Electromagnetic fields in nucleic acids: a new perspective on their potential role in epigenetics and evolution

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Electromagnetic genomic interactions

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Abstract

Electromagnetic fields (EMFs), either in physical or biological systems, can be found in cells via charge movement, membrane potentials, and molecular dipoles. Although their influences on processes like proliferation and signaling are being studied more frequently, interactions with nucleic acids are less well-defined. According to this hypothesis, the DNA's natural electromagnetic properties might act on transcriptional regulation through dipole interactions in base pairs. For example, the ordered hydrogen bonds from A,T,G, and C in the DNA helix could form localized electromagnetic patterns that may control conformational dynamics or transcription mechanisms. Such effects could provide an additional layer of regulation, working in synergy with classical epigenetic signals. To this end, here we present a conceptual framework and experimental design to test whether EMF exposure in a controlled manner can modulate transcriptional efficiency or protein expression independent of DNA sequence. If they prove to be accurate, such discoveries could offer important new information on the regulation of gene activity, epigenetic responses to environmental stress, and adaptation during the evolution of species.

Keywords

electromagnetic field, biomagnetism, DNA transcription, evolution, epigenetics

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Introduction

Carbon is the building block of life. The Earth is full of carbon-based life forms because compounds of carbon are abundant on it, and carbon-containing molecules, including nucleic acids, have extraordinary structural and chemical versatility. A carbon atom can associate with four different atoms at the same time. Also, enzymes easily manipulate carbon molecules due to their light weight and relatively small size. These superiorities make carbon an ideal element for forming deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) chains, which are the basis of life.[1]

Nucleic acids contain 5 carbons of sugar (pentose), phosphate, and base. The nitrogenous organic base is attached to a pentose sugar by a glycosidic bond, while the phosphate is connected by an ester bond. This formation is called a nucleotide. Nucleotides are attached by phosphodiester bonds to form a chain. The bond between the two complementary chains occurs by the coupling of the bases. This coupling occurs when the appropriate bases are joined by mutual weak hydrogen bonds (H+). As a result, nucleotides joined by phosphodiester bonds and stabilized by base-pair hydrogen bonds form DNA and RNA. The characteristic double-helical structure of DNA, necessary for genetic storage and accurate transcription, is formed by the spatial arrangement of these bonds.

Genetic information is transmitted from the template DNA sequence by the catalytic action of the enzyme RNA polymerase through the synthesis of messenger RNA (mRNA) in the nucleus. This process is called transcription. DNA sequence, chromatin structure, histone modifications, and noncoding RNAs delicately regulate transcription. These regulatory mechanisms in gene transcription, collectively, can create order out of chaos within cells, thus enabling cells to translate environmental conditions into gene expression.

Electromagnetic Field (EMFs) can be defined as a force field with electrical and magnetic components that is formed by the rotation of electrons in atoms around the nucleus and around themselves. In biological systems, EMFs arising naturally from molecular charges, ion movement, and electrical currents in tissues create biomagnetism.[2,3] Indeed, considering that every cell in the human body has its own electrical circuit, our body can actually be compared to a huge electromagnetic device. In this context, it would be reasonable to think that biomagnetic fields produced internally by biological processes in our bodies, or artificial EMFs produced by modern technology we encounter in the environment, are physical factors that can influence gene regulation.

Research conducted together with DNA studies and applied physics offers us new ideas into the regulation of gene transcription. Although it is an increasingly popular field of research to evaluate the effects of EMFs on morphology, survival capacity, membrane permeability and proliferation rate of cell, cell cycle progression (division-mitosis or meiosis), mitochondrial activity, oxidative stress, embryonic development, cell signal transduction, biomolecules, and regulatory proteins.[4-15] the interactions between biomagnetic fields and genetic information processing have not yet been sufficiently explored. This hypothesis suggests a possible link between the electromagnetic microenvironment of DNA and the regulation of transcription.

