Toward a Topology-Gated Photonic-Redox Control Plane

A testable ceLLM hypothesis linking mitochondrial DNA topology, ultra-weak photon emission, and cellular state inference

Hypothesis manuscript draft | Prepared from source materials supplied by John Coates (RF Safe) and expanded into a literature-grounded, experimentally falsifiable framework.

Prepared for scientific discussion, critique, and collaborative experimental design.

Working thesis. This manuscript argues that the strongest version of the mtDNA-biophoton idea is not a lone-DNA antenna model, but a nested photonic-redox control plane that is experimentally falsifiable.

Suggested short title: Topology-gated photonic-redox control plane

Abstract

Ultra-weak photon emission (UPE) from living systems is an established biophysical phenomenon arising largely from oxidative metabolism and reactive oxygen species (ROS), yet its functional role in cellular signaling remains unresolved [2,5]. Mitochondria are both major generators of UPE and central integrators of redox, calcium, membrane-potential, and transcriptional signals [2,6-8]. Here we extend the original mtDNA-resonance idea into a broader, more biologically plausible framework. Cells may implement a topology-gated photonic-redox control plane in which mitochondrial redox chemistry generates structured optical and electromagnetic fluctuations. In this model, mtDNA topology, TFAM-dependent nucleoid organization, and the local hydration shell act as a transducer layer, while cytoskeletal aromatic networks, mitochondrial reticula, and nanotunnels route or stabilize local state propagation. Organelle contact sites amplify weak perturbations into Ca2+, membrane-potential, and retrograde signaling events, while condensates plus transcriptional programs store the resulting update to cellular state [2,6-25]. Within the cellular Latent Learning Model (ceLLM), these processes are interpreted as a multiscale state-inference architecture rather than literal transformer-like computation. Human mtDNA provides useful dimensional heuristics for experimental design: a 16,569-bp circular genome has a contour length of about 5.633 μm, a relaxed-circle diameter of about 1.79 μm, and is typically packaged into nucleoids near 100 nm, mapping to free-space guideposts near 53 THz, 167 THz, and 3 PHz, respectively [1,9-15]. These values are not asserted as classical in vivo antenna resonances inside hydrated organelles; instead, they define physically motivated search windows for testing whether geometry and topology modulate mitochondrial sensitivity to narrow-band optical or terahertz perturbations [8,14,15]. The paper reframes the central question from same-frequency resonance to cross-scale frequency conversion: optical excited-state chemistry may be converted at hydrated DNA-protein and membrane interfaces into lower-frequency electrochemical envelopes that cells can amplify, integrate, and remember. We present falsifiable predictions and a concrete experimental program spanning TFAM and topoisomerase perturbation, rho0 depletion and rescue, quartz-versus-glass optical isolation, narrow-band THz exposures with thermal controls and Ca2+ uptake blockade, cytoskeletal perturbation, MERC disruption, and spectral-entropy analysis of photon bursts. If supported, the framework would not merely rehabilitate a biophoton-signaling hypothesis; it would define a new systems-biology problem at the intersection of mitochondrial organization, redox physics, intracellular communication, and cellular decision-making.

Keywords: mitochondrial DNA; biophotons; ultra-weak photon emission; terahertz; nucleoid topology; TFAM; ceLLM; mitochondria-ER contact sites; cytoskeleton; redox signaling

Box 1. A disciplined map of what is known, what is proposed, and what would most directly falsify the model.

What is established	What is proposed here	What would most directly falsify it
• UPE exists and is tightly linked to oxidative metabolism. • Mitochondria are major UPE sources and signaling hubs. • mtDNA is circular, topological, TFAM-packaged, and structurally heterogeneous. • MERCs, retrograde signaling, actin dynamics, and mitochondrial subnetworks are real control layers.	• mtDNA topology plus its hydration shell acts as a geometry-sensitive transducer. • Weak optical events are converted into lower-frequency electrochemical envelopes. • Cells implement a nested photonic-redox control plane rather than a lone-DNA antenna.	• No shift in optical / THz sensitivity after TFAM or topology perturbation. • No dependence on mtDNA abundance or organization in rho0/rescue designs. • No added predictive value from structured UPE variables beyond standard redox readouts.

1. Introduction

A century after Gurwitsch proposed that dividing tissues might exchange ultraviolet signals, the existence of ultra-weak photon emission from living systems is no longer the main controversy; the unresolved question is whether any biologically useful information is embedded in those emissions, and if so how cells could physically

transduce it [2-6]. UPE is now widely interpreted as a consequence of oxidative chemistry, especially excited species generated during ROS-producing metabolism. That baseline interpretation is important because it keeps the problem anchored to known chemistry rather than mysticism. At the same time, it leaves open a serious systems question: whether metabolic light is merely waste, or whether evolution exploited it as a state variable in already existing signaling architectures.

