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Yellow sweet potato enhances insulin sensitivity and reduces type 2 diabetes risk in obese rats

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Abstract

Background As central obesity contributes to insulin resistance and type 2 diabetes, the yellow sweet potato (*Ipomoea batatas*), with a lower glycemic index, higher fibre content, and lower calorie count, is a promising functional food.

Objective This study aimed to evaluate the effects of a diet based on yellow sweet potatoes on biomarkers of insulin resistance in obese rats.

Methods A randomized controlled design was conducted on 28 obese rats, which were allocated into four high-fat dietary groups for 3 weeks: K– (standard feed), K+ (rice-based feed), K1 (steamed yellow sweet potato), and K2 (twice-steamed yellow sweet potato). Blood samples were collected before and after the intervention, whereas tissues and caecum were collected only after intervention. Data were analyzed using SPSS, JASP, and GaphPad Prism.

Results The K2 group demonstrated the most significant improvements across all measured parameters. Total antioxidant levels increased by 5.11 U/mL, while HOMA-IR and glycated albumin(%) decreased by 5.67 and 3.83, respectively. Post-prandial glucose levels also dropped significantly by 184 mg/dL. Furthermore, the K2 group exhibited the highest concentrations of GLUT4 (25.12 ng/mL), acetic acid (150.31 mmol/L), propionic acid (53.20 mmol/L), and butyric acid (27.18 mmol/L). Levels of PPAR- α and PPAR- γ were also highest in the K2 group at 1.94 ng/mL and 0.78 ng/mL, respectively. In contrast, glucose-6-phosphatase (G6P) reached its highest level in the K– group at 9.91 mIU/mL.

Conclusion A twice-steamed yellow sweet potato diet significantly improved insulin sensitivity in obese rats by enhancing antioxidant capacity, GLUT4 expression, and SCFA production, while lowering insulin resistance markers. These findings support its potential as a functional food for metabolic health.

Keywords Antioxidant, Post-prandial glucose, GLUT4, Glycated albumin, HOMA-IR, PPAR, Insulin resistance, SCFA, Obese rats, Yellow sweet potato



1 Introduction

The incidence of obesity in developing countries has tripled over the past 20 years, with Southeast Asia experiencing one of the highest increases in obesity rates [1]. The prevalence of obesity in Indonesia has notably increased over the past fifteen years, reaching 23.4% in 2023, with central obesity at 36.8%. Concurrently, the prevalence of diabetes has risen to 11.7% in the same year, with type 2 diabetes (T2D) constituting 50.2% of all diabetes cases. Indonesia ranks fifth globally, with over 19 million individuals living with diabetes. Corroborating this, a large-scale national study reported that among Indonesian adults who are overweight or obese, 13.9% experience Impaired Glucose Tolerance (IGT), further underscoring the substantial burden of metabolic disorders associated with obesity in Indonesia [2–6].

Central obesity, in particular, is associated with an elevated risk of non-communicable diseases such as type 2 diabetes mellitus, cardiovascular disease, cancer, and osteoarthritis, all of which contribute to increased morbidity and mortality [7–9]. According to the Diabetes Prevention Program (DPP), type 2 diabetes mellitus can be prevented in high-risk populations through weight loss and lifestyle modifications, including dietary regulation and increased physical activity [10].

One of the major consequences of central obesity is insulin resistance, a condition in which the body's cells become less responsive to insulin. Adipose tissue stores lipids in the form of triacylglycerols, derived from chylomicron absorption, and releases non-esterified fatty acids to meet increased energy demands. A prolonged positive energy balance results in fatty acid accumulation that exceeds the adipose tissue's storage capacity, leading to dysfunction. This impairment reduces the availability of insulin needed to facilitate triacylglycerol uptake and suppress endogenous lipolysis. As a compensatory mechanism, insulin secretion increases, resulting in hyperinsulinemia. Excess fatty acids subsequently accumulate in peripheral tissues such as muscle, liver, and pancreas due to impaired lipid buffering [11]. The accumulation of fatty acids and elevated blood glucose levels induce oxidative stress, which arises from an imbalance between the production and neutralization of reactive oxygen species (ROS). Excessive ROS damages cellular components, including proteins, lipids, and DNA. Inadequate antioxidant defenses further exacerbate oxidative stress [12].

To measure insulin resistance, several biomarkers and assessment tools are available. One widely used method is the Homeostasis Model Assessment of Insulin Resistance (HOMA-IR), which estimates insulin sensitivity and β -cell function based on fasting glucose and insulin levels. Central obesity is strongly associated with elevated HOMA-IR values, even in individuals not yet diagnosed with diabetes [11, 13, 14]. In addition to HOMA-IR, glycated albumin (GA) is a valuable marker of insulin resistance. Unlike hemoglobin A1c (HbA1c), GA is unaffected by hemoglobin metabolism disorders and reflects glycemic control over the previous 2–4 weeks [15].

Post-prandial glucose levels also play a critical role in identifying individuals at risk of developing diabetes and its complications. The utility of fasting plasma glucose and HbA1c, with 2-hour post-prandial plasma glucose serving as a primary criterion for diagnosing prediabetes and diabetes [16].

Despite the availability of these biomarkers, dietary interventions targeting insulin resistance have yielded mixed results. Although numerous studies have explored the effects of diet on insulin resistance in both animal models and humans, many

interventions have proven to be less effective or difficult to implement in real-world settings. For instance, a study by Utari et al. (2019) demonstrated that low-calorie and low-glycemic index diets were ineffective in significantly reducing insulin resistance (as measured by HOMA-IR), primarily due to limited monitoring of dietary intake among participants [17].

Given these limitations, there is a growing interest in identifying local, accessible food sources that are rich in fiber, have a low glycemic index, and can serve as viable alternatives to staple foods like rice. One such candidate is sweet potato (*Ipomoea batatas*), which contains approximately one-third the calories of rice, a lower glycemic index (46 vs. 79.6), ten times more fiber, and bioactive compounds such as β -carotene that possess antidiabetic properties [18–20]. In line with these findings, recent research reported that among the three sweet potato varieties compared, yellow sweet potato specifically demonstrated a more prominent antidiabetic potential in diabetes management [21]. To the best of our knowledge, there exists a limited number of preclinical and clinical studies that have specifically investigated the impact of yellow sweet potato consumption on biomarkers of insulin resistance and oxidative stress, particularly within the context of obesity. Notably, even fewer studies have been conducted in Asia, with a particular scarcity in Indonesia.

