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Cytochrome cbb_3 of *Thioalkalivibrio* is a Na^+-pumping cytochrome oxidase

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Cytochrome *c* oxidases (Coxs) are the basic energy transducers in the respiratory chain of the majority of aerobic organisms. Coxs studied to date are redox-driven proton-pumping enzymes belonging to one of three subfamilies: A-, B-, and C-type oxidases. The C-type oxidases (cbb_3 cytochromes), which are widespread among pathogenic bacteria, are the least understood. In particular, the proton-pumping machinery of these Coxs has not yet been elucidated despite the availability of X-ray structure information. Here, we report the discovery of the first (to our knowledge) sodium-pumping Cox (Scox), a cbb_3 cytochrome from the extremely alkaliphilic bacterium *Thioalkalivibrio versutus*. This finding offers clues to the previously unknown structure of the ion-pumping channel in the C-type Coxs and provides insight into the functional properties of this enzyme.

cytochrome *c* oxidase | sodium pumping | cbb_3-type oxidase | alkaliphily

The known terminal oxidases according to the structure of their active centers and their phylogenetic relations are subdivided into two superfamilies (1). One is composed of numerous representatives containing a heme-copper binuclear active center (BNC). Oxidases belonging to the other superfamily have no copper. This superfamily includes bacterial oxidases of the *bd* type. The superfamily of representatives with heme-copper BNC is subdivided in turn into two groups, cytochrome *c* oxidases (Coxs) and quinol oxidases, depending upon the electron donor, which can be either cytochrome *c* or quinol. Quinol oxidases with a heme-copper BNC are found only in prokaryotes, whereas Coxs are widespread among living organisms of all domains: Eukarya (where they are found in mitochondria and chloroplasts), Bacteria, and Archaea. Although terminal oxidases with heme-copper BNC constitute a diverse group of multisubunit enzymes having from 2 to 13 subunits, conservatism and similar architecture are obviously inherent in their main (catalytic) subunit. The catalytic center of the main subunit always contains two hemes and copper as redox active prosthetic groups and a redox active tyrosine covalently bound to histidine in the polypeptide chain (2–5). Iron of one of the hemes and copper constitute the BNC. Coxs are the best-studied group of terminal oxidases. The basic mechanism of energy transduction by Coxs during respiration consists of the oxidation of cytochrome *c* by molecular oxygen (O_2) coupled to transmembrane pumping of protons (H^+). This process results in reduction of O_2 to water by the BNC, where O_2 is bound. In Coxs, it requires four protons ("chemical" H^+ for water production) taken from the inner side of the membrane and can be coupled to the translocation of another four protons ("pumped" H^+) from the inner to the outer side of the membrane into the intermembrane or the periplasmic space of mitochondria or prokaryotic cells, respectively, according to the following equation (6–8):

$$4\mathrm{cyt}c^{2+} + 4\mathrm{H}^+_{\mathrm{in,chem}} + 4\mathrm{H}^+_{\mathrm{in,pump}} + \mathrm{O}_2 \rightarrow 4\mathrm{cyt}c^{3+} + 4\mathrm{H}^+_{\mathrm{out,pump}} + 2\mathrm{H}_2\mathrm{O}.$$

In A-type Coxs, two H^+ pathways in the main subunit were identified, the so-called D channel, conducting all pumped and part of chemical H^+, and the K channel, conducting most of chemical H^+ (9). In C-type Coxs, only a K-channel analog was found (10). The described catalytic events are accomplished through generation of a transmembrane difference in H^+ potentials ($\Delta\bar{\mu}_{H^+}$), which is used as a convertible membrane-linked biological currency. Microorganisms living in an alkaline environment maintain a nearly neutral cytoplasmic pH (11). This presents a problem for alkaliphiles because it gives rise to an inverted pH gradient that decreases the $\Delta\bar{\mu}_{H^+}$ (12, 13). Some alkaliphilic microorganisms solve this problem by using an Na^+-pumping NADH-CoQ reductase (NQR) (14), and perhaps a Na^+-pumping terminal oxidase, as was assumed (15). At present, NQR is the only respiratory chain enzyme for which Na^+ pumping has been directly and undoubtedly established (16). However, NQR is absent in the extremely alkaliphilic bacterium *Thioalkalivibrio versutus* AL2, which inhabits an alkaline (~pH 10) Siberian soda lake at saturating salt

Significance

The majority of aerobic living organisms use oxygen for respiration. The key enzyme, which directly reduces oxygen to water during respiration, is the terminal cytochrome *c* oxidase. It generates a large portion of the utilizable energy provided by the respiratory chain. Accumulation of biologically available energy by means of cytochrome *c* oxidases is believed to be due to the proton-motive force across the mitochondrial or bacterial membrane. Details of this energy conversion are still unclear. Here we report the discovery of a sodium-pumping cytochrome *c* oxidase that converts energy of respiration into sodium-motive force. This finding provides clues to understanding the mechanism of cytochrome *c* oxidase that is not available when applying knowledge of the proton-pumping versions of the enzyme.

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The authors declare no conflict of interest.

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Data deposition: The nucleotide sequences of *Thioalkalivibrio* cbb_3 oxidase have been deposited in the EMBL database (accession no. HE575403.1).

