Original Article

Multidomain Correlates of Telomere Shortening in Adults Receiving Advanced Wellness Programs in Thailand

Tanupol Virunhagarun[1] ; Jira Thawornpradit[2] ; Sureerat Sritangrattanakul[2] ; Natnaree Bunsiraphatsorn[2] ; Pornsawan Prutanopajai[2]

Tanupol Virunhagarun

[1] BDMS Wellness Clinic and BDMS Wellness Resort, Bangkok Dusit Medical Services Public Company Limited (BDMS), Bangkok, Thailand.
[2] Prevention and Wellness Clinic, BDMS Wellness Clinic, Bangkok, Thailand.

*Address Correspondence to author:
Natnaree Bunsiraphatsorn, MD
BDMS Wellness Clinic
2/4 Wireless Rd., Lumpini, Pathumwan,
Bangkok 10330, Thailand.
email: natnaree.bu@bdmswellness.com

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Abstract

OBJECTIVES: To characterize telomere length (TL) and determine biological and clinical factors associated with telomere shortening among individuals leukocyte telomere length (LTL) receiving an advanced wellness program at a clinical wellness institution in Thailand.

MATERIALS AND METHODS: This retrospective study included adults aged ≥18 years who underwent TL assessment as part of advanced wellness programs at two clinical wellness institutions in Thailand. Demographic, hormonal, micronutrient, metabolic, and clinical laboratory data were extracted from electronic medical records and laboratory databases within two weeks before or after TL measurement. Associations between TL and related demographic, hormonal, micronutrient, metabolic, and clinical variables were assessed using Pearson's correlation coefficient. A two-sided p-value < 0.05 was considered statistically significant.

RESULTS: Among 1,684 records, TL –derived biological aging was significantly associated with multiple biological domains. Higher levels of insulin-like growth factor 1 (IGF-1) and dehydroepiandrosterone sulfate (DHEA-S) were positively correlated with slower aging, while cortisol showed no significant association. Markers of glucose metabolism, including fasting glucose, HbA1c, and insulin, demonstrated consistent inverse correlations with TL, indicating accelerated aging with poorer glycemic control. Lipid parameters showed modest associations: total cholesterol and low-density lipoprotein cholesterol (LDL-C) were positively associated with slower aging, whereas triglycerides were inversely associated with faster aging. Ferritin levels were negatively correlated with telomere-related aging, while C-reactive protein (CRP) showed no consistent relationship. Several micronutrients and antioxidants, particularly magnesium, selenium, folate, vitamin D, and coenzyme Q10, exhibited significant inverse associations with accelerated aging, most prominently in the fast-aging group.

CONCLUSION: Telomere shortening was associated with specific biological domains, particularly metabolic regulation and endocrine function, followed by micronutrient status, whereas associations with acute inflammatory markers were limited. These findings support the role of TL as a contextual biomarker for investigating biological aging within clinical wellness institutions in Thailand settings.

Keywords: telomere length, biological aging, metabolic health, micronutrients, glucose metabolism, wellness programs

Telomeres are repetitive nucleotide sequences located at the ends of chromosomes that play a critical role in maintaining genomic stability during cell division. Telomere length (TL) progressively shortens with increasing age and is widely used as a biomarker of cellular and biological aging, reflecting interindividual variability in aging trajectories beyond chronological age. [1]

Accelerated telomere shortening has been associated with an increased risk of multiple chronic diseases and all-cause mortality. Previous studies have demonstrated that TL is influenced by a range of biological and clinical factors, particularly metabolic and cardiometabolic conditions, and

has been linked to cardiovascular disease, diabetes mellitus, neurodegenerative disorders, and cancer.[2,3] However, the strength and patterns of these associations may vary across populations and healthcare contexts.

Despite extensive international evidence, data on TL and its associated determinants in the Thai population remain limited. In particular, individuals receiving care in clinical wellness institutions represent a distinct population that differs from the general community or disease-specific cohorts commonly studied. This population typically undergoes comprehensive clinical and metabolic assessments and may be at a preclinical stage of chronic disease development, providing a unique opportunity to examine biological factors associated with telomere shortening in an early phase of biological aging.

