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REVIEW ARTICLE

A CLOSED NINE-STEPPED CYCLE OF PROTON CONDUCTANCE UNIFIES CELLULAR BIOENERGETICS AND SYSTEMIC PHYSIOLOGY

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ABSTRACT

For more than half a century, proton flow in biology has been treated as a partial process confined to mitochondria. Here we describe a closed nine-stepped cycle of proton conductance that completes this picture by uniting intracellular bioenergetics with systemic physiology. The Ambaga Closed 9-Stepped Cycle tracks every proton and electron from food-derived hydrogen through mitochondrial redox reactions, serum buffering, erythrocyte carbonic exchange, and pulmonary - tissue oxygen substitution, returning the same protons to the next metabolic turn. This continuity fulfills complete proton bookkeeping and integrates the chemiosmotic theory of Mitchell, the binding-change model of Boyer, and the ATP-synthase structure of Walker into a single self-consistent system. The cycle predicts measurable redox-potential transitions (alpha,betta, gamma membrane states) and isotopic proton conservation across compartments. These findings establish a unified framework for energy metabolism, oxygen transport, and soft-drug activation, redefining the proton as the central quantized currency of life.

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INTRODUCTION

Energy transformation is the most fundamental and yet incomplete story in biology. While classical bioenergetic theories - Krebs's cycle, Mitchell's chemiosmotic mechanism, and Boyer and Walker's ATPsynthase models - have revolutionized understanding of oxidative phosphorylation, they leave a conceptual gap: the fate of protons and electrons after mitochondrial ATP synthesis remains unclosed. All known metabolic reactions begin with food-derived hydrogen (CHO → NADH, FADH₂), but their proton and electron equivalents are only partly tracked to oxygen reduction. What happens beyond the mitochondrial membrane - how these protons reappear in systemic buffering, oxygen transport, and cellular renewal - has not been explicitly described. The Ambaga Closed 9-Stepped Cycle of Proton Conductance (C9SCPC) was proposed to fill this missing continuity. It represents the first complete proton bookkeeping model, linking the micro-scale of mitochondrial membranes with the macro-scale of erythrocyte and pulmonary exchange. Each of its nine stages corresponds to an experimentally traceable process governed by membrane redox potential and electrophile - nucleophile complementarity. The C9SCPC asserts that life operates as a closed quantum-biological circuit in which protons and electrons circulate without loss:

- Originating from food molecules
- Transformed through enzymatic and redox potentials
- Equilibrated through bicarbonate buffering and hemoglobin chemistry
- Re-absorbed through oxygen uptake

And returned to mitochondria to begin the next cycle. This closed continuity restores thermodynamic and stoichiometric balance to biological energy accounting and offers a system-wide understanding of oxygen-dependent metabolism.

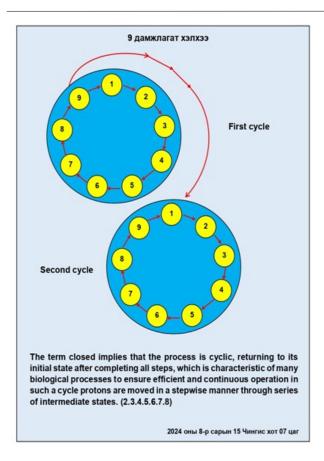
METHODS AND DATA

We used the Model validation, membrane redox potential imaging, Data visualizations.

RESULTS

The chemiosmotic theory (Mitchell, 1961) introduced the concept that a transmembrane proton gradient drives ATP formation. Yet this theory treated proton flow as open-from matrix to intermembrane space - without considering the systemic return path.

Boyer's binding-change model (1977) and Walker's structural elucidation (1997) explained the conformational mechanics of ATP synthase but similarly remained within mitochondrial boundaries. In contrast, the our cycle expands proton dynamics into nine stages that together form a continuous loop, transforming an open, local model into a closed, global system. This extension aligns mitochondrial, serum, erythrocytic, pulmonary, and tissue processes into a single quantitative equation:



Three Versions of the Closed 9-Stepped Cycle of Proton Conductance

Version 1 – Fully Detailed Version (Each Stage Shown Separately)

Food \rightarrow Donor (CHO) and Metabolic Intermediates. Carbohydrates, fats, and amino acids are broken down into acetyl-CoA and Krebs cycle intermediates. Hydrogen Atom Splitting (NADH, FADH2 Formation). Protons (H $^+$) and electrons (e $^-$) are released from hydrogen atoms through NADH/FADH2 formation.

