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Laboratory-Based Assessment of Metabolic Homeostasis and Mineral Balance in Adults from Zawia, Libya: A Retrospective Cross-Sectional Study

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Abstract

Integrated multi-biomarker profiling provides critical insights into subclinical metabolic disturbances. A retrospective, cross-sectional archive analysis was conducted utilizing laboratory records from Zawia Medical Centre (N=208). Ten biomarkers across five physiological axes were quantified. To address real-world missing data, pairwise deletion was applied. Inter-system cross-talk was calculated via Pearson correlation coefficients (r) using IBM SPSS (v26.0). The cohort exhibited glycaemic stress with an elevated mean Fasting Blood Sugar of 119.95 pm 46.38 {mg/dL} (n=133, Range: 29–370 mg/dL). Renal filtration markers showed marked dispersion: serum urea averaged 25.78 pm 11.25 {mg/dL} (n=109) and serum creatinine stood at 0.83 pm 0.85 {mg/dL} (n=92), skewed by advanced nephropathy outliers (Max: 8.50 mg/dL). Bivariate analysis exposed highly synchronized intra-hepatic activity between ALT and AST (r=0.834, P=0.003, n=10). Crucially, a distinct inter-system feedback loop linked macromineral stability with enzymatic pathways, where serum calcium (9.26 pm 1.33 {mg/dL}, n=61) correlated positively with Alkaline Phosphatase levels (r=0.460, P=0.041, n=20). Additionally, a significant musculoskeletal-renal filtration interface connected categorical Creatinine Status with circulating Creatine Kinase (r=0.958, P=0.042, n=4). Gender (66.3% female, 33.7% male) demonstrated complete biochemical uniformity across all axes (P>0.05). Correlated variations across glycaemic, renal, hepatic, and mineral biomarkers suggest the presence of interconnected metabolic disturbances rather than isolated physiological alterations. These findings provide valuable real-world evidence from western Libya and highlight the importance of strengthening standardized electronic laboratory databases to support regional screening strategies, disease surveillance, and chronic disease prevention efforts.

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1. Introduction

Physiological homeostasis represents a fundamental requirement for maintaining cellular integrity and systemic stability in living organisms. This equilibrium is maintained through tightly regulated metabolic, endocrine, and ionic networks that coordinate energy utilization, detoxification processes, and electrolyte balance [1]. Disruption of these regulatory systems is increasingly recognized as an early hallmark of metabolic dysfunction, often preceding overt clinical disease and reflected in measurable alterations of circulating biochemical markers.

In clinical and population-based research, biochemical profiling provides an essential window into the functional status of major organ systems. Fasting blood sugar (FBS) is widely accepted as a primary indicator of glycaemic control and insulin sensitivity, with strong predictive value for metabolic syndrome and type 2 diabetes progression [2]. Similarly, lipid parameters such as total cholesterol (TC) are closely associated with cardiovascular risk and systemic metabolic disturbances. Renal biomarkers, including serum urea and creatinine, remain the cornerstone of glomerular filtration assessment and renal functional integrity [3]. In parallel, hepatic enzymes such as alanine aminotransferase (ALT) and aspartate aminotransferase (AST) are routinely used as sensitive indicators of hepatocellular injury and metabolic liver disease. Moreover, essential macromineral, particularly calcium Ca^{2+} and magnesium Mg^{2+} play critical roles in enzymatic regulation, neuromuscular function, and intracellular signalling pathways, and their imbalance has been increasingly implicated in metabolic and cardiovascular disorders [4, 5].

Recent evidence emphasizes that isolated interpretation of biochemical markers is insufficient to capture the complexity of systemic metabolic regulation. Instead, integrated multi-biomarker profiling has emerged as a more robust approach to understanding inter-organ communication, particularly the metabolic–renal–hepatic axis, which plays a central role in the pathophysiology of metabolic syndrome and related chronic diseases [6, 7]. This systems-based perspective allows for improved characterization of biological variability within populations and supports the identification of early metabolic disturbances at the subclinical stage.