Studying telomere shortening in this setting is therefore particularly important. While most existing studies have focused on community-based populations or patients with established diseases, relatively little is known about telomere dynamics among individuals engaged in preventive and health-promoting care. Investigating TL in conjunction with detailed clinical and metabolic profiles may enhance understanding of early biological aging processes and help identify factors associated with accelerated telomere shortening before overt disease onset. This approach represents a novel contribution in the Thai context and addresses a critical gap in population-specific evidence.

Accordingly, this study aims to characterize TL and identify biological and clinical factors associated with telomere shortening among individuals receiving advanced wellness programs in a clinical wellness institution in Thailand. The findings may support biological risk stratification and inform the development of more personalized preventive and health promotion strategies in the future.[1]

Materials and Methods

This retrospective study included adults aged ≥18 years who underwent wellness health check-up at two clinical wellness institutions in Thailand from January 2021 to December 2024.

Records lacking telomere information were excluded from this study. Data were retrospectively collected from electronic medical records and laboratory databases, including demographic characteristics, health status indicators (growth factors, hormonal balance, and micronutrient levels), and clinical parameters (e.g., complete blood count, fasting blood glucose, and lipid profile) obtained within two weeks before or after TL measurement. TL was measured by the N-Health laboratory service.

LTL was measured using an absolute quantitative real-time polymerase chain reaction (PCR) method. The assay extends the original Cawthon quantitative PCR (qPCR) approach by incorporating synthetic oligomer standards for both the telomere repeat and a single-copy reference gene, allowing calculation of absolute telomere length (aTL) in base pairs per diploid genome. The quality assurance is in line with current recommendations for qPCR-based telomere measurement. All samples were run in triplicate for both telomere and single-copy reactions. Plates with suboptimal amplification efficiency, poor standard-curve linearity, or abnormal melt curves were repeated. A pooled leukocyte deoxyribonucleic acid (DNA) control and short- and long-telomere control samples were included in every set to monitor inter- and intra-assay variability. The biological age index is derived from a telomere-based age estimate using a Thai reference. The reference regression model was constructed from 200 healthy Thai adults aged 20–80 years, each with three telomere measurements. All individuals were free of major chronic disease and had normal standard laboratory profiles according to local reference ranges. Telomere-based biological age is defined as the chronological age at which an average Thai individual would be expected to have the same LTL as the participant. The procedure involves fitting a regression model of chronological age on aTL ($age = \alpha + \beta \cdot aTL$) in the Thai reference population, after confirming approximate linearity. For each participant, we then substituted their aTL into this regression equation and solved for age, obtaining an individual telomere-based biological age.

Descriptive statistics were used to characterize the distribution of TL and to establish age- and sex-specific reference ranges. Associations between TL and related clinical and laboratory variables were assessed using Pearson's correlation coefficients. Statistical significance was defined as a two-sided p-value < 0.05.

To account for biologically relevant heterogeneity in aging, analyses were prespecified across four strata: the overall cohort, individuals aged 40–65 years, those with biological age younger than chronological age (BA < CA), and those with biological age older than chronological age (BA > CA). The overall cohort served as a population-level reference, while analyses restricted to the 40–65-year age group reduced confounding from early-life stability and late-life survivor bias.[4] Stratification by biological age relative to chronological age allowed assessment of effect consistency and potential modification by aging trajectories among individuals of similar calendar age, consistent with emerging evidence that aging is a context-dependent process.

This study was reviewed and approved by the Institutional Review Board (BHQ-IRB No. 2025-05-13).

Results

A total of 1,684 records were included in the analysis, with a balanced sex distribution (49.5% male and 50.5% female). The mean age across records was 53 years, with a wide age range from 19 to 91 years. More than 80% of records were derived from individuals aged 41 years or older, providing an appropriate dataset for analyses related to aging. (Table 1)

Based on biological age assessment, 54.4% of records were classified as slow aging (biological age lower than chronological age), while 45.6% were classified as fast aging (biological age higher than chronological age). This relatively balanced distribution enabled meaningful comparisons between slow and fast aging records. The majority of records were from individuals of Thai nationality (88.4%), indicating that the dataset reflects the Thai population and is suitable for interpretation within national healthcare and policy contexts. The mean TL across records was approximately 6.8 kilobases (kb), with a broad distribution ranging from 3.6 to 11.6 kb. This variability highlights substantial inter-record differences in cellular biological aging.

Table 1: Participant characteristics and telomere length by biological aging status (n = 1,684).

