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An Examination of Sex and Racial/Ethnic Differences in the Metabolic Syndrome among Adults: A Confirmatory Factor Analysis and a Resulting Continuous Severity Score

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Abstract

Objective—The metabolic syndrome (MetS) is typically diagnosed based on abnormalities in specific clustered clinical measures that are associated with increased risk for coronary heart disease (CHD) and Type 2 diabetes mellitus (T2DM). However, current MetS criteria result in racial/ethnic discrepancies. Our goals were to use confirmatory factor analysis (CFA) to delineate differential contributions to MetS by sub-group, and if contributions were discovered, develop sex and racial/ethnic-specific equations to calculate MetS severity.

Research Design and Methods—Using data on adults from the National Health and Nutrition Examination Survey 1999–2010, we performed a CFA of a single MetS factor that allowed differential loadings across groups, resulting in a sex and race/ethnicity-specific continuous MetS severity score.

Results—Loadings to the single MetS factor differed by sub-group for each MetS component ($p < 0.001$), with lower factor loadings among non-Hispanic-blacks for triglycerides and among Hispanics for waist circumference. Systolic blood pressure exhibited low factor loadings among all groups. MetS severity scores were correlated with biomarkers of future disease (high-sensitivity C-reactive-protein, uric acid, insulin resistance). Non-Hispanic-black-males with diabetes had a low prevalence of MetS but high MetS severity scores that were not significantly different from other racial/ethnic groups.

Conclusions—This analysis among adults uniquely demonstrated differences between sexes and racial/ethnic groups regarding contributions of traditional MetS components to an assumed

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single factor. The resulting equations provide a clinically-accessible and interpretable continuous measure of MetS for potential use in identifying adults at higher risk for MetS-related diseases and following changes within individuals over time. These equations hold potential to be a powerful new outcome for use in MetS-focused research and interventions.

Keywords

Metabolic syndrome; Racial/ethnic differences; Epidemiology; Clinical studies; Obesity; Insulin resistance; Risk factors

Introduction

With rising rates of cardiovascular disease (CVD) and type 2 diabetes mellitus (T2DM), there has been significant focus on risk prediction. One way clinicians can identify individuals at higher risk for disease progression is by assessing for the metabolic syndrome (MetS)[1,2], a cluster of cardiovascular risk factors that is associated with insulin resistance [1,3] and that correlates with underlying inflammation [4–7] and oxidative stress [7–11]—additional risk factors for CVD and T2DM. Compared to those without MetS, individuals who are classified as having MetS and followed for 10 years have an odds ratio of 1.2–1.8 for progressing to CVD [12,13] and 4.1 for progressing to T2DM [14], demonstrating its utility as a clinical tool.

Nevertheless, there are significant racial/ethnic differences in MetS that limit its use over time [15–18]. Non-Hispanic blacks have a low prevalence of MetS despite having more insulin resistance, more T2DM and more death from CVD than non-Hispanic whites [17–23]. The binary nature of MetS may contribute to these observed racial/ethnic differences, as it requires extreme values (e.g., triglycerides greater than 150 mg/dL or HDL less than 40 mg/dL for males) that may not be appropriate for all groups, particularly if certain groups have on average lower values of any of the components of MetS (e.g., lower triglyceride levels among non-Hispanic blacks) [24]. Furthermore, a binary MetS classification makes it difficult to follow for a worsening condition over time. Because of this, some have advocated for continuous scores for MetS [25]. The majority of these scores have been composed of a sum of z-scores of the various components of MetS (blood pressure, waist circumference [WC], etc.) [26–28]. This approach does not take into account weighting of how these components correlate together as a manifestation of the processes underlying MetS, nor do they take into account that such weighting may vary by sex or race/ethnicity [29–31].

