scientific reports

OPEN

Dietary patterns derived by Gaussian graphical models and metabolic profiles among overweight and obese individuals

Reyhaneh Mokhtari Hemami[1], Mohammad Asghari-Jafarabadi[2,3,4]✉, Mahdieh Abbasalizad Farhangi[5]✉ & Maedeh Alipour[6]

Background: The increasing prevalence of metabolic syndrome (MetS) and its associated risk factors highlights the critical need to understand dietary patterns that influence health outcomes, particularly among overweight and obese individuals. Identifying dietary networks provides valuable insights into the complex interactions between food groups within typical dietary patterns. This study aimed to derive dietary networks using Gaussian graphical models (GGM) and evaluate their associations with the risk of MetS components in a sample of the Iranian population. **Methods:** This cross-sectional study involved 647 participants who were overweight or obese. The study included assessments of body composition and anthropometric measurements. Dietary fatty acid consumption was evaluated using a validated Food Frequency Questionnaire (FFQ) containing 168 items. Additionally, biochemical parameters, including serum total cholesterol (TC), triglyceride (TG), high-density lipoprotein cholesterol (HDL-C), fasting serum glucose (FSG), and insulin levels, were measured using enzymatic methods. GGM was utilized to explore the networks of participants' dietary intake, and the association between these networks and risk factors related to MetS was assessed using logistic regression. **Results:** GGM analysis identified six major networks of dietary intake, where 28 food items were allocated into six dietary networks of vegetable, grain, fruit, snack, fish/dairy, and fat/oil dietary networks, with raw vegetables, grain, fresh fruit, snack, margarine, and red meat were central to the networks respectively. In the vegetable network, TC was significantly lower in the higher tertiles of this network, and HDL was higher in the third tertile compared with the first tertile in sex, age, and fully adjusted models. In the grain network, lower SBP, DBP, TG, LDL, and higher HDL were shown in the higher tertile ($P < 0.05$). **Conclusion:** This study showed that vegetables and grains are associated with decreased risk of MetS components, including reduced blood pressure and cholesterol. Therefore, these results emphasize that dietary networks can be valuable for analyzing nutritional habits and consumption trends.

Keywords Gaussian graphical models, GGMs, Dietary patterns, Dietary networks, Metabolic syndrome

Metabolic syndrome (MetS) is a collection of related metabolic abnormalities that increases an individual's risk of type 2 diabetes (T2D) and cardiovascular disease (CVD)[1]. Consequently, it is linked to increased morbidity and mortality. MetS is characterized by a combination of risk factors, such as glucose intolerance (including type 2 diabetes mellitus (T2DM), impaired glucose tolerance, or impaired fasting plasma glucose), increased blood pressure (BP), dyslipidemia, insulin resistance (IR), and abdominal obesity[2–4]. Global public health is greatly concerned about this syndrome and the associated chronic illnesses[5]. According to estimates, the prevalence of this syndrome is 3.3% in the general population, 11.9% in children who are obese, and 29.2% in the obese population[6]. The estimated frequency of this illness is between 10% and 30% in Asia, according to data on its

[1]Tabriz Health Services Management Research Center, Tabriz University of Medical Sciences, Tabriz, Iran. [2]Cabrini Research, Cabrini Health, Malvern, VIC 3144, Australia. [3]School of Public Health and Preventive Medicine, Faculty of Medicine, Nursing and Health Sciences, Monash University, Melbourne, VIC 3004, Australia. [4]Department of Psychiatry, School of Clinical Sciences, Monash University, Clayton, VIC 3168, Australia. [5]Department of Community Nutrition, Faculty of Nutrition, Tabriz University of Medical Sciences, Tabriz, Iran. [6]Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran. ✉email: Jafarabadi@monash.edu; Abbasalizad_m@yahoo.com; abbasalizadm@tbzmed.ac.ir

increasing global prevalence[7]. Iran has a greater prevalence of this syndrome than many other countries in the world, around 36.9%[8]. Numerous studies have demonstrated that diet plays a crucial role in the development of MetS. Over the past few decades, various studies have explored the relationship between MetS and the consumption of specific food groups, individual foods, and nutrients[9]. Nutrients and food are also consumed in a variety of combinations. As a result, dietary pattern analysis has emerged as a comprehensive and alternative technique to illustrate the intricate relationship between dietary consumption and chronic disease risk[10]. Numerous studies have explored the connection between dietary patterns and the risk of MetS globally[11,12]. Dietary patterns derived from data reduction techniques such as principal component analysis (PCA) or cluster analysis are commonly used in diet-disease investigations[13–16]. In dietary patterns, individual food groups may be associated with more than one pattern, and the effects of other food groups influence the pairwise correlation between groups. Gaussian Graphical models (GGM) have been introduced as a powerful method for dietary pattern analysis in recent years, revealing conditional independencies between food groups[17]. This analysis has emerged as a comprehensive alternative or supplementary method for understanding the relationship between diet and disease[18–20]. This method for determining diet-disease correlations has been the subject of a few research. According to our literature review, we found nine studies investigating the association between dietary networks and chronic disease risk. These studies identified dietary networks in different populations, showing that higher adherence to healthy dietary networks was associated with a reduced risk of type 2 diabetes[18], central obesity[19], and gastric cancer[21]. Additionally, adherence to networks rich in vegetables, seafood, and fruits demonstrated protective effects against gastric cancer[21]. In contrast, adherence to a dairy and bread network was associated with a lower cancer risk[20]. Conversely, higher adherence to saturated fat networks was linked to an increased likelihood of MetS[22], abdominal obesity[19], and a higher risk of adverse metabolic outcomes in specific populations[23]. Notably, some studies also highlighted differences in dietary patterns between disease-specific groups, such as broader networks in women with breast cancer[24], and revealed demographic factors, such as age and sex, as key contributors to chronic diseases in dietary network analyses[25]. However, none of these studies specifically examined the individual components of MetS or explored the relationship between dietary networks and metabolic parameters, such as lipid profiles, blood glucose levels, or blood pressure. In 2016, Iqbal et al. discovered dietary consumption networks in the adult German population. Red and processed meat, chicken, cooked vegetables, sauces, potatoes, cabbage, mushrooms, legumes, soup, whole grains, and refined bread are among the main networks they have discovered in men and women. However, for women, it also includes fried potatoes[17]. The relationship between the identified networks and the risk of chronic diseases was examined by Iqbal et al. in 2018. Researchers discovered a link between a woman's risk of type 2 diabetes (T2DM) and their level of adherence to Western-type patterns. It is important to note that following a high-fat dairy diet lowers the risk of type 2 diabetes in both men and women[18]. In 2018, Schwedhelm used GGMs to construct meal-specific and habitual dietary networks in the EPIC-Potsdam study. Based on 24-hour recalls from 815 adults, meal networks revealed distinct central foods like bread for breakfast and potatoes for lunch, with stronger partial correlations at the meal level. Overlap with the habitual network varied, being highest for dinner (64.3%) and lowest for snacks (33.3%). The study emphasized that meal-level analyses provide unique insights not fully captured by habitual dietary data, requiring careful interpretation and further validation[23]. In 2020, Gunathilake applied GGMs to investigate dietary networks and their association with gastric cancer (GC) risk in a Korean population. They identified one main network and four subnetworks, including a vegetable and seafood network and a fruit network. Higher adherence to the vegetable and seafood network was associated with a reduced risk of GC, particularly in males. Similarly, the fruit network showed an inverse association with GC risk, emphasizing the protective effects of these dietary patterns against GC development[21]. In 2021, Jayedi et al. identified three dietary networks, with 30 foods grouped into six communities. The identified networks were healthy, unhealthy, and saturated fats, with cooked vegetables, processed meat, and butter central to each. They also reported that greater adherence to the saturated fats network is associated with a higher likelihood of abdominal obesity[19]. In 2022, Jahanmiri et al. expanded on these findings, showing that greater adherence to the saturated fats network was associated with higher odds of (MetS) in the Iranian population[22]. Similarly, in 2023, Hoang T et al. investigated dietary networks in a Korean cohort and their relationship with cancer incidence. Using GGM, they identified dietary communities, including a community composed of dairy products and bread, associated with a reduced risk of cancer. Another network, consisting of poultry, seafood, bread, cakes, sweets, and meat by-products, was also associated with a lower cancer risk in a matched population[20]. Furthermore, in a breast cancer study, Fereidani et al. applied GGMs to analyze food intake networks in women with and without breast cancer. They identified differences between the two groups, revealing that women with breast cancer had a broader dietary network consisting of vegetables, fruits, nuts, processed meat, soft drinks, and fried potatoes, among others. This study highlighted the potential of GGMs to uncover disease-specific dietary patterns[24]. Finally, in a large population study, Hong et al. explored the interrelationships among dietary intake, demographic factors, and comorbidities using GGMs. Their findings emphasized that dietary intake did not play a central role in the network of comorbidities, whereas age and sex were key factors associated with chronic diseases like hypertension, diabetes, and high cholesterol. This study demonstrated the utility of GGMs in integrating dietary and demographic data to examine health outcomes[25].

Although these studies highlight the possible association of dietary networks with MetS, there is no study to evaluate dietary networks in obese populations and to comprehensively investigate its association with anthropometric, metabolic risk factors and individual components of MetS—Moreover, Iran's diversity of cultures and lifestyles results in various dietary patterns and habits. Previous research on dietary networks and MetS has been limited to specific populations and dietary patterns. Therefore, this study aims to expand on these findings by exploring dietary networks and their central food groups among obese individuals and identifying their association with MetS components and glycemic markers.

