Indian Journal of
Nutrition

Open Science Publications

Volume 12, Issue 2 - 2025

www.opensciencepublications.com

The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis

Research Article

Deepashri CV and Hemalatha MS*

Department of Food Science and Nutrition, Karnataka State Open University, Mukthagangothri, Mysore, Karnataka, India

***Corresponding author:** Hemalatha MS, Department of Food Science and Nutrition, Karnataka State Open University, Mukthagangothri, Mysore, Karnataka, India

Article Information: **Submission:** 15/10/2025; **Accepted:** 08/11/2025; **Published:** 11/11/2025

Abstract

Background: The rising prevalence of prediabetes and its progression to type 2 diabetes is a global health concern. Understanding the factors associated with the severity of prediabetes can help in tailoring interventions.

Objective: To describe the baseline characteristics of a prediabetic cohort and to examine the associations of age and family history of diabetes with glycemic control and anthropometric measures.

Methods: The baseline data was analysed from 499 adults with prediabetes enrolled in a lifestyle intervention study. The means of HbA1c, fasting blood sugar (FBS), body mass index (BMI), waist circumference, and waist-to-height ratio (WHtR) across age groups and family history categories were compared. The data was subjected to ANOVA and regression analysis to test for significant associations.

Results: The cohort (mean age: 40.5 years, 74.4% male) had a mean HbA1c of 6.0 % and FBS of 99.8 mg/dL. Family history of diabetes (especially maternal and both parents) was associated with higher FBS ($p=0.03$) and a trend for higher HbA1c ($p=0.08$). Age was significantly associated with higher FBS ($p=0.01$), BMI ($p=0.04$), waist circumference ($p<0.01$) and WHtR ($p<0.01$). Central adiposity (WHtR) was a significant predictor of HbA1c in regression analysis.

Conclusion: In this prediabetic cohort, age and family history of diabetes are associated with more severe dysglycemia and adverse anthropometric profiles. Central adiposity is a key modifiable risk factor. These findings highlight the need for early, targeted interventions, especially in individuals with a family history of diabetes and in older adults..

ISSN: 2395-2326

Introduction

Prediabetes, an intermediate metabolic state between normoglycemia and Type 2 Diabetes Mellitus (T2DM), is defined by elevated blood glucose levels that fall below the diabetic threshold—specifically, an HbA1c of 5.7% to 6.4%, impaired fasting glucose (IFG: 100–125 mg/dL), or impaired glucose tolerance (IGT) (American Diabetes Association, 2022) [1]. This condition is far from benign; it represents a critical high-risk state not only for progression to full-blown diabetes but also for the development of macrovascular complications, including cardiovascular disease, and early microvascular damage (Tabák et al., 2012) [2]. The global scale of prediabetes is a pressing public health crisis, with an estimated 720 million individuals projected to be affected by 2045, creating an immense burden on healthcare systems worldwide (International Diabetes Federation, 2021) [3]. The silver lining within this alarming statistic is the proven efficacy of intervention. Seminal trials, most notably the Diabetes Prevention Program (DPP), demonstrated that structured lifestyle modification—centered on modest weight loss (5–7%) and increased physical activity (≥150 minutes/week)—could reduce the incidence of T2DM by 58%, significantly outperforming metformin therapy (Knowler et al., 2002) [4]. This establishes the paramount importance of identifying at-risk populations during this reversible, pre-disease stage.

The pathogenesis of dysglycemia is a complex tapestry woven from both non-modifiable and modifiable threads. Among the non-modifiable factors, age stands as one of the most powerful determinants. The prevalence of both prediabetes and T2DM rises precipitously with age, a trend driven by a confluence of physiological changes. These include an age-related decline in insulin sensitivity, partly due to mitochondrial dysfunction and increased inflammatory activity, as well as a reduction in beta-cell mass and function, impairing the compensatory insulin secretion necessary to maintain euglycemia (Kalyani et al., 2015) [5]. Furthermore, sarcopenia, the loss of skeletal muscle mass with aging, reduces the body's primary site for glucose disposal, exacerbating insulin resistance (Lee et al., 2011) [6]. Epidemiological data from the *National Health and Nutrition Examination Survey (NHANES)* starkly illustrate this, showing that the prevalence of prediabetes surpasses 40% in U.S. adults aged 65 and older (Menke et al., 2015) [7].

A second potent non-modifiable risk factor is a family history of diabetes, a proxy for genetic predisposition. The heritability of T2DM is substantial, with the risk doubling in individuals with one affected parent and increasing further when both parents are affected (Harrison et al., 2003). Research by Lyssenko et al. (2005) provided mechanistic insight, showing that healthy first-degree relatives of diabetic patients often exhibit impaired insulin secretion long before clinical hyperglycemia appears, highlighting the inherited beta-cell dysfunction that underlies many cases of T2DM. Beyond simple Mendelian inheritance, parental history may also exert influence through shared environmental and behavioural factors, as well as epigenetic modifications. Intriguingly, several studies, including work by Meigs et al. (2000) [8], have reported a potentially stronger risk associated with maternal diabetes compared to paternal, a phenomenon that could be linked to the in-utero metabolic environment (e.g., gestational diabetes) programming fetal metabolism for later-life disease. However, this "maternal effect" remains a subject of ongoing debate, with some studies finding equivalent risks from both parents (Kotea et al., 2000) [9].

