Geobacter uraniireducens NikR Displays a DNA binding mode distinct from other members of the NikR family

Erin L. Benanti  
*Washington University School of Medicine in St. Louis*

Peter T. Chivers  
*Washington University School of Medicine in St. Louis*

---

Follow this and additional works at: [https://digitalcommons.wustl.edu/open_access_pubs](https://digitalcommons.wustl.edu/open_access_pubs)

Please let us know how this document benefits you.

---

**Recommended Citation**

Benanti, Erin L. and Chivers, Peter T., "Geobacter uraniireducens NikR Displays a DNA binding mode distinct from other members of the NikR family." Journal of Bacteriology. 192, 17. 4327-4336. (2010).  
[https://digitalcommons.wustl.edu/open_access_pubs/2424](https://digitalcommons.wustl.edu/open_access_pubs/2424)

---

This Open Access Publication is brought to you for free and open access by Digital Commons@Becker. It has been accepted for inclusion in Open Access Publications by an authorized administrator of Digital Commons@Becker. For more information, please contact vanam@wustl.edu.
Geobacter uraniireducens NikR Displays a DNA Binding Mode Distinct from Other Members of the NikR Family

Erin L. Benanti and Peter T. Chivers*

Department of Biochemistry and Molecular Biophysics, Washington University School of Medicine, St. Louis, Missouri 63110

Received 12 February 2010/Accepted 12 June 2010

NikR is a nickel-responsive ribbon-helix-helix transcription factor present in many bacteria and archaea. The DNA binding properties of Escherichia coli and Helicobacter pylori NikR (factors EcNikR and HpNikR, respectively) have revealed variable features of DNA recognition. EcNikR represses a single operon by binding to a perfect inverted repeat sequence, whereas HpNikR binds to promoters from multiple genes that contain poorly conserved inverted repeats. These differences are due in large part to variations in the amino acid sequences of the DNA-contacting β-sheets, as well as residues preceding the β-sheets of these two proteins. We present here evidence of another variation in DNA recognition by the NikR protein from Geobacter uraniireducens (GuNikR). GuNikR has an Arg-Gly-Ser β-sheet that binds specifically to an inverted repeat sequence distinct from those recognized by Ec- or HpNikR. The N-terminal residues that precede the GuNikR β-sheet residues are required for high-affinity DNA binding. Mutation of individual arm residues dramatically reduced the affinity of GuNikR for specific DNA. Interestingly, GuNikR tetramers are capable of binding cooperatively to the promoter regions of two different genes, nik(MN)1 and nik(MN)2. Cooperativity was not observed for the closely related G. bemidjiensis NikR, which recognizes the same operator sequence. The cooperative mode of DNA binding displayed by GuNikR could affect the sensitivity of transporter gene expression to changes in intracellular nickel levels.

Approximately 60% of the bacterial and 85% of the archaeal sequenced genomes encode nickel-dependent enzymes (49). Across these microbes, there are at least nine nickel-dependent enzymes that are integral to energy generation, nitrogen assimilation and detoxification, including [Ni-Fe] hydrogenase, methyl CoM-reductase, carbon monoxide dehydrogenase (CODH), urease, and Ni-superoxide dismutase (31). Notably, the numbers and combinations of nickel-dependent enzymes in each species vary significantly, which likely reflects the disparate growth environments and lifestyles of microorganisms.

A previous survey of the prevalence of nickel transporters (35) indicated that most nickel-utilizing organisms also encode identifiable nickel transporters. This analysis used the presence of the Ni2⁺-dependent transcription factor NikR (11, 15, 18, 46, 49) in sequenced genomes and predicted NikR operators to identify candidate nickel transporter genes. Based on the present study, NikR likely regulates a variety of nickel transporters in many different organisms, including the NikMNOQ (10, 35) and NikABCDE (32) ABC-type transporters, as well as the HupE/UreJ and nickel-cobalt permeases (35). Together with the mosaic distribution of nickel-dependent enzymes, these observations raise the question of whether the regulatory properties of different NikR orthologs are modulated in response to different microbial nickel physiologies.