Materials and methods

This cross-sectional study included 647 overweight and obese participants in Tabriz and Tehran, Iran. The study protocol was approved and registered by the ethics committee of Tabriz University of Medical Sciences (registration code: IR.TBZMED.REC. 1402.071).

(a) Inclusion-exclusion criteria

Two recent projects were previously conducted in the Tabriz and Tehran cities of Iran[26,27]. Individuals were selected from outpatient clinics through public declaration and the dissemination of posters. The inclusion criteria for this study involved individuals aged between 20 and 50 years with a BMI of 25 kg/m^2 or higher. Specifically, overweight individuals were classified as having a BMI between 25 and 29.9 kg/m^2, and obese individuals as having a BMI of 30 kg/m^2 or higher. Exclusion criteria were specific conditions such as pregnancy, breastfeeding, menopause, recent bariatric surgery, a history of cardiovascular disease (CVD), cancer, hepatic or renal disease, diabetes mellitus, and the use of medications affecting weight. Participants on a weight-loss regimen or taking supplements for at least three months before participating were excluded from the study.

(b) Demographics and anthropometric evaluations

Sociodemographic information, encompassing age, gender, smoking status, educational level, marital status, employment, past medical history, and family size, was collected through a questionnaire administered to participants. Participants' education level and occupational status were categorized using ordered categorical variables, with corresponding scores assigned. For females, education levels ranged from illiterate (0) to higher education[5], while occupational status included housewife[1], worker[2], student[3], freelancer[4], and more[5]. For males, occupational status categories were without a job[1], rancher, farmer, and worker[2], extras[3], employee[4], and independently employed[5]. Family size was scored based on the number of members, and individuals were assigned scores of 1, 2, or 3 for family sizes of 3, 4–5, or 6, respectively. Ownership of a house was scored as one if not owned and two if owned. Body composition was assessed using bioelectrical impedance analysis (BIA) with Tanita BC-418 MA from Tokyo, Japan. Height and weight were measured using a wall-mounted stadiometer and a Seca scale (Seca Co., Hamburg, Germany) to the nearest 0.5 cm and 0.1 kg. Hip circumference (HC) was measured at the broadest part of the buttocks over the greater trochanters, and waist circumference (WC) was measured at the midpoint between the lowest costal border and the iliac crest to the nearest 0.1 cm. Waist-to-hip ratio (WHR) and body mass index (BMI) were calculated. Blood pressure was measured twice in the same arm using a standard, calibrated mercury sphygmomanometer (Riester, Diplomat 1002, Jungingen, Germany) after a rest period of at least 15 min, and the mean of the two measurements was used for analysis. The US National Cholesterol Education Program Adult Treatment Panel III (NCEP-ATP III) criteria defined MetS. Physical activity levels were assessed using the short form of the International Physical Activity Questionnaire (IPAQ)[28].

(c) Dietary assessment and its reliability and validity

Dietary data for the Iranian population were collected using a validated semi-quantitative Food Frequency Questionnaire (FFQ) consisting of 168 questions[29]. Participants maintained diaries recording the frequency and quantity of each food item consumed daily, weekly, monthly, and yearly. The recorded food quantities were converted to grams per day utilizing standard common portion sizes, cooking yield factors, and edible portions of foods specified in the Iranian household measures manual[30]. Daily dietary intakes were analyzed using the NUTRITIONIST IV software (N Squared Computing, California, USA). The reliability and validity of the FFQ used in this study had been previously assessed[29]. Reasonable relative validity was achieved based on the estimated validity coefficients, with men and women showing nearly identical correlation coefficient values for various nutrients. The specified food groups included whole grains, refined grains, potatoes, dairy products, vegetables, fruits, legumes, meats, nuts and seeds, solid fat, liquid oil, tea and coffee, salty snacks, simple sugars, honey and jam, soft drinks, and desserts and snacks. To assess dietary salt consumption, the study considered the frequency with which individuals added salt or salty sauce to food during preparation or cooking, before or during eating, and the frequency of consuming processed foods with high salt content[29].

(d) Biochemical evaluation

Fasting venous blood samples, totaling 10 milliliters, were collected from all participants for biochemical analysis. The levels of total serum cholesterol (TC), triglyceride (TG), high-density lipoprotein cholesterol (HDL-C), and fasting blood glucose (FBG) were determined using a commercial kit (Pars Azmoon, Tehran, Iran). Centrifugation was used to separate the plasma and serum samples at 4,500 rpm for 10 min at 4 degrees Celsius. Before the analysis, aliquots were frozen at 70 degrees Celsius. The Friedewald equation was also used to determine the fraction of low-density lipoprotein cholesterol (LDL-C)[31]. Insulin levels in the blood were assessed using enzyme-linked immunosorbent assay (ELISA) kits sourced from Bioassay Technology Laboratory, Shanghai Korean Biotech, Shanghai City, China. The Quantitative Insulin Sensitivity Check Index (QUICKI) and the Homeostasis Model Assessment of Insulin Resistance (HOMA-IR) were computed by dividing fasting insulin (IU/ml) by 22.5 times fasting glucose (mmol/l) and applying the formula 1/ [log insulin (U/mL) + log glucose (mmol/L) during fasting], respectively.

Statistical analysis

The data was analyzed using SPSS software (IBM SPSS version 26.0) with a significance level set at 0.05. Categorical variables were presented as frequency (percentage), while continuous variables were described as mean [standard deviation (SD)]. Analysis of variance (ANOVA) was employed to assess the association between networks and MetS. To account for the impact of confounding variables, including age, sex, BMI, and total energy intake, covariance (ANCOVA) analysis was used to examine the relationship between networks and

MetS. After constructing the networks, we computed the scores for each network using a principal component-based approach, which involved a linear combination of the item values within each network. Subsequently, we calculated the tertiles of the resulting scores and categorized them into three groups, each containing roughly equal numbers of observations. The sample size was calculated with $\alpha = 0.05$ and $\beta = 0.2$. Therefore, the power was 80%. According to the power of 80%, categorizing the networks into tertiles was the best choice to avoid false positives due to multiple comparisons and false negatives due to inadequate power[32,33]. Multinomial logistic regression was applied to calculate odds ratios (ORs) and corresponding 95% confidence intervals (CIs) for the presence of risk of MetS components across the network tertiles in two multivariable-adjusted models. The risk was assessed in three models: Model I (crude), Model II (adjusted for age and sex), and Model III (adjusted for age, BMI, sex, socioeconomic status (SES), and energy intake).

(a) Network analysis procedure

GGM was utilized to explore the networks of participants' dietary intake. GGMs are graphical models representing the structure of conditional independence in a dataset, where the pairwise correlation between two variables is controlled for all other variables[28]. GGMs can infer a direct relationship between variables without prior information using a given data set by assuming a multivariate normal distribution for the underlying data. A novel and promising approach is to use GGMs to examine conditional independence structures among food consumption variables[29]. The current study categorized participants' food intake into 28 groups (Table 1). R (version 3.4.3) was used to analyze the GGM[30], utilizing "glasso", "huge", and "mgm" packages[31–33]. Two exploratory mixed graphical models (MGM) networks were estimated from participants with complete data ($n = 637$)[34]. Partial correlations, which range from – 1 to 1 (Sup. Table 1), indicate the residual relationship between variables after accounting for all other variables. In a network plot, nodes represent foods or food groups, and edges depict their partial correlations. These edges can be either positive (colored blue) or negative (colored orange). The width of the edges reflects the intensity of the correlations between food groups. Various characteristics of the networks were analyzed, and clusters of strong connections between foods were identified using the spinglass algorithm[35,36]. food group's centrality was evaluated using several metrics (Fig. 1): strength, betweenness, and closeness[37]. Strength centrality measures the sum of a connection of foods' absolute connection weights and reflects how strongly a food or food group is connected to others. Betweenness centrality captures the number of times a food appears in the shortest paths between other foods, highlighting its bridging role. Closeness centrality represents the inverse of the total distance from food to all others, indicating its accessibility within

Food groups
1. Row vegetable
2. Garlic
3. Cooked vegetable
4. Legumes
5. Potato
6. Sweets
7. Cabbage
8. Nuts
9. Grain
10. Organ meat
11. Mushroom
12. Dried fruit
13. Fresh fruit
14. Fruit juices
15. Salty
16. Vegetable oil
17. Snacks
18. Egg
19. Tea
20. Processed meat
21. Fish
22. Coffee
23. Low-fat dairy
24. High-fat dairy
25. Margarin
26. Butter
27. Animal oil
28. Red meat

Table 1. List of food groups included in the analysis of GGM.

