

The regulation of Enzyme IIA^{Glc} expression controls adenylate cyclase activity in *Escherichia coli*

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During the last few years, several genes, such as *pap*, *bgl* and *flhDC*, have been shown to be coregulated by the histone-like nucleoid-structuring (H-NS) protein and the cyclic AMP-catabolite activator protein (cAMP/CAP) complex, suggesting an interaction between both systems in the control of some cellular functions. In this study, the possible effect of H-NS on the cAMP level was investigated. In a CAP-deficient strain, the presence of an *hns* mutation results in a strong reduction in the amount of cAMP, due to a decrease in adenylate cyclase activity. This is caused by the reduced expression of *crr*, which encodes the Enzyme IIA^{Glc} of the phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS), from its specific P2 promoter. This leads to a twofold reduction in the global amount of Enzyme IIA^{Glc}, the adenylate cyclase activator, responsible for the decrease in adenylate cyclase activity observed in the *hns crp* strain.

Keywords: catabolite repression, *cya*, regulatory network

INTRODUCTION

In enterobacteria, the histone-like nucleoid-structuring (H-NS) protein is one of the most abundant DNA-binding proteins involved in the organization of the bacterial chromosome (Bertin *et al.*, 2001). Numerous phenotypes have been associated with *hns* mutations, resulting from a modification in the expression of several genes. Most of them are regulated by environmental parameters, such as pH, osmolarity and temperature, or are known to be involved in bacterial virulence (Atlung & Ingmer, 1997; Laurent-Winter *et al.*, 1997; Hommais *et al.*, 2001).

It has been demonstrated that the H-NS protein interacts with other regulatory systems. For example, the leucine-responsive regulatory protein Lrp regulates the transcription of a number of genes by binding DNA at a specific site located upstream from the transcription start site of the genes (Calvo & Matthews, 1994). Some

of these target genes and the Lrp structural gene itself are regulated by the H-NS protein (Levinthal *et al.*, 1994; Oshima *et al.*, 1995). The H-NS protein also possesses common targets with the cAMP-catabolite activator protein (CAP) complex: *nmpC* and *malT* genes (Coll *et al.*, 1994; Johansson *et al.*, 1998) and *pap*, *bgl*, *mccABCDE* and *flhDC* operons (Forsman *et al.*, 1992; Gonzalez-Pastor *et al.*, 1995; Schnetz & Wang, 1996; Soutourina *et al.*, 1999). In contrast to its role in the control of *flhDC* expression (Bertin *et al.*, 1994; Soutourina *et al.*, 1999), the cAMP-CAP complex acts as an H-NS protein antirepressor in the regulation of *pap* and *bgl* operons (Forsman *et al.*, 1992; Schnetz & Wang, 1996).

The cAMP-CAP complex, which controls the expression of a multitude of genes or operons, has been characterized for its role in catabolite repression. Indeed, high glucose levels reduce Enzyme IIA^{Glc} phosphorylation, which decreases adenylate cyclase activity and cAMP concentration. This results in a repressed synthesis of the enzymes needed for the catabolism of alternative carbon sources. It is now known that CAP is also involved in the expression of genes needed for adaptation to changes in growth conditions. Moreover, CAP regulates the synthesis of some membrane components, numerous proteins involved in various stresses and some regulator-encoding genes. Finally, it is worth

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Abbreviations: CAP, catabolite activator protein; H-NS, histone-like nucleoid-structuring; PTS, phosphoenolpyruvate:carbohydrate phosphotransferase system.

mentioning that many CAP-regulated genes are also controlled by other transcription factors (for a review see Busby & Kolb, 1996).

It has been suggested that the cellular CAP concentration might be somewhat reduced in *hns* strains (Johansson *et al.*, 1998). As it has been demonstrated that the activity of CAP is mainly modulated by the intracellular level of cAMP (Roy *et al.*, 1983; Kolb *et al.*, 1993), we wanted to know whether the H-NS protein could be involved in the control of the intracellular cyclic AMP (cAMP) concentration. In the present paper, we show that the H-NS protein plays a role in this process by acting on *crr* gene expression. The effect on the *crr*-specific P2 promoter was mainly observable in the absence of CAP and, although the H-NS protein has been considered as a transcriptional repressor, our results constitute a new example of a positive effect of this regulatory protein on bacterial physiology. Moreover, we show for the first time that *crr* expression is regulated and that a twofold reduction in the global amount of Enzyme IIA^{Glc} is sufficient to significantly decrease adenylate cyclase activity and the cAMP level.

