Urea Utilization in the Phototrophic Bacterium *Rhodobacter capsulatus* Is Regulated by the Transcriptional Activator NtrC

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The phototrophic nonsulfur purple bacterium *Rhodobacter capsulatus* can use urea as a sole source of nitrogen. Three transposon Tn*5*-induced mutations (Xan-9, Xan-10, and Xan-19), which led to a Ure⁻ phenotype, were mapped to the *ureF* and *ureC* genes, whereas two other Tn*5* insertions (Xan-20 and Xan-22) were located within the *ntrC* and *ntrB* genes, respectively. As in *Klebsiella aerogenes* and other bacteria, the genes encoding urease (*ureABC*) and the genes required for assembly of the nickel metallocenter (*ureD* and *ureEFG*) are clustered in *R. capsulatus* (*ureDABC-orf136-ureEFG*). No homologues of Orf136 were found in the databases, and mutational analysis demonstrated that *orf136* is not essential for urease activity or growth on urea. Analysis of a *ureDA-lacZ* fusion showed that maximum expression of the *ure* genes occurred under nitrogen-limiting conditions (e.g., serine or urea as the sole nitrogen source), but *ure* gene expression was not substrate (urea) inducible. Expression of the *ure* genes was strictly dependent on NtrC, whereas σ⁵⁴ was not essential for urease activity. Expression of the *ure* genes was lower (by a factor of 3.5) in the presence of ammonium than under nitrogen-limiting conditions, but significant transcription was also observed in the presence of ammonium, approximately 10-fold higher than in an *ntrC* mutant background. Thus, *ure* gene expression in the presence of ammonium also requires NtrC. Footprint analyses demonstrated binding of NtrC to tandem binding sites upstream of the *ureD* promoter. Phosphorylation of NtrC increased DNA binding by at least eightfold. Although urea is effectively used as a nitrogen source in an NtrC-dependent manner, nitrogenase activity was not repressed by urea.

Rhodobacter capsulatus is a nonsulfur phototrophic purple bacterium which can grow with a variety of different nitrogen sources, such as ammonium, almost all amino acids, purines (xanthine and hypoxanthine), urea, polyamines (putrescine and spermidine), and molecular nitrogen. Like in many other bacteria, ammonium is a preferred N source, and consequently, the highly energy-demanding nitrogen fixation process is repressed by ammonium.

R. capsulatus measures the cellular nitrogen status (e.g., availability of ammonium) by an Ntr system similar to that of enterobacteria involving the two-component regulatory system NtrB-NtrC (10, 15, 18). NtrC is the transcriptional activator of a number of genes directly or indirectly involved in nitrogen fixation in *R. capsulatus* (*glnB-glnA*, *nifA1*, *nifA2*, *anfA*, and *mopA-modABCD* [3]). These genes code for the signal transduction protein PII (GlnB) and glutamine synthetase (GlnA), the transcriptional activators of the two nitrogenase systems (*nif-* and *anf-*encoded), a molybdenum repressor of the Anf system, and a high-affinity molybdate uptake system. Despite the similarities of the Ntr systems of *R. capsulatus* and of enterobacteria, mutations in *R. capsulatus ntrC* do not produce the "classical" Ntr phenotype of enterobacteria, since the NtrC protein in *R. capsulatus* is not required for the utilization of amino acids as an N source (11, 13, 25).

Under conditions of nitrogen limitation, the NtrB sensor kinase autophosphorylates and transfers the phosphate to the NtrC response regulator. NtrC~P in turn activates transcription of its target genes. Transcriptional activation of these genes requires binding of NtrC~P to enhancer-binding sites distant from the promoters that are activated. Members of the enhancer-binding protein family characteristically activate transcription from promoters recognized by the alternative sigma factor σ⁵⁴ (NtrA). The NtrC protein from *R. capsulatus* (RcNtrC) is a unique enhancer-binding protein that does not require σ⁵⁴ but instead activates transcription of the genes mentioned above together with RNA polymerase containing the σ⁷⁰-like housekeeping sigma factor (RNAP-σ⁷⁰ [3, 8]).

Since an *R. capsulatus ntrC* mutant does not grow with urea as the sole N source (17), genes required for utilization of urea (*ure* genes) were likely targets for NtrC-mediated activation. Degradation of urea is catalyzed by the enzyme urease, which is an inducible enzyme in *R. capsulatus* E1F1 (7). Urease is a nickel-containing enzyme that catalyzes the hydrolysis of urea to form ammonia and carbamate, which spontaneously decomposes to produce carbonic acid and additional ammonia. In *Klebsiella aerogenes* and many other bacteria, the *ureA*, *ureB*, and *ureC* genes encode the catalytically inactive apoenzyme, and the *ureD*, *ureE*, *ureF*, and *ureG* gene products are required for assembly of the nickel metallocenter (5, 22).