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concentrations (17). *T. versutus* is a chemolithotroph that oxidizes sulfur compounds and employs Cox as a terminal component of its aerobic electron transport chain. Here we report that *T. versutus* uses a novel C-type Cox that (*i*) specifically requires Na^+ for its activity and (*ii*) electrogenically exports Na^+ from cells or right-side-out subcellular membrane vesicles, the process being coupled to oxidation of ascorbate by O_2.

Results and Discussion

Experiments were performed using *T. versutus* cells (exhausted of endogenous substrates) and the right-side-out subcellular vesicles derived from them. Thus, both cells and vesicles displayed no respiration without substrate addition. To start respiration at the level of Coxs in respiratory chain, we used the exogenous substrates Wurster's blue [*N,N,N′,N′*-tetramethyl-*p*-phenylenediamine (TMPD)], which is nonspecific for all terminal oxidases, or cytochrome *c*, which is specific for Coxs, both in the presence of a reductant ascorbate. Addition of any of the substrates initiated rapid O_2 consumption (Fig. 1 *A* and *B*) and generation of an electric membrane potential ($\Delta\psi$) (Fig. 1*D*). Similar to the Na^+-motive NQR (14), these activities were specifically Na^+-dependent, showing optimum at alkaline pH (8.5–9.5) (Fig. 1 *C* and *D*). In contrast, the well-known H^+-motive Coxs from *Rhodobacter sphaeroides* (7) and *Paracoccus denitrificans*, used as controls (Fig. S1 *A–C*), as well as from *Pseudomonas stutzeri* (18), showed no Na^+ specificity (*SI Text*, section S1). Cytochrome *c*, unlike TMPD, was inefficient toward *T. versutus* Cox at high salt concentrations, similar to Coxs from other species; therefore, TMPD was used later on. The Cox inhibitor cyanide fully arrested both Cox activities (Fig. 1*D* and Fig. S1*D*). Thus, Cox operating in *T. versutus* membranes is a Na^+-dependent oxidase (Scox) that can be either a Na^+-activated H^+ pump or Na^+-activated redox loop lacking in H^+ pump.

To discriminate between these two possibilities, we tested H^+ pumping by the oxidase. Unlike H^+-pumping Coxs, which acidify the external medium during respiration in the presence of the K^+ ionophore valinomycin (Fig. S2*A*) (see also refs. 7 and 19), Scox did not mediate H^+ extrusion at alkaline pH (Fig. 2*A* and Fig. S2*B*), as shown earlier (20). Instead, Scox evoked alkalinization of the medium in response to O_2 pulse when valinomycin was replaced by protonophore, and H^+ could serve as counter ion instead of K^+ (Fig. 2*B* and inset and Fig. S2*C*). Reversibility of this alkalinization in the time scale (upper green curve, Fig. 2, *Inset*) points that it cannot be attributed to H^+ consumption during respiratory chemical reaction of water production because of irreversibility of the latter reaction. These effects could be explained by assuming that the oxidase is Na^+-motive and electrogenic. In such case, $\Delta\psi$ formed by Na^+ efflux, in the presence of a protonophore, should be counterbalanced by H^+ influx, leading to reversible alkalinization of the outer space. Fig. 2*D* shows these relationships. Consistent with this scheme, a respiration-driven, fully cyanide-sensitive export of $^{22}Na^+$ was found in bacterial cells and vesicles preloaded with this isotope (Figs. 2*C* and 3 *A* and *B*). Export of $^{22}Na^+$ could be stimulated by protonophores [carbonyl cyanide *m*-chlorophenylhydrazone (CCCP) and 2-heptyl-4-hydroxyquinoline *N*-oxide (HQNO), a protonophore operating at alkaline pH (Fig. S3 and *SI Text*, section S2)] as well as valinomycin. Like respiratory activity of *T. versutus* Scox, export of $^{22}Na^+$ occurred at alkaline pH (8.0–10.0) (Fig. 2*C*). These data confirm that *T. versutus* Scox operates as a primary Na^+ pump rather than an Na^+/H^+ antiporter or a K^+ pump.

To identify the Na^+-pumping Scox, we considered the three known types of Coxs (21, 22): A, B, and C (Fig. 4*A*), which are represented by cytochromes aa_3/caa_3, ba_3, and cbb_3, respectively. Because *T. versutus* membranes contained heme B but not heme A (Fig. S4), A- and B-type Coxs can be excluded in our case. Instead, we identified an operon of a cbb_3 oxidase (C-type Cox)

