Energy Transducing Roles of Antiporter-like Subunits in Escherichia coli NDH-1 with Main Focus on Subunit NuoN (ND2)*

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Abstract

The proton-translocating NADH-quinone oxidoreductase (complex I/NDH-1) contains a peripheral and a membrane domain. Three antiporter-like subunits in the membrane domain, NuoL, NuoM, and NuoN (ND5, ND4 and ND2, respectively), are structurally similar. We analyzed the role of NuoN in Escherichia coli NDH-1. The lysine residue at position 395 in NuoN (Lys<sup>395</sup>) is conserved in NuoL (Lys<sup>404</sup>) but is replaced by glutamic acid (Glu<sup>407</sup>) in NuoM. Our mutation study on NuoN<sup>395</sup> suggests that this residue participates in the proton translocation. Furthermore, we found that Glu<sup>497</sup> is also essential and most likely interacts with conserved Arg<sup>175</sup>. Glutamic acids Glu<sup>133</sup>, Glu<sup>144</sup>, and Glu<sup>144</sup> are corresponding residues. Unlike mutants of Glu<sup>144</sup> and Glu<sup>144</sup>, mutation of Glu<sup>133</sup> scarcely affected the energy-transducing activities. However, a double mutant of Glu<sup>133</sup> and nearby Glu<sup>72</sup> showed significant inhibition of these activities. This suggests that Glu<sup>133</sup> bears a functional role similar to Glu<sup>144</sup> and Glu<sup>144</sup> but its mutation can be partially compensated by the nearby carboxyl residue. Conserved prolines located at loops of discontinuous transmembrane helices of NuoL, NuoM, and NuoN were shown to play a similar role in the energy-transducing activity. It seems likely that NuoL, NuoM, and NuoN pump protons by a similar mechanism. Our data also revealed that Lys<sup>395</sup> is one of the key interaction points with helix HL in NuoL. A truncation study indicated that the C-terminal amphipathic segments of TM14 interacts with the β sheet located on the opposite side of helix HL. Taken together, the mechanism of H<sup>+</sup> translocation in NDH-1 is discussed.

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Significance:

- Antiporter-like subunits NuoL, NuoM, and NuoN are structurally similar but whether NuoN functions as a proton pump was uncertain.
- Functionally and structurally important residues in NuoN were identified.
- The mechanism of H<sup>+</sup> translocation in NDH-1 is discussed.

Results:

- The proton-translocating NADH-quinone oxidoreductase (complex I) is the first enzyme of the respiratory chain in most eukaryotic cells. Complex I catalyzes the electron transfer from NADH to quinone, which is coupled to the translocation of protons through the inner mitochondrial membrane.
- This enzyme complex, made up of ~45 different polypeptides, is the largest enzyme of the respiratory chain, with a molecular mass of ~1,000 kDa.
- The physiological importance of complex I is highlighted by the fact that this enzyme is the principal source of reactive oxygen species in mitochondria and that its deficiencies are linked to many human diseases.
- The bacterial enzyme (NDH-1) is composed only of 13–14 subunits with a molecular mass of 500 kDa, all of which are homologous to the 14 subunits that constitute the core of the mitochondrial complex I.
- Both eukaryotic complex I and prokaryotic NDH-1 have a characteristic L-shaped form with two clearly defined domains, a hydrophilic peripheral domain and a hydrophobic domain.
- The hydrophilic domain is projected into the mitochondrial matrix/bacterial cytoplasm and houses all of the cofactors that participate in electron transfer from NADH to quinone, through FMN and a chain of seven conserved Fe/S clusters.
- In Escherichia coli, the hydrophilic domain contains six subunits named NuoB, NuoCD (a fusion of 2 subunits, NuoC and NuoD), NuoE, NuoF, NuoG, and NuoI.
- The hydrophobic membrane domain is embedded in the inner mitochondrial/cytoplasmic membrane and is believed to participate in H<sup>+</sup> translocation and in the binding of quinone and specific inhibitors.

Conclusion:

- Functionally and structurally important residues in NuoN were identified.
- The mechanism of H<sup>+</sup> translocation in NDH-1 is discussed.

Background:

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of the H\(^+\) translocation. The membrane domain of \textit{E. coli} NDH-1 is composed of seven subunits, NuoA, NuoH, NuoJ, NuoK, NuoL, NuoM, and NuoN, which are homologues of the mitochondrial DNA-encoded subunits, ND3, ND1, ND6, ND4L, ND5, ND4, and ND2, respectively.

According to the recently disclosed three-dimensional structures of the transmembrane segment of complex I/NDH-1 (7, 17–19), subunits NuoA, NuoJ, NuoK, and NuoH are located close to the peripheral arm, whereas subunits NuoL, NuoM, and NuoN are in the extended part of the membrane arm. The structural model revealed that NuoL, NuoM, and NuoN share similar structural features with multisubunit antiporters (20, 21) and energy-converting NiFe hydrogenases (22), leading to a hypothesis that they have evolved from a common ancestor (23). This suggests involvement of the antiporter-like subunits in the mechanism of H\(^+\) translocation. Their distal location from the electron transfer pathway and their side-by-side arrangement strongly suggested a long range conformational change as an essential part of the energy-coupling mechanism of complex I/NDH-1 (6, 18, 24).

