differentiate into heterocysts, which are specialized cells for nitrogen fixation. Heterocysts are unable to carry out photosynthesis and are supplied with carbohydrate required for nitrogen fixation from neighbouring vegetative cells. Thus, filament integrity is very important for diazotrophic growth of the heterocystous cyanobacteria. The \textit{pknH} gene (\textit{alr1336}), encoding a putative Ser/Thr protein kinase, was upregulated in heterocysts after nitrogen deprivation. Its expression was developmentally regulated by the \textit{hetR} gene. Expression levels of genes involved in heterocyst maturation, such as \textit{hepA}, \textit{hglE} and \textit{nifH}, in the \textit{pknH} disruptant were similar to those of the wild-type strain. The disruptant was able to form heterocysts with nitrogenase activity, but most heterocysts were detached from filaments. Hence, the \textit{pknH} disruptant showed a growth defect in the medium without combined nitrogen. It is concluded that the \textit{pknH} gene is not involved in the development of heterocyst function but is involved in maintaining connections between heterocysts and vegetative cells.

INTRODUCTION

Cyanobacteria are a large group of eubacteria characterized by oxygen-evolving photosynthesis. Heterocysts are terminally differentiated cells of filamentous cyanobacteria specialized for nitrogen fixation. Upon limitation of combined nitrogen in the medium, particular vegetative cells differentiate into heterocysts with a regular spacing of 10–15 cells (Flores & Herrero, 2010; Kumar \textit{et al.}, 2010). Heterocysts provide the microoxic environment for the oxygen-labile nitrogenase complex, the enzyme responsible for nitrogen fixation (Wolk \textit{et al.}, 1994). In heterocysts, O\textsubscript{2}-evolving photosystem II is inactivated, respiration is enhanced, and a thick envelope consisting of layers of polysaccharide and glycolipid that limits oxygen diffusion into cells is formed outside the cell wall. Because heterocysts are unable to fix CO\textsubscript{2} photosynthetically, vegetative cells supply carbohydrate to heterocysts and, in return, receive nitrogen fixation products from heterocysts. Thus, vegetative cells and heterocysts depend on each other and filament integrity is important for diazotrophic growth.

In the filamentous cyanobacterium \textit{Anabaena} (\textit{Nostoc}) sp. strain PCC 7120 (hereafter \textit{Anabaena} PCC 7120), approximately 10\% of chromosomal genes are upregulated with spatiotemporal regulation in the process of heterocyst development (Ehira \textit{et al.}, 2003; Ehira & Ohmori, 2006a). Although little is known of the regulation of gene expression during heterocyst development, the regulatory network of the early stages of heterocyst development is known in outline. The developmental process is initiated by an increase in the level of 2-oxoglutarate (Laurent \textit{et al.}, 2005). 2-Oxoglutarate binds to NtcA (Zhao \textit{et al.}, 2010), a transcriptional regulator that globally controls nitrogen metabolism in cyanobacteria (Herrero \textit{et al.}, 2004). NtcA activates transcription of the \textit{nrrA} gene, whose product in turn activates \textit{hetR} expression (Ehira & Ohmori, 2006a, b; Muro-Pastor \textit{et al.}, 2006). HetR is a master regulator of heterocyst development, and plays a key role in differentiation and pattern formation (Buikema & Haselkorn, 1991; Buikema & Haselkorn, 2001). HetR is thought to activate expression of many genes involved in heterocyst development (Higa & Callahan, 2010; Huang \textit{et al.}, 2004; Saha & Golden, 2011).

In addition to transcriptional regulation, the importance of post-translational regulation in heterocyst development has...
been recognized in the last decade. The genome of *Anabaena* PCC 7120 contains a large number of genes that encode protein kinases and phosphatases (Ohmori et al., 2001; Wang et al., 2002). Some of these genes are involved in heterocyst development, mostly in heterocyst maturation and function. The *pknE* gene, encoding a Ser/Thr protein kinase, is upregulated by nitrogen deprivation (Ehira & Ohmori, 2006a). A *pknE* inactivation mutant shows a defect in diazotrophic growth (Zhang et al., 1998), and over-expression of *pknE* blocks heterocyst differentiation (Saha & Golden, 2011). A Ser/Thr protein kinase, HepS, is involved in the synthesis of heterocyst envelope polysaccharide (Fan et al., 2006). Two protein kinases, Pkn30 and Pkn44, of the HstK family, which contain a putative Ser/Thr-kinase domain at their N termini and a His-kinase domain at their C termini, are involved in the synthesis of the minor heterocyst-specific glycolipid (Shi et al., 2007). In the present study, we have found that the *pknH* gene (*alr1336*), encoding a putative Ser/Thr protein kinase, is restrictively expressed in heterocysts and is required for diazotrophic growth.

