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Camel milk and microRNAs: a narrative review integrating molecular evidence, bioinformatics, and nutraceutical perspectives on metabolic diseases in the Sahel

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Abstract

Camel milk is increasingly recognized as a promising nutraceutical resource for addressing the double burden of malnutrition and metabolic disease in the Sahel, within a broader context of epidemiological and nutritional transition. This narrative review synthesizes recent evidence published between 2020 and 2024 on the molecular mechanisms underlying the metabolic effects of camel milk, with particular attention to the Sahelian context and Chad. Current evidence indicates that camel milk has a distinctive nutritional profile, characterized by relatively low lactose content, a favorable proportion of unsaturated fatty acids, and the presence of stable extracellular vesicles, including exosomes, enriched in bioactive microRNAs (miRNAs). miRNAs are short non-coding RNA molecules involved in the post-transcriptional regulation of gene expression. Extracellular miRNAs have been identified in bodily fluids, suggesting that they may facilitate epigenetic communication between tissues. Furthermore, miRNAs are highly conserved molecules across animal species, especially among mammals; therefore, it is reasonable to expect that the targets of miRNAs are orthologous genes in different species. In addition to well-described miRNAs such as miR-148a, miR-30d, and miR-21, recent sequencing studies have identified additional conserved miRNAs across camel species, including let-7i-5p, let-7b-5p, miR-200a-3p, and miR-26a-5p. Integrative analysis of experimentally validated and high-confidence predicted target genes suggests convergence on pathways involved in insulin signaling, adipogenesis, inflammatory regulation, growth control, and cellular homeostasis. Preclinical studies and a limited number of clinical trials suggest that camel milk may exert antidiabetic and hypolipidemic effects. However, important challenges remain, including seasonal variability in milk composition, limited preservation infrastructure, the lack of regulatory frameworks supporting health claims, and the absence of clinical evidence generated in Sahelian populations. Overall, camel milk emerges as a biologically relevant food matrix with potential metabolic benefits in environments undergoing rapid dietary transition. Nevertheless, its proposed nutraceutical role remains to be confirmed through locally grounded translational and clinical research addressing exosome miRNA bioavailability, mechanism of action, and context-adapted valorization strategies.

Key words: camel milk; exosomes; microRNAs; metabolic diseases; Sahel; Chad.

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Introduction

The health landscape of Sub-Saharan Africa, and particularly of the Sahelian region, is characterized by a rapid epidemiological transition. While challenges related to infectious diseases and malnutrition persist, the prevalence of non-communicable diseases (NCDs), notably type 2 diabetes and obesity, is increasing at an alarming rate, creating a double burden that places increasing pressure on health systems.[1,2] This situation is closely linked to an ongoing nutrition transition, marked by a gradual shift from traditional diets toward more energy-dense and highly processed foods, especially in rapidly urbanizing African settings. Chad illustrates this duality acutely, with a prevalence of childhood stunting approaching 30% and a documented rise in cardiometabolic risk factors in the urban context.[3,4]

In response to this complexity, identifying innovative, accessible, and culturally grounded nutritional solutions has become a public health priority. In this context, camel milk (*Camelus dromedarius*) emerges as an endogenous resource with underexploited potential. A staple food of Sahelian pastoral communities

for millennia, it has been empirically recognized for its health benefits. Historically, camel milk has supported human survival in arid environments characterized by water scarcity, caloric restriction, and metabolic stress, suggesting a context-specific nutritional role in desert ecosystems. Recent scientific research has begun to substantiate these effects, highlighting promising antidiabetic and hypolipidemic properties.[5,6] Understanding these effects has entered a new era with the investigation of bioactive components of milk. Beyond its distinctive macronutrient composition (low lactose content and a lipid profile rich in unsaturated fatty acids), attention has increasingly focused on extracellular nanovesicles, particularly exosomes. These natural carriers (30-150 nm), present in milk, are recognized for their resistance to digestion and their role in intercellular transfer of signaling molecules.[7,8] Their cargo includes microRNAs (miRNAs), small non-coding RNAs capable of modulating host gene expression, suggesting a sophisticated molecular mechanism of trans-species regulation.[9,10] miRNAs have very similar sequences across mammalian species (highly conserved). It is therefore reasonable to expect that the targets of these probably functionally homologous miRNAs are orthologous genes in the different species. Specific miRNAs such as miR-148a, miR-30d, and miR-21, which are abundant in camel milk, are involved in the regulation of key metabolic and inflammatory human pathways.[11,12] More recently, additional conserved human miRNAs (hsa-let-7i-5p, hsa-let-7b-5p, hsa-miR-200a-3p, and hsa-miR-26a-5p) have been identified across different camel species, reinforcing the hypothesis of a coordinated regulatory network of communication and "epigenetic priming" by camel milk on human gene regulation.[13] However, although the beneficial properties of camel milk are increasingly documented, a critical and up-to-date synthesis linking these emerging molecular mechanisms (exosomes/ miRNAs), evidence of metabolic efficacy, and the challenges of valorization in the Sahelian context is still lacking. In particular, the potential relevance of camel milk within the framework of nutrition transition and adaptive responses to desert environments remains insufficiently explored. Most existing reviews adopt a general approach or focus on only one of these dimensions.