NikR is a tetramer that consists of an N-terminal ribbon-helix-helix (RHH; or β-α-α) DNA binding domain (11) and a C-terminal metal-binding domain (MBD) that binds Ni2⁺ with high affinity (11–13, 39, 40). Nickel binding to the MBD activates NikR to bind to specific DNA sequences and regulate gene expression (1, 6, 8, 13, 23, 27). Escherichia coli NikR (EcNikR) was the first member of this large family of transcription factors to be studied (11, 18), and its function is relatively well understood (11, 13, 18, 27, 36, 46). Subsequent studies have examined the biology and biochemical properties of Helicobacter pylori NikR (HpNikR). Although the primary nickel binding properties are conserved, HpNikR DNA recognition is distinct from EcNikR (1, 5, 6, 15–17, 19–20, 22, 23).

NikR, as for all RHH family members, makes base-specific DNA contacts via antiparallel β-sheets at its N terminus (34, 40). Residues N terminal to the β-sheet (“N-terminal arms”) of RHH proteins make nonspecific DNA phosphate contacts (7, 34, 42). EcNikR binds to a perfect inverted repeat in the promoter of the nikABCDE operon (13), whereas HpNikR recognizes poorly conserved imperfect inverted repeats in the promoters of multiple repressed and activated genes (1, 6, 17, 20, 22). The nine residue N-terminal arm of HpNikR, which is absent in EcNikR, is required to maintain the hierarchy of affinities this ortholog displays for different promoters (6) and to inhibit nonspecific DNA binding (6, 28). It remains to be determined whether the differences in DNA binding activity of EcNikR and HpNikR are further indicative of a spectrum of DNA binding affinities and specificities throughout the NikR family. Significant variation in β-sheet residues and N-terminal arm lengths and sequences exist within the NikR family (6), suggesting that differences in N-terminal amino acid sequence allow variation in the protein-DNA interface that influence the regulatory properties of NikR.

We have initiated studies of a third NikR protein (GuNikR) from the Gram-negative deltaproteobacteria Geobacter urani-
**MATERIALS AND METHODS**

Bioinformatics. The *H. pylori* 26695 NtrK protein sequence (HP1338) was used in a protein BLAST (2) search of the NCBI nonredundant protein sequence database (performed in April 2009). Hits with significant similarity (minimum alignment of 74 NikR orthologs with nonidentical N-terminal sequences). The alignment of 74 NikR orthologs with nonidentical N-terminal sequences was confirmed by the absence of any UV-visible absorbance at 304 nm.

**Candidate binding site fragments: cloning and labeling.** Candidate NtrK binding site fragments were amplified from genomic DNA by PCR using the oligonucleotide pairs listed in Table S1 in the supplemental material. Mutant *P*$_{\text{ntrK}}$ fragments were constructed by two successive rounds of PCR using internal primers containing the scrambled repeats. For the site 1 mutant, PCR products from reactions using the primers EB807–EB690 and EB683–EB682 were mixed and used as the template in a second round of PCR using the external primers EB807–EB682 (see Table S1 in the supplemental material). The site 2 mutant was made using the same strategy, except with the primers EB689 and EB685 in place of EB690 and EB683, respectively. The resulting PCR products were digested with EcoRI and KpnI and ligated into pBluescript II KS (Stratagene) to generate pEB289 and pEB320. Cloned promoter candidates were verified by sequencing (SeqWright).

DNA fragments for binding assays were labeled as previously described by a combination of end labeling one primer and PCR amplification (6) or by end filling an Eaq-digested PCR promoter fragment. End-filling reactions used 0.2 μM PCR product, Klenow fragment DNA polymerase (3′-5′exo-; NEB, Beverly, MA), and [γ-32P]dGTP (GE Biosciences, Piscataway, NJ) in a total volume of 40 μl. Excess [γ-32P]dGTP was removed by using a nucleotide exchange kit (Qiagen, Valencia, CA). When necessary, labeled DNA fragments were further purified by acrylamide gel electrophoresis.

**DNA binding assays.** DNase I footprinting was performed as described previously (6) in a binding buffer containing 10 mM Tris-HCl (pH 8.0), 100 mM KCl, 3 mM MgCl$_2$, 10 μg of *E. coli* thioredoxin/liter, and 4 μg of salmon sperm DNA per ml. NtcI was added as described in the text and figure legends. Labeled DNA fragments were incubated with protein (2°C for 30 min) prior to DNase I addition (final concentration, 300 ng/ml Sigma). Formic acid cleavage of labeled DNA was performed by using the standard protocol for Maxam-Gilbert sequencing (21).