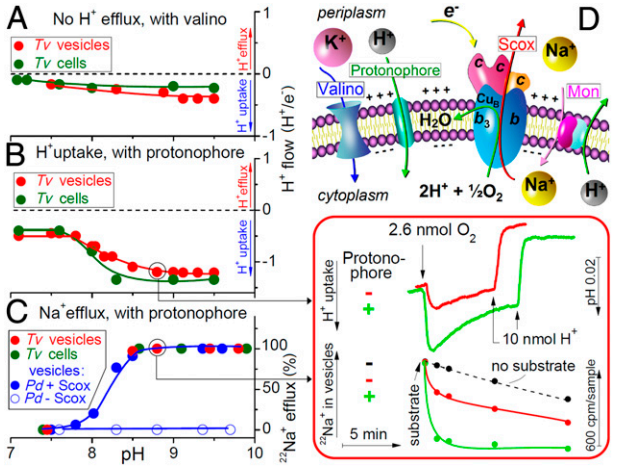

Fig. 2. pH profile of respiration-driven $^{22}Na^+$ efflux and H^+ uptake mediated by *T. versutus* AL2 (*Tv*) Scox. (*A*) The absence of O_2 pulse-induced H^+ pumping in *Tv* cells and right-side-out vesicles ("vesicles") in the presence of 1 μM valinomycin (valino). (*B*) O_2 pulse-induced H^+ uptake in *Tv* cells and vesicles in the presence of protonophore: 50 μM CCCP (cells) or 25 μM HQNO (vesicles). (*C*) Protonophore-supported Na^+ pumping in $^{22}Na^+$-loaded *Tv* cells and vesicles and in *P. denitrificans* vesicles (*Pd*-Scox) and vesicles from Scox-expressing *P. denitrificans* (*Pd*+Scox). $^{22}Na^+$ efflux was assessed for 2 min after substrate addition. Na^+ efflux at pH 9 is defined as 100% in each case. Reactions were started by addition of O_2 as small aliquots of water into an anaerobic reaction mixture (*A* and *B*) or ascorbate and TMPD (*C*). (*Inset*) Time scale, respiration-driven $^{22}Na^+$ efflux (bottom) and H^+ uptake (top) in *Tv* vesicles. For conditions, see Fig. 3 and Fig. S2. (*D*) Orientation of Scox and ion fluxes in bacterial cell and right-side-out membrane vesicles derived therefrom. Scox subunits as defined (Fig. S5): N (navy), O (orange), and P (pink). Scox active site facing the periplasm accepts electrons (e^-) from a substrate and then pumps Na^+ outside the cell; protonophore or K^+ ionophore valino facilitates Na^+ efflux via counter ion influx (H^+ or K^+, respectively); the Na^+/H^+-antiporter monensin (Mon) collapses the Na^+ gradient.

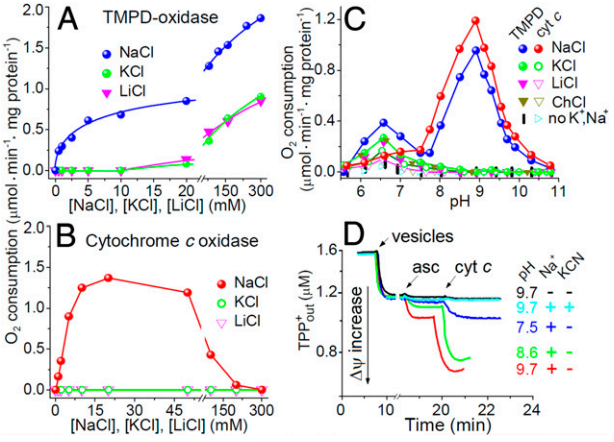

Fig. 1. Na^+ concentration and pH dependence of the respiration-linked characteristics of cytochrome oxidase in *T. versutus* membrane vesicles. (*A–C*) O_2 consumption and (*D*) $\Delta\Psi$ generation measured using tetraphenylphosphonium (TPP^+)-selective electrode; reactions were induced by substrate addition. Reaction media: 50 mM CHES-Tris buffer (pH 9.2) and 0.5 mM EDTA (*A* and *B*) or 50 mM Mops/TAPS/CAPS buffer-KOH, 0.5 mM EDTA, and 20 mM Na, K, Li, or choline (Ch) chloride (*C*) or 50 mM Mops/TAPS/CAPS buffer-KOH, 0.5 mM EDTA, and 30 mM K_2SO_4 (no Na^+) or 20 mM Na_2SO_4, 10 mM K_2SO_4 (+Na^+), 1.6 μM TPP^+, and 10 μM KCN, where indicated (*D*). Vesicle protein concentration: 34 μg/mL (*A–C*); 1 mg/mL (*D*). Substrate final concentrations, 80 μM TMPD (*A* and *C*) or 6 μM horse heart cytochrome *c* (*B–D*), both in the presence of reductant, 2 mM ascorbate-Tris (pH 7) (*A–D*).

