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Biological Age Acceleration as a Marker of Chronic Kidney Disease: A Population-Based Study

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Abstract

Chronic kidney disease (CKD) remains a major global health concern. Biological age (BA), which reflects the functional state of multiple physiological systems, may capture aging-related vulnerability more effectively than chronological age. This study evaluated whether acceleration in BA—estimated by the Klemera–Doubal method (KDM)—is linked to CKD in a nationally representative Chinese cohort. The original number of participants was 17,708. Data were drawn from 6,830 participants in the baseline wave of the China Health and Retirement Longitudinal Study (CHARLS). KDM-based BA acceleration (KDM-BAacc) was calculated as the residual from regressing biological age on chronological age and categorized into quartiles. CKD was identified from self-reported physician diagnoses. Logistic regression models with stepwise adjustment for sociodemographic, lifestyle, and clinical factors were applied to examine the association. Each interquartile range increase in KDM-BAacc was linked with markedly higher odds of CKD (OR = 2.13, 95% CI: 1.68–2.70,$p < 0.001$). Participants in the top quartile of acceleration exhibited a risk of CKD that was over three times greater compared to those in the bottom quartile (OR = 3.10, 95% CI: 1.99–4.85). Restricted cubic spline models supported a steady, approximately linear increase in CKD risk across the entire spectrum of BA acceleration ($p$for non-linearity = 0.758). Subgroup analyses showed consistency across demographic strata, with significant interactions observed for smoking history, education level, and sleep duration. Sensitivity analyses yielded consistent results. KDM-derived biological age acceleration is a strong, independent, and linearly increasing risk factor for CKD, suggesting that BA may hold substantial value for CKD risk prediction and early identification.

Introduction

Chronic kidney disease (CKD) has become an increasingly pressing global health issue, leading to substantial illness burden, premature deaths, and rising healthcare costs[1]. From 1990 to 2017, both the prevalence and mortality of CKD showed marked upward trends—cases increased by nearly one-third and deaths by more than 40%, amounting to approximately 35.8 million disability-adjusted life years (DALYs)[2]. Although chronological age is recognized as a major non-modifiable determinant of CKD—with markedly higher rates observed in older adults[3]—individuals of the same age often exhibit markedly different health statuses. This variability highlights the limitation of measuring aging solely as time elapsed since birth, as it does not fully reflect true physiological decline. To address this, the concept of biological age (BA) has been proposed. BA integrates multiple physiological indicators to better characterize an individual's functional status and degree of aging[4], thereby providing a more nuanced assessment of health than chronological age alone.

Among various approaches, the Klemera–Doubal method (KDM) is a widely used and validated algorithm for estimating BA[5]. It combines a panel of clinical biomarkers into a composite score representing overall physiological integrity. The discrepancy between BA and chronological age, commonly termed BA acceleration, captures whether a person is aging more rapidly or more slowly than expected. A positive acceleration value indicates that an individual's physiological profile resembles that of someone older than their actual age, suggesting an accelerated aging process.

Previous research has shown that individuals with higher biological age tend to experience a greater burden of aging-related diseases, including elevated risks of mortality, cardiovascular disorders, and cognitive impairment[6,7]. However, the specific nature of the association between BA acceleration and CKD risk remains unclear, particularly in terms of the dose-response relationship in large, community-based populations. Clarifying this relationship is important for understanding how systemic physiological dysregulation contributes to renal impairment. To address this research gap, we examined the association between accelerated biological aging and CKD in a population-based sample of middle-aged and elderly Chinese individuals from the China Health and Retirement Longitudinal Study (CHARLS). We employed a comprehensive analytical strategy, incorporating categorical, continuous, and flexible modeling approaches, to rigorously characterize this association.

Results

Baseline characteristics

Table 1 outlines the baseline characteristics of the 6,830 participants, stratified by quartiles of KDM-BAacc. The mean age of the study population was 58.4 years, and 54.1% were female. As BA acceleration increased across quartiles, participants exhibited progressively less favourable health profiles. Individuals in the highest quartile (Q4) were more likely to be male, current smokers, and frequent alcohol drinkers, with all comparisons showing significant differences. Q4 participants also had a substantially higher prevalence of cardiometabolic conditions, including diabetes (13.4% in Q4 vs. 4.9% in Q1), dyslipidemia, and hypertension. In terms of biomarker profiles, those in Q4 demonstrated elevated levels of urea, creatinine, and cystatin C, along with higher glycated hemoglobin, total cholesterol, and LDL-C. They also had lower platelet counts and higher hs-CRP concentrations. Together, these patterns indicate broad physiological dysregulation across multiple systems among individuals with the greatest BA acceleration.