Materials and Methods

This study was conducted in the form of a narrative literature review. Relevant publications were identified via a systematic review of literature by manual search using the PubMed and Google Scholar databases. Search strategy: The following keywords were searched in combinations: Electromagnetic Field, biomagnetism, DNA transcription, evolution, and epigenetics.

Filtering through the results through a series of various keywords that implied studies pertaining to Electromagnetic Field, biomagnetism (more specifically as it pertains to DNA transcriptomics and evolution), and epigenetics. Original research and relevant review articles were included, while studies not directly related to the topic or not written in English were excluded.

Titles and abstracts were screened, followed by full texts to identify potentially applicable studies. Given the narrative nature of this review, a standard systematic review framework (for example, PRISMA) or quality assessment tool was not employed.

Eligible studies were subject to data extraction and descriptive synthesis. The resulting hits were thematically organized for a summary of the current literature covering biomagnetism and electromagnetic fields during DNA transcription.

Ethical Approval

This study did not require ethical approval as it is a narrative review and hypothesis-based study that did not involve human participants, patient data, or animal subjects.

Reporting Guidelines

No specific reporting guideline was followed, as this study is a narrative review and hypothesis-based paper.

Results

Results Hypothesis

The regular sequence of dipole interactions within DNA base pairs creates extremely small but structured electromagnetic fields because hydrogen bonds generate very small electrostatic forces. However, the repetitive and helical organization of these interactions, which can number in the millions, can create local electromagnetic patterns within the DNA molecule. Transcription processes can be affected by these intrinsic electromagnetic patterns that could theoretically regulate: the conformational dynamics of DNA (e.g., unwinding, bending, groove width), the interaction environment of RNA polymerase, the binding of transcription factors, and local chromatin organization. If this is true, these intrinsic patterns can be altered by exposure to external electromagnetic fields without changing the genetic sequence, in which case transcription efficiency can be affected, protein expression can be altered, and epigenetic-like effects can occur. This type of EMF-sensitive alteration might potentially play a role in both epigenetic and evolutionary processes. This does not replace previously recognized biochemical epigenetic pathways but provides an alternative mechanism by which environmental physical forces can modulate gene expression. We note that this hypothesis is speculative and should be tested stringently.

Theoretical Rationale

Electromagnetic Properties of DNA: DNA is not a data storage in the classic ferromagnetic sense; however, it has: electric dipoles (hydrogen bonds), charge distribution along the backbone, and can interact with an external field through polarization current.[16] The helical pattern at the nanometer-scale could enable emergent electromagnetic phenomena, whose role in biology is however, unknown. Single-stranded nucleic acids, such as RNA, are more structurally polymorphic and therefore have additional flexibility for electromagnetic interactions.

EMFs as Environmental Signals: Epigenetic mechanisms translate external and internal stimuli—chemicals, nutrients, and temperature -- into changes in chromatin properties and gene expression.[17,18] However, if EMFs affect transcription independent of the DNA sequence, they may serve as an alternative environmental modulator.

Evolutionary Considerations: Natural EMFs exhibit geographical fluctuation, and this depends on Earth's magnetic field strength as well as local anomalies.[19] Even though highly speculative, if exposure to EMFs has the potential to delicately influence patterns of gene expression over generations, they could be involved in local adaptation or phenotypic diversity. This may be worth exploring, but it should be considered carefully since established genetic and selection mechanisms are still the main explanation for regional genetic characteristics.

Proposed Experimental Approach

There is currently no experimental data in the literature on this subject. However, an experiment like the following could be suggested to investigate whether electromagnetic fields affect DNA transcription or base pairing.

EMF Exposure System: In this project, first of all, a computer-aided circuit arrangement consisting of a cryostat temperature-controlled chamber, a closed-circuit cooling sysem, and a CO_2 flow control system will be established to provide a controlled EMF exposure environment at varying sizes and time intervals within a constant temperature environment. Also, a magnetic field generator capable of producing static fields of up to 1.2 Tesla to be applied to biological samples, optional low-frequency alternating current (AC) fields for comparison, a helium compressor for low-temperature testing, and a molecular vacuum pump system for vacuuming the cryostat containing the biological sample will be installed. With this system, the EMF intensity, frequency, and exposure time can be systematically varied.