This work describes genetic analyses of the *R. capsulatus ure* gene region showing that expression of the *ure* genes is activated under nitrogen-limiting conditions in an NtrC-dependent manner. DNA footprinting studies demonstrate direct binding of NtrC to the *ureD* promoter. This is the first example

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TABLE 1. Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant characteristics[a]	Reference or source
Bacterial strains		
E. coli		
JM83	Host for pUC plasmids	30
S17-1	RP4-2 (Tc::Mu) (Km::Tn7) integrated in the chromosome	29
R. capsulatus		
B10S	Spontaneous Sm^r mutant of *R. capsulatus* B10	14
KS36	Δ*nifHDK*::[Spc]	31
KS111	*ntrA*::[Gm]	16
TD50	*ntrC*::[Gm]	T. Drepper, Bochum (1998)
Xan-9, -10, -19, -20, -22	Tn*5*-induced Ure$^-$ mutants	17
Plasmids		
pUC18	*lacZ*α Ap^r	30
pPHU235	Broad-host-range *lacZ* fusion vector, Tc^r	10
pSUP202	Ap^r Cm^r Tc^r *mob*	29
pSUP301	Ap^r Km^r *mob*	29
pSUP401	Cm^r Km^r *mob*	29
pNIRUB4	13.3-kb *Eco*RI fragment from Xan-10 (*ureC*::Tn5) in pUC18	This work
pNIRUB35	*ureDA-lacZ* fusion in pPHU235, Tc^r	This work
pNIRUB42-I	1.3-kb *Eco*RI fragment carrying the *ureD* promoter in pUC18	This work
pNIRUB46	pSUP202 derivative carrying *lrp2*::[Gm^r], Spc^r	This work
pNIRUB53	10-kb *Bam*HI fragment of Xan-9 (*ureF*::Tn5) in pUC18, Km^r	This work
pNIRUB54	6-kb *Bam*HI fragment of Xan-19 (*ureC*::Tn5) in pUC18, Km^r	This work
pNIRUB55	8-kb *Bam*HI fragment of Xan20 (*ntrC*::Tn5) in pUC18, Km^r	This work
pNIRUB56	10-kb *Bam*HI fragment of Xan-22 (*ntrB*::Tn5) in pUC18, Km^r	This work
pNIRUB73-I/II	pSUP202 derivative carrying *orf136*::[Gm^r], Km^r	This work
pNIRUB76-I/II	pSUP401 derivative carrying *orf433*::[Km^r], Gm^r	This work
pBKRUB1-I/II	pSUP301 derivative carrying Δ(*lrp1-lrp2-ureD*)::[Gm^r], Km^r	This work
pBKRUB15-I	pSUP401 derivative carrying *ureG*::[Km^r], Gm^r	This work
pBKRUB16/17	pUC18 derivative carrying *orf323*::[Km^r], Tc^r *mob*	This work

[a] Abbreviations: Ap^r, ampicillin resistance; Cm^r, chloramphenicol resistance; Gm^r, gentamicin resistance; Km^r, kanamycin resistance; Spc^r, spectinomycin resistance; Sm^r, streptomycin resistance; Tc^r, tetracycline resistance.

of an NtrC-activated target gene in *R. capsulatus* which is not somehow involved in the process of nitrogen fixation.

MATERIALS AND METHODS

Bacterial strains and plasmids. The bacterial strains and plasmids used in this study are listed in Table 1. Methods for conjugational plasmid transfer between *Escherichia coli* and *R. capsulatus* and the procedures for selection of mutants, anaerobic growth conditions, and antibiotic concentrations have been previously described (14, 19, 23, 24).

DNA techniques. DNA isolation, restriction enzyme analysis, and cloning procedures were performed according to standard methods (27). Restriction endonucleases, T4 DNA ligase, and Superscript I reverse transcriptase were purchased from MBI Fermentas (St. Leon-Rot, Germany) or Life Technologies (Karlsruhe, Germany) and were used as recommended by the supplier. DNA sequence analysis was done by the chain termination method with fluorescein-labeled primers for use in the A. L. F. DNA sequencer (Amersham Pharmacia Biotech, Freiburg, Germany) according to the manufacturer's instructions.