Mitochondria are the natural place to ask that question. They generate and respond to redox signals, shape calcium microdomains, regulate membrane potential, communicate with the nucleus, form extended subnetworks, and sit at the center of many cell-fate decisions. They are also major sources of UPE and have shown both light-responsive behavior in isolated preparations and frequency-selective responses to narrow-band terahertz irradiation [2,6-8]. A framework that links mitochondrial organization to weak optical signaling therefore has a plausible empirical foothold, even if the stronger historical claims about coherence or long-range photonic control remain unsettled [4,5].

The original mtDNA-antenna formulation is valuable because it treats mitochondrial DNA not only as a sequence archive but as a physical object with contour, circularity, topology, packaging, and hydration. Those properties matter. Human mtDNA is a 16,569-bp circular genome [1]. Its contour length is about 5.633 μm, its relaxed-circle diameter is about 1.79 μm, and in mammalian cells it is usually compacted into TFAM-organized nucleoids near 100 nm that vary in accessibility and activity [9-13]. The key correction made here is that these are not grounds to claim a literal classical loop antenna operating inside a water-rich organelle. They are grounds to ask a sharper question: can mtDNA geometry and topology change how mitochondria couple to the local optical, terahertz, and electrochemical microenvironment?

To make that question publishable and testable, this paper broadens the scope from mtDNA alone to a topology-gated photonic-redox control plane. In this framework, mtDNA remains central, but as one transducer layer embedded in a richer architecture that includes ETC chromophores, hydration-shell physics, cytoskeletal aromatic networks, mitochondrial reticula, organelle contact sites, and slower transcriptional memory. The ceLLM concept is used here as a systems metaphor for cellular state inference: cells integrate fast variables and slower structural priors to update state, rather than responding as purely local chemical switches. The aim is not to declare a paradigm shift by rhetoric. The aim is to define a coherent hypothesis that can be broken by experiment.

2. Empirical foundation

2.1. UPE is real; the signaling question is still open

UPE is experimentally well established. Modern reviews describe it as a low-intensity broadband emission spanning approximately ultraviolet to near-infrared wavelengths and arising from electronically excited species generated during oxidative metabolism and stress [2,5]. Claims that all UPE is coherent or laser-like remain unsupported by the strongest critical reviews [5], but the existence of the emission itself is not in doubt. That matters because a candidate signaling variable does not need to be perfectly coherent in order to be biologically sampled; it only needs to covary with internal state strongly enough that a cell can integrate it with other channels.

Mitochondria are unusually well positioned to generate such variables. Oxidative phosphorylation produces ROS, excited carbonyls, singlet oxygen, redox oscillations, and membrane-potential fluctuations in a physically confined geometry. Recent isolated-mitochondria experiments suggest that mitochondria can influence one another in non-chemical ways that depend on shielding and ambient-light conditions [6]. Separate photobiomodulation work shows that isolated mitochondria respond directly to 810-nm light [7]. Most strikingly, a 2026 ACS Nano study reported a frequency-selective terahertz effect in which 34.5 THz irradiation promoted mitochondrial biogenesis via calcium influx and the PGC-1alpha-NRF1/2-TFAM axis, whereas a nearby tested

frequency did not produce the same effect [8]. None of these findings proves photonic computation. Together, however, they justify a serious search for topology-sensitive mitochondrial coupling mechanisms.

The detected external UPE intensity is extremely low, which is precisely why the signaling question remains open [2,5]. External counts, however, need not equal local intramitochondrial flux, because many emitted photons may be reabsorbed or scattered before they escape the cell; that possibility remains a plausible inference rather than a settled measurement. In this regime the relevant question is not whether a single photon triggers a deterministic switch, but whether structured fluctuations in burst timing, spectral mix, or entropy bias an already noisy redox/Ca2+ decision landscape. That is the regime in which stochastic resonance becomes physically relevant: in nonlinear threshold systems, added noise can improve detection of weak signals rather than merely degrade it [30]. The present model therefore relies on downstream amplification at contact sites, mitochondrial network junctions, and retrograde pathways rather than on a high-fidelity optical command channel. Hydration-shell dynamics and biomolecular-condensate phase transitions may provide one route across the timescale gap by trapping ultrafast optical or THz perturbations into longer-lived conformational or electrochemical states that millisecond calcium machinery and slower transcriptional programs can sample [14,15,21].