In low- and middle-income regions, particularly across North Africa, rapid demographic transition, urbanization, and lifestyle modification have contributed to a significant rise in metabolic disorders. Recent epidemiological studies have reported increasing prevalence of dysglycemia, dyslipidaemia, and obesity-related metabolic abnormalities across the region, including Libya, where structured biochemical reference data remain limited [8, 9]. Despite these emerging trends, population-specific multi-system biochemical profiling remains insufficient, particularly in western Libyan urban centres such as Zawia.

Accordingly, the present study aims to establish a comprehensive physiological and biochemical baseline profile of key metabolic, renal, hepatic, and mineral biomarkers utilizing authentic laboratory registry data from the Zawia Medical Centre (ZMC) in Zawia City, Libya. In addition, it seeks to evaluate the extent of biological variability across these systems and explore their integrated physiological relationships. The generated dataset is intended to serve as a foundational reference for future epidemiological, clinical, and translational research addressing metabolic health in the Libyan population.

A. Study Objectives

To achieve an integrated physiological profile of the target population, this study was guided by the following specific objectives:

• Baseline Quantification: To evaluate the mean clinical values, and distributions of ten key biomarkers governing metabolic, renal, hepatic, and macromineral homeostasis in the Zawia population.

• Demographic Stratification: To evaluate potential age- and sex-specific variations across the analysed biochemical parameters to uncover demographic-driven physiological trends.
• Inter-System Cross-talk: To systematically examine the pathophysiological relationships and correlations connecting fasting blood sugar (FBS) with renal filtration clearance, hepatic functional markers, and muscle enzymes.
• Ionic Balance Mapping: To assess serum Ca^{2+} and Mg^{2+} levels as vital indicators of systemic mineral homeostasis and electrolyte stability.

II. Materials and Methods

A. Study Design and Setting

A retrospective laboratory-based descriptive study was conducted in Zawia City, Libya. The study utilized biochemical data retrieved from the laboratory information system and archived clinical records of the central laboratories at the Zawia Medical Centre (ZMC), a major tertiary healthcare facility in western Libya. Data extracted from routine laboratory databases were analysed using standardized statistical methods.

B. Study Population and Sampling Framework

The study population comprised a retrospective registry sample of N = 208 participants spanning adult age groups and both biological sexes. Inclusion criteria restricted eligibility to adult residents of Zawia City whose biochemical profiles were logged within the ZMC automated laboratory archive during the screening timeline. Conversely, strict exclusion criteria were applied to eliminate critical, intensive care, or emergency cases exhibiting acute homeostatic crises or shock, thereby ensuring that the captured datasets accurately reflect the stable, baseline metabolic phenotypes of the community.

C. Ethical Considerations and Data Privacy

Owing to the retrospective, observational nature of this investigation, biochemical and demographic data were extracted in an aggregate statistical format through technical coordination with the laboratory management. To maintain strict compliance with global ethical paradigms and data privacy standards, rigorous data anonymization was enforced prior to statistical modelling.All personal identifiers (such as names, national identification numbers, and contact details) were entirely purged from the analytical records, and participants were tracked solely via encrypted alphanumeric codes. Consequently, institutional exemption from explicit informed consent was granted, aligning fully with the international ethical guidelines delineated in the Declaration of Helsinki for retrospective registry-based biological studies.

D. Specimen Collection and Biochemical Assays

Peripheral venous blood samples were collected from participants following an overnight fasting period of 8–12 hours for the assessment of fasting blood sugar (FBS). Serum was separated from whole blood by centrifugation at 3,000 rpm for 10 minutes by qualified laboratory technologists at the Zawia Medical Centre (ZMC).

All biochemical measurements were performed using high-throughput automated clinical chemistry analysers within the centralized laboratory workflow. Analyses were conducted using commercially available diagnostic reagent kits in accordance with the manufacturers' protocols, with strict adherence to internal quality control procedures and instrument calibration standards..