Construction of an *ureDA-lacZ* fusion plasmid. A 3.9-kb *Bam*HI-*Hin*dIII fragment encompassing the *ureD* promoter region (Fig. 1A) was inserted into the mobilizable broad-host-range vector pPHU235, resulting in hybrid plasmid pNIRUB35 (Fig. 1C) carrying an in-frame *ureDA-lacZ* fusion.

β-Galactosidase and in vivo nitrogenase assays. To determine the β-galactosidase activities of *R. capsulatus* strains carrying pNIRUB35 (*ureDA-lacZ*), cultures were grown in RCV minimal medium supplemented with tetracycline (23). For growth under nitrogen-limiting conditions, either serine or urea was added to final concentrations of 9.5 or 4.0 mM, respectively. Nitrogen-sufficient conditions were achieved by addition of 15 mM NH$_4$Cl to the medium. Following growth in the media to late exponential phase, β-galactosidase activities of *R. capsulatus* strains were determined by the sodium dodecyl sulfate-chloroform method (10, 20).

Nitrogenase activities of whole cells were determined by the acetylene reduction assay as described by Wang et al. (31).

RNA isolation and primer extension analysis. RNA was prepared from *R. capsulatus nifHDK* deletion strain KS36 harboring plasmid pNIRUB35 (*ureDA-lacZ*). For this purpose, cells were grown in RCV minimal medium containing 4 mM urea as the sole nitrogen source under photoheterotrophic conditions until the early exponential growth phase. Cells were harvested and RNA was isolated according to the method described by Chomczynski and Sacchi (4). The primer extension procedure was performed with Superscript I reverse transcriptase (Life Technologies), using a 5′ fluorescein-labeled oligonucleotide (5′-TGCGTCCGAATCAAGCCCATAGC-3′, corresponding to codons 35 to 42 of the *ureD* gene). Conditions for primer extension were as described by Myöhänen and Wahlfors (26). Analysis of primer extension products next to a sequencing ladder generated with the same oligonucleotide was performed using the A. L. F. DNA sequencer (Amersham Pharmacia Biotech).