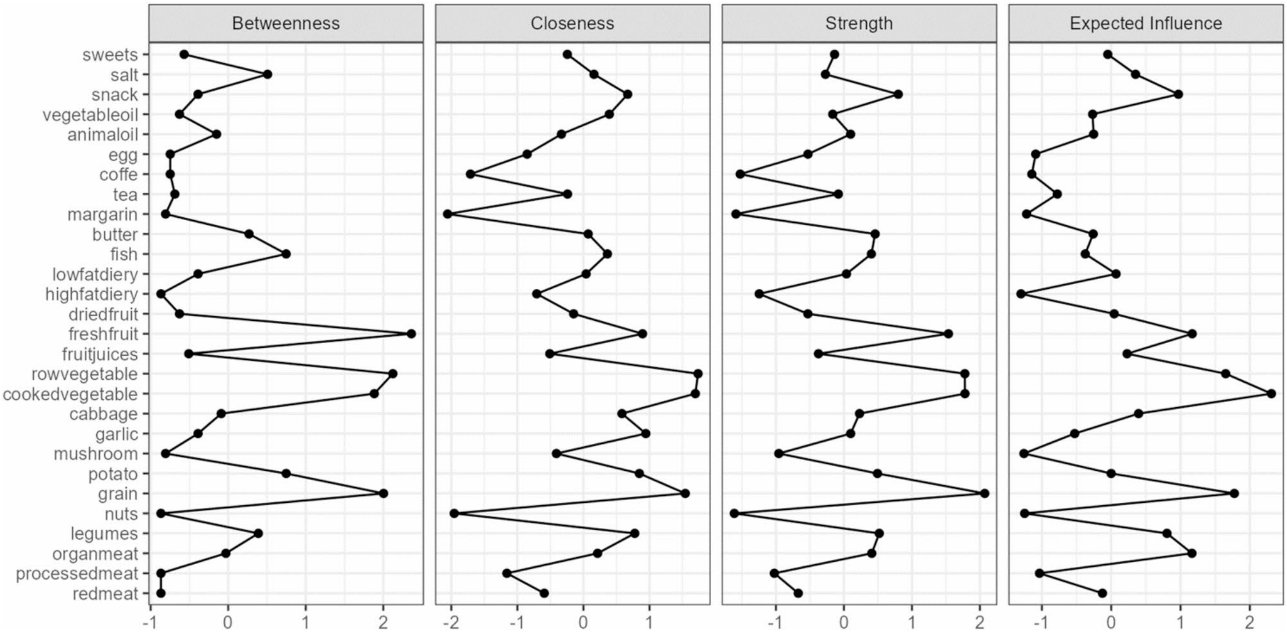

Fig. 1. The centrality of each variable in the network is indicated by the strength (i.e., the z-score of the sum of the absolute connection weights of a node, with higher values indicating stronger connectivity of a node), betweenness (the number of times a node appears in the shortest paths between other nodes), and closeness (the inverse of the sum of the distances between a node and all other nodes).

the network. Strength is highlighted in the main text because this index has demonstrated the highest stability among centrality measures[38]. In network analysis, centrality measures are used to quantify the importance or prominence of connections of foods within a network. Strength centrality is one measure that focuses on the weighted connections of foods[34] (Tables 2 and 3).

Results

(a) Demographics and anthropometric evaluations

Sociodemographic information, encompassing age, gender, smoking status, educational level, marital status, employment, past medical history, and family size, was collected through a questionnaire administered to participants. Participants' education level and occupational status were categorized using ordered categorical variables, with corresponding scores assigned. For females, education levels ranged from illiterate (0) to higher education[5], while occupational status included housewife[1], worker[2], student[3], freelancer[4], and more[5]. For males, occupational status categories were without a job[1], rancher, farmer, and worker[2], extras[3], employee[4], and independently employed[5]. Family size was scored based on the number of members, and individuals were assigned scores of 1, 2, or 3 for family sizes of 3, 4–5, or 6, respectively. Ownership of a house was scored as one if not owned and two if owned. Body composition was assessed using bioelectrical impedance analysis (BIA) with Tanita BC-418 MA from Tokyo, Japan. Height and weight were measured using a wall-mounted stadiometer and a Seca scale (Seca Co., et al.) to the nearest 0.5 cm and 0.1 kg. Hip circumference (HC) was measured at the broadest part of the buttocks over the greater trochanters, and waist circumference (WC) was measured at the midpoint between the lowest costal border and the iliac crest to the nearest 0.1 cm. Waist-to-hip ratio (WHR) and body mass index (BMI) were calculated. Blood pressure was measured twice in the same arm using a standard, calibrated mercury sphygmomanometer (Riester, Diplomat 1002, Jungingen, Germany) after a rest period of at least 15 min, and the mean of the two measurements was used for analysis. The US National Cholesterol Education Program Adult Treatment Panel III (NCEP-ATP III) criteria defined MetS. Physical activity levels were assessed using the short form of the International Physical Activity Questionnaire (IPAQ)[28].

(b) Network results

GGM analysis identified six major networks of dietary intake (Fig. 2), where 28 food groups were grouped into six networks. The identified networks were vegetable, grain, fruit, snack, fish/ dairy, and fat/oil networks, wherein raw vegetables, grain, fresh fruit, snack, margarine, and red meat were, respectively, central to the networks (Fig. 3). The centrality of these particular food groups indicates their crucial role in the dietary networks that have been identified. The vegetable network includes foods primarily associated with vegetables, with raw vegetables serving as the central food group. The strongest correlations within this network were between raw vegetables and garlic (partial correlation = 0.28), cooked vegetables and cabbage (0.26), and raw and cooked vegetables (0.20). An inverse relationship was observed between raw vegetables and processed meat (partial correlation = -0.08). The grain network, with grains at its center, exhibited significant positive correlations between grains and garlic (partial correlation = 0.27) and grains and organ meat (0.19). A negative correlation was identified between

Variables	Network 1 (Vegetable network)				Network 2 (Grain network)						Network 3 (Fruit network)				
	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*
Age (year)	42.19 (9.39)	41.91 (8.30)	37.82 (9.21)	**<0.001**		39.93 (8.78)	40.52 (9.27)	41.48 (9.47)	0.44		40.68 (8.89)	40.91 (9.25)	40.35 (9.46)	0.90	
Education (≤ 12 y)	51 (91.1)	57 (90.5)	65 (95.6)	0.94***		78 (89.7)	68 (97.1)	27 (90.0)	**0.01*****		51 (96.2)	64 (92.8)	58 (89.3)	0.17***	
Marital status (% Single)	13 (11.3)	7 (6.3)	25 (22.1)	**0.01*****		11 (9.6)	18 (15.9)	16 (14.2)	0.53***		16 (14.0)	16 (14.3)	13 (11.4)	0.52***	
Gender (%Male)	57 (49.6)	67 (59.8)	72 (63.7)	0.08***		53 (46.5)	65 (57.5)	78 (69.0)	**<0.001*****		67 (58.8)	68 (60.7)	61 (53.5)	**0.01*****	
Weight (kg)	90.83 (13.02)	92.93 (14.50)	93.42 (14.91)	0.13	0.35	89.99 (14.95)	92.36 (12.44)	94.81 (14.71)	**<0.001**	0.79	91.21 (13.59)	92.33 (14.22)	93.63 (14.71)	0.21	0.26
Height (cm)	163.81 (14.79)	166.46 (11.83)	166.72 (10.10)	0.03	0.86	166.02 (10.84)	165.75 (14.93)	165.22 (11.18)	0.79	0.48	164.68 (14.94)	164.48 (11.73)	167.82 (9.90)	**<0.001**	0.34
BMI (kg/m^2)	33.73 (4.66)	33.46 (4.35)	33.26 (6.47)	0.65	0.70	32.72 (5.40)	33.67 (4.47)	34.05 (5.70)	0.02	0.82	33.24 (6.10)	33.81 (4.62)	33.40 (4.89)	0.526	0.66
WC (cm)	105.51 (9.11)	106.40 (9.68)	107.72 (10.46)	0.06	0.45	105.65 (9.41)	105.68 (9.77)	108.30 (9.99)	**<0.001**	0.43	106.30 (9.58)	106.85 (9.55)	106.48 (10.27)	0.84	0.16
HC (cm)	116.70 (12.38)	115.67 (11.87)	115.37 (10.23)	0.48	0.08	115.53 (11.79)	114.89 (11.31)	117.25 (11.47)	0.10	0.18	115.16 (11.30)	117.25 (11.83)	115.31 (11.41)	0.13	0.08
WHR	0.91 (0.09)	0.92 (0.09)	0.93 (0.06)	0.02	0.06	0.92 (0.08)	0.92 (0.08)	0.92 (0.09)	0.57	0.34	0.92 (0.08)	0.91 (0.08)	0.93 (0.09)	0.32	0.35
FM (kg)	36.14 (9.20)	34.41 (10.22)	35.07 (9.92)	0.26	0.47	36.91 (10.90)	34.36 (9.44)	35.16 (9.36)	0.10	0.57	35.35 (9.31)	35.36 (9.62)	35.03 (10.47)	0.94	0.52
FFM (kg)	56.82 (12.35)	60.12 (12.55)	58.92 (14.72)	0.06	**0.01**	56.96 (12.01)	59.00 (11.58)	58.96 (15.14)	0.38	0.81	56.46 (13.62)	58.02 (12.47)	61.39 (13.32)	<0.001	0.10
BMR (kcal)	7464.56 (1404.81)	8019.27 (1415.26)	7639.60 (1750.45)	0.03	**<0.001**	7558.84 (1379.10)	7630.32 (1468.43)	7882.75 (1755.54)	0.26	0.81	7559.46 (1423.16)	7570.12 (1667.91)	8039.16 (1606.39)	0.03	0.21

