Acupuncture and Herbal Medicine

Tongue age: a new dimension for disease risk assessment based on tongue-coating microbiome and image features

Yanfei Liu[1,2], Yiwen Li[3], Jianqing Ju[1], Yanwu Xu[4], Yue Liu[1,2,*]

[1]National Clinical Research Center for Chinese Medicine Cardiology, Xiyuan Hospital, Chinese Academy of Chinese Medical Sciences, Beijing, China; [2]The Second Department of Geriatrics, Xiyuan Hospital of China Academy of Chinese Medical Sciences, Beijing, China; [3]Beijing Key Laboratory of Traditional Chinese Medicine Basic Research on Prevention and Treatment for Major Diseases, Experimental Research Center, China Academy of Chinese Medical Sciences, Beijing, China; [4]School of Future Technology, South China University of Technology, Guangzhou, China

Cardiovascular disease (CVD) is characterized by high incidence, disability burden, and mortality. Early warning and precise prognosis assessment are crucial for reducing disease burden[1]. According to Traditional Chinese Medicine (TCM), tongue appearance changes can reflect organ functions such as blood circulation and nutrient metabolism. The tongue surface provides an accessible window for host physiology. Advances in tongue-coating microbiomes and digital imaging have enabled the development of multimodal, non-invasive biomarkers by integrating these quantitatively captured oral phenotypes.

Currently, "biological age"[2] (such as telomere length, DNA methylation age, and gut microbiota age) has become an important marker for evaluating the aging state and disease risk, reflecting the deviation between physiological and chronological ages through biomarkers. Based on this, we propose the concept of "tongue age" which evaluates biological aging by constructing a quantitative model integrating tongue-coating microbiota and tongue image phenotypes[3–5]. While tongue age is conceptually consistent with biological age, it differs in data modality and intended use. Epigenetic clocks are highly informative, but require laboratory assays of blood or tissue, limiting scalability and monitoring. Tongue age integrates two non-invasive and complementary modalities, the tongue-coating microbiome and standardized tongue imaging phenotypes, thereby linking a readily observable oral phenotype to the underlying microbial ecology. Tongue age is not proposed as a replacement for aging clocks; it aims to provide an intuitive, accessible, and repeatable readout that may complement existing markers for the screening and longitudinal monitoring of cardiovascular health.

Core connotation and definition of tongue age

Tongue age does not reflect the developmental age of the tongue, but a comprehensive biological age indicator based on the tongue-coating microbiome and image phenotypes (Figure 1). Tongue age comprises the following: (1) physiological tongue age, describing age-associated patterns in tongue-coating microbial profiles and tongue phenotypes observed in healthy individuals; (2) pathological tongue age, referring to elevation tongue age relative to chronological age under disease-relevant conditions, potentially reflecting accelerated biological aging. Compared with many existing biological age indicators, tongue age is based on an observable oral surface and can be obtained through non-invasive, convenient, and repeatable sampling and imaging, enabling large-scale screening and longitudinal monitoring[3].

The rationale for tongue age is supported by convergent evidence from oral microbiome profiling and tongue imaging studies. TCM theory suggests the tongue relates to internal organ function and shows regular differences in tongue phenotypes among different age groups. Studies have documented age-associated shifts in the oral microbiome across multiple oral sites, relating to aging-associated traits such as frailty[6–7]. Moreover, tongue imaging phenotypes associate with CVD status and lesion severity, with tongue color parameters correlating to coronary stenosis burden or post- percutaneous coronary intervention changes[8]. Advances in digital tongue imaging and machine learning enable objective extraction of tongue phenotypes. Tongue images have been used to predict chronological age, supporting an age-related signal in tongue appearance.

Yanfei Liu and Yiwen Li contributed equally to this work.