DNase I footprinting. PCR was used to generate a 286-bp fragment spanning the *ureD* promoter region with oligonucleotide primers ureD.F (5′-CGGGGTC GGGCAGATCGAAG-3′) and ureD.R (5′-CACAAGACCCTTCAGACGCG-3′) using pNIRUB42-I as a template. In each reaction, one of the primers ureD.F and ureD.R was end labeled with T4 polynucleotide kinase (Epicentre Technologies, Madison, Wis.) and [γ-^{32}P]dATP. DNA binding reactions with the unphosphorylated RcNtrC were carried out by the addition of various concentrations of RcNtrC to binding buffer (50 mM Tris-HCl [pH 7.5], 0.1 mM EDTA, 10 mM MgCl$_2$, 50 mM KCl, 10 mM dithiothreitol, 0.5 mM phenylmethylsulfonyl fluoride) which contained either upper- or lower-strand end-labeled probe (approximately 20,000 cpm), either 0 or 1 mM ATP, and 100 ng of poly(dI-dC) as a nonspecific competitor. Complexes were allowed to form for 10 min at 23°C in a total volume of 50 μl, after which DNase I digestion and DNA purification were performed as described previously (8). DNA binding reactions with phosphorylated RcNtrC were performed by incubation of maltose-binding protein-RcNtrB (MBP-RcNtrB; 1 μM) in binding buffer that contained 1 mM ATP as
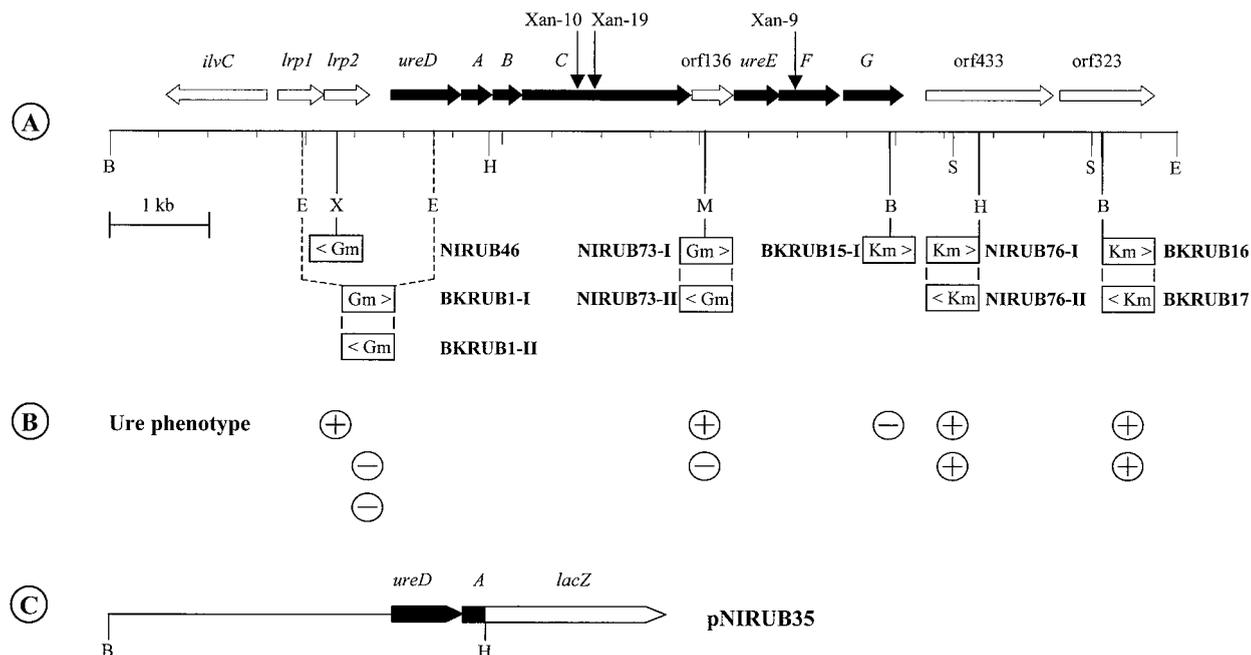
FIG. 1. Physical and genetic map of the *R. capsulatus* *ure* gene region. Abbreviations: B, *Bam*HI; E, *Eco*RI, H, *Hin*dIII; M, *Sma*I; S, *Sal*I; X, *Xho*I. (A) The localizations of genes and open reading frames are given by arrows carrying their respective gene designations. Black arrows emphasize the highly conserved structural and accessory *ure* genes found in many bacteria (22). Vertical arrows above the genetic map indicate the locations of Tn5 insertions in mutant strains Xan-9, Xan-10, and Xan-19 (17) resulting in an Ure⁻ phenotype. Below the map, the locations of interposon insertions are shown. The interposon cassettes (Gm, gentamicin resistance; Km, kanamycin resistance) are not drawn to scale. The directions of transcription of interposon resistance genes are symbolized by arrowheads, indicating polar and nonpolar insertions. (B) The ability of the corresponding *R. capsulatus* mutant strains to grow with urea as the sole nitrogen source is indicated by + or −. (C) Hybrid plasmid pNIRUB35 carrying an in-frame *ureDA-lacZ* fusion is based on the mobilizable broad-host-range plasmid pPHU235.

described previously (6). DNase I digestion reactions were analyzed on an 8% sequencing gel.

RESULTS AND DISCUSSION

Genetic organization of the *R. capsulatus ure* gene region. Random transposon Tn5 mutagenesis of an *R. capsulatus nifHDK* mutant strain (deleted for the structural genes of the molybdenum nitrogenase) led to the identification of five mutants (Xan-9, Xan-10, Xan-19, Xan-20, and Xan-22) unable to grow with urea as the sole nitrogen source (17). Tn5-containing DNA fragments from these mutants were cloned, and the sites of transposon insertions were determined by nucleotide sequence analyses. Comparison with the *R. capsulatus* genome sequence (http://wit.mcs.anl.gov/WIT2/CGI/org.cgi) showed that the Tn5-induced mutations in Xan-9, Xan-10, and Xan-19 mapped within the *ureF* and *ureC* genes (Fig. 1A). Due to the close proximity of the *ureDABC-orf136-ureEFG* genes, it seems likely that the *ure* genes are cotranscribed in *R. capsulatus* from a promoter upstream of *ureD* (see below). The organization of *ure* genes in *R. capsulatus* is similar to that of *K. aerogenes* and many other bacteria (22), except for the presence of an additional open reading frame (*orf136*) located between *ureC* and *ureE*. This *orf* did not show homology to any known *ure* gene or any other gene in the databases, indicating that *orf136* might be specific for *Rhodobacter*. The remaining mutants Xan-20 and Xan-22 carried the transposon within the *ntrC* and *ntrB* genes, respectively (data not shown).