Our goal was to examine the differences between sexes and among racial/ethnic groups with respect to how the traditional MetS components correlate with a single MetS — “factor” via a confirmatory factor analysis, utilizing data from adults in the National Health and Nutrition Examination Survey (NHANES). Rather than explore whether or not there are multiple factors or examine whether additional components should be added to MetS, we instead operated under the framework that a single metabolic syndrome exists and is made up of the components utilized in common definitions such as the Adult Treatment Panel III (ATP-III) [1,32]— namely WC, systolic blood pressure (SBP), triglycerides, HDL-

cholesterol, and fasting blood glucose. Such a statistical exploration then would not only allow for an examination of sex- and racial/ethnic differences in how these components correlate with the hypothesized single MetS factor, but it also would take into account any observed differences in producing a continuous MetS score from this analysis – thus providing in essence a sex- and race/ethnicity-specific risk or severity score that can followed over time in individuals either clinically or in research settings. Our hypothesis was that the contribution of MetS components to such a factor would vary by sex and race/ethnicity in a way that could improve on correlations between MetS and clinically-relevant measures related to insulin resistance, CVD risk and disease diagnosis.

Methods

Data were obtained from NHANES (1999–2010), a complex, multistage probability sample of the US population [33]. These annual cross-sectional surveys are conducted by the National Center for Health Statistics (NCHS) of the Centers for Disease Control (CDC), with randomly-selected subjects undergoing anthropometric and blood pressure measurements, answering questionnaires and undergoing phlebotomy. The NCHS ethics review board reviewed and approved the survey and participants gave informed consent prior to participation. WC, SBP, and laboratory measures of triglycerides, HDL-cholesterol, and fasting glucose were obtained using standardized protocols and calibrated equipment [33]. For SBP, the mean of up to four readings taken on each individual was used. All blood samples used for analyses were obtained following a fast 8 hours prior to the blood draw.

Data from non-Hispanic-white, non-Hispanic-black, or Hispanic (Mexican-American/other Hispanic) participants 20–64 years old were analyzed. For the initial confirmatory factor analysis described below, participants were excluded if they were pregnant, had known diabetes or unknown diabetes (fasting plasma glucose >125 mg/dL), or were taking antihyperlipidemic or anti-diabetic medications all of these situations all likely to alter lipid and insulin levels. For the confirmatory factor analysis, individuals who reported having congestive heart failure (CHF) or coronary heart disease (CHD), or ever having had a myocardial infarction (MI) or a stroke, were also excluded.

We combined all data sets from the 6 two-year cycles (1999–2010) for statistical analyses to increase sample size. Prevalence rates of MetS were calculated by sex, race/ethnicity, and age group, according to ATP III criteria [1], and mean levels (95% CI's) of the MetS components of interest (WC, SBP, HDL, triglycerides, and glucose) as well as the surrogate outcomes (hsCRP, uric acid, homeostasis model of insulin resistance [HOMA-IR][3]) were calculated by sex, race/ethnicity, and age group.

The general methods for the formulation of this score have been reported previously [29]. The previous study [29] found racial/ethnic as well as sex differences in the how traditional components are correlated with MetS, among adolescents ages 12–19. We felt it essential to validate these findings and examine if similar differences were found among adults, when MetS and its ability to predict future disease is more relevant. In addition, the previous study [29] used BMI z-scores as a measure of obesity, as in children and adolescents it is essential to use relative measures of obesity, and no precise z-score/percentile calculation is available

for waist circumference (WC). In adults, no such relative measure is necessary, and waist circumference is a better measure of central obesity that correlates well with insulin resistance [1,26,32]. Therefore, a series of confirmatory factor analyses were performed on the five identified MetS components in adults: WC, SBP, HDL, triglycerides, and glucose. We selected these five components exclusively because of their inclusion in the most prominently used MetS criteria [1,26,32] and due to their clinical accessibility. With such a factor analysis, both SBP and diastolic blood pressure should not be included together, as the two are highly correlated with each other [34]. We chose SBP given it is more strongly associated with insulin resistance [35] and other outcomes [36]. Triglycerides were log-transformed, and all variables were standardized (mean=0, SD=1) over the entire sample. The inverse of HDL was used when standardizing, so a higher factor loading score would be similar in interpretation to the other measures in the model. The variables were not standardized within groups to allow for potential overall higher standardized scores within individual sex- and race/ethnic-specific groups. A one-factor model formed the basis of all confirmatory factor analyses performed; measurement errors between the five components were assumed not to be correlated. The factor loadings were of interest, indicating the magnitude of association between each component and the underlying “MetS” factor. Factor loadings >0.4 were considered clinically meaningful.

