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·CLINICAL RESEARCH·

Correlation of the features of metabolic syndrome with type 2 diabetes mellitus among the elderly**★

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Abstract

BACKGROUND: The cluster of multiple metabolic disorders, namely raised blood pressure, overweight or obesity, raised triglyceride level, reduced high density lipoprotein cholesterol (HDL-C) level were the predictor of type 2 diabetes mellitus (DM). However, similar data especially the old people's data is relatively rare in China.

OBJECTIVE: To analyze the relationship between the components of metabolic syndrome (MetS), their clusters and the risk of diabetes among Chinese old population.

DESIGN: Cross-sectional study.

SETTING: Beijing Institute of Geriatrics, Beijing Hospital, Ministry of Public Health.

PARTICIPANTS: The study was carried out from February 2001 until November 2001.4 499 volunteers aged 60 and over were recruited from the academic institutes in Beijing Xicheng, Haidian and Shijingshan districts through cluster sampling methods. They were selected after excluding those who did not have integral data.

METHODS: Diabetes was considered when fasting glucose was ≥7.0 mmol/L and was treated for or diagnosed as DM. Chi-square tests were performed to compare the categorical data. Age and sex adjustment were taken in the comparison of the levels of blood pressure, waist circumference (WC), The body mass index (BMI), and lab variables, Multifactor stepwise (backward) Logistic regression analyses were used to select the factors which would have association with the risk of DM. When analyzing the relationship between number of clustering of the traits of MetS and DM, the group without any metabolic abnormalities was set as control group. The dummy variables were set for 1,2,3,4 clusters of metabolic abnormalities. The Logistic regression model was used again to test the relationship and adjusted by age and the family history of DM.

MAIN OUTCOME MEASURES: The blood glucose, waist, BMI, blood pressure, triglyceride (TG), HDL-C, and family history of diabetes of subjects.

RESULTS: 4 444 people in the mean age of 65±5 were retrieved. 556 cases of DM were found in this survey. Age, family history of diabetes, systolic blood pressure, waist and TG were independently associated with the risk of DM, with *OR* (95%*CI*) being 1.02 (1.00-1.04), 3.48 (2.76-4.39), 1.02 (1.01-1.02), 1.03 (1.00-1.03), 1.13 (1.05-1.21), respectively. When TG was not in the model, HDL-C was also inversely associated with DM (*OR*=0.67, 95%*CI* 0.49-0.91). The risk of DM increased with clustering of abdominal obesity, raised blood pressure, raised TG, and reduced HDL-C level in individuals.

CONCLUSION: In addition to age and genetic factors, metabolic factors, especially their clusters are closely related to the risk of diabetes. Therefore, the features of MetS are important indicators for the risk of DM in aged people.

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INTRODUCTION

There is no doubt that type 2 diabetes mellitus (DM)has been rising to an epidemic level in China. Old people account for major part of type 2 DM. Evidences have been accumulated for the risk factors of DM. In the last two decades, there were reports suggested the cluster of multiple metabolic disorders, namely raised blood pressure, overweight or obesity, raised triglyceride (TG) level, reduced high density lipoprotein cholesterol (HDL-C) level were the predictors of DM [1-7]. However, similar data especially in the old people is relatively scarce in China. The occurrence of DM is insidious and usually many years passed before diagnosis. If the metabolic disorder(metabolic syndrome, MetS) is the early sign of DM, it will help to identify risk individuals who need intervention to prevent the development of DM, therefore to reduce the morbidity and mortality caused by this disease. The purpose of this study was to analyze the relationship between the components of MetS, its clusters and the risk of diabetes among Chinese old population.

SUBJECTS AND METHODS

Subjects

The study was carried out from February 2001 until November 2001.4 444 participants aged 60 and over were recruited from the academic institutes in Beijing Xicheng, Haidian and Shijingshan districts through cluster sampling methods voluntary. They were selected after excluding those who did not have integral data. There were 2 643 men and 1 801 women. The mean age of the population was (65±5) years old.