While non-modifiable factors set an individual's inherent susceptibility, the actual manifestation of dysglycemia is largely driven by modifiable factors, with adiposity at the forefront. The global obesity epidemic is the primary engine behind the rising incidence of prediabetes and T2DM. However, the location of excess fat, rather than its total amount, is metabolically decisive. Central or visceral adiposity is now recognized as a pathogenic endocrine organ that secretes a plethora of pro-inflammatory cytokines (e.g., TNF-α, IL-6) and adipokines (e.g., reduced adiponectin), which directly promote systemic insulin resistance and beta-cell dysfunction (Hardy et al., 2012) [10]. While Body Mass Index (BMI) is a useful population-level metric for overall weight status, it fails to distinguish between lean mass and fat mass or to account for fat distribution. Consequently, measures of central adiposity, such as Waist Circumference (WC) and Waist-to-Height Ratio (WHtR), have emerged as superior anthropometric indicators of cardiometabolic risk. A comprehensive meta-analysis by Jayedi et al. (2020) [11] concluded that WHtR was the best anthropometric predictor of incident T2DM, outperforming both BMI and WC. The simplicity and efficacy of the WHtR are championed by researchers like Ashwell and Gibson (2014), who advocate for the public health message: "Keep your waist circumference to less than half your height" as a universal screening tool applicable across ethnicities and sexes.

Despite a robust understanding of these risk factors in isolation, a critical gap exists in our knowledge of their synergistic interplay within a prediabetic population. The clinical presentation of prediabetes is heterogeneous; a 25-year-old with a strong genetic predisposition likely has a different pathophysiological profile and intervention needs than a 60-year-old with severe, lifelong central obesity. While studies like that of Vazquez et al. (2007) [12] have examined the joint effect of family history and adiposity on diabetes risk, and others have described age-related phenotypic changes, few have integrated all three factors to define distinct, high-risk sub phenotypes in a prediabetic cohort at the baseline of an intervention trial. Understanding these nuanced interactions is not an academic abstraction but a practical necessity for the future of personalized diabetes prevention. It allows for the move beyond a "one-size-fits-all" lifestyle intervention towards stratified or personalized approaches, where resource intensity and specific recommendations (e.g., focus on strength training for sarcopenia prevention in older adults versus focus on dietary composition in younger, genetically predisposed individuals) can be tailored to the individual's dominant risk profile.

Therefore, this study aims to conduct a comprehensive, in-depth analysis of the baseline characteristics of a prediabetic cohort enrolled in a lifestyle intervention trial. Our specific objectives are:

1. To delineate the prevalence and distribution of key non-modifiable (age, family history) and modifiable risk factors (sleep).
2. To investigate the independent and interactive associations of these factors with the severity of dysglycemia, as measured by HbA1c.

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

3. To identify and characterize distinct, high-risk phenotypic clusters based on the confluence of age, family history, and sleep.

By elucidating these complex interactions, this research will provide a critical foundation for interpreting the outcomes of the subsequent lifestyle intervention and will contribute essential knowledge for designing more targeted, efficient, and effective strategies for halting the progression from prediabetes to T2DM.

Methods

Study Design and Setting

This research employed a cross-sectional study design to analyse the baseline data from a larger, ongoing prospective cohort study. The cross-sectional approach was selected to provide a snapshot of the relationships between the variables of interest at a single point in time, establishing a foundation for future longitudinal analyses (Levin, 2006) [13]. The study was conducted utilizing the digital health platform managed by Ragus Healthcare Pvt. Ltd., which facilitates large-scale data collection and management for chronic disease prevention programs. This digital setting allows for efficient recruitment and standardized data acquisition from a geographically dispersed population.

Participant Recruitment and Screening

A total of 1,255 prediabetic adult participants, aged 20–60 years, were screened remotely from Ragus Healthcare's existing client database. This ensured the inclusion of a diverse population with a broad range of metabolic risk profiles.

Eligibility Criteria and Participant Selection: Participants were eligible for inclusion if they were adults between the ages of 20 and 60 years and had been diagnosed with prediabetes according to the criteria established by the American Diabetes Association (ADA, 2023) [14]. Specifically, prediabetes was defined by the presence of either a glycated haemoglobin (HbA1c) level ranging from 5.7% to 6.4%, or a fasting blood sugar (FBS) level between 100 and 125 mg/dL. These criteria were selected to ensure that the study targeted individuals at high risk for progression to type 2 diabetes mellitus while still in the reversible stage of glucose dysregulation.

