Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy

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ORIGINAL RESEARCH

Interaction between dietary patterns and *TCF7L2* polymorphisms on type 2 diabetes mellitus among Uyghur adults in Xinjiang Province, China

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Purpose: This study aimed to characterize dietary patterns in the Uyghur population and examined the relationship between dietary pattern, *TCF7L2* single-nucleotide polymorphisms (SNPs), and the risk of type 2 diabetes mellitus (T2DM).

Patients and methods: Dietary patterns were defined using factor analysis, and associations between dietary patterns were evaluated using multivariate logistic regression analyses. Genotyping of seven SNPs of *TCF7L2* (rs11196205, rs12255372, rs12573128, rs4506565, rs7895340, rs7901695, and rs7903146) was conducted, and the association between these seven SNPs and the risk of T2DM was evaluated. Interactions between SNPs, homeostasis model assessment-insulin resistance, and dietary patterns were also analyzed.

Results: A total of 828 participants were enrolled in this study, including 491 people with T2DM and 337 healthy controls. Five dietary patterns were defined, and the results indicated that the "fruit" and "vegetables" dietary patterns were associated with a significant decrease in the risk of T2DM, whereas the "meats" and "grains" dietary patterns were associated with an increased risk of T2DM. Moreover, the "dairy product" dietary pattern showed no association with the risk of T2DM. Furthermore, our results revealed that the *TCF7L2* SNP, rs12573128, is associated with an increased risk of T2DM. SNPs rs4506565 and rs7903146 significantly interacted with dietary pattern.

Conclusion: Our studies suggest that dietary pattern and genetic polymorphisms of *TCF7L2* are associated with the development of T2DM in the Uyghur population of China.

Keywords: type 2 diabetes mellitus, dietary patterns, *TCF7L2*, polymorphism, Uyghur

Introduction

Type 2 diabetes mellitus (T2DM) is a chronic metabolic disorder that is characterized by high blood sugar, insulin resistance, and a relative lack of insulin.[1] Although T2DM is not life-threatening, it can cause numerous complications and reduce the quality of life.[2,3] The morbidity rate due to T2DM is also growing every year. T2DM is the result of interactions between genetic and lifestyle factors.[4] Therefore, it is important to explore population-specific genetic factors and lifestyle risk factors in the context of T2DM.

Dietary patterns, which reflect the complexity of dietary intake, are considered an alternative method to human diet alone for investigating the association between diet and risk of disease.[5] Although there have been studies on the association between dietary pattern and the risk of T2DM in different countries,[6–10] data for the Chinese population are limited, and the majority of them were focused on eastern Chinese and Han nationalities.[6,11,12] Uyghur people live primarily in Xinjiang Province of China

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and have their own genetic background, lifestyle, and dietary habits.[13,14] They eat a lot of carbohydrates, including pasta, naan, noodles, and roasted buns. Milk and dairy products, beef, and mutton are also consumed a lot. These significant differences between the dietary patterns of the Uyghur and Han populations mean that there is a need to investigate the association between dietary pattern and the risk of T2DM in the Uyghur population.

Several studies have been conducted to assess the relationship between genetic risk factors and T2DM risk in Chinese minority ethnicities, including the Uyghur,[15,16] Hui,[17] and Dong[18] ethnic populations. *TCF7L2*, formerly known as *TCF4*, is a member of the TCF family that affects the expression of pro-glucagon and consequently blood glucose regulation.[19] In previous studies, strong associations between *TCF7L2* single-nucleotide polymorphisms (SNPs) and the risk of T2DM have been found in different ethnic populations.[20–24] However, only one study was conducted on Uyghur people, and only two *TCF7L2* SNPs (rs12255372 and rs7901695) were investigated in that study.[14]

Recent studies have begun to pay attention to the relationship between genetic factors and lifestyle factors, such as diet and physical activity, on the risk of T2DM. The current study aimed to define the dietary patterns for the Uyghur population and to examine the association between dietary patterns and risk of T2DM. We also examined the polymorphisms of *TCFL2* gene in the Uyghur population and sought to determine whether the association between genetic variants of *TCFL2* and T2DM risk is affected by the dietary pattern.

Patients and methods

Study population

This study was conducted on Uyghur national residents in Urumqi, the capital of Xinjiang Province, China from November 2016 to February 2018. Participants were selected from six Community Health Centers in Tianshan and Saybagh districts using a stratified cluster random-sampling method. Physical examination records of the community health centers were reviewed, and individuals who conformed to the following inclusion criteria were selected: 1) fasting plasma glucose (FPG) ≥7.0 mmol/L but without T2DM history; 2) no diagnosis of DM or other diseases that could affect their dietary habits; 3) no diseases related to blood glucose and insulin metabolism, such as abnormal thyroid function and severe obesity, and no other severe diseases of the gastrointestinal tract, cardiovascular, kidney, liver, or pancreas; 4) no history of taking drugs that affect blood glucose metabolism; and 5) Uyghur nationality. Participants with mental disease, who had difficulty in moving or communicating, and women who were pregnant or breast-feeding were also excluded. Selected participants were invited to our center and an oral glucose tolerance test (OGTT) was conducted to confirm the diagnosis. T2DM was defined using the diagnostic criteria of American Diabetes Association standards 2016 (FPG ≥7.0 mmol/L and OGTT ≥11.1 mmol/L).[25] For the normal control group, participants were selected from people who were assessed during the same physical examination period. This study was approved by the Ethics Committee of the Fifth Affiliated Hospital of Xinjiang Medical University. It was conducted in accordance with the Declaration of Helsinki, and all participants provided written informed consent to be included in this study.

Dietary intake investigation

In accordance with the dietary characteristics of Uyghur national residents in Urumqi, a specific semi-quantitative food frequency questionnaire (SQFFQ), comprising 84 items in 17 food groups (Table 1), was designed. The validity and reliability of the SQFFQ was evaluated via a preliminary survey conducted within the same region from September 2016 to October 2016. One hundred and fifty participants who had undergone physical examination were randomly selected, and three 24-hour dietary reports (two working days and one rest day) were compared with the results of the SQFFQ. After eliminating incomplete data, results from 137 participants were analyzed. The average Pearson correlation coefficients (PCCs) between the SQFFQ and dietary reports ranged from 0.19 to 0.83, with an average value of 0.45 for the major food groups. Results showed that the SQFFQ provided a reasonably valid measurement of dietary intakes. The interscorer reliability of the SQFFQ was evaluated after 4 weeks. Ninety-eight of the 110 participants completed the test. Pearson correlation analysis showed that the PCCs between dietary intake of all food groups from the second survey and those from the first survey ranged from 0.52 to 0.91, with an average of 0.73. This indicates that the interscorer reliability of the SQFFQ is relatively high.