Methods

The investigators were trained before the survey started. The questionnaire was designed with demographic data, lifestyle data, history of diseases data, physical and lab examination data. The lifestyle data included physical exercise (moderate or more, at least once a week and lasting for 30 minutes or over), and smoking (≥1/d) [4]. The data of disease history included having or not having self-reported DM (ever-diagnosed or currently taking medicine to control glucose level), and hypertension (ever-diagnosed, or taking medicine to control blood pressure), and family history of DM and hypertension. Weight and standing height were measured with the subjects wearing light clothes and no shoes. The body mass index (BMI) was calculated as the weight in kilograms divided by the square of the height in meters (kg/m^2). The subjects were considered as overweight or obesity if their BMI ≥25 kg/m^2. When the waist circumference was taken, the subjects stood and measures were made at the level of umbilicus and at the end of expiration. Abdominal obesity was considered if the waist circumference (WC) was greater or equal to 90 cm for men and 80 cm for women. The blood pressures were measured twice and the mean values were used. If a person had ever-diagnosed hypertension, or systolic blood pressure (SBP) ≥130 mm Hg(1 mm Hg=0.133 kPa), or diastolic blood pressure (DBP) ≥85 mm Hg, the raised blood pressure was determined. The blood samples were taken after fasting at least 12 hours. The lab tests were done in the internationally standardized laboratory. Raised TG was defined if plasma TG≥1.70 mmol/L. A subject was classified as having reduced HDL-C if the HDL-C level was less than 1.03 mmol/L for men and 1.29 mmol/L for women. The criteria for DM was fasting glucose ≥7.0 mmol/L, or having ever diagnosed diabetes. The 2005 International Diabetes Federation (IDF) consensus worldwide definition of the MetS was referred to diagnose each abnormality.

Statistical analysis: All the statistical analyses were carried out using SAS software. Chi-square tests were performed to compare the categorical data. Age and sex adjustment were taken in the comparison of the levels of blood pressure, WC, BMI, and lab variables, Multifactor stepwise (backward) Logistic regression analyses were used to select the factors which would have association with the risk of DM. When analyzing the relationship between MetS and DM, the group without any metabolic abnormalities was set as control group. The dummy variables were set for 1,2,3,4 clusters of metabolic abnormalities. The Logistic regression model was used again to test the risk of DM in MetS adjusting age and the family history of DM.

RESULTS

Characteristics of diabetes and non-diabetes

There were 4 499 persons taking part in the survey. Among them, 4 444 persons had complete data, with the response rate being 91.1%. The results of the comparisons of the characteristics between the group with DM (DM+) and without DM (DM−) are in Table 1.

Table 1 The comparison of the characteristics between DM− group and DM+ group

Item	DM−	DM+	*P*
Men (*n*/%)	2 287/86.53	356/13.47	
Women(*n*/%)	1 601/88.90	200/11.10	0.019 3
Age(yr)	65.4±4.7	66.1±4.8	0.001 2
SBP(mm Hg)	128.2±0.3	134.0±0.7	< 0.000 1
DBP(mm Hg)	79.1±0.1	79.8±0.4	0.076 4
WC(cm)	84.9±0.2	88.0±0.4	< 0.000 1
BMI(kg/m^2)	24.1±0.1	24.9±0.1	< 0.000 1
TG(mmol/L)	1.67±0.02	1.92±0.04	< 0.000 1
HDL-C(mmol/L)	1.38±0.01	1.30±0.01	< 0.000 1
LDL-C(mmol/L)	3.23±0.01	3.18±0.04	0.147 7
TC(mmol/L)	5.36±0.01	5.35±0.04	0.815 8
Family history of DM(*n*/%)	314/8.08	130/23.38	< 0.000 1
Family history of HP(*n*/%)	1 459/37.53	227/40.83	0.133 5
Exercise(*n*/%)	2 232/57.41	329/59.17	0.430 8
Smoking(*n*/%)	496/12.76	60/10.79	0.190 1

DM+: with diabetes mellitus(DM); DM−: without DM; SBP:systolic blood pressure ; DBP: diastolic blood pressure; WC: waist circumference; TG: triglyceride; HDL-C: high density lipoprotein cholesterol; LDL-C :low density lipoprotein cholesterol; TC: total cholesterol; DM: diabetes; HP: hypertension

There were totally 556 cases in DM+ group, among them 442 were the previously diagnosed cases, and 114 were newly diagnosed. There were 3 888 persons in the control group (DM−). The mean age for the two groups was (66±5) years for DM+, and (65±5) years for DM− respectively. Men is more prevalent for DM than women (13.47% *vs.* 11.10%, *P*=0.019 3). Although the mean age was higher (*P*=0.001 2) in the DM+ group, the difference was only one year. The level of SBP, WC, BMI, TG, were significantly higher and HDL-C lower in the DM+ group. Also, the family history of DM was significantly associated with DM. On the other hand, the level of low-density-lipoprotein-cholesterol (LDL-C), total cholesterol (TC), and family history of hypertension(HP), physical exercise, and smoking were not significantly different between the two groups. The reason of the physical exercise showing no protective effect may be contributed by the low level of energy expenditure among the old people, or since the DM was diagnosed (442 ever-diagnosed cases), people were more likely to take part in the exercise.