This narrative review therefore aims to: i) synthesize recent scientific evidence on the molecular mechanisms underlying the metabolic effects of camel milk, with particular emphasis on the role of nanovesicles and miRNAs; ii) evaluate its nutraceutical potential for the prevention and management of metabolic diseases; and iii) propose perspectives and recommendations for research and development of this sector in the specific context of the Sahel and Chad by identifying knowledge gaps and actionable levers.

Methods

This narrative review followed a structured literature search strategy to synthesize current knowledge on the molecular mechanisms and nutraceutical potential of camel milk in the context of metabolic diseases in the Sahel, with particular emphasis on Chad.

Context and complementary sources

Initially, reports from international and national organizations (WHO, UNICEF, INSEED Chad) were consulted to define the epidemiological context of the double burden of malnutrition in the region.

Systematic search of the scientific literature

A targeted bibliographic search was conducted in July 2024 using PubMed/MEDLINE, Web of Science, and Scopus. The search strategy combined terms related to camel milk, exosomes, miRNAs, metabolic diseases, and the Sahel/Chad, using Boolean operators.

Selection criteria

Priority was given to peer-reviewed scientific publications published between 2020 and 2024, including original research articles, systematic or narrative reviews, and short communications. Publications prior to 2020, considered foundational or essential for understanding core concepts (*e.g.*, early studies on the stability of milk-derived miRNAs or the role of exosomes), were selectively included to ensure completeness of the theoretical framework. Particular attention was paid to studies conducted in Africa and within the Sahelian context (Table 1).

Analysis and synthesis

Data from the 30 selected publications were extracted and organized thematically to construct the narrative synthesis presented herein, structured around the following axes: i) composition and variability, ii) role of nanovesicles, iii) miRNA mechanisms, iv) evidence of metabolic efficacy, and v) challenges related to valorization.

Results

This section presents a critical analysis of the selected scientific publications (2020-2024), organized according to the four predefined thematic axes.

Table 1. Article selection process for the narrative review.

Process stage	Number of articles	Criteria/actions
1. Identification	142	Articles identified through database searches (PubMed, Web of Science, Scopus) and screening of reference lists
2. Screening	65	Title and abstract screening to assess relevance to the following themes: camel milk, molecular mechanisms (exosomes, miRNAs), metabolic diseases, and the Sahelian context
3. Eligibility	30	Full-text assessment of selected articles with strict application of inclusion and exclusion criteria
4. Inclusion (final corpus)	30	Articles included in the qualitative synthesis, comprising publications up to July 2024 and selected pre-2020 studies retained for their foundational value

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Biochemical composition and variability in the Sahelian environment

Recent studies confirm the uniqueness of camel milk and its adaptation to environmental constraints.

Recent reviews have consistently reported that camel milk exhibits a lipid profile favorable to cardiometabolic health, characterized by a high proportion of unsaturated fatty acids, including linoleic acid.[14]

However, this composition is not static. A study conducted in Sudan revealed significant seasonal variability, with marked decreases in fat content and bioactive proteins, such as lactoferrin, during the dry season, in direct correlation with forage availability and quality.[15] This variability, intrinsic to extensive pastoral systems, represents a major challenge for standardization while also reflecting the adaptive physiology of camels in resource-constrained environments.

