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Impact of Magnetic Fields on the Proteome of Human Cells: A Pilot and Feasibility Study

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Abstract

Background: Magnetic field therapies have gained attention for their non-invasive potential to modulate biological processes, yet the underlying molecular mechanisms remain poorly understood, particularly at the proteomic level.

Objective: This pilot study aimed to assess whether short-term exposure to low-frequency magnetic fields affects the proteomic profile of human buccal cells and to evaluate the methodological viability of using buccal cell proteomics as a monitoring tool.

Methods: Nine participants were assigned to either a control group (n=3) or an intervention group (n=6) exposed to the Vitori mat (7.83 Hz Schumann frequency) for five consecutive days. Buccal cell samples were collected pre- and post-intervention, with a follow-up sample collected three days later in the intervention group. Samples were analyzed via LC-MS/MS using a data-independent acquisition (DIA) workflow and processed with DIA-NN [1]. Statistical comparisons employed Wilcoxon rank-sum and Friedman tests.

Results: A total of 108 protein groups differed significantly between groups after exposure ($p<0.05$), while 67 proteins showed significant temporal changes within the intervention group. Thirteen proteins were identified across both comparisons, implicating biological pathways related to immune regulation, cell proliferation, and stress response. Principal component analysis indicated partial reversibility of proteomic shifts following a short washout phase.

Conclusions: The study confirms both the biological responsiveness of buccal cells to magnetic field exposure and the feasibility of integrating non-invasive sampling with high-resolution proteomic analysis. These findings support future investigations into the molecular mechanisms of magnetic field therapies and the development of minimally invasive monitoring tools.

Keywords: Magnetic field exposure; Proteomics; Electromagnetic fields; Buccal cells; Non-invasive biomarker; Schumann frequency; Immune response

Introduction

The therapeutic use of electromagnetic fields (EMFs), particularly in the form of low-frequency or pulsed electromagnetic fields (PEMFs), has gained increasing recognition for its non-invasive nature and broad potential across various medical domains [2]. These applications include promoting tissue regeneration, alleviating chronic pain, managing mood disorders such as depression, improving sleep, and modulating inflammation and circulation [3-7]. Clinically, EMFs have shown promise as alternative or complementary treatments to pharmacological and physical therapies, with controlled studies demonstrating symptom improvement across musculoskeletal [4, 8], neurological [6], and cardiovascular conditions [8]. The ease of application and favourable safety profile of EMF-based therapies further support their growing adoption in clinical settings.

Despite promising clinical observations and decades of research, the molecular and cellular mechanisms by which electromagnetic fields (EMFs) exert their effects remain poorly understood and underexplored. While many studies focus on symptom outcomes or gene expression, proteomic changes and other molecular indicators of EMF response are often overlooked. Early experimental and clinical findings have suggested that EMFs can influence cell signalling, proliferation, gene expression, inflammatory pathways, protein synthesis, and even neuroendocrine functions [5, 6, 8, 9]. Specifically, low-frequency and pulsed EMFs—such as those in the Schumann resonance range (7.83 Hz)—have shown potential to enhance tissue repair, modulate immune responses, and influence emotional regulation [7], blood perfusion [4], and inflammatory cascades [10]. This frequency corresponds to the Earth's natural electromagnetic resonance, which has been hypothesized to interact with neural and circadian oscillations in humans [11, 12]. Beyond organ-specific effects, extremely low-frequency EMFs have also been associated with modulation of human brain activity, including encephalographic patterns, pain perception, and mood regulation [13, 9, 14, 11]. These ultra-low-frequency fields may entrain neural oscillations and modulate central nervous system dynamics, suggesting a broader resonance between human physiology and environmental electromagnetic signatures [15, 16]. However, inconsistencies across studies—often stemming from variability in field strength, frequency, exposure duration, tissue type, and population heterogeneity—underscore the urgent need for more rigorous, standardized molecular investigations to clarify EMF mechanisms.

Proteomic profiling offers an opportunity to characterize the cellular responses to EMF exposure at a systems level. Human buccal cells represent a convenient, minimally invasive model for monitoring systemic molecular effects [17, 18]. Therefore, this pilot study aimed to assess whether magnetic field exposure alters the buccal cell proteome and to explore the biological pathways affected.