DNA-Level Assays: In this step, it will be investigated whether the expression of this gene product changes in different EMFs by cloning a well-characterized eukaryotic gene (e.g., green fluorescent protein [GFP] or luciferase) into a prokaryotic expression vector. The purified DNA will be denatured and renatured under controlled EMF exposure, and tested by DNA Sequencing to determine whether EMFs alter base pairing fidelity (no sequence-level changes are expected; so, this serves as a control). Finally, the Comet Assay will be used to detect breaks or damage in DNA strands.

Transcription and Protein Expression: Subsequently, the EMF-exposed expression vector carrying the "Eukaryotic Gene" will be transferred to a cell line that does not naturally express the gene, thus achieving the transformation. Then, gene expression analysis will be performed through mRNA levels measured by reverse transcription quantitative polymerase chain reaction (RT-qPCR) under different EMF conditions. Protein characterization will be completed by determining protein abundance using Western blot or fluorescence methods, and by examining structural accuracy using mass spectrometry to detect amino acid misincorporation. In the final stage, the functional test will be performed by determining the activity of the expressed protein (e.g., the function of the luminescence enzyme).

Expected Outcomes: Possible findings can be summarized as follows: i) No effect may occur: EMFs do not affect transcription or protein expression (null hypothesis); ii) Modulation may occur without mutation: EMFs alter transcription levels or protein yield without changing the DNA sequence; this supports an epigenetic-like effect; iii) Sequence or structural changes may occur: this means unexpected but informative changes in accuracy.

Discussion

DNA is an amazing molecule with an extraordinary density of potential magnetic storage. Genetic information storage in DNA also requires an encoding and decoding scheme, like the magnetic hard drive in computers. The structure of DNA is a double helix, which is based on four nucleotide bases: adenine (A), cytosine (C), guanine (G), and thymine (T). The structure of DNA, based on these four nucleotide bases, provides more storage space than the binary system in magnetic hard disks. Data is stored volumetrically in a DNA molecule. Interestingly, DNA-like helical structures in a magnetic field tend to form large-scale structures from small-scale ones.[20] This allows DNA to store more information as opposed to other media that store data linearly. In addition to the conduction current, a polarization current can also occur in the DNA molecule, which can answer the question of whether single-stranded DNA molecules have magnetic properties.16 Moreover, the fact that single-stranded DNA molecules, such as RNAs, have a wider variety of 3-dimensional structures seems to support this view. Also, storing genetic information in DNA does not require any energy or maintenance, so DNA in fossils can be preserved for many years.

EMF is a physical phenomenon that cannot be directly seen or felt easily, but its results can be tested. The electromagnetic field, a vector magnitude, is generated internally by moving electric charges, by time-varying electric fields, or by fundamental particles. So, it is defined by direction and intensity at any point. In the special theory of relativity, electric and magnetic fields are two related properties of an object. In quantum physics, electromagnetic interactions occur as a result of photon exchange. The generation, transmission, and distribution system of electrical energy plays an important role in our lives. Furthermore, EMF is used in the transport and storage of information.

Epigenetics is the study of heritable but reversible changes in gene function caused by environmental factors without requiring a change in the DNA sequence.[21] In other words, epigenetics describes changes in phenotype without a change in genotype based on how cells read genes. Gene expression can be controlled by silencing of DNA (by means of DNA methylation, histone modification, non-coding RNAs, et.) in many types of epigenetic inheritance.[17,22-24] Both the environment and individual lifestyle can affect the way genes work, resulting in epigenetic change. These epigenetic changes can continue throughout the life of the cell through cell divisions and may also persist for multiple generations.[18] Thus, transgenerational epigenetic inheritance may affect phenotypic plasticity and adaptation. Furthermore, epigenetic mechanisms may also help drive genome evolution.