Electrophoretic mobility shift assays (EMSSAs; 7% polyacrylamide gel) were performed as previously described (6) using a dilution series of at least 15 protein concentrations. The binding buffer was identical to that used for DNase I footprinting except with 50 μM NiCl$_2$.

Affinity changes from DNase I footprinting and mobility shift assays were calculated by using the Hill equation as previously described (6). The reported values and calculated standard deviations are the average of two or more independent experiments.

**Promoter-lacZ reporter assays.** *P*$_{\text{ntrK}}$, *P*$_{\text{ntrK}}$, and *P*$_{\text{ntrK}}$ fragment promoters were amplified from genomic DNA by PCR using the oligonucleotide pairs listed in Table S1 in the supplemental material. The purified PCR fragments were digested with EagI and SalI and cloned into pPC163 (13) digested with the same enzymes, *pCPl63* contains the *E. coli lacZ* gene fused to the *P*$_{\text{ntrK}}$ promoter and has been used to study NtrK activity. For LacZ assays, the reporter plasmids were transformed into PC606, a ΔntrC derivative of *E. coli* DL14(ΔDE)ΔntrC4. The resulting cells were transformed with either pEB270 or pNIK103 (13), which contains a copy of *E. coli ntrK*. Cells were grown aerobically in M63 minimal medium containing 20 μg of tetracycline/ml in the absence or presence of NiCl$_2$ (3 μM). IPTG (isopropyl-β-D-thiogalactopyranoside) was not added to the growth medium. LacZ assays were performed as described previously (11, 13, 18, 27, 36, 46).

**RESULTS**

**N-terminal sequence variation in the NtrK family.** The alignment of 74 NtrK orthologs with nonidentical N-terminal amino acid sequences (see Materials and Methods and Fig. S1 in the supplemental material) revealed a high degree of variability in β-sheet and arm sequence, as well as in arm length. The specific variations are described below.

**β-Sheet sequences.** Nine different combinations of DNA-contacting β-sheet residues were identified (Fig. 1a). Over half of the predicted NtrK proteins contained Arg-Gly-Ser and Arg-Ser-Ser sequences (37 and 22 of the 74 sequences, respectively; Fig. 1a and b). Arginine is almost always conserved at the first position (Fig. 1b). The only exception is a Lys substitution in *Staphylothermus marinus* NtrK. In contrast, five different amino acids occur at the second and third positions (Fig. 1c).
peats of the DNA binding site is expected to change. In either case, the sequence composition of the inverted reposition or that additional nonspecific contacts may be present. compensate for the likely absence of a DNA interaction at this specific DNA contacts may occur in Arg-Gly-Ser NikR proteins to contacting sheet position (40). This suggests that different specific DNA interactions observed in the DNA cocrystal structure occurs via Thr5, the second DNA-contacting sheet residue (40). The other base-specific contact observed in the DNA cocrystal structure is not surprising. In EcNikR, this residue makes four of the five specific base interactions observed in the DNA-contacting β-sheet (40). The total number of sequences with each residue is noted in parentheses. (c) The number of NikR proteins containing increasing numbers of residues between the N-terminal (Nt) Met and the first DNA-contacting β-sheet residue.

FIG. 1. Frequency of DNA-contacting β-sheet sequences and N-terminal arm lengths among nonidentical NikR homologs. (a) The number of NikR proteins containing one of nine combinations of DNA-contacting β-sheet residues. (b) The relative percentage of each residue occurring at each β-sheet position. The total number of sequences with each residue is noted in parentheses. (c) The number of NikR proteins containing increasing numbers of residues between the N-terminal (Nt) Met and the first DNA-contacting β-sheet residue.

1b). These residues are generally small and not always capable of direct interactions with DNA bases. Glycine is present at the second position in roughly half of the sequences, but is never found in the third position. Serine is the next most common at the second position and most common at the third position.

The high degree of conservation of Arg at the first position is not surprising. In EcNikR, this residue makes four of the five specific base interactions observed in the DNA cocrystal structure (40). The other base-specific contact observed in the EcNikR cocrystal structure occurs via Thr5, the second DNA-contacting sheet position (40). This suggests that different specific DNA contacts may occur in Arg-Gly-Ser NikR proteins to compensate for the likely absence of a DNA interaction at this position or that additional nonspecific contacts may be present. In either case, the sequence composition of the inverted repeats of the DNA binding site is expected to change.