Participants were invited to a separate air-conditioned room after breakfast. For nutrition assessment, ten professional investigators, who majored in medicine and nutrition and were fluent in the local language, were trained using a combination of theoretical teaching and practical operation prior to the investigation. Participants were asked to recall the frequencies (per day, per week, per month, per year) and portion sizes of all food consumed within the previous 12 months, with the help of visual measurement aids. Answers were transformed

Table 1 Food grouping used in the dietary pattern analyses

Food groups	Food items
Grains	Rice, pilaf, rice soap, porridge, pancake, fired noodles, steamed bun, steamed stuffed bun, dumplings, wonton, fired bread stick, deep-fried dough cake, maize meal, millet, oat, wheat, buckwheat, corn
Bean	Soybean, miscellaneous beans, bean sprouts, tofu, dried bean curd, soybean milk
Vegetables	Green vegetables, cowpea, green bean, sweet potato, potato, Chinese yam, green peppers, tomato, Chinese cabbage, radish, cucumber, eggplant, pumpkin, cauliflower, broccoli, carrot, radish, onion, pickled vegetables
Fruit	Apple, pears, oranges, bananas, watermelon, grapes, peach, apricots, pomegranate, cherries, cantaloupe, strawberries, etc
Dairy product	Milk, milky tea, yogurt, cheese, butter
Meats	Mutton, beef, chicken, duck meat, goose meat
Organ meats	Animal pluck
Fish and seafood	Fishes, shrimp, crab, shellfish
Eggs	Duck eggs, chicken eggs, goose eggs, quail eggs, pigeon eggs
Pastry	Bread, cookies, cake
Nuts and dried fruit	Walnut, peanuts, almonds, melon seeds, pistachio nuts, raisin, red dates, dried apricot
Salt	Salt
Oil	Vegetable oil, animal oil
Beverage	Fruits juice, sodas, tea, water, wine, beer

to an average daily intake (grams) for all subsequent analyses. One specific person was responsible for quality control of the dietary survey, including checking for errors, missed items, and unclear items, all of which were corrected in a timely manner.

Dietary pattern identification

Dietary patterns were identified using factor analysis (principal component analysis) in dimensionality reduction analysis of SPSS 21.0 as described elsewhere.[26] Briefly, factors were rotated using varimax rotation to ensure that there was no association between factors and to improve interpretability. Factors were extracted by combing eigenvalue, interpretability, and scree plot. Factor groups with factor loading $\geq|0.5|$ were considered to contribute significantly and served as a reference for labeling the dietary patterns.[27] Factor scores were categorized into quartiles (Q1–Q4), and differences between Q1 and Q4 in every dietary pattern were compared by single factor difference analysis. Multivariate logistic regression analysis was used to examine the association between dietary patterns and T2DM by adjusting for sex, age, education level (primary and lower, junior, senior, and college and higher), physical activity level (light, moderate, and heavy), smoking status (never, current, and former), body mass index (BMI), and total energy intake.

Physical activity assessment

The physical activity level of all participants was evaluated using the validated international physical activity questionnaire (Chinese version, IPAQ).[28,29] Participants were divided into vigorously active, moderately active, or sedentary groups according to their physical activity over the past 7 days.

Anthropometric and laboratory measurement

Demographic and anthropometric data were collected for all participants. Demographic data including age, gender, smoking status, alcohol consumption, marital status, education, occupation, household income, and disease history were collected via an interviewer-administered questionnaire. Anthropometric data including height (mm), weight (kg), diastolic blood pressure (DBP, mmHg), systolic blood pressure (SBP, mmHg), waist circumference (WC, cm), and hip circumstance (HC, cm) were measured in an air-conditioned room with participants wearing light clothing and no shoes. BMI was calculated as weight divided by height squared (kg/m^2). Waist–hip ratio (WHR) was calculated as WC/HC. Blood samples were obtained from all participants in the morning after 12 hours of fasting. Total cholesterol (TC, mmol/L), triglycerides (TG, mmol/L), low-density lipoprotein-cholesterol (LDL-C, mmol/L), high-density lipoprotein-cholesterol (HDL-C, mmol/L), and FPG (mmol/L) were measured using a Beckman Coulter AU5800 clinical chemistry system (Beckman, Newark, NJ, USA). Fasting insulin (FINS, pmol/L) was measured using a Roche Diagnostics Kit and a Roche Cobas e-601 analyzer (GmbH, Mannheim, Germany). Homeostasis model assessment-insulin resistance (HOMA-IR) was calculated as (FINS× FPG)/22.5.

SNP genotyping

TCF7L2 SNPs were searched for on the NCBI database (http://www.ncbi.nlm.nih.gov/SNP) and 1000 Genomes database (http://www.internationalgenome.org/) by referencing genomes obtained from Chinese Han and European populations. SNP information was imported into Haploview 4.2 software and seven SNPs (rs11196205, rs12255372, rs12573128, rs4506565, rs7895340, rs7901695, and rs7903146) were selected based on the criteria of linkage disequilibrium parameter $r^2 \geq 0.8$ and minimum allele frequency ≥0.05. DNA was extracted from whole blood using a TIANamp Genomic DNA Kit (Tiangen, Beijing, China), and *TCF7L2* genotyping was performed using improved multiplex ligation detection reaction (iMLDR, Genesky, Shanghai, China) as previously described.[30] Quality control procedures, including internal consistency and external validation, were applied to ensure accurate genotyping results. Approximately 5% of samples were randomly selected in duplicate with an internal consistency rate of 100%, and another 5% were randomly selected for Sanger sequencing. Genotyping results showed 100% reproducibility.

Statistical analysis

All statistical analyses were conducted using the SPSS 21.0 software (IBM Corporation, Armonk, NY, USA). Normal distribution of quantitative data was examined using a one-sample Shapiro–Wilk test. Data following a normal distribution were expressed as mean ± SD, and data that did not follow a normal distribution were expressed as median and quartile range. Differences between two groups were compared by independent-sample *t*-test or Mann–Whitney *U* test where appropriate. Qualitative data were expressed as frequencies (percentages) and compared using the chi-squared test or Fisher's exact test. Dietary patterns were extracted by factor analysis. OR and 95% CIs were calculated by multivariable logistic regression to assess the association between dietary pattern and risk of T2DM. Genotype frequencies between T2DM participants and control participants, as well as Hardy–Weinberg equilibrium (HWE), were assessed using a chi-squared test. Interaction analyses between SNPs and dietary factors/physical activity were carried out using Spearman correlation analysis and logistic regression models. $P<0.05$ was regarded as statistically significant.

Results

Demographic and clinical characteristics

A total of 932 participants were initially included in the study. After excluding participants with abnormal glucose tolerance, incomplete information of general conditions, physical examination, laboratory tests, and dietary data, as well as those with extreme physical activity and dietary energy identified during data processing, a final number of 828 participants were enrolled for subsequent analyses. Table 2 shows the demographic and clinical characteristics of patients with T2DM (n=337) and control participants (n=491). There was no significant difference in terms of age, gender, polyunsaturated fatty acids, marital status, monthly income, or alcohol intake ($P>0.05$), whereas BMI, WHR, SBP, DBP, TC, TG, LDL-C, FINS, HOMA-IR, energy, protein, fat, total fatty acids, saturated fatty acids (SFA), and monounsaturated fatty acids (MUFA) levels were significantly higher in patients with T2DM than in control participants ($P<0.05$). It is interesting to note that participants in the T2DM group on average had a higher level of education, a higher incidence of T2DM in the family, were less physically active, and tended to smoke less than those in the control group (all $P<0.05$).