Variable	Overall n = 1,684[1]	Slow aging n = 916[1]	Fast aging n = 768[1]
Gender			
Male	833 (49.5)	420 (45.9)	413 (53.8)
Female	851 (50.5)	496 (54.1)	355 (46.2)
Age (years)			
Mean±SD	53.4 ± 13.4	57.2 ± 12.1	48.8 ± 13.5
Median (Q1, Q3)	54.0 (43.0, 63.0)	57.5 (49.0, 65.0)	47.0 (38.0, 59.0)
Min–Max	19 – 91	20 – 91	19 – 86
Age Category			
>18-30	76 (4.5)	13 (1.4)	63 (8.2)
31-40	242 (14.4)	61 (6.7)	181 (23.6)
41-50	379 (22.5)	195 (21.3)	184 (24.0)
51-60	459 (27.3)	294 (32.1)	165 (21.5)
60+	528 (31.4)	353 (38.5)	175 (22.8)
Biological Age (years)			
Mean ± SD	53.9 ± 13.5	47.0 ± 12.4	54.9 ± 13.5
Median (Q1, Q3)	49.0 (41.0, 59.0)	46.0 (38.0, 55.0)	53.0 (45.0, 65.0)
Min – Max	10–91	10– 85	26 – 91
Nationality			
Thai	1,489 (88.4)	839 (91.6)	650 (84.6)
Non-Thai	195 (11.6)	77 (8.4)	118 (15.4)
Telomere Length (kb)			
Mean ± SD	6.8 ± 1.2	7.2 ± 1.1	6.2 ± 1.1
Median (Q1, Q3)	6.7 (5.9, 7.6)	7.1 (6.4, 7.9)	6.1 (5.4, 6.9)
Min – Max	3.6–11.6	4.2 – 11.6	3.6 – 9.5

[1] n/N (%)

Table 2 shows correlations between TL–derived biological aging and biomarkers across multiple biological domains for the overall cohort (n = 1,684) and predefined subgroups, including records from individuals aged 40–65 years (n = 350), slow aging (n = 916), and fast aging (n = 768).

Fasting glucose, HbA1c, and insulin levels showed significant inverse associations with TL across the overall cohort and all aging strata, with HbA1c demonstrating the most robust correlations (r ranging from −0.179 in the overall cohort to −0.253 in the fast-aging group).

In the hormonal and growth factor domain, IGF-1 and dehydroepiandrosterone sulfate (DHEA-S) showed consistent positive correlations with slower biological aging across all analytic strata in our cohort, with notably stronger associations in individuals aged 40–65 years, while cortisol showed no significant association. IGF-1 demonstrated moderate correlations with TL in the overall cohort ($r = 0.245$, $p < 0.001$) that increased in the fast aging group ($r = 0.373$), while DHEA-S exhibited a similar pattern (overall $r = 0.220$, $p < 0.001$; fast aging $r = 0.431$). Thyroid-stimulating hormone (TSH) demonstrated weak inverse correlations, primarily in the slow aging group.

Total cholesterol and LDL-C showed weak positive correlations with TL (total cholesterol: $r = 0.139$, $p < 0.001$; LDL-C: $r = 0.124$, $p < 0.001$), with stronger positive associations in the slow aging group (total cholesterol: $r = 0.231$, $p < 0.001$; LDL-C: $r = 0.228$, $p < 0.001$). In contrast, triglycerides showed weak inverse associations, notably in the fast-aging subgroup ($r = -0.082$, $p < 0.05$), whereas high-density lipoprotein cholesterol (HDL-C) showed limited and inconsistent associations with TL across strata.

Within the inflammation and iron status domain, ferritin demonstrated a consistent inverse association with TL across analytic strata in our cohort. Ferritin correlated negatively with TL ($r = -0.103$, $p < 0.001$), with stronger inverse associations in the fast aging subgroup ($r = -0.151$, $p < 0.001$). In contrast,

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CRP showed no significant association with TL across strata, with correlation coefficients close to zero in both the overall cohort and aging subgroups.