Milk-derived nanovesicles (exosomes): isolation, characterization, and stability

The characterization of extracellular nanovesicles from camel milk has progressed significantly. A 2022 study succeeded in isolating and characterizing their proteome, revealing an abundance of membrane proteins involved in vesicular trafficking and a lipid composition rich in cholesterol and sphingomyelin, suggesting enhanced structural stability.[16] This stability is fundamental to their bioactivity. Studies conducted under simulated gastrointestinal conditions suggest that camel milk-derived bioactive components may exhibit substantial stability, supporting their potential for oral delivery.[17]

Bioactive miRNAs and mechanisms of action

The molecular cargo of these exosomes is particularly rich in miRNAs. Comprehensive profiling using high-throughput sequencing identified highly conserved and abundant miRNAs, including miR-148a, miR-30d, and miR-21.[18] Mechanistic studies attribute key roles in metabolic regulation to these miRNAs. miR-148a and miR-30d display context-dependent roles, acting as tumor suppressors or oncogenic regulators depending on tissue and disease state. miR-148a has been identified as a negative regulator of adipogenesis by directly targeting the expression of the transcription factor PPARγ, a master regulator of adipocyte differentiation.[18,19] miR-30d, in turn, enhances insulin signaling by inhibiting the expression of PTEN, a major negative regulator of the phosphoinositide 3-kinase/protein kinase B (PI3K/Akt) pathway, which is essential for insulin action.[18] Finally, miR-21, classically considered an oncomiR, which consistently represses tumor-suppressor genes, modulates the inflammatory response by attenuating activation of the nuclear factor (NF)-κB pathway through negative regulation of its activator PDCD4, thereby linking camel milk consumption to a reduction in low-grade inflammation.[20] Table 2 summarizes the miRNAs identified in camel milk exosomes and their principal biological pathways based on literature synthesis and bioinformatics-supported target interpretation.

Conserved miRNA expression and anti-proliferative mechanisms

Target gene analysis of conserved miRNAs

Five miRNAs were consistently expressed across all four camel species:[18] hsa-miR-148a-3p, hsa-let-7i-5p, hsa-let-7b-5p, hsa-miR-200a-3p, and hsa-miR-26a-5p. Target gene analysis utilized experimentally validated targets from miRTarBase and high-confidence predictions from RPmirDIP (top 1% of >2,500 genes). Analysis revealed that hsa-miR-148a-3p, hsa-let-7i-5p, and hsa-let-7b-5p converge on shared target genes, while hsa-miR-200a-3p and hsa-miR-26a-5p exhibit non-overlapping target profiles, suggesting functionally distinct regulatory roles.

Convergent targeting of growth-regulatory pathways

For the miRNA trio with overlapping targets, we identified eight experimentally validated common genes (*ARID3A*, *ARL8B*, *COLEC12*, *FAM104A*, *MYC*, *SLC12A7*, *USP38*, *WASL*) and two high-confidence predicted targets (*GMPS*, *SLC25A33*). Functional analysis suggests coordinated suppression of cellular proliferation through five complementary mechanisms.

Metabolic suppression: *GMPS* and *SLC25A33* targeting restricts nucleotide biosynthesis, creating a metabolic bottleneck that constrains DNA/RNA synthesis and shifts cells from expansive toward maintenance metabolic states.[21]

Growth arrest: *MYC* and *ARID3A* suppression halts transcriptional programs required for cell cycle progression and biomass accumulation, establishing strong anti-proliferative signals.[22]

Motility restriction: *WASL* and *SLC12A7* inhibition disrupts cytoskeletal dynamics and cell volume regulation, effectively limiting morphological changes required for migration.[23]

Trafficking disruption: *ARL8B* and *FAM104A* targeting impairs vesicle trafficking and protein localization, potentially preventing the secretion of matrix-degrading enzymes and altering the compartmentalization of growth signals.[24]

Protein turnover acceleration: *USP38* suppression enhances proteasomal clearance of pro-growth regulatory proteins, shortening the half-life of proliferative signals.[25]

These coordinated effects may create a cellular "stability state" characterized by tissue consolidation, balanced resource utilization, and reduced sensitivity to pro-growth stimuli even when such signals are present.

