

Distribution and cardiovascular risk correlates of hemoglobin A_{1c} in nondiabetic younger adults: the Bogalusa Heart Study

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Received 25 July 2007; accepted 9 April 2008

Abstract

Excess glycated hemoglobin (HbA_{1c}), an indicator of long-term glucose homeostasis, is recognized as a risk factor for cardiovascular (CV) disease and mortality even among persons without diabetes. However, information is scant regarding its distribution and correlates of CV risk in nondiabetic younger adults. This aspect was examined in a biracial (black-white) community-based sample of 1111 younger adults (mean age: 36.2 years; 71% white, 43% male) enrolled in the Bogalusa Heart Study. Blacks vs whites and women vs men had higher HbA_{1c} values ($P < .0001$). In bivariate analysis adjusted for age, race, sex, and smoking status, significant adverse trends were noted for body mass index, waist circumference, low-density lipoprotein cholesterol, high-density lipoprotein cholesterol (HDL-C), total cholesterol to HDL-C ratio, insulin, glucose, and homeostasis model assessment of insulin resistance across HbA_{1c} quartiles; trends were not significant for mean arterial blood pressure, triglycerides, C-reactive protein, adiponectin, and estimated glomerular filtration rate. In multivariate analysis, besides race and sex, total cholesterol to HDL-C ratio and waist circumference were independent correlates of HbA_{1c}. Furthermore, the prevalence of excess (top decile) HbA_{1c} was 1.6-fold ($P < .05$) higher among those with metabolic syndrome defined by the National Cholesterol Education Program Adult Treatment Panel III and 2.1-fold ($P < .01$) and 1.5-fold ($P < .05$) higher, respectively, among those with positive parental history of CV disease and type 2 diabetes mellitus. These findings underscore the potential value of HbA_{1c} in risk assessments of CV disease and type 2 diabetes mellitus in nondiabetic, apparently “healthy” younger adults.

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1. Introduction

That elevated levels of blood glucose are associated with excess risk of cardiovascular (CV) disease even among persons without diabetes is well recognized [1]. Glycosylated hemoglobin A_{1c} (HbA_{1c}) is an indicator of the status of glucose homeostasis over the preceding 2 to 3 months. In addition, it reflects oxidative stress and protein glycation of tissues including the vasculature [2]. Compared with fasting glucose, it has less intraindividual variation and tracks well over time [3,4]. Furthermore, measurement of HbA_{1c} is simple to perform and inexpensive, and does not require overnight fasting. Therefore, HbA_{1c} is considered useful as a measure of dysglycemia and related risk in population studies [5].

Although normative distribution of HbA_{1c} and its correlates of CV risk have been described for pediatric [6], and middle- and older-aged groups [7], such data for the US nondiabetic black and white younger adults are scant. The present study examines this aspect as part of the Bogalusa Heart Study, a biracial (black-white) community-based investigation of the early natural history of CV disease [8].

2. Methods

2.1. Study population

Individuals ($n = 1203$) aged 24 to 43 years, residing in the biracial (65% white, 35% black) community of Bogalusa, LA, were examined in 2000 to 2001 as part of long-term cohort follow-up study. Diabetic individuals ($n = 70$) with fasting glucose levels greater than 125 mg/dL, with HbA_{1c} levels greater than or equal to 7%, or on medications for diabetes were excluded from the study. Individuals ($n = 4$) with C-reactive protein (CRP) levels greater than 10 mg/L

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were also excluded to minimize the effect of any acute infection. These exclusions along with nonfasting status resulted in 1111 fasting individuals (mean age: 36.2 years; 71% white, 43% male) who had data on HbA_{1c} along with other variables of metabolic syndrome for the study. The Institutional Review Board of the Tulane University Health Sciences Center approved this study. All participants gave their informed consent.

2.2. General examination

Subjects were instructed to fast for 12 hours before the screening, with compliance ascertained by an interview on the day of examination. Standardized protocols were used by trained examiners. All measurements were made in replicate, and mean values were used. Height and weight were measured to calculate body mass index (BMI; weight in kilograms divided by the square of height in meters) as a measure of overall adiposity. Waist circumference was measured as an indicator of abdominal visceral fat. Blood pressure measurements were obtained on the right arm of the subjects in a relaxed, sitting position. Systolic and diastolic blood pressures were measured using a mercury sphygmomanometer. Blood pressure levels were reported as the mean of 6 replicate readings taken by each of 2 randomly assigned examiners. Mean arterial pressure (MAP), calculated as diastolic blood pressure plus one third of the pulse pressure, was used in the analysis.