The three-dimensional structure also showed that the longest subunit, NuoL, possesses a long amphipathic \(\alpha\)-helix (110 Å in case of \textit{E. coli}), called helix HL, spanning and making a bridge among NuoK, NuoN, NuoM, and NuoL (7). On the opposite side of helix HL, there are long \(\beta\) sheets in NuoM and NuoL linking themselves to neighboring subunits NuoN and NuoM, respectively. Sazanov and co-workers (7, 17) have hypothesized that helix HL can work in a piston-like mechanism, together with the \(\beta\) sheets, driving the conformational changes along the antiporter-like subunits.

Our mutation studies of membrane domain subunits NuoA, NuoJ, NuoK, NuoH, NuoM, and NuoL showed that NuoK, NuoM, and NuoL are directly involved in the H\(^+\) translocation (25–31). The stoichiometry of the H\(^+\) translocation in NDH-1/complex I is long believed to be 4H\(^+\)/2e\(^-\) per NADH oxidized (32). Recently, an alternative stoichiometry of 3H\(^+\)/2e\(^-\) under certain conditions was reported (2). Yet another study reported that NDH-1/complex I lacking both NuoL and NuoM can pump two protons with a stoichiometry of H\(^+\)/2e\(^-\) = 2 (33, 34). These data suggest that NDH-1/complex I may contain either 3 or 4 H\(^+\) translocation sites, also implying the possibility of the H\(^+\) translocation in NuoN.

The NDH-1 crystal structure showed that NuoN is located close to the NuoAJK bundle (7, 17). Previously Amaranh and Vik (35) reported that conserved lysine residues in the middle of the transmembrane helices were required for the energy-transducing NDH-1 activity and that mutation of conserved \(\text{Glu}^{33}\) in the membrane helix only moderately (30%) reduced the energy-transducing NDH-1 activities. On the other hand, we and others showed that mutations of corresponding glutamic acids in NuoM and NuoL lead to almost total elimination of energy-transducing NDH-1 activities (24, 27, 36). These reports suggest the difference in the functional role of the three homologous antiporter-like subunits (NuoN, NuoM, and NuoL).

In the present work, we investigated the functional and structural roles of the charged residues in H\(^+\) translocation in NuoN, together with a few residues in NuoM and NuoL. We also examined the connecting parts in NuoN linking it to the neighboring subunits, accompanied by prolines in the discontinuous helices in NuoN, NuoM, and NuoL. Along with the previous results of mutation studies, the present work highlights similarities and differences among NuoN, NuoM, and NuoL. Furthermore, possible H\(^+\) translocation pathways in the three antiporter-like subunits of the NDH-1 are discussed.

**EXPERIMENTAL PROCEDURES**

**Materials**—PCR product, DNA gel extraction, and plasmid purification kits were from Qiagen (Valencia, CA). The pGEM\(^{®}\)-T Easy Vector System was from Promega (Madison, WI). The Taq DNA polymerase and Rapid DNA Dephos & Ligation Kit were from Roche Applied Science (Indianapolis, IN). The pCRScript cloning kit and the site-directed mutagenesis kit (QuikChange\(^{®}\) II XL kit) were from Stratagene (Cedar Creek, TX). The pKO\(_3\) vector was a generous gift from Dr. George M. Church (Harvard Medical School, Boston, MA). The endonucleases were from New England Biolabs (Beverly, MA). p-Nitro blue tetrazolium was from EMD Biosciences (La Jolla, CA). The Mini-PROTEAN\(^{®}\) TGX\(^{TM}\) Precast Gels (4–20%) and Trans-Blot\(^{®}\) Turbo\(^{TM}\) Transfer Pack were from Bio-Rad. The BCA protein assay kit was from Pierce. Bis-(3-propyl-5-oxo-isoxazol-4-yl)pentamethine oxonol (oxonol VI) and 9-amino-6-chloro-2-methoxyacridine (ACMA) were obtained from Molecular Probes (Eugene, OR). Capecsaicin-40 was a generous gift from Dr. Hiokyo Miyoshi (Kyoto University, Kyoto, Japan). Squamotacin was a generous gift from Dr. Subhash Sinha (The Scripps Research Institute, La Jolla). \(\beta\)-Dodecyl \(\beta\)-maltoside was from Biozynth International Inc. All other chemicals including dNADH, NADH, and the antibiotics were from Sigma. The antibodies against \textit{E. coli} NDH-1 subunits NuoB, NuoCD, NuoE, NuoF, NuoG, NuoL, NuoK, NuoM, and NuoL were obtained previously in our laboratory (27, 37, 38). Oligonucleotides were synthesized by Valuegene (San Diego, CA). \textit{E. coli} MC4100 (F\(^{-}\), araD139, D\((\text{arg F-lac})U169, ptsF25, relA1, flb5301, rpsL150\(\lambda\)\(^{-}\)) was used to generate \textit{nuoK}, \textit{nuoL}, \textit{nuoM}, and \textit{nuoN} site-specific mutations.