Association between KDM-BAacc and CKD

Logistic regression analyses validated a significant association between KDM-BAacc and CKD. In the initial univariate analysis (Model 1), every interquartile range increment in KDM-BAacc demonstrated a significant 43% elevation in the likelihood of developing CKD (OR = 1.43, 95% CI: 1.26–1.63,$p < 0.001$). This robust correlation persisted with minimal variation following the incorporation of sociodemographic covariates in Model 2 (OR = 1.43, 95% CI: 1.25–1.63,$p < 0.001$). After further adjustment for lifestyle and clinical factors in Model 3, the association strengthened markedly, with each IQR increase in KDM-BAacc linked to a 113% increase in the odds of CKD (OR = 2.13, 95% CI: 1.68–2.70,$p < 0.001$). Stratification by KDM-BAacc quartiles demonstrated a significant dose-dependent association with CKD risk. In the fully adjusted multivariate model (Model 3), when compared to individuals in the lowest quartile (Q1), the adjusted odds ratios for CKD incidence progressively increased across higher quartiles: 1.47 (95% CI: 1.04–2.09) for Q2, 1.38 (0.94–2.04) for Q3, and 3.10 (1.99–4.85) for Q4. Although the OR for Q3 was slightly lower than that for Q2, the overall trend across quartiles remained highly significant ($p < 0.001$),

showing a consistent increase in risk (Table 2). This pattern was further supported by the restricted cubic spline (RCS) analysis.

Dose-response relationship analysis

RCS analysis showed a significant overall association between KDM-BAacc and CKD risk (Wald χ^2 = 28.81, 2 df,p < 0.0001). The test for non-linearity was non-significant ($p$for non-linearity = 0.7576), indicating that a linear relationship adequately described the association. As illustrated in Fig. 1, the OR for CKD increased steadily across the full range of KDM-BAacc values, reinforcing the dose-response pattern observed in the quartile analyses. No threshold or saturation effect was evident. In Fig. 1, the solid line illustrates the OR for CKD, while the shaded region indicates the associated 95% confidence interval. The OR is standardized to a value of 1 at the median of the KDM-BAacc measure. The model was adjusted for age, sex, education, residential location, marital status, alcohol consumption, smoking status, and sleep duration.

Subgroup and interaction analyses

Subgroup analyses showed a consistently positive association between KDM-BAacc (per IQR increase) and CKD across nearly all examined strata, including age (< 65 vs. ≥65 years), sex, residential location, and smoking. In all subgroups, the odds ratios exceeded 1.9 and reached statistical significance (p < 0.05) (Fig. 3). The association appeared stronger among married individuals and participants reporting more than 6 hours of sleep per night. Interaction analyses further revealed significant effect modification by smoking history (particularly among former smokers), education level (primary school and high school groups), and sleep duration, as indicated by significant interaction terms (p for interaction < 0.05) (Fig. 3).

Sensitivity analyses

Sensitivity analyses demonstrated a robust positive association between KDM-BAacc and CKD across the majority of examined subgroups. In the fully adjusted model (Model 3), an interquartile range (IQR) increment in KDM-BAacc corresponded to a 92% elevated risk of CKD (OR = 1.92, 95% CI: 1.60–2.30). A statistically significant dose-response pattern was evident across KDM-BAacc quartiles (P for trend < 0.001). This linear association was further substantiated by restricted cubic spline (RCS) modeling (P for nonlinearity = 0.758). Significant effect modification was observed, with interactions identified for smoking status, educational attainment, and sleep duration (P for interaction < 0.05 for each), suggesting that the relationship between KDM-BAacc and CKD risk is modified by these factors (Supplementary materials).

Discussion

This epidemiological investigation revealed a statistically significant correlation between KDM-BAacc and the development of CKD. Baseline comparisons showed progressively poorer health profiles across increasing KDM-BAacc quartiles, including higher prevalences of diabetes, hypertension, and dyslipidemia, accompanied by adverse biomarker patterns. Logistic regression analyses demonstrated that each interquartile range increase in KDM-BAacc was associated with a substantially elevated odds of CKD, an association that became stronger after full adjustment for sociodemographic, lifestyle, and clinical factors (OR = 2.13). Both the quartile-based analyses and RCS models supported a linear dose–response relationship, with no indication of threshold or saturation effects. Subgroup analyses further confirmed the consistency of this association across a wide range of demographic and behavioral characteristics, while interaction analyses revealed significant effect modification by smoking history, education level, and sleep duration. Sensitivity analyses confirmed consistent results, further supporting the main results. Collectively, these findings establish KDM-BAacc as an independent and robust risk factor for CKD and highlight its potential value in risk stratification and early prevention strategies.