However, despite growing interest, the precise molecular pathways modulated by electromagnetic fields remain largely unexplored, particularly at the proteomic level in human models. Previous studies have primarily focused on functional outcomes or gene expression, with very limited proteomics investigations, which when performed have shown only modest or inconsistent protein-level changes [19-21].

Despite growing clinical and mechanistic support for EMF effects, a critical need remains to investigate how magnetic fields influence the human proteome, particularly through accessible biosamples such as buccal cells, to better understand the biological mechanisms underlying EMF-based therapies.

This pilot study addresses a critical gap in the field by systematically profiling proteomic changes in human buccal cells following short-term exposure to the Vitori mat [22], which emits magnetic fields at the Schumann frequency (7.83 Hz). Using high-throughput LC-MS/MS and non-parametric statistical analysis, we aim to explore the biological mechanisms underlying electromagnetic field therapies and evaluate the feasibility of using proteomic biomarkers to monitor EMF-induced molecular responses. The primary objectives are to (1) determine whether exposure induces consistent and measurable changes in the buccal cell proteome, (2) identify which biological pathways are most affected, and (3) assess whether these proteomic changes persist after a short washout period.

Specifically, this study addresses the following research questions: Does exposure to magnetic fields induce measurable changes in the proteomic profile of human buccal cells? Which biological pathways are most affected by magnetic field exposure at the proteomic level? Are the observed proteomic changes sustained after cessation of EMF exposure?

We hypothesize that magnetic field exposure induces significant changes in the proteomic signature of human buccal cells, particularly affecting immune system regulation and metabolic pathways. Some of these effects may be sustained beyond the immediate exposure phase.

This paper represents an essential step in exploring the biological mechanisms underlying electromagnetic field therapies through proteomic analysis. By piloting a novel approach using buccal cell samples from human participants (using Epi-Proteomics Test kit from MOLEQLAR Analytics [23]), we aim to evaluate the feasibility of detecting molecular responses to magnetic field exposure while identifying key biological pathways that may be affected.

In the following sections, we present related work and the methodology used in this pilot study, summarize the proteomic findings, and discuss their implications for advancing molecular research on EMFs, supporting future validation studies, and guiding the development of targeted therapeutic protocols.

Background

The connections between electromagnetic fields (EMFs) and biological systems have increased attention over the past decades, particularly its therapeutic medical applications [24-26]. Bassett's [27] work was crucial in establishing a viable treatment for bone nonunions using pulsed electromagnetic fields (PEMFs), marking a foundational contribution to the field of magnetotherapy. Similarly, Aaron, Ciombor, and Simon [28] demonstrated that electric and electromagnetic fields could effectively stimulate bone healing in orthopaedic contexts. These early studies laid the groundwork for using EMFs in clinical practice, particularly in musculoskeletal rehabilitation.

Pall provided further mechanistic insight [29], who proposed that EMFs exert their biological effects primarily through the activation of voltage-gated calcium channels (VGCCs), triggering downstream cascades including oxidative stress, nitric oxide synthesis, and inflammation. This VGCC-mediated model offers a unifying hypothesis for beneficial and adverse EMF effects observed across tissues.

Expanding beyond orthopaedic applications, Markov's [24] work provided a comprehensive review of PEMF therapy, highlighting its utility in bone regeneration and managing chronic pain and inflammation. Vavken et al. [30] later contributed a meta-analysis of randomized controlled trials confirming PEMF therapy's effectiveness in reducing osteoarthritis symptoms, further validating EMF applications in degenerative joint conditions.

At the cellular level, Fitzsimmons et al. (1995) [31] investigated the effects of combined magnetic fields on human osteosarcoma cells. They demonstrated that electromagnetic stimulation can enhance the production of insulin-like growth factor-II (IGF-II), a key regulator of bone cell activity. Their findings suggest that magnetic fields may influence signal transduction pathways relevant to cellular proliferation and bone tissue development. Building on this, Reale et al. [32] demonstrated that extremely low-frequency EMFs could modulate immune responses in neuronal cells, suggesting broader effects of EMFs on inflammatory and neuroimmune functions. In support of the potential neuroplastic effects of EMFs, Cuccurazzu et al. [33] demonstrated that exposure to extremely low-frequency electromagnetic fields (50 Hz) enhanced adult hippocampal neurogenesis in mice, suggesting that EMFs may modulate brain plasticity and cognitive function under specific conditions.