Definition of dietary patterns in the Uyghur population

The dietary intakes of all participants were analyzed using factor analysis. Kaiser–Meyer–Olkin index (KMO =0.703>0.5) and Bartlett's test of sphericity (χ^2=1,060.491, df=92, $P<0.001$) suggested the food groups were not independent but significantly correlated with each other and that a factor analysis was applicable.[31] Five types of dietary pattern were derived from the principal component analysis, which accounted for 95.22% of the variance among food items (Table 3). The first pattern was named the "fruit" pattern and was characterized by a high intake of fruits, nuts and dried fruit, and a low intake of salt, oil, and beverages. The second pattern was termed the "meats" pattern and was characterized by a high intake of meat, animal pluck, fish, and seafood and a low intake of fruits and dairy products. The third pattern was named the "dairy product" pattern and was characterized by a high intake of dairy products and eggs, with a low intake of salt and beverages. The fourth pattern was named the "vegetables" pattern and was characterized by a high intake of vegetables, and a low intake of salt, meat, oil, and beverages. The final pattern was called the "grains" pattern and was characterized by a high intake of grains.

Association between dietary pattern and general characteristics

The general characteristics of all participants across quartile categories of dietary pattern scores are summarized in Table 4. Participants in the highest quartile of the "fruit" dietary pattern were mostly male, with lower FPG and TC, higher levels of energy, protein, fat, total fatty acids, SFA, MUFA, and polyunsaturated fatty acids (PUFA), and a lower incidence of T2DM and hypertension than those in the lowest

Table 2 Demographic and clinical characteristics of participants with and without T2DM

Variables	Participants in control group (N=491)	Participants in T2DM group (N=337)	Z/χ^2	*P*-value
Age, years	48.00 (43.00–57.00)	50.00 (42.00–57.00)	–0.060	0.952
Gender, n				
Male	215	162	1.478	0.224
Female	276	175		
BMI, kg/m^2	25.97 (22.77–29.05)	27.89 (25.07–30.79)	–6.103	<0.001
WHR	0.88 (0.83–0.93)	0.94 (0.89–0.98)	–9.966	<0.001
SBP, mmHg	120.00 (110.00–132.00)	133.00 (122.00–145.50)	–8.379	<0.001
DBP, mmHg	76.00 (70.00–82.00)	80.00 (75.00–89.00)	–6.826	<0.001
FPG, mmol/L	5.10 (4.76–5.50)	7.70 (7.20–9.28)	–24.472	<0.001
TC, mmol/L	4.28 (3.64–5.04)	4.95 (4.20–5.76)	–8.166	<0.001
TG, mmol/L	1.60 (1.25–2.28)	2.40 (1.67–3.18)	–8.830	<0.001
LDL-C, mmol/L	2.38 (1.88–2.63)	2.91 (2.22–3.55)	–9.776	<0.001
HDL-C, mmol/L	1.43 (1.19–1.88)	1.19 (0.95–1.55)	–8.057	<0.001
FINS, pmol/L	9.04 (5.79–12.59)	11.94 (7.52–18.29)	–6.548	<0.001
HOMA-IR	2.03 (1.32–2.85)	4.56 (2.74–6.83)	–15.148	<0.001
Energy, Kcal	2,389.49 (1,925.67–2,984.22)	2,581.22 (2,128.15–3,115.74)	–3.893	<0.001
Protein, g	87.80 (68.33–112.45)	93.53 (74.66–121.33)	–2.771	0.006
Fat, g	82.42 (63.35–103.68)	86.71 (69.12–113.53)	–2.956	0.003
Total fatty acids, g	75.42 (58.24–95.07)	80.04 (62.83–105.06)	–3.050	0.002
SFA, g	17.70 (13.37–22.69)	18.93 (13.98–25.83)	–2.924	0.003
MUFA, g	25.27 (19.70–31.39)	28.15 (22.31–37.12)	–4.764	<0.001
PUFA, g	31.02 (22.79–40.27)	30.97 (24.49–42.49)	–1.465	0.143
Occupation, n				
Leader	8	10	46.141	<0.001
Professional	53	27		
Businessman and service staff	179	102		
Worker	105	36		
Other	100	84		
Retired	46	78		
Education level, n				
Primary and lower	219	139	10.182	0.017
Middle school	240	157		
College and higher	31	39		
Marital status, n				
Unmarried	8	5	2.993	0.393
Married	435	292		
Widowed or divorced	48	40		
Monthly income per person, RMB				
<3,000	364	242	5.306	0.257
3,000–6,000	119	89		
>6,000	8	6		
Family history of T2DM, n				
No	426	259	13.728	<0.001
Yes	65	78		
Hypertension, n				
No	435	249	30.088	<0.001
Yes	56	88		
Smoking status, n				
Never	364	254	8.745	0.013
Current	111	59		
Former	16	24		
Alcohol intake, n				
No	438	302	0.035	0.851
Yes	53	35		
Physical activity, n				
Light	12	13	12.336	0.002
Moderate	311	246		
Vigorous	168	78		

Notes: Smoker was defined as one who smokes more than 10 cigarettes per week for more than 6 months. Former smoker was defined as one who stopped smoking for more than 6 months. Alcohol intake was defined as one who drinks at least once a week, for more than 6 months. Differences between these two groups were compared by chi-squared test, and $P<0.05$ indicated statistically significant difference.

Abbreviations: BMI, body mass index; DBP, diastolic blood pressure; FINS, fasting insulin; FPG, fasting plasma glucose; HDL-C, high-density lipoprotein-cholesterol; HOMA-IR, homeostasis model assessment-insulin resistance; LDL-C, low-density lipoprotein-cholesterol; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; SBP, systolic blood pressure; SFA, saturated fatty acids; T2DM, type 2 diabetes mellitus; TC, total cholesterol; TG, triglycerides; WHR, waist–hip ratio.