Using PROC CALIS in SAS, the parameters of the confirmatory factor analyses were estimated via maximum likelihood. Two multi-group one-factor confirmatory factor analyses were fit:

1. Model 1: constrained the factor loadings to be equal across the six combinations of sex and race/ethnicity;
2. Model 2: allowed the factor loadings to vary across the six groups.

Chi-square tests of the equality of the factor loadings across the six groups in Model 2 were performed. The two models were compared using various fit statistics, both overall and by group. Chi-square and Akaike's Information Criteria (AIC) were used for model comparisons; smaller chi-square and AIC values indicated a better fit. A chi-square difference test was calculated; a significant difference between two nested models implies that the model with more paths explains the data better [37]. Other goodness of fit indices included the Root Mean Square Error of Approximation (RMSEA; >0.06 indicates a poor fit), the Standardized Root Mean Square Residual (SRMR; >0.08 poor fit), the Goodness of Fit Index (GFI; <0.90 poor fit), and the Bentler-Bonett Normed Fit Index (NFI; <0.90 poor fit)[38]. A final model was chosen among the two based on an examination of the model fits.

The standardized factor coefficients from the final chosen model were used to calculate the MetS factor score on each individual. This score can be interpreted as a Z-score (mean 0, SD=1), with higher scores representing an increased risk, or severity, of MetS. Receiver operating characteristic (ROC) analysis was used to assess the ability of this new score to discriminate against the traditional ATP-III definition of MetS. Overall predictive performance was measured by the area under the curve (AUC) of the ROC curve, with 0.5 and 1.0 indicating no and perfect predictive ability, respectively. We considered AUC values

>0.90 to be very accurate. We expected high values, particularly since we were validating this continuous score on the same data set from which it was derived, but it was important to ensure that this score could be viewed as a continuous representation of the traditional metabolic syndrome. Given our hypothesis of sex and racial/ethnic differences, we did not expect perfect ($AUC \approx 1.0$) ability of a new severity score to predict traditional MetS that does not allow for these differences.

The resulting equations could then be used to calculate a MetS score on a more expansive set of individuals – including those who reported having any of the aforementioned conditions that led to their exclusion in the series of confirmatory factor analyses (T2DM, CHD, CHF, MI, stroke). On this larger set of individuals, excluding only individuals with “extreme” MetS scores (<-5 or >5), we examined the relationship between the resulting MetS score and surrogate markers of disease risk, including hsCRP, uric acid and HOMA-IR. To do this, a series of linear regressions were fit, using a natural log transformation for hsCRP and HOMA-IR. We did this from both the Model 1 severity score—in effect a continuous version of traditional MetS that does not account for sex and/or racial/ethnic differences—as well as from the factor analysis that does account for these differences. In addition, we estimated mean severity scores from both models among NHANES participants reported to have diabetes, and compared these mean scores across groups (sex and race/ethnicity) while adjusting for highest level of household education and income-to-poverty ratio. Along with reporting prevalences of traditional MetS across these groups, this first validation provides insight into the magnitude of the benefit of accounting for sex and racial/ethnic differences while producing a MetS severity score.

Statistical significance was defined as a p -value < 0.05 . Statistical analysis was performed using SAS (version 9.3, Cary, NC). Descriptive statistics and all linear regressions as well as mean MetS score comparisons used SAS survey procedures (SURVEYMEANS, SURVEYFREQ, SURVEYREG), which accounts for the survey design when estimating standard errors to obtain population-based estimates. The confirmatory factor analysis itself did not account for the survey design due to the inability of standard software to perform multigroup confirmatory factor analyses within subpopulations while also accounting for the survey design.

Results

The sample of participants utilized in the series of confirmatory factor analyses consisted of 6,870 male and female non-Hispanic blacks, non-Hispanic whites, and Hispanics age 20–64 years old with complete data for MetS components (Supplementary Table 1). The overall prevalence of MetS in this sample was 25.8% according to ATP-III criteria [1]. The prevalence of ATP-III-based MetS was considerably lower among non-Hispanic-black males.