Additional work by Blank and Goodman [34] revealed that electromagnetic fields can act as cellular stressors, triggering protective responses such as the upregulation of heat-shock proteins. Funk, Monsees, and O¨ zkucur [35] synthesized similar findings across cell types, showing that EMFs may alter ion channel behaviour, calcium signaling, and reactive oxygen species (ROS) dynamics, processes that are central to inflammation and cell survival. Furthermore, Consales et al. [36] work highlights how sustained EMF exposure may increase reactive oxygen species (ROS) production, potentially contributing to neuronal damage and ageing-related pathologies, linking EMF exposure to oxidative stress pathways implicated in neurodegeneration.

Despite growing interest, relatively few studies have explored the impact of EMFs at the proteomic level. Lantow et al. [37] demonstrated that electromagnetic field exposure could induce oxidative stress and modulate the expression of heat shock proteins in primary human immune cells, highlighting a potential cellular stress response pathway activated by EMFs.

Moreover, Gye et al. [38] emphasized that EMF responses are context-dependent, influenced by factors such as field strength, exposure duration, biological sex, and tissue type. These insights underscore the need for standardized protocols and establish biomarker-based evaluation methods.

Human buccal cells offer a promising but underutilized model for investigating systemic biological responses to EMFs. Bollati et al. [18] and Sullivan et al. [39] demonstrated the value of buccal cells in molecular epidemiology and biomarker research, citing their non-invasive collection and responsiveness to environmental and physiological factors. However, their application in EMF-related proteomic research remains limited. In addition to cellular mechanisms, Ohkubo and Okano [40] investigated the clinical effects of static magnetic fields on circulatory function, reporting modulation of blood flow and cardiovascular regulation. These findings suggest that magnetic fields may exert broader physiological influences beyond localized tissue effects.

In addition to their convenience and non-invasive collection, buccal cells have proven responsive to environmental and physiological exposures at the molecular level, including epigenetic and oxidative stress markers [18]. However, their use in EMF-related proteomic research remains limited. Furthermore, EMFs have been shown to influence not only gene expression but also protein stability, phosphorylation status, and intracellular signalling networks, particularly in immune and neural cells [41, 36]. These findings suggest that a proteomic approach, particularly using accessible tissues such as buccal cells, may reveal key post-transcriptional mechanisms through which EMFs modulate human physiology.

To address the gaps existing in the literature, the present study builds upon prior work in electromagnetic field biology and emerging proteomic methodologies by investigating the effects of magnetic field exposure on the human buccal cell proteome [20, 19]. Through a controlled experimental design and the application of data-independent acquisition mass spectrometry [42, 1], this study seeks to identify specific protein expression patterns and biological pathways that are modulated by EMF exposure in human epithelial cells.

Methodology

This study employed a randomized controlled pilot design to explore the molecular effects of magnetic field exposure on human buccal cell proteomes. The methodology was developed to assess the feasibility of using buccal cells as a non-invasive sampling method (using the Epi-Proteomics Test kit from MOLEQLAR Analytics [23]) and the sensitivity of proteomic analysis in detecting exposure-related biological changes. The following subsections describe the participant recruitment, experimental intervention, sample collection procedures, proteomic workflow, and statistical analyses used to evaluate differential protein expression.

Study Design and Participants

This study was conducted as a pilot design study to evaluate the applicability of proteomic analysis as a monitoring tool and the potential biological effects of repeated exposure to a magnetic field-generating device. The primary goal was to assess whether magnetic field exposure through the Vitori mat [22] induces measurable epigenetic and proteomic changes in human buccal cells and to determine whether these changes persist after a short washout phase. The study aimed to identify candidate biomarkers that could be validated in future, larger-scale investigations.

Nine adult participants were recruited, randomized and allocated into two groups: an intervention group of six female participants and a control group comprising three individuals (two men and one woman). The intervention group exclusively comprised female participants aged between 28 and 55 years, while the control group included one female and two males aged between 47 and 48 years.