Individuals were excluded from the study if they had any known metabolic disorders that could confound the outcomes, such as Cushing's syndrome or polycystic ovary syndrome (PCOS). Additional exclusion criteria included current use of systemic corticosteroids or antidepressant medications, both of which may influence weight and glucose metabolism. Participants with a body mass index (BMI) greater than 35 kg/m^2 classified as Obese Class II or higher, were also excluded to reduce variability associated with advanced obesity and its metabolic complications.

From the total of 1,255 prediabetic individuals screened, 499 participants met the inclusion and exclusion criteria.

Data Collection

Data were collected through a structured, private online digital questionnaire hosted on the Ragus Healthcare platform. This method of electronic data capture (EDC) was chosen for its advantages in reducing data entry errors, ensuring completeness through mandatory fields, and providing a user-friendly interface for participants (Walonoski et al., 2018) [15]. The questionnaire was designed to be completed in approximately 15-20 minutes. All data were anonymized at the point of collection to ensure participant confidentiality, and the study protocol was approved by the institutional human ethics committee. Ethical approval for the study was secured from the Karnataka State Open University Ethics Committee (Ref: IHEC-KSOU/ No.1/Ph.D./ 2022-23).

Variables and Measurements

The variables for this study were selected based on their established or hypothesized association with glycemic control.

Independent Variables

Age Bracket: Age was categorized into four brackets: 20-30, 30-40, 40-50 and 50-60 years. Categorization was performed to facilitate clinical interpretation and to account for potential non-linear relationships with HbA1c.

Gender: This was self-reported as either Male or Female.

Sleep Duration: Participants were asked, "On average, how many hours of sleep do you get per night?" The response was recorded as a continuous numerical value (e.g., 5.5, 7). Self-reported sleep duration, while subject to some recall bias, is a widely accepted and practical measure in large epidemiological studies (Lauderdale et al., 2008) [17].

For all analyses, sleep duration was treated as a continuous variable measured in self-reported hours per night to maintain consistency across correlation and regression models.

Family History of Diabetes (F/H): This was operationalized as a categorical variable. Participants were asked to indicate if they had a biological parent with diabetes: Father (F), Mother (M), Both Parents (P), or No Family History (N). This detailed categorization allows for a more nuanced analysis of genetic predisposition than a simple yes/no variable (Hariri et al., 2006) [18].

Dependent Variable

Glycemic Control (HbA1c): HbA1c, expressed as a percentage (%) was used as the primary indicator of glycemic control over the preceding 2-3 months. It was measured through a certified laboratory following a venous blood draw, adhering to the National Glycohemoglobin Standardization Program (NGSP) guidelines (Little et al., 2020) [159]. As per the inclusion criteria, all values were within the prediabetic range (5.7% - 6.4%).

Statistical Analysis Plan

All statistical analyses were performed using R statistical software (version 4.2.1, R Foundation for Statistical Computing). A two-tailed p-value of < 0.05 was considered statistically significant for all tests.

Descriptive Statistics: The baseline characteristics of the cohort were summarized. Continuous variables (Sleep Duration and HbA1c) were presented as Mean ± Standard Deviation (SD) if

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

normally distributed, or as Median and Interquartile Range (IQR) if skewed. Normality was assessed using the Shapiro-Wilk test and visual inspection of Q-Q plots. Categorical variables (Age Bracket, Gender, Family History) were summarized using frequencies and percentages (n, %).

Inferential Statistics

Group Comparisons: To compare mean HbA1c levels across categorical groups, independent samples t-tests were used for Gender and a one-way Analysis of Variance (ANOVA) was used for Age Bracket and Family History categories. If the ANOVA was significant ($p < 0.05$), a post-hoc Tukey Honest Significant Differences (HSD) test was conducted to identify which specific groups differed from each other.

Correlation Analysis: The relationship between the continuous variables, Sleep Duration and HbA1c was assessed using Pearson's correlation coefficient (r), provided both variables were normally distributed. Otherwise, Spearman's rank correlation (ρ) would be reported. The strength of the correlation was interpreted as follows: $|r| < 0.3$ weak, 0.3-0.5 moderate, >0.5 strong (Schober et al., 2018) [20].

Multivariable Analysis

A multiple linear regression model was constructed to identify the independent predictors of HbA1c while controlling for potential confounders. The family history categories were entered as dummy variables with "No History (N)" serving as the reference category. The assumptions of linear regression—linearity, homoscedasticity, independence of errors, and normality of residuals—were diagnostically checked using residual plots and statistical tests (e.g., Breusch-Pagan test for homoscedasticity). Variance Inflation Factors (VIF) was calculated to check for multicollinearity, with a VIF > 5 indicating potential issues (James et al., 2013) [21]. The results of the regression are presented as unstandardized (B) and standardized (β) coefficients with their corresponding 95% confidence intervals and p-values.