**Corresponding author. Yue Liu, E-mail: liuyueheart@hotmail.com.*

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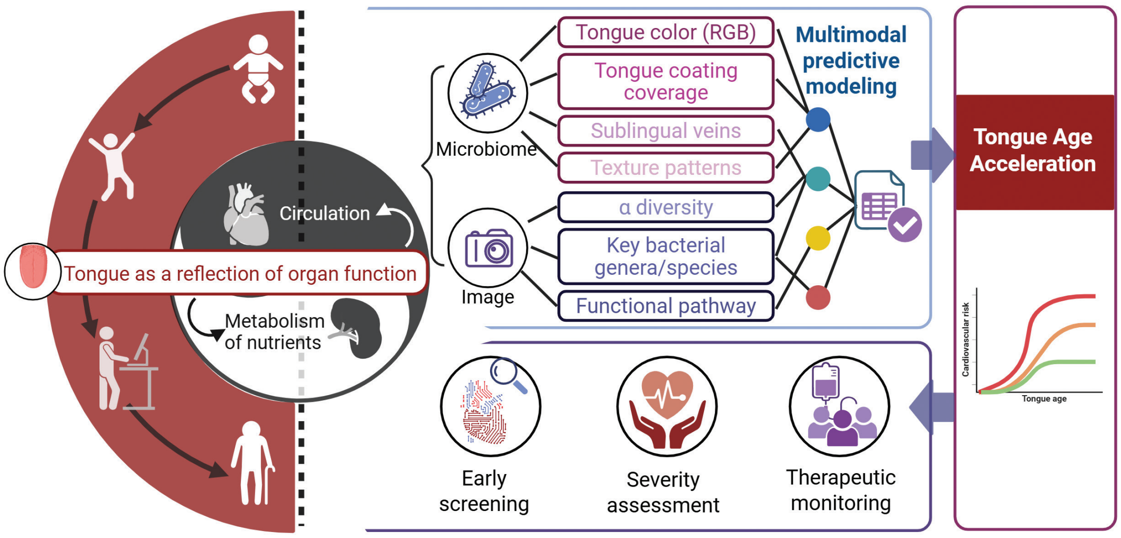

Figure 1. Conceptual framework of tongue age as a multimodal aging metrics.

These convergent observations support integrating tongue-coating microbiome profiles with standardized tongue imaging phenotypes into an interpretable multimodal aging-related metric (Figure 1). Cross-site interactions between the oral and gut microbial ecosystems have been linked to aging and cardiometabolic health[9], supporting a systemic relay pathway.

Construction of quantitative evaluation system for tongue age

Core indicators of tongue age require high specificity, quantifiability, and repeatability. Microbiome indicators include tongue-coating microbiome diversity, taxonomic abundance, and functional pathways, whereas image indicators include tongue body color (red–green–blue [RGB] and hue–saturation–value [HSV] color spaces), tongue-coating coverage rate/thickness, and tongue morphology parameters. A standardized process across pre-collection controls, tongue-coating sampling[3], image acquisition, and data processing and quality control[10] is necessary to ensure data quality and comparability.

Multimodal predictive models[11] can be trained in healthy cohorts to estimate tongue age using chronological age as the target, tongue-coating microbiome profiles, and standardized tongue imaging phenotypes as inputs. Candidate models include regularized regression, tree-based ensemble learners (gradient boosting), and deep-learning–based multimodal fusion frameworks. To mitigate overfitting, model development should emphasize robust internal and external validations in independent populations. An effective model should provide accurate age estimates in healthy cohorts and capture clinically meaningful deviations in patients.

The deviation between tongue age and chronological age serves as evaluation standard, which can be divided into three levels: (1) Normal aging: deviation within ±2 years, indicating a good physiological state; (2) Mild accelerated aging: tongue age is 2 to 5 years higher than chronological age[12–13], indicating early pathological changes, requiring enhanced monitoring; (3) Severe accelerated aging: tongue age over 5 years higher, indicating a significantly increased disease risk, requiring clinical intervention. These categories are intended as illustrative strata, with optimal cutoffs to be calibrated and validated in prospective cohorts, similar to frameworks used for other biological aging markers[14–16].

Potential value of tongue age in the prevention and treatment of CVD

Early warning of CVD

Early CVD often lacks typical symptoms, particularly in patients with diabetes. Tongue age may capture age-related changes that are not fully reflected by conventional indicators and complement cardiovascular 1.5-level prevention[17]. Oral dysbiosis may contribute to cardiovascular pathology through low-grade systemic inflammation *via* microbial products (lipopolysaccharide and outer membrane vesicles), activating immune-sensing pathways, and affecting tongue phenotypes. Elevated tongue age acceleration may indicate higher cardiovascular risk and warrant further clinical evaluation.