Inclusion criteria required participants to be adults in generally good health. Some participants reported mild or chronic conditions such as back pain or sleep disorders, but no acute or unstable illnesses were present. None of the participants reported current medication use. Physical activity levels varied, with some individuals reporting regular or occasional engagement in activities such as walking or swimming. One intervention group participant (Part 8) was later excluded due to incomplete sampling, resulting in a final sample of eight participants. The small sample size was appropriate for a pilot and feasibility study focused on method validation and exploratory analysis.

Buccal cell samples were collected from all participants through non-invasive swabbing procedures, using the Epi-Proteomics Test kit from MOLEQLAR Analytics [23]. The experimental design followed a pre-post model with an additional follow-up time point. Participants in the intervention group underwent magnetic field exposure for five consecutive days, doing three sessions (S1, S2 and S3) during this period. In the intervention group, samples were collected at three distinct time points (Figure 1): before the magnetic field exposure (P1), immediately after five consecutive days of exposure (P2), and three days following the cessation of the intervention (P3), marking a "fade-out" phase. In contrast, the control group (Figure 2), which did not undergo any magnetic field exposure, provided samples at two corresponding time points (P1 and P2), five days apart, to mirror the overall duration of the intervention schedule. Figure 3 shows the schematic design of the study.

All participants were instructed to maintain consistent daily routines and avoid introducing lifestyle changes during the study period. Before participation, written informed consent was obtained from all individuals by ethical standards for human subjects research. The sample composition reflects a gender imbalance favouring female participants in the intervention group, which is acknowledged as a limitation of this pilot study.

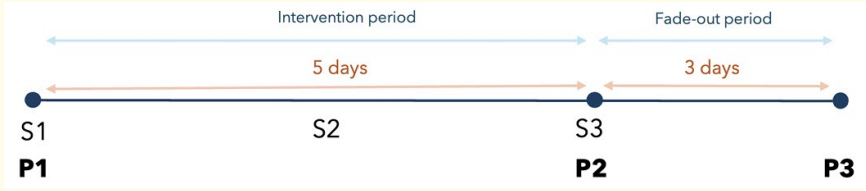

Figure 1: Intervention Group- Sample Collection Timeline.

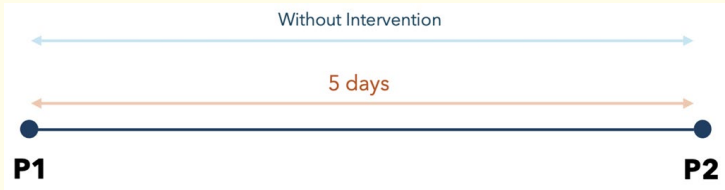

Figure 2: Control Group- Sample Collection Timeline.

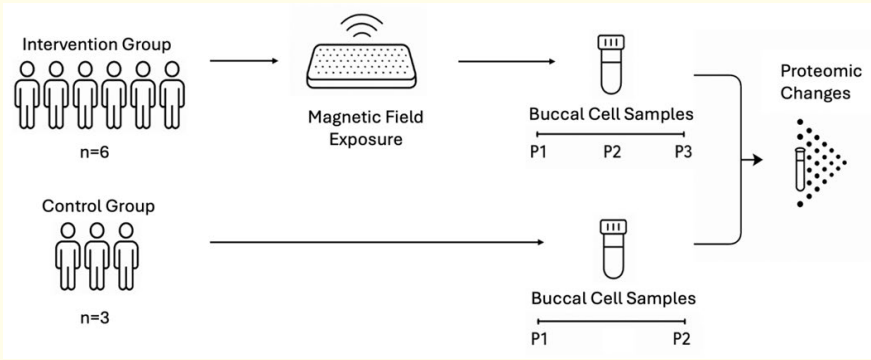

Figure 3: Schematic Design of the Study.

Electromagnetic Field Exposure Protocol

The intervention group used the Vitori mat [22], a non-invasive wellness device that emits magnetic fields at the Schumann frequency (7.83 Hz) [12, 43, 11]. No other functional settings were enabled. Each participant used the mat for 60 minutes daily for five consecutive days. Each session involved one hour of exposure per day, followed by a 30-minute rest period before sample collection to minimize immediate post-intervention biological fluctuations. The sessions could take place in the location of the participant's choice, provided the environment was quiet and free from interruptions. Participants were advised to lie supine on the mat, which could be placed on the floor or a cushioned surface, and to wear light, comfortable clothing or as little clothing as possible to allow optimal field exposure. A glass of water was to be consumed before each session.