**Preparation of Knock-out and Mutagenesis of the \textit{nuoK}, \textit{nuoL}, \textit{nuoM}, and \textit{nuoN} Genes in the \textit{E. coli} Chromosome—**The strategies used for generating knock-out mutants (\(\textit{nuoK}\), \(\textit{nuoL}\), \(\textit{nuoM}\), and \(\textit{nuoN}\) mutations. The mutated \(\textit{nuoN}\) genes were in principle similar to those we reported previously (15, 25–30, 39). The knock-out mutants were generated by employing the pKO\(_3\) system according to the method described by Link et al. (40) and Kao et al. (25) along with minor modifications. In brief, the \textit{spc} gene was inserted into the \textit{nuoN} gene using a HindIII restriction site to disrupt the \textit{nuoN} gene as described in a previous report (27), leading to the construction of the \textit{E. coli} \(\textit{nuoK}\). In parallel, the \textit{nuoN} gene together with a 1-kb DNA segment, both upstream and downstream, was cloned into the pGEM\(^{®}\)-T Easy Vector System to generate a template for the site-specific \textit{nuoN} mutations. The mutated \textit{nuoN} fragments were inserted into pKO\(_3\) using the restriction site NotI to construct pKO\(_3\) (\(\textit{nuoN}\) mutants). Likewise, stop codons were introduced by the site-directed mutagenesis for the stop mutants (\(\text{Val}^{589}\)stop, \(\text{Ile}^{27}\)stop, and \(\text{Ala}^{381}\)stop). For evaluating the entire process of gene manipulation on the
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*E. coli* chromosome, we also constructed a control mutant (sKO-rev) that employed unmutated gene pKO(snuoN), instead of pK0(snuoN mutants), in the recombination process. Then, the above pK0 plasmids were used to replace the psp gene in *E. coli* sKO by recombination. The *E. coli* sE133A/sKO mutant was obtained by transforming pKO(snuoK:spc) into the sE133A mutant, and the double mutant sE133A/E72A was obtained by using pK0(snuoK-E72A) (26). The mutagenesis of nuoL, and the nuoM gene were done in a similar manner as written in previous reports (24, 27). The point mutations in *E. coli* NDH-1 as well as three antiporter-like subunits that are known to be similar to each other. Our previous studies identified conserved charged residues in NuoM (NGLU144, NLYS234, and NLYS265) and NuoL (NGLU144, NLYS228, and NLYS399) that are involved in energy transduction (24, 27). As highlighted in the sequence alignment, NuoN has conserved charged residues at corresponding positions (NGLU133, NLYS217, NLYS247, and NLYS395). Our first aim was to clarify whether these residues are part of the mechanism of H+ translocation by using a mutagenesis approach (Fig. 2, blue rectangles). In addition, to understand the perspective of key residues in NuoL, NuoM, and NuoN, conserved residues that have not been investigated in these subunits, MGLU407, LARG175, and LLYS342, were also studied.

NuoN, NuoM, and NuoL are known to be structurally similar. One unique feature shared by the three subunits is the presence of two discontinuous helices (17), which were hypothesized to participate in ion translocation. We attempted to elucidate the role of conserved prolines that are located in the loop of those helices (Fig. 2, orange pentagons).

Last, the three-dimensional structural model of NDH-1 places residues NLYS158 and NHIS224 near helix HL (17). Also, NVAL469 seems to interact with a β sheet in NuoM. We investigated contributions of these residues to structural integrity of NDH-1 (Fig. 2, green oval).

**Conserved Charged Residues in TM in NuoN and Neighboring Subunits**—We analyzed *E. coli* membranes on SDS-PAGE by immunoblotting using subunit-specific antibodies (Fig. 3). As expected, membrane vesicles from the knock-out mutants of NuoK, NuoM, and NuoN (sKO, sKO, and sKO) totally lacked all the subunits tested except NuoCD, confirming essential roles of these membrane subunits in the structure of NDH-1. On the other hand, sKO showed the presence of all tested subunits except NuoL and NuoM, as reported earlier (29). No detectable differences in the contents of analyzed subunits were seen in the mutants of the conserved charged residues in NuoN and NuoM (NGLU133, NLYS217, NLYS247, NLYS395, and NGLU407). It is important to note that the sKO-rev and sE133A/KKO-rev mutants also showed subunit contents almost comparable with the WT, validating the chromosomal homologous recombination procedure adopted here. On the other hand, the NuoL mutants (R175A and K342A) contained considerably

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**Enzymatic Assays**—The activity assays were conducted according to the methods described previously (44). In brief, dNADH oxidase activity of membrane samples were assayed at 340 nm in 10 mM potassium phosphate buffer (pH 7.0) containing 1 mM EDTA, 150 mM dNADH, and 1 mM K3Fe(CN)6 at 420 nm absorption.