Therefore, this study aims to investigate the potential of yellow sweet potato as a functional food to improve insulin resistance and oxidative stress in obesity. Specifically, we evaluate the effects of yellow sweet potato consumption on total antioxidant capacity, insulin resistance (HOMA-IR), glycated albumin (GA), post-prandial glucose, GLUT4 expression, glucose-6-phosphatase (G6P), short-chain fatty acids (SCFA), and the expression of peroxisome proliferator-activated receptors (PPAR- α and PPAR- γ).

2 Materials and methods

2.1 Materials

Yellow sweet potatoes (*Ipomoea batatas* L.), specifically the Sari variety, were obtained from CV Arindo Makmur in Malang, East Java, Indonesia. The tubers were harvested at 3–4 months of age and certified under the variety purification certificate No. Ubjl.R.3514010.0288.0068/PV. For the steamed yellow sweet potato (SYSP) preparation, the tubers were peeled, sliced into 4 cm pieces, and steamed at approximately 70 °C for 15 min. Meanwhile, for the resistant starch-rich SYSP (SYSP-RS), the sweet potatoes underwent steaming for 15 min at 70 °C, followed by cooling at 4 °C for 24 h, and were subsequently re-steamed for 15 min under the same temperature condition. The processed sweet potatoes were then incorporated into the experimental diet.

2.2 Biochemical analysis of steamed yellow sweet potato and animal diet

Resistant starch components and antioxidant total of the steamed yellow sweet potato and SYSP-RS were analyzed in duplicate following standard methods by AOAC 2002.02 [22] and AOAC 2012.04 [23]. The nutrient composition of the steamed yellow sweet potato (SYSP) and the high-resistant starch yellow sweet potato (SYSP-RS) diets was calculated based on their formulated feed ingredients (Table 1).

Table 1 Composition of standard feed ingredients AIN 93 [24] and yellow sweet potato feeding

Material	Standard feed (%)	Feed high fat (%)	SYSP (%)	SYSP-RS (%)	Rice feed (%)
Corn Starch-dextrin	62	1.6	-	-	-
Dextrin	-	15.5	15.5	15.5	15.5
Casein	14	14	14	14	14
Sucrose	10	10	10	10	10
Powdered cellulose	5	5	5	5	5
Soybean oil	4	46.9	4	4	4
AIN-93 mineral mix	3.5	3.5	3.5	3.5	3.5
AIN 93 vitamin mix	1	1	1	1	1
Choline bitartrate	0.25	0.25	0.25	0.25	0.25
L-cystine	0.18	0.18	0.18	0.18	0.18
t-Butylhydroquinone	0.0008	0.0008	0.0008	0.0008	0.0008
Cholesterol	-	2	-	-	-
Rice	-	-			46.6
Yellow Sweet Potato			46.6		
Twice-steamed yellow sweet potato				46.6	
Total	99.93	99.93	100.03	100.03	100.03
Energy (kcal)	4000	6241	4004	4004	4004
Protein (%)	14	14	14	14	14
Fat (%)	4	48.9	4	4	4
Carbohydrate (%)	77	32	77.1	77.1	77.1

2.3 Animal handling

This study utilized male Sprague Dawley rats aged approximately 8 weeks. All animals were obtained in a healthy and active condition and were maintained in individual cages to monitor dietary intake and avoid feed competition. The animals underwent a 7-day acclimatization period under controlled conditions, including a room temperature of 25 °C, 12-hour light/dark cycle, and free access to water and standard AIN-93 M chow. During acclimatisation, behavioural observations were conducted to assess the animal's health status. Inclusion criteria included a Lee Index > 310, indicating an obese phenotype, while exclusion criteria were mortality or abnormal behavioral signs during the acclimatization and intervention period. The rat model was utilized in this study, as it provides a reliable platform for conducting well-controlled investigations.

This study has obtained ethical approval for animal experimentation from the Health Research Ethics Committee of Diponegoro University, Semarang, Indonesia, with the following number: 075/EC-H/KEPK/FK-UNDIP/VII/2024.

2.4 Experimental design

The minimum number of animals per group was determined using the Federer formula, resulting in six rats per group, with an additional rat included as a reserve ($n = 7$). After acclimatisation, obesity was induced by administering a high-fat diet for three weeks, which consisted of 48.9% fat, 32% carbohydrates, and 19.1% protein. Cholesterol powder (Sigma-Aldrich) was used as the primary lipid source. After induction phase, rats were randomly assigned into four experimental groups and switched to standard diet and standard diet supplemented with rice or steamed yellow sweet potato or yellow sweet potato rich in resistant starch. Group K1 (Treatment Group 1) was provided with a diet in which 100% of the corn starch was substituted with steamed yellow sweet potato.

Group K2 (Treatment Group 2) received a diet where all corn starch was replaced by yellow sweet potato rich in resistant starch, processed using a steam–cool–steam method. The K + group (Positive Control) was given a diet with complete replacement of corn starch by rice (Platinum Raja brand), while the K – group (Negative Control) was maintained on a standard AIN-93 M chow diet. All diets were provided at a fixed quantity of 15 g/rat/day, and water was available ad libitum throughout the intervention period. Body weight and naso-anal length were recorded weekly to calculate the Lee Index as a measure of obesity progression and intervention efficacy. The following is the formula for calculating the Lee index [25].

$$\text{Lee index} = [\text{Body Weight (g)} \times 1000 / \text{Naso - anal Length (cm)}]^{1/3}$$

Rice, compared to sweet potatoes, has several characteristics that can contribute to increased insulin resistance. Rice is a staple food in Indonesia, so the author studied the differences between rats fed rice and those fed sweet potatoes. The hope is that rice can be replaced by sweet potatoes as a staple to help prevent insulin resistance.