Among trace elements and minerals, copper showed a modest positive association with TL in the overall cohort, with a stronger correlation in individuals with slow biological aging (overall r = 0.059, $p < 0.05$; slow aging r = 0.126, $p < 0.05$). In contrast, magnesium, selenium, and chromium levels were inversely associated with TL, with markedly stronger correlations observed among individuals with accelerated biological aging (fast aging group, magnesium: r = -0.143, $p < 0.001$; selenium: r = -0.114, $p < 0.01$; chromium: r = - 0.134, $p < 0.001$)

Antioxidants and vitamins mostly showed inverse association with TL, with stronger associations in individuals with accelerated biological aging, while vitamin B12 showed no association with TL across aging strata. Among all, folate, vitamin E (α-tocopherol), beta-cryptoxanthin, beta-carotene, and vitamin A exhibited a high inverse correlation on TL in fast aging group (folate: r = -0.203, $p < 0.001$; vitamin E (α-tocopherol): r = -0.116, $p < 0.01$; beta-cryptoxanthin: r = -0.156, $p < 0.001$; beta-carotene: r = -0.171, $p < 0.001$; vitamin A: r = -0.192, p< 0.001), while vitamin D, especially vitamin D2 showed a high negative correlation on TL in slow aging group (r = -0.169, $p < 0.001$).

Table 2: Associations between biomarkers and telomere length across analyses, grouped by biological domain (n = 1684).

Biological domain	Biomarker	Overall (n = 1,684)	Age 40–65 years (n = 350)	Slow Aging (BA < CA) (n = 916)	Fast Aging (BA > CA) (n = 768)
Hormonal & Growth factors	TSH	-0.050*	-0.029	-0.110**	0.008
	Cortisol	-0.005	0.021	-0.03	-0.008
	DHEA-S	0.220***	0.132*	0.254*	0.431*
	IGF-1	0.245***	0.122*	0.288*	0.373*
Glucose & insulin metabolism	Insulin	-0.065*	-0.027	-0.089*	-0.026
	HbA1c	-0.179***	-0.114**	-0.240***	-0.253***
	Glucose (fasting)	-0.159***	-0.097*	-0.217***	-0.198***
Lipid metabolism	Triglycerides	-0.023	0.034	-0.025	-0.082*
	HDL-C	0.074**	0.003	0.074*	0.064
	LDL C	0.124***	0.077	0.228***	0.092*
	Total cholesterol	0.139***	0.088*	0.231***	0.081*
Inflammation & iron status	Ferritin	-0.103***	-0.023	-0.110**	-0.151***
	CRP	-0.031	0.061	-0.058	-0.009
Trace elements & minerals	Zinc	-0.037	-0.001	-0.031	-0.049
	Selenium	-0.056*	-0.053	-0.064	-0.114**
	Magnesium	-0.086***	-0.055	-0.069*	-0.143***
	Chromium	-0.032	0.022	-0.037	-0.134***
	Copper	0.059*	0.108*	0.126*	0.038
Vitamins & antioxidants	Coenzyme Q10	-0.056*	-0.091*	-0.071*	-0.113**
	Total Vitamin E	-0.102***	-0.048	-0.149***	-0.086
	Total Vitamin D	-0.107***	-0.048	-0.157***	-0.089*
	Vitamin D3	-0.002	-0.031	-0.022	-0.01
	Vitamin D2	-0.126***	-0.031	-0.169***	-0.092*
	Vitamin B12	-0.014	-0.013	-0.022	-0.034
	Folate	-0.124***	-0.058	-0.177***	-0.203***
	Vitamin E (γ-tocopherol)	-0.064*	-0.078	-0.058	-0.088*
	Vitamin E (α-tocopherol)	-0.035	-0.030	-0.017	-0.116**
	Vitamin C	-0.018	-0.044	-0.026	-0.085*
	Lycopene	-0.009	-0.046	-0.016	-0.074*
	Lutein + Zeaxanthin	-0.024	0.012	-0.007	-0.068
	Beta-cryptoxanthin	-0.022	-0.071	-0.015	-0.156***
	Beta-carotene	-0.011	-0.007	0.024	-0.171***
	Alpha-carotene	-0.040	0.001	-0.091**	-0.048
	Vitamin A	-0.063*	-0.063	-0.055	-0.192***

*$p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

Discussion

These results extend existing international evidence by demonstrating that telomere shortening is more closely associated with metabolic regulation, endocrine reserve, and micronutrient status than with markers of acute inflammation, highlighting the importance of underlying biological regulation in telomere attrition within preventive and wellness-oriented clinical settings.