**Measurement of Membrane Potential and H+ -pumping Activity**—Generation of membrane potential by the NDH-1 mutants was monitored optically using a reaction mixture containing 0.33 mg/ml of *E. coli* membrane samples in 50 mM MOPS (pH 7.3), 10 mM MgCl2, 50 mM KCl, and 2 mM oxonol VI as described previously (15). The reaction was started by addition of 200 μM dNADH. Uncoupler FCCP was added at a final concentration of 2 μM to dissipate the potential. The H+ pump activity was followed by ACMA fluorescence quenching (35). Fifty-μg of protein/ml of membrane vesicles, 2 μM ACMA, and 200 μM dNADH were used for the assay. Fluorescence was monitored with excitation at 410 nm and emission at 480 nm on a SpectraMax M2 fluorescence microplate reader (Molecular Devices Corp.).

**Other Analytical Procedures**—Protein concentrations were determined by the BCA protein assay kit (Pierce) with bovine serum albumin as standard, according to the manufacturer’s instructions. Any variations from the procedures and other details are described in the figure legends.

**Results**

The *E. coli* NuoN subunit (the counterpart of the mitochondrial ND2 subunit) consists of 485 amino acid residues, including 14 transmembrane regions. Fig. 1 shows the deduced amino acid sequence alignment of NuoN from several species spanning from bacteria to human. It also includes NuoL and NuoM of *E. coli* NDH-1 as well as three antiporter-like subunits that are known to be similar to each other. Our previous studies identified conserved charged residues in NuoM (NGLU144, NLYS234, and NLYS265) and NuoL (NGLU144, NLYS228, and NLYS399) that are involved in energy transduction (24, 27). As highlighted in the sequence alignment, NuoN has conserved charged residues at corresponding positions (NGLU133, NLYS217, NLYS247, and NLYS395). Our first aim was to clarify whether these residues are part of the mechanism of H+ translocation by using a mutagenesis approach (Fig. 2, blue rectangles). In addition, to understand the perspective of key residues in NuoL, NuoM, and NuoN, conserved residues that have not been investigated in these subunits, MGLU407, LARG175, and LLYS342, were also studied.

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lower amounts of NuoL and NuoM in their membranes, suggesting that these mutations make NuoL and NuoM unstable.

The assembly of NDH-1 complex in the mutants was investigated by BN-PAGE followed by NADH dehydrogenase activity staining (Fig. 4A). Of the two bands that appeared in the WT membrane, only the upper band was recognized by the antibody to the peripheral subunit NuoB in the immunoblotting of BN-PAGE (Fig. 4B). Along with the results from the membrane isolated from the NKO mutant, we regard the upper band as assembled NDH-1. The lower band might be an oligomeric form of NDH-2 but has not been verified. Membranes isolated from the majority of mutants of the charged residues showed a comparable upper band with that from the WT, assuring they contain well assembled NDH-1. On the other hand, mutants LR175A and LK342A exhibited a significantly reduced amount of assembled NDH-1, indicative of partially degraded subcomplexes as reported previously for some other NuoL mutants (24).

In addition to the above analyses, we estimated the amount of the peripheral domain associated with the membrane by measuring the dNADH-K3Fe(CN)6 reductase activity, which derives from the NADH dehydrogenase segment of NDH-1. Here, we used dNADH as the substrate to eliminate contribution from the alternative NADH-quinone oxidoreductase that exists in *E. coli* (45). As shown in Table 1, NKO and NE133A/KKO mutants exhibited, respectively, only 25 and 20% dNADH-K3Fe(CN)6 reductase activity as compared to WT, indicating the absence of a functionally active

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**Figure 1.** Comparison of the amino acid sequences among the NuoN (ND2) subunits and other homologous antiporters. The alignment around helices that contain conserved charged residues presumably involved in H+/H1 translocation was carried out by using the Clustal W program (54). Helices are depicted above the alignment based on the three-dimensional structure of *E. coli* NuoN (17), highlighting the candidates of essentially charged residues for energy-coupled NDH-1 activities (dark colored) and prolines in discontinuous helices (P). Black boxes with white letters illustrate similar residues among at least eight listed organisms. Dashes represent gaps to facilitate alignment. Amino acids mutated in this study are marked by arrows with the numbering in *E. coli* NuoN. Sequence sources and their UniProtKB/Swiss-Prot accession numbers are:

- *E. coli*-NuoN, *E. coli* K-12 NuoN subunit (P0AFF0);
- P.a-NuoN, *Pseudomonas aeruginosa* NuoN subunit (Q9I0I9);
- T.t-Nqo14, *Thermus thermophilus* Nqo14 subunit (Q56229);
- P.d-Nqo14, *Paracoccus denitrificans* Nqo14 subunit (A1B479);
- R.c-NuoN, *Rhodobacter capsulatus* NuoN subunit (P50973);
- N.t-ND2, *Nicotiana tabacum* GN Nad2 subunit (Q5MA39);
- B.t-ND2, *Bos taurus* ND2 subunit (P03892);
- H.s-ND2, *Homo sapiens* ND2 subunit (B1NU62);
- X.l-ND2, *Xenopus laevis* ND2 subunit (P03894);
- Y.l-ND2, *Yarrowia lipolytica* ND2 subunit (Q9B6C8);
- C.e-ND2, *Caenorhabditis elegans* ND2 subunit (P24889);
- E.c-NuoM, *E. coli* K-12 NuoM subunit (P33607);
- M.b-EchA, *Methanosarcina barkeri* EchA subunit (O59652);
- B.s-MrpA, *Bacillus subtilis* MrpA subunit (Q9K2S2);
domain. The residual activities of the two KO mutants were most likely diaphorase activities unrelated to NDH-1 because membranes of KO mutants did not contain NuoF (the NADH-binding subunit) or NuoE that is required for the dNADH-K₃Fe(CN)₆ reductase activity of NDH-1 (38, 46). Slight reduction in the activity was seen for some point mutants (NK247A, NK395A, ME407A, LR175A, and LK342A mutants). The remaining single mutants listed in Table 1 exhibited dNADH-K₃Fe(CN)₆ reductase activity more or less similar to that of WT.