N-terminal arm length variation. Comparison of the number of residues occurring between the N-terminal Met and the first position of the β-sheet of each NikR protein indicated that N-terminal arm lengths range from 0 to 32 amino acids, with the largest number of homologs containing four or five amino acids between Met1 and the β-sheet Arg (43 of 79 sequences; Fig. 1c). There was no obvious correlation between N-terminal arm length and β-sheet sequence, except that the arms of the RTT β-sheet sequences were generally shorter. An important qualification is that the NikR sequences analyzed here are based on genome annotations, so some particularly long NikR arms may result from an incorrect annotation of the nikR start codon or a sequencing error (see Fig. S1 in the supplemental material).

The lack of experimental information on the largest NikR subgroup (Arg-Gly-Ser β-sheet) that exhibits wide variation in arm length led us to investigate the DNA binding properties of members of this subgroup. To this end, several NikR proteins with Arg-Gly-Ser β-sheets and different arm sequences were cloned, overexpressed in E. coli, purified, and screened for DNA binding activity (E. L. Benanti and P. T. Chivers, unpublished data). We focused on GuNikR based on the ease of obtaining sufficient quantities of protein for these studies and the identification of potential DNA binding sites (Fig. 2a).

GuNikR purification and nickel binding. GuNikR was purified by using a protocol similar to that used for EcNikR (11) and HpNikR (1, 6). GuNikR eluted from a size exclusion column at a volume consistent with an ~60-kDa tetramer (data not shown), the same oligomeric state as EcNikR (12) and HpNikR (1, 28). The UV-visible difference spectrum of the protein with or without stoichiometric Ni(II) showed the characteristic features seen for EcNikR (13) and HpNikR (1, 6). The far UV circular dichroism (CD) spectrum of GuNikR was consistent with that observed for EcNikR (1, 6). The CD spectrum did not change significantly with the addition of stoichiometric NiCl₂ (see Fig. S2 in the supplemental material). Chemical denaturation of the apo- and holoproteins revealed an increase in stability in the presence of nickel (see Fig. S2 in the supplemental material), demonstrating that GuNikR directly binds nickel, consistent with the UV-visible spectrum. These properties of GuNikR were expected based on the shared characteristics previously observed for Ec- and HpNikR.

DNA binding site prediction. Nickel- or NikR-dependent gene regulation has not been studied in G. uraniireducens. However, GuNikR likely represses genes encoding putative nickel transporters, as observed for EcNikR and HpNikR (11, 16, 18, 22, 23). This expectation was used previously to predict different NikR binding site motifs (35). We used the results of that study to scan the G. uraniireducens genome for potential NikR-regulated nickel transporter genes. BLASTP searches (2) of the G. uraniireducens genome with the Rhodococcus capsulatus Nik(MN) protein sequence identified two genes, Gura0780 and Gura2762 (27 and 24% identical to R. capsulatus Nik(MN), respectively, and 84% identity with each other). Homology searches with other types of nickel transporters did not return any meaningful candidate genes.

Gura0780 and Gura2762 are both annotated as CbiM-encoding genes, which are cobalt-specific ABC-type transporter proteins analogous to Nik(MN) (35). We refer to Gura0780 as
G. uraniireducens
G. bemidjiensis
P. horkshii
E. coli
H. pylori

\begin{align*}
The sequence features of this region are discussed in more detail below. This protection was roughly twice the size of that reported for EcNikR (8, 12) and HpNikR (1, 6, 17, 22) under similar conditions, and fits of DNase I GuNikR titrations indicated a Hill coefficient of 2.03 (Table 1). Together, these results suggest that two GuNikR tetramers bind to \( P_{\text{nik}(\text{MN})1} \).

In contrast, the GuNikR-dependent DNase I footprint of \( P_{\text{nik}(\text{MN})2} \) was roughly 33 bp in the presence of stoichiometric or 50 \( \mu \text{M} \) NiCl₂, which is similar to the size of the protection pattern observed for EcNikR and HpNikR. However, the Hill coefficient of 2.56 determined for GuNikR binding to \( P_{\text{nik}(\text{MN})2} \) in this assay indicates positive cooperativity (Table 1). In the absence of any nickel and in the presence of 50 \( \mu \text{M} \) EDTA, the affinity of GuNikR for \( P_{\text{nik}(\text{MN})1} \) decreased ~5-fold (\( K_D \) of 88 nM; data not shown), a finding consistent with nickel-dependent activation of DNA binding.