Glucose and Insulin Metabolism

Markers of glucose and insulin metabolism emerged as some of the strongest and most consistent correlates of telomere-related aging in this study, with HbA1c demonstrating the most robust correlations. These findings highlight the importance of cumulative glycemic burden, rather than transient glucose fluctuations, in driving telomere attrition and cellular aging.

This observation is consistent with a comprehensive meta-analysis of 37 observational studies, which reported that individuals with type 2 diabetes mellitus exhibited substantially shorter TL than non-diabetic controls, with a pooled standardized mean difference of −3.70 (95% CI: −4.20 to −3.20; $p < 0.001$).[5] Similarly, an earlier meta-analysis demonstrated a significant overall association between diabetes status and telomere shortening (SMD: −3.41, 95% CI: −4.01 to −2.80) across diverse populations.[3] Mechanistically, chronic hyperglycemia and insulin resistance promote oxidative stress, mitochondrial dysfunction, and low-grade inflammation, all of which accelerate telomere erosion. The consistency of inverse glycemic–telomere associations across aging strata in the present study suggests that impaired glucose regulation represents a universal biological stressor, while the magnitude of its impact may be amplified in individuals with accelerated biological aging.

Together, these findings strengthen the central role of metabolic health in shaping aging trajectories and support glycemic control as a critical target for interventions aimed at slowing biological aging and telomere shortening.

Hormonal and Growth Factors

Among hormonal and growth-related biomarkers, IGF-1 and DHEA-S showed consistent positive correlations with slower biological aging across all analytic strata in our cohort, with notably stronger associations in individuals aged 40–65 years. These findings align with existing evidence that both IGF-1 and TL diminish with advancing age and are positively correlated, reflecting interconnected declines in anabolic hormonal reserve and telomere integrity.[6,7] Mechanistically, IGF-1 supports cellular proliferation, DNA repair, and mitochondrial function, whereas DHEA-S has been implicated in antioxidative, immune-modulatory, and anti-inflammatory pathways that collectively contribute to genomic stability.[8,9] The consistency between our findings and previous studies on endocrine aging suggests that maintaining anabolic and adrenal hormonal function may help protect against telomere shortening and cellular aging.

In contrast, cortisol showed no significant association with telomere-related aging across strata in our study (correlation near zero), suggesting that single time-point assessments of stress hormones may not fully capture the chronic burden of stress relevant to telomere dynamics. Previous reviews have similarly noted that associations between cortisol and TL are complex and inconsistent across studies, potentially dependent on the intensity, duration, and timing of exposure, as well as methodological differences in hormone assessment.[10] Likewise, TSH exhibited only weak inverse correlations with TL[6] (e.g., overall r = −0.050 and r = −0.110 in the slow aging group), with attenuation in fast aging records. This pattern may reflect early dysregulation of the hypothalamic–pituitary–thyroid axis in accelerated biological aging, whereby hormonal signaling becomes progressively uncoupled from downstream cellular effects.[11] Together, these suggest that while anabolic hormones such as IGF-1 and DHEA-S show robust positive relationships with telomere preservation, catabolic stress hormones like cortisol and regulatory hormones such as TSH may not demonstrate consistent telomere associations in cross-sectional settings, underscoring the need for longitudinal and mechanistic studies to clarify these dynamics.[6]

Lipid Metabolism

Within the lipid metabolism domain, total cholesterol and LDL-C showed modest positive correlations with slower aging, whereas triglycerides demonstrated weak inverse associations, particularly in the fast aging group; associations with HDL-C were limited. These findings show that having lower lipid levels does not necessarily mean a person is experiencing healthier biological aging. Instead, lipids appear to play a more complex role: they are not only metabolic fuels but also important markers of nutritional health and the body's overall anabolic status.

This complexity is supported by broader biological evidence on lipid metabolism and aging. Lipids are essential for cellular homeostasis, contributing to energy production, membrane integrity, steroidogenesis, and intracellular signaling pathways, and they interact dynamically with metabolic and inflammatory processes that influence aging phenotypes.[7,13] Furthermore, evidence from large epidemiological and genetic studies of circulating lipoproteins suggests that distinct lipoprotein fractions and lipid ratios are differentially associated with TL, reinforcing that lipid–telomere relationships depend on lipoprotein class and metabolic context rather than uniformly reflecting beneficial or adverse biological aging.[14]

Beyond observational patterns, causal inference analyses have provided complementary insights. A recent Mendelian randomization and mediation analysis demonstrated that unfavorable lipid profiles were causally associated with

alterations in TL, and that TL significantly mediated the relationship between lipid metabolism disorders and the risk of certain cancers, particularly lung and hematologic cancers.[15] Mediation analysis from this study further confirmed TL as a significant mediator in the pathway linking lipid profiles to cancer development ($p < 0.05$).