Evaluation of CVD severity

Tongue age relates to CVD severity. Tongue imaging phenotypes vary across coronary disease states and correlate with angiographic severity or myocardial injury[18]; tongue phenotypes associate with heart failure severity and prognosis[19]. In addition, oral–gut microbial transmission links to CVD[20–22], supporting a plausible systemic relay pathway. Dynamic monitoring of tongue age helps to evaluate disease progression and severity.

Evaluation of disease prognosis

Tongue age may serve as a dynamic marker for monitoring the disease trajectory and treatment response.

Changes in oral microbiota and images occur after clinical interventions[23], suggesting potential utility for longitudinal follow-up. However, whether tongue age dynamics can predict recurrent cardiovascular events and whether the magnitude of change is clinically meaningful remains to be established in adequately powered cohorts.

Personalized management integrating macroscopic phenotypes and microbiome

Integrating tongue phenotypes with tongue-coated microbiome profiles may support individualized risk stratification and treatment tailoring. Rather than relying on a single visual sign, a multimodal readout can link observable tongue features to the underlying microbial ecology (diversity and taxonomic/functional patterns)[24], enabling more reproducible patient subtyping. These subtypes can guide therapeutic strategies, follow-up intensity, and adjunctive lifestyles or interventions. These therapeutic links remain hypothesis-generating and require validation in prospective cohort and interventional studies.

Challenges and prospects

Tongue age research faces several key challenges: most studies have small sample sizes and high population heterogeneity, affecting model generalizability; tongue-coating microbiota and images are affected by factors such as diet, oral hygiene, and drugs, requiring strict control of confounding factors; the relationship between tongue age and CVD remains unclear; and lack of unified evaluation standards limits clinical promotion.

Future research should focus on the following aspects: conducting multicenter large-sample cohort studies to establish a standardized database and optimize model accuracy; establishing age-stratified reference ranges and assessing test–retest reliability/longitudinal sensitivity under standardized acquisition; exploring the biological mechanism of tongue age in depth by combining multiomics technologies; developing an intelligent platform integrating image collection, microbiota detection, and evaluation for primary care; verifying tongue age effectiveness in disease prevention and treatment through clinical trials with adjudicated endpoints and evaluation of incremental predictive value over established risk models; and promoting clinical translation.

Tongue age is a novel biological age indicator that integrates TCM tongue examination and modern technology, with the advantages of quantification, noninvasiveness, and dynamic reflection of health status, and has potential in the early warning, evaluation, and intervention of CVDs. In the future, through in-depth mechanistic research, standardized evaluation, and promoted technology integration, tongue age could become an important tool for the prevention and treatment of CVDs.

Conflict of interest statement

The authors declare no conflict of interest.

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Author contributions

Yanfei Liu and Yiwen Li contributed to writing and revising the original draft. Yanwu Xu and Jianqing Ju participated in conceptual discussion. Yue Liu contributed to conceptualization, review and editing, funding acquisition. All authors have read and agreed to the published version of the manuscript.

Ethical approval of studies and informed consent

Not applicable.

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Data availability

Not applicable.

Declaration of generative AI in scientific writing

The conception and writing of this article were carried out collaboratively by all authors. Artificial intelligence was utilized exclusively for refining sentence coherence and amending punctuation. All citations in this manuscript were manually searched for and incorporated. After utilizing the aforementioned tools/services, the authors thoroughly reviewed and revised the content and take full responsibility for the entirety of this publication.

References

[1] Xu S, Liu Y, Zhu M, et al. Global burden of atherosclerotic cardiovascular disease attributed to lifestyle and metabolic risks. *Sci China Life Sci* 2025;68(9):2739–2754.

[2] Rutledge J, Oh H, Wyss-Coray T. Measuring biological age using omics data. *Nat Rev Genet* 2022;23(12):715–727.

[3] Li Y, Zhu M, Wang W, et al. Comparable tongue coating microbiota profiles from a simplified single-swab versus different sampling approaches: a pilot study. *Clin Oral Investig* 2025;29(11):543.

[4] Xie J, Jing C, Zhang Z, et al. Digital tongue image analyses for health assessment. *Med Rev (2021)* 2021;1(2):172–198.