Activities during the intervention were not restricted; participants were free to sleep, meditate, listen to music, read, or engage in other restful tasks. Any adverse events, such as dizziness, sweating, or palpitations, were to be reported immediately, and in such cases, participants were instructed to discontinue the study.

Data Processing and Quality Control

All samples were processed and analysed as a single batch to minimise technical variation. Protein identification and quantification were performed using the DIA-NN software platform following LC-MS/MS acquisition in data-independent acquisition (DIA) mode.

Raw intensity data were normalised using median-centering to reduce inter-sample variation. Missing values were imputed using random draws from a Gaussian distribution centred around a minimal intensity value. This approach ensured the preservation of variance structure while enabling downstream statistical analyses.

Protein groups with more than 90% missing values across all samples were excluded from further analysis to ensure data reliability. Samples with high missingness clustered separately in unsupervised principal component analysis (PCA), further supporting their lower data quality.

PCA was also used to explore global trends, evaluate clustering across time points, and assess the reversibility of changes following the intervention fade-out phase.

Statistical Analysis

Due to the pilot nature of the study and the low sample size, non-parametric tests were employed. Two complementary statistical approaches were used to assess intervention-related effects.

First, between-group effects were evaluated by calculating log2 fold changes in protein expression from P1 to P2 for each individual, then comparing these values between the intervention and control groups using the Wilcoxon rank-sum test.

Second, the Friedman test was applied to the intervention group's three time points (P1, P2, P3) to examine within-subject changes across time.

Proteins found significant in both tests were further analysed for functional relevance. Enrichment of Gene Ontology (GO) biological processes among these proteins revealed associations with immune regulation, cell proliferation, and antimicrobial activity. Time-course trends for selected proteins were visualised to illustrate expression trajectories across intervention and washout phases.

Results

Proteomic Profiling and Between-Group Differences

A total of 22 buccal cell samples from eight participants were analysed using LC-MS/MS with data-independent acquisition (DIA). After quality control and filtering, between 2000 and 4000 protein groups were identified per sample. Following normalisation and imputation, 108 protein groups differed significantly between the control and intervention groups, based on log2 fold changes from P1 to P2 and the Wilcoxon rank-sum test ($p < 0.05$, unadjusted).

These differentially expressed proteins showed a variety of up- and down-regulation patterns in response to magnetic field exposure. Most proteins identified had fold changes greater than 0.5 in either direction, indicating biologically relevant alterations.

Longitudinal Changes Within the Intervention Group

The Friedman test analysed proteomic data from the intervention group's three time points (P1, P2, and P3). This longitudinal analysis revealed 67 protein groups with significant temporal changes across the intervention and washout phases ($p < 0.05$). While pairwise comparisons between individual time points were not statistically significant after correction, a large effect size (Kendall's $W \geq 0.5$) was observed, suggesting meaningful intra-individual shifts.

Principal component analysis (PCA) demonstrated that P2 samples clustered apart from baseline (P1), indicating a response to magnetic field exposure. Notably, P3 (fade-out phase) samples tended to shift back toward the P1 cluster, suggesting partial reversibility of the observed effects. However, some variability persisted, indicating that the three-day washout may not be sufficient for a full return to baseline.

Overlap of Significant Proteins and Functional Analysis

An intersection of proteins found significant in the Wilcoxon and Friedman analyses yielded 13 overlapping protein groups. These proteins were associated with diverse cellular processes, including immune modulation, cell growth, and antimicrobial defence.

- ***CHAD (O15335)*** - Involved in chondrocyte attachment and proliferation.
- ***RNASE3*** - Displays antimicrobial activity, particularly against Gram-negative bacteria.
- ***POC1B*** - Plays a key role in centriole assembly and mitotic spindle formation.
- ***MUC20*** - Modulates the MET signalling cascade and MAPK activation.
- ***EHF*** - Regulates epithelial differentiation and proliferation.
- ***KIDIN220 (Q9ULH0)*** - Involved in neuronal growth and EPHA4-mediated signaling.
- ***HSD17B11*** - Participates in steroid metabolism and has been identified as a tumor associated antigen.
- ***CAMSAP1*** - Stabilizes microtubules and influences cell structure.
- ***TRPM4 (Q8TD43)*** - Regulates calcium oscillations in T-cell activation and insulin secretion.