2.2. mtDNA geometry and nucleoid organization provide a physically meaningful substrate

mtDNA itself is not static packaging. Super-resolution work showed that mammalian nucleoids are relatively uniform in size and often contain a single mtDNA molecule [9]. Subsequent studies showed that only a minority of nucleoids are transcriptionally or replicatively active at a given moment, and that inactivity correlates with high TFAM-to-mtDNA ratios consistent with stronger compaction [10]. More recent structural work found that single-nucleoid architecture is heterogeneous rather than monolithic [11], while mechanistic studies demonstrated sequence-specific DNA bending in TFAM-mediated packaging and transcription initiation [12]. Topology control by mitochondrial topoisomerases provides yet another layer of physical regulation [13]. In other words, the mtDNA system already behaves like a tunable structural state variable before any photonic hypothesis is imposed on it.

Hydration adds an underappreciated physical bridge. Terahertz spectroscopy studies show that the DNA hydration shell differs measurably from bulk water [14], while long-range DNA-water interaction studies indicate that hydrated DNA supports low-frequency collective modes sensitive to temperature and hydration state [15]. This does not demonstrate information-bearing resonance. It does suggest that the relevant coupling problem is not simply a bare DNA loop in vacuum. The physically interesting object is the DNA-protein-water interface, where excited-state chemistry, local field fluctuations, and structural dynamics coexist.

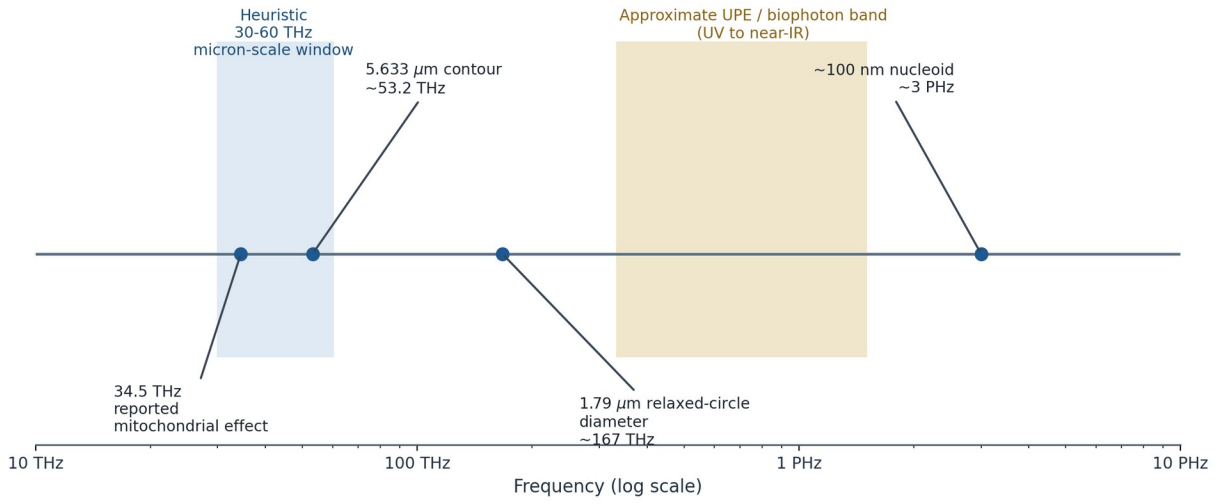

Figure 1. Multiscale frequency markers derived from human mtDNA geometry. The plotted values are dimensional guideposts only: a 5.633 μm contour maps to about 53.2 THz, a 1.79 μm relaxed-circle diameter to about 167 THz, and a 100

nm nucleoid scale to about 3 PHz. The shaded 30-60 THz band highlights the micron-scale window emphasized in the original engineering argument, while the broad UPE band spans the approximate UV-to-near-IR range reported in the biophoton literature. These are not asserted as classical in vivo resonant peaks.

2.3. Candidate routing and amplification layers already exist in mainstream cell biology

The intracellular context also offers credible routing and amplification partners. Electronic energy migration has been measured in microtubules over a scale comparable to a tubulin dimer [16], and ultraviolet superradiance has been proposed and experimentally probed in large tryptophan-rich biological architectures including tubulin systems [17]. These findings do not prove long-range optical waveguiding inside cells, but they make aromatic cytoskeletal networks plausible short-range relays or sinks for optical excitation. Actin, meanwhile, appears particularly important as a state-distribution system: an interphase actin wave has been shown to promote mitochondrial content mixing, maintain polarization and oxygen consumption, and suppress excess ROS [18]. That makes actin a powerful candidate for converting local optical-redox perturbations into spatially distributed mitochondrial state changes.