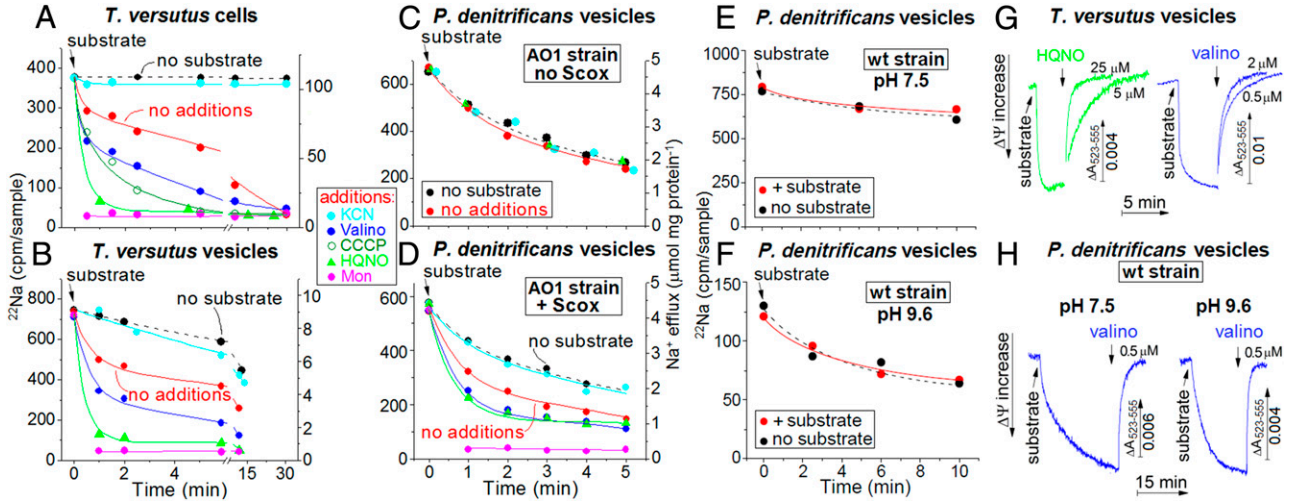

Fig. 3. Evidence of a primary Na^+ pump in *T. versutus* (*Tv*). (*A*) Substrate-induced Na^+ efflux from ^{22}Na-loaded *Tv* cells, (*B*) *Tv* vesicles, (*C*) *P. denitrificans* AO1 vesicles without *Tv* cbb_3 (no Scox), (*D*) *P. denitrificans* AO1 vesicles with *Tv* cbb_3 (+Scox), and (*E* and *F*) WT *P. denitrificans* vesicles was assessed by radioactivity of ^{22}Na retained in cells or vesicles after substrate addition. (*G*) Substrate-induced $\Delta\psi$ generation in vesicles from *Tv* and (*H*) WT *P. denitrificans* monitored by spectral changes of safranine O (10 μM). A pH 9.2 (*A–D* and *G*), 7.5 (*E* and *H*), and 9.6 (*F* and *H*) reaction medium for "Na^+ transport measurements" was used (*Materials and Methods*). Additions (final concentrations): valinomycin, 0.5 μM (*B*, *D*, *G,* and *H*) or 2 μM (*A* and *G*); protonophores: HQNO, 5 μM (*G*), 25 μM (*B–D* and *G*) or 50 μM (*A*), and CCCP, 38 μM (*A*); monensin, 0.1 μM (*B* and *D*) or 38 μM (*A*); KCN, 1 mM (*B–D*) or 10 mM (*A*); protein of cells, 2.7 mg/mL (*A*), vesicles, 0.7 mg/mL (*B*), 1 mg/mL (*C–F*), 50 μg/mL (*Left*) or 76 μg/mL (*Right*) (*G*), and 50 mg/mL (*H*). Arrows at "0" time show substrate addition: TMPD, 40 μM (*A*, *B*, *G,* and *H*), or 3 mM (*C–F*) in the presence of ascorbate, 3 mM (*B, G,* and *H*) or 10 mM (*A* and *C–F*).

in the *T. versutus* genome (EMBL accession no. HE575403.1) and detected its expression product (Fig. S5 and *SI Text*, section S1; for the enzyme pattern, see Fig. 2*D*), which might operate in this bacterium as a Na^+ pump. Consistent with our hypothesis, *P. denitrificans* AO1 vesicles, which lack all Coxs and displayed no active Na^+ transport (Figs. 2*C* and 3*C*), became capable of

