Real-World Diet Tracking with CGM Reveals Macronutrient–Glycemia Dynamics and Microbiome Profiles in a Korean Cohort

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Abstract:

Background: Daily dietary intake and the gut microbiome are pivotal in shaping glucose metabolism. However, integrated data linking continuous glucose monitoring (CGM), real-life dietary assessment, and microbiome composition in Asian populations remain limited.

Methods: We recruited 525 participants with normal glucose tolerance (NGT), prediabetes (PD), or newly diagnosed, treatment-naïve type 2 diabetes (T2DM) (HbA1c 5.0–7.0%). All participants wore a 14-day CGM and recorded daily meals through a custom-developed mobile application, yielding 10,689 meals for analysis. A subset of 348 participants underwent additional biochemical testing, including a 75-g oral glucose tolerance test (OGTT), HbA1c, fasting plasma glucose, lipid profiles, and gut microbiota profiling from stool samples. Postprandial glycemic responses were quantified by incremental area under the curve (iAUC), slope, and peak glucose, and analyzed in relation to both absolute and proportional macronutrient intake using spline models (df=4). Microbiome analyses included α- and β-diversity and subgroup comparisons by insulin resistance (HOMA-IR ≤ 2.5 vs. > 2.5) and obesity status (BMI ≤ 25 vs. > 25 kg/m²).

Results: A total of 525 participants were enrolled, and among the 348 with full biochemical and microbiome data, the mean age was 56.0 ± 11.6 years, mean BMI was 24.6 ± 3.9 kg/m², and 69.3% were female. When examining CGM data according to dietary intake, carbohydrate intake exhibited a plateau pattern, with iAUC rising at lower levels but stabilizing beyond 50–100 g. Lipid intake was consistently associated with attenuated iAUC, whereas protein showed a U-shaped association, reducing glycemic excursions at moderate intake but not at higher levels. Fiber demonstrated heterogeneous effects: very low intake was linked to exaggerated iAUC, moderate intake (10–20 g/day) attenuated responses, while higher intake showed variable associations, with significant elevations observed in elderly participants (>65 years) and women. Gut microbiome diversity (α- and β-diversity) did not differ significantly across NGT, PD, and T2DM groups. Similarly, no diversity differences were observed when stratified by insulin resistance (HOMA-IR ≤ 2.5 vs. > 2.5) or obesity status (BMI ≤ 25 vs. > 25).