Next, the dNADH oxidase and dNADH-DB reductase activities were measured to assess the effect of mutations on the energy-coupled activities of NDH-1 (see Table 1). Overall, the dNADH oxidase and dNADH-DB reductase activities behaved in a similar manner among all the mutants tested, implying that the observed effects solely reflect NDH-1 mutations. The mutation of the highly conserved $N_{\text{Glu}}^{133}$ to alanine in TM5 showed a small (~28%) decrease in the activities, which is in good agreement with an earlier study by Amarneh and Vik (35). Mutation of the highly conserved $N_{\text{Lys}}^{217}$ to alanine, cysteine, or arginine all resulted in reduced activities (in the range of 44–61%). The results are in contrast to that of Amarneh and Vik (35) in which the NK217C mutant was shown to have null energy-coupled activities. The mutation of the other conserved lysine residue to alanine ($N_{\text{K247A}}$) led to only about 30% remaining activity. The mutation of the same residue to arginine resulted in almost complete restoration in the activities similar to the WT. Among the other candidates of essential residues in NuoN, mutation of the highly conserved $N_{\text{Lys}}^{395}$ (present in the TM12) to $N_{\text{K395A}}$ strikingly caused almost a complete loss in activity, whereas the arginine mutant ($N_{\text{K395R}}$) showed moderately reduced activities in the 37–43% range. When we mutated the highly conserved $N_{\text{Glu}}^{407}$ located...
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In the TM12 (position equivalent to \(_{\text{N}}\text{Lys}^{395}\) to alanine, almost total abolishment of the activities was observed. Likewise, mutation of the highly conserved charged residues \(_{\text{L}}\text{Arg}^{1775}\) and \(_{\text{L}}\text{Lys}^{342}\) to alanine (\(_{\text{R}}\text{R175A}\) and \(_{\text{K}}\text{K342A}\)) resulted in greatly reduced activities (~15%).

To ascertain the effects of the mutations on the energy-coupled activities of NDH-1 further, we examined the generation of membrane potential (\(\Delta\Psi\)) and \(\text{H}^+\) translocation activity. As shown in Fig. 5A, addition of dNADH to the membrane vesicles from the WT led to generation of \(\Delta\Psi\), which was then dissipated by an uncoupler FCCP. The \(\text{H}^+\) translocation activity in the inverted membrane vesicles of different mutants was monitored by ACMA, where the membranes from the WT showed a maximum quenching after the addition of dNADH, followed by a reversion of the signal when FCCP was added (Fig. 6A). The mutation of highly conserved \(_{\text{M}}\text{Glu}^{407}\) and \(_{\text{M}}\text{Lys}^{395}\) to alanine resulted in a significant loss in \(\Delta\Psi\) generation and no \(\text{H}^+\) pumping activity (only ~10% as compared with the WT). Those of \(_{\text{R}}\text{R175A}\) and \(_{\text{K}}\text{K342A}\) exhibited only a small \(\Delta\Psi\) generation and \(\text{H}^+\) pumping activity (~30%). In contrast, other mutants of highly conserved residues including \(_{\text{E}}\text{E133A}, _{\text{N}}\text{K217A}, \) and \(_{\text{K}}\text{K247A}\) exhibited \(\Delta\Psi\) and \(\text{H}^+\) pumping activity almost comparable with that of the WT. These results were largely consistent with the data of the energy-coupled activities.