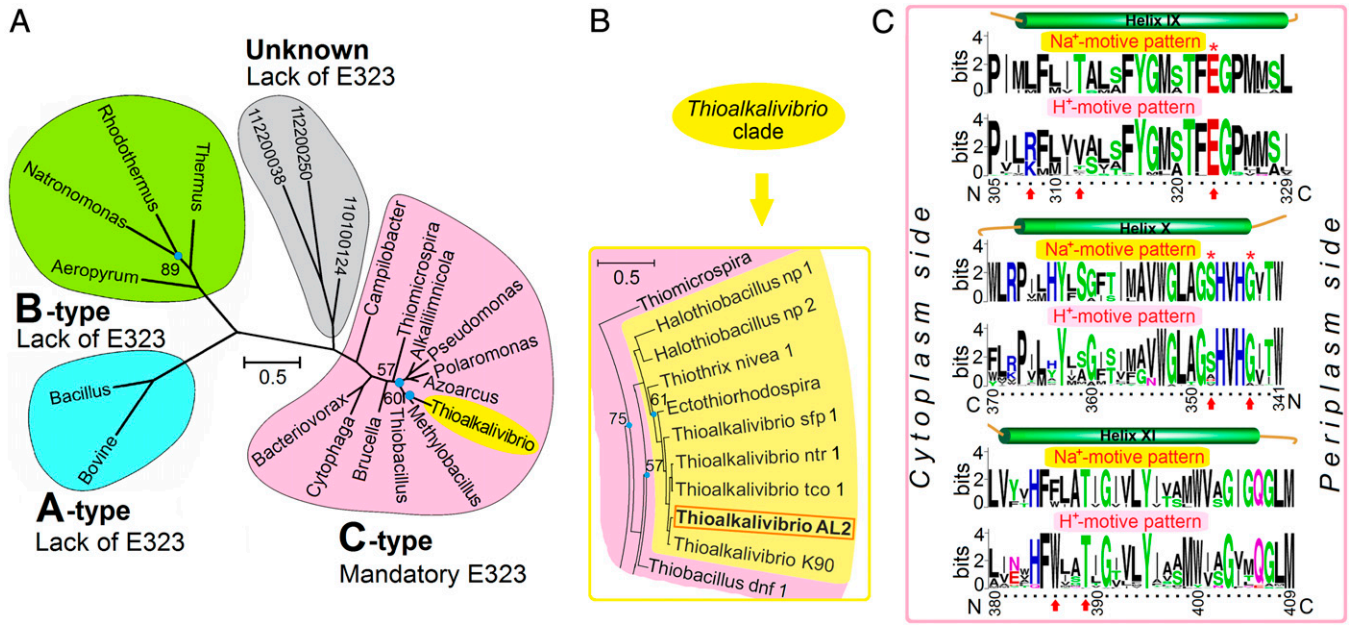

Fig. 4. Phylogenetic relationships of representative Coxs based on catalytic subunit protein sequences (Table S1). (*A*) The brief phylogenetic tree with representative Coxs: A-type (blue), B-type (green), and C-type (pink). *Thioalkalivibrio* clade (yellow, see also *B*) with R(K)308L(M) substitution is inside C-type Coxs. The sequences given in ref. 10 (gray) cluster separately from C-type Coxs (Unknown). E323 is conserved only in the catalytic subunit of C-type Coxs (see *C*); residue numbering corresponds to *P. stutzeri* cbb_3 (here and elsewhere). (*B*) Inset derived from the detailed phylogenetic tree with representative Coxs (Fig. S6); *T. versutus* cbb_3 Scox is orange-contoured. Blue spheres indicate nodes with clade credibility values <90; other nodes have clade credibility values ≥90. (Scale bar: 0.5 substitutions per residue.) (*C*) Amino acid sequences of helices IX–XI of catalytic subunit of C-type Coxs aligned using WebLogo software (23). The upper panels of each pair under an individual α-helix contain representatives of the Na^+-motive-like cbb_3 Coxs (yellow-colored in the C-type cluster); the lower panels contain all other representatives of the C-type cluster that are H^+-motive-like (pink-colored in the C-type cluster). Red arrows show R(K)308L(M) substitution and conservative T312, G344, S348, and T389 in the Na^+-motive-like representatives, E323 conserved in both groups, W386 conserved among H^+-motive-like representatives. Red asterisks in the Na^+-motive template indicate residues forming Na^+ coordination shell (shown in Fig. 5*B*).

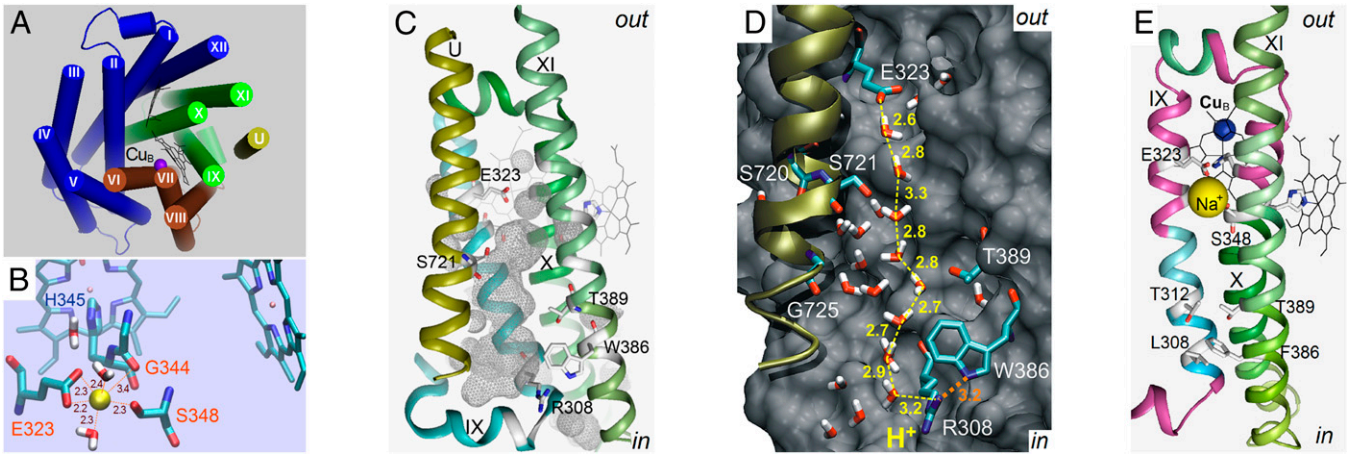

Fig. 5. Structural model of the ion-pumping channel in cbb_3 oxidases. (*A*) Cylindrical helix model of *P. stutzeri* cbb_3 catalytic subunit (ccoN) and α-helix U (olive), viewed from periplasm (PDB ID code 3MK7). Helices VI–VIII (brown) form a "K channel" that conducts H^+ for water production in the active center of all cbb_3 Coxs; helices IX–XI (green) form the proposed Na^+-pumping channel in Na^+-motive cbb_3 Coxs. (*B*) Na^+ (yellow ball)-binding coordination shell in the active center in ccoN of *T. versutus* cbb_3. It involves Glu323, Gly344, Ser348, and two water molecules as evaluated by VMD (27). (*C*) Large cavity (gray network) within α-helices IX–XI (green and cyan) and U (olive) of *P. stutzeri* cbb_3. Helix U, unresolved in the X-ray structure (26), was assigned to the ccoH sequence of *P. stutzeri* cbb_3 (*SI Text*, section S3 and ref. 28) (see also *D*). (*D*) Transient H^+-conducting network predicted at the interface between ccoN and the α-helix U (olive) of H^+-motive *P. stutzeri* cbb_3. (*E*) Assumed Na^+-translocating pathway in *T. versutus* cbb_3; yellow ball marks hydrated Na^+ ion. Regions in α-helices lacking regularity (magenta) were predicted using DisEMBL Predictor (29). Images were made using PyMol (30) (*A*, *C*, and *E*) and VMD (27) (*B* and *D*).

