The Metabolic Syndrome Defined by Factor Analysis and Incident Type 2 Diabetes in a Chinese Population With High Postprandial Glucose

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OBJECTIVE — The aim of this study was to examine how the major components of the metabolic syndrome relate to each other and to the development of diabetes using factor analysis.

RESEARCH DESIGN AND METHODS — The screening survey for type 2 diabetes was conducted in 1994, and a follow-up study of nondiabetic individuals at baseline was carried out in 1999 in the Beijing area. Among 934 nondiabetic and 305 diabetic subjects at baseline, factor analysis was performed using the principle components analysis with varimax orthogonal rotation of continuously distributed variables considered to represent the components of the metabolic syndrome. Fasting insulin was used as a marker for insulin resistance. Of the 559 subjects without diabetes at baseline, 129 developed diabetes during the 5-year follow-up. Factors identified at baseline were used as independent variables in univariate and multivariate logistic regression models to determine risk factor clusters predicting the development of diabetes.

RESULTS — Four factors were identified in nondiabetic and diabetic subjects. Fasting insulin levels, BMI, and waist-to-hip ratio were associated with one factor. Systolic and diastolic blood pressures were associated with the second factor. Two-hour postload plasma glucose (2-h PG) and serum insulin and fasting plasma glucose were associated with the third factor. Serum total cholesterol and triglycerides were associated with the fourth factor. The first and the third factors predicted the development of diabetes. In diabetic patients at baseline, the combination of systolic and diastolic blood pressure was the most important factor, and urinary albumin excretion rate clustered with fasting and 2-h PG levels.

CONCLUSIONS — Insulin resistance alone does not underlie all features of the metabolic syndrome. Different physiological processes associated with various components of the metabolic syndrome contain unique information about diabetes risk. Microalbunuria is more likely to be a complication of type 2 diabetes or hypertension than a marker for the metabolic syndrome.

Diabetes Care 27:2429–2437, 2004

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Received for publication 4 February 2004 and accepted in revised form 29 June 2004.

Abbreviations: 2-h PG, 2-h postload glucose; DBP, diastolic blood pressure; FPG, fasting plasma glucose; IGR, impaired glucose regulation; IGT, impaired glucose tolerance; NGT, normal glucose tolerance; OGTT, oral glucose tolerance test; SBP, systolic blood pressure; UAER, urinary albumin excretion rate; WHR, waist-to-hip ratio.

A table elsewhere in this issue shows conventional and Système International (SI) units and conversion factors for many substances.

The clustering of hypertension, dyslipidemia, glucose intolerance, insulin resistance, hyperinsulinemia, microalbuminuria, and obesity, particularly central obesity, has been termed the metabolic syndrome (1). Controversies still exist as to whether microalbuminuria is a component of the syndrome (2–4). An important feature of the syndrome is insulin resistance, which is characterized by increased serum fasting insulin levels among nondiabetic individuals in epidemiological studies (5,6). Thus, it has been called syndrome X or insulin resistance syndrome (7,8). Despite that the underlying mechanism of the syndrome is not completely understood, obesity and sedentary lifestyle coupled with unbalanced diet and still largely unknown genetic factors interact to produce the syndrome (9,10). It has been proposed that this syndrome is a powerful determinant of type 2 diabetes and cardiovascular disease (7,8,11). Recently, factor analysis, a statistical technique for studies including interrelating variables, has been applied to investigate the risk factor clustering in the metabolic syndrome (12–18) and to predict coronary heart disease or total and cardiovascular disease mortality (19,20). However, little information is currently available on the mechanism with which the major components of the metabolic syndrome, including urinary albumin excretion rate (UAER), relate to each other in nondiabetic and diabetic individuals. Furthermore, there are only few prospective studies evaluating the extent to which the metabolic syndrome or its individual components predict the development of type 2 diabetes (21,22). Therefore, we applied factor analysis to investigate how the major components of the metabolic syndrome relate to each other and to the development of diabetes in a Chinese population. We have also compared our findings in women and men and in nondiabetic and diabetic participants separately.