KDM-BAacc has increasingly been used to quantify the pace of biological aging and has been examined in relation to several age-related diseases, including cardiovascular, neurodegenerative, and renal disorders[8,9]. Previous research on aging markers and CKD has primarily focused on epigenetic aging indicators such as Horvath's clock[10,11]. In contrast, evidence on KDM-BAacc, which is based on clinical biomarkers rather than DNA methylation profiles, remains limited. Some prospective cohort studies have reported associations between epigenetic age acceleration and renal function decline or CKD incidence, although effect sizes were generally modest (ORs around 1.1–1.3 per IQR increase) and often estimated without extensive adjustment for confounders[12,13]. A major strength of the present study is its demonstration of a comparatively strong association between KDM-BAacc and CKD risk in a large community-based sample, with a fully adjusted OR of 2.13 and a clearly delineated linear dose–response relationship. These findings are consistent with the few comparable studies available[14], though the magnitude of association observed here is notably larger, potentially reflecting more comprehensive covariate adjustment or population-specific influences. Furthermore, prior studies seldom evaluated effect modification by lifestyle or psychosocial factors, whereas our analysis identified significant interactions with smoking history, education level, and sleep duration. These results underscore the possibility that the impact of accelerated biological aging on renal health may differ across population subgroups, suggesting avenues for more tailored risk assessment. Overall, our findings strengthen the evidence supporting the utility of KDM-BAacc in predicting CKD risk and indicate that it may offer advantages over certain traditional aging metrics.

The mechanisms linking KDM-BAacc to CKD are likely multifactorial and may involve several interconnected physiological pathways. Firstly, accelerated aging is characterized by key biological processes such as cellular senescence, telomere shortening, and elevated oxidative stress, all of which can directly damage glomerular and tubular structures, promote renal fibrosis, and contribute to progressive loss of kidney function[15,16]. Secondly, the strong correlations observed in this study between KDM-BAacc and cardiometabolic risk factors, including diabetes, hypertension, and dyslipidemia, suggest that metabolic dysregulation and chronic inflammation may act as important mediators. Elevated hs-CRP

and glycated hemoglobin levels among individuals with high BA acceleration reflect systemic inflammation and impaired glucose metabolism, both well-recognized contributors to renal microenvironment injury[17,18]. Additionally, accelerated biological aging may influence CKD risk through epigenetic mechanisms, such as aberrant DNA methylation patterns that modify the expression of genes involved in renal homeostasis[19]. Another relevant mechanism concerns the interplay between physiological dysregulation and the natural age-related decline in renal function. Individuals with accelerated biological aging often demonstrate multisystem impairment, as reflected in the elevated urea and creatinine levels and hematological abnormalities observed in this study. Such cumulative organ dysfunction likely heightens susceptibility to CKD progression[20]. Finally, lifestyle factors identified as effect modifiers, particularly smoking and insufficient sleep, may further amplify the detrimental impact of BA acceleration on renal health by intensifying oxidative stress, inflammation, and immune dysregulation[21]. Together, these pathways form a plausible mechanistic framework supporting the strong and linear association observed between KDM-BAacc and CKD risk.

There are several notable strengths in this study. This study utilizes a comprehensive, nationally representative dataset, which strengthens the external validity of its conclusions. The use of detailed multivariable adjustment strengthens the robustness of the observed associations, while the application of RCS analysis provides compelling evidence for a linear dose–response relationship that extends beyond simple linear assumptions. Furthermore, subgroup and interaction analyses offer valuable insights into potential effect modification, contributing to a more nuanced understanding of how BA acceleration may influence CKD risk among different population groups. Nevertheless, several limitations should be acknowledged. Firstly, the cross-sectional design precludes causal inference. Prospective cohort studies or interventional trials are needed to confirm whether KDM-BAacc predicts CKD incidence or progression. Secondly, although extensive covariates were included, the possibility of residual confounding, such as genetic susceptibility, unmeasured environmental exposures, or medication use, cannot be excluded. For instance, the biological mechanisms underlying interactions with sleep duration and marital status remain unclear and warrant further investigation. Additionally, the study population's specific characteristics may limit generalizability to other demographic or ethnic groups. Future research should incorporate multi-omics data, including genomic and epigenomic markers, to deepen mechanistic insights. Developing dynamic measures of BA acceleration that capture changes over time would also enhance understanding of aging trajectories. From a clinical perspective, integrating KDM-BAacc or similar biomarkers into CKD risk assessment tools could facilitate earlier identification of high-risk individuals and support targeted preventive strategies.

Methods

Study population

The dataset was obtained from the initial 2011 survey of the China Health and Retirement Longitudinal Study (CHARLS), which represents a nationally representative cohort of Chinese residents aged 45 years or older. This cohort was constructed using a rigorous, multi-stage probability sampling methodology to

ensure population representativeness[22]. The study collects detailed information on participants' demographic background, socioeconomic circumstances, health status, and biochemical indicators. For the current analysis, we included individuals who provided blood samples and had complete biomarker data necessary for computing KDM-based biological age as well as for determining CKD status. The original number of participants was 17,708. After applying these criteria, 6,830 participants remained eligible for inclusion. The CHARLS project received ethical approval from the Peking University Institutional Review Board (IRB00001052–11015), and written informed consent was obtained from all participants.