These findings suggest that lipid metabolism influences telomere biology through multiple pathways related to metabolic health and disease risk. This underscores the need to interpret lipid–telomere associations within their biological context, rather than assuming that lipid levels alone directly reflect biological aging

Inflammation and Iron Status

Within the inflammation and iron status domain, Ferritin levels were inversely correlated with biological aging. These findings are corroborated by studies showing that high body iron status is associated with shorter telomeres, particularly in older adults. In the study by Zhan et al.,[16] elevated systemic iron biomarkers were linked to significantly shorter LTL, with the strongest associations observed in individuals aged 65 years or older. The biological plausibility of this relationship is supported by the role of iron in catalyzing oxidative reactions that generate reactive oxygen species and promote DNA damage, including at telomeric regions.

In contrast, CRP showed no consistent association. This finding suggests that acute-phase or low-grade systemic inflammation, as reflected by single-time-point CRP measurements, may not adequately capture the chronic biological processes driving telomere attrition in relatively health-screened populations. This observation differs from findings in disease-specific cohorts. For example, in patients with coronary artery disease, impaired collateral circulation was associated with both shorter telomeres and elevated CRP levels, indicating that CRP may reflect inflammation-mediated telomere shortening in populations with established vascular pathology.[17]

Furthermore, an integrative analysis in aging research proposed that CRP may act as a central mediator linking cardiovascular risk factors to LTL, particularly under conditions of sustained inflammatory stimulation.[18] The absence of a detectable CRP–telomere association in our study likely reflects differences in baseline inflammatory burden and health status.

Micronutrients, Trace Elements and Vitamin

Our findings demonstrate that associations between micronutrients and TL are heterogeneous and strongly modified by biological aging status, rather than reflecting uniform or universally protective effects. This pattern is consistent with conceptual frameworks suggesting that LTL is most informative as a marker of biological age when interpreted alongside other aging-related indicators, and that its biological relevance varies across different metabolic and aging contexts. [1]

Among trace elements, copper showed a modest positive association with TL in the overall cohort, with a stronger correlation in individuals with slow biological aging, whereas no significant association was observed in those with fast biological aging. This pattern suggests that copper may support mitochondrial bioenergetics and redox balance primarily in biologically resilient individuals, consistent with mechanistic evidence indicating that copper-dependent processes become increasingly dysregulated with advancing biological aging.[19]

These findings align with population-based studies reporting longer TL among individuals with higher dietary copper intake, particularly in metabolically stable adult populations.[20] In contrast, zinc showed no association with TL across any analytic strata, underscoring that essential trace elements may differ substantially in their relevance to telomere biology.

Conversely, circulating magnesium, selenium, and chromium levels were inversely associated with TL, with markedly stronger correlations observed among individuals with accelerated biological aging. These inverse associations contrast with prior nutritional epidemiology studies reporting positive relationships between dietary magnesium or selenium intake and TL.[21, 22] This discrepancy likely reflects differences in exposure assessment, as circulating micronutrient levels may be influenced by supplement use, altered metabolism, or underlying disease states, rather than representing long-term nutritional adequacy.[23]

A similar pattern was observed within the vitamins and antioxidants domain. Multiple micronutrients—including folate, vitamin A, vitamin D (particularly vitamin D2), beta-carotene, and coenzyme Q10—showed inverse associations with TL, with consistently stronger effects in individuals with accelerated biological aging. This pattern is compatible with the concept that accelerated aging is characterized by heightened oxidative stress and disrupted redox homeostasis, in which elevated circulating antioxidant-related micronutrients may reflect compensatory responses, altered utilization, or disease-related supplementation rather than direct telomere-protective effects.[23]

While folate and vitamin D have been implicated in genomic stability, immune modulation, and telomere maintenance in prior mechanistic and epidemiological studies, [24,25] the inverse associations observed in our cohort—particularly for circulating vitamin D2—may reflect clinical behavior, supplementation patterns, or altered nutrient handling in health-screened populations, rather than causal effects on telomere dynamics. This interpretation is supported by classic metabolic studies demonstrating that circulating vitamin levels often reflect physiological context and utilization rather than intake alone.[26] Consistent with this framework,

vitamin B12 showed no meaningful association with TL across aging strata, further indicating that not all vitamins exert primary or uniform effects on telomere biology.