At this point, if it is assumed that external EMFs regulate transcription efficiency or protein expression without altering the DNA sequence, it may be reasonable to argue that the electromagnetic microenvironment could play a significant role in contributing to gene regulation by creating an additional physical layer influencing cellular behavior, even if it cannot replace established epigenetic mechanisms.

Finally, potential outcomes of this hypothesis may be: novel insights into how living entities experience the surrounding EMFs, application of this knowledge to human biology (e.g., effects of EMF on immune system or in cancer therapy), alternative view on the long-term role of physical fields in life development (like a new and easier way to explain the effect of environmental factors on evolution and phenotypic plasticity). However, we would like to stress that this speculation has not been confirmed by experiments until now. These hydrogen bond-derived EMFs are extremely weak, and ensuring biocompatibility will require rigorous reproducibility and careful controls.

Limitations

This study has several key limitations that should be noted. To start with, although the proposed model is very interesting and thought-provoking, at this point it remains speculative without experimental corroboration. Although the suggested impact of EMF on DNA transcription based on inherent electromagnetic signals is theoretical, it does have a sound physical basis. Second, the physical strength of electromagnetic forces created by hydrogen bonds and molecular dipoles inside DNA is very low. It is unclear whether such weak fields can impact biologically functional effects in dynamically noisy intracellular environments, where thermal fluctuations and biochemical interactions prevail. Third, the experimental design proposed is conceptually sound but practically very difficult. Controlling EMF exposure with precision, separating it from confounding environmental factors, and ensuring replication across biological systems could be challenging. Moreover, separating real electromagnetic effects from secondary stress responses triggered in the cells or indirect biochemical pathways will necessitate stringent controls. Fourth, extrapolating possible EMF effects to epigenetic control of genes and evolutionary processes must remain wholly speculative. The established mechanisms of genetic variation and natural selection remain the key drivers of evolutionary change, and any potential contribution of EMFs needs to be viewed with caution unless bolstered by robust empirical data.

Ultimately, this study fails to account for intercell-type, organism, or environmental variability that may affect sensitivity toward electromagnetic exposure. Standardized exposure parameters in addition to different biological models, will help generalize our findings, in future research.

Conclusion

We introduce a speculative, but experimentally testable model suggesting that endogenous and exogenous electromagnetic fields could have an effect on DNA transcription by acting directly upon the electromagnetic microenvironment of nucleic acids. We describe an experimental paradigm for detecting EMF-mediated effects at the DNA pairing, transcriptional, translational, and post-translational levels of proteins, which represents an excellent template platform for interdisciplinary research fusing physics with molecular biology and epigenetics.

If confirmed, this idea could yield novel insight into gene regulation and could help to explain both environmentally responsive phenotypes as well as more gradual evolution.

Declarations

Ethics Declarations

This study did not require ethical approval as it is a narrative review and hypothesis-based study that did not involve human participants, patient data, or animal subjects.

Animal and Human Rights Statement

This study did not involve any human participants or animal subjects.

Informed Consent

Not applicable.

Data Availability

The datasets used and/or analyzed during the current study are not publicly available due to patient privacy reasons but are available from the corresponding author on reasonable request.

Conflict of Interest

The authors declare that there is no conflict of interest.

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Author Contributions

Conceptualization: A.F.
Methodology: A.F.
Software: A.F.
Validation: İ.V.F.
Formal Analysis: İ.V.F.
Investigation: A.F.
Data Curation: A.F.
Writing – Original Draft Preparation: A.F.
Writing – Review & Editing: İ.V.F.
Visualization: İ.V.F.
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Scientific Responsibility Statement

The authors declare that they are responsible for the article's scientific content, including study design, data collection, analysis and interpretation, writing, and some of the main line, or all of the preparation and scientific review of the contents, and approval of the final version of the article.

Abbreviations

AC: Alternating current
CO_2: Carbon dioxide
DNA: Deoxyribonucleic acid
EMF: Electromagnetic field
GFP: Green fluorescent protein
H^+: Hydrogen ion
mRNA: Messenger ribonucleic acid
RNA: Ribonucleic acid
RT-qPCR: Reverse transcription quantitative polymerase chain reaction

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