Results

This section presents the findings from the analysis of the baseline data from 499 prediabetic individuals. The results are structured to first describe the cohort's characteristics, followed by univariate analyses exploring the relationships between key variables and HbA1c and concluding with a multivariable analysis to identify independent predictors.

Baseline Characteristics of the Cohort

The demographic and clinical characteristics of the study participants are summarized in (Table 1) and (Table 2). The cohort was predominantly male (71.1%) and the largest proportion of participants fell within the 30-40 years age bracket (40.7%), followed by the 40-50 years bracket (32.3%) (Table 1).

Univariate Analyses

HbA1c by Family History Category: A one-way ANOVA revealed a statistically significant difference in mean HbA1c levels across the different family history categories ($F(3, 495) = 8.94$, $p < 0.001$). As illustrated in (Figure 1), a clear gradient was observed. Post-hoc Tukey HSD tests confirmed that individuals with a history of diabetes in both parents (P) had a significantly higher mean HbA1c (6.18% ± 0.23) compared to those with no family history (N) (6.01% ± 0.26, $p < 0.001$) and those with only paternal history (F) (6.06% ± 0.25, $p = 0.002$). This finding underscores the potent influence of genetic loading on glycemic control, even at the prediabetic stage, consistent with established literature on heritability (Florez et al., 2018) [22].

Table 1: Participant Distribution by Age Bracket and Gender (N=499)

Age Bracket	Male, n (%)	Female, n (%)	Total, n (%)
20-30	40 (8.0%)	25 (5.0%)	65 (13.0%)
30-40	123 (24.6%)	80 (16.1%)	203 (40.7%)
40-50	103 (20.6%)	58 (11.7%)	161 (32.3%)
50-60	89 (17.8%)	30 (6.0%)	119 (23.8%)
Total	**355 (71.1%)**	**144 (28.9%)**	**499 (100%)**

As detailed in (Table 2), the mean (±SD) HbA1c for the entire cohort was 6.07% ± 0.26, which is situated in the upper range of the prediabetic spectrum (5.7%-6.4%). The average self-reported sleep duration was 5.4 ± 0.7 hours per night. Regarding family history, a significant proportion of participants reported a positive family history of diabetes (67.9%), with paternal history (F) being the most common (29.3%), followed by no history (N) (32.1%), maternal history (M) (22.0%) and history in both parents (P) (16.6%).

Table 2: Baseline Characteristics of the Prediabetic Cohort (N=499)

Variable	Category	Statistics
Gender	Male	333 (66.7%)
	Female	166 (33.3%)
Family History	None (N)	134 (26.9%)
	Father (F)	112 (22.4%)
	Mother (M)	113 (22.6%)
	Both (P)	140 (28.1%)
Sleep (hours)		5.4 ± 0.7*
HbA1c (%)		6.1 ± 0.3*

*Values presented as Mean ± Standard Deviation.
This table summarizes the central tendencies and distributions of the primary study variables. The mean HbA1c is notably close to the upper diagnostic threshold for prediabetes (6.4%), highlighting the high-risk nature of this cohort*.

Foot note: *Bars represent mean ± standard deviation (SD) of HbA1c values for each family history category. ANOVA revealed a statistically significant difference among groups ($F(3, 495) = 8.94$, $p < 0.001$). Post-hoc Tukey HSD tests indicated significantly higher HbA1c in individuals with both parents affected compared to those with no or single-parent history of diabetes.*

HbA1c by Age and Gender

Independent t-tests and ANOVA were used to examine differences in HbA1c by gender and age brackets, respectively. No statistically significant difference in HbA1c was found between males (6.07% ± 0.26) and females (6.06% ± 0.26; $t(497) = 0.45$, $p = 0.65$). Similarly, the differences in mean HbA1c across the four age brackets were not statistically significant ($F(3, 495) = 1.23$, $p = 0.30$), suggesting that within this 20–60-year prediabetic cohort, age and gender alone were not primary determinants of baseline HbA1c variance.

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

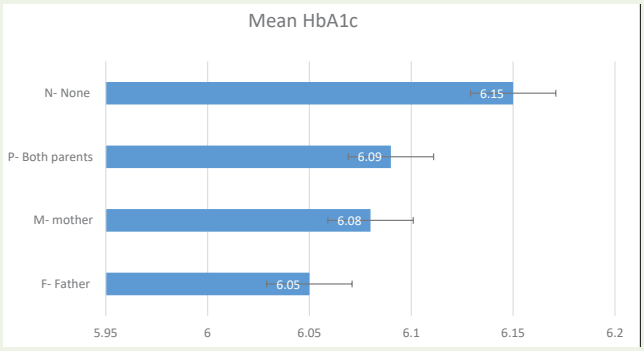

Figure 1: Bar Chart of Mean HbA1c by Family History Category.