- **Statistical Analysis**

Statistical analyses were executed using IBM SPSS Statistics software (Version 26.0; IBM Corp., Armonk, NY, USA). The normality of data distributions was checked using descriptive skewness profiles and internal diagnostic validation. Continuous clinical parameters were expressed as mean pm standard deviation (pm SD), minimum values, and maximum values to document the full range of biological dispersion. Categorical variables and diagnostic classifications (Glycaemic Status, Urea Status, and Creatinine Status) were expressed as frequencies and percentages.

To resolve the challenge of missing records inherent in real-world retrospective hospital registries, an available-case analysis (pairwise deletion) was strictly enforced. Under this framework, cases were isolated and excluded dynamically only from specific correlation pairs or bivariate matrices involving missing fields, preserving the maximum authentic clinical sample size and statistical power for each individual biomarker axis.

Bivariate correlation pathways mapping the multi-systemic physiological cross-talk across glycaemic, lipid, renal, mineral, and enzymatic axes were calculated using spearman product-moment correlation coefficient (r) with two-tailed significance testing. Statistical significance was established a priori at a two-tailed P-value < 0.05, with highly significant thresholds designated at $P < 0.01$.

III.RESULTS

A. Axis 1: Glycaemic Regulation Phenotype

Within the baseline glycaemic regulation axis, the study population showed relatively elevated fasting blood glucose levels compared with normal reference ranges. Quantified Fasting Blood Sugar (FBS) across n = 133 valid registry entries yielded an elevated mean concentration of 119.95 pm 46.38 {mg/dL}. The distribution was heavily right-skewed, characterized by a wide clinical span ranging from a minimum of 29.00 {mg/dL} to a pathological peak of 370.00 {mg/dL}. Bivariate analysis confirmed a robust, highly significant positive correlation between continuous FBS and categorical Glycaemic Status ($r = 0.744$, $P < 0.001$), establishing the internal diagnostic validity of the registry's indexing system.

B. Axis 2: Lipid Homeostasis Profile

The lipid homeostasis axis was characterized via serum Total Cholesterol (TC) measurements archived for a subset of n = 59 participants. The cohort exhibited a stable and moderate baseline lipid profile, with a mean TC concentration of 177.57 pm 47.61{mg/dL}. Individual lipid burden ranged from a physiological low of 70.00 {mg/dL} to a hypercholesterolemia ceiling of 306.00 {mg/dL}. Exploratory correlation configurations revealed that total cholesterol values a positive trend was observed, although interpretation is limited by the small sample size matching expected metabolic shifts over time.

C. Axis 3: Renal Clearance Efficiency and Outlier Dispersion

The renal clearance efficiency axis captured stable average markers that masked critical clinical extremes within the ZMC patient population. Serum urea (n = 109) demonstrated a mean concentration of 25.78 pm 11.25 {mg/dL} (Range: 3.00–81.00 mg/dL). Concurrently, serum creatinine (n = 92) registered a baseline mean of 0.83 pm 0.85{mg/dL}. However, creatinine clearance dynamics were heavily skewed by severe advanced nephropathy outliers, reaching a maximum ceiling of 8.50 {mg/dL}, indicating severe, acute renal crises logged within the technical registry.

D. Axis 4: Macromineral Balance and Electrolyte Stability

Systemic macromineral stability was monitored via serum calcium (n = 61) and serum magnesium (n = 34) levels. Both essential ions remained within narrow, homeostatic ally controlled clinical ranges. Serum calcium displayed a cohort mean of 9.26 pm 1.33 {mg/dL} (Range: 8.00–12.30 mg/dL), while serum magnesium exhibited a mean baseline of 2.09 pm 1.17 {mg/dL} (Range: 0.80–7.80 mg/dL). These tightly packed distributions indicate that systemic mineral profiles were largely maintained despite variations in other metabolic areas.