Calculation of KDM-BA acceleration

BA was estimated utilizing the Klemera–Doubal method (KDM), an established algorithm that integrates multiple biomarkers representing the functional status of various physiological systems. Following prior research, the KDM-BA algorithm was trained via data from the China Health and Nutrition Survey (CHNS), which included adults aged 20–79 years. For the CHARLS population, we applied an adapted and previously validated version of the KDM - BA model for Chinese adults[23]. The revised predictive model integrated eight key clinical indicators: serum cholesterol levels, triglyceride concentrations, glycated hemoglobin (HbA1c), blood urea, serum creatinine, high - sensitivity C - reactive protein (hsCRP), platelet count, and systolic arterial pressure measurements[23]. These biomarkers capture renal function (e.g., creatinine), metabolic status (e.g., HbA1c and lipid profiles), inflammation (hsCRP), and hematopoietic function (platelet count), all of which were available in the CHARLS dataset. KDM - based BA acceleration (KDM-BAacc) was calculated as the residual from a linear regression of KDM-estimated BA on chronological age. A positive residual indicates accelerated aging, meaning that an individual's BA exceeds their chronological age; conversely, a negative residual reflects slower than expected aging. For statistical analyses, KDM-BAacc was examined both as a continuous variable—standardized by its interquartile range to improve interpretability—and as a categorical variable divided into quartiles, with Q1 indicating the slowest aging and Q4 the fastest.

Assessment of CKD

CKD was identified based on participants' self - reported physician diagnosis. Participants who had been previously diagnosed with chronic kidney disease prior to the study's initiation in 2011 were excluded in the cohort. For the remaining participants, CKD status was validated during the 2015 follow - up, where respondents directly confirmed the accuracy of their previously reported diagnosis.

Covariates

Drawing on prior literature and guided by directed acyclic graphs, we selected a comprehensive set of covariates to address potential confounding. Sociodemographic factors included chronological age (treated as a continuous variable), sex, educational attainment (categorized as college or above, high school, or primary school and below), place of residence (urban or rural), and marital status (married versus unmarried, separated, or widowed). Lifestyle characteristics considered in the models were smoking behaviour (current, former, or never smoker), alcohol consumption (never, occasional use—less

than once per month—or more frequent intake), and average sleep duration per night (hours, continuous). Clinical indicators incorporated into the adjustment set were systolic and diastolic blood pressure (both continuous, mmHg). These covariates were included to minimize residual confounding as much as possible.

Statistical analysis

Baseline characteristics of the study population were summarized overall and across quartiles of KDM-BAacc. Depending on their distribution, continuous variables were presented as mean ± standard deviation or median (interquartile range), with between - group comparisons performed using parametric ANOVA or non-parametric Kruskal–Wallis tests as appropriate. For categorical variables, we reported absolute numbers and proportions, with statistical significance assessed through Pearson's chi - square tests. The association between KDM-BAacc and CKD was evaluated using multivariable logistic regression. Three progressively adjusted regression models were developed with sequential covariate adjustments: The baseline Model 1 contained no covariates; Model 2 incorporated adjustments for key sociodemographic characteristics including age, gender, educational attainment, geographic residence, and marital status; while Model 3 extended these adjustments to encompass behavioral and clinical covariates such as tobacco use, alcohol intake, nightly sleep duration, and both systolic and diastolic blood pressure measurements. Results were presented as odds ratios (ORs) with 95% confidence intervals (CIs). A p value for linear trend across KDM-BAacc quartiles was obtained by modeling the quartile variable as a continuous term. To assess the dose - response relationship between continuous KDM-BAacc and CKD risk without assuming linearity, restricted cubic spline (RCS) models with three knots positioned at the 10th, 50th, and 90th percentiles of the KDM-BAacc distribution were fitted, adjusting for all covariates included in Model 3. Linearity was evaluated using a likelihood ratio test comparing the spline model with a corresponding linear model. Subgroup analyses were performed by applying Model 3 within strata of key demographic and clinical characteristics. Multiplicative interactions were assessed by introducing cross- product terms into the regression models and evaluating significance using Wald tests. For sensitivity analysis,to handle potential bias from missing data and verify the robustness of our findings, we employed multiple imputation using the $mice$ package (m = 5 imputations, maxit = 10, method = "pmm"). The regression analysis and subgroup analysis were repeated across the imputed datasets, and the results were pooled. All statistical analyses were conducted using R software (version 4.1.0; R Foundation for Statistical Computing, Vienna, Austria). Statistical significance was defined as a two - sided p - value of less than 0.05.

Declarations

Data availability

The data that support the findings of this study are available from the China Health and Retirement Longitudinal Study (CHARLS) but restrictions apply to the availability of these data, which were used under license for the current study, and so are not publicly available. Data are however available from the corresponding author upon reasonable request and with permission of CHARLS.

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Author contributions

QZ, MCC: Conceptualization, Methodology, Formal analysis, Writing – original draft.