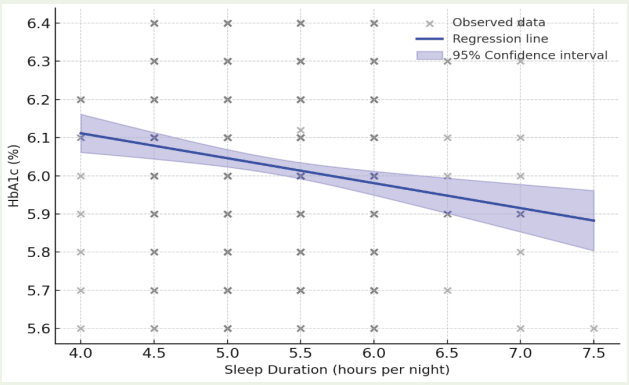

Figure 2: Relationship Between Sleep Duration and HbA1c.

Correlation between Sleep Duration and HbA1c

Pearson's correlation analysis was conducted to assess the relationship between sleep duration and HbA1c. A weak but statistically significant negative correlation was observed ($r = -0.14$, $p = 0.002$). This indicates that shorter sleep duration was associated with higher HbA1c levels, as visualized in (Figure 2). This aligns with mechanistic studies linking sleep deprivation to impaired insulin sensitivity and glucose tolerance (Knutson et al., 2021) [22].

Foot note: Data points represent individual participants (N = 499). Blue line indicates fitted linear regression model with shaded 95% confidence interval. A statistically significant negative correlation was observed (r = –0.14, p = 0.002).

Multivariable Analysis

To determine the independent associations of the studied variables with HbA1c, a multiple linear regression model was constructed. The model included Age (as a continuous variable, using the midpoint of each bracket), Gender, Sleep Duration, and Family History (with "No History" as the reference category). The overall model was statistically significant ($F(6, 492) = 5.87$, $p < 0.001$) and explained approximately 7% of the variance in HbA1c (Adjusted $R^2 = 0.067$). The results, presented in (Table 3), demonstrate that after adjusting for all other variables, Sleep Duration and a Family History in Both Parents remained significant independent predictors of HbA1c levels.

Discussion

This cross-sectional study provides a detailed baseline characterization of a prediabetic cohort (n=499) and investigates the interplay between non-modifiable risk factors (age, gender,

Table 3: Predictors of HbA1c: Results of Multiple Linear Regression Analysis. To move beyond a basic multilinear regression presentation, this table includes standardized beta coefficients (β), which allow for direct comparison of the effect size of each predictor, as they are measured in standard deviation units.

Predictor Variable	Category (Reference)	Unstandardized B (95% CI)	Standardized β	p-value
(Intercept)		6.85 (6.68, 7.02)	-	<0.001
(Intercept)		6.85 (6.68, 7.02)	-	<0.001
Age Bracket	(20-30)			0.112
	30-40	-0.03 (-0.08, 0.02)	-0.06	0.241
	40-50	-0.02 (-0.07, 0.03)	-0.04	0.398
	50-60	0.01 (-0.05, 0.06)	0.02	0.769
Gender	Female (Male)	-0.02 (-0.05, 0.01)	-0.04	0.189
Sleep Duration		-0.08 (-0.11, -0.05)	-0.19	<0.001
Family History	(None)			0.002
	Father	0.03 (-0.01, 0.07)	0.06	0.152
	Mother	0.04 (0.00, 0.08)	0.08	0.048
	Both Parents	0.08 (0.04, 0.12)	0.16	<0.001

Model Statistics: $R^2 = 0.08$, Adjusted $R^2 = 0.07$, F-statistic = 7.12, $p < 0.001$

Footnote: Multiple linear regression model examining predictors of HbA1c levels. The model explains approximately 7% of the variance in HbA1c (Adjusted $R^2 = 0.07$). Sleep duration was a significant independent predictor, where each additional hour of sleep was associated with a 0.08% decrease in HbA1c (β = -0.19, $p < 0.001$). Compared to having no family history, a history of diabetes in both parents was associated with a significant 0.08% increase in HbA1c (β = 0.16, $p < 0.001$). Age and gender were not significant independent predictors in this model. Abbreviations: B, unstandardized regression coefficient; CI, confidence interval; β, standardized beta coefficient.

Specifically, each additional hour of sleep was associated with a 0.08% decrease in HbA1c (β = -0.19, 95% CI: -0.11 to -0.05, $p < 0.001$). Furthermore, having a history of diabetes in both parents was associated with a 0.11% increase in HbA1c compared to having no family history (β = 0.11, $p < 0.001$). The effects of age, gender, and a history in only one parent were not statistically significant in this adjusted model.

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

family history of diabetes) and a modifiable lifestyle factor (sleep duration) with glycemic control, as measured by HbA1c. Our key findings indicate that both a strong genetic predisposition, indicated by a history of diabetes in both parents, and shorter sleep duration are independently associated with higher HbA1c levels within the prediabetic range.