RESEARCH DESIGN AND METHODS

The First National Diabetes Survey was carried out in China in 1980 (23). The second National Diabetes Survey (24), comprising a population of ~250,000 in 19 provinces and areas, was launched in 1994. In April 1994, a workshop was held to standardize the protocol and methodology, and a 3-day training course took place for the investigators in each location before the baseline survey. The results from the previous Da Qing Impaired Glucose Tolerance and Diabetes study on 2,692 subjects with 2-h postprandial plasma glucose values of 6.67–7.7 mmol/l showed 9 (0.3%) cases of diabetes and 31 (1.2%) cases of impaired glucose tolerance (IGT) based on 1985 World Health Organization criteria (25). Thus, the subjects with 2-h postprandial capillary glucose <6.67 mmol/l would be expected to have an extremely low percentage of diabetes or IGT. In this context, a fingerstick prescreening using the One Touch II glucose meter after breakfast containing at least 80 g of carbohydrate was used in our screening survey to maximize the yield of abnormal glucose tolerance at a 75-g oral glucose tolerance test (OGTT). In the participants whose 2-h postprandial capillary blood glucose was ≥6.67 mmol/l, the OGTT was performed. The Beijing Project, as part of the National Diabetes Survey, was carried out between July 1994 and January 1995 (26). The participants and design of the Beijing Project have been described previously in more details (24,26,27). Briefly, 76 units in the Beijing area, including 33 villages, 15 factories, 11 military camps, and 17 urban communities, were randomly ascertained with a multistage sampling method. In these units, 20,682 inhabitants aged 25–82 years (64% were aged 25–44 years) participated in the finger blood glucose screening survey. The participation rate was 92%. A total of 2,499 participants aged 25–80 years, who at the screening had a 2-h capillary blood glucose ≥6.67 mmol/l, were invited to participate in the OGTT. Among them, the OGTT was performed in 1,566 (62.7%) subjects. Of these 1,566 subjects, after excluding 106 with known diabetes and 221 currently taking antihypertensive or hypolipidemic drugs, 305 with newly diagnosed diabetes and 934 without diabetes were included in this study (Fig. 1).

From October 1999 to January 2000, the 5-year follow-up survey was carried out in subjects who participated in the OGTT at baseline. Of the initial 1,566 subjects, 483 had moved out of Beijing and 181 individuals could not be followed up because of logistic reasons. The remaining 902 (57.6%) individuals participated in the follow-up examination. The nonparticipants did not differ significantly from participants in age, sex, BMI, waist-to-hip ratio (WHR), plasma fasting and 2-h postload glucose (2-h PG), serum fasting and 2-h postload insulin, triglycerides, total cholesterol, timed 2-h UAER, and the frequency of diabetes, hypertension, and obesity at baseline. Of the 902 subjects who participated in the follow-up study, 275 with diabetes at baseline and 68 currently taking antihypertensive or hypolipidemic drugs were excluded in this study. Thus, 559 subjects without diabetes at baseline and who were not receiving antihypertensive or hypolipidemic treatment were included in the study (Fig. 1). Of them, 129 had developed type 2 diabetes (61 men and 68 women) during the 5-year follow-up. The enrollment and examination of subjects were conducted in accordance with the Helsinki Declaration. All subjects with diabetes were diagnosed according to the 1999 World Health Organization criteria for diabetes (1).

Anthropometric measurements

The anthropometric measurements and laboratory methods were similar at both the baseline and the follow-up surveys. The physicians completed the interview questionnaire, which included questions about past medical history, family history of diabetes, history of pharmacological treatment, smoking habits, occupation, and education. Family history of diabetes and antihypertensive and hypolipidemic medication were dichotomized. Smoking status included current smoker and nonsmoker. Occupation was classified as white- or blue-collar work. Three education categories were created according to the total number of school years: 0–6, 7–12, and ≥13 years.

Body weight of the subjects wearing light clothing without shoes was measured with a 0.1-kg precision. Height was measured to the nearest 0.5 cm. BMI was calculated as the weight in kilograms divided by the square of the height in meters. Waist girth was defined as the average of two measurements taken after inspiration and expiration at the midpoint between the lowest rib and iliac crest. Hip circumference was measured at the point of trochanter major. The WHR was defined as waist girth to hip circumference. Obesity was defined as WHR >0.90 and/or BMI >30 kg/m^2 (for men) or WHR >0.85 and/or BMI >30 kg/m^2 (for women) (1). After each subject had been seated for 5 min, blood pressure was measured twice to the nearest 2 mmHg from the left arm of the participant using a standard sphygmomanometer. The average of the two measurements was used for all analyses. Diastolic blood pressure (DBP) was recorded at the fifth Korotkoff sound. Hypertension was defined as systolic blood pressure (SBP) ≥140 mmHg and/or DBP ≥90 mmHg (1).