In performing confirmatory factor analysis of MetS components in this sample we generated two models with increasingly better fit of the data (Model 1 and Model 2; Table 1). Model 2 allowed factor loading of the individual components of MetS to vary by race/ethnicity and sex, providing substantial improvements in fit compared to Model 1, both overall and by

group. Because SBP presented with factor loadings below 0.40 (particularly among males), an additional model was performed without SBP as a component; this provided the best fit in terms of chi-square and AIC (data not shown). However, for the remainder of the analysis the severity score generated from Model 2 was used because of its consistency with traditional MetS definitions that include SBP, because the loadings for SBP were close to being meaningful for females, and because the Model 2 MetS scores fit the outcomes-based data (reported subsequently) slightly better than the model without SBP. There were notable differences in the magnitude of factor loadings among the six sex and ethnic groups. Most notably, WC had lower factor loadings among Hispanic males and females, indicating that WC is less correlated with MetS among Hispanic individuals. In addition, among both males and females, non-Hispanic blacks had lower loadings for triglycerides compared to non-Hispanic whites and Hispanics. HDL appeared to be more correlated with MetS among males overall compared to females, and glucose was only a meaningful component (factor loadings > 0.40) for females. SBP loadings were less than 0.40 for all groups, but were above 0.30 for females.

The resulting equations from Model 2 can be viewed as a continuous version of the traditional MetS criteria while also accounting for sex and racial/ethnic differences. Equations based on the factor coefficients from Model 2 are presented in Table 2, and can be used to calculate what is called a MetS severity score based on the clinically-used components of MetS. For ease of clinical use, these equations are based on the actual values of the variables and not the standardized measures that went into the factor analysis; they were derived by back-transforming the coefficients that resulted from the standardized factor analysis.

ROC analysis of the Model 2 risk score among our validation data set (removing many of the exclusions used to develop the score itself) demonstrated excellent ability to predict a traditional MetS classification (AUC values = 0.93 for racial/ethnic groups; figures not shown). However, these values are not particularly close to 1, which is to be expected if the severity score accounting for sex and racial/ethnic differences is an improvement over the traditional MetS criteria. For cross-sectional age, Model 2 severity scores exhibited a statistically significant albeit modest linear increase for each race/ethnicity (R^2 values between 0.06 and 0.15; Table 3). Severity score values were significantly correlated with $\ln(\text{hsCRP})$, uric acid, and $\ln(\text{HOMA-IR})$ (Figure 1; Table 3), with lower R^2 values for $\ln(\text{hsCRP})$ and for uric acid among Hispanics (Table 3).

Because MetS is strongly associated with risk for diabetes, we next evaluated the the MetS status of NHANES participants reported to have diabetes—a group that was excluded from formulation of the MetS severity score. Figure 2A displays the prevalence of traditionally-defined MetS among NHANES participants with diabetes. A significantly ($p < 0.05$) lower rate of MetS was observed among NHB males in this subgroup. Figure 2B confirms this result: mean Model 1 scores among participants with diabetes were significantly lower among NHB participants (males and females), accounting for any confounding influence of household education and income. Males with diabetes also had significantly higher overall mean Model 1 scores compared to females. In contrast, the severity score from Model 2 that

accounts for sex and racial/ethnic differences was not observed to be significantly different among diabetics across racial/ethnic groups (Figure 2C).