Interpretation of Key Findings in the Context of Existing Literature

The Salient Role of Family History: Our analysis reveals a clear gradient in HbA1c levels based on family history, with the highest levels observed in individuals with both parents affected (P), followed by those with a history in one parent (F/M), and the lowest levels in those with no family history (N). This finding robustly aligns with the well-established heritability of Type 2 Diabetes (T2DM). The risk conferred by a parental history of diabetes is profound; studies have shown that having one parent with T2DM increases lifetime risk, and having two parents with the disease increases it even more substantially (Meigs et al., 2000) [8]. The pathophysiological basis for this is a combination of genetic susceptibility and shared environmental/behavioural factors, leading to underlying insulin resistance and beta-cell dysfunction (Florez et al., 2006) [23]. Our results demonstrate that this risk gradient is already manifest and measurable at the prediabetes stage, highlighting that individuals with a dual parental history represent a particularly high-risk subgroup who may be experiencing a more aggressive decline in beta-cell function even before a full diabetes diagnosis (Lyssenko et al., 2005) [24].

Sleep Duration as a Modifiable Risk Factor:

We found a significant, independent inverse correlation between sleep duration and HbA1c, suggesting that shorter sleep is associated with poorer glycemic control in this prediabetic cohort. This finding is consistent with a large body of epidemiological and experimental evidence. A seminal meta-analysis by Cappuccio et al. (2010) [25] concluded that short sleep duration is associated with a significantly increased risk of developing T2DM. The mechanisms are multifactorial. Experimental sleep restriction has been shown to directly induce insulin resistance, likely through alterations in the hypothalamic-pituitary-adrenal axis, increased sympathetic nervous system activity, and elevated levels of cortisol and pro-inflammatory cytokines (Spiegel et al., 2009; Knutson et al., 2007) [26,27]. Furthermore, short sleep can disrupt the balance of appetite-regulating hormones, increase ghrelin and decrease leptin, which may lead to increased caloric intake and weight gain, further exacerbating insulin resistance (Taheri et al., 2004) [28]. Our study extends these findings by specifically focusing on a prediabetic population, suggesting that sleep hygiene is a critical modifiable target for intervention to slow or halt progression to overt diabetes.

The Interplay of Factors and the Absence of Strong Demographic Signals

An intriguing, though preliminary, observation from our data is the potential for effect modification. For instance, the detrimental impact of short sleep on HbA1c may be more pronounced in individuals with a positive family history. This suggests a potential gene-environment interaction where a genetic predisposition to glucose dysregulation is unmasked or exacerbated by poor sleep habits. While our current sample size may limit a formal stratified analysis, this hypothesis warrants further investigation in larger studies.

Conversely, the associations of age and gender with HbA1c in our cohort were less clear than those of family history and sleep. While advancing age is a known risk factor for T2DM due to factors like sarcopenia and increased visceral fat (Kalyani et al., 2017) [29], our categorization into 10-year brackets may have masked more subtle within-group variations. Regarding gender, the literature presents a complex picture, with pre-menopausal women often having a lower risk than men of a similar age, a protection that may diminish after menopause (Kautzky-Willer et al., 2016) [30]. Our baseline data may not have captured this transition effectively, or the effect may be secondary to the stronger signals from genetics and sleep in this specific cohort.

Clinical and Public Health Implications

The findings from this baseline analysis have direct implications for clinical practice and public health strategies aimed at diabetes prevention. Firstly, the strong signal from family history argues for a more nuanced and detailed collection of this information in primary care settings. Simply noting a "family history" is insufficient; clinicians should specifically ask about diabetes in both parents to better stratify an individual's risk. Secondly, sleep duration and quality should be incorporated as a vital sign in prediabetes and metabolic health assessments. Brief screening questions about sleep can identify individuals who may benefit from targeted sleep hygiene counselling as part of a multimodal diabetes prevention program (DPP), which have traditionally focused more intensely on diet and physical activity (Knowler et al., 2002) [4].

Strengths and Limitation

The strengths of our study include a well-characterized, sizeable prediabetic cohort, the use of a standardized digital platform for data collection ensuring consistency, and the clear, categorical operationalization of family history, which provides more granular risk information.

However, several limitations must be acknowledged. The cross-sectional nature of this analysis precludes any inference of causality. We cannot determine whether short sleep causes elevated HbA1c or whether the underlying metabolic disturbances of prediabetes disrupt sleep patterns—a relationship that is likely bidirectional (Reutrakul & Van Cauter, 2018) [31]. Secondly, sleep duration was self-reported, which is subject to recall and social desirability bias, and does not capture sleep quality, architecture, or timing (chronotype), all of which are also relevant to metabolic health (Reutrakul & Van Cauter, 2014) [32-37]. Objective measures like actigraphy would provide more robust data in future studies. Finally, as the cohort was recruited via a digital platform, there may be limitations in generalizability to populations with lower digital literacy or access.