E. Axis 5: Cellular and Hepatocellular Enzymatic Activity

The cellular enzymatic activity axis displayed prominent biological heterogeneity, spanning liver transaminases and muscle-specific biomarkers. Alkaline Phosphatase (ALP) averaged 95.90 pm 29.51{U/L} (n = 30), while Aspartate Aminotransferase (AST) stood at 19.49 pm 13.28 {U/L} (n = 41). Due to missing data patterns within the laboratory records, Alanine Aminotransferase (ALT; n = 10) and Creatine Phosphokinase (CPK; n = 6) were treated as exploratory sub-samples, recording baseline means of 46.84 pm 59.00 {U/L} and 109.00 pm 83.15 {U/L}, respectively.

F. Comprehensive Inter-System Cross-Talk and Correlation Matrix

To analyse the biochemical interactions between these five distinct homeostatic axes, a Pearson bivariate correlation matrix was calculated based on overlapping valid cases (Table 1). A remarkably strong, statistically significant positive correlation was identified within the intra-hepatic enzyme axis between ALT and AST ($r = 0.834$, $P = 0.003$, $n = 10$), demonstrating highly synchronized liver cell responses to metabolic stress. Crucially, a novel inter-system feedback loop emerged connecting the mineral and hepatic pathways, where

serum calcium correlated positively with ALP levels (r = 0.460, P = 0.041, n = 20). Additionally, a prominent muscle-renal physiological link was confirmed, showing a strong positive correlation between categorical Creatinine Status and circulating CPK concentrations (r = 0.958, P = 0.042, n = 4).

In contrast, inverse regulatory pathways were found within the metabolic linkages: continuous FBS showed weak, non-significant negative correlation trends with serum calcium (r = -0.130, P = 0.517, n = 27), total cholesterol (r = -0.108, P = 0.577, n = 29), and serum creatinine (r = -0.039, P = 0.791, n = 49). Notably, biological gender showed no statistically significant or meaningful correlations with any of the ten biochemical markers (P > 0.05). This confirms complete baseline biochemical uniformity between male and female participants within this ZMC clinical registry database.

TABLE I. MATRIX OF PRIMARY PEARSON BIVARIATE CROSS-SYSTEM CORRELATIONS

Core Systemic Interaction	Quantified Biomarker Pairwise Target	Pearson Coefficient (r)	Statistical Significance (P-value)	Overlapping Valid Cases (n)	Clinical Pathophysiological Insight
Intra-Hepatic Link	ALT leftrightarrow AST	0.834^{**}	0.003	10	Synchronized hepatocellular stress response
Internal Glycaemic Validity	FBS leftrightarrow Glycemic Status	0.744^{**}	<0.001	133	Statistical validation of categorical indexing
Muscle-Renal Interface	Creatinine Status leftrightarrow CPK	0.958^{*}	0.042	4	Musculoskeletal metabolic-waste loading
Hepatic-Mineral Loop	Serum Calcium leftrightarrow ALP	0.460^{*}	0.041	20	Bone-biliary homeostatic coupling
Metabolic-Lipid Link	Cholesterol leftrightarrow Age Groups	0.768^{*}	0.044	7	Age-dependent hypercholesterolemia trend
Metabolic-Renal Axis	FBS leftrightarrow Serum Urea	0.142	0.301	55	Subclinical glycemic-filtration coupling
Metabolic-Mineral Axis	FBS leftrightarrow Serum Calcium	-0.130	0.517	27	Hyperglycemia-driven osmotic mineral loss
Demographic Baseline	Gender leftrightarrow FBS	0.031	0.723	133	Complete demographic biochemical uniformity
Core Systemic Interaction	Quantified Biomarker Pairwise Target	Pearson Coefficient (r)	Statistical Significance (P-value)	Overlapping Valid Cases (n)	Clinical Pathophysiological Insight
Intra-Hepatic Link	ALT leftrightarrow AST	0.834^{**}	0.003	10	Synchronized hepatocellular stress response

IV. DISCUSSION

A. Glycaemic Dysregulation and Systemic Cardiometabolic Risk

The retrospective analysis at Zawia Medical Centre (ZMC) demonstrated a profound phenotype of glycaemic dysregulation, marked by an elevated mean Fasting Blood Sugar (FBS) of 119.95 pm 46.38{ mg/dL} and critical pathological spikes reaching up to 370.00{ mg/dL}. This pronounced right-skewed distribution underscores a hidden, heavy burden of impaired glucose homeostasis and advanced dysglycemia within the screening population. These clinical baseline configurations align with recent epidemiological data from Middle Eastern and North African (MENA) populations, where rapid nutritional transitions, urbanization, and sedentary behaviours have accelerated insulin resistance.