Discussion

We report here a comprehensive analysis showing that under the assumption of a single MetS factor, the components that make up the traditional MetS definition are correlated differently according to sex and race/ethnicity. This analysis allows for the utilization of a continuous MetS severity score that is tailored to how MetS is manifest among particular sex- and racial/ethnic groups. While racial/ethnic differences have long been noted in individual components of MetS [17,24] and while a classification of MetS has been shown to more poorly predict disease risk factors among non-Hispanic blacks [3,4,8,39], to our knowledge this represents the first MetS scoring system among adults that differentiates by sex and race/ethnicity based on the unique contribution of individual MetS components to their underlying MetS factor. Prior confirmatory factor analyses by race/ethnicity failed to demonstrate inter-ethnicity differences, potentially because of less statistical power [30,35]. Our analysis confirms inter-group variation that had been suggested by differences in the prevalence of certain risk factors by sub-group, with early indication that these inter-ethnicity differences may have clinical importance for risk identification related to the degree of metabolic derangement. This analysis of adults confirms our previous work in adolescents [29], but we also observed more pronounced inter-ethnicity and sex differences that we did not see previously in children. Most notably, when using an improved measure of central obesity, waist circumference, significant differences were observed in the correlation between this measure and the underlying single MetS factor that were not seen in adolescents. Central obesity as measured by WC was far less correlated with the MetS factor for Hispanics, but was strongly correlated for NHB and NHW participants, females in particular. In addition, glucose was found to be associated with this MetS factor, as expected, but was not found to be associated with a MetS factor in adolescents [29]. Moreover, this association in adults was strongest among females. Overall, however, we noted similar factor loadings for MetS components for the adult and adolescent scores, suggesting stability in how these components cluster over the lifespan by sex and race/ethnicity.

A major drawback to the use of the traditional MetS criteria clinically has been that individuals may be labeled as low-risk despite having component measurements with broad elevations that were just shy of cut-off values to classify the individual as having MetS. Several previous continuous risk scores have tried to mitigate this disadvantage by summing z-scores for the individual components [26–28], but failed to take into account 1) that the components may differ in their involvement in processes underlying MetS and 2) that some components (most notably triglycerides among non-Hispanic blacks) vary significantly by race/ethnicity making the degree of associated risk unclear [24,34].

Our approach addressed these prior problems by using confirmatory factor analysis to reveal multiple differences in how the individual MetS components contributed to an overall MetS score by racial/ethnic group—potentially revealing variations in how MetS is manifest in each group. While HDL-cholesterol had high factor loadings overall—particularly among

males—non-Hispanic-black females exhibited lower factor loadings for HDL. Triglycerides also had high factor loadings overall except among non-Hispanic-black males and females. These inter-ethnicity differences in factor loadings for lipids are notable given that compared to other racial/ethnic groups non-Hispanic blacks exhibit lower rates of HDL suppression [17] and lower levels of triglycerides at baseline and in the setting of MetS [24]. Thus, these aspects of our race/ethnicity-specific risk score may confirm previously-known differences in how MetS is manifest between racial/ethnic groups.

Factor loadings for WC also differed by race/ethnicity and sex, being lower among Hispanics and higher among women. In the case of Hispanics, it is not clear if this reflects a lower role of WC in MetS or whether the high prevalence of elevated WC in the cohort made other MetS components better at differentiating between those with further-advanced processes associated with MetS. In the case of females, the overall higher factor loadings for WC may reflect women with a higher degree of central obesity as compared to those with more subcutaneous fat depots as seen in the gynecoid body habitus [40].

SBP exhibited lower factor loadings overall than any of the other components, although in females the correlation of SBP loadings with the latent MetS factor approached what we considered to be meaningful (loadings > 0.3). These lower loadings for SBP may not be surprising given relatively high rates of essential hypertension independent of MetS [41]. Because of the low factor loadings, we generated a model omitting SBP that exhibited improved fit statistics. Nevertheless, in testing for correlations between the severity score and other surrogates of chronic disease (elevations in hsCRP, uric acid and HOMA-IR), the severity score from Model 2 (with SBP included) correlated slightly better with other risk factors than the model without SBP. Thus, SBP does not segregate as well as other components with the underlying MetS factor in the overall analysis but when included in the score itself slightly improved the score's performance in its correlating with other surrogates of chronic disease. This may indicate that BP is a risk factor that is frequently separate from MetS but which provides an additive effect on the ability of the MetS score to assess risk.

The cross-sectional nature of NHANES prevented our analysis of temporal changes in this severity score; nevertheless, we did note that progressively older individuals had higher MetS scores. This underscores the potential for this score to be used—potentially via internet site or smart phone application—to follow for worsening of metabolic disarray over time in a given individual. This intra-individual application will require validation in longitudinal cohorts, but could ultimately indicate use of this MetS score as an outcome to assess improvements in MetS in research studies.