Laboratory methods

After a 10- to 12-h overnight fast, each subject voided and then the fasting blood sample was collected. A 75-g anhydrous glucose dissolved in 300 ml of water was given orally over the course of 5 min, and a second blood sample was drawn 2 h later for the glucose and insulin determinations. A urine sample was collected immediately after the 2-h blood collection to quantify timed 2-h UAER. Blood samples were immediately centrifuged and processed further. Plasma glucose was detected in duplicate within 2 h by a glucose oxidase method at the Laboratory Center of Beijing Tongren Hospital. Serum insulin was determined by a double-antibody radioimmunoassay (Huaxi, Sichuan, China). Urinary albumin concentration was measured by radioimmunoassay (MA kit; 401, Beijing, China). Their intra- and interassay coefficients of variation were <6 and <8% for insulin and <5 and <7% for urinary albumin. Microalbuminuria was defined as UAER ≥20 μg/min (1). Serum total cholesterol level and triglyceride were measured by enzymatic methods using Zhongsheng reagents (Zhongsheng, Beijing, China).

Diagnosis of diabetes and study groups

According to the 1999 World Health Organization criteria (1), the participants were classified into the categories of glycemic status based on fasting plasma glucose (FPG) and 2-h PG: normal fasting glucose and normal glucose tolerance (NGT) (FPG <6.1 mmol/l and 2-h PG <7.8 mmol/l); impaired glucose regula-