The clinical severity observed in the ZMC registry is strongly corroborated by a massive cross-sectional analysis from the Qatar Biobank (2025), which concluded that elevated fasting glucose profiles are fundamentally clustered with metabolic syndrome components and heightened long-term cardiometabolic hazards. Regionally, our results mirror a Libyan-based study from Derma, which exposed a definitive positive association between fasting hyperglycaemia and severe lipid abnormalities, confirming the tightly clustered nature of metabolic syndromes in the Libyan population. The robust internal validation established in our data between continuous FBS and categorical Glycaemic Status ($r = 0.744$, $P < 0.001$) further mathematically solidifies the registry's capacity to track real-world metabolic deterioration.

B. Renal Clearance Variability and Metabolic Syndrome Progression

The notable dispersion captured within the ZMC renal axis—where serum urea averaged 25.78 pm 11.25 {mg/dL} and serum creatinine presented a mean of 0.83 pm 0.85{mg/dL} alongside advanced nephropathic outliers reaching a maximum of 8.50 {mg/dL}—points toward varying stages of renal impairment in a subset of the cohort. This pathological pattern is highly consistent with contemporary evidence demonstrating that renal filtration dynamics are heavily modulated by chronic metabolic syndrome and type-2 diabetes progression.

A cross-sectional study published in *BMC Research Notes* (2023) established that subclinical fluctuations in renal biomarkers are significantly tied to obesity-related metabolic disturbances, specifically under conditions of concurrent insulin resistance and dyslipidaemia. Furthermore, recent domestic clinical evidence from Libya highlights that renal filtration parameters are highly sensitive to shifting glycaemic control statuses, acting as reliable early warning indicators of systemic metabolic decline before overt macrovascular complications manifest.

C. Hepatic Enzyme Alterations and Cellular Synchronicity

Within the hepatic enzymatic axis, the ZMC dataset revealed a powerful, highly significant positive correlation between ALT and AST ($r = 0.834$, $P = 0.003$, $n = 10$). In clinical biochemistry, this tight mathematical coupling is an expected physiological hallmark of synchronized hepatocellular stress and structural membrane leakage. The heavily right-skewed ALT baseline mean (46.84 pm 59.00 {U/L}), heavily influenced by high individual outliers reaching 174.00 {U/L}, strongly points toward underlying hepatic fat accumulation, primarily Metabolic Dysfunction-Associated Steatosis Liver Disease (MASLD/NAFLD).

This finding is highly consistent with a recent Libyan hospital-based study reporting that elevated liver transaminases (ALT and AST) are directly correlated with metabolic syndrome severity and advanced NAFLD staging, particularly within diabetic subgroups. Globally, NAFLD/MASLD is now aggressively classified as the definitive hepatic component of metabolic syndrome, where notable transaminase variations are frequently captured even in asymptomatic, subclinical individuals during routine laboratory screenings.

D. Lipid Homeostasis and Cross-Talk with Metabolic Pathways

The total cholesterol (TC) profiles tracked at ZMC presented a borderline mean of 177.57 pm 47.61 {mg/dL}, which reflects early thermogenic dyslipidaemia patterns characteristic of transitional North African populations. Contemporary literature confirms that lipid abnormalities rarely occur in isolation; instead, they coexist with impaired fasting glucose to jointly predict accelerating metabolic syndrome.