Gene Ontology Enrichment

Enrichment analysis of the 108 significantly differentially expressed proteins revealed over-representing biological processes related to immune response, cell proliferation, and stress signalling. These results suggest that magnetic field exposure may modulate pathways associated with immunological activation and tissue remodelling.

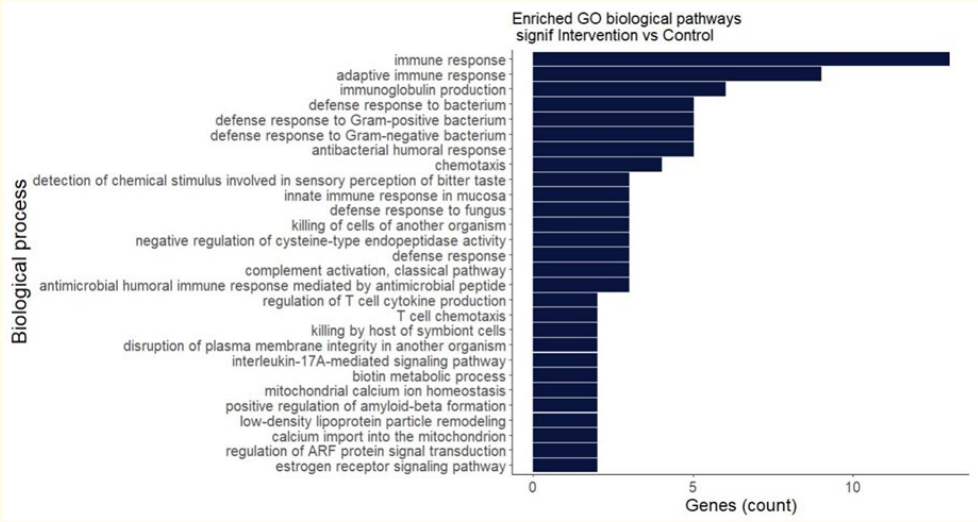

Figure 4: Enriched GO biological pathways from the 108 protein groups different between the control and intervention (before and after).

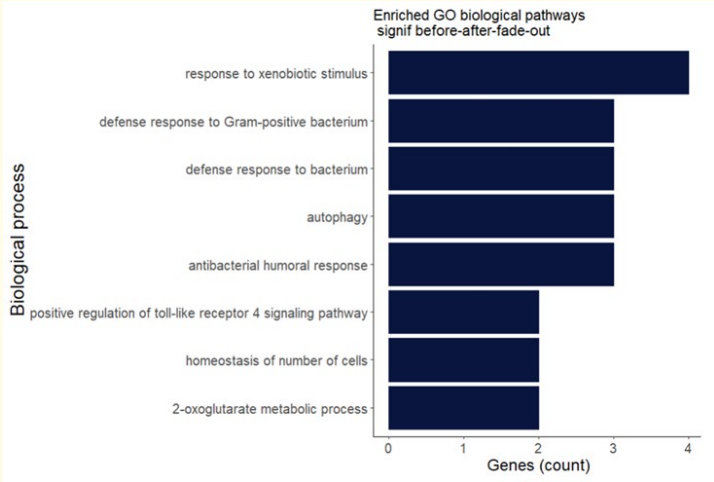

Figure 5: Enriched GO biological pathways from the 108 protein groups different between the control and intervention in the fade-out period (before and after) in the intervention group.

Protein Expression Dynamics

Three example proteins with distinct expression dynamics are illustrated in Figure 6:

- ***TRPM4 (Q8TD43)*** increased after exposure (P2) and decreased again after the fade-out period (P3), indicating a transient response.
- ***KIDIN220 (Q9ULH0)*** showed a stable increase from P1 through P3, suggesting a potentially sustained effect.
- ***CHAD (O15335)*** decreased after exposure and did not return to baseline levels by P3.