Table 3 Factor loadings and explained variations of dietary patterns from principal component analysis

Foods groups	**Dietary patterns**				
	Fruit	**Meats**	**Dairy product**	**Vegetables**	**Grains**
Grains	0.134	0.235	0.066	–0.033	**0.960**
Bean	0.186	0.037	0.155	0.122	0.063
Vegetables	0.152	0.096	0.021	**0.979**	0.095
Fruits	**0.984**	–0.059	0.046	0.156	0.037
Dairy product	0.179	–0.016	**0.983**	0.010	–0.033
Organ meats	0.254	0.285	0.105	–0.071	0.137
Meats	0.229	**0.963**	0.141	–0.016	0.000
Fish and sea food	0.045	0.184	0.165	0.021	0.022
Eggs	0.192	0.109	0.203	–0.024	0.056
Pastry	0.269	0.031	0.075	0.050	0.003
Nut and dried fruit	0.310	0.097	0.179	0.122	0.022
Salt	–0.055	0.071	–0.013	–0.136	0.064
Oil	–0.081	0.075	0.012	–0.065	0.030
Beverage	–0.030	0.154	–0.020	–0.006	0.077

Note: The bold number indicates the largest component in principal component analysis.

quartile. Individuals in the highest quartile of the "meats" dietary pattern were more likely to be male, smokers, drinkers, and have higher WHR, FPG, TG, HOMA-IR, energy, protein, fat, total fatty acids, SFA, MUFA, and PUFA, lower levels of HDL-C, and a higher incidence of T2DM than those in the lower quartile. Subjects in the highest quartile of the "dairy product" pattern tended to have a lower BMI, WHR, and TG, a low family history of T2DM, higher levels of energy, protein, fat, total fatty acids, SFA, MUFA, and PUFA, and a higher education level and higher economic income than those in the lowest quartile. Participants in the highest quartile of the "vegetables" pattern were more likely to have a lower BMI, WHR, FPG, TC, TG, LDL-C, and HOMA-IR, a lower economic income, low incidence of T2DM and hypertension, and higher levels of HDL-C, energy, protein, fat, SFA, and PUFA than those in the lower quartile. Individuals in the highest quartile of the "grains" pattern were younger, more likely to be female, smokers, drinkers, had higher WHR, SBP, DBP, FPG, LDL-C, HOMA-IR, energy, protein, fat, total fatty acids, and MUFA, a higher economic income, and higher incidence of T2DM and hypertension, but lower levels of HDL-C than those in the lower quartile.

Association between dietary pattern and T2DM risk

Multivariable logistic regression analysis was conducted to evaluate the relationship between dietary pattern and T2DM risk. As shown in Table 5, participants in the highest quartile of the "fruit" and "vegetables" dietary pattern scores had a lower incidence of T2DM than those in the lowest quartiles (OR =0.238; 95% CI: 0.144–0.395; *P*<0.001 and OR =0.187, 95% CI: 0.118–0.295; *P*<0.001, respectively), after adjustment for sex, age, education level, physical activity level, smoking status, BMI, and total energy intake. Subjects in the highest quartile of the "meats" and "grains" dietary pattern scores had a higher incidence of T2DM than those in the lowest quartiles (OR =2.389; 95% CI: 1.487–3.838; *P*<0.001 and OR =10.239; 95% CI: 5.142–20.388; *P*<0.001, respectively). The "dairy product" pattern showed no association with the risk of T2DM (OR =0.672; 95% CI: 0.423–1.066; *P*=0.091).

Association between *TCF7L2* SNPs and T2DM risk

The genotypic distribution for all seven SNPs of the *TCF7L2* gene was consistent with the predicted HWE (*P*>0.05 in both T2DM and control groups, Table S1). Table 6 shows the distribution of genotypes and alleles for the seven SNPs in the T2DM and control groups within the Uygur population. The distribution of rs12573128 genotyping (*P*=0.041), dominant model (AG + AA vs GG, *P*=0.031), and additive model (AG vs GG, *P*=0.013) showed a significant difference between the T2DM and control groups. However, the distribution of the other six SNPs showed no statistical significance between the two groups (*P*>0.05).

Interaction between *TCF7L2* SNPs and dietary pattern on T2DM risk

Next, interactions between the seven *TCF7L2* SNPs and dietary pattern on T2DM risk were further assessed. As shown in Table 7, the interaction between the additive model of rs4506565 and dietary pattern, and between the additive model of rs7903146, were statistically significant ($P_{\text{interaction}}$=0.033, $P_{\text{interaction}}$=0.031, respectively). Conversely, the interaction between the dominant model of the seven SNPs and dietary pattern was not statistically significant ($P_{\text{interaction}}$ >0.05).

Discussion

In this study, we defined five dietary patterns from the diet of the Uyghur population. Multivariable logistic regression analysis indicated that the "fruit" and "vegetables" dietary patterns were associated with a significantly decreased risk of T2DM, whereas the "meats" and "grains" dietary patterns were associated with an increased risk of T2DM. Moreover, the "dairy product" dietary pattern showed no association with the risk of T2DM. Given the limited research that has been conducted on the Uyghur population, our studies represent a unique contribution to the pathogenesis of T2DM in this nation.

Uyghur people live primarily in the Xinjiang Province located in west China, and they have their own genetic background, lifestyle, culture, language, and dietary habits.[13,14] The traditional Uyghur dietary pattern involves a high consumption of wheat-based foods (such as naan and noodles) and animal products (such as mutton and beef, and milk products such as butter and cheese), but a low intake of fruits and vegetables.[32] In accordance with these national food habits, three dairy patterns, "grains," "meats," and "dairy product," were defined in the current study. Multivariable regression analysis revealed that the "meats" and "grains" dietary patterns were associated with a high risk of T2DM, whereas the "dairy product" pattern showed no association with the risk of T2DM. The positive association between the "meats" and "grains" pattern and T2DM could be due to unhealthy constituents, such as red meat. Naan and noodles are made of flour and contain a large amount of carbohydrates, and beef and mutton are rich in saturated fatty acids and cholesterol. These foods provide sufficient materials for the synthesis of fat in the body, which could result in a high risk for T2DM.[32]

In addition to the three traditional dietary patterns, we also defined two others, namely the "vegetables" and "fruit" patterns. The "fruit" pattern is characterized by a high intake of fruits, nuts, and dried fruit and low intake of salt, oil, and beverages. This is in line with the variety of fruits in Xinjiang Province, such as grapes and Hami melon, and a characteristic high consumption of dried fruits, such as raisins, walnuts, and red dates. Multivariable regression analysis suggested the "vegetables" and "fruit" dietary patterns are associated with a low risk of T2DM. This finding is consistent with previous studies that demonstrated a positive effect of "fruit" and "vegetables" in decreasing the risk of T2DM. The "fruit" and "vegetables" dietary patterns are similar to dietary patterns in loading structure termed "vegetable, fruit, and soy-rich pattern" in a Singapore Chinese population study,[33] "prudent" in a Finnish study[34] or a US study.[35] All of these studies demonstrated an inverse association between dietary pattern and risk of T2DM. In another study in China, Shu et al identified three dietary patterns in the Zhejiang Province, and a traditional southern Chinese dietary pattern, which is characterized by a high intake of refined grains, vegetables, fruits, and pickled vegetables and has similarities to the "fruit" and "vegetables" patterns in the current study. However, in contrast to the current study, they found that this pattern was associated with the risk of T2DM. One reason for this could be that the traditional southern Chinese diet also includes a high intake of pickled vegetables, which contain a large amount of salt, known to cause hypertension and T2DM.[36–38] Regardless of these differences, fruits and vegetables are abundant in dietary fiber, which are associated with a decreased risk of T2DM.[39,40]