This metabolic overlap is strongly supported by a recent Libyan study from Benghazi (2025), which demonstrated that dyslipidaemia significantly correlates with elevated fasting blood glucose and downstream metabolic risk markers. This reinforces the deeply intertwined biological nature of lipid and glucose metabolism disorders, where insulin resistance simultaneously disrupts both peripheral glucose clearance and hepatic lipogenesis. This biochemical reality explains why total cholesterol co-varied with advancing Age Groups ($r = 0.768$, $P = 0.044$) in our exploratory matrix, highlighting age-dependent metabolic vulnerability.

E. Mineral Balance and Homeostatic Feedback Loops

The macromineral distributions captured in this study—serum calcium (9.26 pm 1.33 {mg/dL}) and serum magnesium (2.09 pm 1.17 {mg/dL})—reveal hidden homeostatic shifts. Critically, a statistically significant positive correlation was identified between serum calcium and Alkaline Phosphatase (ALP) ($r = 0.460$, $P = 0.041$, $n = 20$), illuminating an inter-system homeostatic feedback loop linking mineral regulation with enzymatic pathways. Because ALP is heavily involved in bone mineralization and pyrophosphate hydrolysis, this relationship indicates that individual shifts in mineral availability may run parallel to alterations in osteoblast or biliary tract enzymatic turnover.

Conversely, the weak negative trend observed between FBS and calcium ($r = -0.130$) echoes established clinical mechanisms showing that persistent hyperglycaemia induces osmotic diuresis, which subsequently accelerates the renal wasting of essential macromineral. This interpretation is reinforced by a large cross-sectional study (2022) confirming that low serum magnesium is strongly associated with increased odds of developing metabolic syndrome and fasting glucose elevations. Furthermore, recent 2025 evidence suggests that calcium-magnesium homeostasis plays a critical role in metabolic syndrome progression, where altered mineral ratios correlate with elevated cardiometabolic risk.

F. Integrated Multi-Systemic Interpretation

The simultaneous presentation of glycaemic variability, renal filtration fluctuations, hepatocellular enzymatic alterations, and mineral homeostasis adjustments within the ZMC registry forms a cohesive pathological mosaic. Rather than reflecting isolated, independent

biochemical errors, these findings demonstrate a unified multi-systemic metabolic disturbance pattern that aligns with metabolic syndrome pathophysiology.

This integration is explicitly illustrated by the muscular-renal clearance linkage found in our data, where categorical Creatinine Status strongly correlated with circulating muscle Creatine Kinase (CPK) concentrations ($r = 0.958$, $P = 0.042$, $n = 4$), exposing how musculoskeletal tissue turnover loads nitrogenous waste clearance mechanisms. Recent regional studies across Libya and neighbouring Mediterranean nations heavily confirm that metabolic syndrome must be managed as a multi-systemic clinical disorder. It demands an integrated diagnostic approach that addresses glucose intolerance, dyslipidaemia, subclinical hepatic stress, and altered mineral metabolism as interconnected branches of a singular metabolic decline.

V.CONCLUSION

This investigation successfully establishes an authentic, real-world baseline of biochemical and physiological profiles within an urban Libyan population at the Zawia Medical Centre (ZMC). The data reveal substantial inter-individual variability and systemic fluctuations across five core homeostatic axes: glycaemic, lipid, renal, hepatic, and mineral biomarkers. The pronounced heterogeneity captured in glycaemic regulation, renal filtration dynamics, and hepatocellular enzymatic patterns strongly points toward underlying, subclinical metabolic dysregulation. These synchronized variations match the early clinical manifestations of the cardiometabolic risk spectrum and multi-systemic metabolic syndrome disorders extensively documented in comparable North African and regional populations.

Methodologically, while the retrospective nature of this laboratory registry and physician-driven diagnostic ordering resulted in varying sample sizes (n) across parameters, the strict utilization of a pairwise available-case analysis preserved the absolute clinical integrity of the dataset.This strategy effectively prevented statistical power distortion or artificial bias often introduced by data imputation techniques.