METHODS

Bacterial strains, plasmids and growth conditions. The *Escherichia coli* K-12 derivative strains and the plasmids used in this work are listed in Table 1. Mutations *hns-1001* and *hns-118* were introduced by P1 transduction as described previously (Bertin *et al.*, 1994). For reasons of incompatibility with the kanamycin resistance marker of the resident plasmid, the *hns-118* mutation was used instead of the *hns-1001* mutation in β -galactosidase experiments. All strains were grown at 37 °C in M63 medium (Miller, 1972), supplemented with glucose (0.4%), thiamine (5 μ g ml⁻¹) and Casamino acids (0.1%). When required, kanamycin and ampicillin were added at 25 and 100 μ g ml⁻¹, respectively. Plasmid pDIA3350 was constructed by insertion of the *Sall*-*Bam*HI fragment of

pDIA3238, corresponding to the full phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS) operon with promoters P0, P1 and P2, into plasmid pDIA3240 (De Reuse *et al.*, 1986). All experiments were performed in accordance with the European regulation requirements concerning the contained use of Genetically Modified Organisms of Group I (agreement no. 2735).

cAMP assay. Total cAMP production was determined by a radioimmunological assay from at least four samples of exponentially growing cells as described by Guidi-Rontani *et al.* (1981) and Crasnier *et al.* (1994).

In vitro adenylate cyclase assay. Exponentially growing cell cultures were centrifuged at 9000 *g* for 10 min at 20 °C. The pellet, corresponding to 0.5 g bacteria, was resuspended in 3 ml 25 mM Tris/HCl, 10 mM MgCl₂, pH 8.3, (Tris-Mg buffer) to obtain a 20 mg ml⁻¹ protein concentration. Bacteria were then broken with the FastPrep System and FastProtein Blue (Bio-101) and centrifuged at 13000 *g* at 4 °C. Protein (0.4–0.8 mg) of the bacterial supernatant was added to 1.2 ml of assay mixture (125 mM Tris/HCl, pH 8.3, 50 mM MgCl₂, 5 mM dithiothreitol, 5 mM ATP) and 4.68 ml Tris-Mg buffer. During incubation at 28 °C, several samples of 1 ml were taken between 0 and 60 min and heated for 5 min at 100 °C, according to the method of Joseph *et al.* (1982). The cAMP synthesized was quantified with the cAMP^[125I]-RIA kit (NEN).

β -Galactosidase assay. β -Galactosidase activity was determined by the method of Miller (1992) on exponentially growing cells. The assay was performed on more than three samples from at least two independent cultures.

Determination of the phosphorylation state of Enzyme IIA^{Glc}. The phosphorylation state of Enzyme IIA^{Glc} was determined with a Western blotting experiment with anti-IIA^{Glc} antibodies (kindly provided by P. Postma, University of Amsterdam, The Netherlands) on 20 μ l protein extracts from strains grown to an OD₆₀₀ of precisely 0.400 (Takahashi *et al.*, 1998). Immunoblots were scanned with a JX-330 Sharp scanner and quantified using PDI software, PDQuest, based on a SUN computer system.