We chose to perform this confirmatory factor analysis on a group that was relatively healthy and free from medications that could produce perturbations in MetS-related measures so as not to mask potential important relationships. In evaluating severity score levels, however, we evaluated both the full database including both healthy and diseased individuals and a sub-set of NHANES participants with diabetes. Given the dichotomous nature of traditional MetS criteria, it is challenging to compare ATP-III MetS classification to a severity score with respect to differences in sex and race/ethnicity. However, in comparing the severity score that results from Model 1, which is in effect a continuous version of the traditional

MetS criteria, we were able to show the benefit when calculating a MetS severity score of accounting for sex and race/ethnicity. Most strikingly, in a group of individuals with diabetes that would be expected to have extremely high prevalences of MetS, observed racial/ethnic differences in MetS disappeared when utilizing the Model 2 severity score.

While we have purposely avoided setting a cut-off level to stratify risk for this MetS score, we recognize that for clinical application having an empirically-determined cut-off would be important. Ideally such a cut-off would be based on longitudinal data determining thresholds of increased risk for concerning outcomes such as development of new CVD or T2DM. This type of analysis is part of our future directions.

Our study had multiple limitations, including the cross-sectional nature of the data. We assumed one latent “MetS” factor with traditional MetS components due to the large body of research dedicated to this factor [26–28,35] and the clinical accessibility of the measures involved. The additional risk factors (hsCRP, uric acid, HOMA-IR) we assessed to demonstrate racial/ethnic variations in the score have other underlying causes independent of MetS [12,14,41] and are not an ideal validation of the score’s clinical utility. However, our analysis had multiple strengths as well, including a large, representative population sample with significant representation from the three racial/ethnic groups analyzed.

In conclusion, the sex- and race/ethnicity-specific MetS severity score generated from this confirmatory factor analysis may hold clinical relevance in the manner in which MetS is manifest in each sub-group. Following validation in longitudinal cohorts, this score may be useful as a screening tool for risk identification. Even more so, however, this continuous score provides a potential means of following changes in MetS-related abnormalities in a given individual over time.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Abbreviations

AIC	Akaike’s Information Criteria
ATP-III	Adult Treatment Panel III
AUC	Area under the curve
CDC	Centers for Disease Control

CFA	Confirmatory Factor Analysis
CHD	Coronary heart disease
CHF	Congestive heart failure
CVD	Cardiovascular disease
GFI	Goodness of Fit Index
Hisp	Hispanic
HOMA-IR	Homeostasis model of insulin resistance
hsCRP	High-sensitivity C-reactive protein
MetS	Metabolic syndrome
MI	Myocardial infarction
NFI	Bentler-Bonett Normed Fit Index
NHANES	National Health and Nutrition Examination Survey
NHB	Non-Hispanic Black
NHW	Non-Hispanic White
RMSEA	Root Mean Square Error of Approximation
ROC	Receiver operating characteristic
SBP	Systolic blood pressure
SRMR	Standardized Root Mean Square Residual
T2DM	Type 2 diabetes mellitus
WC	Waist circumference

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Figure 1.

MetS Severity Score Validation Studies: Age and Associated Serum Risk Markers by Racial/Ethnic Group. Each scatter plot represents Model 2 MetS severity score for each racial/ethnic group for each of the following analyses: A: correlation with cross-sectional age; B: correlation with ln(HOMA); C: correlation with ln(hsCRP); D: correlation with uric acid. See Table 3 for R^2 values by sex and racial/ethnic group. Abbreviations: high-sensitivity C-reactive protein: hsCRP; HOMA: homeostasis model of insulin resistance.

Figure 2.

ATP-III MetS Prevalence and MetS Severity Score Levels Among Participants with Diabetes. Data shown are by sex- and racial/ethnic subgroup among NHANES participants with diabetes: (A) Prevalence of ATP-III MetS; (B) Model 1 score (i.e., without racial/ethnic specificity); (C) Model 2 MetS severity score (accounting for sex and racial/ethnic differences). Mean model scores presented are estimated from linear models that adjust for highest household education and household income (values presented for those with a highest household education = high school and an income-to-poverty ratio value of 2).