Table 2. miRNAs identified in camel milk exosomes and associated biological functions.

miRNA	Level of conservation	Main biological pathways involved	References
miR-148a-3p	High (across camel species)	Adipogenesis (PPARγ), insulin signaling, epigenetic regulation	11, 18, 19
miR-30d	High	Insulin signaling (PTEN/PI3K-Akt), autophagy	18, 19
miR-21	High	Inflammation (NF-κB), immune modulation	21, 40
hsa-let-7i-5p	Inter-species conserved	Cell proliferation control, metabolic regulation	18
hsa-let-7b-5p	Inter-species conserved	Cell cycle regulation, differentiation	18
hsa-miR-200a-3p	Inter-species conserved	Cellular plasticity, metabolic stress response	18
hsa-miR-26a-5p	Inter-species conserved	Energy metabolism, growth control	18

Hsa-miR-148a-3p exhibits expression levels approximately five-fold higher than other conserved miRNAs, suggesting a potentially dominant regulatory role. This miRNA is well characterized as a tumor suppressor involved in the regulation of DNA methyltransferases, immune checkpoints, and epithelial-mesenchymal transition.[26] The convergence of multiple miRNAs on overlapping anti-proliferative targets suggests evolutionary conservation and potentially amplified effects through redundant targeting.

The high expression of these miRNAs in camel milk may reflect regulatory features associated with camel adaptation to desert environments. Camel's express miRNAs, such as miR-148a and let-7e, that contribute to cellular stress resistance, potentially supporting tissue homeostasis under conditions of dehydration and resource limitation. The growth-restrictive regulatory profile described above may help reduce metabolic expenditure during periods of environmental stress, a physiological strategy that could contribute to the remarkable ability of camels to tolerate water loss exceeding 25% of body weight without circulatory failure, conditions that are fatal to most other mammals at approximately 12% dehydration.

These miRNAs have also demonstrated therapeutic relevance in human studies. miR-148a functions as a tumor suppressor across multiple cancer types, including gastric, colorectal, breast, and cervical cancers, through signal transducer and activator of transcription 3 (STAT3) and Akt pathway modulation.[27,28] Members of the let-7 family target oncogenes, including *RAS*, *HMGA2*, *c-Myc*, and *CCND1*, while regulating metabolism, proliferation, and apoptosis.[29,30] Let-7a has also been shown to influence cancer metabolism by downregulating anabolic enzymes and promoting oxidative phosphorylation, mechanisms that may also intersect with pathways involved in metabolic syndrome.

The consumption of dromedary camel milk by African populations presents an intriguing intervention scenario. Chad faces dual nutritional challenges, with approximately 31.1% of children under five affected by stunting, while metabolic diseases are emerging in urban settings.[3,4] Sub-Saharan Africa is undergoing a rapid nutrition transition toward Westernized diets, yet relatively few cancer epidemiology studies exist for the region.[31] Camel milk-derived miRNAs could theoretically provide protective regulatory signals during this transition; however, such benefits remain entirely dependent on their bioavailability.[18]

The realization of these mechanisms in human consumers depends critically on miRNA bioavailability. Dietary miRNAs must survive digestive degradation, cross intestinal barriers, and reach target tissues in functionally relevant concentrations. Although exosomal encapsulation may protect miRNAs and facilitate cellular uptake, the efficiency of absorption, tissue distribution, and achievable concentrations following dietary intake remains incompletely understood. This represents a major knowledge gap that requires validation through in vitro, in vivo, and clinical studies before nutraceutical claims related to cancer prevention or metabolic disease management can be substantiated in any population, including Sahelian communities.[8,32]

The principal experimentally supported and predicted shared targets of these conserved miRNAs and their functional implications are summarized in Table 3.

Evidence of efficacy on metabolic parameters

The effects suggested by cellular models are substantiated in more complex biological systems. A 2022 preclinical study demonstrated that oral administration of purified camel milk exosomes to streptozotocin-induced diabetic rats led to significant improvements in glucose tolerance, increased insulin sensitivity, and reduced hepatic lipid accumulation, supporting a potential causal contribution of this vesicular fraction in the observed metabolic improvements.[11] In humans, a three-month randomized controlled clinical trial provided robust evidence: daily consumption of 500 mL of camel milk by patients with type 2 diabetes resulted in a significant mean reduction in glycated hemoglobin of 1.1% and an improvement in lipid profiles, in contrast to the placebo group.[33] An associated pilot study (2022) suggests that these benefits may be partially mediated by positive modulation of the gut microbiota, with an observed increase in beneficial bacterial genera such as Bifidobacterium.[34]