QZ,XJH: Data curation, Validation, Writing – review & editing.

XJH, ETL: Supervision, Project administration, Funding acquisition.

All authors reviewed and approved the final manuscript.

Competing interests

The authors declare no competing interests.

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Tables

Table 1. Baseline Characteristics of Study Participants Stratified by KDM Biological Age Acceleration Quartiles

Characteristic	Overall (N=6830)	Q1 (Slowest) (N=1708)	Q2 (N=1707)	Q3 (N=1707)	Q4 (Fastest) (N=1708)	p-value
Demographics						
Age, years (Mean (SD))	58.4 (8.6)	58.9 (8.7)	57.8 (8.4)	58.3 (8.6)	58.7 (8.4)	0.001
Male, n (%)	3135 (45.9)	469 (27.5)	646 (37.8)	924 (54.1)	1096 (64.2)	<0.001
Education, n (%)						<0.001
Primary school or below	4789 (70.1)	1299 (76.1)	1194 (69.9)	1151 (67.4)	1145 (67.0)	
High school	1840 (26.9)	378 (22.1)	465 (27.2)	495 (29.0)	502 (29.4)	
College or above	201 (2.9)	31 (1.8)	48 (2.8)	61 (3.6)	61 (3.6)	
Location, n (%)						<0.001
City/Town	1087 (15.9)	200 (11.7)	258 (15.1)	312 (18.3)	317 (18.6)	
Village	5735 (84.1)	1507 (88.3)	1446 (84.9)	1394 (81.7)	1388 (81.4)	
Marital Status, n (%)						0.677
Married	6088 (89.2)	1515 (88.8)	1533 (90.0)	1518 (88.9)	1522 (89.2)	
Never/Separated/Widowed	737 (10.8)	192 (11.2)	171 (10.0)	189 (11.1)	185 (10.8)	
Lifestyle Factors						
Smoking Status, n (%)						<0.001
Current Smoker	2008 (29.9)	356 (21.0)	440 (26.3)	567 (34.0)	645 (38.7)	
Ex-smoker	545 (8.1)	87 (5.1)	112 (6.7)	160 (9.6)	186 (11.2)	
Non-smoker	4153 (61.9)	1255 (73.9)	1122 (67.0)	940 (56.4)	836 (50.1)	
Drinking Status, n (%)						<0.001
>Once/month	1332 (20.7)	221 (13.5)	279 (17.2)	397 (25.0)	435 (27.6)	
≤Once/month	534 (8.3)	114 (7.0)	144 (8.9)	128 (8.1)	148 (9.4)	

Characteristic	Overall (N=6830)	Q1 (Slowest) (N=1708)	Q2 (N=1707)	Q3 (N=1707)	Q4 (Fastest) (N=1708)	p-value
Never	4555 (70.9)	1297 (79.5)	1202 (74.0)	1063 (66.9)	993 (63.0)	
Sleep Time, hours (Mean (SD))	6.4 (1.9)	6.3 (1.9)	6.4 (1.9)	6.4 (1.8)	6.5 (1.8)	0.008
Clinical Measures						
SBP, mmHg (Mean (SD))	129.1 (21.1)	112.0 (11.5)	122.3 (12.7)	132.0 (14.3)	150.7 (20.9)	<0.001
DBP, mmHg (Mean (SD))	75.3 (12.2)	66.8 (9.1)	72.3 (9.4)	77.4 (9.9)	85.0 (11.6)	<0.001
Comorbidities, n (%)						
Diabetes	579 (8.6)	82 (4.9)	97 (5.8)	176 (10.6)	224 (13.4)	<0.001
Dyslipidemia (Mean (SD))	0.2 (0.4)	0.2 (0.4)	0.2 (0.4)	0.3 (0.4)	0.3 (0.5)	<0.001
Hypertension (Mean (SD))	0.4 (0.5)	0.1 (0.3)	0.2 (0.4)	0.5 (0.5)	0.8 (0.4)	<0.001
Cardiovascular Disease	894 (13.2)	203 (12.0)	212 (12.6)	216 (12.7)	263 (15.5)	0.013
Biomarkers (Mean (SD))						
Total Cholesterol, mg/dL	193.2 (38.3)	183.5 (35.5)	191.6 (37.7)	195.2 (37.3)	202.5 (40.2)	<0.001
LDL-C, mg/dL	116.2 (34.7)	107.3 (31.5)	114.7 (32.4)	118.1 (33.7)	124.5 (38.4)	<0.001
HDL-C, mg/dL	50.9 (15.3)	50.5 (14.5)	51.5 (15.1)	51.4 (16.0)	50.2 (15.5)	0.032
Triglycerides, mg/dL	134.7 (110.2)	137.7 (142.3)	131.0 (104.3)	132.0 (95.6)	138.3 (90.4)	0.119
Urea, mmol/L	4.4 (1.2)	3.6 (0.9)	4.1 (0.9)	4.6 (1.0)	5.3 (1.3)	<0.001
Creatinine, mg/dL	0.8 (0.2)	0.7 (0.1)	0.7 (0.1)	0.8 (0.1)	0.9 (0.2)	<0.001
Cystatin C, mg/L	1.0 (0.2)	0.9 (0.2)	1.0 (0.2)	1.0 (0.2)	1.0 (0.2)	<0.001
Glycated Hemoglobin, %	5.3 (0.8)	5.1 (0.5)	5.2 (0.7)	5.3 (0.8)	5.5 (1.1)	<0.001
hs-CRP, mg/L	0.1 (0.2)	0.0 (0.1)	0.0 (0.1)	0.1 (0.1)	0.1 (0.3)	<0.001
Platelet Count, 10^9/L	212.5 (76.4)	234.8 (91.8)	216.6 (70.1)	204.1 (68.5)	194.4 (66.4)	<0.001