**METHODS**

**Bacterial strains and culture conditions.** *Anabaena* sp. strain PCC 7120 and its derivatives were grown in the BG-11 medium (containing NaN3 as nitrogen source), as described previously (Ehira & Ohmori, 2006a). Liquid cultures were bubbled with air containing 1.0 % (v/v) CO2. For nitrogen-deprivation experiments, cells grown in BG-11 medium until they reached OD675 0.4–0.5 were washed with nitrogen-free medium (BG-11o) and then resuspended in BG-11o medium. Spectinomycin was added to the medium at a final concentration of 10 μg mL–1, when required.

**Mutant and plasmid construction.** All primers listed in Table S1, available with the online version of this paper, were designed based on genome data from Cyanobase (Nakao et al., 2010). A plasmid, pRHetRS, for hetR gene disruption was constructed as follows. A DNA fragment containing the hetR gene was amplified by PCR using the primer pair hetR-uF and hetR-RB (Table S1) and cloned between the *Sac*I–*Xho*I sites of plasmid pRL271 (Black et al., 1993) to construct pRhetRS. A plasmid, pR1336S, for *pknH* gene disruption was constructed as follows. DNA fragments upstream and downstream of the *pknH* gene were amplified by PCR using the primer pairs 1336-5F and 1336-5R, and 1336-3F and 1336-3R, respectively (Table S1). The upstream fragment was cloned between the *Sac*I and *Bam*HI sites of pBluescript II KS + (Agilent Technologies), and then the downstream fragment was cloned between the *Bam*HI and *Xho*I sites of pBluescript II KS + (Agilent Technologies), and then the downstream fragment was cloned between the *Sac*I and *Xho*I sites of pRL271 to construct pR1336S. pRhetRS and pR1336S were transferred by conjugation into *Anabaena* PCC 7120 containing plasmid pAM505 (Yoon & Golden, 1998) to construct pA1336.

Plasmid pA1336G was used to express a *pknH*-gfp transcriptional fusion. An upstream fragment of the *pknH* gene was amplified by PCR using the primer pair 1336-5F and 1336-5R, and then cloned between the *Sac*I and *Kpn*I sites of shuttle vector pAM505 (Yoon & Golden, 1998) to construct pA1336G.

**Acetylene reduction assays.** Acetylene activity was determined by acetylene reduction assays using GC (GC-8A gas chromatograph, Shimadzu), as described previously (Ehira & Ohmori, 2001).

**Nitrogenase activity was determined by acetylene reduction assays using GC (GC-8A gas chromatograph, Shimadzu), as described previously (Ehira & Ohmori, 2001).**

**RESULTS**

**Expression of pknH is upregulated in heterocysts**

In the previous study, changes in whole-gene expression of *Anabaena* PCC 7120 by nitrogen deprivation were investigated using a DNA microarray (Ehira & Ohmori, 2006a). The results showed induction of *alr1336*, encoding a putative Ser/Thr kinase, by nitrogen deprivation. In this study, spatiotemporal expression of *alr1336* was closely analysed by qRT-PCR and the use of a gfp transcriptional fusion gene. Expression of *alr1336* was induced 8 h after nitrogen deprivation, with increases in the transcript level of about ninefold after 24 h (Fig. 1). Fig. 2 shows the spatial regulation of *alr1336* expression. In *Anabaena* PCC 7120 containing plasmid pA1336G, the gfp gene is transcribed from a promoter of *alr1336*. No GFP fluorescence was observed when the filaments were grown with nitrate or subjected to nitrogen deprivation for 3 h (Fig. 2e, f). After 12 h of nitrogen deprivation, differentiating cells were structurally distinguishable from vegetative cells and slight GFP fluorescence was detected in those cells, while vegetative cells showed no detectable fluorescence (Fig. 2c, g). After 24 h, fluorescence levels increased only in heterocysts, though fluorescence from some heterocysts was weak (Fig. 2d, h). This indicated that expression of *alr1336* is restrictively induced in heterocysts by nitrogen deprivation.

The product of *alr1336* has a Ser/Thr protein kinase domain at its N terminus and a DUF323 domain at its C terminus (Zhang et al., 2007). Ser/Thr kinases with the DUF323 domain are found in filamentous cyanobacteria,
but not in unicellular strains (Zhang et al., 2007). The kinase domain of Alr1336 shows 42% amino acid identity with SpkC of *Synechocystis* sp. PCC 6803, which has been shown to phosphorylate both itself and general substrate proteins (Kamei et al., 2002). Moreover, the well-conserved 12 amino acid residues in the catalytic domains of Ser/Thr kinases are completely conserved in the deduced amino acid sequence of the *alr1336* product (Hanks & Hunter, 1995). Thus, we designated *alr1336* as *pknH* (**protein kinase expressed in heterocysts**).