TCF7L2 encodes a transcription factor that plays a key role in the canonical WNT signaling pathway. Previous studies have demonstrated that this pathway is important for β-cell proliferation and insulin secretion,[41,42] and T2DM is known to be caused by impaired insulin secretion due to defective β-cell mass or function. In the current study, we assessed the association of seven *TCF7L2* SNPs with T2DM risk in the Uygur population. To our knowledge, our study included the largest number of *TCF7L2* SNPs ever investigated in this population. A previous study conducted by Yao et al demonstrated an association between two *TCF7L2* SNPs (rs12255372 and rs7901695) and the risk of T2DM in the Uygur population. However, in our study, we did not find a significant association between these two SNPs and T2DM risk. Among the seven SNPs, only the distribution of rs12573128 genotypes (P=0.041), dominant model (AG + AA vs GG, P=0.031), and additive model (AG vs GG, P=0.013) showed a significant difference between the T2DM and control groups. Our study is consistent with previous work showing that *TCF7L2* rs12573128 alone, or in combination with dietary fat intake, influenced insulin sensitivity, and glucose tolerance.[43] Our result suggests that SNP rs12573128 affects WNT signaling to impact essential functions of *TCF7L2* during insulin secretion and may also impact the maturity and proliferation of pancreatic β-cells associated with T2DM pathogenesis.

Table 4 General characteristics of study participants for lowest and highest quartiles of the major dietary pattern scores

Variables	**Fruit pattern score**		***P*-value**	**Meats pattern score**		***P*-value**	**Dairy product pattern score**
	Q1 (lowest) (n=207)	**Q4 (highest) (n=207)**		**Q1 (lowest) (n=207)**	**Q4 (highest) (n=207)**		**Q1 (lowest) (n=207)**
Age, years	51.00 (42.00–58.00)	48.00 (42.00–58.00)	0.51	49.00 (43.00–57.00)	48.00 (41.00–56.00)	0.067	51.00 (43.00–58.00)
Gender, n			0.006			<0.001	
Male	82	110		66	133		92
Female	125	97		141	74		115
BMI, kg/m^2	27.34 (24.30–30.39)	27.12 (24.32–30.45)	0.946	27.06 (24.00–31.14)	26.51 (24.24–29.37)	0.165	27.49 (24.52–31.11)
WHR	0.90 (0.86–0.95)	0.90 (0.85–0.95)	0.172	0.89 (0.84–0.94)	0.91 (0.86–0.96)	0.004	0.92 (0.87–0.96)
SBP, mmHg	128.00 (114.00–140.00)	125.00 (114.00–136.00)	0.106	126.00 (114.00–140.00)	126.00 (116.00–140.00)	0.577	127.00 (114.00–140.00)
DBP, mmHg	80.00 (70.00–87.00)	78.00 (69.00–85.00)	0.084	78.00 (70.00–84.00)	78.00 (70.00–86.00)	0.673	78.00 (70.00–88.00)
FPG, mmol/L	7.00 (5.10–7.92)	5.47 (4.97–7.17)	<0.001	5.60 (4.99–7.06)	7.00 (5.16–8.50)	<0.001	5.80 (5.01–7.45)
TC, mmol/L	4.80 (4.05–5.42)	4.34 (3.85–5.27)	0.027	4.39 (3.88–5.29)	4.65 (3.96–5.46)	0.190	4.53 (3.99–5.37)
TG, mmol/L	1.96 (1.40–2.75)	1.82 (1.34–2.49)	0.295	1.84 (1.30–2.54)	2.01 (1.41–2.97)	0.017	2.06 (1.51–2.99)
LDL-C, mmol/L	2.53 (2.13–3.23)	2.38 (2.11–2.87)	0.065	2.41 (2.05–3.15)	2.54 (2.04–3.25)	0.435	2.50 (2.05–3.20)
HDL-C, mmol/L	1.26 (1.00–1.79)	1.36 (1.11–1.80)	0.062	1.36 (1.09–1.84)	1.27 (1.01–1.66)	0.015	1.34 (1.09–1.79)
FINS, pmol/L	10.02 (6.53–15.86)	9.74 (6.09–15.11)	0.664	9.74 (6.27–14.50)	9.95 (6.45–15.96)	0.494	10.02 (6.61–15.57)
HOMA-IR	2.83 (1.79–5.19)	2.54 (1.59–4.31)	0.083	2.53 (1.49–4.20)	2.79 (1.78–5.33)	0.026	2.62 (1.66–5.07)
Energy, Kcal	2,139.22 (1,823.41–2,638.45)	2,878.49 (2,382.67–3,615.14)	<0.001	2,166.57 (1,830.08–2,743.64)	2,991.04 (2,478.85–3,666.34)	<0.001	2,203.27 (1,751.28–2,762.03)
Protein, g	79.23 (61.64–97.79)	109.29 (87.80–138.03)	<0.001	71.37 (59.68–91.13)	128.54 (108.88–158.21)	<0.001	79.79 (57.55–103.39)
Fat, g	72.73 (56.73–95.60)	97.18 (73.98–124.33)	<0.001	73.71 (56.11–93.39)	108.355 (84.78–129.74)	<0.001	70.993 (54.62–93.31)
Total fatty acids, g	66.53 (51.67–88.58)	89.47 (67.45–114.62)	<0.001	68.185 (51.251–86.388)	98.507 (78.016–119.272)	<0.001	65.212 (49.552–86.373)
SFA, g	15.62 (12.10–20.44)	21.23 (16.32–28.82)	<0.001	14.81 (12.10–19.06)	25.38 (20.54–31.28)	<0.001	13.67 (10.53–18.99)
MUFA, g	23.57 (18.50–29.84)	28.68 (22.41–37.19)	<0.001	22.64 (17.21–29.40)	33.53 (27.20–41.79)	<0.001	22.49 (17.79–29.31)
PUFA, g	26.37 (20.13–36.56)	37.03 (26.82–49.44)	<0.001	28.39 (20.21–38.08)	36.37 (27.51–47.78)	<0.001	27.54 (20.06–36.78)
Occupation, n			0.035			0.012	
Leader	6	5		6	4		2
Professional	26	15		22	24		22
Businessman and service staff	57	78		56	90		74
Worker	28	41		37	30		32
Other	53	42		55	34		45
Retired	37	26		31	25		32
Education level, n			0.127			0.251	
Primary and lower	94	96		93	82		105
Junior	57	64		62	77		61
Senior	38	23		29	34		24
College and higher	16	24		21	14		15
Marital status, n			0.351			0.055	
Unmarried	1	5		1	6		1
Married	182	176		178	181		176
Widowed	16	15		20	10		17
Divorced	8	11		8	10		13
Monthly income per person, RMB			0.118			0.088	
<1,500	81	56		74	49		69
1,500–3,000	72	87		85	94		98