Table 2. General characteristics and anthropometric measurements of study participants across different tertiles of dietary networks. BMI, Body mass index; BMR, Basal Metabolic Rate; FM, Fat Mass; FFM, Fat Free Mass; LC-CFA, long chain combined fatty acids; PUFA, polyunsaturated fatty acid; SES, socioeconomic status, SFA, saturated fatty acid; WC, Waist Circumference; WHR, waist-to-hip ratio. All data are mean (± SD) except marital status and gender, which are presented as the number and percent of single and males respectively in each group. * P values derived from One-Way ANOVA. ** P values derived from ANCOVA after adjustment for confounders (age, gender, BMI, physical activity, and energy intake). *** P values derived from chi-squared test.

grains and mushrooms (partial correlation = -0.13). In the fruit network, fresh fruit was central, showing key positive correlations with dried fruit (partial correlation = 0.22) and fruit juice (0.16), emphasizing its strong connections with other fruit-based food groups. The snack network centered on snacks showed the strongest correlation among all networks between snacks and tea (partial correlation = 0.80). Additionally, snacks were positively associated with vegetable oil (0.17), highlighting common pairings within this network. For the fish/ dairy network, margarine served as the central food group. Key relationships included positive correlations between fish and organ meat (partial correlation = 0.15) and low-fat dairy and legumes (0.12). A slight inverse relationship was observed between high-fat and low-fat dairy (partial correlation = -0.08). Lastly, the fat/oil network featured red meat as the central food group. Positive correlations were observed between red meat and butter (partial correlation = 0.16) and red meat and fish (0.12), indicating their significant roles in this network.

(c) Comparison of biochemical variables

Sup. Tables 2 and 3 compare biochemical variables in crude and energy, age, gender, and BMI-adjusted models. Tables 4 and 5 and supplementary Tables 4–7 examined the odds of biochemical variables in the second and third tertile versus the first in 6 networks. In the vegetable network (Table 4), TC was lower in the second tertile than the first, and the difference was significant in all three models ($P \le 05$). HDL was higher in the third tertile compared with the first tertile in sex, age, and fully adjusted models (OR = 1.024; CI = 1.002–1.048; $P = 0.03$, respectively). In the grain network (Table 5), individuals at the first and second tertiles of this network were more likely to have lower SBP in all three models ($P < 0.05$). Also, lower DBP was observed in the third tertile versus the first tertile of this network in all three models ($P \le 05$). TG was lower in the third tertile than the first. In all three models ($P \le 05$). In the third tertile of this network, HDL was higher in all three models ($P = 0.01$ in the model I and II models for all variables). Also, LDL was lower in the third tertile than the first in all three models ($P \le 0.05$). The multinomial logistic regression models revealed no significant associations for the biochemical variables in the snacks, fruit, fish/ dairy, and fat/oil networks (Sup. Tables 4–7).

(d) Correlation between dietary networks and food groups

Sup. Tables 8 and 9 compare dietary macronutrients and some micronutrients across different tertiles of dietary networks. As expected, there was an increase in almost all of the food ingredients in different tertiles of the three networks.

Discussion

As far as we know, this research was the first to examine the relationship between dietary networks identified by the GGM and the risk of MetS components among overweight and obese individuals in Iran. In this cross-sectional study, six networks were detected, i.e., vegetable, grain, fruit, snack, fish/dairy, and fat/oil. However, this discussion primarily focused on the vegetable and grain networks. This focus was chosen because these two networks demonstrated significant associations with metabolic components, whereas the other four networks showed no notable relationship. Based on our findings, participants in the higher tertile of the vegetable network had higher BMR and FFM. Also, these patients had lower TC. Also, Individuals in the upper tertile of the grain network had lower SBP, DBP, TG, LDL, and higher HDL. The findings from this study are also consistent with the eating habits of Iranians. The eating habits of Iranians, as revealed by the dietary networks derived from Gaussian Graphical Models (GGM), provide a realistic and interconnected image of their dietary intake. Unlike isolated dietary patterns, these networks emphasize the interrelationships between food groups, offering a deeper understanding of how various foods are consumed together in typical Iranian diets. Six major networks were identified: vegetable, grain, fruit, snack, fish/dairy, and fat/oil. The vegetable network is centered on raw vegetables, which play a crucial role in Iranian diets. Strong positive correlations were observed between raw vegetables and garlic, cooked vegetables and cabbage, and raw and cooked vegetables. An inverse relationship was noted between raw vegetables and processed meat, reflecting a dietary habit of pairing vegetables with healthier choices while avoiding processed meats. Grains were central in the grain network, showcasing significant positive relationships with garlic and organ meat, commonly used in traditional Iranian dishes. Conversely, grains showed a negative correlation with mushrooms, indicating a less common pairing in the Iranian dietary context. Fresh fruit served as the centerpiece of the fruit network, with strong connections to dried fruit and fruit juice. This reflects the preference for natural and minimally processed fruit-based foods, a staple in Iranian eating habits. Snacks, particularly paired with tea, demonstrated the strongest correlation among all networks, highlighting a quintessential Iranian habit of consuming snacks like sweets, nuts, or bread with tea, a culturally significant and widely practiced tradition. Additionally, snacks were positively associated with vegetable oil, suggesting the frequent use of oil-based snacks in Iranian diets. The fish/dairy network centered on margarine, with key correlations between fish and organ meat, as well as low-fat dairy and legumes. Interestingly, there was a slight inverse relationship between high-fat and low-fat dairy, pointing to distinct dietary preferences in this network. Red meat was the central food group in the fat/oil network, showing strong correlations with butter and fish. These findings resonate with common Iranian dishes like (chelo kabab), a traditional meal where red meat and butter are integral. This network reflects the widespread consumption of red meat and butter in Iranian cuisine, underscoring their cultural significance. The snack network, in particular, provides an excellent snapshot of Iranian eating habits, where tea is a ubiquitous companion to snacks. Similarly, the fat/oil network highlights the popularity of rich and hearty dishes featuring red meat and butter, a hallmark of traditional meals. These networks collectively illustrate the dietary patterns and the cultural and social dimensions of eating in Iran. We observed that individuals in the higher tertile of the vegetable network had higher FFM and BMR. FFM has a direct and positive relationship with BMR. This means that as FFM increases, BMR also tends to increase. Muscle tissue, a significant component of FFM, is metabolically active and requires more energy to maintain than fat tissue[35,36]. Several studies have supported the hypothesis. In a cross-sectional study, Michael Yu et al. reported

Variables	Network 4 (Snacks network)					Network 5 (Fish/dairy network)					Network 6 (Fat /oil network)				
	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*	1st tertile)*n* = 213)	2nd tertile (*n* = 212)	3rd tertile (*n* = 220)	**P*	***P*
Age (year)	39.77 (9.24)	40.19 (9.86)	40.34 (9.60)	0.81		39.10 (9.17)	38.37 (7.714)	38.00 (8.26)	0.60		38.67 (8.88)	38.30 (7.85)	38.80 (8.45)	0.90	
Education (≤ 12 y)	39 (18.3)	48 (22.6)	40 (18.2)	0.42***		18 (16.1)	28 (24.3)	21 (18.6)	0.33***		17 (15.6)	17 (15.5)	29 (26.4)	0.11***	
Marital status (% Single)	84 (39.4)	104 (49.1)	124 (48.4)	**< 0.001*****		52 (46.4)	56 (48.7)	55 (48.7)	0.92***		47 (43.1)	60 (54.5)	50 (45.5)	0.20***	
Gender (%Male)	39.77 (9.24)	40.19 (9.86)	40.34 (9.60)	0.81		39.10 (9.17)	38.37 (7.714)	38.00 (8.26)	0.60		38.67 (8.88)	38.30 (7.85)	38.80 (8.45)	0.90	
Weight (kg)	163.59 (9.72)	165.46 (16.47)	167.93 (9.53)	**< 0.001**	0.07	165.59 (11.66)	165.25 (15.22)	166.16 (9.89)	0.74	0.40	165.87 (9.68)	165.79 (15.25)	165.34 (11.81)	0.89	0.62
Height (cm)	32.82 (6.16)	33.38 (4.26)	34.25 (5.04)	0.01	**0.03**	33.71 (5.12)	32.99 (5.11)	33.75 (5.48)	0.25	0.71	33.90 (4.98)	33.52 (4.77)	33.03 (5.89)	0.23	0.11
BMI (kg/m^2)	107.25 (10.85)	106.64 (8.87)	105.75 (9.54)	0.28	0.15	106.53 (9.41)	105.85 (9.07)	107.25 (10.80)	0.34	0.63	107.07 (10.03)	106.34 (9.99)	106.22 (9.36)	0.62	0.43
WC (cm)	116.83 (12.95)	116.55 (11.02)	114.35 (10.36)	0.06	0.41	117.09 (12.76)	115.55 (10.29)	115.14 (11.40)	0.21	0.91	116.58 (10.62)	115.76 (11.81)	115.44 (12.16)	0.60	0.21
HC (cm)	0.92 (0.09)	0.92 (0.08)	0.92 (0.08)	0.61	0.46	0.91 (0.10)	0.92 (0.08)	0.93 (0.06)	0.20	0.53	0.92 (0.06)	0.92 (0.08)	0.92 (0.10)	0.83	0.55
WHR	35.80 (10.57)	34.65 (9.03)	35.22 (9.54)	0.55	0.38	36.61 (9.96)	34.24 (9.48)	34.84 (9.75)	0.71	0.74	36.13 (10.17)	34.63 (9.56)	35.08 (9.61)	0.37	0.22
FM (kg)	58.41 (12.10)	58.28 (12.36)	58.99 (15.51)	0.88	0.90	57.27 (12.69)	58.40 (13.27)	60.06 (13.75)	0.16	0.94	60.77 (12.94)	58.16 (12.49)	56.92 (14.04)	**0.03**	0.08
FFM (kg)	7464.09 (1792.15)	7856.57 (1429.52)	7888.33 (1389.81)	0.06	0.46	7800.02 (1410.30)	7852.48 (1445.14)	7566.16 (1742.28)	0.30	0.50	7933.32 (1486.40)	7672.17 (1485.31)	7505.93 (1725.86)	0.10	0.10
BMR (kcal)	40.28 (9.41)	40.15 (9.84)	39.28 (9.05)	0.50	0.70_	40.28 (10.00)	40.26 (9.18)	39.18 (9.10)	0.39	0.45 _	40.2 (9.17)	39.56 (8.85)	39.93 (10.25)	0.76	0.34 _