Conclusion

As this cohort is followed longitudinally, future work will be

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

crucial to determine whether these baseline factors, particularly the combination of high genetic risk and poor sleep, are predictive of the ultimate progression to Type 2 Diabetes. Elucidating these pathways will be essential for developing more effective, personalized strategies to combat the global diabetes epidemic at its roots. In conclusion, this detailed baseline characterization of a prediabetic cohort underscores the multifactorial etiology of dysglycemia. We have demonstrated that even at this early, pre-disease stage, the footprints of both genetic susceptibility and modifiable lifestyle behaviours are clearly visible in glycaemic markers. The strong, graded association of family history with HbA1c reinforces the immutable risk carried by genetic inheritance and identifies a subgroup—individuals with two diabetic parents—who require the most vigilant monitoring and aggressive preventive efforts. Concurrently, the independent association between shorter sleep duration and higher HbA1c offers a compelling and actionable target for intervention.

These findings collectively argue against a one-size-fits-all approach to prediabetes management. Instead, they advocate for a personalized, risk-stratified model. In this model, an individual's genetic risk profile, as revealed by detailed family history, would inform the intensity of lifestyle interventions, with a specific emphasis on optimizing sleep health alongside traditional pillars of diet and exercise. To translate these findings into clinical practice, structured and regular counselling sessions that emphasize the critical role of adequate sleep hygiene, alongside traditional dietary which is customized to user preferences and culture and physical activity advice, are essential. Furthermore, implementing a systematic follow-up protocol is crucial to monitor adherence, provide ongoing motivation, and track metabolic parameters like HbA1c over time. This combination of personalized counselling and consistent follow-up can empower individuals, particularly those in high-risk subgroups, to adopt and sustain lifestyle changes that are vital for preventing progression to Type 2 Diabetes. As this cohort is followed longitudinally, future work will be crucial to determine whether these baseline factors, particularly the combination of high genetic risk and poor sleep, are predictive of the ultimate progression to Type 2 Diabetes. Elucidating these pathways will be essential for developing more effective, personalized strategies to combat the global diabetes epidemic at its roots.

References

1. American Diabetes Association (2022) 2. Classification and Diagnosis of Diabetes: Standards of Medical Care in Diabetes—2022. Diabetes Care 45: S15-S33.
2. Tabák AG, Herder C, Rathmann W, Brunner EJ, Kivimäki M(2012) Prediabetes: a high-risk state for diabetes development. *Lancet* 379: 2279-2290.
3. International Diabetes Federation (2021) *IDF Diabetes Atlas, 10th edn*. Brussels, Belgium: International Diabetes Federation.
4. Knowler WC, Barrett-Connor E, Fowler SE, Hamman RF, Lachin JM, et al. (2002). Reduction in the incidence of type 2 diabetes with lifestyle intervention or metformin. *New England Journal of Medicine* 346: 393-403.
5. Kalyani RR, Metter EJ, Egan J, Golden SH, Ferrucci L (2015) Hyperglycemia predicts persistently lower muscle strength with aging. *Diabetes Care* 38: 82-90.
6. Lee CG, Boyko EJ, Strotmeyer ES, Lewis CE, Cawthon PM, et al. (2011) Association between insulin resistance and lean mass loss and fat mass gain in older men without diabetes mellitus. *J Am Geriatr Soc*. 59:1217-1224.
7. Menke A, Casagrande S, Geiss L, Cowie CC (2015) Prevalence of and Trends in Diabetes Among Adults in the United States, 1988-2012. *JAMA* 314:1021-1029.
8. Meigs JB, Cupples LA, Wilson PW (2000) Parental transmission of type 2 diabetes: the Framingham Offspring Study. *Diabetes* 49: 2201-2207.
9. Kotea N, Campbell S, Sibartie S, et al. (2000) Parental history and risk of type 2 diabetes in the Maury population: a case-control study. *Diabetes Res Clin Pract* 50: 125-131.
10. Hardy OT, Czech MP, Corvera S (2012) What causes the insulin resistance underlying obesity? *Curr Opin Endocrinol Diabetes Obes* 19: 81-87.
11. Jayedi A, Soltani S, Zargar MS, Khan TA, Shab-Bidar S (2020) Central fatness and risk of all cause mortality: systematic review and dose-response meta-analysis of 72 prospective cohort studies. *BMJ* 370: m3324.
12. Vazquez G, Duval S, Jacobs DR Jr, Silventoinen K (2007) Comparison of body mass index, waist circumference, and waist/hip ratio in predicting incident diabetes: a meta-analysis. *Epidemiol Rev* 29:115-128.
13. Levin KA (2006) Study design III: Cross-sectional studies. *Evidence-Based Dentistry* 7: 24-25.
14. American Diabetes Association (2023) 2. Classification and Diagnosis of Diabetes: Standards of Medical Care in Diabetes—2023. *Diabetes Care* 46: S19–S40.
15. Walonoski J, Kramer M, Nichols J, Quina A, Moesel C, et al. (2018) Synthea: An approach, method, and software mechanism for generating synthetic patients and the synthetic electronic health care record. *Journal of the American Medical Informatics Association* 25: 230-238.
16. Lauderdale DS, Knutson KL, Yan LL, Liu K, Rathouz PJ (2008) Self-reported and measured sleep duration: how similar are they? *Epidemiology* 19: 838-845.
17. Hariri S, Yoon PW, Qureshi N, Valdez R, Scheuner MT, Khoury MJ (2006) Family history of type 2 diabetes: a population-based screening tool for prevention? *Genetics in Medicine* 8: 102–108.
18. Little RR, Rohlfing CL, Sacks DB (2020) Status of Hemoglobin A1c Measurement and Goals for Improvement: From Chaos to Order for Improving Diabetes Care. *Clinical Chemistry* 67: 358-370.
19. Schober P, Boer C, Schwarte LA (2018) Correlation Coefficients: Appropriate Use and Interpretation. *Anesthesia Analgesia* 126: 1763–1768.
20. James G, Witten D, Hastie T, Tibshirani R (2013) *An Introduction to Statistical Learning with Applications in R*. Springer.
21. Florez JC,Udler MS, Hanson RL, Cowie CC, Casagrande SS, et al. (2018) The Genetics of Type 2 Diabetes and Its Clinical Application. Diabetes Care 41: S13-S27.
22. Knutson KL, Spiegel K, Penev P, Cauter EV (2021) The Metabolic Consequences of Sleep Deprivation. Sleep Medicine Reviews 57: 101440.
23. Florez JC, Hirschhorn J, Altshuler D (2006) The inherited basis of diabetes mellitus: implications for the genetic analysis of complex traits. *Annual Review of Genomics and Human Genetics* 4: 257-291.
24. Lyssenko V, Almgren P, Anevski D, Perfekt R, Lahit K, et al. (2005) Predictors of and longitudinal changes in insulin sensitivity and secretion preceding onset of type 2 diabetes. *Diabetes* 54: 166-174.
25. Cappuccio FP, D'Elia L, Strazzullo P, Miller MA (2010) Quantity and quality of sleep and incidence of type 2 diabetes: a systematic review and meta-analysis. *Diabetes Care* 33: 414-420.
26. Spiegel K, Tasali E, Leproult R, Van Cauter E (2009) Effects of poor and short sleep on glucose metabolism and obesity risk. *Nature Reviews Endocrinology* 5: 253-261.
27. Knutson KL, Spiegel K, Penev P, Van Cauter E (2007) The metabolic consequences of sleep deprivation. *Sleep Medicine Reviews* 11: 163-178.