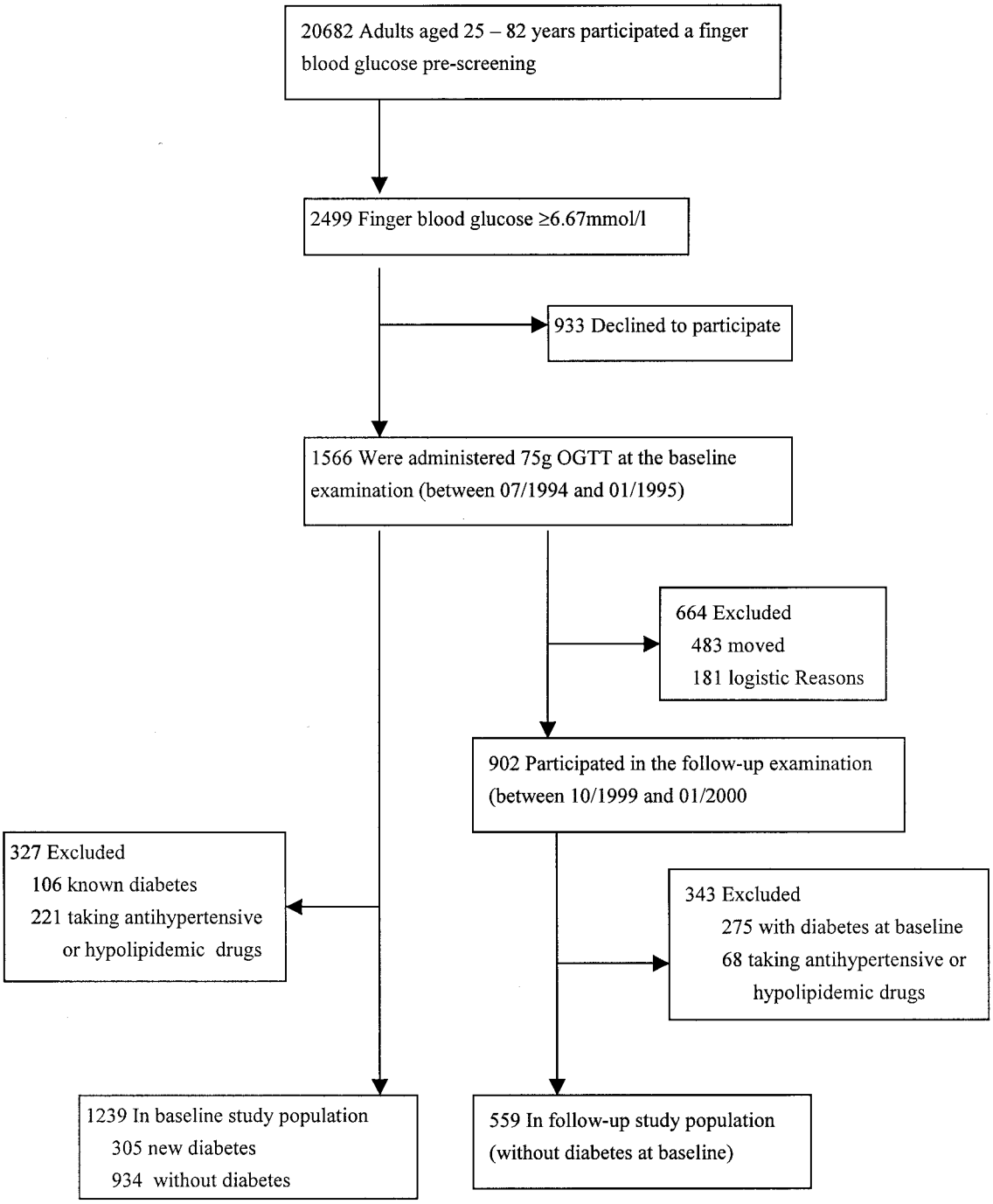

Figure 1—*Study population at the baseline and at the follow-up examination.*

tion (IGR), which consists of impaired fasting glucose and/or IGT (FPG 6.1–7.0 mmol/l and/or 2-h PG 7.8–11.1 mmol/l); and diabetes (FPG ≥7.0 mmol/l and/or 2-h PG ≥11.1 mmol/l). At baseline, the two study groups were defined as follows: the nondiabetic group comprised the participants with both normal fasting glucose and NGT and those with IGR at baseline, and the diabetic group comprised the participants with newly diagnosed diabetes at baseline.

Statistical analyses

All statistical analyses were performed separately by sex with SPSS 11.5 software (SPSS, Chicago, IL). Log-transformed values were used for variables skewed toward the high values such as UAER, serum triglecerides, fasting, and 2-h postload insulin. Group means were compared by Student's *t* test, and the differences in proportions were compared by χ^2 test. Individual associations

Table 1—*Comparison of characteristics by sex in 934 nondiabetic and 305 diabetic subjects at baseline*

	Nondiabetic			Diabetic		
	Men	Women	*P*	Men	Women	*P*
n	449	485		132	173	
Age (years)	49 ± 12	47 ± 11	0.007	51 ± 10	52 ± 11	<0.001
BMI (kg/m^2)	24.6 ± 3.6	24.6 ± 4.0	NS	25.1 ± 3.0	26.1 ± 4.7	0.011
WHR	0.91 ± 0.07	0.89 ± 0.09	0.004	0.92 ± 0.1	0.90 ± 0.1	0.044
SBP (mmHg)	127 ± 23	127 ± 23	NS	131 ± 21	143 ± 29	<0.001
DBP (mmHg)	80 ± 13	78 ± 12	0.007	84 ± 20	84 ± 12	NS
UAER (μg/min)*	5.4 (4.8–6.0)	4.6 (4.1–5.2)	NS	7.8 (6.4–9.5)	7.9 (6.4–9.8)	NS
Cholesterol (mmol/l)	5.0 ± 2.2	4.9 ± 1.6	NS	5.0 ± 1.7	5.5 ± 1.8	0.007
Triglycerides (mmol/l)*	1.4 (1.3–1.5)	1.4 (1.3–1.4)	NS	1.8 (1.6–2.0)	1.8 (1.6–1.9)	NS
Fasting insulin (pmol/l)*	44 (42–46)	48 (45–50)	0.02	53 (48–58)	63 (58–69)	0.007
2-h insulin (pmol/l)*	154 (144–164)	200 (189–213)	<0.001	195 (171–223)	234 (210–261)	0.035
Fasting glucose (mmol/l)	5.7 ± 0.6	5.5 ± 0.8	<0.001	8.2 ± 2.1	8.6 ± 2.6	NS
2-h PG (mmol/l)	6.5 ± 2.0	7.1 ± 2.3	<0.001	10.6 ± 4.5	12.0 ± 4.9	0.009
Smoking (%)	53	8	<0.001	52	14	<0.001
Family history of diabetes (%)	13	19	NS	18	13	NS
IGR (%)	52	49	NS			
Hypertension (%)	39	42	NS	56	60	NS
Obesity (%)	55	61	NS	68	78	0.02
Serum triglycerides ≥1.7 mmol/l (%)	43	41	NS	56	57	NS
Microalbuminuria (%)†	13	10	NS	25	21	NS

Data are means ±SD or percentage. Impaired glucose regulation, FPG 6.1–6.9 mmol/l and/or 2-h PG 7.8–11.0 mmol/l; hypertension, SBP ≥140 mmHg and/or DBP ≥90 mmHg; obesity, WHR >0.90 and/or BMI >30 kg/m^2 (for men) or WHR >0.85 and/or BMI >30 kg/m^2 (for women); microalbuminuria, UAER ≥20 μg/min. *Geometric mean (95% CI); †$P < 0.01$, diabetic versus nondiabetic men or diabetic versus nondiabetic women.