To determine the correlation between *pknH* expression and heterocyst development, the transcript level of *pknH* in the *nrrA* disrupted DR4312S (Ehira & Ohmori, 2006a) and the *hetR* disrupted DRhetRS was determined (Fig. 1). Heterocyst development is delayed in DR4312S (Ehira & Ohmori, 2006a) and completely abolished in DRhetRS, as reported elsewhere (Buikema & Haselkorn, 1991). Induction of the *pknH* gene was delayed to 24 h after nitrogen deprivation in DR4312S, and abolished in DRhetRS (Fig. 1). It is concluded that the expression of *pknH* is developmentally regulated and that *hetR* is necessary for the induction of *pknH*.

**The *pknH* gene is required for diazotrophic growth**

The *pknH* gene-deficient mutant DR1336S was constructed by homologous recombination. DR1336S grew normally in nitrate-containing medium (Figs 3a and 4d), while the rate of growth of DR1336S was much slower than that of the wild-type (WT) strain in medium without combined nitrogen (Fig. 3b). After 18 h of nitrogen deprivation, when the WT starts nitrogen fixation (Ehira & Ohmori, 2011), heterocysts were stained with Alcian blue, which specifically stains the polysaccharide layer of the heterocyst envelope (Fig. 4b). In DR1336S, heterocysts were visually detectable and stained with Alcian blue, indicating that the polysaccharide layer of the heterocyst had formed (Fig. 4e). However, the filament length of DR1336S was reduced and many heterocysts were detached from filaments (Fig. 4e). These phenotypes were emphasized by prolonged cultivation in nitrogen-free medium (Fig. 4f), and even in a static culture, fragmentation was

![Fig. 1. Changes in the transcript level of the *pknH* gene after nitrogen deprivation. The relative transcript levels of *pknH* at the indicated times were determined by qRT-PCR in the WT strain (●), the *nrrA* disrupted DR4312S (▲) and the *hetR* disrupted DRhetRS (○). The transcript levels were determined in duplicate using three independently grown cultures. The transcript level of the WT strain at 0 h was taken as 1.](http://mic.sgmjournals.org)
observed (data not shown). Shuttle vector pA1336, in which the pknH gene is the only coding region, was transferred into DR1336S, resulting in a complemented strain that showed elongated filaments with heterocysts similar to those of the WT (data not shown). These results indicate that pknH is required for the stability of the connection between heterocysts and vegetative cells.

In fragmentation mutants of *Anabaena* PCC 7120, heterocyst differentiation is impaired (Flores et al., 2007; Jang et al., 2007; Merino-Puerto et al., 2010; Nayar et al., 2007). Fig. 5 shows developmental regulation of genes involved in heterocyst differentiation, including hetR, hepA, hglE and nifH, in DR1336S. Expression of hetR was upregulated within 3 h after nitrogen deprivation, and the hetR transcript level reached the maximum level at 8 h, and then decreased (Fig. 5a). In DR1336S, the increase in the hetR transcript was delayed to 8 h, and the transcript level remained high even after 24 h (Fig. 5a). Expression of hepA, which is essential for the formation of the polysaccharide layer of heterocysts (Holland & Wolk, 1990), was induced at 8 h. The induction of hepA was also detected in DR1336S, although the transcript level was lower than in the WT (Fig. 5b). Expression of hglE, which is required for the synthesis of the glycolipid layer of heterocysts (Campbell et al., 1997), and nifH, encoding a subunit of nitrogenase, was induced at 24 h in both the WT and DR1336S (Fig. 5c, d). Thus, heterocyst maturation is likely to be unaffected by disruption of the pknH gene. Indeed, DR1336S developed appreciable nitrogenase activity 24 h after nitrogen deprivation, although the activity in DR1336S [1.3 ± 0.5 μmol ethylene (mg Chl\(^{-1}\)) h\(^{-1}\)] was very low compared with the WT [22.4 ± 1.7 μmol ethylene (mg Chl\(^{-1}\)) h\(^{-1}\)]. The nitrogenase activity of DR1336S was increased to 2.5-fold during the following 24 h of incubation [3.2 ± 0.4 μmol ethylene (mg Chl\(^{-1}\)) h\(^{-1}\)] and reached one quarter of the WT level [12.9 ± 3.3 μmol ethylene (mg Chl\(^{-1}\)) h\(^{-1}\)]. It is concluded that DR1336S is able to form mature heterocysts with nitrogenase activity.