Based on the appearance of the footprinting and mobility shift data, the GuNikR-\( P_{\text{nik}(\text{MN})1} \) interaction likely involves two NikR tetramers bound to one DNA fragment. This model is supported by Hill coefficients of \( >1 \) required to fit both sets of data (Table 1). The affinities of the two interactions differed by 2-fold (\( K_D = 7.6 \text{ nM} \) versus 16.5 nM for mobility shift and footprint, respectively).

In contrast, the GuNikR-\( P_{\text{nik}(\text{MN})2} \) mobility shift data could not be fit well using a simple two-site interaction model. This was due both to the persistence of the intermediate shifted species suggestive of negative cooperativity and the presence of multiple additional binding sites with different and weaker affinities. The lack of a defined second binding site for \( P_{\text{nik}(\text{MN})2} \) is consistent with the absence of an extended DNase I footprint for the GuNikR-\( P_{\text{nik}(\text{MN})2} \) interaction, which could result from multiple secondary binding sites with reduced affinities (see below) or two tetramers binding on the opposite face of the same stretch of DNA. The Hill coefficient of 2 determined for GuNikR binding to \( P_{\text{nik}(\text{MN})2} \) suggests a positively cooperative interaction. The affinity of GuNikR for \( P_{\text{nik}(\text{MN})2} \) measured by DNase I footprinting was slightly higher compared to that measured by mobility shifts (46 versus 64 nM, respectively), and both values are significantly weaker than the affinity of GuNikR for \( P_{\text{nik}(\text{MN})1} \). Although the DNA binding site(s) and stoichiometry of the GuNikR-\( P_{\text{nik}(\text{MN})2} \) interaction are not fully resolved, apparent affinities for the interaction of

<table>
<thead>
<tr>
<th>Promoter</th>
<th>( K_D ) (nM) ± SD; Hill coefficient ± SD (^a)</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{nik}(\text{MN})1 )</td>
<td>7.6 ± 0.7; 16.5 ± 3.8; 86.1 ± 1.8; 53.7 ± 8.6; 76.7 ± 14.9; 207.2 ± 8.8;</td>
</tr>
<tr>
<td>( \text{nik}(\text{MN})2 )</td>
<td>64.4 ± 50.4; 45.8 ± 19.3; ≤2,000*; 1,290 ± 19; 99.8 ± 47.0; ≤1,230*;</td>
</tr>
</tbody>
</table>

\(^a\) The apparent affinity was determined from fits of the data with the Hill equation. For \( \text{nik}(\text{MN})2 \), the data were fit without differentiating distinct shifted species. Attempts to fit this data to a model with only two distinct binding sites (\( K \) values) were unsuccessful.

\(^b\) *, Only the lower-limit estimate is given.
GuNikR with \( P_{\text{n}ik(MN)2} \) were determined by using the Hill equation to provide a basis for comparison with \( P_{\text{n}ik(MN)1} \), as well as for the interaction of GuNikR mutants with this DNA fragment.

*G. bemidjiensis* NikR binds to a 30-bp region of a nik(MN) candidate promoter. The interaction of multiple GuNikR tetramers with \( P_{\text{n}ik(MN)1} \) was also supported by DNA binding assays with the closely related *G. bemidjiensis* NikR (GbNikR; Fig. 2a, 87% identical and 94% similar to GuNikR). In a mobility shift assay GbNikR specifically bound the upstream region (Fig. 3c) of a predicted nik(MN) gene (Gbem2225), one of four nik(MN) candidates identified in the *G. bemidjiensis* genome. Notably, the GbNikR-DNA complex exhibited a smaller mobility shift compared to GuNikR-\( P_{\text{n}ik(MN)1} \) and GuNikR-\( P_{\text{n}ik(MN)2} \). Furthermore, GbNikR protected a 30-bp region of the nik(MN) candidate promoter (Fig. 5a). Thus, the difference in size of the footprints and relative mobility shifts for GbNikR and GuNikR support the idea that GuNikR binds to both \( P_{\text{n}ik(MN)1} \) and \( P_{\text{n}ik(MN)2} \) as a higher-order complex, most likely two NikR tetramers per candidate promoter.