2.5 Blood, adipose tissue and caecum content samples collection

Blood samples were collected on Day 0 and Day 22 of the intervention period. Rats were anesthetized using ketamine (60 mg/kg BW) during the light phase, and approximately 3 mL of blood was drawn via the orbital sinus using glass capillary tubes. Samples were centrifuged at 4000 rpm for 15 min at 4 °C to separate the serum. The supernatant was aliquoted and stored at – 80 °C for further biochemical analyses. At the end of the intervention, rats were sacrificed, and both cecal contents and adipose tissue were collected. Luminal contents of the caecum were obtained by rinsing with phosphate-buffered saline (1X PBS, pH 7.4) and stored at – 80 °C for short-chain fatty acids (SCFAs) analysis using gas chromatography. Adipose tissue samples were preserved for post-intervention evaluation of insulin signaling and metabolic-related protein expressions.

2.6 Biomedical analysis of blood and caecum content samples

Fasting blood glucose was measured using an enzymatic photometric test based on the glucose oxidase-peroxidase (GOD-PAP) method (Glucose GOD FS, DiaSys Diagnostic Systems GmbH, Germany) with catalogue number : 2500 99 10 021. Serum insulin levels were determined using a sandwich ELISA kit (FineTest® Rat Insulin ELISA Kit, Wuhan Fine Biotech Co., Ltd., China) catalogue number : ER1113. HOMA-IR was calculated using the formula: (fasting glucose (mg/dL) × fasting insulin (μU/mL)) / 405, with HOMA-IR values above 3.9 considered indicative of insulin resistance in rats. Glycated albumin was analyzed using the FineTest® Rat GA QuickTest ELISA Kit (Wuhan Fine Biotech Co., Ltd., China) catalogue number : QT-ER1851. Total antioxidant capacity (TAC) was evaluated using the Trolox Equivalent Antioxidant Capacity (TEAC) method with ABTS (2,2-azino-bis-3-ethylbenzthiazoline-6-sulphonic acid) as the radical source, and absorbance was measured using a UV-Vis spectrophotometer (Genesys 150, Thermo Fisher Scientific, USA). Post-prandial glucose levels were assessed 120 min after feeding on Day 0 and Day 22 using the same GOD-PAP enzymatic method. The normal post-prandial glucose level for rats was set at 5.65 mmol/L (218.5 mg/dL). SCFAs, including acetate, propionate, and butyrate, were analyzed in caecum content samples after the intervention. The concentrations were measured using gas chromatography.

2.7 Protein expression analysis for GLUT4, G6P, PPAR- α , and PPAR- γ

The expression levels of GLUT4 and PPAR- γ proteins were analyzed from adipose tissue samples, while G6P and PPAR- α proteins were measured from liver tissue. All protein expression levels were determined using sandwich enzyme-linked immunosorbent assay (ELISA) kits (FineTest® Rat ELISA Kits: GLUT4 catalogue number : ER0999, G6P catalogue number : ER0967, PPAR- α catalogue number : ER1283, and PPAR- γ catalogue number : ER1284; Wuhan Fine Biotech Co., Ltd., China), following the manufacturer's protocols.

2.8 Statistical analysis

Statistical analysis was performed using SPSS software version 25.0 (IBM Corp., Armonk, NY, USA), while graphical illustrations were generated using GraphPad Prism version 9.0 (GraphPad Software Inc., USA) and JASP 2025 version 0.19.3.0 (JASP Team 2025). All data were expressed as mean $\pm$ standard deviation (SD). The normality of data distribution was assessed using the Shapiro–Wilk test, considering that the number of subjects in each group was fewer than 50. For intra-group comparisons, the paired t-test was used for normally distributed data. Between-group comparisons were conducted using one-way ANOVA, followed by Bonferroni or Tamhane's T2 post hoc test, depending on the homogeneity of variance based on Levene's test results. Non-normally distributed variables were analysed using the Kruskal–Wallis test, followed by the Mann–Whitney U test for pairwise comparisons. Pearson Product-Moment correlations were performed to assess the association between insulin resistance and SCFA levels (acetate, butyrate, and propionate). A p-value of <0.05 was considered statistically significant.

3 Results

3.1 Resistant starch and antioxidant total

The results of the resistant starch and total antioxidant content tests on feed, where rice, SYSP, and SYSP-RS were replaced, are presented in Table 2. This table shows that SYSP-RS has the highest resistant starch and total antioxidants.

3.2 Baseline characteristics

A total of 28 Wistar rats with diet-induced obesity were included in this study, with seven rats in each group. No significant differences were observed at baseline among the groups for body weight, Lee index, total antioxidant, glycated albumin, and postprandial glucose levels ($p > 0.05$). However, a significant difference was found in HOMA-IR values between groups at baseline ($p = 0.026$), although the overall mean values remained indicative of insulin resistance in all groups (Table 3). The results of the Lee index test showed no significant differences, meaning that all groups had the same obesity characteristics before the intervention stage.

Data were expressed as mean $\pm$ standard deviation (SD) and measured before the treatment period; K1 (Treatment Group 1): normal diet + 100% of corn starch replaced by

Table 2 The results of resistant starch and total antioxidant content

Materials	Rice	SYSP	SYSP-RS
Resistant Starch	0.49%	2.12%	2.35%
Total Antioxidant	12.3%	15.7%	20.2%

Table 3 Baseline characteristics

Parameters	Group				P value
	K-	K+	K1	K2	
Bodyweight (g)	275.00 ± 11.31	265.85 ± 21.58	269.14 ± 16.92	270.57 ± 23.56	0.839
Lee index	325.72 ± 1.43	325.70 ± 2.26	323.14 ± 3.32	325.37 ± 3.18	0.238
Antioxidant total (U/mL)	1.59 ± 0.01	1.56 ± 0.04	1.57 ± 0.03	1.58 ± 0.03	0.545
HOMA-IR	9.32 ± 0.14	9.29 ± 0.21	9.06 ± 0.08	9.14 ± 0.20	0.026
Glycated albumin (%)	7.34 ± 0.34	7.33 ± 0.49	7.34 ± 0.27	7.33 ± 0.37	0.901
Post-prandial Glucose (mg/dL)	290.61 ± 2.11	289.43 ± 3.13	289.08 ± 2.62	288.26 ± 1.53	0.357
Fasting Glucose (mg/dl)	262.04 ± 2.64	262.04 ± 4.09	261.22 ± 3	261.98 ± 2.93	0.954
Fasting Insulin (pg/ml)	480.34 ± 4.49	478.99 ± 6.91	468.72 ± 6.32	471.1 ± 7.34	0.004

SYSP; K2 (Treatment Group 2): normal diet + 100% of corn starch replaced by SYSP-RS; K+ (Positive Control): normal diet + 100% of corn starch replaced by rice; K- (Negative Control): standard AIN-93 M chow; n: 7; $p < 0.05$ was considered significant with One Way ANOVA test.