between variables were assessed using Pearson's correlation coefficients adjusted for age. Factor analyses were conducted to determine risk factor clusters by diabetes status and sex using the baseline survey data. All the continuous variables considered to represent the components of the metabolic syndrome including UAER and fasting insulin were included. If there is a single underlying cause for the clustering of the risk variables, factor analyses should only identify one dominant factor. Factor analysis involves three procedures: *1*) extraction of the initial components, *2*) rotation of the principal components, and *3*) interpretation of the factors identified. Principal component analysis first transformed a set of correlated risk factors to a linear combination of the variables accounting for the maximum proportion of the total variance and thus formed a new set of uncorrelated components. The components with eigenvalues >1.0 were retained in the analysis. Eigenvalues are the sum of squared correlations between the original independent variables and the principal components obtained, and they represent the amount of variance attributable to the components of a factor. Each of the components is rotated to facilitate their interpretation and then referred to as factors. A varimax orthogonal rotation was used in this analysis to obtain the factors. To interpret the results from factor analyses, the pattern of factor loadings was examined to determine which original variables represent primary constituents of each factor. An absolute loading value ≥0.40 was used to interpret the resulting factor pattern (28).

Finally, based on the follow-up data, factors identified were used as independent variables in univariate and multivariate logistic regression models to determine risk factor clusters predicting the development of diabetes adjusting for age, smoking, family history of diabetes, education, and occupation.

RESULTS — The characteristics of the nondiabetic and diabetic subjects at baseline by sex are presented in Table 1. In nondiabetic participants, men were older than women, whereas in diabetic participants, men were younger. Over one-half of both nondiabetic and diabetic men were current smokers. As expected, men had higher WHR than women. High BMI and obesity were more common in diabetic women compared with men. Women had higher fasting and 2-h insulin values and 2-h PG compared with men. SBP was higher in diabetic women than men, whereas in nondiabetic participants, mean FPG was lower in women than men. No differences in the prevalence of IGR, hypertension, high serum triglycerides (≥1.7 mmol/l), and microalbuminuria were observed between men and women. The prevalence of hypertension, obesity, high serum triglycerides (≥1.7 mmol/l), and microalbuminuria was higher in both men and women with diabetes than those without.

Factor analyses in nondiabetic participants

After adjustment for age, BMI and WHR correlated with SBP, DBP, and fasting and 2-h insulin in both men and women. Fasting and 2-h insulin correlated significantly with most other variables, especially in men. Serum cholesterol had low correlations with most other parameters. Both SBP and DBP correlated significantly with UAER in men but not in women (data not shown). The factor patterns were consistent in analyses between men and women (Table 2 and Fig. 2). There were four factors determined with eigenvalues >1, which accounted for 59% of the variance in the original vari-

Table 2—*Factor loadings for original variables with rotated factors by diabetes status and sex at baseline*

	Men								Women							
	Nondiabetic				Diabetic				Nondiabetic				Diabetic			
	Factor 1	Factor 2	Factor 3	Factor 4	Factor 1	Factor 2	Factor 3	Factor 4	Factor 1	Factor 2	Factor 3	Factor 4	Factor 1	Factor 2	Factor 3	Factor 4
BMI	**0.657**	0.170	0.1000	0.007	0.121	−0.101	**0.637**	0.242	**0.702**	0.112	0.096	0.143	0.160	−0.156	**0.602**	0.214
WHR	**0.662**	0.227	0.029	0.011	0.032	0.087	**0.778**	−0.052	**0.761**	0.073	0.000	0.033	0.016	0.064	**0.755**	−0.002
SBP	−0.003	**0.811**	0.243	−0.152	**0.855**	0.032	0.180	0.049	0.248	**0.778**	0.185	0.261	**0.856**	0.013	0.102	0.057
DBP	0.224	**0.768**	0.128	0.011	**0.853**	−0.012	−0.020	0.071	0.182	**0.735**	0.207	0.298	**0.858**	0.08	−0.042	0.047
UAER*	0.210	0.299	−0.173	0.272	0.390	**0.534**	0.009	0.052	−0.014	0.263	−0.085	−0.279	0.372	**0.417**	0.097	−0.025
Total cholesterol	−0.180	−0.030	0.146	**0.771**	0.200	0.305	0.185	**0.411**	0.026	−0.032	0.105	**0.757**	0.241	0.331	0.162	**0.482**
Triglycerdies*	0.276	0.016	0.024	**0.654**	−0.019	**0.482**	0.344	−0.066	0.080	0.130	−0.036	**0.665**	0.017	0.349	**0.436**	−0.125
Fasting insulin*	**0.676**	0.078	−0.031	0.241	0.086	0.072	**0.445**	**0.667**	**0.649**	0.098	0.183	−0.038	0.057	0.062	**0.413**	**0.598**
2-h postload insulin*	0.256	0.186	**0.630**	0.378	0.008	−0.048	−0.144	**0.856**	0.278	−0.060	**0.738**	0.028	0.013	−0.021	−0.141	**0.812**
FPG	**0.563**	−0.184	**0.419**	−0.203	−0.108	**0.613**	−0.164	−0.137	0.062	0.287	**0.434**	−0.228	−0.085	**0.731**	−0.095	−0.109
2-h PG	−0.006	0.130	**0.885**	0.045	0.022	**0.727**	0.029	0.215	−0.003	0.119	**0.773**	0.197	0.052	**0.780**	0.012	0.184
Variance	17.4%	15.2%	13.6%	12.4%	17.3%	15.8%	14.6%	13.3%	15.2%	14.6%	13.4%	12.4%	15.5%	14.3%	13.0%	12.3%