Table 1. *E. coli* strains and plasmids used in this study

Strain or plasmid	Description	Source
Strains		
TP2101	F ⁻ <i>xyl</i> Δ <i>lacX74</i> <i>argH1</i>	Laboratory collection
BE1522	F ⁻ <i>xyl</i> Δ <i>lacX74</i> <i>argH1</i> <i>hns-1001</i> ::Tn5 <i>seq1</i>	This study
TP2139	F ⁻ <i>xyl</i> Δ <i>crp39</i> Δ <i>lacX74</i> <i>argH1</i> <i>ilvA</i>	Roy <i>et al.</i> (1983)
BE1420	F ⁻ <i>xyl</i> Δ <i>crp39</i> Δ <i>lacX74</i> <i>argH1</i> <i>ilvA</i> <i>hns-1001</i> ::Tn5 <i>seq1</i>	This study
BE1421	F ⁻ <i>xyl</i> Δ <i>crp39</i> Δ <i>lacX74</i> <i>argH1</i> <i>ilvA</i> <i>hns-118</i> ::Tn10	This study
Plasmids		
pDIA1973	<i>cyaA-lacZ</i> operon fusion	Roy <i>et al.</i> (1988)
pDIA3226	<i>ptsH-ptsI-lacZ</i> protein fusion	De Reuse & Danchin (1988)
pDIA3238	<i>ptsH-ptsI-crr-lacZ</i> protein fusion	De Reuse & Danchin (1988)
pDIA3247	<i>ptsH-lacZ</i> protein fusion	De Reuse & Danchin (1988)
pDIA3241	<i>ptsH-lacZ</i> operon fusion	De Reuse & Danchin (1988)
pDIA3242	<i>ptsH-ptsI-lacZ</i> operon fusion	De Reuse & Danchin (1988)
pDIA3350	<i>ptsH-ptsI-crr-lacZ</i> operon fusion	This study
pDIA4705	pBR322 derivative carrying <i>crr</i> under anti-Tc ^r promoter	Zeng <i>et al.</i> (1992)

RESULTS

Effect of *crp* and/or *hns* mutations on cAMP level

To determine whether the H-NS protein modulates cAMP synthesis, the total cAMP level was measured in exponentially growing cells of wild-type TP2101 and isogenic strains deficient for the H-NS protein (BE1522), CAP (TP2139) or both regulators (BE1420), by using a radioimmunological method. As expected (Potter *et al.*, 1974; Joseph *et al.*, 1982), the presence of a *crp* mutation in TP2139 resulted in an important increase in cAMP concentration (more than 300-fold). In contrast, no significant difference was observed in the *hns* strain BE1522 (Table 2). Moreover, compared to the strain carrying the sole *crp* mutation, the presence of both *crp* and *hns* mutations in BE1420 resulted in a more than sixfold reduction in the cAMP concentration (Table 2). This result was confirmed by a cAMP excretion test on MacConkey maltose medium (data not shown). This suggests that the repression by the cAMP-CAP complex seems to be epistatic with regard to the activation by the H-NS protein. However, at least in a *crp* background, the H-NS protein affects the level of cAMP.

Table 2. cAMP levels in H-NS protein-deficient and/or CAP-deficient strains

Data are the mean values of four samples from two independent cultures that differed by less than 20%.

Strain	Relevant genotype	Total cAMP [pmol (mg protein) ⁻¹]
TP2101	Wild-type	314
BE1522	<i>hns</i>	415
TP2139	<i>crp</i>	97 625
BE1420	<i>crp hns</i>	15 069

Positive effect of the H-NS protein on the activity and the synthesis of adenylate cyclase in a *crp* strain

Adenylate cyclase plays a major role in the control of cAMP level in bacterial cells. This enzyme is known to be regulated by CAP at the level of its activity and at the transcriptional level (Aiba, 1985; Inada *et al.*, 1996; Takahashi *et al.*, 1998).

Adenylate cyclase activity was measured with an *in vitro* assay on exponentially growing cells. A more than 30-fold increase in enzyme activity was measured in the *crp* strain TP2139 [12 600 pmol cAMP (mg protein)⁻¹ min⁻¹] compared to the wild-type TP2101 [400 pmol cAMP (mg protein)⁻¹ min⁻¹], in accordance with the results of others (Rephaeli & Saier, 1976; Joseph *et al.*, 1982). In contrast, an eightfold decrease in activity was measured in the *crp hns* double mutant BE1420 [1600 pmol cAMP (mg protein)⁻¹ min⁻¹] compared to the *crp* strain. These results are in agreement with the total cAMP level measured in bacterial cultures (Table 2).