3.3 Effects of SYSP intervention on Lee index

The Lee index, was significantly affected by the intervention across all groups. As presented in Table 1, the K1 and K2 groups exhibited markedly lower Lee index values post-intervention compared to both control groups. Specifically, the K1 group showed a Lee index of 309.59 ± 3.03 , while the K2 group demonstrated an even lower value of 308.02 ± 2.47 . In contrast, the negative control (K-) and positive control (K+) groups maintained higher indices of 331.16 ± 1.36 and 331.02 ± 2.00 , respectively. The change (Δ) in Lee index post-treatment was -13.55 in the K1 group and -17.35 in the K2 group, indicating a significant reduction in body fat accumulation compared to the K- ($\Delta = 5.44$) and K+ ($\Delta = 5.32$) groups. The statistical analysis confirmed that these differences were highly significant, with $P < 0.000$ for both within-group and between-group comparisons. These findings suggest that the intervention effectively reduced adiposity in a dose-dependent manner, with the greatest improvement observed in the K2 group.

3.4 Effects of SYSP intervention on antioxidant total, glycated albumin, HOMA-IR, and post-prandial glucose

The effect of the intervention on antioxidant status and metabolic parameters was evaluated by comparing post-intervention values among groups. As shown in Fig. 1A, total antioxidant levels were significantly higher in both intervention groups (K1 and K2) compared to the negative control (K-) and positive control (K+). The K2 group exhibited the highest antioxidant capacity (6.69 ± 0.10 U/mL), followed by K1 (5.93 ± 0.20 U/mL), with both showing statistically significant differences from K- and K+ ($P < 0.0001$). There was also a significant difference between K1 and K2, indicating a dose-dependent effect. In terms of insulin resistance (Fig. 1B), post-intervention HOMA-IR values were markedly lower in the K1 (4.21 ± 0.13) and K2 (3.47 ± 0.12) groups compared to K- (9.35 ± 0.13) and K+ (9.36 ± 0.26) groups ($P < 0.0001$). Furthermore, K2 demonstrated significantly lower HOMA-IR than K1, suggesting a more pronounced improvement in insulin sensitivity with higher intervention dose. Similarly, glycated albumin levels (Fig. 1C) were significantly reduced in K1 ($4.20 \pm 0.79\%$) and K2 ($3.51 \pm 0.66\%$) groups compared to the control groups (K-: $7.38 \pm 0.31\%$; K+: $7.17 \pm 0.45\%$), with $P < 0.0001$ for all comparisons. The K2 group exhibited the lowest glycated albumin level, indicating

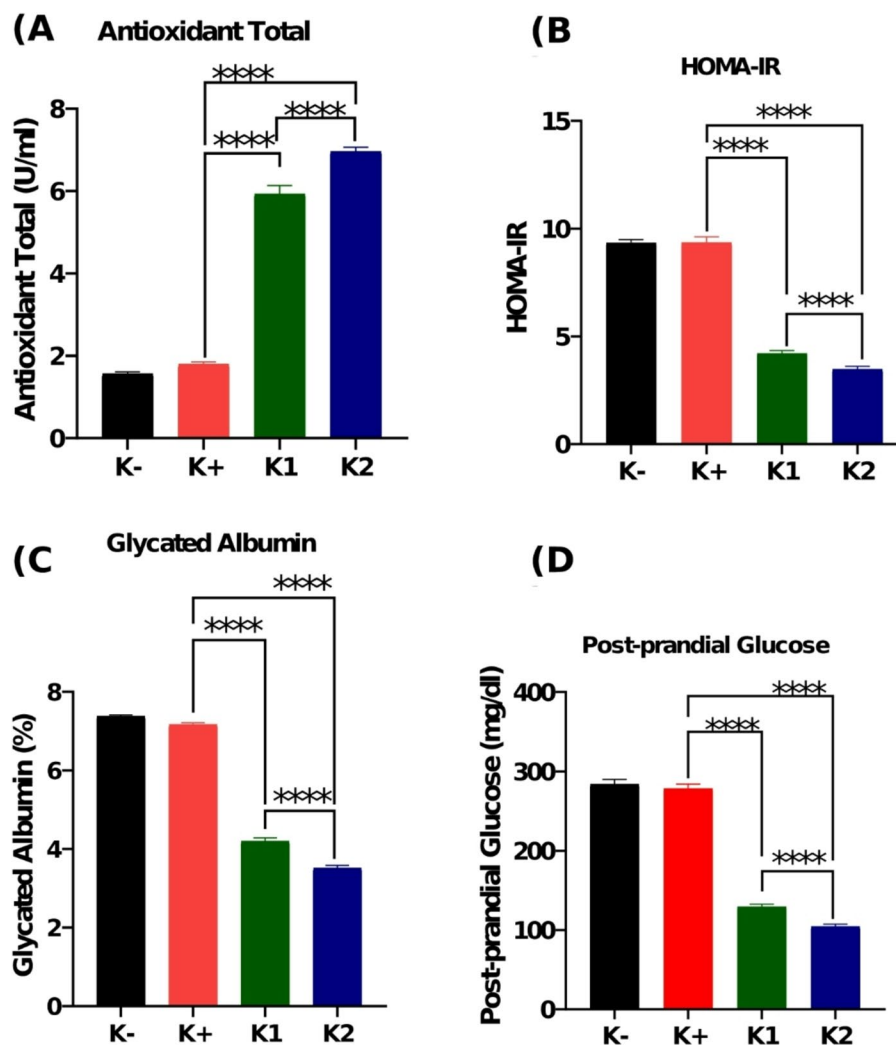


Fig. 1 Effects of SYSP on antioxidant capacity and metabolic parameter. **A** Total antioxidant capacity, **B** HOMA-IR (insulin resistance), **C** Glycated albumin (%), and **D** Post-prandial glucose levels (mg/dL) in each experimental group after the intervention. Data are presented as mean $\pm$ SD. Significant differences were observed between the positive control group (K+) and both intervention groups (K1; K2), as well as between K1 and K2, as indicated by **** ($P < 0.0001$). One-way ANOVA followed by Tukey's post hoc test was used for statistical analysis