Mutational analysis of the *R. capsulatus* urease gene region. As mentioned above, urease catalyzes the hydrolysis of urea to form ammonia and carbamate, which spontaneously decomposes to produce carbonic acid and additional ammonia. Although this process might produce free ammonium within the cell, urea did not prevent nitrogenase synthesis or activity in *R. capsulatus* at least under the conditions used in this study (Table 2). This is similar to the situation in *Azotobacter vinelandii*, where urea has been used as a nonrepressing nitrogen source (e.g., references 1 and 12). Since urease contains a nickel cofactor, different amounts of $NiCl_2$ (Table 2) were added to the *R. capsulatus* medium to rule out that the nickel concentration was limiting urease activity. In other studies

TABLE 2. In vivo nitrogenase activities of *R. capsulatus* B10S in the presence of urea

Nitrogen source	Nickel added (μM)	Nitrogenase activity[a] (nmol of ethylene produced/ [mg of protein × h])
Ammonium	None	3.6 ± 1.7
Serine	None	1,069.4 ± 19.6
Urea	None	665.9 ± 50.2
Urea	0.4	941.9 ± 82.7
Urea	6.0	995.1 ± 85.2
Urea	100.0	688.6 ± 145.7

[a] In vivo nitrogenase activities were analyzed by the acetylene reduction assay as described by Wang et al. (31). The results represent the means and standard deviations of at least three independent measurements.

TABLE 3. Transcriptional analysis of *R. capsulatus* wild-type and mutant strains carrying an in-frame *ureDA-lacZ* fusion (pNIRUB35)

Strain (pNIRUB35)	Relevant genotype	β-Galactosidase activity with[a]:				
		NH$_4^+$	Serine	Urea	Urea plus NH$_4^+$	Urea plus serine
B10S	Wild type	434.4 ± 47.8	1,556.7 ± 109.1	1,529.1 ± 166.1	448.3 ± 53.3	1,577.9 ± 373.5
TD50	*ntrC*$^-$	49.2 ± 4.7	31.6 ± 4.6	67.7 ± 9.0	62.8 ± 12.3	28.8 ± 6.6
KS111	*ntrA*$^-$	556.5 ± 25.5	3,369.4 ± 138.2	2,638.4 ± 287.9	782.7 ± 124.6	2,412.1 ± 196.3
KS36	Δ*nifHDK*	256.7 ± 15.9	1,471.0 ± 104.3	1,503.8 ± 59.1	309.5 ± 41.7	1,787.9 ± 111.9

[a] β-Galactosidase activities (in Miller units) were determined in late-exponential-phase *R. capsulatus* cultures grown photoheterotrophically with the indicated N sources. Miller units (20) and standard deviations were calculated from three independent assays for each strain.

nickel has been added in the micromolar range (e.g., 200 μM for *E. coli* carrying the *K. aerogenes ure* gene cluster [5]).

R. capsulatus exhibited growth rates in media containing urea without nickel supplementation comparable to those in media with ammonium (data not shown), demonstrating that sufficient amounts of nickel were present due to impurities of the other chemicals used for the preparation of the media. However, nickel concentrations of up to 100 μM did not significantly affect nitrogenase activities or increase growth rates of *R. capsulatus* (Table 2; data not shown). At present it remains speculative whether intracellular ammonium cannot be detected by the Ntr system or if ammonium assimilation (via GlnA) is faster than ammonium production by urease.

To avoid any interference between the activities of urease and nitrogenase, all mutations in the *ure* gene region (see below) were analyzed in the genetic background of the *R. capsulatus nifHDK* mutant strain KS36. Owing to the deletion of *nifHDK*, which encode the apoproteins of nitrogenase, this strain is unable to fix molecular dinitrogen, and thus growth is dependent on added nitrogen sources such as urea.