SD: Standard Deviation; SBP: Systolic Blood Pressure; DBP: Diastolic Blood Pressure; LDL-C: Low-Density Lipoprotein Cholesterol; HDL-C: High-Density Lipoprotein Cholesterol; hs-CRP: high-sensitivity C-Reactive

Protein.

Q1-Q4: Quartiles of KDM Biological Age Acceleration.

p-values are derived from ANOVA for continuous variables and Chi-square test for categorical variables.

Table 2. Multivariable Logistic Regression Analysis of the Association Between KDM Biological Age Acceleration and Chronic Kidney Disease Risk

Variable	Model 1 (Crude) OR (95% CI)	Model 2 (Sociodemographic)† OR (95% CI)	Model 3 (Fully Adjusted)‡ OR (95% CI)
KDM_BAacc (per IQR)	**1.43 (1.26, 1.63)***	**1.43 (1.25, 1.63)***	**2.13 (1.68, 2.70)***
KDM_BAacc Quartiles			
Q1 (Reference)	1.00	1.00	1.00
Q2	1.22 (0.88, 1.70)	1.31 (0.94, 1.82)	**1.47 (1.04, 2.09)***
Q3	1.11 (0.79, 1.55)	1.12 (0.79, 1.57)	1.38 (0.94, 2.04)
Q4	**2.06 (1.54, 2.78)***	**2.08 (1.54, 2.83)***	**3.10 (1.99, 4.85)***
P for trend	**<0.001**	**<0.001**	**<0.001**

†Model 2 adjusts for: Age, Sex, Education, Location, Marital Status.

‡Model 3 adjusts for all variables in Model 2 plus: Smoking, Drinking, Sleep_time, SBP, DBP.

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

OR: Odds Ratio; CI: Confidence Interval; IQR: Interquartile Range.