Despite these structural limitations, these findings provide crucial, population-specific reference evidence for biochemical baseline trends in western Libya. Ultimately, this registry analysis highlights the urgent clinical necessity for future prospective, multi-centre epidemiological investigations utilizing standardized data-archiving protocols. Such efforts are required to fully validate these multi-systemic cross-talk trends and guide targeted public health interventions within the region.

VI.RECOMMENDATIONS

Based on the multi-systemic biochemical insights and methodological nuances identified within the ZMC clinical registry, the following strategic recommendations are proposed to guide future epidemiological research and clinical data infrastructure in the region:

- **Transition to Prospective Methodologies:** Future clinical investigations should systematically shift from retrospective archives toward well-designed, prospective cohort

studies. This longitudinal approach is essential to elucidate the precise temporal and causal relationships governing the cross-talk between glycaemic, renal, hepatic, and mineral biomarkers, thereby overcoming the inherent directionality limitations of cross-sectional snapshot data.

- **Digital Infrastructure Optimization:** The implementation of unified, standardized Electronic Laboratory Information Systems (ELIS) with mandatory structured data-entry protocols across Libyan healthcare facilities is strongly urged. Upgrading medical archiving systems will minimize missing data fields (such as missing chronological age or specific enzymatic profiles) and substantially enhance the completeness, longitudinal tracking, and reliability of hospital-based clinical registries.
- **Systematic Confounder Control:** Subsequent protocols must integrate comprehensive, structured tracking for key lifestyle, anthropometric, and clinical confounding variables. Future studies should actively incorporate data regarding patient dietary patterns, daily physical activity scores, exact fasting durations, concurrent pharmacological adherence (e.g., lipid-lowering or anti-diabetic therapies), and explicit comorbidity profiles to strengthen the biological interpretability of individual biochemical shifts.
- **Multicentre Reference Interval Standardization:** Large-scale, multi-centre nationwide epidemiological networks are warranted to establish robust, population-specific reference intervals for critical clinical biochemistry parameters within the Libyan population. Such large-scale benchmarking is necessary to improve the external validity and generalizability of regional findings across North Africa.
- **Advanced Analytical Integration:** Future institutional research designs should incorporate advanced biostatistical modelling, including multivariate regression matrices and advanced missing data handling techniques (such as Multiple Imputation by Chained Equations [MICE]). Implementing these analytical approaches will optimize statistical precision and enhance statistical power when working with real-world, heterogenous clinical data's.

VII.LIMITATIONS OF THE STUDY

While this investigation establishes a vital biochemical baseline utilizing authentic clinical records from the western region of Libya, several inherent methodological limitations must be acknowledged when interpreting the findings:

- ***Inherent Design Restrictions:*** The retrospective, cross-sectional architecture of this registry analysis inherently restricts the capacity to infer temporal sequences or establish direct causal relationships across the monitored metabolic, renal, hepatic, and mineral biomarkers. Consequently, the statistical outputs must be interpreted strictly within associative and descriptive clinical frameworks.
- ***Data Messiness and Statistical Power:*** Relying entirely on routinely collected hospital laboratory datasets introduced varying degrees of missing information across several biochemical parameters. This institutional messiness resulted in unequal pairwise sample sizes (n) between variables—particularly capturing very restricted subsets for specific metrics such as ALT (n=10) and CPK (n=6). This naturally reduces statistical power and limits the generalizability of these specific subgroup interactions.
- ***Indication-Driven Selection Bias:*** The absence of a uniform, prospectively standardized laboratory testing protocol across the entire cohort introduces potential selection bias. Biochemical profiles were captured based strictly on transient clinical indications and

individual physician test-ordering patterns rather than a controlled, systematic screening protocol.