Two genes (*lrp1* and *lrp2*) coding for Lrp-like proteins were identified upstream of *ureD*, and two genes (*orf433* and *orf323*) coding for putative periplasmatic proteins were located downstream of *ureG* (Fig. 1A). Orf433 is of special interest since it shows similarity to the FmdD protein of *Methylophilus methylotrophus*, which is thought to comprise part of a high-affinity, binding-protein-dependent active-transport system for short-chain amides and urea (21). To determine the role of these four genes and of *orf136* in urea utilization, interposon cassettes carrying gentamicin (Gm) or kanamycin (Km) resistance genes were used to construct corresponding mutant strains in an *nifHDK* deletion background (Fig. 1A). Both interposons were previously shown to induce polar or nonpolar mutations depending on their orientation (10, 28). Growth of the parental strain KS36 (Δ*nifHDK*) and its derivatives was determined in RCV minimal medium containing urea as the sole N source under phototrophic growth conditions (see Materials and Methods). The corresponding Ure phenotype is given in Fig. 1B. Mutations in *ureD* (BKRUB1-I and BKRUB1-II) and *ureG* (BKRUB15-I) resulted in a Ure$^-$ phenotype in *R. capsulatus* regardless of the orientation of the interposon. Depending on the orientation of the interposon, insertions within *orf136* resulted either in a Ure$^+$ (NIRUB73-I) or Ure$^-$ (NIRUB73-II) phenotype, suggesting that *orf136* itself is not essential for urea utilization but that *orf136* is cotranscribed with a gene essential for this process (e.g., *ureG*). Mutations in *lrp2* (NIRUB46), *orf433* (NIRUB76-I and NIRUB76-II), and *orf323* (BKRUB16 and BKRUB17) did not affect growth with urea (4 mM) as an

N source, indicating that none of these genes is essential for urea utilization. The Ure$^+$ phenotype of *lrp2* mutant NIRUB46 indicates that *lrp2* and the *ure* genes are not cotranscribed, suggesting that the *ure* promoter is located in the intergenic region between *lrp2* and *ureD* (see below).

Since Orf433 is thought to be part of a high-affinity urea transport system, the urea concentrations in the growth medium were lowered. The parental strain KS36 and the *orf433* mutant strains did not differ in growth within the range from 4 to 0.25 mM urea (data not shown). All strains were unable to grow with less than 0.25 mM urea. However, this does not necessarily exclude the possibility that there are differences between the parental strain and the *orf433* mutant strains in urea uptake in the micromolar range.