Finally, mitochondria already participate in established mesoscale signaling networks. Mitochondria-ER contact sites regulate exchange, calcium coupling, redox homeostasis, and metabolic transitions [19]. Mitochondria also form sites of contact with the nucleus that help organize retrograde signaling [20]. In muscle, the mitochondrial reticulum behaves like a subcellular energy-distribution network [22], and nanotunnels may provide another route for inter-mitochondrial interaction under constrained motility [23]. Beyond the single cell, connexin-43-associated contacts and other mechanisms can support intercellular mitochondrial transfer [24]. Even biomolecular condensates have been shown to reshape electrochemical equilibria and membrane-associated state variables [21]. These observations together motivate a layered framework in which weak optical events need not carry the full signaling burden themselves; they may simply bias, trigger, or synchronize networks that already have powerful classical amplifiers.

Table 1. Empirical status of the major components used in the hypothesis.

Component	Status	Role in this model	Key uncertainty
UPE from living cells	Strong	Fast optical/redox state variable	Whether UPE is ever functional rather than byproduct
Mitochondria as major UPE sources	Moderate to strong	Primary emitter and integrator	Relative contribution by context and cell type
Circular mtDNA and nucleoid organization	Strong	Physical substrate for topology-sensitive transduction	How geometry couples in hydrated organelles
TFAM compaction affects nucleoid activity	Strong	Slow prior controlling transducer state	Exact coupling between compaction and field sensitivity
Narrow-band THz mitochondrial effects	Moderate	Experimental foothold for frequency selectivity	Whether mtDNA is the critical mediator
Microtubule energy migration / aromatic networks	Moderate	Possible short-range routing or excitonic relay	Distance, specificity, and biological relevance in vivo
Actin-dependent mitochondrial mixing	Strong	Spatial distribution of local perturbations	Whether it carries optical-state information specifically
MERCs / NAMs / retrograde signaling	Strong	Classical amplification layer	Which hubs are necessary for any optical leg

Component	Status	Role in this model	Key uncertainty
Condensate electrochemistry	Emerging	Memory / persistence layer	Extent of generalization to mammalian mitochondrial signaling
Intercellular mitochondrial transfer / Cx43 contacts	Moderate	Hybrid amplifier across cells	When direct hardware exchange dominates over optical leakage
Large-scale UPE coherence claims	Weak / disputed	Not required by core model	Whether any nonclassical statistics survive rigorous testing

3. Hypothesis: from lone antenna to control plane

The central claim of this paper is therefore narrower, stronger, and more testable than a literal loop-antenna narrative. The claim is that mitochondrial redox chemistry generates structured optical and electromagnetic microfluctuations; that mtDNA topology, TFAM-dependent nucleoid organization, and the local hydration shell form a topology-gated transducer layer sensitive to those fluctuations; and that downstream mitochondrial and cellular signaling networks amplify the resulting perturbations into stable state updates.

This model is easiest to understand in layers. The source layer is conventional mitochondrial biophysics: ETC activity, ROS production, excited-state chemistry, membrane-potential oscillation, and UPE generation [2,6-8]. The transducer layer is the mtDNA-nucleoid complex, including circular geometry, supercoiling and topological control, TFAM compaction, DNA bending, and the hydration shell [1,9-15]. The routing layer includes candidate short-range relays such as microtubules, actin-dependent mitochondrial rearrangement, mitochondrial reticula, and nanotunnels [16-18,22,23]. The amplification layer includes MERCs, calcium microdomains, membrane-potential changes, and retrograde signaling to the nucleus [19,20]. The memory layer includes condensate state, transcriptional reprogramming, nucleoid accessibility, and other slow variables that preserve the consequences of brief perturbations [10-12,21].

Within this architecture, the most plausible physics is not same-frequency resonance across all components. A more interesting possibility is cross-scale frequency conversion. Optical excited-state chemistry may be converted at hydrated DNA-protein and membrane interfaces into lower-frequency structural or electrochemical envelopes, which then propagate through calcium, redox, and membrane-potential networks. One plausible bridge is non-radiative relaxation: optically excited states produced by ROS chemistry can dump energy through internal conversion and vibrational energy redistribution into low-frequency collective modes and solvent-coupled phonons in the THz band, providing a candidate route from UV/visible UPE chemistry to THz-scale structural dynamics [14,15,33]. In engineering language, the cell may behave less like a narrowband radio and more like a heterogeneous mixer, envelope detector, and adaptive controller. This shift in framing resolves an apparent mismatch. Measured UPE often occupies UV-visible-near-IR ranges, whereas mtDNA contour and relaxed-circle heuristics point to lower THz-to-far-IR windows. The mismatch may itself be the clue if biological function depends on transduction between scales rather than direct one-band resonance.

The dimensional heuristics still matter. Taking human mtDNA as a circular object with contour length 5.633 μm gives a free-space guidepost near 53.2 THz. Treating the relaxed circle diameter as 1.79 μm gives a guidepost near 167 THz. Nucleoid compaction near 100 nm maps to around 3 PHz [1,9-15]. In hydrated organelles these values will shift, broaden, and damp. They are useful not as claims of in vivo resonant peaks but as experimental search windows, especially in light of the reported 34.5 THz mitochondrial effect [8]. A serious program would ask whether perturbing nucleoid compaction, topology, or mtDNA abundance shifts the sensitivity of mitochondrial readouts within or near those windows.