In good agreement with an earlier report (35), our present results relating to the conserved charged residues on the NuoN subunit showed that \(_{\text{N}}\text{Lys}^{395}\) located in the TM12 is an essential residue for the energy-transducing NDH-1 activity. \(_{\text{N}}\text{Lys}^{395}\) is also conserved in NuoM (\(_{\text{N}}\text{Lys}^{399}\)) but in the homologous NuoM subunit the equivalent residue is a glutamic acid (\(_{\text{M}}\text{Glu}^{407}\). Our studies demonstrated that both \(_{\text{M}}\text{Glu}^{407}\) and \(_{\text{M}}\text{Lys}^{395}\) interacts with the essential residue \(_{\text{L}}\text{Arg}^{1775}\), whereas \(_{\text{N}}\text{Lys}^{395}\) interacts with the essential residue...
The conserved residue $\varepsilon$Glu$^{133}$ was seemingly non-essential for the energy-transducing NDH-1 activity unlike the corresponding glutamic residues in NuoM and NuoL ($\varepsilon$Glu$^{144}$ and $\varepsilon$Glu$^{144}$) that had been shown to be essential (24, 27, 28, 36). Accordingly, the strong reduction of $\Delta\Psi$ and H$^+$ translocation activity of the double mutant were observed (Figs. 5A and 6A). These results suggest an essential role of the pair of these two highly conserved glutamic acids on the energy-coupled NDH-1 activity. Thus we postulate that $\varepsilon$Glu$^{133}$ is important for function similarly to the corresponding residues in NuoM and NuoL ($\varepsilon$Glu$^{144}$ and $\varepsilon$Glu$^{144}$) but its role can be compensated by another residue, $\varepsilon$Glu$^{72}$. It should also be noted that a compensatory effect exerted by two conserved charged residues has been reported for the two nearby conserved carboxyl residues (Asp$^{79}$ and $\varepsilon$Glu$^{81}$) located in the NuoA subunit (25) but never for a pair of residues located in different subunits like in the current case. These results strongly suggest that NuoN has function of the H$^+$ translocation like NuoM and NuoL.

**Prolines in Discontinuous Helices of Subunits NuoN, NuoM, and NuoL**—It has recently been demonstrated that discontinuous membrane helices ($\alpha$-helix–loop–$\alpha$-helix motif) are present in Ca$^{2+}$-ATPase and secondary transporters such as NhaA (47). The three-dimensional structural models of these transporters led to a hypothesis that the loops are involved in recognition, binding, and translocation of ions. Similar to the secondary antiporters (17), NuoN, NuoM, and NuoL all have two discontinuous helices in their TM7 and TM12 sections, which are located close to essential charged residues, thus implying a key role for conformational changes in these subunits (see Figs. 2 and 7B). As highly conserved prolines are located at the bend-

$\varepsilon$Glu$^{144}$ (27), rationalizing the necessity of the opposite charges between $\varepsilon$Lys$^{395}$ and $\varepsilon$Glu$^{407}$.
ing of the discontinuous helices in NDH-1 (NPro222, NPro387, MPro239, MPro399, LPro234, and LPro390) (Fig. 2), replacing them with alanine, which is a strong helix-forming residue, might possibly force the helices into a less kinked structure. Therefore, we made mutations NP222A, NP387A, MP239A, MP399A, LP234A, and LP390A, along with a glycine mutant NP387G.

The analysis of SDS-PAGE (Fig. 3), BN-PAGE (Fig. 4), and dNADH-K3Fe(CN)6 reductase activity (Table 2) confirm that all of the proline mutants had normal subunit contents and assembly. As expected, mutation of each of the conserved prolines to alanine moderately reduced the dNADH oxidase and the dNADH-DB reductase activities (50–80%, Table 2). Likewise, these mutants gave a slight reduction of and H translocation (Figs. 5B and 6B). The energy-coupled activities of a mutation of NPro387 to glycine (NP387G) as well as the extent of H translocation were comparable with WT, suggesting that replacement with glycine, which has no side chain and is thus relatively flexible, perhaps did not deprive the helix of kink enough to cause a significant activity loss.

The remaining activities of mutation of the prolines to alanine indicated their similar roles among the antiporter-like subunits. However, their relatively high activities do not seem to support the hypothesis (17) that the individual proline residues are indispensable for the energy-coupled NDH-1 activities. It might be possible that replacement of a proline residue by alanine in a different discontinuous helix only partially affects the kinked structure of NDH-1. In addition, we could not exclude a possibility that discontinuous helices do not make a significant contribution to the energy coupling mechanism.

Structural Elements in NuoN—The x-ray structure of E. coli NDH-1 displayed at least two connection elements among NuoK, NuoN, NuoM, and NuoL, which are considered to contribute to the stability of the antiporter-like subunits and help in coupling electron transfer with H translocation (17, 29, 48, 49). One is a rod-like helix HL in NuoL, and the other is β sheets in NuoL and NuoM located on the opposite side of the domain from helix HL (17) (Fig. 2). In NuoN subunit, residues NLYS158 and NHis224 are placed near helix HL according to the x-ray structural model. Also, NVal1469 (or the α-helix in TM14 from NVal1469 to the C-terminal) seem to interact with the β sheet.

We investigated the possible connecting elements (NLYS158 and NHis224) of NuoN with the helix HL in NuoL by producing mutants NLK158A, NLK158R, and NLH224A. When we measured dNADH oxidase and dNADH-DB reductase activities, a mod-
The decrease was observed for NVal469 and NVal475 mutants (~50%, Table 3). The NH224A mutant displayed a slight decrease in the energy-coupled activities (~70%). Similarly, ΔΨ and the H+ translocation activity were only slightly reduced by these mutations (Figs. 5C and 6C). Interestingly, mutants NVal158A and NVal158R showed significantly decreased levels of the intact NDH-1 activity on BN-PAGE (Fig. 4A) despite the detection of fully assembled NDH-1 as seen in immunoblotting (Fig. 4B), the normal subunit contents (Fig. 3) and the dNADH-KFe(CN)6 reductase activity (Table 3). This discrepancy might be due to the extraction procedures in BN-PAGE, which requires dissociation of the membrane using dodecyl maltoside as described previously (26). The loss of connecting residue NVal158 could reduce the stability of helix HL resulting in an altered architecture in that part of NDH-1. Along with the three-dimensional structural model of membrane subunits, these results strongly suggested that NVal158 plays a critical role in the interaction with helix HL. On the other hand, alanine mutation of the conserved histidine residues, NHis241 (27) and NHis224 (this work), seemed to imply that their involvement in the interaction with helix HL may be less significant compared with that of NVal158.