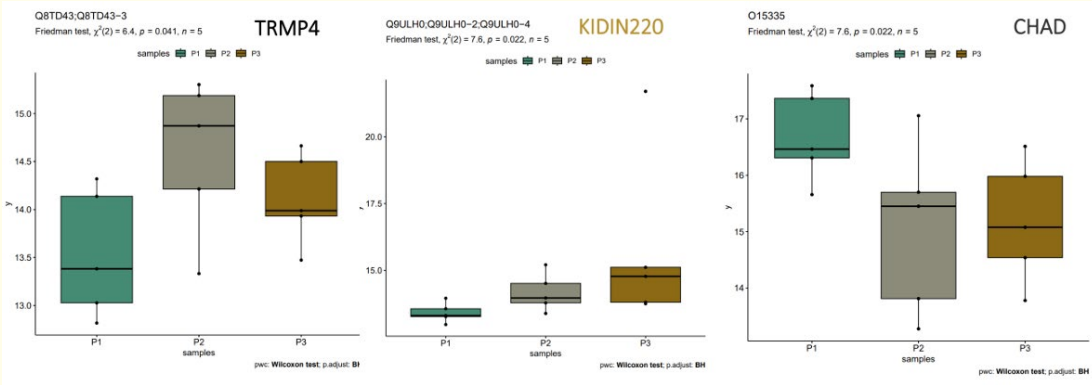

Figure 6: Examples of protein expression changes across intervention time points.

These expression patterns highlight the variability of molecular responses to magnetic field exposure and suggest that some effects may be reversible while others could be longer lasting.

Discussion

This pilot and feasibility study investigated the effects of repeated exposure to a magnetic field-generating Vitori mat [22] on the proteomic profile of human buccal cells. Using a controlled pre-post-follow-up design with an intervention group and a control group, we observed measurable and biologically meaningful changes in protein expression associated with immune processes, cellular growth, and stress response.

Principal Findings and Biological Interpretation

Exposure to magnetic fields over five consecutive days resulted in significant proteomic alterations. One hundred eight protein groups differed between the intervention and control groups following the exposure phase, with fold changes exceeding 0.5 and $p < 0.05$. Additionally, 67 proteins showed significant longitudinal changes across the intervention and washout phases, as revealed by the Friedman test. Principal component analysis (PCA) indicated a clear divergence in the proteomic profile immediately post-intervention (P2), with a partial reversion during the fade-out period (P3), suggesting that some effects may be transient while others could be more persistent.

Notably, 13 proteins were identified as significant in both statistical analyses. These proteins were functionally diverse, associated with chondrocyte attachment (CHAD), immune activity (RNASE3), neuronal signalling (KIDIN220), and T-cell calcium signalling (TRPM4). These findings suggest that magnetic field exposure may influence immune regulation, tissue remodelling, and neuroimmune communication pathways.

Beyond these core proteins, several additional targets identified in both statistical tests offer further insight into the potential biological effects of magnetic field exposure. POC1B, a centrosomal protein, is necessary for centriole assembly and stability, implicating magnetic fields in regulating cell division and cytoskeletal integrity. CAMSAP1, a microtubule-binding protein, is similarly involved in maintaining cell architecture, suggesting possible modulation of structural protein dynamics in epithelial cells.

MUC20 interacts with the MET signalling pathway, which governs cell proliferation and epithelial repair. Its regulation may reflect EMF-induced changes in epithelial homeostasis or mucosal surface responses. EHF, an ETS-family transcription factor, is associated with epithelial differentiation and barrier function — processes relevant to buccal mucosa integrity and stress adaptation.

At the metabolism and endocrine interaction level, HSD17B11 is involved in steroid metabolism and has been identified as a tumour-associated antigen in cutaneous lymphoma. While speculative, this finding may indicate subtle EMF interactions with lipid signalling or hormone pathways. These observations and TRPM4's involvement in calcium dependent signalling and immune activation suggest that magnetic field exposure can influence various functional systems — including immune surveillance, tissue remodelling, and cell cycle control.

Enriching proteins associated with immune function suggests that magnetic field exposure may stimulate or modulate the innate immune system, even without external pathogens or stressors. The involvement of proteins such as TRPM4 and KIDIN220 further raises the possibility of EMF-induced changes in calcium signalling and neuroimmune cross-talk. These mechanisms are particularly interesting in neurorehabilitation, inflammation, and tissue repair.

The return of proteomic profiles toward baseline after a three-day washout phase indicates that the intervention's effects are at least partially reversible. However, not all proteins returned to baseline, which suggests that exposure duration, intensity, or individual susceptibility may influence the persistence of effects.