Table 3. General characteristics and anthropometric measurements of study participants across different tertiles of dietary networks. BMI, Body mass index; BMR, Basal Metabolic Rate; FM, Fat Mass; FFM, Fat-Free Mass; LC-CFA, long chain combined fatty acids; PUFA, polyunsaturated fatty acid; SES, socioeconomic status, SFA, saturated fatty acid; WC, Waist Circumference; WHR, waist-to-hip ratio. All data are mean (± SD) except marital status and gender, presented as the number and percent of single and males in each group. * P values derived from One-Way ANOVA. ** P values derived from ANCOVA after adjustment for confounders (age, gender, BMI, physical activity, and energy intake). *** P values derived from chi-squared test.

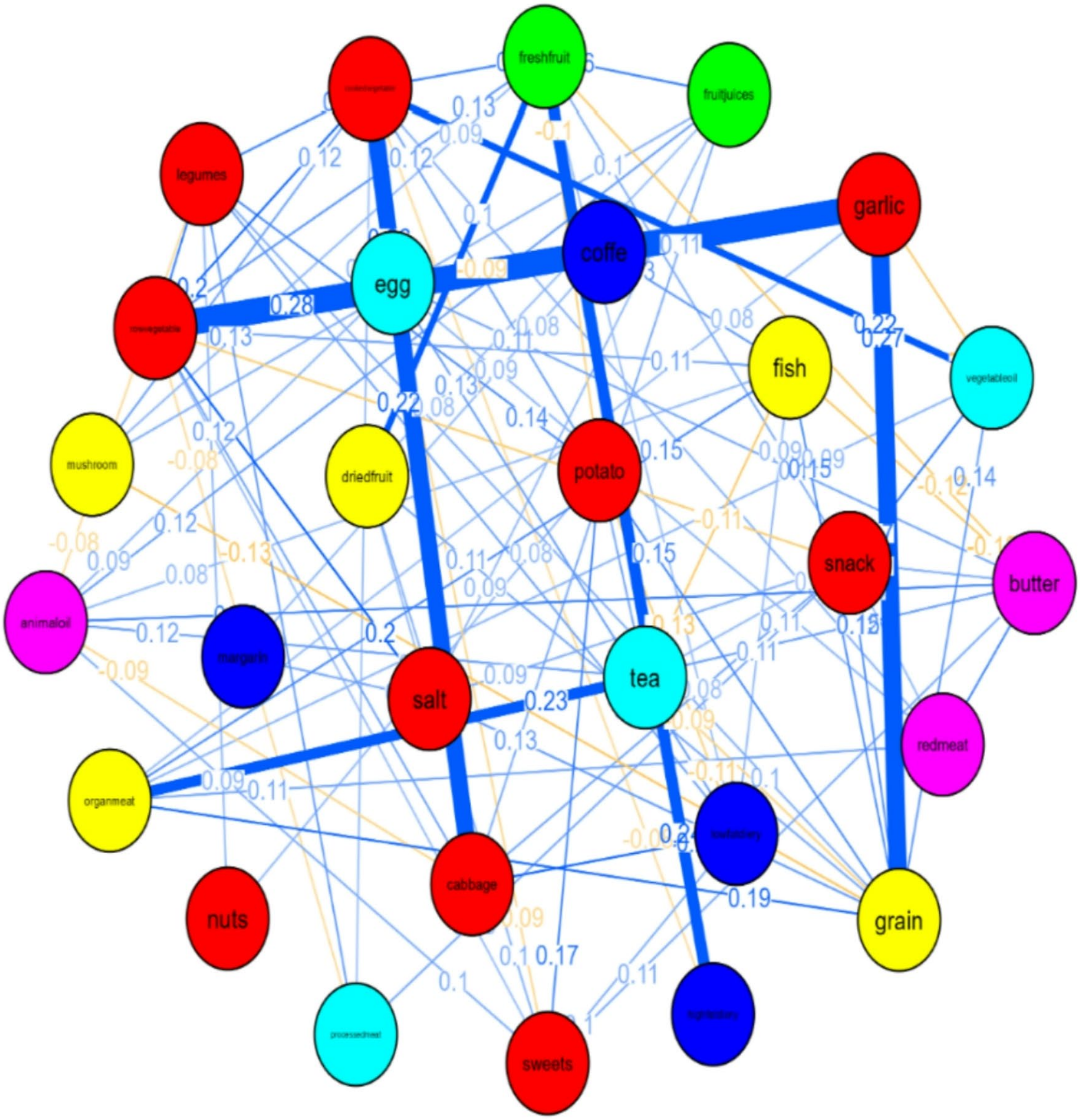

Fig. 2. Dietary networks identified through Gaussian graphical model in Iranian adults (n = 647).

that Consuming vegetables consistently showed a reverse association with anthropometric measurements, fat mass, obesity, and abdominal obesity[1]. Also, a Cross-Sectional Study by Moore et al. found a positive association between vegetable intake and FFM among adults. Higher vegetable consumption is associated with greater FFM, suggesting that vegetables may promote muscle mass[37]. Despite the strong evidence, some studies have presented conflicting results: Wang et al. conducted a meta-analysis of observational studies examining the association between vegetable consumption and muscle strength or mass. They found Contradictory results, with some studies showing a positive association while others showed no significant correlation between vegetable intake and FFM[38]. Therefore, additional research is required to explore this relationship. The possible mechanisms are as follows: Vegetables are rich in bioactive compounds such as polyphenols, flavonoids, and carotenoids, which possess potent anti-inflammatory properties[39]. Chronic inflammation is a critical factor in muscle catabolism and loss of FFM. These compounds can inhibit the activity of pro-inflammatory cytokines (e.g., TNF-α, IL-6) and enzymes (e.g., COX-2), thereby reducing inflammation and muscle degradation. Polyphenols are abundant in many vegetables and have been shown to attenuate inflammation by modulating signaling pathways such as NF-κB and MAPK, which are involved in the inflammatory response[40].

Additionally, participants in the higher tertile of the vegetable network had lower TC. Numerous studies have highlighted the cholesterol-lowering benefits of vegetable consumption. The Dietary Approaches to Stop Hypertension (DASH) study found that a diet rich in fruits, vegetables, and low-fat dairy products significantly reduced total cholesterol and LDL cholesterol levels[41].