Loadings ≥0.40 in bold type; *log-transformed values.

ables in men and for 56% in women. Factor loadings after varimax rotation showed that the first factor correlated with BMI, WHR, and fasting insulin levels, the second factor with SBP and DBP, the third factor with FPG, 2-h PG, and 2-h insulin, and the fourth factor with serum cholesterol and triglycerides. In men, FPG also loaded on the first factor. These four factors were interpreted as obesity/insulin resistance, blood pressure, glucose/2-h insulin, and lipid factor, respectively.

Factor analyses in diabetic participants

Although most correlations were similar in nondiabetic and diabetic subjects, some differences were noted. UAER correlated with FPG and 2-h PG in diabetic but not in nondiabetic men and women. Serum cholesterol and triglycerides correlated strongly with 2-h PG in both diabetic men and women. No significant correlations were found between insulin and glucose in diabetic men and women (data not shown). There were also four factors determined with eigenvalues >1 that accounted for 61% of the variance in the original variables in men and 55% in women. The factor patterns showed some differences in separate analysis among men and women compared with the nondiabetic group (Table 2 and Fig. 2). On the first factor, SBP and DBP had positive loadings. On the second factor, UAER, FPG, and 2-h PG had strong loadings both in men and women, whereas triglycerides loaded on this factor in men also (loading = 0.482). On the third factor, WHR, BMI, and fasting insulin had positive loadings in both men and women, whereas triglycerides also were linked to this factor in women. On the fourth factor, fasting and 2-h insulin and cholesterol had positive loadings in both sexes. These four factors were interpreted as blood pressure, glucose, obesity/insulin resistance, and insulin factor, respectively.

Table 3 shows the results of logistic regression models when factors obtained from factor analyses were analyzed as independent variables for predicting the development of diabetes during the 5-year follow-up. Among 272 men who were originally nondiabetic and who participated in the follow-up study, both obesity/insulin resistance and glucose/2-h insulin factors were significantly associated with future diabetes in univariate lo-