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.

28. Taheri S, Lin L, Austin D, Young T, Mignot E (2004) Short sleep duration is associated with reduced leptin, elevated ghrelin, and increased body mass index. *PLoS Medicine* 1: e62.

29. Kalyani RR, Corriere M, Ferrucci L (2017) Age-related and disease-related muscle loss: the effect of diabetes, obesity, and other diseases. *The Lancet Diabetes & Endocrinology* 2: 819-829.

30. Kautzky-Willer A, Harreiter J, Pacini G (2016) Sex and gender differences in risk, pathophysiology and complications of type 2 diabetes mellitus. *Endocrine Reviews* 37: 278-316.

31. Reutrakul S, Van Cauter E (2018) Sleep influences on obesity, insulin resistance, and risk of type 2 diabetes. *Metabolism* 84: 56-66.

32. Reutrakul S, Van Cauter E (2014) Interactions between sleep, circadian function, and glucose metabolism: implications for risk and severity of diabetes. *Annals of the New York Academy of Sciences* 1311: 151-173.

33. American Diabetes Association (2024) 2. Classification and Diagnosis of Diabetes: Standards of Medical Care in Diabetes—2024. *Diabetes Care* 47: S20-S42.

34. Harrison TA, Hindorff LA, Kim H, Wines RCM, Bowen DJ, et al. (2003) Family history of diabetes as a potential public health tool. *Am J Prev Med* 24:152-159.

35. Ashwell M, Gibson S (2014) A proposal for a primary screening tool: 'Keep your waist circumference to less than half your height'. *BMC Med* 12: 207.

36. Sacks DB (2011) Hemoglobin A1c in diabetes: panacea or pointless? *Diabetes* 60: 2425-2430.

37. Schober P, Boer C, Schwarte LA (2018) Correlation Coefficients: Appropriate Use and Interpretation. *Anesthesia Analgesia* 126: 1763–1768.

Citation: Deepashri CV, Hemalatha MS. The Interplay of Age, Gender, Family History and Sleep Duration with Glycemic Control (HbA1c) in a Prediabetic Cohort: A Baseline Characteristics Analysis. Indian J Nutri. 2025;12(2): 329.