Factors which contribute to diabetes risk(Table 2)

The factors demonstrating significant difference between the two groups in Table 1 were allowed to compete in the multi-variable stepwise Logistic regression model. The results show in addition to traditional risk factors, *i.e.* age and family history of DM, the components of MetS, SBP, WC, TG were associated with the risk of DM independent of the other variables. The HDL-C was not left in the model. But when TG was not put in the model, HDL-C was inversely, just as expected, associated with the occurrence of DM with only little change of the *ORs* for the other variables (data not show). The reason TG and HDL-C was not left in the model simultaneously may be explained by the strong association between them. For the value of *ORs*, the family history show 3 folds of increase in the risk of DM, which is much higher than the other variables, may be due to it entered the model as categorical variable.

Table 2 The multi-factor Logistic regression model

Variables	β	Stderr	Chi-Square	*OR* (95% *CI*)	*P*
Intercept	−7.8065	0.739 4	111.473 3	–	< 0.000 1
Age	0.0216	0.009 4	5.293 5	1.02(1.00–1.04)	0.021 4
DM history	1.2470	0.118 7	110.360 6	3.48(2.76–4.39)	< 0.000 1
SBP	0.0147	0.002 7	30.121 8	1.02(1.01–1.02)	< 0.000 1
WC	0.0245	0.004 7	26.892 6	1.03(1.00–1.03)	< 0.000 1
TG	0.1185	0.037 7	9.889 5	1.13(1.05–1.21)	0.001 7
*HDL-C	−0.4076	0.157 9	6.661 0	0.67(0.49–0.91)	0.009 9

DM: diabetes mellitus; SBP:systolic blood pressure; WC: waist circumference; TG: triglyceride; HDL-C: high density lipoprotein cholesterol; * The model with age, sex, family history of DM, SBP, WC, HDL-C

Clustering of MetS components in DM(Table 3)

Table 3 The Logistic regression model for the MetS and the risk of DM

No. of components of MetS	DM−	DM+	β	Stderr	Chi-Square	*OR* (95% *CI*)	*P*
0	653	47	–	–	–	–	
1	1 137	142	0.551 1	−0.175 3	9.882 3	1.74(1.23–2.45)	0.001 7
2	1 132	161	0.681 0	0.172 9	15.511 8	1.98(1.41–2.77)	< 0.000 1
3	664	128	0.985 1	0.179 2	30.209 2	2.68(1.89–3.81)	< 0.000 1
4	302	78	1277 7	0.197 3	41.923 6	3.59(2.44–5.28)	< 0.000 1

DM+: with diabetes mellitus(DM); DM−: without DM: MetS: metabolic syndrome

Table 3 shows the cluster of MetS components increases the risk of DM. While those having only one component were about 1.5 times more likely to have DM with the *OR* being 1.74(1.23–2.45), those having 2, 3 or all 4 disorders were close to 2, 2.5, 3.6 times higher increased risk of DM. The *ORs* were 1.98(1.41–2.77), 2.68(1.89–3.81) and 3.59(2.44–5.28), respectively. When the analysis was performed after adjusted for age and family history of DM, the *ORs*, and the direction of association were the same as in tables 2. This result indicates along with the cluster of MetS components, namely raised blood pressure, abdominal obesity, raised TG level, and reduced HDL-C level, the risk of DM increased, independently of age and family history of DM.

DISCUSSION

The prevalence of type 2 diabetes is rising to an epidemic level all over the world while large part is un-diagnosed (35% of diabetic subjects in the U.S.). High frequency of diabetes-related complications at diagnosis, increased coronary artery disease mortality associated with impaired fasting glucose(IFG) and impaired glucose tolerance(IGT) were noted. Early detection is the new preventive strategy at current state of time. Meanwhile, the evidence from preventive studies demonstrating that the modification of life style can prevent or delay the onset of DM further highlights the importance of early detection[8].

However, how to identify the risk of DM at early stage is still under investigation. There are many proposed methods to be used for early detection of DM[6,9]. The oral glucose tolerance test (OGTT) is the standard method for identifying subjects at risk for type 2 diabetes in clinical setting. However, OGTT is not widely used in clinical practice because it is inconvenient and costly. In order to minimize the use of OGTT, some other methods such as the Diabetes Predicting Model[6], have been proposed to identify individuals at risk. But the model and risk scores need validation in different population, Therefore, their applications are compromised. Saydah *et al*[9] evaluated their strategy using BMI in combination with fasting plasma glucose (FPG) and HbA1C measurements. They found that different combination of variables resulted in different proportion of the population recommended for OGTT, and detected different proportion of IGT in the OGTT candidates. The optimal method should become more apparent over the next few years as additional information becomes available. At present, for preventive perspective, it is important to consider using more convenient, more easily available information to evaluate the risk of DM.