Transcriptional analysis of the *R. capsulatus ure* operon. Since expression of the *ure* operon appears to depend on a promoter located directly upstream of *ureD*, pNIRUB35 carrying an in-frame *ureDA-lacZ* fusion was constructed (Fig. 1C; Materials and Methods). This broad-host-range reporter plasmid was introduced into the *R. capsulatus* wild type and selected mutants, and β-galactosidase activity was determined in cultures grown with different nitrogen sources. The results shown in Table 3 can be summarized as follows. (i) Maximum expression of the *ure* genes occurred under nitrogen-limiting conditions (serine or urea as the sole nitrogen source). (ii) Transcription of urease genes was not substrate (urea) inducible in *R. capsulatus* B10S. As mentioned above, urease is an inducible enzyme in *R. capsulatus* E1F1 (7). However, the two *R. capsulatus* strains differ in several aspects (e.g., their susceptibilities to several bacteriophages) from each other, including those concerning the general nitrogen metabolism. *R. capsulatus* E1F1 is able to grow with nitrate as the sole source of nitrogen, whereas *R. capsulatus* B10S is devoid of any nitrate reductase activity. Therefore, it seems not unlikely that regulatory circuits also differ from each other in these two *R. capsulatus* strains. (iii) Expression of the *ureDA-lacZ* fusion was down-regulated (3.5-fold) under nitrogen-sufficient conditions, but significant expression remains in the presence of ammonium. (iv) NtrC is essential for expression of the *ure* genes under both nitrogen-limiting and nitrogen-sufficient conditions, suggesting that expression of the *ure* genes in the presence of ammonium somehow requires NtrC. At present it remains a matter of speculation whether ammonium-grown *R. capsulatus* cells contain low amounts of phosphorylated NtrC sufficient for partial activation of promoters with high affinity to NtrC~P. As shown by footprint analysis (see below), NtrC~P indeed efficiently binds to the *ureD* promoter. (v) σ^{54} (NtrA or RpoN) is not essential for urease activity or expres-
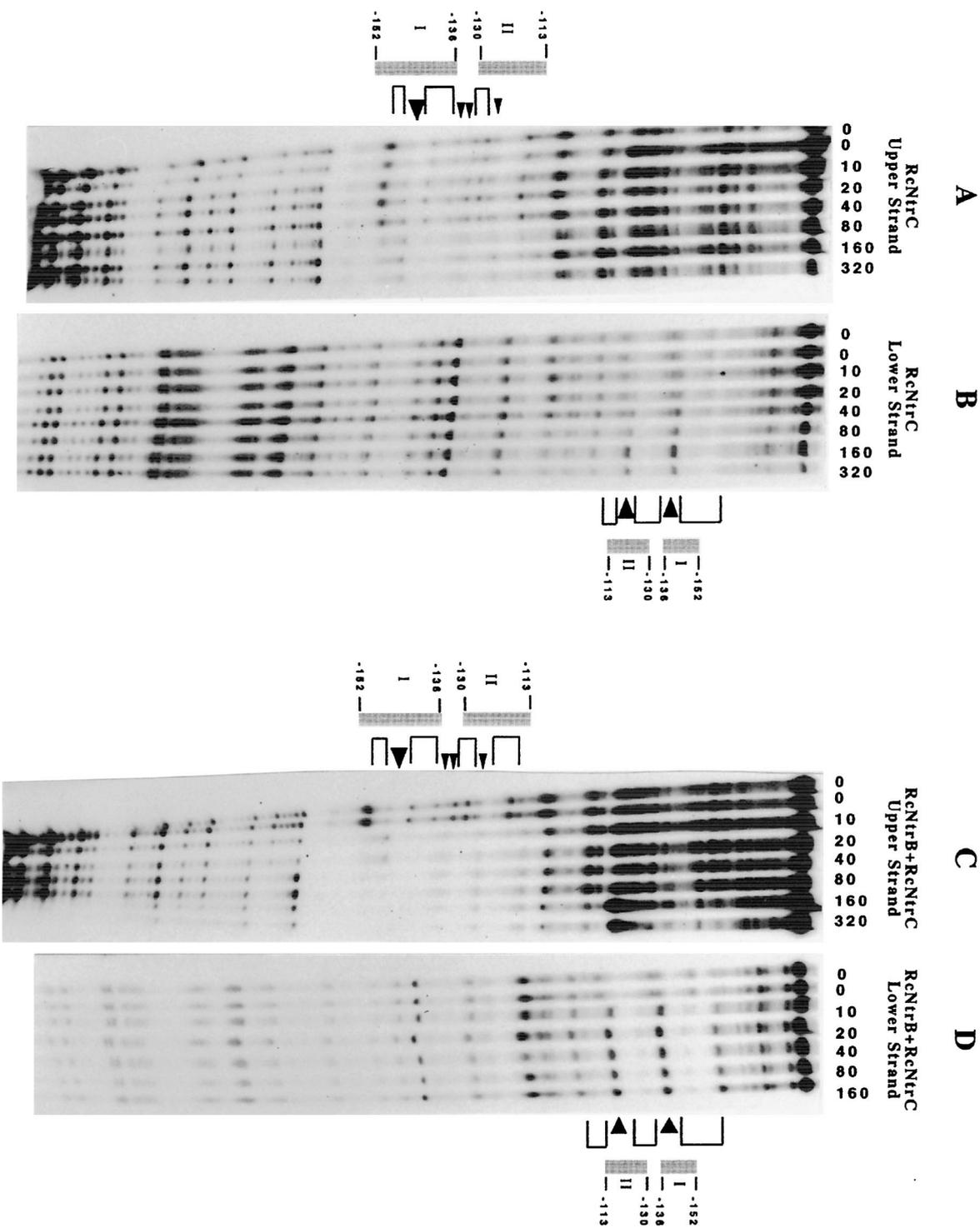
FIG. 2. Protection of the *ureD* promoter region by ReNtrC from DNase I digestion. (A) Upper-strand protection by ReNtrC at the indicated concentrations (nM); (B) lower-strand protection by ReNtrC at the indicated concentrations; (C) upper-strand protection by the indicated concentrations of ReNtrC with 1 μM MBP-ReNtrB and 1 mM ATP; (D) lower-strand protection by the indicated level of ReNtrC with 1 μM MBP-ReNtrB and 1 mM ATP. The concentration of DNA probe was approximately 0.1 nM for each reaction. Shaded bars indicate potential ReNtrC binding sites (see text); numbers refer to the distance from the transcription start site; arrowheads mark areas of increased DNase I sensitivity. Brackets indicate regions of protection at 160 nM ReNtrC (A and B) or 10 nM ReNtrC with 1 μM MBP-ReNtrB and 1 mM ATP (C and D).

sion of *ureD*. Expression of *ureDA-lacZ* was somehow enhanced in an *ntrA* mutant background, but this was typically less than twofold.