To investigate the role of the H-NS protein on the transcription of the adenylate cyclase encoding gene, we measured the activity of a *cyaA-lacZ* operon fusion from plasmid pDIA1973 (Roy *et al.*, 1988). Compared to the wild-type TP2101 [6320 Miller units (mg protein)⁻¹], a moderate increase in β -galactosidase activity was observed in the *crp* strain TP2139 (Table 3), in agreement with the data of others (Kawamukai *et al.*, 1985). In contrast, in the *crp hns* double mutant BE1421 (Table 3), a more than twofold decrease in β -galactosidase activity was observed compared to that in the *crp* strain.

Regulation of adenylate cyclase activity by the H-NS protein via the Enzyme IIA^{Glc} level

Adenylate cyclase activity is known to be regulated by the PTS via Enzyme IIA^{Glc} and the cAMP-CAP complex (Levy *et al.*, 1990; Saier *et al.*, 1996; Reddy & Kamireddi,

Table 3. Effect of the H-NS protein on β -galactosidase synthesis rate of gene fusions between *cyaA*, *ptsH*, *ptsI* or *crr* and *lacZ*

Data are the mean values of more than three samples from at least two independent cultures that differed by less than 10%.

Plasmid	<i>lacZ</i> fusion	β -Galactosidase activity [Miller units (mg protein) ⁻¹] in:	
		TP2139 (<i>crp</i>)	BE1421 (<i>crp hns</i>)
pDIA1973	<i>cyaA</i> operon	8950	3470
pDIA3241	<i>ptsH</i> operon	2730	2000
pDIA3247	<i>ptsH</i> protein	5370	3870
pDIA3242	<i>ptsH-ptsI</i> operon	2190	2150
pDIA3226	<i>ptsH-ptsI</i> protein	1420	1910
pDIA3350	<i>ptsH-ptsI-crr</i> operon	10 690	2870
pDIA3238	<i>ptsH-ptsI-crr</i> protein	6210	3150

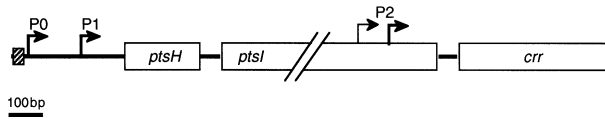


Fig. 1. Organization of the *pts* operon (De Reuse & Danchin, 1988; De Reuse *et al.*, 1992). Open boxes represent the *ptsH*, *ptsI* and *crr* coding regions. The transcriptional start sites from P0, P1 and P2 promoters are indicated by arrows. The major transcriptional start sites are indicated by bold arrows and the binding site for the CAP-cAMP complex is shown by a hatched box.

1998). The HPr protein could also be involved in this process (Peterkofsky *et al.*, 1995). Although the three PTS genes *ptsH*, *ptsI* and *crr*, which encode the proteins HPr, Enzyme I and Enzyme IIA^{Glc}, respectively, are considered to be part of a single operon, transcription is known to be initiated from three distinct promoters, P0, P1 and P2 (Fig. 1) (De Reuse & Danchin, 1988; De Reuse *et al.*, 1992). As the decrease in *cyaA-lacZ* activity does not seem to be sufficient to explain the strong decrease in adenylate cyclase activity measured in the *crp hns* double mutant BE1421 (see above), the expression level of *ptsH*, *ptsI* and *crr* was analysed using protein and operon fusions (De Reuse & Danchin, 1988). In the *crp* strain, the lack of H-NS protein had only a minor effect on the expression of both *ptsH-lacZ* and *ptsI-lacZ* fusions, which are exclusively under the control of promoters P0 and P1, i.e. a 1.3-fold decrease and 1.3-fold increase, respectively (Table 3). In contrast, *crr* expression, which is under the control of the three promoters, showed a 3.7-fold and twofold decrease in the β -galactosidase activity of the *crr-lacZ* transcriptional and protein fusion, respectively, in the *crp hns* double mutant BE1421 compared to the *crp* strain (Table 3). This suggests that the H-NS protein exerts a positive and specific effect on *crr* transcription from the P2 promoter.