The ceLLM language offers a disciplined systems interpretation. Let x_t denote the latent cellular state at time t. Let r_t encode redox variables, p_t encode structured photon variables such as spectral mix and burst entropy, c_t encode calcium and membrane-potential variables, and g_t encode slowly varying genomic or topological priors such as nucleoid compaction, contact-site density, and condensate organization. The update $x_{t+1} = F(x_t, r_t, p_t, c_t, g_t)$ need not be computationally exotic. It simply states that cells update state by integrating fast fluctuating inputs through slower structural constraints. In that sense, ceLLM is a language for probabilistic state integration, not a claim that cells implement software large language models.

Figure 2. Proposed topology-gated photonic-redox control plane

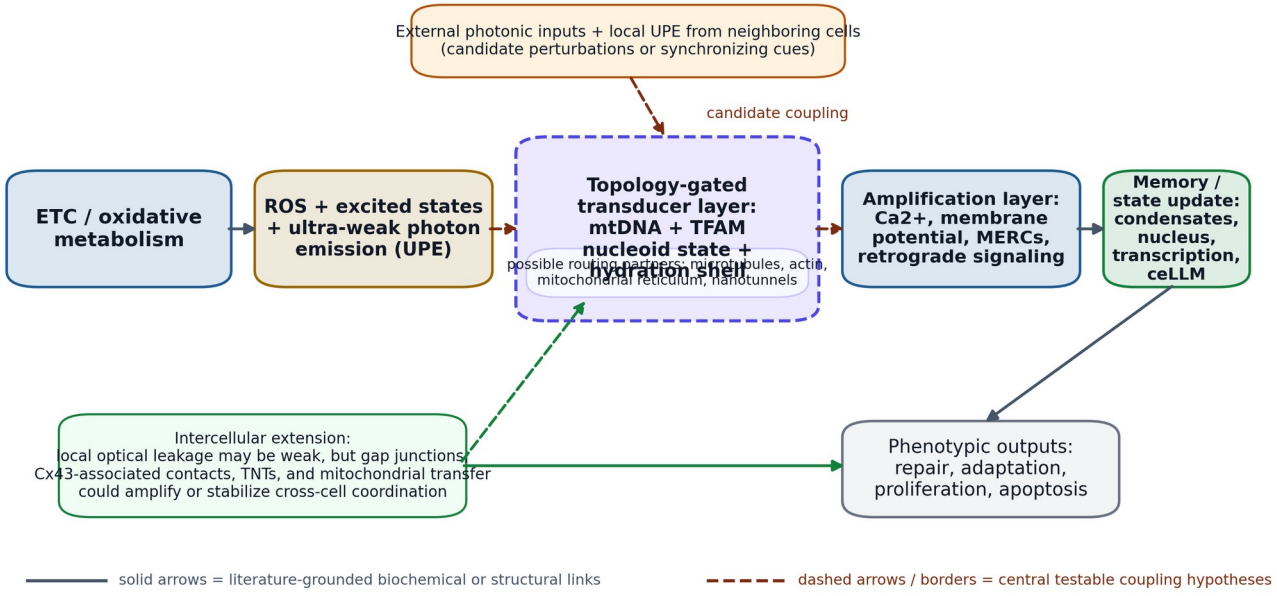

Figure 2. Proposed topology-gated photonic-redox control plane. Solid arrows indicate links already grounded in mitochondrial, contact-site, and transcriptional biology. Dashed borders and arrows mark the central hypothesis tested here: mtDNA topology, TFAM-dependent nucleoid state, and the local hydration shell may form a geometry-sensitive transducer layer that samples weak optical or terahertz-scale perturbations and feeds them into stronger classical amplifiers.

This framing also places the hypothesis inside current bioelectricity research rather than outside it. Emmons-Bell et al. showed that transient gap-junctional blockade in planaria can stochastically induce species-specific head morphologies that persist for weeks before remodeling back toward the native state, illustrating how fast membrane-level perturbations can be transduced into longer-lived (yet still reversible) morphological memory without changes in DNA sequence [35]. Likewise, depolarization of resting membrane potential is increasingly treated not merely as a downstream consequence of oncogenic transformation but as an instructive bioelectric variable that can regulate proliferation, migration, and metastatic state switching [36,37]. In that light, the proposed mitochondrial control plane is not meant to replace classical bioelectric circuits. It offers a candidate subcellular mechanism by which fast photonic-redox fluctuations could bias the distributed electrochemical envelopes that cells already use as actionable summaries of internal state.