DNase I footprint analysis of the *ureD* promoter region. Since transcription of *ureDA-lacZ* was dependent on the *ntrC* gene, we predicted that RcNtrC might directly contact the *ureD* promoter upstream of the transcriptional start site. To verify this assumption, DNase I footprinting was performed with unphosphorylated RcNtrC to identify DNA sequences involved in contacting RcNtrC. Labeled DNA fragments containing the *ureD* upstream region from −227 to +59 were incubated with increasing concentrations of purified RcNtrC and subjected to DNase I digestion. The DNase I protection patterns were localized by comparison with dideoxy DNA sequence ladders generated with the ureD.F primer for the upper strand (Fig. 2A) and the ureD.R primer for the lower strand (Fig. 2B). A DNase I-hypersensitive site could be seen at −148 on the upper strand at an RcNtrC concentration of 10 nM and at −118 and −139 on the lower strand at an RcNtrC concentration of 20 nM. At a higher RcNtrC concentration (160 nM), several minor hypersensitive sites were observed on the upper strand. Full protection of the *ureD* upstream region was observed between −157 and −115 (upper strand) and between −155 and −110 (lower strand) at concentrations of RcNtrC of 80 nM and higher (Fig. 2A and B). This RcNtrC concentration (80 nM) is similar to that reported for complete protection of the *glnB* (160 nM), *nifA1* (80 nM to 160 nM), and *nifA2* (80 nM to 160 nM) promoter regions (6, 8). These regions of DNase I protection by RcNtrC encompass the consensus tandem RcNtrC binding sites described previously (Fig. 2A and B, regions I and II [3]).

To determine whether the phosphorylated RcNtrC protein has enhanced DNA binding activity, as described previously for the *glnB* promoter (6), a comparison between the DNase I protection patterns of unphosphorylated and phosphorylated RcNtrC was performed. The labeled *ureD* upstream region was incubated with various concentrations of RcNtrC that was phosphorylated with 1 μM MBP-RcNtrB and 1 mM ATP. Complete protection of both the upper and lower strands of the *ureD* upstream region by phosphorylated RcNtrC was detected at the 10 nM concentration, as compared to 80 nM for the unphosphorylated RcNtrC (Fig. 2, compare panels A and B [80 nM RcNtrC] with panels C and D [10 nM RcNtrC]). We conclude that at the *ureD* promoter, phosphorylation of RcNtrC increases DNA binding by at least eightfold. Previously, an increase in binding affinity of at least fourfold at the *glnB* promoter was observed upon phosphorylation of RcNtrC (6). Increased oligomerization at the enhancer tandem binding sites by phosphorylation of RcNtrC may modulate the response to nitrogen via transcriptional activation of RNAP at this promoter.

NtrC-dependent *ure* gene expression in *K. aerogenes* occurs indirectly via the action of the positive regulator NAC (nitrogen assimilation control) (2, 9). Under nitrogen-limiting conditions, *K. aerogenes* NtrC activates expression of the *nac* gene in concert with RNAP-σ⁵⁴, and in turn, NAC activates expression of the *ure* genes together with RNAP-σ⁷⁰. Thus NAC acts as a bridge between RNAP-σ⁷⁰-dependent operons and the RNAP-σ⁵⁴-dependent Ntr system in *K. aerogenes*. Since RcNtrC acts directly with RNAP-σ⁷⁰ (3) and directly on the *ure* operon,

FIG. 3. Summary of the *R. capsulatus ureD* promoter region analysis. Boldfaced letters indicate oligonucleotide primers used to generate the indicated probe for DNase I protection experiments. Arrowheads represent major and minor DNase I-hypersensitive sites, and potential RcNtrC binding sites are indicated by horizontal shaded bars. The horizontal arrows show the direction of transcription, with +1 indicating the *ureD* transcriptional start site. Putative "−10" and "−35" regions are boxed. The asterisk marks the translational stop codon for the *lrp2* gene.

as shown here, there appears to be no requirement for a NAC-like protein in *R. capsulatus*.

To further confirm that the transcriptional start point of the *ure* operon is located within the intergenic region between *lrp2* and *ureD* (Fig. 1A), primer extension analysis was carried out (see Materials and Methods). As shown in Fig. 3, putative "−10" and "−35" regions for a σ^{70}-RNAP were identified at reasonable distances upstream of the transcriptional start site of the *ureD* gene. The "−35" region contains at least four of the optimal nucleotides of a "−35" hexamer identified by mutagenesis of the *R. capsulatus nifA1* promoter, which are also present in the corresponding promoter elements of the *R. capsulatus nifA2* and *glnB* genes (3).

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