Identified challenges for valorization in the Sahelian context

Despite this promising potential, the literature highlights critical obstacles specific to the Sahel. Natural compositional variability compromises the reproducibility of effects, underscoring the need for context-appropriate standardization protocols.[15] Technological constraints are substantial: the absence of cold-chain infrastructure and the use of traditional thermal processing methods (boiling) significantly compromise the integrity of thermosensitive components such as exosomes and bioactive proteins.[35] From a regulatory standpoint, there is a clear gap regarding health claims specific to camel milk, which hinders the development of a structured nutraceutical value chain.[36] Finally, a fundamental evidence gap remains: no randomized clinical trial has been published specifically involving Sahelian or Chadian populations, which considerably limits the transposability of the encouraging results obtained in other geographical and genetic contexts.[15,33]

Table 3. Shared target genes of conserved miRNAs (miR-148a-3p, let-7i-5p, let-7b-5p) and functional implications.

Target gene	Evidence type	Main biological function	Expected physiological impact
MYC	Experimental	Cell proliferation, metabolic regulation	Growth arrest
ARID3A	Experimental	Transcriptional regulation, cell cycle control	Tissue stabilization
GMPS	Predicted (high confidence)	Nucleotide biosynthesis	Metabolic restraint
SLC25A33	Predicted (high confidence)	Mitochondrial nucleotide transport	Energy limitation
WASL	Experimental	Cytoskeletal dynamics	Reduced cell migration
SLC12A7	Experimental	Ion transport, cell volume regulation	Cellular immobilization
ARL8B	Experimental	Vesicular trafficking	Inhibition of invasive signaling
FAM104A	Experimental	Protein localization and trafficking	Restriction of growth signals
USP38	Experimental	Protein turnover regulation	Accelerated clearance of pro-growth signals

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Discussion

This narrative review, based on a targeted corpus of recent publications (2020-2024), and supported by bioinformatics-based target interpretation, reveals that the nutraceutical potential of camel milk for the Sahel rests on a convergent triptych: a distinctive compositional matrix, stable nanometric vehicles (exosomes), and a cargo of regulatory molecules (miRNAs) whose molecular targets coincide with the pathogenic pathways of metabolic diseases. This discussion aims to interpret the strength and coherence of the available evidence and to derive concrete implications for research and public health in the region.

The synthesized data suggest a mode of action that is not linear but rather integrated and synergistic. The milk matrix itself, with its low lactose load and favorable lipid profile, creates a nutritional context that is less conducive to systemic inflammation and lipotoxicity.[14,37] Within this context, exosomes act as targeted delivery systems, protecting and transporting specific miRNAs (miR-148a, miR-30d, and miR-21) whose cellular targets identified *in vitro* form a coherent regulatory network: PPARγ (adipogenesis), PTEN (insulin signaling), and NF-κB/PDCD4 (inflammation).[19,38] This concordance between the molecular targets of miRNAs and the key dysfunctions of metabolic syndrome (insulin resistance, adipose tissue inflammation, and dyslipidemia) provides a plausible and elegant mechanistic basis for the empirically and clinically observed effects. However, this hypothesis of a "matrix effect", combining nutrients and dietary epigenetic signals, requires direct validation through studies comparing the effects of whole milk with those of its isolated fractions.

Although the proposed mechanistic framework is compelling, its level of translational evidence in humans and particularly in Sahelian populations remains to be strengthened. *In vitro* and preclinical studies provide convincing support,[11,19] but the missing link is the direct demonstration of systemic bioavailability and *in vivo* functional activity of camel milk-derived exosome miRNAs in humans. The clinical trial by Zheng *et al.*[33] demonstrates a strong correlation between consumption and clinical improvement, but does not establish a direct molecular causal relationship with exosomes. Pharmacokinetic studies using labeled exosomes, along with assessments of target gene expression in peripheral tissues of consumers, are therefore required.