oxidase-driven primary $^{22}Na^+$ pumping (Figs. 2*C* and 3*D*) similar to that of *T. versutus* vesicles (Figs. 2*C* and 3*B*) after expression of *T. versutus* cbb_3. We checked whether the observed $^{22}Na^+$ export from the energized cells and vesicles could be explained by a Δψ-potentiated $^{22}Na^+/Na^+$ exchange or specified by a potential-dependent Na^+ channel. Because dissipation of Δψ by valinomycin, as well as by protonophore (Fig. 3*G*), increased $^{22}Na^+$ export in *T. versutus* vesicles (Fig. 3*B*), a passive Δψ-potentiated $^{22}Na^+/Na^+$ leakage or $^{22}Na^+$ transfer through a Δψ-activated Na^+ channel can be excluded. Consistent with this conclusion is the absence of Δψ-driven $^{22}Na^+$ export in $^{22}Na^+$-loaded WT *P. denitrificans* vesicles that lack *T. versutus* Scox (Fig. 3 *E, F*, and *H*). The data also reveal that *P. denitrificans* aa_3 and cbb_3 Coxs, expressed in the used growth conditions (*Materials and Methods*), do not pump Na^+. Thus, these experiments directly demonstrated that *T. versutus* cbb_3 is a primary Na^+ pump.

The cbb_3 oxidases studied previously were shown to operate as H^+ pumps (7, 19, 24, 25). However, an individual pathway of pumped H^+ analogous to the D channel in A-type Coxs has not been identified (10, 24). Only a K-pathway analog, involved in delivering chemical H^+ to BNC to produce water in Coxs of all types, has been experimentally and structurally (10, 25, 26, 31) defined in C-type Coxs (depicted by brown-colored helices in Fig. 5*A*). Based on these data (10, 33), the K-channel analog in C-type Coxs was proposed to also fulfill the role of the D channel. To localize a possible Na^+-pumping pathway in Scox, we compared Na^+- and H^+-motive structural models. Before comparing the two models, we performed phylogenetic analyses of the C-type Cox protein sequences. Evidently, *T. versutus* Scox clusters with eight other sequences from extremely haloalkaliphilic species deep in the type-C phylogeny, and thus it constitutes the *Thioalkalivibrio* clade (yellow-colored, Fig. 4 *A* and *B*). Taking into consideration such clustering, we divided all protein sequences of the C-type Cox main subunit into two groups for further comparison: yellow-colored *Thioalkalivibrio* clade (including *T. versutus* AL2) and other, pink-colored clades (Fig. 4*C* and Fig. S7). The sequences were compared in view of 3D structure of C-type Cox. Because the catalytic subunit (ccoN) of the two cbb_3 Coxs—Na^+-motive from *T. versutus* and H^+-motive from *P. stutzeri*—are highly similar (69% identity), we modeled the 3D structure of the *T. versutus* subunit based on *P. stutzeri* X-ray data (26). We analyzed in detail the membrane-spanning parts of the model to identify the substitutions that govern ion specificity. Because the "K channel" formed by helices VI–VIII (Fig. 5*A*) does not contain specific substitutions across the cbb_3 cluster (Fig. S7), the "K channel" is not likely to mediate Na^+ pumping. Instead, we found indications of the tentative Na^+-pumping channel located within helices IX–XI in the catalytic subunit of *T. versutus* and of homologs that occupy the same clade: (*i*) a unique substitution, R(K)308L(M), near the cytoplasmic entrance of the tentative Na^+ channel and (*ii*) conservatism of residues T312, G344, S348, and T389 (Fig. 4*C*). Accordingly, we propose that within C-type Coxs these five residues serve as a fingerprint that distinguishes two templates of catalytic subunits: Na^+-motive-like (*Thioalkalivibrio* clade) and H^+-motive-like (all other C-type members). Additionally, W386 seemed to be fully conserved among the H^+-motive-like but not in the Na^+-motive-like C-type members.

Another indication that the Na^+-pumping channel is located within helices IX–XI in the *T. versutus* Scox is provided by the observation that there is a unique conserved, ionizable, membrane-embedded residue, E323, that is found in the middle of helix IX (Fig. 4*C*). This E323 is surrounded by several polar residues that form a Na^+-coordination shell and could function as Na^+ chelators (Fig. 5*B*). In the *R. sphaeroides* H^+-motive cbb_3, the corresponding glutamate (E383) was initially suggested to participate in H^+ pumping (24). However, its functional role in H^+ pumping was challenged later based on the absence of E323 in some putative C-type Coxs (10). To resolve discrepancies about the role of E323, we performed phylogenetic analyses of the C-type Cox sequences used in ref. 10 where the study was limited to sequence-alignment level. We found that the previously assigned C-type Cox sequences that lack E323 do not actually cluster with other C-type enzymes in the phylogenetic tree and form a phylogenetically distinct clade (gray-colored, Fig. 4*A* and Fig. S6), which we tentatively define as a group with unknown function. In our designation, the C-type Cox family covers the sequences from *Campylobacter* to *Bacteriovorax* in the phylogenetic tree (pink and yellow clusters, Fig. 4 *A* and *B* and Fig. S6). Significantly, E323 is fully conserved in these C-type sequences, but it is never present in other Cox types.