To assess the other possible connecting element (NVal469) in the NuoN subunit, we also made the mutation and truncations of the NuoN subunit (NVal469A, NVal469 stop, NAla475 stop, and NVal475 stop). The amount of membrane and peripheral subunits were reduced for the C-terminal truncation NVal469 stop and NVal475 stop mutants (Fig. 3). In contrast, the truncation mutant NAla475 stop and a point mutant NVal469A showed subunit contents mostly comparable with that of the WT. We also found a reduced amount of completely assembled NDH-1 in BN-PAGE (Fig. 4) and partially reduced dNADH-KFe(CN)6 reductase activity (60%, Table 3) for the NVal469 stop and NVal475 stop mutants. In line with the above analysis, NVal469 stop or NAla475 stop mutants displayed a significant decrease in the energy-coupled NDH-1 activities (~30%), whereas the NAla475 stop and NVal469A mutants showed relatively higher activities (~65%). The data on ΔΨ generation and H+ translocation ability exhibited similar tendencies with the energy-coupled activities (Figs. 5C and 6C). These results indicated that the C-terminal amphipathic helix starting from NVal469 in NTM14 interacts with the Mβ sheet. Interestingly, the loss of NuoL and NuoM in NDH-1 was detected in C-terminal truncation mutants of NuoM (29) but not in the C-terminal truncation mutants of NuoN.

table 2

<table>
<thead>
<tr>
<th>Mutation</th>
<th>dNADH-O2</th>
<th>dNADH-DB</th>
<th>dNADH-KFe(CN)6</th>
<th>IC50 (cap)</th>
<th>IC50 (squ)</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>812 ± 25 (100%)</td>
<td>854 ± 37 (100%)</td>
<td>1546 ± 27 (100%)</td>
<td>0.19</td>
<td>0.0023</td>
</tr>
<tr>
<td>P222A</td>
<td>503 ± 21 (62%)</td>
<td>655 ± 15 (77%)</td>
<td>1400 ± 19 (91%)</td>
<td>0.20</td>
<td>0.0027</td>
</tr>
<tr>
<td>P387A</td>
<td>479 ± 31 (59%)</td>
<td>442 ± 14 (52%)</td>
<td>1288 ± 34 (83%)</td>
<td>0.19</td>
<td>0.0023</td>
</tr>
<tr>
<td>P387G</td>
<td>705 ± 65 (87%)</td>
<td>780 ± 56 (91%)</td>
<td>1594 ± 60 (103%)</td>
<td>0.18</td>
<td>0.0028</td>
</tr>
<tr>
<td>P239A</td>
<td>477 ± 14 (59%)</td>
<td>621 ± 17 (73%)</td>
<td>1343 ± 50 (87%)</td>
<td>0.18</td>
<td>0.0047</td>
</tr>
<tr>
<td>P399A</td>
<td>422 ± 28 (52%)</td>
<td>540 ± 12 (63%)</td>
<td>1204 ± 87 (78%)</td>
<td>0.20</td>
<td>0.0044</td>
</tr>
<tr>
<td>P343A</td>
<td>422 ± 15 (52%)</td>
<td>569 ± 46 (67%)</td>
<td>1340 ± 67 (85%)</td>
<td>0.16</td>
<td>0.0025</td>
</tr>
<tr>
<td>P390A</td>
<td>485 ± 35 (60%)</td>
<td>578 ± 65 (68%)</td>
<td>1399 ± 51 (90%)</td>
<td>0.15</td>
<td>0.0030</td>
</tr>
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</table>

# DISCUSSION

Based on the empirical findings in this study, we concluded that NuoN is involved in H+ translocation similar to the other antiporter-like subunits, NuoM and NuoL. Our data also suggested that NAla133 and NVal395 in NuoM may be involved in H+ translocation. Together with the results from our previous work, we summarized the candidate residues that may be part of the mechanism of H+ translocation as shown in Fig. 7B. Besides the aforementioned residues in NuoN, we are Gly36, Gly44, Lys234, Gly407, Glu133, Arg175, Lys229, Lys342, and Lys395. In addition, Asp83, Glu81, and Glu72 were also considered to be essential residues based on the data using the double mutants. Most of the residues are located not only in the middle of the TM but also at the interface of adjacent subunits, suggesting that the core elements of the H+ translocation machinery lie around the borders of contiguous membrane domains (52). Recently, Verkhovsky and Bloch (53) proposed a “wave-spring” model that involves conformational changes driven by the reduction of quinone transmitted through charged residues located in the middle of the TMs, from the NuoAK(H) bundle to NuoL. In this model, electrochemical transmission has to cover the distance between the two closest charged residues. There exist large gaps around the border of subunits, especially between TM8 and TM12. Sazanov’s group (19) suggested a “river” of water molecules and histidine residues that assist formation of a continuous hydrophilic axis in the membrane (see the green arrow in Fig. 7B). Therefore, it is possible that replacements of the charged residues by site-directed mutagenesis at the interface of adjacent subunits had a critical impact on energy-
coupled activities because of the gaps with adjacent charged residues. Thus, H⁺ can be translocated through the inside of the antiporter-like subunits (NuoL, NuoM, and NuoN) and also through the aforementioned NuoAJK(H) bundle, powered by the horizontal array of charged/polar groups in conjunction with conformational changes in different membrane subunits (Fig. 7B).