[5] Ren Y, Chen M, Wang Z, et al. Oral microbiota in aging and diseases. *Life Med* 2024;3(3):lnae024.

[6] Xu Q, Wang W, Li Y, et al. The oral-gut microbiota axis: a link in cardiometabolic diseases. *NPJ Biofilms Microbiomes* 2025;11(1):11.

[7] Liao C, Rolling T, Djukovic A, et al. Oral bacteria relative abundance in faeces increases due to gut microbiota depletion and is linked with patient outcomes. *Nat Microbiol* 2024;9(6):1555–1565.

[8] Xia Y, Wang Q, Feng X, et al. Tongue diagnosis based on hue-saturation value color space: controlled study of tongue appearance in patients treated with percutaneous coronary intervention for coronary heart disease. *Intell Med* 2023;3(4):252–257.

[9] Zhao M, Wang M, Fan L, et al. An explainable dual-modal diagnostic model for coronary artery disease: a feature-gated approach using tongue and facial image features. *Front Artif Intell* 2025;8:1662577.

[10] Qi Z, Tu LP, Chen JB, et al. The classification of tongue colors with standardized acquisition and ICC profile correction in traditional Chinese medicine. *Biomed Res Int* 2016;2016:3510807.

[11] Teoh JR, Dong J, Zuo X, et al. Advancing healthcare through multimodal data fusion: a comprehensive review of techniques and applications. *PeerJ Comput Sci* 2024;10:e2298.

[12] Cumplido-Mayoral I, García-Prat M, Operto G, et al. Biological brain age prediction using machine learning on structural neuroimaging data: multi-cohort validation against biomarkers of Alzheimer's disease and neurodegeneration stratified by sex. *eLife* 2023;12:e81067.

[13] Jawinski P, Forstbach H, Kirsten H, et al. Genome-wide analysis of brain age identifies 59 associated loci and unveils relationships with mental and physical health. *Nat Aging* 2025;5(10):2086–2103.

[14] Hao M, Zhang H, Wu J, et al. Gompertz law-based biological age (GOLD BioAge): a simple and practical measurement of biological ageing to capture morbidity and mortality risks. *Adv Sci (Weinh)* 2025;12(32):e01765.

[15] Poganik JR, Zhang B, Baht GS, et al. Biological age is increased by stress and restored upon recovery. *Cell Metab* 2023;35(5):807–820.e5.

[16] Wang T, Shi Z, Ren H, et al. Divergent age-associated and metabolism-associated gut microbiome signatures modulate cardiovascular disease risk. *Nat Med* 2024;30(6):1722–1731.

[17] Zhang Y, Wu J, Liu Y, et al. Cardiovascular 1.5-level prevention: a comprehensive screening and intervention for early cardiovascular organ damage. *Sci Bull (Beijing)* 2025;70(9):1380–1383.

[18] Zhou M, Li J, Lim J, et al. A machine learning model integrating tongue image features and myocardial injury markers predicts major adverse cardiovascular events in patients with coronary heart disease. *Int J Gen Med* 2025;18:3739–3765.

[19] Yunhu C, Moqing Y, Lihua F, et al. Mirror-like tongue is an important predictor of acute heart failure: a cohort study of acute heart failure in Chinese patients. *J Tradit Chin Med* 2023;43(6):1243–1251.

[20] Li Y, Liu Y, Cui J, et al. Oral-gut microbial transmission promotes diabetic coronary heart disease. *Cardiovasc Diabetol* 2024;23(1):123.

[21] Chen BY, Lin WZ, Li YL, et al. Roles of oral microbiota and oral-gut microbial transmission in hypertension. *J Adv Res* 2023;43:147–161.

[22] Li YL, Chen BY, Feng ZH, et al. Roles of oral and gut microbiota in acute myocardial infarction. *J Adv Res* 2025;74:319–332.

[23] Chen H, Ma Y, Li M, et al. Tongue-coating microbiome reflects cardiovascular health and determines outcome in blood pressure intervention. *J Genet Genomics* 2023;50(10):803–806.

[24] Tu S, Yin Y, Ma L, et al. Diagnosis of non-puerperal mastitis based on "whole tongue" features: non-invasive biomarker mining and diagnostic model construction. *Front Cell Infect Microbiol* 2025;15:1602883.