Confirmatory Factor Analysis Results (Adults age 20–64, n = 6,870) *

Model Fit Indices	Model 1					Model 2				
	Males			Females		Males			Females	
	Overall	NHW	NHB	Hisp	NHW	NHB	Hisp	NHW	NHB	Hisp
Chi-square (df)	1498.4 (80)									
Akaike's Information Criteria (AIC)	1518.4									
Root Mean Square Error of Approximation (RMSEA)	0.125									
Standardized Root Mean Square Residual (SRMR)	0.134	0.131	0.132	0.170	0.089	0.162	0.133	0.075	0.069	0.080
Goodness of Fit Index (GFI)	0.917	0.921	0.902	0.896	0.944	0.869	0.931	0.952	0.957	0.950
Bentler-Bonett Normed Fit Index (NFI)	0.649	0.661	0.444	0.552	0.803	0.322	0.722	0.817	0.785	0.792
Factor Loadings								p-value		
Waist Circumference			0.57					0.49	0.67	0.36
SBP			0.26					0.17	0.16	0.19
HDL			0.54					0.60	0.64	0.57
Triglycerides			0.59					0.73	0.45	0.70
Glucose			0.38					0.26	0.37	0.27

* Model 1: Single factor, loadings constrained to be equal across all six sex-race/ethnicity groups

Model 2: Single factor, loadings allowed to vary across all six groups

Chi-square test (5 df) p-value of the equivalency of the factor loadings across the six groups
**:

NHW = Non-Hispanic White; NHB = Non-Hispanic Black; Hisp = Hispanic

Table 2
Equations for New Sex and Race/Ethnic-Specific Metabolic Syndrome Risk Z-Score using Model 2.

Males	
Non-Hispanic White	$= -5.4559 + 0.0125 * \text{Waist Circumference} - 0.0251 * \text{HDL} + 0.0047 * \text{SBP} + 0.8244 * \ln(\text{Tri}) + 0.0106 * \text{Glu}$
Non-Hispanic Black	$= -6.3767 + 0.0232 * \text{Waist Circumference} - 0.0175 * \text{HDL} + 0.0040 * \text{SBP} + 0.5400 * \ln(\text{Tri}) + 0.0203 * \text{Glu}$
Hispanic	$= -5.5541 + 0.0135 * \text{Waist Circumference} - 0.0278 * \text{HDL} + 0.0054 * \text{SBP} + 0.8340 * \ln(\text{Tri}) + 0.0105 * \text{Glu}$
Females	
Non-Hispanic White	$= -7.2591 + 0.0254 * \text{Waist Circumference} - 0.0120 * \text{HDL} + 0.0075 * \text{SBP} + 0.5800 * \ln(\text{Tri}) + 0.0203 * \text{Glu}$
Non-Hispanic Black	$= -7.1913 + 0.0304 * \text{Waist Circumference} - 0.0095 * \text{HDL} + 0.0054 * \text{SBP} + 0.4455 * \ln(\text{Tri}) + 0.0225 * \text{Glu}$
Hispanic	$= -7.7641 + 0.0162 * \text{Waist Circumference} - 0.0157 * \text{HDL} + 0.0084 * \text{SBP} + 0.8872 * \ln(\text{Tri}) + 0.0206 * \text{Glu}$

Table 3
Linear Relationships between Metabolic Syndrome Severity Score (Model 2) ^{*} and Biomarkers of Disease ^{**}

	Model R ² Values			
	Age	CRP	HOMA	Uric Acid
Males				
Non-Hispanic White	0.04	0.11	0.39	0.06
Non-Hispanic Black	0.11	0.19	0.43	0.07
Hispanic	0.06	0.07	0.37	0.02
Females				
Non-Hispanic White	0.11	0.28	0.48	0.24
Non-Hispanic Black	0.10	0.22	0.43	0.20
Hispanic	0.15	0.17	0.35	0.07

^{*} Model 2: Metabolic syndrome severity score accounting for sex and racial/ethnic differences

^{**} See Figure 1 for overall relationships