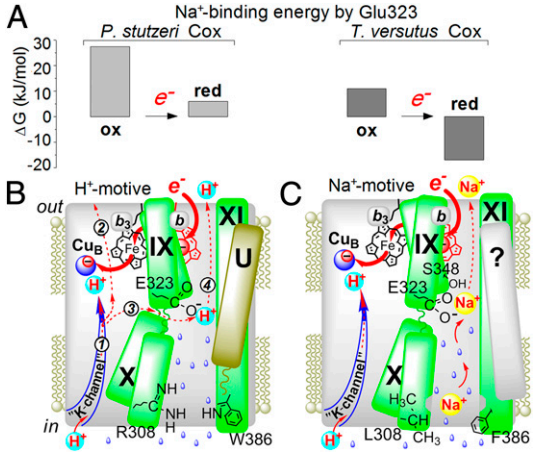

Fig. 6. Putative mechanism of ion translocation by the H^+-motive (*P. stutzeri*) and Na^+-motive (*T. versutus*) cbb_3 Coxs for a single electron transfer. (*A*) Free energy of Na^+ binding by E323 in ccoN of *P. stutzeri* (left) and *T. versutus* cbb_3 (right), estimated by the free energy perturbation method within MD modeling of the complexes in 1 M Na^+ solution (Table S2). (*B*) Combined models of the H^+-pumping channel in the H^+-motive cbb_3 by several hypotheses (circled numbers): *1* (10) + *2* (26) or *1* + *3* (26, 32) + *4* (24). (*C*) Functional model of the sodium pumping in the Na^+-motive cbb_3 (this study) formed by α-helices IX–XI (green) of the catalytic subunit; α-helix (question-marked rectangle) in the Na^+-motive Cox analogous to the auxiliary α-helix U (olive) in the H^+-motive Cox is presumed. In the H^+-motive and Na^+-motive cbb_3 Coxs, a large gray rectangle depicts helices I–VIII and XII: "K channel" (blue) delivers chemical H^+ to the active center to produce water during reduction of O_2.

Notably, helices IX and X of the catalytic subunit of *P. stutzeri* cbb_3 (H^+-motive pattern) as well as of *T. versutus* cbb_3 (Na^+-motive pattern) contain features that disrupt regularity of the helices, conferring flexibility that might be necessary for ion transfer (Fig. 5*E*). Additionally, in *P. stutzeri* cbb_3 the only large cavity seems to be located within helices IX–XI of the main subunit (Fig. 5*C*) and the recently identified auxiliary subunit U (26) (for details, see *SI Text*, section S3). When water-filled, this cavity could link the critical residues R(K)308 and E323, providing a water-filled H^+-translocation pathway (Fig. 5*D*). These facts allow us to assume that in the Na^+-motive cbb_3 such cavity could serve as the Na^+-pumping channel. Finally, we evaluated the Na^+-binding capacity of the H^+-motive and Na^+-motive cbb_3 Coxs using molecular dynamics (MD). MD simulations predicted that the main subunit of *T. versutus*, but not that of *P. stutzeri*, can bind Na^+ in the E323 site in a redox-linked manner (Fig. 6 *A* and *B* and Table S2). According to the prediction, one electron coming into the metal active center switches the enzyme from a Na^+-nonbinding oxidized (ox) state to a Na^+-binding reduced (red) state. Under the tentative model, the subsequent entry of H^+ to the active center via the chemical reaction through the "K channel" results in Na^+ extrusion (Fig. 6*B*). The predicted coupling stoichiometry is one electron for each pumped Na^+, which is consistent with the experimental data (Fig. 2*B* and Fig. S2 *B* and *C*) according to which Scox operation fits in best with the following equation:

$$4\mathrm{cyt}c^{2+} + 4\mathrm{H}^+_{\mathrm{in,chem}} + 4\mathrm{Na}^+_{\mathrm{in,pump}} + \mathrm{O}_2 \rightarrow 4\mathrm{cyt}c^{3+} + 4\mathrm{Na}^+_{\mathrm{out,pump}} + 2\mathrm{H}_2\mathrm{O}.$$

Evidently, the capacity of *T. versutus* Scox to bind Na^+ is provided by the E323-involving Na^+-coordination shell (see Fig. 5*B*), which is absent in *P. stutzeri* Cox due to S348(A) substitution.

The fact that the Na^+-pumping function was revealed among C-type Coxs may shed light on evolution of Coxs. At present, the phylogenomics-based evolutionary scenario of Coxs remains obscure (1, 22, 34). Therefore, in our reasoning we take into consideration several independent markers of possible Cox evolution and generally accepted facts: (*i*) geological evidence on oxygen-free atmosphere on the Earth preceded an oxygen atmosphere (35), (*ii*) close relationship between nitric oxide reductases and C-type Coxs and their far distance from A- and B-type Coxs (1, 36, 37), and (*iii*) the conclusion that Na^+ energetics appeared before H^+ energetics (38). If we believe the mentioned facts and views are true, then C-type Coxs—which include Na^+-motive and H^+-motive representatives—might be the ancestors of H^+-motive A- and B-type Coxs, as assumed earlier (37). C-type Coxs were shown to bind O_2 much more tightly than A-type Coxs (39). Owing to this property C-type Coxs operate under low O_2 conditions and would be the first energy-transducing enzymes capable of oxygen reduction when the early atmosphere of the Earth was formed, being gradually filled with O_2.