- Nutrients are transformed into hydrogen-carrying molecules (NADH, FADH₂).
- Mitochondrial Electron-Proton Separation
- Electrons move along the respiratory chain; protons are pumped to form the gradient.
- Energy Conversion (ATP + Heat + Water)
- Proton return through ATP synthase produces ATP and heat.
- CO2 Transport and Blood Buffering
- CO₂ leaves mitochondria → forms HCO₃⁻ in serum → transported via erythrocytes.
- Systemic Oxygen Exchange
- O₂ uptake (lungs) and O₂ release (tissues) complete the closed proton-electron loop.

Version 3 – Integrated / Condensed Systemic Model

- Stages 1–5: Cellular / Mitochondrial Energy Production (Food → ATP → CO₂ + H₂O)
- Stages 6–7: Systemic CO₂ Conversion and Buffering (Carbonic Anhydrase + Hamburger Shift)
- Stages 8–9: Oxygen Exchange (O₂ Uptake + O₂ Release)

These three domains form one Closed Proton Conductance Cycle linking food, mitochondria, blood buffering, and oxygen exchange as a continuous system of energy and life.

Relation to Quantum Biology: Within this model, the Membrane Redox Potential Three-State Line System (α, β, γ) regulates proton conductance quantum-mechanically.

 $\alpha ext{-State:}$ electrophilic; promotes oxygen attraction and water formation.

 β -State: nucleophilic; supports electron donation and proton pumping.

γ-State: transitional equilibrium; acts as a synchronizer between α and β .

Philosophical and Methodological Context: Following Karl Popper's falsification principle, the Ambaga Cycle is not assumed true but tested by its failure to be disproved. If isotopic and redox experiments cannot break the predicted closure of proton bookkeeping, the cycle stands as a verified natural law. Moreover, the C9SCPC integrates classical and modern frameworks:

Stage	Compartment	Key Process	Equivalent Phenomenon
1-5	Mitochondria	Donor oxidation → Membrane redox potential → ATP + Heat	Chemiosmotic + ATP synthase (Mitchell - Boyer -
		$+ H_2O + CO_2$	Walker)
6	Mitochondria → Serum	$CO_2 + H_2O \leftrightarrow H_2CO_3 \rightarrow H^+ + HCO_3^-$	Carbonic anhydrase buffering
7	Serum ↔ Erythrocyte	H ⁺ binds Hb; HCO ₃ ⁻ exchange	Hamburger shift
8	Lung capillary	O2 uptake via electrophilic substitution	Bohr/Haldane effects
9	Tissue capillary	O ₂ release via nucleophilic substitution	Proton return to mitochondrial donors

Electron Transfer Chain Initiation. Electrons enter the mitochondrial inner membrane electron transport system, creating a proton gradient. Proton Pumping to the Intermembrane Space. Electrons reduce cytochrome complexes, while protons are pumped outward, building membrane potential. ATP and Heat Formation (Ambaga Equation Fulfilled). ADP + Pi + O₂ + H $^+$ \rightarrow ATP + Heat + CO₂ + H₂O + Matrix H $^+$ - energy is synthesized and balanced. CO₂ and Metabolic Water Exit from Mitochondria. CO₂ diffuses out and reacts with water under carbonic anhydrase to form carbonic acid (H₂CO₃).

Bicarbonate Formation and Hamburger Shift. H_2CO_3 dissociates into H^+ and HCO_3^- ; bicarbonate moves into erythrocytes to maintain charge balance. Oxygen Uptake at Pulmonary Capillaries (Electrophilic Substitution). Oxygen binds Fe^{2+} in hemoglobin through electrophilic substitution at the lung–blood interface. Oxygen Release at Tissue Capillaries (Nucleophilic Substitution). Protons and CO_2 act as nucleophiles to release O_2 from hemoglobin; O_2 enters mitochondria to restart the next cycle.