In the last 16 years, studies demonstrated the constellation of multiple metabolic abnormalities called MetS is able to predict the occurrence of diabetes [1-7]. This evidence has consistently been confirmed across different ethnic populations, in different countries, among men and women, and in all age groups[1-7]. However, similar data is relatively scarce in China. Our study showed besides the traditional factors, namely age and family history of DM, high level of blood pressure, WC, TG, and low level of HDL-C, especially their clusters were independently associated with the risk of DM. Therefore, it indicates DM is associated with the features of MetS in Chinese population [1-7].

The features of MetS have the advantage in assessing the risk of DM. First, the measure of indices can be easily available in both clinical practice setting and population study. Second, the constellation of multiple metabolic disorders is an important condition suggesting the risk of diabetes [1-7]. In prospective data, Boyko *et al*[5] and Lorenzo *et al*[7] reported the features of MetS predicted the development of DM independent of the level of insulin, although insulin level is a marker of insulin resistance (IR) and IR is a potential risk factor of DM. Kekalainen *et al*[3] indicated hyperinsulinemia clustered the traits of MetS predicted DM independent of family history of DM. Stern *et al*[6] suggest the exhibition of MetS can predict future diabetes development at least as well as and may be better than IGT. Third, MetS is also risk factor for cardiovascular disease, therefore early detection and lifestyle modification also results favorable benefit for its adverse outcome.

Although our data has limitations because it is cross-sectional data, and it lacked OGTT data, which might underestimate the association, the significance of this research is that our results confirm the association between the features of MetS and diabetes among Chinese old population. In conclusion, abdominal obesity, raised blood pressure, raised TG level, reduced HDL-C level especially in their combinations are the high risk status for DM, the application of intervention is important for not only the prevention of DM itself but also for its complications.

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代谢综合征特征指标与老年人2型糖尿病的相关性*★

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摘要

背景:代谢综合征指标即血压升高、腹部肥胖、三酰甘油水平升高,高密度脂蛋白胆固醇水平降低,在个体中聚集存在,是糖尿病的预测因子。但类似老年人的资料相对较少。

目的: 分析代谢综合征各特征指标与老年人2型糖尿病危险性的相关性,为糖尿病的一级预防提供依据。

设计:横断面调查。

单位:卫生部北京老年医学研究所。

对象:调查于2001-02/11完成,选择北京市西城、海淀、石景山科研单位年龄60岁以上老年人共4 499名作为调查对象,均自愿参加调查。排除调查资料不全者。

方法:对调查人群进行观察性分析,用调查问卷收集相关信息。糖尿病的诊断标准为空腹血糖≥ 7.0 mmol/L或有糖尿病现患史。计数资料用χ^2检验进行分析，计量资料均数的比较用调整年龄、性别的协方差分析。应用非条件多因素Logistic逐步回归法分析与糖尿病独立相关的指标。分析代谢紊乱的聚集与糖尿病的关系时，以无任何因素聚集为对照,按1,2,3,4个聚集数设亚变量,用Logistic回归模型分析各种聚集数目时糖尿病的危险程度,并调整年龄、糖尿病家族史、受教育水平的影响。

主要观察指标:调查对象的血糖、腹围、体质量指数、血压、血清三酰甘油、高密度脂蛋白胆固醇、糖尿病现患史及家族史。

结果:有4 444名老年人进入结果分析。①调查共检出556名糖尿病患者。②统计结果显示年龄、糖尿病家族史、血压、腹围和血清三酰甘油与糖尿病独立相关[*OR*(95%*CI*)=1.02(1.00~1.04), 3.48(2.76~4.39), 1.02(1.01~1.02), 1.03(1.00~1.03), 1.13(1.05~1.21)]。③当血清三酰甘油不在模型中，高密度脂蛋白胆固醇与糖尿病成显著负相关,*OR* (95%*CI*)= 0.67(0.49~0.91)。④随腹部肥胖、血压升高、三酰甘油水平升高、高密度脂蛋白胆固醇水平降低这4个变量在个体内聚集数目的增加，糖尿病的危险性亦逐渐增大。

结论:除遗传和年龄因素外,代谢综合征指标尤其是指标的聚集与糖尿病密切相关,是提示糖尿病危险性的重要指征。

主题词:代谢疾病;综合征;糖尿病,非胰岛素依赖型

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