better long-term glycemic control. Post-prandial glucose concentrations (Fig. 1D) were also substantially decreased in both intervention groups. The K2 group had the lowest glucose level (104.55 ± 2.75 mg/dL), followed by K1 (129.41 ± 3.30 mg/dL), both of which were significantly lower than the values observed in K- (284.19 ± 5.65 mg/dL) and K+ (278.49 ± 5.36 mg/dL) groups ($P < 0.0001$). The reduction in post-prandial glucose was greater in K2 compared to K1, highlighting a dose-dependent glycemic-lowering effect.

3.5 Effects of SYSP intervention on adipose tissue GLUT4 and PPAR- γ

The SYSP intervention significantly altered the expression levels of GLUT4 and PPAR- γ in adipose tissue across all treatment groups (Fig. 2A–B). Post-intervention analysis revealed a marked increase in GLUT4 expression in the K1 and K2 groups compared to both the negative control (K-) and positive control (K+) groups. Specifically, GLUT4 levels were significantly higher in K1 (23.19 ± 0.51) and K2 (25.12 ± 0.43) groups than

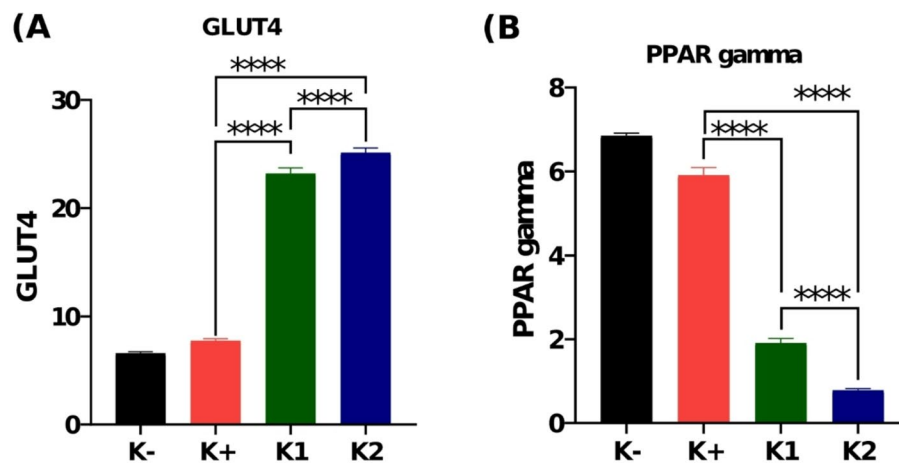


Fig. 2 SYSP intervention modulates expression of glucose transport and insulin sensitivity markers in adipose tissue. **A** GLUT4 and **B** PPAR- γ expression levels post-intervention. Data are shown as mean $\pm$ SD. SYSP treatment significantly increased GLUT4 expression and decreased PPAR- γ expression in a dose-dependent manner, with **** indicating $P < 0.0001$ for comparisons between K+ and K1/K2, and between K1 and K2. Statistical analysis was performed using one-way ANOVA followed by Tukey's post hoc test

in K- (6.58 ± 0.15) and K+ (7.74 ± 0.18) groups ($P < 0.000$). Notably, the highest GLUT4 expression was observed in the K2 group, suggesting a dose-dependent effect of the SYSP intervention (Fig. 2A). Conversely, the expression of PPAR- γ was significantly reduced in the K1 and K2 groups compared to the K- and K+ groups. The PPAR- γ levels in the K2 group (0.78 ± 0.03) were significantly lower than in K1 (1.90 ± 0.11), K+ (5.90 ± 0.17), and K- (6.84 ± 0.06) groups ($P < 0.000$), with the K2 group showing the most substantial suppression (Fig. 2B). These findings suggest that the SYSP intervention may enhance insulin sensitivity and glucose transport activity in adipose tissue by upregulating GLUT4 and downregulating PPAR- γ in a dose-dependent manner.

3.6 Effects of SYSP intervention on liver tissue G6P and PPAR- α

Post-intervention analysis demonstrated significant differences in liver G6P and PPAR- α levels across all groups (Fig. 3). G6P expression was markedly decreased in the K+ group (0.80 ± 0.02) compared to the K- group (9.91 ± 0.48). Interestingly, administration of SYSP in both treatment groups (K1 and K2) restored G6P levels to values significantly higher than K+ (7.76 ± 0.22 and 8.67 ± 0.41 , respectively; $P < 0.000$), although not fully to the level of the K- group (Fig. 3A). Among the treatment groups, K2 exhibited the highest G6P level, indicating a possible dose-dependent effect of SYSP intervention. In contrast, hepatic PPAR- α levels were significantly downregulated in the K1 and K2 groups (2.93 ± 0.11 and 1.94 ± 0.08 , respectively) when compared to K- (9.38 ± 0.08) and K+ (8.06 ± 0.25) groups ($P < 0.000$). The lowest expression was observed in the K2 group, suggesting that the SYSP intervention suppressed PPAR- α more effectively at the higher dose (Fig. 3B). This pattern may reflect a modulatory role of SYSP in hepatic lipid metabolism through downregulation of PPAR- α expression.