	P-value	Vegetables pattern score		*P*-value	Grains pattern score		*P*-value
Q4 (highest) (n=207)		**Q1 (lowest) (n=207)**	**Q4 (highest) (n=207)**		**Q1 (lowest) (n=207)**	**Q4 (highest) (n=207)**	
48.00 (41.00–57.00)	0.103	52.00 (42.00–57.00)	48.00 (44.00–58.00)	0.905	51.00 (44.00–59.00)	47.00 (42.00–55.00)	0.006
	0.921			1			<0.001
93		97	97		48	144	
114		110	110		159	63	
26.78 (23.60–29.05)	0.043	27.64 (24.45–30.82)	26.143 (23.01–29.37)	0.003	26.24 (23.44–29.41)	26.83 (23.79–29.07)	0.927
0.89 (0.84–0.94)	0.002	0.93 (0.87–0.97)	0.89 (0.84–0.92)	<0.001	0.88 (0.83–0.93)	0.92 (0.87–0.97)	<0.001
128.00 (112.00–140.00)	0.713	129.00 (116.00–141.00)	126.00 (114.00–135.00)	0.071	120.00 (110.00–131.00)	128.00 (118.00–138.00)	0.002
80.00 (70.00–86.00)	0.761	78.86±11.44	78.46±12.60	0.578	74.00 (68.00–82.00)	80.00 (72.00–87.00)	<0.001
5.75 (5.04–7.60)	0.756	7.10 (5.32–8.19)	5.28 (4.78–5.98)	<0.001	5.26 (4.80–5.80)	7.00 (5.10–8.52)	<0.001
4.47 (3.80–5.37)	0.386	4.88 (4.20–5.64)	4.34 (3.61–5.13)	<0.001	4.30 (3.63–5.34)	4.53 (4.04–5.28)	0.077
1.80 (1.30–2.64)	0.016	2.13 (1.48–3.01)	1.65 (1.23–2.47)	<0.001	1.73 (1.33–2.46)	1.96 (1.27–2.82)	0.118
2.38 (1.90–3.12)	0.171	2.65 (2.19–3.48)	2.38 (1.98–2.74)	<0.001	2.38 (1.84–2.81)	2.46 (2.10–3.12)	0.003
1.34 (1.070–1.73)	0.681	1.20 (0.97–1.62)	1.42 (1.12–1.85)	<0.001	1.42 (1.21–1.88)	1.25 (1.04–1.63)	<0.001
9.70 (6.45–14.80)	0.384	10.52 (6.72–15.63)	9.58 (6.17–14.33)	0.189	9.54 (6.41–13.61)	10.03 (5.59–16.08)	0.342
2.73 (1.69–4.21)	0.790	3.26 (2.06–5.28)	2.31 (1.45–3.78)	<0.001	2.17 (1.48–3.49)	2.70 (1.51–5.47)	0.001
2,791.29 (2,339.86–3,408.95)	<0.001	2,508.10 (1,921.19–2,927.28)	2,676.97 (2,072.03–3,316.18)	0.008	2,040.03 (1,679.95–2,479.72)	3,116.55 (2,651.93–3,715.92)	<0.001
105.67 (85.14–134.92)	<0.001	88.86 (63.17–113.20)	97.28 (75.14–129.05)	0.005	79.96 (56.37–100.46)	112.45 (89.10–136.22)	<0.001
100.659 (83.88–122.43)	<0.001	84.10 (58.64–109.95)	87.23 (69.50–114.43)	0.049	81.96 (64.77–100.96)	89.23 (68.27–115.65)	0.012
92.548 (76.442–112.127)	<0.001	77.280 (53.659–102.136)	80.371 (63.495–105.252)	0.056	75.416 (60.189–94.460)	81.069 (62.049–105.464)	0.046
23.84 (19.18–29.00)	<0.001	17.10 (12.62–24.31)	19.63 (14.84–24.92)	0.012	19.02 (13.97–23.68)	18.99 (13.83–25.31)	0.394
30.87 (26.00–37.58)	<0.001	26.69 (19.15–34.37)	27.12 (20.61–35.03)	0.409	25.32 (20.42–31.87)	27.08 (20.67–35.58)	0.028
36.31 (27.45–45.68)	<0.001	30.04 (21.52–41.04)	34.67 (24.59–44.27)	0.022	30.30 (22.17–39.53)	32.26 (24.18–44.15)	0.067
	0.748			0.047			0.002
6		4	3		3	6	
20		19	20		17	24	
68		63	73		68	86	
36		23	41		27	40	
43		62	48		55	33	
34		36	22		37	18	
	0.005			0.380			0.119
73		86	89		83	104	
67		66	71		68	54	
40		31	33		34	35	
26		23	13		21	13	
	0.101			0.391			0.498
5		4	5		5	6	
183		177	185		181	183	
13		16	8		13	7	
6		10	9		8	11	
	0.016			0.002			
58		84	56		75	46	0.014
82		70	104		85	97	

(*Continued*)

Table 4 (*Continued*)

Variables	Fruit pattern score		*P*-value	Meats pattern score		*P*-value	Dairy product pattern score
	Q1 (lowest) (n=207)	Q4 (highest) (n=207)		Q1 (lowest) (n=207)	Q4 (highest) (n=207)		Q1 (lowest) (n=207)
3,000–4,500	29	38		28	36		25
4,500–6,000	22	22		18	24		10
>6,000	3	4		2	4		5
T2DM, n	109	70	<0.001	62	106	<0.001	91
Hypertension, n			0.025			0.499	
No	158	176		172	177		171
Yes	49	31		35	30		36
Smoking status, n			0.066			<0.001	
Never	159	146		173	127		158
Current	35	53		30	72		37
Former	13	8		4	8		12
Alcohol intakes, n			0.056			0.001	
No	191	179		189	165		189
Yes	16	28		18	42		18
Physical activity, n			0.157			0.439	
Light	8	3		7	3		10
Moderate	148	141		137	139		139
Vigorous	51	63		63	65		58

Notes: Smoker was defined as one who smokes more than 10 cigarettes per week for more than 6 months. Former smoker was defined as one who stopped smoking for more than 6 months. Alcohol intake was defined as one who drinks at least once a week, for more than 6 months. Differences between these two groups were compared by chi-squared test, and *P*<0.05 indicated statistically significant difference.

Abbreviations: BMI, body mass index; DBP, diastolic blood pressure; FINS, fasting insulin; FPG, fasting plasma glucose; HDL-C, high-density lipoprotein-cholesterol; HOMA-IR, homeostasis model assessment-insulin resistance; LDL-C, low-density lipoprotein-cholesterol; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids; SBP, systolic blood pressure; SFA, saturated fatty acids; T2DM, type 2 diabetes mellitus; TC, total cholesterol; TG, triglycerides; WHR, waist–hip ratio.