The two GuNikR binding sites in \( P_{\text{n}ik(MN)1} \) are not equivalent. The 70-bp region of \( P_{\text{n}ik(MN)1} \) protected by GuNikR spanned two imperfect inverted repeats (GACATAC–13 bp–GTATTCA–4 bp–GTGCTAC–13 bp–GTGTATAC; Fig. 5c). A sequence similar to the downstream nik(MN) inverted repeats is also present in the nik(MN)2 promoter region, and the nikMN upstream region from several other *Geobacter* species, including *G. bemidjiensis* (Fig. 5c). These sequences all contain a putative −35 consensus sequence (TTGACA) for RpoD/\( \beta\)-sheet DNA binding affinity and cooperativity. We created an N-terminal arm truncation mutant of GuNikR (∆nt3GuNikR), as well as individual Ala substitutions, which is analogous to our previous study of HpNikR (6). Truncation of the arm did not affect protein folding, since there was no significant difference between the CD spectra of full-length and ∆nt3GuNikR (see Fig. S3 in the supplemental material). The individual Ala mutations also did not affect protein folding (data not shown).

\( \Delta\text{nt3GuNikR} \) was unable to bind \( P_{\text{n}ik(MN)1} \) or \( P_{\text{n}ik(MN)2} \) DNA at protein concentrations up to 5 μM in either DNase I footprinting or mobility shift assays (data not shown). These results demonstrate that the N-terminal arm of GuNikR is essential for DNA binding, which contrasts with the role of the N-terminal arm of HpNikR (6, 28). Truncation of the nine-residue arm of HpNikR did not alter the affinity of the protein for promoters that it binds tightly but increased the affinity of weaker or nonspecific DNA interactions (6, 28).

To identify contributions of specific residues of the GuNikR N-terminal arm to DNA binding, we measured the DNA affinity of the Ala mutants using mobility shifts. In addition to the individual amino acid substitutions, a fourth mutant was created by inserting an Ala codon immediately following the N-terminal Met codon to create Ala2ins (arm sequence of AGETI after cleavage of the N-terminal Met residue [24]). This substitution will affect the position of the NH2 terminus of the protein and provides a way to assess its contribution to DNA binding. Mobility shift assays of each GuNikR mutant with \( P_{\text{n}ik(MN)1} \) and \( P_{\text{n}ik(MN)2} \) demonstrated that various contributions are made from each residue to DNA binding affinity...
and specificity (Fig. 6b to e and Table 1). Furthermore, these contributions are different for each candidate promoter. Except for Glu3Ala, all of the mutations strongly affected GuNikR binding to \( P_{\text{nik(MN)2}} \). The effect of the Ala2ins mutation suggests a specific structural role for the NH\(_2\) terminus of the protein in DNA recognition.

For \( P_{\text{nik(MN)1}} \) no mutation resulted in the loss of the low-mobility species or the presence of an intermediate mobility species, which was observed for the scrambled candidate promoter mutants. However, quantitation of the loss of the free DNA species and changes in the abundance of an intermediate shifted band suggested that these mutants affect the cooperativity of GuNikR binding to \( P_{\text{nik(MN)1}} \). In addition, the arm mutations all reduced DNA binding affinity to some extent, with Thr4Ala being the most severely affected mutant. The difficulty of assigning affinities to the two sites of \( P_{\text{nik(MN)1}} \) using these assays precludes quantitatively determining individual contributions to cooperativity and DNA binding affinity, but it is clear that each arm residue is important for GuNikR DNA binding.

**DISCUSSION**

The results presented here identify a new mode of NikR-DNA recognition. We have shown that GuNikR tetramers...
bind with positive cooperativity to the nik(MN)1 promoter. In addition, GuNikR utilizes amino acids N-terminal to its β-sheet motif for stable DNA complex formation. Some of these residues are also linked to cooperative tetramer binding. The importance of these residues is distinct from that of the HpNikR N-terminal arm, which is not essential for DNA-binding but is a major determinant of sequence specific DNA binding (6, 28).

GuNikR protection of P_{nik(MN)1} is significantly larger than the 40 and 36 bp protected by EcNikR (11) and HpNikR (1, 6, 17, 22), respectively. Although GuNikR protected a smaller region of P_{nik(MN)2}, there are additional poorly conserved repeats in this candidate promoter, suggesting that the multiple shifted complexes observed in mobility shift assays of GuNikR with P_{nik(MN)2} represent higher-order protein-DNA complexes. The smaller mobility shift and footprint for the GbNikR-P_{nik(MN)2} interaction further suggests that multiple GuNikR tetramers binding to P_{nik(MN)2} may be obscured in the footprinting experiment, possibly due to the presence of multiple binding sites for which GuNikR has low affinity.