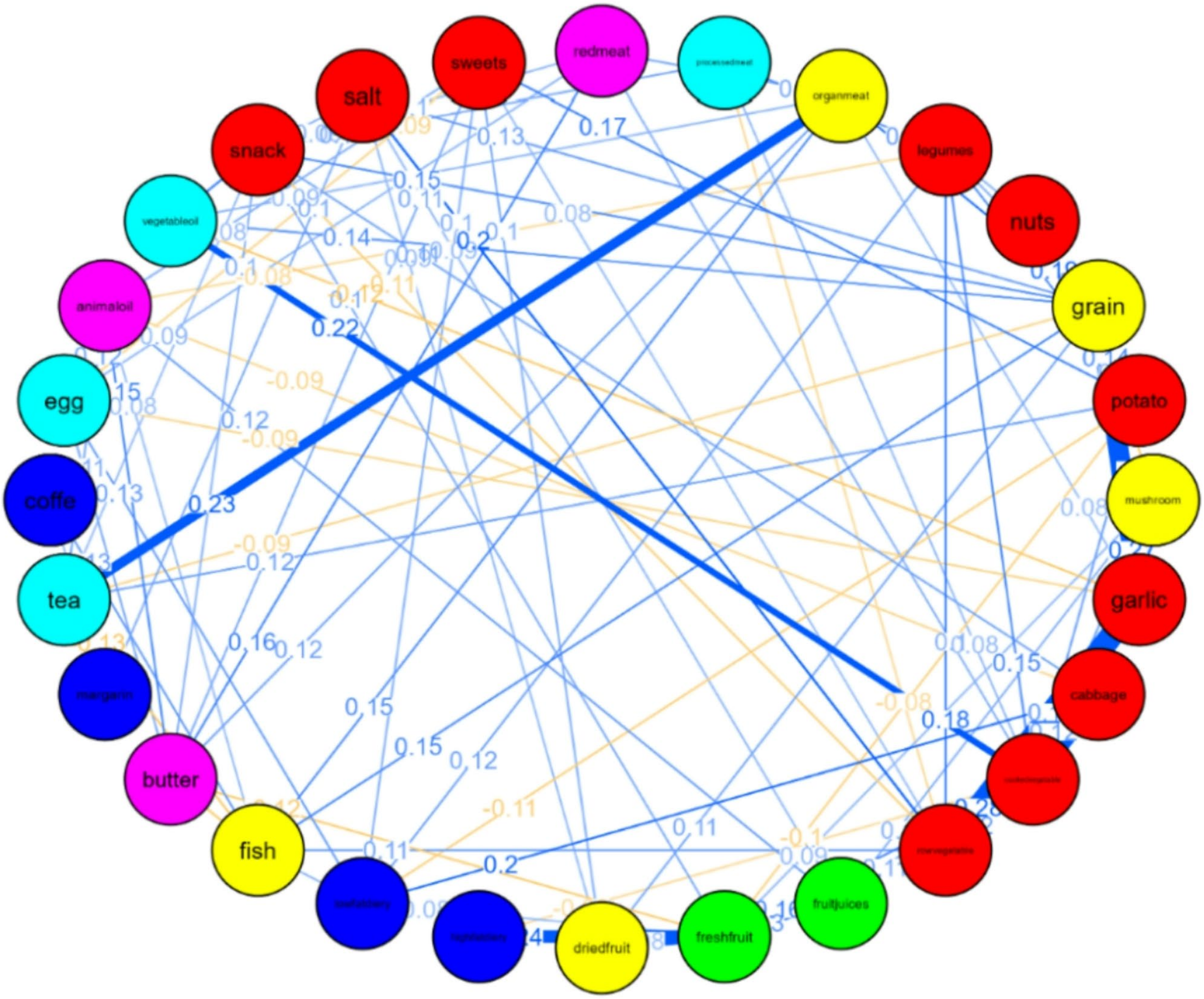

Fig. 3. Detailed characteristics of six dietary networks identified by Gaussian graphical model. Nodes represent food groups. Edges represent conditional dependencies between food groups revealed by partial correlation coefficients. These edges can be either positive (colored blue) or negative (colored orange). The width of the edges reflects the intensity of the correlations between food groups.

Vegetables may also lower cholesterol through their soluble fiber content, which binds to bile acids and reduces cholesterol absorption[42]. This study found that participants in the upper tertile of the grain network had lower SBP and DBP. The recent meta-analysis reviewed randomized controlled trials by Wu et al. examining the effects of whole grain consumption on cardiovascular risk factors, including blood pressure. The study found that a higher intake of whole grains was associated with significant reductions in SBP and DBP[43]. A study by Choi et al. investigated the relationship between whole grain consumption and various cardiovascular risk factors, including blood pressure, in a Korean population. The results showed that higher whole grain intake was associated with lower blood pressure and improved cardiovascular health[44]. However, a meta-analysis of randomized controlled trials by Marshall et al. found no significant effect of whole grain consumption on blood pressure, suggesting that the impact of whole grains on SBP and DBP may be limited or negligible[45]. Also, an umbrella review of meta-analyses of randomized controlled trials by Lingmeng Fu et al. found a weak association between total dietary fiber intake and lower blood pressure. However, the results were not statistically significant for all fiber sources, including grains[46]. While numerous studies support the beneficial effects of whole grain consumption on blood pressure, these more recent studies present mixed or non-supportive findings. The discrepancies might be due to differences in study design, population demographics, dietary assessment methods, and genetic factors.

The findings of this study indicated that individuals in the higher tertile of the grain network had lower TG, LDL, and higher HDL, suggesting significant benefits of whole grain consumption on lipid profiles. Several recent studies support these benefits. A study by Giacco et al. demonstrated that individuals consuming a high amount of whole grains had significantly lower TG and LDL levels and higher HDL levels, attributing these benefits to the high fiber and nutrient content in whole grains[47]. Similarly, a meta-analysis of 25 randomized controlled trials found consistent evidence that whole grain consumption significantly reduces TG and LDL

Variable		**Tertiles of Network 1 (Vegetable network)**				
		1st tertile)*n* = 213)	**2nd tertile (*n* = 212)**		**3rd tertile (*n* = 220)**	
			OR(CI)	**P-value**	**OR(CI)**	**P-value**
SBP (mmHg)	Model I	**1 REF**	1.012 (0.997–1.027)	0.11	1.009 (0.995–1.024)	0.20
	Model II		1.014 (0.998–1.031)	0.08	1.009 (0.994–1.025)	0.23
	Model III		1.032 (0.997–1.067)	0.07	1.037 (1.000-1.075)	0.05
DBP (mmHg)	Model I	**1 REF**	1.015 (0.995–1.036)	0.14	1.000 (0.981–1.020)	0.96
	Model II		1.019 (0.997–1.042)	0.08	1.000 (0.980–1.021)	0.99
	Model III		1.024 (0.983–1.067)	0.24	1.014 (0.969–1.061)	0.54
FBS (mg/dl)	Model I	**1 REF**	0.995 (0.986–1.004)	0.26	1.002 (0.995–1.010)	0.56
	Model II		0.994 (0.985–1.003)	0.21	1.001 (0.994–1.009)	0.73
	Model III		0.989 (0.976–1.003)	0.11	0.987 (0.972–1.002)	0.08
TC (mg/dl)	Model I	**1 REF**	0.991 (0.983–0.992)	**0.04**	0.990 (0.982–0.998)	**0.01**
	Model II		0.992 (0.983–0.991)	**0.03**	0.991(0.983–0.990)	**0.04**
	Model III		0.984 (0.970–0.997)	**0.01**	0.987 (0.973–1.001)	0.07
TG (mg/dl)	Model I	**1 REF**	1.002 (1.000-1.004)	0.08	1.001 (0.999–1.003)	0.44
	Model II		1.002 (0.999–1.004)	0.16	1.000 (0.998–1.003)	0.72
	Model III		1.002 (0.996–1.008)	0.47	1.003 (0.996–1.010)	0.394
HDL (mg/dl)	Model I	**1 REF**	1.005 (0.988–1.023)	0.56	1.017 (1.000-1.035)	0.05
	Model II		1.008 (0.991–1.026)	0.35	1.021 (1.003–1.039)	**0.01**
	Model III		1.011 (0.992–1.030)	0.25	1.024 (1.002–1.048)	**0.03**
LDL (mg/dl)	Model I	**1 REF**	1.005 (1.000-1.010)	0.06	1.007 (1.002–1.012)	**0.01**
	Model II		1.005 (1.000-1.010)	0.06	1.007 (1.002–1.012)	**0.01**
	Model III		1.005 (0.996–1.013)	0.29	1.000 (0.990–1.010)	0.98
Insulin (mIU/l)	Model I	**1 REF**	1.005 (0.991–1.019)	0.46	1.008 (0.995–1.021)	0.25
	Model II		1.005 (0.991–1.019)	0.49	1.007 (0.994–1.021)	0.30
	Model III		0.988 (0.964–1.012)	0.31	1.003 (0.981–1.025)	0.80
HOMA-IR	Model I	**1 REF**	1.044 (0.938–1.162)	0.42	1.001 (0.896–1.118)	0.98
	Model II		1.038 (0.929–1.159)	0.51	0.996 (0.888–1.118)	0.95
	Model III		1.024 (0.899–1.167)	0.72	1.047 (0.938–1.168)	0.41
QUICKI	Model I	**1 REF**	0.997 (0.981–1.013)	0.80	0.988 (0.970–1.006)	0.34
	Model II		0.996 (0.979–1.013)	0.57	0.989 (0.969–1.007)	0.25
	Model III		0.998 (0.919–1.003)	0.44	0.988(0.956-1.018)	0.22

Table 4. Biochemical variables of study participants across different tertiles of network 1 (Vegetable network). SBP, Systolic Blood Pressure; DBP, Diastolic Blood Pressure; TC, Total Cholesterol; TG, Triglyceride; HDL-C, High Density Lipoprotein Cholesterol; LDL-C, Low Density Lipoprotein Cholesterol; HOMA-IR, Homeostatic Model Assessment for Insulin Resistance; QUICKI, Quantitative Insulin sensitivity Check Index; OR, odds ratio; CI, confidence interval, SFA, saturated fatty acid; PUFA, polyunsaturated fatty acid; LC-CFA, long chain combined fatty acids. The multivariate multinomial logistic regression was used to estimate ORs and confidence interval (CI). Model I: crude, Model II: adjusted for age and sex, Model III: adjusted for age, BMI, sex, SES, physical activity, and energy intake.

levels while increasing HDL levels[48]. However, some studies present conflicting results. A systematic review and meta-analysis of randomized controlled studies by Hollænder et al. found that whole-grain diets lower LDL cholesterol and TC, but not HDL cholesterol or triglycerides, compared with non-whole-grain control diets[49]. Several mechanisms can explain the beneficial effects of whole grains on lipid profiles and reduce the risk of hypertension. Whole grains are high in dietary fiber, particularly soluble fiber, which can bind to bile acids in the intestine. This leads to increased excretion of bile acids and decreased cholesterol synthesis in the liver, lowering LDL cholesterol levels[50]. They also contain antioxidants such as ferulic acid and phytic acid, which help reduce oxidative stress and inflammation, lowering LDL and TG levels and improving HDL levels[51]. Beta-glucan, a soluble fiber found in oats and barley, has significantly lowered LDL cholesterol by increasing the intestinal contents' viscosity and reducing cholesterol absorption[52]. Moreover, the complex carbohydrates in whole grains slow the digestion and absorption of sugars, leading to better glycemic control, which can help reduce triglycerides and improve overall lipid profiles[53].