Table 5 Multivariable regression analyses of dietary patterns and T2DM risk

Fruit			Meats			Dairy product			Vegetables			Grains		
Q1	Q4, OR (95% CI)	*P*-value	Q1	Q4, OR (95% CI)	*P*-value	Q1	Q4, OR (95% CI)	*P*-value	Q1	Q4, OR (95% CI)	*P*-value	Q1	Q4, OR (95% CI)	*P*-value
1	0.238 (0.144–0.395)	<0.001	1	2.389 (1.487–3.838)	<0.001	1	0.672 (0.423–1.066)	0.091	1	0.187 (0.118–0.295)	<0.001	1	10.239 (5.142–20.388)	<0.001

Notes: Multivariable regression analyses were adjusted for sex, age, education level (primary and lower, junior, senior, college and higher), physical activity level (light, moderate, and heavy), smoking status (never, current, and former), BMI, and total energy intake. Q4, the highest quartile of dietary patterns; Q1, the lowest quartile of dietary patterns (reference). Smoker was defined as one who smokes more than 10 cigarettes per week for more than 6 months. Former smoker was defined as one who stopped smoking for more than 6 months. Drinker was defined as one who drinks at least once a week, for more than 6 months.

Abbreviations: BMI, body mass index; T2DM, type 2 diabetes mellitus.

T2DM results from a combination of genetic and lifestyle factors, such as dietary pattern. However, few studies have investigated the relationship between SNPs and dietary patterns. In the present study, we assessed the interaction between the seven SNPs of *TCF7L2* and dietary patterns. The results showed that two of the SNPs, rs4506565 and rs7903146, were significantly interact with dietary patterns. The genetic variants of *TCF7L2* influence both insulin secretion and insulin sensitivity.[44] Insulin secretion depends on blood glucose levels, which can be significantly affected by carbohydrates in the diet. Therefore, we speculate that the quality and quantity of carbohydrates may affect the relationship between *TCF7L2* SNPs and the risk of T2DM.

There are some limitations to our study. First, the sample size was relatively small: only 828 participants were included in the full analysis, which may have led to weak statistical significance when estimating ORs. Second, the causal associations between dietary pattern and risk of T2DM could

	***P*-value**	**Vegetables pattern score**		***P*-value**	**Grains pattern score**		***P*-value**
Q4 (highest) (n=207)		**Q1 (lowest) (n=207)**	**Q4 (highest) (n=207)**		**Q1 (lowest) (n=207)**	**Q4 (highest) (n=207)**	
37		30	35		31	36	
26		18	11		14	21	
4		5	1		2	7	
86	0.619	127	49	<0.001	28	107	<0.001
	0.451			0.003			0.015
165		160	183		170	187	
42		47	24		37	20	
	0.488			0.141			<0.001
155		164	158		177	128	
44		30	42		24	67	
8		13	7		6	12	
	0.411			0.485			<0.001
184		191	187		197	173	
23		16	20		10	34	
	0.249			0.284			0.085
4		5	5		6	7	
140		166	153		150	129	
63		36	49		51	71	

Table 6 Genotype and allele distributions in participants with and without T2DM

Variants	**T2DM, n**	**Control, n**	χ^2	***P*-value**
rs11196205 genotypes				
CC	25	36	1.150	0.563
GC	115	190		
GG	156	218		
Allele				
G	427	626	0.461	0.497
C	165	262		
Additive model				
GC	115	190	0.231	0.631
CC	25	36		
GG	156	218	0.011	0.915
CC	25	36		
Recessive model				
GG	156	218	0.923	0.337
CC + CG	140	226		
Dominant model				
GC + GG	271	408	0.027	0.870
CC	25	36		
rs12255372 genotypes				
GG	207	305	0.228	0.892
GT	79	126		
TT	9	13		
Allele				
T	97	152	0.116	0.734
G	493	736		
Additive model				
TG	79	126	0.219	0.640
GG	207	305		
TT	9	13	0.002	0.964
GG	207	305		
Recessive model				
TT	9	13	0.009	0.923
GG + GT	286	431		
Dominant model				
TG + TT	88	139	0.181	0.670
GG	207	305		
rs12573128 genotypes				
GG	58	61	6.376	0.041
GA	128	228		
AA	110	157		
Allele				
A	348	542	0.580	0.446
G	244	350		
Additive model				
AG	128	228	6.118	0.013
GG	58	61		

(*Continued*)

Table 6 (*Continued*)

Variants	T2DM, n	Control, n	χ^2	*P*-value
AA	110	157	1.904	0.168
GG	58	61		
Recessive model				
AA	110	157	0.297	0.586
GG + GA	186	289		
Dominant model				
AG + AA	238	385	4.627	0.031
GG	58	61		
rs4506565 genotypes				
AA	196	287	3.882	0.144
AT	85	147		
TT	15	12		
Allele				
T	115	171	0.015	0.903
A	477	721		
Additive model				
TA	85	147	1.021	0.312
AA	196	287		
TT	15	12	2.364	0.124
AA	196	287		
Recessive model				
TT	15	12	2.867	0.090
AA + AT	281	434		
Dominant model				
TA + TT	100	159	0.273	0.601
AA	196	287		
rs7895340 genotypes				
GG	159	221	1.228	0.541
GA	113	187		
AA	24	35		
Allele				
A	161	257	0.574	0.449
G	431	629		
Additive model				
AG	113	187	1.218	0.270
GG	159	221		
AA	24	35	0.028	0.866
GG	159	221		
Recessive model				
AA	24	35		
GG + GA	272	408	0.010	0.919
Dominant model				
AG + AA	137	222	1.041	0.307
GG	159	221		
rs7901695 genotypes				
CC	14	12	3.663	0.160
CT	82	145		
TT	200	289		
Allele				
T	482	723		
C	110	169	0.031	0.860
Additive model				
TC	82	145	3.112	0.078
CC	14	12		
TT	200	289	1.704	0.192
CC	14	12		
Recessive model				
TT	200	289	0.607	0.436
CC + CT	96	157		
Dominant model				
TC + TT	282	434	2.188	0.139
CC	14	12		
rs7903146 genotypes				
CC	197	287	4.996	0.082
CT	83	147		
TT	16	12		
Allele				
T	115	171	0.015	0.903
C	477	721		
Additive model				
TC	83	147	1.393	0.238
CC	197	287		
TT	16	12	2.945	0.086
CC	197	287		
Recessive model				
TT	16	12	3.611	0.057
CC + CT	280	434		
Dominant model				
TC + TT	99	159	0.381	0.537
CC	197	287		

Abbreviations: SNP, single-nucleotide polymorphism; T2DM, type 2 dietary mellitus. Differences between these two groups were compared by chi-squared test.

not be evaluated. Besides, although several confounding factors were adjusted in the statistical analyses, we could not completely eliminate the potential influence of other factors on our results. Further studies with larger sample sizes will be required to validate our findings.