![Fig. 3. Growth of *Anabaena* PCC 7120 (●) and DR1336S (○) on different nitrogen sources. Growth was measured as OD\(_{750}\). (a) Growth on nitrate as the nitrogen source. (b) Growth on dinitrogen as the nitrogen source. Nitrate-grown filaments were transferred to nitrogen-free medium at time zero. Data are expressed as averages of the results of two independent cultures.](image-url)

![Fig. 4. Heterocyst development after nitrogen deprivation in the wild-type strain (a–c) and the pknH disruptant DR1336S (d–f). Nitrate-grown filaments were transferred to nitrogen-free medium. Micrographs were taken before (a, d) or 18 h (b, e) and 44 h (c, f) after nitrogen deprivation. The polysaccharide layer of heterocysts was stained with Alcian blue.](image-url)
Expression of the *pknH* gene was developmentally regulated (Fig. 1). Disruption of the *hetR* gene abolished the induction of *pknH*. The *pknE* (*alr3732*) gene, encoding another Ser/Thr protein kinase, is also upregulated in heterocysts (Saha & Golden, 2011). HetR is known to interact with the *pknE* promoter. The inverted repeat sequence that is recognized by HetR has been determined for the promoter region of *hetP* (Higa & Callahan, 2010). Since the HetR-recognition sequence is not found within the upstream region of the *pknH* gene, transcription of the *pknH* gene could be regulated by a transcriptional regulator that is under the control of HetR.

In the *pknH* disruptant, heterocysts were formed 18 h after nitrogen deprivation and had normal morphology and Alcian blue staining (Fig. 4). Expression of genes involved in heterocyst maturation, such as *hepA*, *hglE* and *nifH*, was similar to that of the WT (Fig. 5). The *pknH* disruptant showed nitrogenase activity even in the presence of oxygen, although the levels were lower than those of the WT, indicating that the *pknH* disruptant differentiated mature heterocysts. However, most heterocysts of the *pknH* disruptant were detached from filaments (Fig. 4). These results support the conclusion that the *pknH* gene is required for the connections between heterocysts and vegetative cells rather than for heterocyst maturation. Heterocysts have a thick envelop outside the cell wall, which limits oxygen diffusion, but they are connected to the adjacent vegetative cells at the polar region through a special structure to allow the exchange of metabolites between heterocysts and vegetative cells (Walsby, 2007). Proteins constituting the cell–cell joining structure have been identified over the past few years (Flores et al., 2007; Mariscal et al., 2011; Merino-Puerto et al., 2011). Since PknH is predicted to be a cytosolic protein by the secondary structure prediction system SOSUI (Hirokawa et al., 1998), PknH itself is unlikely to constitute the cell–cell joining structure. PknH could regulate activities and/or localization of proteins involved in cell–cell connections by phosphorylation.

Two Ser/Thr protein kinases, encoded by *pknE* and *alr4668*, are expressed in differentiating cells (Saha & Golden, 2011), as well as the *pknH* gene (Fig. 2), and a Ser/Thr protein phosphatase DevT accumulates in mature heterocysts (Espinosa et al., 2010). The *pknE* mutant strain can grow in nitrogen-free medium, although its growth rate is slightly slower than that of the WT, and overexpression of *pknE* blocks heterocyst differentiation (Saha & Golden, 2011). The *devT* mutant strain can form morphologically mature heterocysts, but it cannot fix nitrogen (Espinosa et al., 2010). Thus, the phosphorylation of Ser/Thr residues of certain proteins in heterocysts plays important roles in heterocyst differentiation and function, and a phosphorylation network might regulate various aspects of heterocyst development. In order to understand the role of these protein kinases and phosphatases, the signals activating them as well as their target proteins need to be addressed.

**DISCUSSION**

In the present study, we characterized the *pknH* gene of *Anabaena* PCC 7120, encoding a Ser/Thr protein kinase. Expression of *pknH* was upregulated in heterocysts by nitrogen deprivation (Figs 1 and 2). The *pknH* disruptant was capable of differentiating heterocysts with nitrogenase activity (Fig. 4), but it showed a defect in diazotrophic growth (Fig. 3). After nitrogen deprivation, filaments of the *pknH* disruptant were fragmented, and most heterocysts were detached from filaments (Fig. 4). This indicates that the *pknH* gene is required for the stability of the connection between heterocysts and vegetative cells.

Expression of the *pknH* gene was developmentally regulated (Fig. 1). Disruption of the *hetR* gene abolished the induction of *pknH*. The *pknE* (*alr3732*) gene, encoding another Ser/Thr protein kinase, is also upregulated in heterocysts (Saha & Golden, 2011). HetR is known to interact with the *pknE* promoter. The inverted repeat sequence that is recognized by HetR has been determined for the promoter region of *hetP* (Higa & Callahan, 2010). Since the HetR-recognition sequence is not found within the upstream region of the *pknH* gene, transcription of the *pknH* gene could be regulated by a transcriptional regulator that is under the control of HetR.

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