3.7 Effects of SYSP intervention on caecum SCFAs

Post-intervention analysis revealed significant differences in caecal short-chain fatty acid (SCFA) concentrations among groups ($P < 0.000$), as shown in Fig. 4. The K2 and K1 groups, which received SYSP intervention, exhibited markedly higher levels of

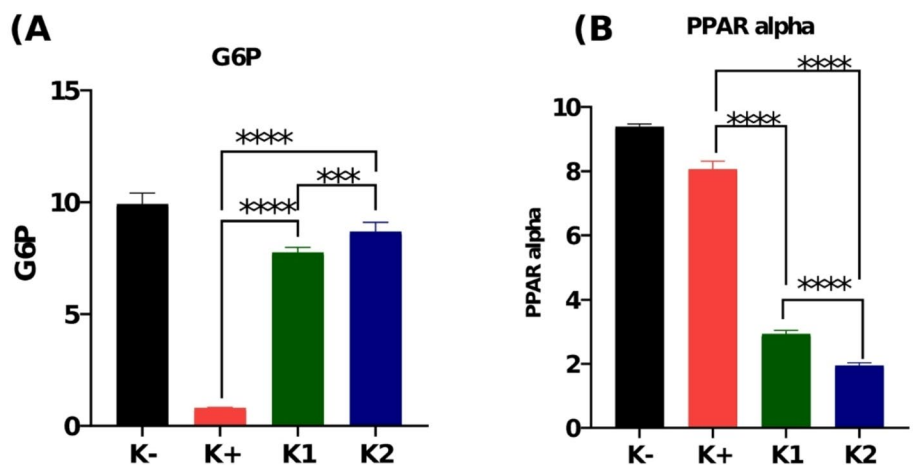


Fig. 3 Liver expression of G6P and PPAR-α following SYSP intervention. **A** G6P and **B** PPAR-α levels post-intervention. Data are expressed as mean ± SD. SYSP treatment restored G6P levels and suppressed PPAR-α expression significantly, with K2 showing the most prominent effect. Asterisks (****) indicate $P < 0.0001$ for all significant group comparisons (K+ vs. K1/K2 and K1 vs. K2). One-way ANOVA with Tukey's post hoc test was applied

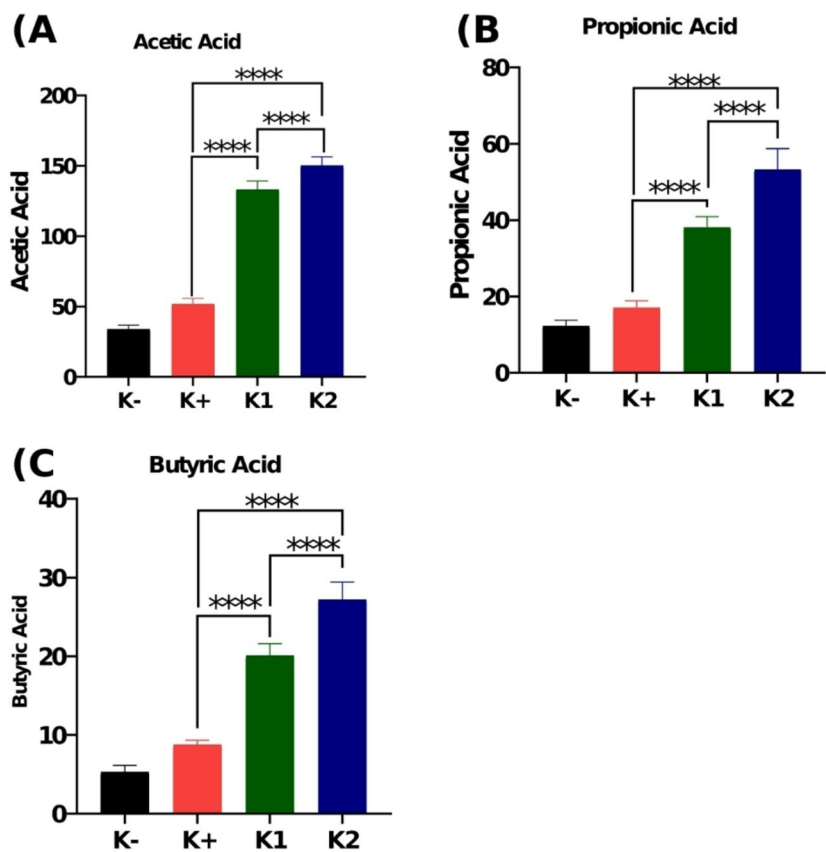


Fig. 4 SYSP enhances caecal SCFA concentrations in a dose-dependent manner. Concentrations of **(A)** Acetic acid, **(B)** Propionic acid, and **(C)** Butyric acid measured in caecal samples post-intervention. Results are presented as mean ± SD. SYSP intervention significantly increased SCFA levels, particularly in the K2 group. Significant differences between K+ and both K1/K2, as well as between K1 and K2, are denoted by **** ($P < 0.0001$). Data were analyzed using one-way ANOVA with Tukey's post hoc test

acetic acid, propionic acid, and butyric acid compared to the K[−] and K⁺ groups. Specifically, acetic acid levels were highest in the K2 group (150.31 ± 6.08 mmol/kg), followed by K1 (133.16 ± 5.98 mmol/kg), K⁺ (51.82 ± 4.01 mmol/kg), and K[−] (34.18 ± 1.06 mmol/kg). A similar trend was observed for propionic acid, with concentrations in K2 (53.20 ± 5.54 mmol/kg) and K1 (38.10 ± 2.78 mmol/kg) substantially surpassing those in K⁺ (17.09 ± 1.75 mmol/kg) and K[−] (12.23 ± 1.52 mmol/kg). Likewise, butyric acid levels were significantly elevated in the SYSP-treated groups, with the highest level observed in K2 (27.18 ± 2.23 mmol/kg), followed by K1 (20.09 ± 1.50 mmol/kg), K⁺ (8.80 ± 0.52 mmol/kg), and K[−] (5.32 ± 0.81 mmol/kg). These findings suggest that SYSP supplementation enhances microbial SCFA production in a dose-dependent manner, particularly in the caecum.

The relationship between SCFA and insulin sensitivity is as follows: a significant negative correlation between posttest HOMA IR and propionic acid was observed ($p \leq 0.0001$ $r = -0.950$), a significant negative correlation between post-test HOMA IR and butyrate acid was observed ($p \leq 0.0001$ $r = -0.958$), a significant negative correlation between posttest HOMA IR and acetate acid was observed ($p \leq 0.0001$ $r = -0.986$). The correlation test results indicate a negative relationship between HOMA-IR and SCFA (acetate, butyrate, and propionate), as shown in Fig. 5a–c, suggesting that higher SCFA levels are associated with lower HOMA-IR indices.