We categorized three areas/regions of essential charged residues that could comprise the key elements in the H⁺ translocation pathway (see Fig. 7A). They are: 1) a negatively charged region formed by essential residues Glu₁₃₃, Glu₇₂, Glu₃₆, Lys₃₄₂, and Lys₃₉₉; 2) a positively and negatively charged region near the end of NuoL formed by residues Glu₁₃₃, Glu₇₂, and Lys₃₄₂, and/or in subunit NuoH (19). Along with the fact that the set of Glu₁₃₃ and Glu₇₂ are the propensity of essential charged residues (whose double mutations led to a significant loss of activity) to be located at the interface of adjacent subunits, it seems reasonable to imagine that H⁺ translocation occurs through the interface between two adjacent subunits, as shown in Fig. 7B. Our results on the site-directed mutagenesis suggest that Lys₃₄₂ and Lys₃₉₉ are also involved in the maintenance of architecture of NDH-1. From the mutation experiments on NuoL and NuoM (adjacent to Lys₃₉₉) was considered to be involved in H⁺ translocation (24). Further research would help establish whether this region participates in H⁺ translocation and/or structural stability of NDH-1.

In conclusion, the results of the present study suggested that (a) the NuoN subunit is involved in the H⁺ translocation in a similar manner to NuoM and NuoL, (b) conserved chargeable residues including those at the interface of adjacent subunits play key roles in the mechanism of H⁺ translocation, as the requisites for horizontal energy transmission and/or H⁺ translocation pathways, (c) conserved prolines in the loops of discontinuous helices are not essential for the energy transduction of NDH-1, and (d) a lysine residue and the C terminus region in NuoN bear structural roles.

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REFERENCES


TABLE 3

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<tr>
<th>Mutation</th>
<th>dNADH-O₂</th>
<th>dNADH-DB</th>
<th>dNADH-K₂Fe(CN)₆</th>
<th>IC₅₀ (cap)</th>
<th>IC₅₀ (squ)</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT</td>
<td>812 ± 25 (100%)</td>
<td>854 ± 37 (100%)</td>
<td>1546 ± 27 (100%)</td>
<td>0.19</td>
<td>0.0023</td>
</tr>
<tr>
<td>K₁₅₈A</td>
<td>435 ± 45 (50%)</td>
<td>489 ± 54 (57%)</td>
<td>1224 ± 16 (79%)</td>
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<tr>
<td>H₂₂₄R</td>
<td>330 ± 43 (41%)</td>
<td>350 ± 60 (41%)</td>
<td>1155 ± 127 (75%)</td>
<td>0.13</td>
<td>0.0022</td>
</tr>
<tr>
<td>V₄₆₉A</td>
<td>567 ± 65 (70%)</td>
<td>623 ± 49 (73%)</td>
<td>1391 ± 92 (90%)</td>
<td>0.15</td>
<td>0.0032</td>
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<tr>
<td>L₅₃₉STOP</td>
<td>152 ± 13 (37%)</td>
<td>162 ± 52 (72%)</td>
<td>1358 ± 95 (88%)</td>
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<td>0.0031</td>
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<td>L₅₃₉STOP</td>
<td>307 ± 9 (38%)</td>
<td>354 ± 13 (41%)</td>
<td>970 ± 87 (63%)</td>
<td>0.18</td>
<td>0.0031</td>
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<td>NK₁₅₈R</td>
<td>504 ± 52 (62%)</td>
<td>562 ± 52 (72%)</td>
<td>923 ± 88 (60%)</td>
<td>0.14</td>
<td>0.0032</td>
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<td>NK₁₅₈R</td>
<td>505 ± 31 (62%)</td>
<td>575 ± 28 (67%)</td>
<td>1267 ± 37 (82%)</td>
<td>0.15</td>
<td>0.0025</td>
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</table>

a Activity in nanomole of K₂Fe(CN)₆/mg of protein/min.
b Activity in nanomole of dNADH/mg of protein/min.
c Concentration of capsaicin-40 (cap) that causes 50% inhibition on dNADH-oxidase activity (µM).
d Concentration of squatamacin (squ) that causes 50% inhibition on dNADH-oxidase activity (µM).
Essential and Connecting Elements of NuoN in E. coli NDH-1


Energy Transducing Roles of Antiporter-like Subunits in *Escherichia coli* NDH-1 with Main Focus on Subunit NuoN (ND2)

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