Conclusion

We provide the first direct demonstration to our knowledge that the *T. versutus* cytochrome cbb_3 (Cox) is a primary Na^+ pump. This finding is collectively based on the observation of (*i*) specific Na^+ dependence of Cox activity, (*ii*) protonophore- or valinomycin-stimulated Na^+ pumping in *T. versutus* cells and vesicles, (*iii*) no H^+ pumping in them in the presence of valinomycin and reversible alkalinization of the outer space in the presence of protonophore without valinomycin, (*iv*) expression of the *T. versutus* cbb_3 in *P. denitrificans* cells with the result that membranes of this bacterium are competent in protonophore/valinomycin-activated respiration-supported Na^+ pumping, and (*v*) a Na^+-binding coordination shell in the active center of Cox. These results raise the question of whether Na^+ pumping is inherent in some other C-type Coxs. In this context, whether the Na^+ transport in *Vitreoscilla* (40) is evoked by a primary Na^+-pumping *bo*-type quinol oxidase or by a secondary pumping Na^+/H^+ antiporter is still unclear for the lack of ionophore tests after *bo* oxidase expression in *Escherichia coli*, which contains self-Na^+/H^+ antiporters (41) (for details, see *SI Text*, section S2). Our findings are consistent with the hypothesis of using Na^+-motive energy transducers in organisms living under low ΔpH and high salinity (12) and might stimulate further progress in the study of energy-transduction mechanisms of Coxs.

Materials and Methods

Cultivation of bacterial strains, phylogenetic analysis, molecular dynamic simulations, and other methods are detailed in *SI Materials and Methods*.

Bacterial Strains. *T. versutus* AL2 and *P. denitrificans* strain AO1 [expresses no cytochrome *c* oxidase activity (42)] and WT strain (PD 1222) were batch-cultured aerobically as previously described (17, 43).

Membrane Vesicle Isolation. Right-side-out membrane vesicles were isolated from freshly grown cells in a medium containing 50 mM CAPSO-KOH (pH 9.9), 50 mM K_2SO_4, 0.1 M sucrose, 0.1 mM EGTA, and 0.35 M Na_2SO_4 by disruption in a French press cell according to a standard procedure.

Expression of Coxs in *P. denitrificans*. For heterologous expression of *T. versutus* cbb_3 Cox in *P. denitrificans*, the *T. versutus* AL2 *ccoNOQP* operon was identified (HE575403.1) and amplified by PCR. The PCR fragment was cloned into the XbaI-HindIII–digested derivative of the broad host-range plasmid pBBR1MCS (42, 43) to produce the pBBR1/*ccoNOQP* plasmid. For protein expression, the recombinant plasmid pBBR1/*ccoNOQP* was transferred by conjugation into the *Paracoccus* recipient strain AO1. Exogenously expressed *T. versutus* cbb_3 Cox in strain AO1 reached a level comparable to that in *T. versutus* AL2 strain, as monitored using Western blotting. Expression of self-cbb_3 Cox in *P. denitrificans* WT strain grown aerobically (this study) reached the same high level as in semiaerobically grown cells (44), as quantified by real-time quantitative PCR. Each self-Cox level, aa_3 and cbb_3, reached 70 pmol Cox/mg of membrane protein as determined by CO-reduced minus reduced spectra using extinction coefficients of 7 $mM^{-1} \cdot cm^{-1}$

(aa_3, 595–606 nm) (45) and 7.6 $mM^{-1} \cdot cm^{-1}$ (cbb_3, 558–572 nm) (46). Self-Coxs presence was confirmed by the laser-flash photolysis method (47).

Na^+ transport measurements were performed with starved bacterial cells exhausted of endogenous substrates and loaded with $^{22}Na^+$ (PerkinElmer Life Sciences) on ice as reported (48). Membrane vesicles were loaded with $^{22}Na^+$ by passive diffusion (incubation medium: 50 mM CAPSO/TRICINE/Mops-KOH, 50 mM K_2SO_4, 0.1 M sucrose, 0.1 mM EGTA, and 0.6 M Na_2SO_4) at 6 °C overnight. Then $^{22}Na^+$-loaded cells or vesicles were added to the "cold"-Na^+-containing incubation medium and the reaction was started by addition of substrate together with ascorbate (at 22°C). Samples of 25 μL were withdrawn from the incubation mixture at the appointed time and cells or vesicles were separated from the incubation medium by rapid vacuum filtration (1–3 s) through nitrocellulose filters (Millipore). Radioactivity was counted using a liquid scintillation counter (LKB Wallac 1215 RackBeta). Each curve shown in figures is the average of three to eight independent experiments.

Electrical membrane potential generation in right-side-out membrane vesicles was monitored by the safranine method (49) or by tetraphenylphosphonium-selective electrode (50) at 25 °C.

H^+ release in intact cells and membrane vesicles in O_2-pulse experiments was assessed by a standard method (51) in 1 mL of anoxic incubation mixture. Respiration of samples was initiated by addition of water (5–20 μL) saturated with air O_2 at 25 °C. The evoked changes in pH in the incubation mixture were estimated by titration with argon-saturated 0.5 mM H_2SO_4.

Respiratory activity was assessed using a Clark-type electrode at 25 °C.

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