Feasibility Outcomes

This pilot study also confirmed the methodological feasibility of conducting proteomic analysis using buccal cell samples collected via at-home kits, utilising the Epi-Proteomics Test kit from MOLEQLAR Analytics [23]. Sample collection adherence was high, with only one participant excluded due to incomplete submission. Based on data-independent acquisition (DIA) and DIA-NN analysis, the proteomics workflow yielded robust protein identification (ranging from 2000 to 4000 protein groups per sample), confirming the method's sensitivity in a minimally invasive context. Normalisation and imputation procedures were successfully applied, and most samples passed quality control despite the known challenges of working with buccal material. The combined experimental protocol—including the magnetic field intervention, sampling timeline, and mass spectrometry analysis—was executed without technical or procedural complications. These findings support the viability of using this approach in larger-scale studies and suggest that buccal cells are a practical and responsive biosource for detecting short-term molecular effects of EMF exposure.

Comparison with Previous Literature

Our findings align with prior studies suggesting that electromagnetic fields (EMFs) can modulate biological activity at the cellular and molecular level. Earlier work has demonstrated that pulsed or extremely low-frequency EMFs may affect gene expression, apoptosis, and inflammatory signalling [32, 34]. The observed changes in immune-related proteins and those involved in cell proliferation are consistent with reported effects of EMFs on macrophage activation, cytokine release, and cellular metabolism [44, 32, 45].

To date, relatively few studies have applied high-resolution proteomics to evaluate human responses to electromagnetic field exposure, highlighting a methodological gap in the field [32, 44, 46]. This study addresses that gap by demonstrating the technical feasibility of proteomic profiling using non-invasively collected buccal samples and provides novel candidate protein markers responsive to magnetic field exposure.

Limitations

Several limitations must be acknowledged. First, the sample size was small, and the gender distribution was unbalanced, with only female participants in the intervention group. This limits the generalizability of the findings and precludes subgroup analysis. Second, while the proteomic analysis was rigorous, the absence of a matched epigenetic dataset limits the interpretation of broader regulatory mechanisms.

Additionally, although exposure was standardized in duration and frequency (Schumann frequency, 7.83 Hz), the intensity and spatial distribution of the magnetic field were not quantified in physical units. This fact restricts comparability with other EMF studies and should be addressed in future experimental setups.

Future Directions

The observed changes support the feasibility of using buccal cell proteomics as a sensitive, noninvasive method to track biological responses to magnetic field exposure. Future studies should include larger, gender-balanced cohorts and extended follow-up periods to examine long-term effects and dose dependence. Parallel gene expression and epigenetic modification analysis would provide a more comprehensive view of the regulatory cascades involved.

In addition, quantifying and calibrating magnetic field intensity, including physiological endpoints (e.g., HRV, inflammation markers), and exploring clinical relevance in specific patient populations (e.g., pain, neuroinflammation) would enhance translational potential.

Conclusion

This study provides preliminary evidence that short-term exposure to low-frequency magnetic fields via the Vitori mat [22] induces significant proteomic changes in human buccal cells. Using a controlled pre-post-follow-up design, we identified 108 differentially expressed proteins between the control and intervention groups and 67 proteins with significant temporal changes within the intervention group. Enrichment analysis revealed biological pathways related to immune function, stress regulation, and cellular remodelling, with several protein expression trends suggesting partial reversibility following a short washout period.

In addition to its biological insights, the study confirmed the methodological feasibility of combining non-invasive buccal cell sampling with high-resolution mass spectrometry and statistical proteomics. The successful implementation of this workflow—across participant recruitment, sample collection, magnetic field exposure, and proteomic analysis—demonstrates the practicality of this approach for future molecular studies involving human participants.

The findings highlight the potential of buccal cell proteomics as a sensitive tool for capturing short-term molecular responses to electromagnetic field exposure. By identifying candidate protein markers linked to immune signalling and cell stress, this work lays the foundation for larger-scale investigations and supports the future development of EMF-based therapeutic monitoring strategies. Further research is warranted to validate these findings in more diverse populations, extend follow-up durations, and incorporate complementary genomic and physiological endpoints.

Ultimately, this study advances the emerging field of bioelectromagnetic research by offering new molecular evidence and a scalable methodological framework to explore the therapeutic and biological effects of magnetic field interventions in humans.

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