Certain limitations should be considered when interpreting our findings. Firstly, the cross-sectional design of our study prevents us from establishing a causal relationship between fatty acid patterns and MetS. To better understand the direction of this association, further research with a prospective design is needed. Secondly, although we used a validated FFQ to assess dietary and fatty acid intakes, the closed-ended format of the

Variable		**Tertiles of Grain network**				
		1st tertile)*n* = 213)	**2nd tertile (*n* = 212)**		**3rd tertile (*n* = 220)**	
			OR (CI)	**P-value**	**OR (CI)**	**P-value**
SBP (mmHg)	Model I	**1** **REF**	0.968 (0.954–0.983)	< **0.001**	0.959 (0.944–0.974)	< **0.001**
	Model II		0.976 (0.961–0.992)	< **0.001**	0.962 (0.946–0.978)	< **0.001**
	Model III		0.974 (0.959–0.991)	< **0.001**	0.960 (0.943–0.977)	< **0.001**
DBP (mmHg)	Model I	**1** **REF**	0.971 (0.953–0.990)	< **0.001**	0.950 (0.931–0.970)	< **0.001**
	Model II		0.984 (0.964–1.005)	0.14	0.958 (0.937–0.979)	< **0.001**
	Model III		0.983 (0.963–1.004)	0.11	0.959 (0.938–0.981)	< **0.001**
FBS (mg/dl)	Model I	**1** **REF**	1.004 (0.996–1.012)	0.31	1.000 (0.992–1.009)	0.97
	Model II		1.006 (0.997–1.014)	0.19	1.001 (0.992–1.010)	0.81
	Model III		1.005 (0.996–1.013)	0.26	0.999 (0.989–1.008)	0.76
TC (mg/dl)	Model I	**1** **REF**	0.999 (0.995–1.004)	0.71	0.995 (0.990-1.000)	**0.03**
	Model II		0.999 (0.995–1.004)	0.78	0.995 (0.990-1.000)	**0.04**
	Model III		1.000 (0.996–1.005)	0.89	0.995 (0.990-1.000)	0.04
TG (mg/dl)	Model I	**1** **REF**	0.997 (0.983–0.995)	**0.01**	0.993 (0.990–0.996)	< **0.001**
	Model II		0.997 (0.978–0.996)	**0.03**	0.993 (0.990–0.996)	< **0.001**
	Model III		1.000 (0.995–1.006)	0.86	0.993(0.987–0.993)	**0.03**
HDL (mg/dl)	Model I	**1** **REF**	1.015 (0.997–1.033)	0.09	1.023 (1.005–1.041)	**0.01**
	Model II		1.015 (0.997–1.033)	0.11	1.023 (1.005–1.042)	**0.01**
	Model III		1.019 (0.984–1.055)	0.29	1.028 (1.005–1.064)	**0.01**
LDL (mg/dl)	Model I	**1** **REF**	0.996 (0.992–1.001)	0.16	0.993 (0.988–0.998)	< **0.001**
	Model II		0.997 (0.991–1.002)	0.18	0.993 (0.988–0.998)	< **0.001**
	Model III		1.001 (0.992–1.009)	0.87	0.989 (0.980-0.0.994)	**0.03**
Insulin (mIU/l)	Model I	**1** **REF**	1.003 (0.991–1.016)	0.61	1.002 (0.990–1.015)	0.70
	Model II		1.005 (0.991–1.019)	0.48	1.003 (0.990–1.017)	0.63
	Model III		1.000 (0.983–1.018)	0.95	0.999 (0.983–1.016)	0.93
HOMA-IR	Model I	**1** **REF**	0.982 (0.883–1.092)	0.74	1.010 (0.916–1.113)	0.84
	Model II		0.979 (0.876–1.094)	0.71	1.002 (0.903–1.112)	0.97
	Model III		0.978 (0.878–1.088)	0.67	1.001 (0.902–1.111)	0.98
QUICKI	Model I	**1** **REF**	1.004 (1.000-1.007)	0.10	1.003 (0.999–1.005)	0.85
	Model II		1.002 (0.999–1.005)	0.19	1.002 (0.999–1.006)	0.98
	Model III		1.001 (0.993–1.010)	0.94	1.008 (1.008–1.016)	0.55

Table 5. Biochemical variables of study participants across different tertiles of Network 2 (Grain network). SBP, Systolic Blood Pressure; DBP, Diastolic Blood Pressure; TC, Total Cholesterol; TG, Triglyceride; HDL-C, High Density Lipoprotein Cholesterol; HOMA-IR, Homeostatic Model Assessment for Insulin Resistance; LDL-C, Low Density Lipoprotein Cholesterol; QUICKI, Quantitative Insulin sensitivity Check Index; OR, odds ratio; CI, confidence interval. The multivariate multinomial logistic regression was used to estimate ORs and confidence interval (CI). Model I: crude, Model II: adjusted for age and sex, Model III: adjusted for age, BMI, sex, SES, physical activity, and energy intake.

questionnaires may have increased the likelihood of misclassification. Nonetheless, any misclassifications would have a neutral effect on the odds ratios. Lastly, despite our efforts to control for various confounding factors, we cannot entirely rule out the potential influence of residual confounders.

Conclusion

In conclusion, the dietary networks derived from GGM effectively represent dietary patterns and can identify central food groups. This study showed that the vegetable and grain networks are associated with decreased risk of MetS components. This study highlights the significance of dietary networks in understanding the interrelationships between food groups, which offers a more holistic view of dietary habits, particularly in Iranian diets. These findings underline the complexity of food choices and the cultural and social dimensions of eating in Iran. Therefore, additional prospective studies are needed to confirm our findings, particularly with a prospective design.

Data availability

The datasets generated and analyzed during the current study are not publicly available due to privacy and ethical considerations but can be available from the corresponding author upon reasonable request.