4. Intercellular extension and relation to circadian / photobiomodulation narratives

The model also suggests a restrained but important intercellular extension. A pure free-space biophoton-communication thesis is physically difficult because photon counts are low and tissue environments are lossy. A hybrid network is more plausible. Local UPE may provide synchronization, directional bias, or state leakage over short distances, while gap junctions, calcium waves, direct contacts, tunneling nanotubes, and mitochondrial transfer amplify or stabilize the effect [6,19,20,24]. In this reading, Gurwitsch's onion-root experiments become

historically provocative but not dispositive: they motivate the search for an optical leg in cell-cell communication without proving the modern mechanism.

This hybrid framing also helps place the model alongside established external-light pathways rather than against them. In mammals, circadian photoentrainment is initiated primarily by retinal photoreceptors, especially melanopsin-containing intrinsically photosensitive retinal ganglion cells, while cryptochromes remain core clock flavoproteins and blue-light photoreceptors in other taxa [27,28]. Likewise, photobiomodulation literature often treats cytochrome c oxidase as a principal mitochondrial photoacceptor, or at minimum a central node, for red/near-IR responses [7,29].

The present framework operates at a different scale and with different inputs. It asks how endogenous ultra-weak photon emission generated by mitochondrial ROS chemistry might be sampled by the nucleoid-cristae-cytoskeletal architecture inside the organelle and then amplified into redox, Ca2+, membrane-potential, and transcriptional updates. In that sense, mitochondria are not merely ATP factories; they are dynamic sensors and integrators. External photons and internally generated UPE need not be rival stories; they may converge on the same mitochondrial control plane.

Brown adipose tissue, for example, need not possess a unique signaling chemistry for its putative 'biophoton' role. Its heightened thermogenesis may simply raise ROS-linked photon output and thereby increase local coupling opportunities within the same general architecture.

5. Falsifiable predictions and experimental program

A credible hypothesis paper must make itself vulnerable. The present model can be falsified, narrowed, or strengthened by a focused experimental program that distinguishes source, transducer, routing, amplification, and memory layers.

First, topology dependence should be tested directly. TFAM overexpression, TFAM depletion, and topoisomerase perturbation should alter nucleoid compaction or topology without necessarily abolishing respiration outright [10-13]. If the model is correct, such perturbations should shift the relationship between optical or terahertz input and mitochondrial readouts such as ROS, membrane potential, calcium handling, and transcriptional activation. A null result across well-controlled perturbations would weigh against the transducer claim.

Second, mtDNA itself should be made experimentally dispensable and then restored. rho0 or mtDNA-depleted systems, followed by rescue where feasible, can test whether the candidate coupling layer depends on mtDNA abundance or organization rather than only on membranes and canonical photoacceptors. If narrow-band or optical effects survive complete loss of mtDNA with unchanged magnitude and structure, the strongest version of the mtDNA-centered hypothesis would fail; such persistence would instead implicate alternative chromophores such as flavins, porphyrins, or cytochrome c oxidase [29,31].

Third, routing candidates should be separated from sources. Microtubule perturbation and actin perturbation should be combined with simultaneous imaging of UPE, ROS, calcium, membrane potential, and mitochondrial morphology [16-18]. The key question is not merely whether the cytoskeleton changes emission intensity, but whether it changes propagation, anisotropy, synchronization, or the spatial spread of downstream state changes. A routing role predicts altered correlation structure even when mean emission changes are modest.

Fourth, amplification hubs should be attacked. MERC disruption, altered calcium-handling proteins, and perturbation of retrograde signaling should test whether any weak optical coupling requires classical organelle-contact amplification to become functionally relevant [19,20]. If disrupting amplification abolishes a candidate effect while source emission persists, the theory gains a mechanistic foothold: photons may bias a control plane whose biological meaning is created downstream by established signaling circuits.

Fifth, the known 34.5 THz mitochondrial-biogenesis result provides a ready-made frequency window to separate transducer from amplification layers. Co-application of targeted mitochondrial Ca2+ uptake inhibitors - for example Ruthenium Red, Ru360, or MCU inhibitors such as DS16570511 - during narrow-band THz exposure should abolish downstream PGC-1alpha-NRF1/2-TFAM induction and biogenesis if the effect requires the Ca2+ amplification node [8,32]. If the topology-gated transducer hypothesis is correct, the same Ca2+ blockade should leave any upstream changes in UPE statistics or nucleoid-localized coupling intact, whereas TFAM or topoisomerase perturbation should shift the THz sensitivity window even when Ca2+ influx is permitted. This experiment directly leverages existing mechanistic detail and creates a clean double dissociation between amplification and transducer layers.