Figures

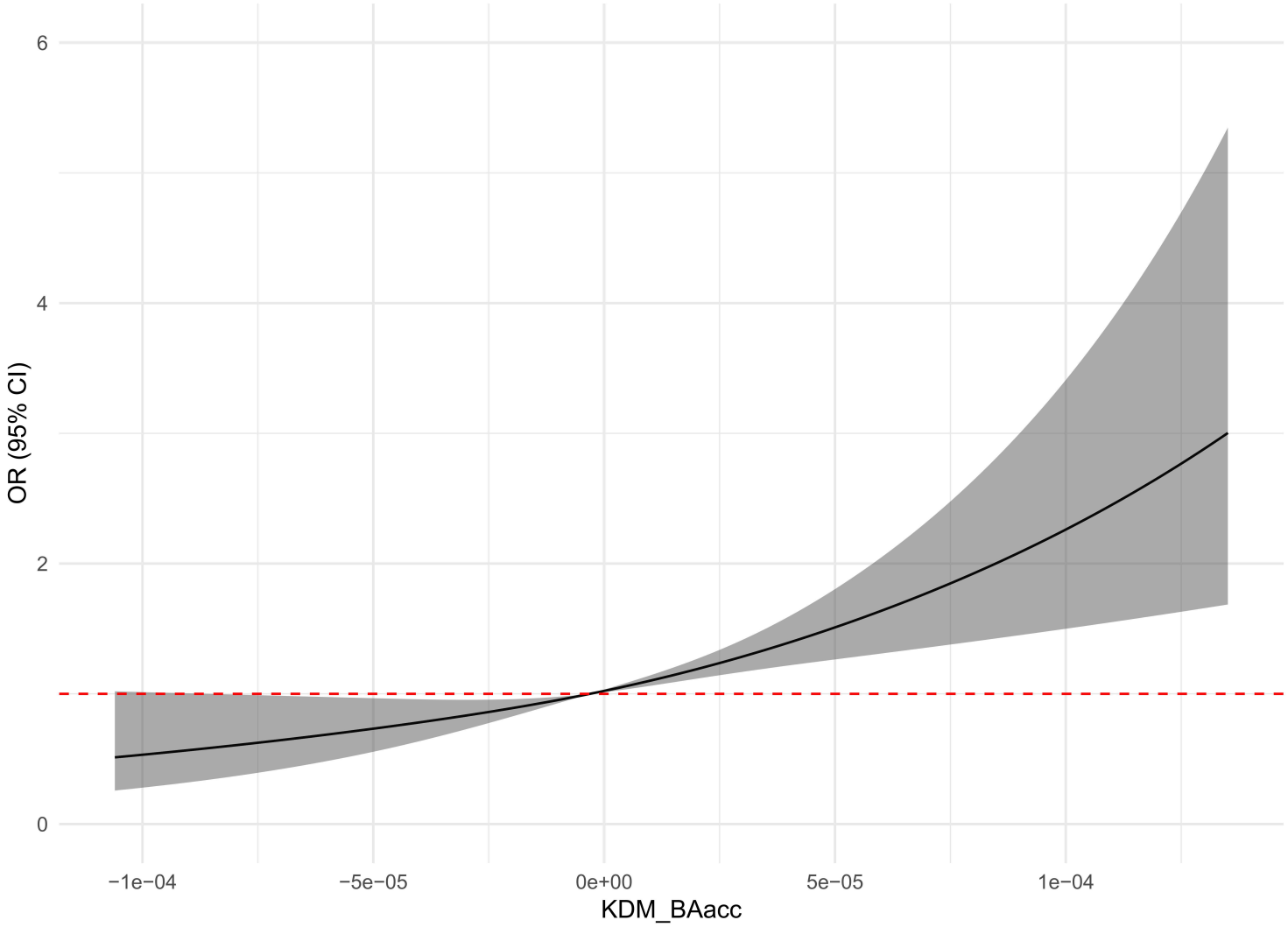


Figure 1

Dose-response relationship between KDM-BAacc and CKD risk.

The solid line represents the odds ratio (OR) for CKD, and the shaded area indicates the 95% confidence interval. The OR is set to 1 at the median of KDM-BAacc. The model is adjusted for age, sex, education, residence, marital status, alcohol consumption, smoking, and sleep duration.

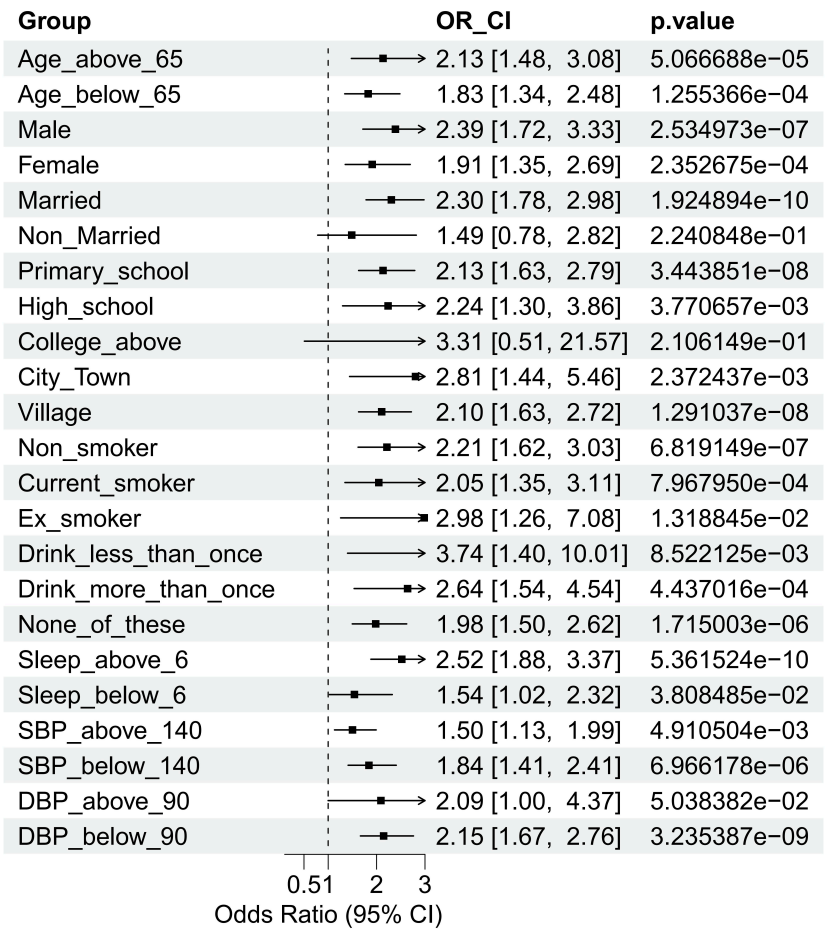


Figure 2

Subgroup analysis of the association between KDM-BAacc and CKD risk.
Forest plot displays odds ratios (OR) with 95% confidence intervals for CKD across demographic, behavioral, and clinical subgroups. The association was positive and statistically significant in most subgroups, including all age, sex, and residential categories. Non-significant associations were observed for non-married status and college education or above. All estimates are derived from multivariable logistic regression models adjusted for covariates in Model 3 (age, sex, education, residence, marital status, alcohol consumption, smoking, and sleep duration).