Received: 15 July 2024; Accepted: 27 February 2025

References

1. Mondal, S. M. S. *Metabolic Syndrome 2023.*
2. Mohamed, S. M. et al. Metabolic syndrome: risk factors, diagnosis, pathogenesis, and management with natural approaches. *Food Chem. Adv.* **3**, 100335 (2023).
3. Meloni, A. et al. Gender differences and cardiometabolic risk: The importance of the risk factors. *Int. J. Mol. Sci.* **24**(2) (2023).
4. Cornier, M. A. et al. The metabolic syndrome. *Endocr. Rev.* **29** (7), 777–822 (2008).
5. Ford, E. S. Prevalence of the metabolic syndrome defined by the international diabetes federation among adults in the U.S. *Diabetes Care.* **28** (11), 2745–2749 (2005).
6. Grabia, M., Markiewicz-Żukowska, R. & Socha, K. Prevalence of metabolic syndrome in children and adolescents with type 1 diabetes mellitus and possibilities of prevention and treatment: A systematic review. *Nutrients* **13**(6). (2021).
7. Liyanage, T. et al. Prevalence of chronic kidney disease in Asia: A systematic review and analysis. *BMJ Glob. Health* **7**(1) (2022).
8. Ferns, G. A. A. & Ghayour-Mobarhan, M. Metabolic syndrome in Iran: A review. *Translational Metabolic Syndrome Res.* **1**, 10–22 (2018).
9. Wei, L. et al. The effect of dietary pattern on metabolic syndrome in a suburban population in Shanghai, China. *Nutrients* **15**(9). (2023).
10. Zheng, P. F. et al. Dietary patterns and chronic obstructive pulmonary disease: A Meta-analysis. *Copd* **13** (4), 515–522 (2016).
11. Wei, Z. Y., Liu, J. J., Zhan, X. M., Feng, H. M. & Zhang, Y. Y. Dietary patterns and the risk of metabolic syndrome in Chinese adults: a population-based cross-sectional study. *Public. Health Nutr.* **21** (13), 2409–2416 (2018).
12. Chupanit, P., Muktabhant, B. & Schelp, F. P. Dietary patterns and their association with the components of metabolic syndrome: A cross-sectional study of adults from Northeast Thailand. *F1000Res* **7**, 905 (2018).
13. Varraso, R. et al. Assessment of dietary patterns in nutritional epidemiology: principal component analysis compared with confirmatory factor analysis. *Am. J. Clin. Nutr.* **96** (5), 1079–1092 (2012).
14. Ocké, M. C. Evaluation of methodologies for assessing the overall diet: dietary quality scores and dietary pattern analysis. *Proc. Nutr. Soc.* **72** (2), 191–199 (2013).
15. Lesani, A., Djafarian, K., Akbarzade, Z., Janbozorgi, N. & Shab-Bidar, S. Meal-specific dietary patterns and their contribution to habitual dietary patterns in the Iranian population. *Br. J. Nutr.* 1–10 (2022).
16. Shahinfar, H. et al. Interaction between major dietary patterns and cardiorespiratory fitness on metabolic syndrome in Iranian adults: a cross-sectional study. *Nutr. J.* **20** (1), 36 (2021).
17. Iqbal, K. et al. Gaussian graphical models identify networks of dietary intake in a German adult population. *J. Nutr.* **146** (3), 646–652 (2016).
18. Iqbal, K. et al. Gaussian graphical models identified food intake networks and risk of type 2 diabetes, CVD, and cancer in the EPIC-Potsdam study. *Eur. J. Nutr.* **58** (4), 1673–1686 (2019).
19. Jayedi, A., Janbozorgi, N., Djafarian, K., Yekaninejad, M. S. & Shab-Bidar, S. Dietary networks identified by Gaussian graphical model and general and abdominal obesity in adults. *Nutr. J.* **20** (1), 86 (2021).
20. Hoang, T., Lee, J. & Kim, J. Differences in dietary patterns identified by the Gaussian graphical model in Korean adults with and without a Self-Reported Cancer diagnosis. *J. Acad. Nutr. Diet.* **121** (8), 1484–96e3 (2021).
21. Gunathilake, M., Lee, J., Choi, I. J., Kim, Y. I. & Kim, J. Identification of dietary pattern networks associated with gastric Cancer using Gaussian graphical models: A case-control study. *Cancers (Basel)* **12**(4). (2020).
22. Jahanmiri, R., Djafarian, K., Janbozorgi, N., Dehghani-Firouzabadi, F. & Shab-Bidar, S. Saturated fats network identified using Gaussian graphical models is associated with metabolic syndrome in a sample of Iranian adults. *Diabetol. Metab. Syndr.* **14** (1), 123 (2022).
23. Schwedhelm, C., Knüppel, S., Schwingshackl, L., Boeing, H. & Iqbal, K. Meal and habitual dietary networks identified through semiparametric Gaussian copula graphical models in a German adult population. *PLoS One.* **13** (8), e0202936 (2018).
24. Fereidani, S. S. et al. Gaussian graphical models identified food intake networks among Iranian women with and without breast cancer: A Case-Control study. *Nutr. Cancer.* **73** (10), 1890–1897 (2021).
25. Hoang, T., Lee, J. & Kim, J. Network analysis of demographics, dietary intake, and comorbidity interactions. *Nutrients* **13**(10). (2021).
26. Abbasalizad Farhangi, M., Vajdi, M., Nikniaz, L. & Nikniaz, Z. The interaction between dietary inflammatory index and 6 P21 rs2010963 gene variants in metabolic syndrome. Eating and weight Disorders-Studies on anorexia. *Bulimia Obes.* **25**, 1049–1060 (2020).
27. Khodarahmi, M., Asghari-Jafarabadi, M. & Abbasalizad Farhangi, M. A structural equation modeling approach for the association of a healthy eating index with metabolic syndrome and cardio-metabolic risk factors among obese individuals. *PloS One.* **14** (7), e0219193 (2019).
28. Craig, C. L. et al. International physical activity questionnaire: 12-country reliability and validity. *Med. Sci. Sports Exerc.* **35** (8), 1381–1395 (2003).
29. Mirmiran, P., Esfahani, F. H., Mehrabi, Y., Hedayati, M. & Azizi, F. Reliability and relative validity of an FFQ for nutrients in the Tehran lipid and glucose study. *Public. Health Nutr.* **13** (5), 654–662 (2010).
30. Alipour Nosrani, E. et al. The association between meal-based diet quality index-international (DQI-I) with obesity in adults. *BMC Nutr.* **8** (1), 156 (2022).
31. Rifai, N. *Tietz Textbook of Clinical Chemistry and Molecular Diagnostics-E-Book* (Elsevier Health Sciences, 2017).
32. Burke, J. F., Sussman, J. B., Kent, D. M. & Hayward, R. A. Three simple rules to ensure reasonably credible subgroup analyses. *BMJ* **351**. (2015).
33. Dijkman, B., Kooistra, B. & Bhandari, M. How to work with a subgroup analysis. *Can. J. Surg.* **52** (6), 515 (2009).
34. Peng, S. et al. Influence analysis in social networks: A survey. *J. Netw. Comput. Appl.* **106**, 17–32 (2018).
35. Johnson, K. O. et al. An increase in fat-free mass is associated with higher appetite and energy intake in older adults: A randomised control trial. *Nutrients* **13**(1). (2021).
36. James, W. P. T. Energy requirements. In *Encyclopedia of Human Nutrition* (Caballero B, ed.). 3rd Ed. 186 – 192. (Academic Press, 2013).
37. Moore, D. R. et al. Ingested protein dose response of muscle and albumin protein synthesis after resistance exercise in young men. *Am. J. Clin. Nutr.* **89** (1), 161–168 (2009).
38. Wang, X. et al. Fruit and vegetable consumption and mortality from all causes, cardiovascular disease, and cancer: systematic review and dose-response meta-analysis of prospective cohort studies. *Bmj* **349**, g4490 (2014).
39. Samtiya, M., Aluko, R. E., Dhewa, T. & Moreno-Rojas, J. M. Potential health benefits of plant food-derived bioactive components: An overview. *Foods* **10**(4). (2021).
40. Ganesan, K. & Xu, B. Polyphenol-Rich dry common beans (Phaseolus vulgaris L.) and their health benefits. *Int. J. Mol. Sci.* **18** (11), 2331 (2017).
41. Appel, L. J. et al. A clinical trial of the effects of dietary patterns on blood pressure. DASH collaborative research group. *N Engl. J. Med.* **336** (16), 1117–1124 (1997).

42. Ras, R. T., Geleijnse, J. M. & Trautwein, E. A. LDL-cholesterol-lowering effect of plant sterols and Stanols across different dose ranges: a meta-analysis of randomised controlled studies. *Br. J. Nutr.* **112** (2), 214–219 (2014).
43. Wu, H. et al. Association between dietary whole grain intake and risk of mortality: two large prospective studies in US men and women. *JAMA Intern. Med.* **175** (3), 373–384 (2015).
44. Choi, C. K., Kweon, S. S., Cho, S. H., Kim, H. Y. & Shin, M. H. Association between ALDH2 polymorphism and gastric Cancer risk in a Korean population. *J. Korean Med. Sci.* **35** (17), e148 (2020).
45. Marshall, S. et al. The effect of replacing refined grains with whole grains on cardiovascular risk factors: A systematic review and Meta-Analysis of randomized controlled trials with GRADE clinical recommendation. *J. Acad. Nutr. Diet.* **120** (11), 1859–83e31 (2020).
46. Fu, L., Zhang, G., Qian, S., Zhang, Q. & Tan, M. Associations between dietary fiber intake and cardiovascular risk factors: an umbrella review of meta-analyses of randomized controlled trials. *Front. Nutr.* **9**, 972399 (2022).
47. Giacco, R., Della Pepa, G., Luongo, D. & Riccardi, G. Whole grain intake in relation to body weight: from epidemiological evidence to clinical trials. *Nutr. Metab. Cardiovasc. Dis.* **21** (12), 901–908 (2011).
48. McRae, M. P. Health benefits of dietary whole grains: an umbrella review of Meta-analyses. *J. Chiropr. Med.* **16** (1), 10–18 (2017).
49. Hollænder, P. L., Ross, A. B. & Kristensen, M. Whole-grain and blood lipid changes in apparently healthy adults: a systematic review and meta-analysis of randomized controlled studies. *Am. J. Clin. Nutr.* **102** (3), 556–572 (2015).
50. Soliman, G. A. Dietary fiber, atherosclerosis, and cardiovascular disease. *Nutrients* **11**(5). (2019).
51. Bumrungpert, A., Lilitchan, S., Tuntipopipat, S., Tirawanchai, N. & Komindr, S. Ferulic acid supplementation improves lipid profiles, oxidative stress, and inflammatory status in hyperlipidemic subjects: A randomized, double-blind, placebo-controlled clinical trial. *Nutrients* **10**(6). (2018).
52. El Khoury, D., Cuda, C., Luhovyy, B. L. & Anderson, G. H. Beta glucan: health benefits in obesity and metabolic syndrome. *J. Nutr. Metab.* **2012**, 851362 (2012).
53. Mustad, V. A., Huynh, D. T. T., López-Pedrosa, J. M., Campoy, C. & Rueda, R. The role of dietary carbohydrates in gestational diabetes. *Nutrients* **12**(2):385–402 (2020).

Acknowledgements

The authors wish to thank all the study participants for their sincere collaboration. We also thank Research Undersecretary of Tabriz University of Medical Sciences for their financial support (Grant number: 71552).

Author contributions

All authors approved the final version of the article. MAF contributed to study design, supervision, statistical analysis, and manuscript writing. RM was involved in revision and English language revision. MAJ performed the statistical analysis and was involved in hypothesis generation. He also supervised the project and was involved in revision. MA was also involved in revision and part of data collection. All authors read the final version of article and agreed to its submission.

Funding

A grant from Tabriz University of Medical Sciences financially supported the present study. (Code: IR.TBZMED.REC.1402.071 and grant number: 71552). The funders had no role in hypothesis generation, recruiting, and designing the study.

Declarations

Competing interests

The authors declare no competing interests.

Ethics approval and consent to participate

There is no conflict of interest, according to the authors. All subjects provided a written informed consent before participation in the study. We confirm that methods were performed in accordance with declaration of Helsinki's guidelines and regulations. Also, legal guardians of the illiterate participants provided a written informed consent.

Additional information

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1038/s41598-025-92361-6.

Correspondence and requests for materials should be addressed to M.A.-J. or M.A.F.