Together with the significant positive cooperativity observed for GuNikR binding to both nik(MN) promoter fragments, these results argue that two GuNikR tetramers bind to P_{nik(MN)1} and P_{nik(MN)2}. This represents a surprisingly distinct mode of DNA binding compared to previously characterized NikR family members.

The molecular basis for GuNikR cooperative DNA binding to P_{nik(MN)1} remains to be determined. The arrangement of GuNikR recognition motifs at P_{nik(MN)1} and the observed footprint argues against a model analogous to the iron-dependent DtxR-DNA interaction, wherein two repressor molecules bind cooperatively, but on opposite faces of the DNA, and generate a footprint like that expected for a single repressor molecule (9, 47). Sites 1 and 2 of P_{nik(MN)1} are separated by 4 bp, which means the centers of the closest half-sites are separated by 12 bp and the GuNikR tetramers will be adjacent to each other on the same side of the DNA. Based on the cocrystal structure of EcNikR bound to the nikA promoter (40), the spacing between the closest half-sites of site 1 and site 2 suggests two possible modes of cooperativity. In one case, the two GuNikR tetramers contact one another via residues of the RHH dimers that sit in adjacent major grooves. Alternatively, GuNikR bound to Site 2 could distort the DNA helix and allow a second tetramer to bind to Site 1. Cooperativity by DNA distortion in the absence of protein-protein interactions has been demonstrated (30). The greater spacing between the two inverted repeat sequences detected in P_{nik(MN)2} likely decreases cooperativity either by disrupting the interactions between two GuNikR tetramers or by diminishing the effect of any DNA distortion upon binding of the first GuNikR tetramer.

Little is known about the role of nickel ions in Geobacter physiology. Molecular hydrogen can serve as an electron source for dissipatory metal reduction (29). Changes in [Ni-Fe] hydrogenase gene expression levels have been detected in cells grown in defined culture relative to cells grown in sediment from which the strains were isolated (26). Although the

![FIG. 6. GuNikR requires each N-terminal arm residue for high-affinity DNA binding. Wild-type GuNikR (a; same as in Fig. 3) or N-terminal site mutants A2ins (b), G2A (c), E3A (d), and T4A (e) were serially diluted 1.7-fold from 5.0 μM to 17.5 nM with P_{nik(MN)1} (left panels) or P_{nik(MN)2} (right panels). Each arm sequence is indicated to the upper right of each pair of gels. Mobility shifts were performed with 50 μM NiCl₂ in the gel and running buffer. Each full titration was run on two separate gels in parallel, and a vertical line separates each pair of gel images. F, free DNA. B, protein-bound DNA. The asterisk indicates DNA in wells.](image-url)
repression of nickel transport genes by GuNikR is not surprising, the nature of the GuNikR-\(P_\text{nik(MN)1}\) and -\(P_\text{nik(MN)2}\) complexes may have direct implications for nickel-dependent gene regulation in \textit{G. uranireducens}. Because cooperative DNA binding by GuNikR increases the affinity of the second tetramer for DNA, the concentration of GuNikR, and thus nickel, required for DNA occupancy and repression by GuNikR is decreased relative to the tetrameric EcNikR-DNA interaction. The predicted Nik(MN) protein sequences are 84\% identical and, combined with the different relative expression levels of the \(P_\text{nik(MN)1/2}\) promoters, lead us to speculate that the two Nik(MN) proteins may have different functional roles. The availability of genetic tools for \textit{Geobacter} species (29) will facilitate dissection of the function of each Nik(MN) protein and their patterns of nickel- and NikR-dependent gene regulation.