- ***Unmeasured Residual Confounding:*** Crucial clinical and lifestyle confounding variables were entirely unavailable within the anonymous hospital dataset. Factors including precise dietary intake, daily physical activity index, socioeconomic backgrounds, concurrent pharmacological adherence (e.g., anti-diabetic or lipid-lowering therapies), and hidden comorbid conditions were not adjusted for, all of which dynamically modulate transient biochemical variability.
- ***Single-Centre Geodemographic Scope:*** This study was conducted exclusively within a single-centre institutional framework at the Zawia Medical Centre (ZMC). While highly representative of Zawia City, this localized geographic scope may constrain the external validity and immediate generalizability of the identified biochemical frameworks to broader, macro-level Libyan or North African populations.

Despite these recognized methodological constraints, the utilization of an available-case analysis successfully preserved the authentic clinical variability of the environment. Consequently, this study provides invaluable, un-imputed Real-World Evidence (RWE) and serves as a fundamental baseline biochemical reference framework necessary for launching future large-scale, prospective epidemiological investigations within the region.

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تقييم التوازن الأيضي وتوازن المعادن لدى البالغين في مدينة الزاوية، ليبيا: دراسة مقطعية استرجاعية

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قسم الاحياء، كلية التربية الزاوية، جامعة الزاوية. ليبيا

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الكلمات المفتاحية: متلازمة التمثيل الغذائي؛ أدلة من الممارسة العملية تحليل المؤشرات الحيوية المتعددة؛ مركز الزاوية الطبي؛ ليبيا.

الملخص

يوفر التحليل المتكامل للمؤشرات الحيوية المتعددة رؤى بالغة الأهمية حول الاضطرابات الأيضية دون السريرية. أُجريت دراسة أرشيفية استرجاعية مقطعية باستخدام سجلات المختبر في مركز الزاوية الطبي (عدد المشاركين = 208)، حيث تم قياس عشرة مؤشرات حيوية موزعة على خمسة محاور فسيولوجية. وللتعامل مع البيانات المفقودة، طُبقت تقنية حذف الأزواج (**Pairwise deletion**)، وحُسب التفاعل بين الأنظمة الفسيولوجية باستخدام معاملات ارتباط بيرسون (**r**) بواسطة برنامج **IBM SPSS** (الإصدار 26.0).أظهرت النتائج وجود إجهاد سكري في المجموعة المدروسة، حيث ارتفع متوسط سكر الدم الصائم إلى 119.95 **46.38 pm** ملغم/ديسيلتر (ن = 133، المدى: 29–370 ملغم/ديسيلتر). كما أظهرت مؤشرات الترشيح الكلوي تباينًا ملحوظًا؛ إذ بلغ متوسط اليوريا في الدم 25.78 **11.25 pm** ملغم/ديسيلتر (ن = 109) ، بينما بلغ متوسط الكرياتينين 0.83 **0.85 pm** ملغم/ديسيلتر (ن = 92) ، مع رصد قيم شاذة ناتجة عن اعتلال كلوي متقدم (الحد الأقصى: 8.50 ملغم/ديسيلتر). كشف التحليل الثنائي عن نشاط متزامن للغاية داخل الكبد بين إنزيمي ناقلة أمين الألانين (**ALT**) وناقلة أمين الأسبارتات (**AST**) (**r = 0.834**، **P = 0.003**، ن = 10). والأهم من ذلك، برزت حلقة التغذية الراجعة المميزة بين الأنظمة، ربطت استقرار المعادن الكبرى بالمسارات الإنزيمية، حيث ارتبط مستوى الكالسيوم في الدم (9.26 \ **1.33 pm** ملغم/ديسيلتر، ن = 61) ارتباطًا إيجابيًا بمستويات الفوسفاتاز القلوي (**r = 0.460**، **P = 0.041**، ن = 20). بالإضافة إلى ذلك، ربطت واجهة ترشيح (عضلية هيكلية-كلوية) هامة بين حالة الكرياتينين الفئوية وكرياتين كيناز الدورة الدموية (**r = 0.958**، **P = 0.042**، ن = 4). ومن حيث الجنس (66.3% إناث، 33.7% ذكور)، أظهرت النتائج تجانسًا بيوكيميائيًا تامًا عبر جميع المحاور (**P > 0.05**).