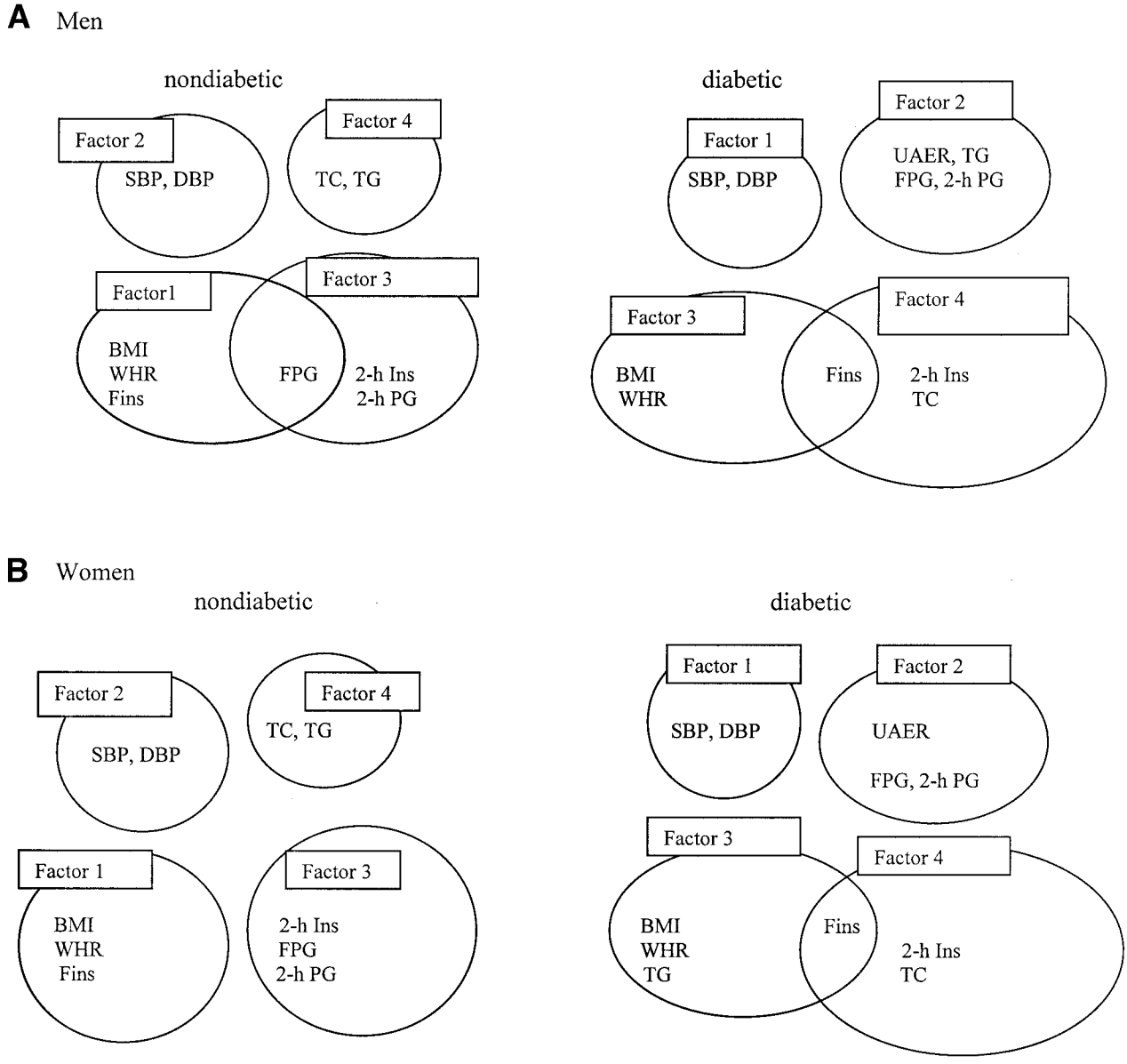

Figure 2—*Clusters of the risk variables of the metabolic syndrome in men* (A) *and women* (B) *with and without diabetes. TC, total cholesterol; TG, triglycerides; Fins, fasting insulin; 2-h Ins, 2-h postload insulin.*

gistic regression analysis with odds ratio (OR) 1.67 (95% CI 1.18–2.37) and 2.58 (1.74–3.81), respectively. Neither blood pressure factor nor lipid factor significantly predicted the development of diabetes (1.26 [0.91–1.74] and 1.17 [0.83–1.64], respectively). Multiple adjustments for age, smoking, family history of diabetes, education, and occupation did not significantly change the outcomes in these analyses. Among 287 women without diabetes at baseline, the OR in univariate model for obesity/insulin-resistance factor was 1.50 (1.08–2.07). Blood pressure factor had a significant association with risk of developing diabetes in univariate logistic regression model (1.39 [1.03–1.88]), but this association was no longer significant after adjustment for age, smoking, family history of diabetes, education, and occupation. Glucose/2-h insulin factor in the univariate analysis was associated with the progression to diabetes (1.67 [1.20–2.31]). Similar to the male subjects, lipid factor was not significantly associated with the prediction of diabetes (1.13 [0.84–1.54]). No significant changes in ORs for other factors were found in the adjusted model except the blood pressure factor.

CONCLUSIONS — To our knowledge, this is the first application of factor analysis to describe the clustering of the disorders characterizing the metabolic syndrome among nondiabetic and diabetic individuals in a Chinese population. This study is characterized by introducing a capillary glucose prescreening before the application of an OGTT at baseline. This selection procedure has two advantages. First, the yield of abnormal glucose

Table 3—*OR (95% CI) for factors by factor analyses to predict the development of diabetes during 5-year follow-up in 272 nondiabetic men and 287 nondiabetic women at baseline*

	Univariate			Adjusted*		
	OR	95% CI	*P*	OR	95% CI	*P*
Men (n = 272)						
Obesity/insulin resistance	1.67	1.18–2.37	0.004	1.78	1.20–2.61	0.004
Blood pressure	1.26	0.91–1.74	0.17	1.36	0.90–2.05	0.144
Glucose/2-h insulin	2.58	1.74–3.81	<0.001	2.84	1.84–4.39	<0.001
Lipids	1.17	0.83–1.64	0.365	1.10	0.77–1.57	0.589
Women (n = 287)						
Obesity/insulin resistance factor	1.50	1.08–2.07	0.016	1.51	1.05–2.18	0.026
Blood pressure factor	1.39	1.03–1.88	0.029	1.31	0.90–1.89	0.157
Glucose/2-h insulin factor	1.67	1.20–2.31	0.002	1.68	1.19–2.39	0.004
Lipid factor	1.13	0.84–1.54	0.403	1.17	0.84–1.65	0.339