Sixth, intercellular optical claims should be forced into competition with classical explanations. Quartz-versus-glass or other optical-isolation assays should be paired with chemical diffusion controls, optical shielding, gap-junction blockade, TNT inhibition, and Cx43 perturbation [3,6,24]. A hybrid-network hypothesis predicts partial separability: some effects should survive chemical isolation and depend on optical transmission, whereas others should disappear when classical contact-mediated amplification is disabled.

Seventh, signal structure should be tested against simple intensity metrics. UPE research often reduces measurements to photon counts, but a control-plane model predicts that burst timing, spectral composition, entropy, and cross-correlation with ROS or calcium events may outperform raw counts as predictors of state transitions [2,25]. The decisive question is whether mtDNA-nucleoid variables - topology, TFAM compaction, hydration-shell state, or their perturbation history - add predictive power beyond standard redox, Ca2+, and membrane-potential readouts. If TFAM or topoisomerase perturbation shifts the relationship between structured UPE variables or narrow-band THz input and downstream state transitions while respiration and bulk ROS remain controlled, the topology-gated transducer claim gains support. If no such shift occurs, the model narrows toward a simpler redox/membrane-only mechanism. This is where AI-enabled analysis can contribute immediately: state-space models, sequence models, and graph-temporal models can determine whether structured photon variables plus topology state improve prediction beyond conventional metabolic measurements.

Finally, the computational program should run in parallel with wet-lab work. Multiscale electrodynamic and molecular simulations can bound plausible coupling regimes for hydrated nucleoids and membrane interfaces. At the systems level, latent-state models can ask whether including UPE-derived variables improves forecasting of mitochondrial or cellular fate. Such modeling will not prove mechanism, but it will sharpen experimental priors and identify which observables are worth expensive measurement.

Table 2. Decisive experiments, readouts, and what their outcomes would mean.

Perturbation	Core readouts	Prediction if the model is correct	If negative, the model narrows to
TFAM up/down perturbation; topoisomerase perturbation	UPE spectrum, ROS, membrane potential, Ca2+, transcription, nucleoid imaging	Sensitivity to optical / THz input shifts with nucleoid topology or compaction	No change implies weak support for a topology-gated transducer

Perturbation	Core readouts	Prediction if the model is correct	If negative, the model narrows to
rho0 depletion and rescue	Same readouts plus mtDNA abundance / organization controls	Specific coupling effects weaken or disappear without mtDNA and recover on rescue	Persistence of effect without mtDNA points to membranes or protein chromophores (flavins, porphyrins, CCO) instead
Microtubule and actin perturbation	Spatial anisotropy, correlation length, timing, mitochondrial mixing	Routing metrics change more than source intensity alone	Pure transport/mechanics explanation becomes more likely
MERC disruption / altered Ca2+ handling	Ca2+ microdomains, dehydrogenase activity, retrograde signals, phenotype	Weak optical effects require classical amplification hubs	Optical observations without downstream dependence may be epiphenomenal
34.5 THz exposure +/- mitochondrial Ca2+ uptake inhibitors +/- TFAM/topology perturbation	PGC-1alpha-NRF1/2-TFAM induction, mitochondrial biogenesis markers, UPE statistics, nucleoid imaging, Ca2+ microdomains	Ca2+ blockade abolishes downstream biogenesis while preserving any upstream UPE or nucleoid changes; topology perturbation shifts THz sensitivity independently of Ca2+ influx	Effect is purely Ca2+-channel mediated with no topology dependence (model narrows to membrane-only mechanism)
Quartz-vs-glass optical isolation plus gap-junction / TNT / Cx43 blockade	Intercellular respiration, ROS, UPE, fate markers	Partial separability of optical and contact-mediated components	Loss of all effects under diffusion/contact controls argues against an optical leg
Sequence or state modeling of photon bursts (with vs. without TFAM perturbation)	Spectral mix, entropy, burst timing, cross-correlation with ROS / Ca2+	Structured UPE variables plus topology state outperform raw counts or standard redox readouts for state prediction	No added predictive value weakens the topology-gated control-plane framing

6. Physical constraints and alternative explanations

Several constraints need to be stated plainly. Hydrated cytoplasm and the mitochondrial matrix are lossy, screened, thermally noisy environments. Early validation will therefore rely on isolated mitochondria, 2D cultures, and tightly controlled optical-isolation assays, because intact tissues are highly scattering and absorptive media in which photonic effects are difficult to separate cleanly from diffusion, heating, and contact-mediated signaling in vivo [34]. Terahertz fields couple strongly to water and collective vibrational modes, so any in vivo effect is more likely to involve dielectric, hydration-shell, interfacial, or channel-gating physics than classical free-space antenna behavior. The free-space dimensional markers used here - 5.633 μm contour length to about 53 THz, 1.79 μm relaxed-circle diameter to about 167 THz, and 100 nm nucleoid scale to about 3 PHz - are therefore experimental search windows rather than direct predictions of in vivo resonant peaks [8,14,15]. The

recent frequency-selective THz result is consistent with this caution: 34.5 THz, but not 36.1 THz, promoted mitochondrial biogenesis through calcium influx and the PGC-1alpha-NRF1/2-TFAM axis rather than through demonstrated direct mtDNA absorption [8].