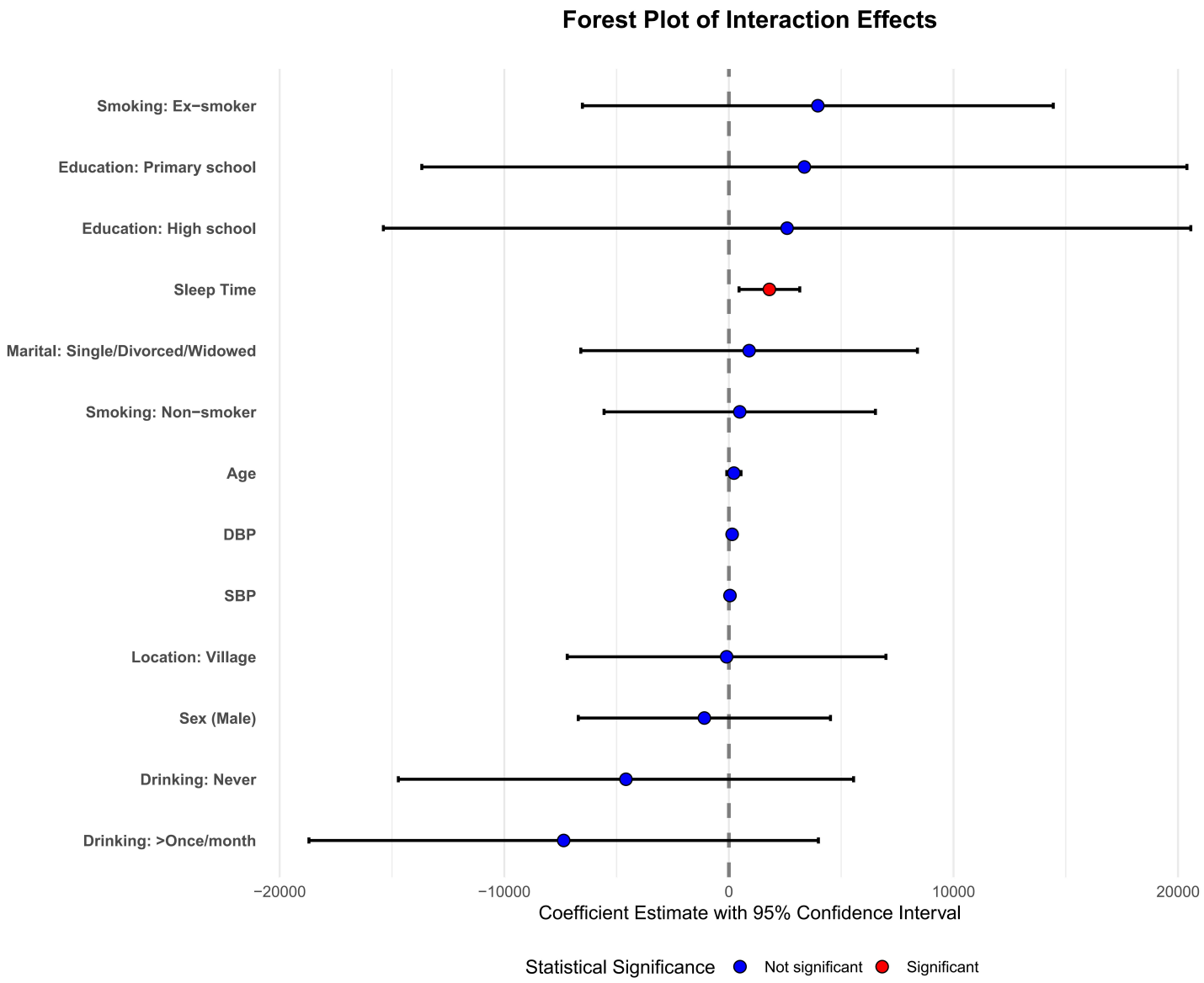


Figure 3

Interaction analysis between KDM-BAacc and selected covariates on CKD risk.
The forest plot illustrates the coefficient estimates (beta) with 95% confidence intervals for multiplicative interaction terms introduced into the fully adjusted logistic regression model. Statistically significant interactions (p for interaction < 0.05) were identified for smoking history (especially ex-smoker status), education level (primary and high school groups), and sleep duration. No significant interaction was found for marital status, age, sex, blood pressure, residence, or alcohol consumption. The analysis suggests that the magnitude of the association between KDM-BAacc and CKD risk may be modified by these specific lifestyle and socioeconomic factors.