Version 2 - Simplified Functional Representation

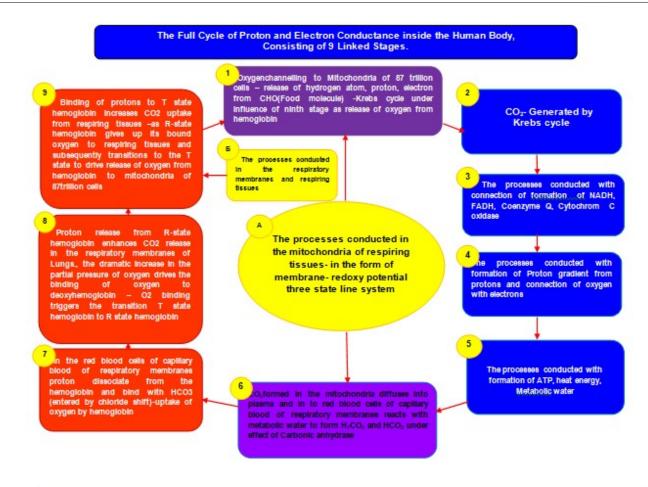
Food Breakdown → Electron and Proton Donors

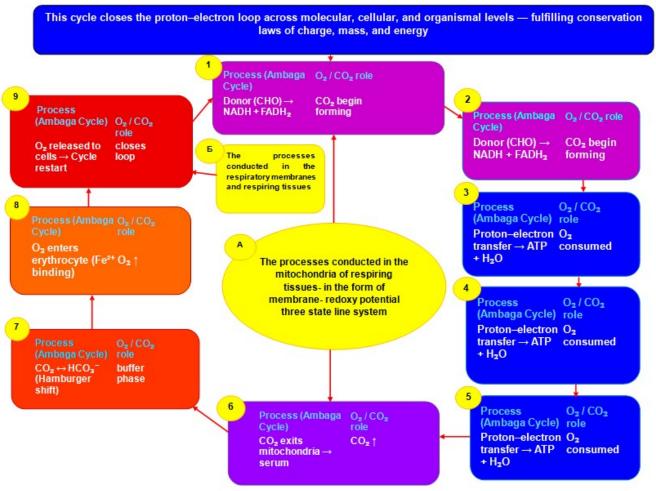
- Krebs Cycle: substrate oxidation (Stages 1–2).
- Mitchell: chemiosmotic proton gradient (Stages 3–5).
- Boyer/Walker: ATP formation mechanism (Stage 5).
- Ambaga: systemic proton return (Stages 6–9).

Thus, Ambaga's discovery does not reject earlier models; it fulfills them by providing closure and continuity across scales.

DISCUSSION

Quantitative proton bookkeeping: every proton released in Stage 2 reappears in Stage 9. Redox potential regulation: three-state membrane system governs α (electrophilic), β (nucleophilic), γ (equilibrium) transitions. Integration: situates Mitchell, Boyer, Walker, Lane theories as open segments within Ambaga's closed system. Pharmacological implications: activation of soft drugs within the same proton cycle. The Ambaga Closed 9-Stepped Cycle fulfills proton - electron conservation from molecule to organism. Provides the long-missing closure uniting biochemistry, physiology, and





quantum bioenergetics. Offers a new metric for evaluating metabolism, disease, and drug action. Defines proton-based unification of chemistry and biology. May serve as framework for next-generation pharmacology (AmbagaBiotargeting). Opens a "Tree of Proton-Dependent Theories" ending in systemic closure.

Summarize the key novelty: Classical bioenergetics accounts for partial proton flow (up to mitochondrial chemiosmosis). The Ambaga model completes proton bookkeeping, linking mitochondrial, erythrocytic, and systemic oxygen exchange. Demonstrates continuity of proton–electron dynamics through nine linked stages, each experimentally traceable. Integrates Mitchell, Boyer, and Walker theories within a closed, conservative system. Predicts measurable physiological variables (pH buffering, O2/CO2 exchange ratios, isotopic H+ tracing). Implications: fundamental for metabolism, pharmacology, and biomedicine.

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