*Adjusted for age, smoking, family history of diabetes, education, and occupation.

tolerance at OGTT can be maximized in a large population survey. Second, the follow-up study may be more efficient because more high-risk cases can be included at baseline only at cost of missing a small number of individuals with diabetes or IGT (25). Therefore, the study sample in this study represents a population-based high-risk segment identified by raised postprandial glucose. In keeping with results from the Insulin Resistance Atherosclerosis Study (12), this study also showed that the subjects with NGT had similar factor patterns to those with IGR (data not shown).

Factor analysis can reveal underlying patterns or structures among variables showing high degrees of intercorrelation. If an analysis reveals only one underlying factor, this may be interpreted as supporting the unity hypothesis—that one unifying physiology (perhaps insulin resistance) underlies and accounts for the metabolic risk variable clustering. Finding more than one factor contradicts the unity hypothesis (13). Insulin resistance has been proposed as the underlying pathophysiological mechanism of the metabolic syndrome (7). Fasting insulin, used in our study, is a marker for insulin resistance in individuals with and without diabetes (6). The present factor analyses did not, however, identify a single factor only but identified a total of four factors that resulted in the clustering of the basic risk variables. These results suggest that insulin resistance alone does not underlie all features of the metabolic syndrome and that more than one pathophysiological mechanism are present for the full expression of the metabolic syndrome among the Chinese population. Similar findings have been shown in a Korean population in whom obesity clustered with fasting insulin levels and the blood pressure factor was independent of other factors (18). Also in several populations, an independent blood pressure factor has been identified (12,14–16).

Although the factor patterns were consistent in the analyses among men and women separately, there was a remarkable contrast in the patterns between the subjects with and without diabetes. Among diabetic subjects, blood pressure was the most important factor and UAER was linked with glucose factor. As expected, the prevalence of microalbuminuria was higher in diabetic than nondiabetic subjects. Previous studies have shown that microalbuminuria in nondiabetic subjects was associated with atherosclerotic risk factors (29–31) and suggested that microalbuminuria might be a feature of the metabolic syndrome (1,32,33). Nevertheless, it is still controversial whether microalbuminuria is a marker for this syndrome or merely a complication of hypertension or diabetes (34). The majority of these studies have been performed in Caucasians (31,35), and only few data exist from Asian populations (29,36). One factor analysis study identified microalbuminuria as an independent factor among nondiabetic subjects (21), but another study did not (12). Our results imply that in the Chinese population, microalbuminuria is most likely to be a complication of hyperglycemia rather than a marker of the metabolic syndrome.

Regarding multifactorial diseases, it has been the epidemiologist's convention to consider the independent weight of each risk factor in turn by multivariate analysis, thus also adjusting for bias introduced by confounding variables. Such an approach, however, fails to take into account the manner in which related factors may confer the risk in concert and obscures attempts to gain understanding about the factors (15). Because factor analysis reduces a large number of correlated variables to fewer uncorrelated factors, it can address some of these challenges. So far, there are only two studies relating the clustering of risk factors for the metabolic syndrome to incident diabetes using factor analysis (21,22). However, these studies did not analyze the data separately by sex, and the Pima Indian study did not include UAER among the variables. The present study showed that glucose/2-h insulin and obesity/insulin-resistance factor are strong risk factors for type 2 diabetes, whereas blood pressure factor and lipid factor were not associated with the development of diabetes. This implies that different physiological processes associated with various components of the metabolic syndrome contain unique information about the diabetes risk in the Chinese population.

In summary, factor analysis revealed consistent clusters of variables that were different in nondiabetic and diabetic subjects in the Chinese population. UAER was associated with glucose factor in diabetic subjects. Blood pressure was not linked with insulin resistance. Obesity and glucose/insulin factor were the strongest predictors of type 2 diabetes. These findings suggest that insulin resistance is not the single unifying factor for the clustering of the components of the metabolic syndrome. Different physiological processes associated with various components of the metabolic syndrome contain unique information about diabetes risk. Microalbunuria is more likely to be a complication of the type 2 diabetes or hypertension than a marker of the metabolic syndrome.

Acknowledgments— This work was supported by a grant from the Bureau of Public Health of Beijing, the Preventive and Treatment Office of Beijing, and the Academy of Finland (46558, 77618, 204274, and 205657).

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