The Enzyme IIA^{Glc} is known to be phosphorylated by the phosphorylated HPr protein (HPr-P), which is itself phosphorylated by Enzyme I-P (Postma & Lengeler, 1985). Phosphorylated Enzyme IIA^{Glc} is known to activate adenylate cyclase while the unphosphorylated form has no effect on enzyme activity (Den Blaauwen & Postma, 1985; Crasnier & Danchin, 1990; Reddy & Kamireddi, 1998; Takahashi *et al.*, 1998). Moreover, it has been supposed that the global regulation of adenylate cyclase activity depends on the sole phosphorylation state of Enzyme IIA^{Glc}. Indeed, the major effect of the cAMP-CAP complex on adenylate cyclase activity results from the decrease in Enzyme IIA^{Glc} phosphorylation (Saier *et al.*, 1996; Crasnier-Mednansky *et al.*, 1997; Reddy & Kamireddi, 1998; Takahashi *et al.*, 1998). To determine the phosphorylated state of Enzyme IIA^{Glc} in the different strains, a Western blotting experiment was performed with anti-IIA^{Glc} antibodies on protein extracts from strains grown to an OD₆₀₀ of 0.400 (Takahashi *et al.*, 1998). After quantification, only 14% of Enzyme IIA^{Glc} was phosphorylated in wild-type

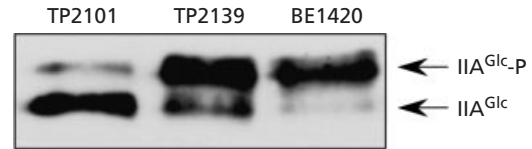


Fig. 2. Phosphorylation state and amount of Enzyme IIA^{Glc} in wild-type (TP2101), *crp* (TP2139) and *crp hns* (BE1420) strains. The two forms of the enzyme were visualized on a Western blot using anti-Enzyme IIA^{Glc} antibodies and quantified using PDI software, PDQuest. The result is representative of two experiments performed with 20 μ l protein extract from two independent cultures at an OD₆₀₀ of precisely 0.400.

strain TP2101, while 82 and 93% was phosphorylated in the *crp* (TP2139) and *crp hns* (BE1420) strains, respectively (Fig. 2). The proportion of the two forms of Enzyme IIA^{Glc} was similar in both *crp* and *crp hns* mutant strains. This suggests that the small variation observed on *ptsH* and *ptsI* expression has no effect on the phosphorylation state of Enzyme IIA^{Glc}. No significant difference in the amount of Enzyme IIA^{Glc} was observed between wild-type and *crp* strains (Fig. 2). In contrast, a twofold decrease in the amount of Enzyme IIA^{Glc} was measured in the *crp hns* double mutant compared to the *crp* strain (Fig. 2). This result is in agreement with the reduced expression of the *crr-lacZ* fusions observed in such a strain (Table 3). Similarly, a 51% reduction in the amount of Enzyme IIA^{Glc} was measured in the *hns* strains compared to that in the wild-type.

To discover whether the reduced amount of Enzyme IIA^{Glc} measured in the *crp hns* strain (Fig. 2) was sufficient to explain the decrease in adenylate cyclase activity, we determined this activity in the double mutant BE1420 containing plasmid pDIA4705 carrying the *crr* gene. The presence of this plasmid in a Δ *crr* strain has been shown to restore the wild-type cAMP level and glucose transport (Zeng *et al.*, 1992). The activity measured in the *crp hns* mutant containing plasmid pDIA4705, 11400 pmol cAMP (mg protein)⁻¹ min⁻¹, was similar to that obtained in the TP2139 *crp* strain [12600 pmol cAMP (mg protein)⁻¹ min⁻¹]. This is consistent with the Western blotting experiment which showed that a similar amount of Enzyme IIA^{Glc} was present in both TP2139 and BE1420(pDIA4705) (data not shown). This demonstrated that the variation in adenylate cyclase activity resulting from an *hns* mutation depends on the reduced amount of Enzyme IIA^{Glc} present in the cells rather than the effect the H-NS protein on *cyaA* gene expression (Table 2).