Alternative explanations are also real. Reported terahertz effects may act primarily through water, membranes, ion channels, or canonical chromophores such as flavins, porphyrins, and cytochrome c oxidase rather than mtDNA specifically [29,31]. Cytoskeletal perturbations may alter mitochondrial behavior through transport or mechanics rather than optical routing. UPE may remain a passive byproduct in many contexts. The coherence question remains unresolved, and the field has a history of overinterpretation [4,5]. These are not reasons to avoid the problem; they are reasons to design experiments that distinguish mechanisms rather than merely accumulating suggestive correlations.

The same discipline applies to environmental electromagnetic-field claims. It is reasonable to ask whether exogenous RF or broader electromagnetic noise could perturb a mitochondrial control plane, but current systematic-review evidence linking RF-EMF exposure to oxidative-stress biomarkers remains overall of very low certainty and highly inconsistent [26]. For that reason, external-RF implications belong in discussion and follow-up work, not in the evidentiary core of the present hypothesis.

7. Discussion

If the model proves partly correct, the payoff is substantial even without any appeal to exotic coherence. A demonstration that nucleoid topology modulates sensitivity to optical or terahertz perturbations would establish mtDNA organization as an active physical control variable rather than merely a genetic repository. A demonstration that structured UPE variables outperform simple intensity in predicting mitochondrial state would transform biophoton measurements from curiosity to systems-biology readout. A demonstration that weak optical effects require MERCs or retrograde signaling would reveal how fragile physical perturbations are translated into robust biological meaning.

As introduced earlier, the multi-timescale architecture of the proposed control plane offers a physical lens for macro-scale phenomena such as morphological memory. Emmons-Bell et al. showed that transient gap-junctional blockade in Girardia dorotocephala can induce temporary species-specific head morphologies in genetically wild-type animals [35], a result that fits Levin's broader view of bioelectric networks as reprogrammable morphogenetic circuits [36]. Within the present framework, the induced state can be interpreted as a fast, bioelectrically maintained short-term memory, whereas reversion toward the native morphology could reflect reassertion of deeper, genetically canalized priors reinforced by coordinated nuclear and mitochondrial retrograde signaling [20,36]. Future in vivo studies could test this bridge directly by asking whether controlled structured electromagnetic perturbations accelerate the decay of such transient bioelectric memories, thereby degrading the fidelity of the electrochemical envelopes normally integrated by the proposed photonic-redox network.

More broadly, the framework offers a way to merge several literatures that currently talk past one another: mitochondrial redox biology, photobiomodulation, biophoton emission, nucleoid organization, cytoskeletal energy transport, organelle-contact biology, and AI-style state inference. The important discovery may not be that cells communicate by light alone. It may be that cells possess a nested photonic-redox control plane in which light, redox chemistry, topology, and classical signaling are inseparable parts of one regulatory architecture.

The hypothesis presented here is therefore ambitious but not unconstrained. It asks the field to move beyond the false choice between 'biophotons are mystical' and 'biophotons are meaningless waste.' A more rigorous middle position is available: ultra-weak optical events may be biologically relevant when, and only when, they are embedded in geometry-sensitive mitochondrial networks with strong downstream amplifiers. That proposition can be tested. If it fails, the field becomes sharper. If it succeeds, mitochondrial biology will have acquired a new control variable.

8. Conclusion

This manuscript proposes that the most defensible expansion of the mtDNA-biophoton idea is a topology-gated photonic-redox control plane. In this framework, mitochondrial redox chemistry generates weak but structured optical and electromagnetic fluctuations; mtDNA topology, TFAM, and the hydration shell form a candidate transducer; cytoskeletal and mitochondrial subnetworks distribute local perturbations; organelle contact sites amplify them into canonical signaling variables; and slower transcriptional and condensate states store the update. The ceLLM concept enters as a state-inference description of that multiscale integration, not as a claim of literal machine-learning hardware in the cell.

The paper is intentionally written so that its core claims can be broken. The decisive issues are whether nucleoid topology changes coupling, whether mtDNA is required, whether routing and amplification layers can be separated experimentally, and whether structured UPE variables carry more state information than simple photon counts. Those are tractable questions. Answering them cleanly would move the discussion from metaphor to mechanism.

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