Furthermore, a major geographical bias limits the scope of current conclusions. Advanced mechanistic evidence and the cited clinical trial originate from research conducted outside Africa.[11,33] To date, no randomized clinical trial has been published specifically involving Sahelian or Chadian populations.[15,33] This absence is critical, as factors such as genetic background, baseline diet, micronutrient status, and gut microbiome composition may significantly modify the response to intervention. Although data on local resource variability exist,[15] they cannot be linked to health outcomes in the absence of population-specific clinical studies. This gap represents the primary barrier to the transposability of promising findings and should be considered an absolute research priority. However, the identified challenges of variability, bioactive

Table 4. Strategic framework for research and integration of camel milk in public health (Chad and Sahel region).

Strategic axis	Primary objective	Proposed key actions
Local fundamental research	Establish a local scientific reference framework	Characterization of the miRNome and vesiculome of camel milk according to agro-pastoral zones and livestock management practices in Chad
Translational and clinical research	Evaluate efficacy and underlying biological mechanisms	Multicenter randomized clinical trials in the Sahel integrating metabolic parameters (HbA1c, lipid profile) and mechanistic biomarkers
Participatory technological innovation	Improve accessibility and sustainability	Co-development of low-cost, low-energy stabilization solutions in collaboration with herders and cooperatives
Public health integration	Strengthen prevention and nutrition strategies	Promotion of camel milk in national nutrition and NCD prevention strategies, and evaluation as a supplement in rural prediabetes management

HbA1c, hemoglobin; NCD, non-communicable disease.

Table 5. Implementation framework: from scientific validation to public health integration.

Strategic axis	Key objective	Priority actions
Local evidence generation	Scientifically validate health benefits	Launch the "Camel Milk Sahel" program; characterize exosomes and miRNAs; conduct the first RCT in prediabetic and type 2 diabetic patients
Context-appropriate innovation	Preserve milk bioactivity	Deploy solar-powered mobile cold-stabilization and freeze-drying micro-units
Equitable valorization framework	Protect producers and traditional knowledge	Initiate a PGI for "Sahelian camel milk"
Public health integration	Strengthen nutrition and NCD prevention	Integrate camel milk into national nutrition programs as a "double-duty" food
Governance and coordination	Ensure sustainability	Establish a multidisciplinary consortium (herders, researchers, policymakers, industry)

RCT, randomized controlled trial; PGI, protected geographical indication; NCD, non-communicable disease.