DISCUSSION

In *E. coli*, adenylate cyclase activity is known to be very low in a wild-type genetic context. Indeed, Enzyme IIA^{Glc}, which is the major activator of this activity, is mainly in an unphosphorylated form due to the presence

of a high concentration of cAMP-CAP complex (Saier *et al.*, 1996; Crasnier-Mednansky *et al.*, 1997; Reddy & Kamireddi, 1998; Takahashi *et al.*, 1998). Only the phosphorylated form of the enzyme plays a role as activator. This phosphorylation results from a transfer of the phosphoryl group from phosphoenolpyruvate to Enzyme IIA^{Glc} via Enzyme I and HPr (Postma & Lengeler, 1985). The three PTS genes *ptsH*, *ptsI* and *crr*, which encode the proteins HPr, Enzyme I and Enzyme IIA^{Glc}, respectively, belong to a single operon. However, transcription is initiated from three distinct promoters (Fig. 1). Both *ptsH* and *ptsI* depend on P0 and P1 promoters, while *crr* is controlled by the three promoters, P2 being responsible for 80% of total *crr* mRNA synthesis (De Reuse & Danchin, 1988; De Reuse *et al.*, 1992). Transcriptional regulation by glucose, the cAMP-CAP complex and the global repressor Mlc has been observed on promoter P0 (De Reuse *et al.*, 1992; Ryu & Garges, 1994; Tanaka *et al.*, 1999), while promoter P1 is known to be regulated by the fructose repressor FruR (Ryu *et al.*, 1995). However, no regulatory mechanism has been shown to affect promoter P2.

Our results demonstrate, for the first time, that *crr* is regulated at the transcriptional level. This regulation only affects the P2-specific promoter and has almost no effect on the two other promoters of the PTS operon. The H-NS protein controls the expression of numerous genes involved in bacterial adaptation to environmental changes (Hommais *et al.*, 2001) and it is generally considered as a transcriptional repressor. Although the mechanism, which could be indirect, remains to be determined, our results constitute a new example of the positive effect of this regulatory protein on bacterial physiology. Recently, the existence of a complex between HhA and the H-NS protein has been shown to be involved in the regulation of the haemolysin operon in *E. coli* (Nieto *et al.*, 2000). Moreover, an *hha* mutation results in a fivefold decrease in Enzyme IIA^{Glc} in rich medium under high osmolarity conditions (Balsalobre *et al.*, 1999). Taken together, these observations may suggest an interaction of both proteins in the regulation of *crr* expression. However, in contrast to the H-NS protein (Table 3 and Fig. 2), the effect of HhA on Enzyme IIA^{Glc} was only observed in conditions of high osmolarity, suggesting that the two regulatory proteins affect *crr* expression by a different mechanism. Finally, the repression by the cAMP-CAP complex is predominant with regard to the activation by the H-NS protein. Indeed, in the presence of the cAMP-CAP complex, only a small fraction of Enzyme IIA^{Glc} was phosphorylated (Fig. 2). This suggests that adenylate cyclase has its lowest activity in the wild-type strain, which could explain that a twofold alteration in the amount of Enzyme IIA^{Glc} in *hns* strains has no major effect on adenylate cyclase activation.

We also showed that, despite a large excess of Enzyme IIA^{Glc} in the cell [about 15000 Enzyme IIA^{Glc} phosphorylated molecules in comparison with 15–50 adenylate cyclase molecules (Yang & Epstein, 1983; Mitchell *et al.*, 1987)], a twofold variation in its accumulation

level resulted in an eightfold decrease in adenylate cyclase activity. In a glucose-rich medium, the phosphorylated form of Enzyme IIA^{Glc} interacts preferentially with the glucose permease (Enzyme IIBC^{Glc}) to allow the entry of glucose into the cell. This suggests that the affinity of phosphorylated Enzyme IIA^{Glc} is much lower for adenylate cyclase, or for the putative intermediary that could activate it (Saier *et al.*, 1996), than for glucose permease. Depending on environmental conditions, adenylate cyclase may be regulated either by the amount or by the phosphorylation of Enzyme IIA^{Glc}.

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