4 Discussion

This study provides compelling evidence that SYSP supplementation significantly enhances insulin sensitivity and improves glycemic control, as demonstrated by reductions in glycated albumin, fasting glucose, and post-prandial glucose levels [15–17]. These results contribute to the growing body of literature emphasizing the metabolic benefits of dietary interventions that modulate gut microbiota-derived metabolites and host metabolic pathways. The discussion below explores the mechanistic basis of these effects, focusing on short-chain fatty acids (SCFAs) in the caecum and the regulation of key metabolic genes, including GLUT4, PPAR- α , PPAR- γ , and G6P.

Carbohydrate substitution with sweet potato variety 2 (twice steamed) showed relatively higher levels of resistant starch (2.35%) and antioxidant activity (DPPH, 20.2%). Steaming has been shown to markedly increase the antioxidant activity of orange sweet potatoes by up to 70%, a level significantly higher than that of purple varieties ($p < 0.05$) [26]. Heat treatment also improves digestibility, alters the chemical composition, and enhances the bioavailability of phenolic compounds [27], indicating that cooking plays a critical role in maximizing the metabolic and antioxidant benefits of SYSP.

A key finding of this study is the elevated concentration of SCFAs—acetate, propionate, and butyrate—in the caecum. These metabolites, produced through microbial fermentation of dietary fiber in the colon [28], are essential regulators of host energy metabolism, gut barrier integrity, and immune modulation. Increased SCFA levels have been consistently linked to improved insulin sensitivity through multiple mechanisms. Butyrate, for example, serves as a primary energy source for colonocytes and exhibits potent anti-inflammatory activity, reducing metabolic endotoxemia—a contributor to systemic insulin resistance [29, 30]. Propionate and acetate further influence hepatic gluconeogenesis and lipid metabolism, partly via activation of G-protein-coupled receptors GPR41 and GPR43 [31, 32].

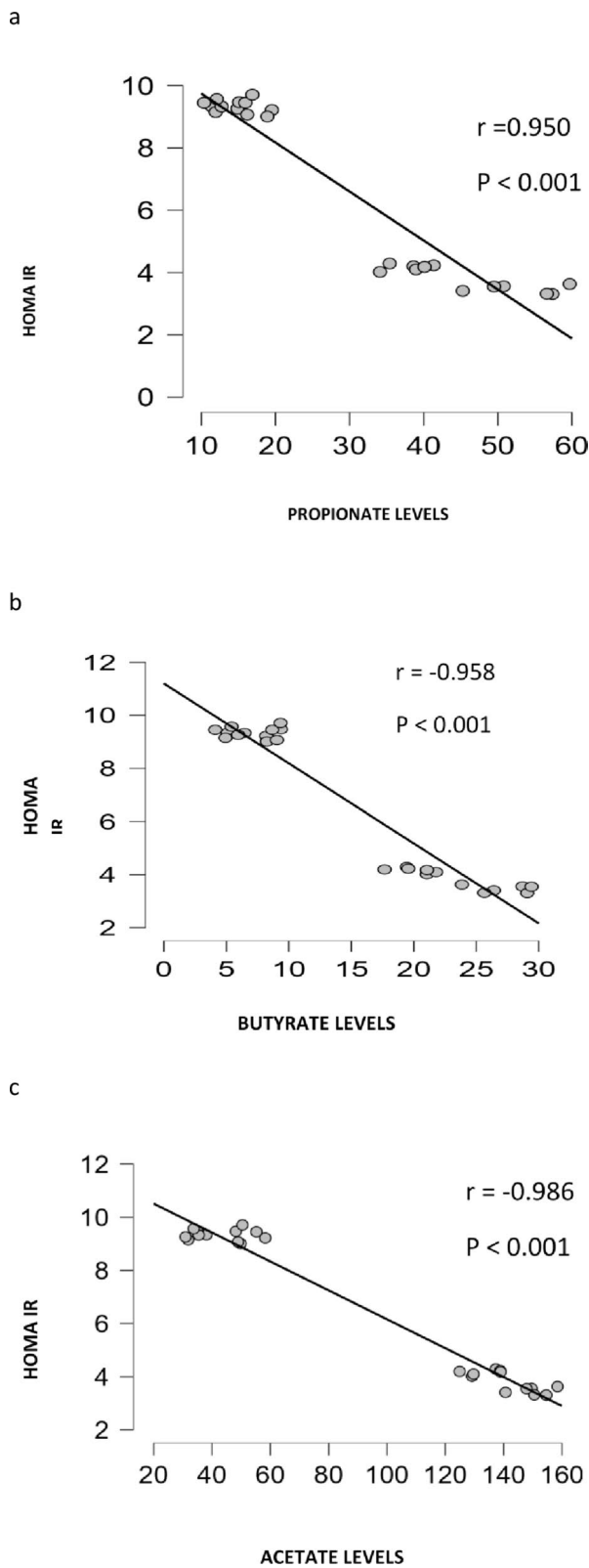


Fig. 5 **a.** The Correlation between HOMA IR and Propionate Levels. **b.** The Correlation between HOMA IR and Butyrate Levels. **c.** The Correlation between HOMA IR and Acetat Levels

SCFAs also interact with G protein–coupled receptors to enhance immune responses and reduce inflammation, which typically increases in obesity due to adipose accumulation and elevated levels of interleukin-6 (IL-6) and tumor necrosis factor- α (TNF- α). This low-grade chronic inflammation is a key driver of insulin resistance and metabolic dysfunction [28, 29]. Additionally, SCFAs stimulate the secretion of glucagon-like peptide-1 (GLP-1) and peptide YY (PYY), hormones that regulate satiety and insulin secretion. GLP-1, in particular, promotes glucose-dependent insulin secretion and delays gastric emptying, thereby improving post-prandial glucose control [33]. The elevated caecal SCFA concentrations observed in this study likely played a pivotal role in the enhanced insulin sensitivity and glycemic regulation.