Overall, these findings suggest that micronutrients and antioxidants influence TL as part of interconnected metabolic and redox systems, rather than acting as isolated factors that directly protect telomeres. Disruption of these systems appears to be more biologically relevant to telomere shortening in individuals with accelerated biological aging, in whom circulating micronutrient levels may reflect oxidative–metabolic stress, altered nutrient processing, or compensatory supplement use. Accordingly, these results highlight the need for cautious interpretation of micronutrient biomarkers in relation to TL, taking into account biological aging status, the method of measurement (dietary intake versus circulating levels), supplement use, coexisting metabolic conditions, and the possibility of context-dependent or nonlinear relationships.

Limitations

The strengths of this study include a large dataset derived from real-world records of an advanced wellness program, comprehensive biomarker coverage across multiple biological domains, and pre-specified stratification by biologically meaningful aging categories. Although several correlations reached statistical significance, most effect sizes were small ($|r| < 0.30$), suggesting limited clinical relevance, as well as in our research data collected from healthy individuals, which show weaker association effects compared with disease-based participants. In addition, the absence of multivariable adjustment precludes assessment of independent associations and potential confounding effects. The retrospective design and incomplete availability of certain laboratory parameters may limit causal inference and introduce variability across analyses.

Conclusion

In this population, TL–derived biological aging is closely associated with metabolic regulation, hormonal reserve, micronutrient, and antioxidant status, rather than acute inflammation. The differential patterns observed across biological aging strata reinforce the importance of context-dependent aging trajectories and support the application of personalized, metabolism-focused preventive strategies. These findings contribute to a growing body of evidence positioning TL as a valuable integrative marker in aging research and clinical practice.

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Conflict of Interest

The authors declare no **conflict of interest** related to this study

References

1. Vaiserman A, Krasnienkov D. Telomere length as a marker of biological age: state-of-the-art, open issues, and future perspectives. *Front Genet*. 2020;11:630186. doi: 10.3389/fgene.2020.630186.
2. Batsis JA, Mackenzie TA, Vasquez E, et al. Association of adiposity, telomere length and mortality: data from the NHANES 1999-2002. *Int J Obes (Lond)*. 2018;42(2):198-204. doi: 10.1038/ijo.2017.202.
3. Wang J, Dong X, Cao L, et al. Association between telomere length and diabetes mellitus: A meta-analysis. *J Int Med Res*. 2016;44(6):1156-73. doi: 10.1177/0300060516667132.
4. Shen X, Wang C, Zhou X, et al. Nonlinear dynamics of multi-omics profiles during human aging. Nature Aging. 2024;4(11):1619-34. doi: 10.1038/s43587-024-00692-2.
5. He X, Cao L, Fu X, et al. The association between telomere length and diabetes mellitus: accumulated evidence from observational studies. *J Clin Endocrinol Metab*. 2024;110(1):e177-e85. doi: 10.1210/clinem/dgae536.
6. Aulinas A, Ramírez MJ, Barahona MJ, et al. Telomeres and endocrine dysfunction of the adrenal and GH/IGF-1 axes. *Clin Endocrinol (Oxf)*. 2013;79(6):751-9. doi: 10.1111/cen.12310.
7. Vasunilashorn S, Cohen AA. Stress responsive biochemical anabolic/catabolic ratio and telomere length in older adults. *Biodemography Soc Biol*. 2014;60(2):174-84. doi: 10.1080/19485565.2014.950722.
8. Winn N, Paul A, Musaró A, et al. Insulin-like growth factor isoforms in skeletal muscle aging, regeneration, and disease. *Cold Spring Harb Symp Quant Biol*. 2002;67:507-18. doi: 10.1101/sqb.2002.67.507.
9. Lin S-YJ, Cui H, Yusta B, et al. IGF-I signaling prevents dehydroepiandrosterone (DHEA)-induced apoptosis in hypothalamic neurons. *Mol Cell Endocrinol*. 2004;214(1):127-35. doi: 10.1016/j.mce.2003.10.064.
10. Jiang Y, Da W, Qiao S, et al. Basal cortisol, cortisol reactivity, and telomere length: A systematic review and meta-analysis. *Psychoneuroendocrinology*. 2019;103:163-72. doi: 10.1016/j.psyneuen.2019.01.022.
11. Monzani F, Del Guerra P, Caraccio N, et al. Age-related modifications in the regulation of the hypothalamic-pituitary-thyroid axis. *Horm Res*. 1996;46(3):107-12. doi: 10.1159/000185005.
12. Alonso-Pedrero L, Ojeda-Rodríguez A, Zalba G, et al. Association between ideal cardiovascular health and telomere length in participants older than 55 years old from the SUN cohort. *Rev Esp Cardiol (Engl Ed)*. 2022;75(4):308-15. doi: 10.1016/j.rec.2021.04.002.
13. Agmon E, Stockwell BR. Lipid homeostasis and regulated cell death. *Curr Opin Chem Biol*. 2017;39:83-9. doi: 10.1016/j.cbpa.2017.06.002.