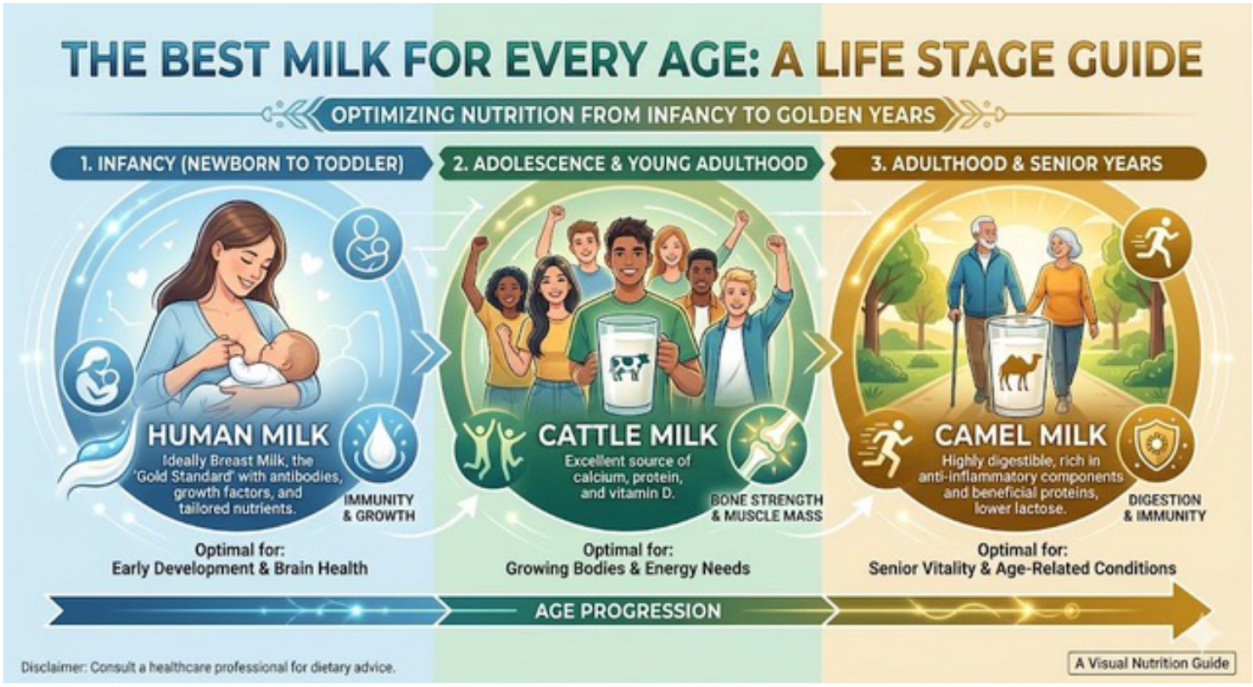

Figure 1. Illustrative image of milk consumption for different age groups.

instability, and the lack of a normative framework[15,35,36] should not be viewed as dead ends, but rather as entry points for context-adapted innovation.

Seasonal variability, which is well documented,[15] could be managed through enhanced traceability and product segmentation. Colostrum or rainy-season milk, richer in immunological and bioactive factors, could be directed toward high-value-added niche markets (nutraceutical applications), while dry-season milk could be stabilized for routine consumption. In particular, preservation of thermosensitive bioactive requires an adapted technological shift. Findings by Devarajan *et al.*[17] on exosome stability and by Arab *et al.*[35] on heat sensitivity argue for moving away from systematic boiling toward decentralized micro-processing units equipped with solar-powered cold storage and gentle drying technologies (freeze-drying), deployable in pastoral settings.

The regulatory gap, while a constraint, also represents an opportunity to design a tailored framework. The establishment of a protected geographical indication for "Sahelian camel milk", coupled with standards incorporating bioactivity markers (*e.g.*, minimum lactoferrin concentration or specific miRNA profiles), would help ensure quality, protect traditional knowledge, guarantee fair remuneration, and ground health claims in objective criteria.[36] Table 4 reports research perspectives and public health integration of camel milk, and Table 5 reports strategic recommendations for the valorization of camel milk in the Sahel region.

Limitations

As a qualitative narrative review, this work provides an interpretive synthesis of recent evidence rather than a formal systematic assessment of all available studies. Although a structured literature search strategy was adopted, the review remains subject to selection bias and to the inherent limitations of heterogeneous preclinical, mechanistic, and clinical evidence. In addition, the emphasis on literature indexed in major international databases may have led to the underrepresentation of unpublished, regional, or non-indexed studies from Sahelian settings.

Conclusions

This narrative, bioinformatics-driven review highlights camel milk as a distinctive nutraceutical matrix whose potential relevance to metabolic health in the Sahel is supported by converging nutritional, molecular, and adaptive considerations. Beyond its unique composition, camel milk contains stable exosomes enriched in bioactive miRNAs, including miR-148a, miR-30d, miR-21, and additional conserved miRNAs identified across camel species. Integrative analyses of their target genes suggest coordinated regulation of pathways involved in metabolic control, growth modulation, and cellular stability.

Within the context of nutrition transition in the Sahel, these molecular features may reflect adaptive biological strategies shaped by long-term exposure to desert environments characterized by resource scarcity and metabolic stress. In populations increasingly exposed to energy-dense diets, camel milk could represent a biologically congruent food, potentially supporting metabolic homeostasis. However, this interpretation remains hypothesis-generating and should be considered with caution.

Despite encouraging preclinical and limited clinical evidence, important gaps persist. The bioavailability and functional integration of milk-derived miRNAs in humans remain incompletely understood, and most clinical data originate from non-Sahelian

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populations. The absence of randomized clinical trials conducted in Chad constitutes a major limitation.

Future research should prioritize locally grounded translational approaches integrating molecular characterization, clinical evaluation, and context-adapted processing strategies. Addressing these gaps will be essential to support evidence-based valorization of camel milk and to assess its potential contribution to strategies aimed at mitigating the double burden of malnutrition and metabolic disease in the Sahel.

An additional conceptual perspective emerging from this review is that different mammalian milks may have age-specific functional relevance across the human life course (Figure 1). Within this framework, camel milk deserves particular attention in later adulthood because of its proposed metabolic regulatory properties. However, this hypothesis remains exploratory and requires validation through clinical and translational research.

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