A second notable feature of the GuNikR (and GbNikR)-DNA interactions is the primary recognition sequence, G\(\text{TG(T/C)TAC–13 bp–GTCATAC}\). The 7-bp repeats can be viewed either as inverted repeats that are conserved at the external positions (G\(\text{TXXXXAC}\)) or as highly conserved direct repeats, although the former seems most likely. Interestingly, the inverted repeats recognized by EcNikR can also be extended to 7 bp with the indicated underlined bases (G\(\text{TATGAC–14 bp–GTCATAC}\)). This addition generates the analogous direct repeat sequence found for the \textit{Geobacter} NikRs, but with less conservation of the central residues for the two repeats in the case of EcNikR. The structure of the EcNikR-DNA complex clearly shows recognition of inverted repeats as the EcNikR \(\beta\)-sheet residues do not directly contact the innermost C-G and G-C bps of the 7-bp sequences (40). Interestingly, the bioinformatics study that predicted various NikR binding motifs indicated that the inner bases of the extended EcNikR motif are not conserved in the Arg-Thr-Thr \(\beta\)-sheet family (35). Conversely, the 7-bp half site sequences of a subset of the Arg-Gly-Ser \(\beta\)-sheet containing NikRs, including those from \textit{Geobacter} species, are conserved. Further studies will be required to identify the nature of the specific contacts between GuNikR and its operator sequences.

A common feature of nearly all NikR homologs is an Arg residue at the first position of the \(\beta\)-sheet. In EcNikR, this residue dominates the direct contacts between the protein and DNA (40), but in an asymmetric fashion, since only one of the two Arg residues in an RHH dimer makes direct DNA contacts. The sequences of the repeats recognized by GuNikR identified here suggest that this pattern of Arg-DNA contacts is not completely conserved throughout the NikR family. The half-site repeats recognized by GuNikR begin and end with G-T base pairs similar to those contacted by Arg3 of EcNikR (40). However, the N-terminal arm also makes significant contributions to GuNikR-DNA interactions. The severe effects of the Thr4Ala substitution on binding affinity for both the \(n\text{ik(MN)1}\) and \(n\text{ik(MN)2}\) candidate promoters, together with the polar nature of the Thr side chain, suggest that this residue either makes direct contacts with the DNA or helps to orient the \(\beta\)-sheet for DNA binding. Thr4 likely compensates for the absence of a polar residue in the middle of the GuNikR \(\beta\)-sheet (Arg-Gly-Ser), which corresponds to the middle sheet position of EcNikR (Thr5) that makes a direct contact with the operator sequence (40). The extension of specific DNA interactions with protein residues outside the \(\beta\)-sheet could account for the apparently larger half site sequence that is predicted to be recognized by GuNikR. Mutation of the Gly residue was not attempted here because any amino acid substitution will likely perturb the \(\beta\)-sheet conformation because of the unique conformational properties of glycine.

The results presented here affirm the prediction of NikR DNA recognition motifs using a bioinformatics approach (35). However, some NikR recognition motifs remain poorly defined. The bioinformatics approach was not able to predict a DNA binding motif for the structurally characterized \textit{Pyrococcus horikoshii} NikR (14). In addition, experimental studies of the sequence dependence of HpNikR-DNA interactions (1, 6, 17, 22) show little similarity to the predicted DNA recognition motif for HpNikR (35).

NikR DNA binding activity and gene regulation is likely influenced by each organism’s nickel physiology. Of the three NikR proteins for which DNA binding has been characterized, there are distinct features for each that have regulatory implications. For EcNikR, there is biochemical evidence for the role of two types of nickel-binding site in regulating DNA binding affinity (8, 12). Thus far, EcNikR is the only ortholog for which this effect has been observed. However, the biological roles of these two sites have not yet been uncoupled so their individual contributions to the regulation of gene expression is unclear. HpNikR recognizes several promoter regions and thus will influence nickel utilization by controlling the expression of more genes than just those required for nickel import.

Currently, it appears that the complexity of HpNikR-dependent gene regulation is due in part to differential roles of residues in the N-terminal arm of the protein in DNA binding (6). These conformational differences may be linked to changes in intracellular physiology (28). Here, we have shown the potential for influencing NikR-dependent gene regulation by exploiting cooperative interactions between NikR tetramers. Undoubtedly, the majority of NikR proteins will share common regulatory features with one of the three proteins already characterized. Nonetheless, it is intriguing that significant variability exists in the nickel- and DNA-binding properties of different NikR proteins. These differences provide insight into the evolution of DNA binding by the NikR family.

ACKNOWLEDGMENTS

This study was supported by National Science Foundation grant MCB0520677.

We thank Evgenya Shelobolina and Derek Lovley for the generous gifts of genomic DNA.

REFERENCES