The observed upregulation of GLUT4, PPAR- α , PPAR- γ , and G6P following SYSP supplementation provides mechanistic insight into its metabolic effects. These genes are central to glucose and lipid metabolism and are closely linked to the pathophysiology of insulin resistance and metabolic syndrome. GLUT4, an insulin-responsive glucose transporter in adipose and muscle tissues, facilitates glucose uptake—a process impaired in insulin-resistant states [34]. Its upregulation suggests improved peripheral glucose utilization, consistent with previous reports showing that prebiotic and polyphenol-rich diets enhance GLUT4 expression via AMPK and PPAR signaling pathways [35].

PPAR- α primarily regulates hepatic lipid metabolism by promoting fatty acid β -oxidation, thereby reducing lipid accumulation and lipotoxicity. SYSP-induced upregulation of PPAR- α may thus mitigate hepatic steatosis and improve overall metabolic function. PPAR- γ , a key regulator of adipocyte differentiation and lipid storage, also maintains insulin sensitivity [36]. Its modulation by SYSP indicates beneficial effects with a favorable safety profile. Meanwhile, G6P catalyzes the final step of gluconeogenesis and glycogenolysis, influencing hepatic glucose output. Although excessive activation may exacerbate hyperglycemia, the regulation observed here may reflect a compensatory adaptation to increased glucose utilization [37]. Further studies are needed to clarify the context-dependent modulation of G6P expression.

While the association between SCFAs and gene regulation in glucose and lipid metabolism is biologically plausible, a causal relationship remains to be established. SCFAs may influence metabolic gene expression via receptor-mediated mechanisms, but direct evidence remains lacking. Future studies using receptor antagonists or germ-free models are essential to delineate these pathways and determine whether SCFAs act as primary effectors or modulators within the metabolic network. The gut–metabolic axis provides a practical conceptual framework linking microbiota, diet, and host metabolism. SYSP appears to modulate this axis by promoting SCFA production and regulating host gene expression. This dual mechanism not only enhances systemic metabolic function but also strengthens intestinal integrity and reduces low-grade inflammation—factors known to contribute to insulin resistance [38, 39].

Emerging evidence suggests that diet-induced microbial shifts can influence host gene expression through epigenetic and metabolite-mediated pathways [38]. SYSP may favor the proliferation of beneficial microbes, such as *Akkermansia muciniphila* and *Faecalibacterium prausnitzii*, both of which are associated with improved mucosal and metabolic health [40]. However, because the gut microbiome was not analyzed in this study, future research should investigate these microbial dynamics directly.

Compared to pharmacological agents such as metformin or thiazolidinediones, SYSP represents a promising dietary alternative with fewer potential side effects. While conventional drugs remain central to T2D management, adjunct nutritional approaches targeting both the microbiota and host metabolism show substantial promise [41]. Nonetheless, the precise bioactive components within SYSP responsible for its metabolic benefits remain unidentified. As a complex mixture of polysaccharides, polyphenols, and fermentation-derived metabolites, SYSP's efficacy may result from synergistic interactions among these compounds. Isolation and characterization of individual bioactives will enhance reproducibility, enable dose–response studies, and clarify specific mechanisms underlying their metabolic effects.

Another limitation of this study is the reliance on gene expression profiling without a corresponding assessment of protein abundance or activity. Because transcriptional changes do not always translate into functional outcomes, future studies integrating proteomic and phosphoproteomic analyses are warranted to elucidate better SYSP's impact on insulin signaling and glucose metabolism. Multi-omics approaches could reveal post-translational modifications, protein stability, and pathway activation, offering a more complete picture of the molecular mechanisms underlying SYSP's metabolic actions. Finally, interventions that modulate PPARs and GLUT4 expression have demonstrated synergistic benefits in metabolic disease models [34, 35]. The multifaceted effects of SYSP highlight its potential as a holistic metabolic intervention. However, translating these preclinical findings into clinical applications will require well-designed trials to assess long-term safety, efficacy, and optimal dosing in humans.

5 Conclusion

This study demonstrated that consumption of steamed yellow sweet significantly improved metabolic health in obese rats. The intervention enhanced total antioxidant levels, GLUT4 expression, and SCFAs concentrations, while reducing insulin resistance (HOMA-IR), glycated albumin, post-prandial glucose, and PPAR- α/γ levels. These findings support the potential of yellow sweet potato as a functional food to improve insulin sensitivity and mitigate T2D risk factors, suggesting its inclusion in dietary interventions to manage obesity-related metabolic disorders.

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Author contributions

HSK, MS, HN, SS, DNA, EM, TIW, AP conceptualized the study; HSK performed the animal intervention and collected the data; HSK, AP, MS, and HN interpreted the data analysis; HSK and AP wrote and drafted the manuscript; MS, HN, SS, DNA, EM, TIW reviewed and edited the manuscript; HSK and AP finalized the manuscript; all authors have approved the final manuscript.

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declaration.

No funding was received to conduct this experiment.

Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate

All experimental procedures involving animals were conducted at the Animal Experiment Laboratory of the Center for Nutrition and Food Studies, Universitas Gadjah Mada. The study protocol was approved by the Health Research Ethics

Committee of the Faculty of Medicine, Diponegoro University, Semarang, Indonesia. Ethical approval was granted under the reference number 075/ECH/KEPK/FK-UNDIP/VII/2024. All research activities were conducted in accordance with the principles outlined in the Declaration of Helsinki and the guidelines set forth by the Council for International Organizations of Medical Sciences (CIOMS).

Plant ethics

This study applies plant ethics in accordance with plant guidelines by treating plants with respect, paying attention to sustainability, avoiding environmental damage, preserving biodiversity, and promoting the common good and scientific integrity. It also includes ensuring data integrity and preventing damage to the ecosystem during sampling. This study focuses on balancing scientific benefits with the conservation of biological resources in accordance with the Declaration of Helsinki. The collection of the plants/plant materials used in our study complied with local and national guidelines. The yellow sweet potatoes used in this study are of the Sari variety, sourced from Malang, East Java, Indonesia, the second-largest sweet potato-growing region in Indonesia. It is located between 112° 06' – 112° 07' East Longitude (EL) and 7° 06' – 8° 02' South Latitude (SL).

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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