Conclusion

In conclusion, our results identified five dietary patterns among the Uygur population in China. We found that the "fruit" and "vegetables" dietary patterns were associated with a significant decrease in the risk of T2DM, whereas the "meats" and "grains" dietary patterns were associated with an increased risk. Moreover, the "dairy product" dietary pattern showed no association with the risk of T2DM. In addition, our results indicate that SNP rs12573128 in the *TCF7L2* gene is associated with an increased risk of T2DM in the Chinese Uygur population and could therefore poten-

Table 7 Interactions of the seven *TCF7L2* SNPs with dietary patterns under additive and a dominant model of analysis

SNPs	**Groups**	**Genotypes**	**N**	**Dietary patterns**					**Additive model**				**Dominant model**
				Fruit	**Meats**	**Dairy product**	**Vegetables**	**Grains**	$P_{\text{association}}$, **GG vs GC**	$P_{\text{association}}$, **GG vs CC**	$P_{\text{association}}$, **GC vs CC**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **GG + GC vs CC**
rs11196205	T2DM	CC	25	3	4	7	2	9	0.877	0.614	0.683	0.222	0.629
		GC	115	15	25	20	22	33					
		GG	156	22	31	37	18	48					
	Control	CC	36	6	6	4	9	11	0.848	0.081	0.135		0.090
		GC	190	43	28	41	44	34					
		GG	218	53	22	49	68	26					
									$P_{\text{association}}$, **TT** vs **GT**	$P_{\text{association}}$, **TT** vs **GG**	$P_{\text{association}}$, **TG vsGG**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **TT**+ GT vs **GG**
rs12255372	T2DM	GG	207	29	42	46	25	65	0.769	0.944	0.781	0.126	0.810
		GT	79	11	15	13	17	23					
		TT	9	0	2	5	0	2					
	Control	GG	305	70	36	69	91	39	0.785	0.607	0.495		0.440
		GT	126	30	16	24	28	28					
		TT	13	2	4	1	2	4					
									$P_{\text{association}}$, **AA** vs **GA**	$P_{\text{association}}$, **AA** vs **GG**	$P_{\text{association}}$, **AG** vs **GG**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **AA**+ GA vs **GG**
rs12573128	T2DM	GG	58	7	6	17	11	17	0.301	0.207	0.647	0.237	0.360
		GA	128	15	28	27	16	42					
		AA	110	18	26	20	15	31					
	Control	GG	61	14	10	14	17	6	0.880	0.347	0.353		0.319
		GA	228	50	30	46	68	34					
		AA	157	38	16	35	37	31					
									$P_{\text{association}}$, **TT** vs **AT**	$P_{\text{association}}$, **TT** vs **AA**	$P_{\text{association}}$, **TA vsAA**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **TT**+ AT vs **AA**
rs4506565	T2DM	AA	196	27	43	43	23	60	0.930	0.650	0.549	0.033	0.490
		AT	85	12	14	16	18	25					
		TT	15	1	3	5	1	5					
	Control	AA	287	66	31	63	90	37	0.548	0.482	0.994		0.869
		AT	147	34	22	31	30	30					
		TT	12	2	3	1	2	4					
									$P_{\text{association}}$, **AA** vs **GA**	$P_{\text{association}}$, **AA** vs **GG**	$P_{\text{association}}$, **AG** vs **GG**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **AA**+ GA vs **GG**

(*Continued*)

Table 7 (*Continued*)

SNPs	Groups	Genotypes	N	Dietary patterns					Additive model				Dominant model
				Fruit	**Meats**	**Dairy product**	**Vegetables**	**Grains**	$P_{\text{association}}$, **GG vs GC**	$P_{\text{association}}$, **GG vs CC**	$P_{\text{association}}$, **GC vs CC**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **GG + GC vs CC**
rs7895340	T2DM	GG	159	22	32	37	19	49	0.869	0.794	0.882	0.267	0.830
		GA	113	15	24	20	21	33					
		AA	24	3	4	7	2	8					
	Control	GG	221	53	23	49	70	26	0.102	0.060	0.911		0.507
		GA	187	43	27	41	42	34					
		AA	35	6	5	4	9	11					
									$P_{\text{association}}$, **TT** vs **CT**	$P_{\text{association}}$, **TT** vs **CC**	$P_{\text{association}}$, **TC** vs **CC**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **TT**+ CT vs **CC**
rs7901695	T2DM	CC	14	1	3	4	1	5	0.481	0.607	0.886	0.072	0.680
		CT	82	12	13	15	17	25					
		TT	200	27	44	45	24	60					
	Control	CC	12	2	3	1	2	4	0.933	0.490	0.534		0.498
		CT	145	33	22	31	31	28					
		TT	289	67	31	63	89	39					
									$P_{\text{association}}$, **TT** vs **CT**	$P_{\text{association}}$, **TT** vs **CC**	$P_{\text{association}}$, **TC** vs **CC**	**Overall** $P_{\text{interaction}}$	$P_{\text{association}}$, **TT**+ CT vs **CC**
rs7903146	T2DM	CC	197	27	43	43	23	61	0.961	0.700	0.649	0.031	0.591
		CT	83	12	14	15	18	24					
		TT	16	1	3	6	1	5					
	Control	CC	287	66	31	63	90	37	0.548	0.481	0.994		0.869
		CT	147	34	22	31	30	30					
		TT	12	2	3	1	2	4					

Abbreviations: SNP, single-nucleotide polymorphism; T2DM, type 2 dietary mellitus.

tially serve as a clinically important prediagnostic marker. The interactions between *TCF7L2* rs4506565 and rs7903146 and dietary pattern were found to be statistically significant. Given the limited amount of research that has been done within the Uyghur population, our studies provide a unique contribution to the pathogenesis of T2DM in this nation.

Data availability

The data sets analyzed during the current study are available from the corresponding author on reasonable request.

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Author contributions

All authors contributed to data analysis, drafting and revising the article, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

Disclosure

The authors report no conflicts of interest in this work.

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Supplementary material

Table S1 The HWE test of the seven SNPs in DM group and control group

SNP	Groups	Wild homozygote	Heterozygote	Mutant homozygote	χ^2	*P*-value
rs11196205		CC	GC	GG		
	Control group	36	190	218	0.366	0.545
	DM group	25	115	156	0.336	0.562
rs12255372		GG	GT	TT		
	Control group	305	126	13	0.000	0.998
	DM group	207	79	9	0.189	0.664
rs12573128		GG	GA	AA		
	Control group	61	228	157	2.318	0.128
	DM group	58	128	110	3.427	0.064
rs4506565		AA	AT	TT		
	Control group	287	147	12	1.800	0.180
	DM group	196	85	15	2.023	0.155
rs7895340		GG	GA	AA		
	Control group	221	187	35	0.275	0.600
	DM group	159	113	24	0.383	0.536
rs7901695		CC	CT	TT		
	Control group	12	145	289	1.528	0.216
	DM group	14	82	200	2.110	0.146
rs7903146		CC	CT	TT		
	Control group	287	147	12	1.800	0.180
	DM group	197	83	16	3.217	0.073

Note: HWE was assessed by chi-squared test, and $P>0.05$ indicated the SNP obeyed HWE.

Abbreviations: DM, diabetes mellitus; HWE, Hardy–Weinberg equilibrium; SNP, single-nucleotide polymorphism.