14. Chen Y-F, Zhou K-W, Yang G-z, Chen C. Association between lipoproteins and telomere length in US adults: data from the NHANES 1999–2002. *Lipids Health Dis.* 2019;18(1):80. doi: 10.1186/s12944-019-1030-7.
15. Liu S, Fu Z, Liu H, et al. Lipid profiles, telomere length, and the risk of malignant tumors: a mendelian randomization and mediation analysis. *Biomedicines.* 2024;13(1):13. doi: 10.3390/biomedicines13010013.
16. Liu B, Sun Y, Xu G, et al. Association between body iron status and leukocyte telomere length, a biomarker of biological aging, in a nationally representative sample of US adults. *J Acad Nutr Diet.* 2019;119(4):617-25. doi: 10.1016/j.jand.2018.09.007.
17. Solorio S, Murillo-Ortíz B, Hernández-González M, et al. Association between telomere length and C-reactive protein and the development of coronary collateral circulation in patients with coronary artery disease. *Angiology.* 2011;62(6):467-72. doi: 10.1177/0003319710398007.
18. Tedaldi AM, Behrouzi P, Grootswagers P. Diet, lifestyle and telomere length: using Copula Graphical Models on NHANES data. *Aging (Albany NY).* 2025;17(2):329-56. doi: 10.18632/aging.206194.
19. Ruiz LM, Libedinsky A, Elorza AA. Role of copper on mitochondrial function and metabolism. *Front Mol Biosci.* 2021;8:711227. doi: 10.3389/fmolb.2021.711227.
20. Lin Z, Gao H, Wang B, et al. Dietary copper intake and its association with telomere length: a population based study. *Front Endocrinol (Lausanne).* 2018;9:404. doi: 10.3389/fendo.2018.00404.
21. Liang C, Zhao R, Du J, et al. The association between dietary selenium intake and telomere length in hypertension. *J Clin Hypertens (Greenwich).* 2024;26(8):990-6. doi: 10.1111/jch.14861.
22. Zhao G, Guo D, Li L, et al. The Association between dietary magnesium intake and telomere length in adults with hypertension. *J Nutr Health Aging.* 2022;26(11):1010-5. doi: 10.1007/s12603-022-1856-y.
23. Intake – Center for Dietary Assessment. Assessing the relationship between dietary nutrient intake and nutrient biomarker data in population surveys [Internet]. Washington, DC: Intake/FHI 360; February 2024 [cited 2024]. Available from: https://www.intake.org/innovations.
24. Mazidi M, Michos ED, Banach M. The association of telomere length and serum 25-hydroxyvitamin D levels in US adults: the National Health and Nutrition Examination Survey. *Arch Med Sci.* 2017;13(1):61-5. doi: 10.5114/aoms.2017.64714.
25. Zhu H, Manson JE, Cook NR, et al. Vitamin D3 and marine ω-3 fatty acids supplementation and leukocyte telomere length: 4-year findings from the vitamin D and omegA-3 triaL (VITAL) randomized controlled trial. *Am J Clin Nutr.* 2025;122(1):39-47. doi: 10.1016/j.ajcnut.2025.05.003.
26. Pelletier O. Vitamin C status of cigarette smokers and nonsmokers. *Am J Clin Nutr.* 1970;23(5):520-4. doi: 10.1093/ajcn/23.5.520.