2.3. Laboratory analyses

Cholesterol and triglycerides (TG) levels in the serum were assayed using enzymatic procedures on a Hitachi 902 Automatic Analyzer (Roche Diagnostics, Indianapolis, IN). Serum lipoprotein cholesterol levels were analyzed by a combination of heparin-calcium precipitation and agar-agarose gel electrophoresis procedures [9]. The laboratory is being monitored for the precision and accuracy of lipid measurements by the Lipid Standardization and Surveillance Program of the Centers for Disease Control and Prevention (Atlanta, GA). A commercial radioimmunoassay kit was used for measuring plasma immunoreactive insulin levels (Phadebas; Pharmacia Diagnostics, Piscataway, NJ); adiponectin levels were measured by radioimmunoassay (Linco Research, St Charles, MO). Glucose and creatinine levels were measured as part of a multiple chemistry profile (SMA20) with the multichannel Olympus Au-5000 analyzer (Olympus, Lake Success, NY). Plasma high-sensitivity CRP was measured by latex particle-enhanced immunoturbidimetric assay on a Hitachi 902 Automatic Analyzer; HbA_{1c} in whole blood was measured by turbidimetric immunoinhibition assay on a Hitachi 902 Automatic Analyzer (Tinaquant, Roche Diagnostics). Insulin resistance status was assessed as homeostasis model assessment of insulin resistance (HOMA-IR) according to the formula described previously [10]: [insulin (in microunits per milliliter) × glucose (in millimoles per liter)/22.5]. The estimated glomerular

filtration rate (EGFR) was assessed by a reexpressed 4-variable Modification of Diet in Renal Disease study equation [11]: $EGFR \text{ (in milliliters per minute per } 1.73 \text{ m}^2) = 175 \times (\text{serum creatinine in milligrams per deciliter})^{-1.154} \times \text{age}^{-0.203} (\times 0.742 \text{ if female}) (\times 1.21 \text{ if black})$. On the basis of 10% blind duplicate determinations of study sample, intraclass correlation coefficient of reliability was 0.98 for HbA_{1c}; thus, reported measurements reflected 98% of the (true) interindividual variability among this study cohort.

2.4. Statistical analysis

All statistical analyses were performed with SAS version 9.1 (SAS Institute, Cary, NC). General linear models were used to examine race and sex differences in risk factor variables. All *P* values were 2-tailed and adjusted for covariates where appropriate. Wherever race-sex interaction was present, separate models were used by race or sex. The trends of CV risk factors by HbA_{1c} quartiles were examined by using multiple linear regression adjusted for age, race, sex, and smoking status (yes/no). Individuals were considered smokers if they reported current use of cigarettes or having stopped smoking within the past year.

Models assessing the independent relation between CV risk factor variables and HbA_{1c} were constructed using multiple linear regression. The independent variables included in these models were age, race, sex, smoking status, MAP, ratio of total cholesterol (TC) to high-density lipoprotein cholesterol (HDL-C), HOMA-IR, CRP, adiponectin, and EGFR, without (model 1) or with (model 2) waist circumference. The TC/HDL-C ratio was chosen as a measure of dyslipidemia because it is a marker of insulin resistance characteristic of metabolic syndrome [12]. Continuous variables were tested for normality using a Kolmogorov-Smirnov test. Values of HbA_{1c} and other continuous risk factor variables, except age, used in the analyses were log transformed to improve normality.

Relationship of metabolic syndrome to HbA_{1c} was examined by comparing the prevalence of individuals at top decile of HbA_{1c} by metabolic syndrome status (yes/no) using χ^2 tests. Likewise, association of excess (top decile) HbA_{1c} with parental history of CV disease (myocardial infarction, coronary artery bypass surgery, angioplasty, angina, and stroke) or type 2 diabetes mellitus was examined by using χ^2 test. Top decile of the distribution was arbitrarily chosen to denote excess HbA_{1c}. Metabolic syndrome risk factors and their cutoff values were used in this analysis as defined by the National Cholesterol Education Program Adult Treatment Panel III [13].

3. Results

Mean levels of anthropometric, hemodynamic, and metabolic variables are presented in Table 1 by race and sex. There was no significant age difference among the race-sex groups. Blacks vs whites had higher BMI (women only),

Table 1
Characteristics of study cohort by race and sex

| Variable (mean \pm SD) | White men (n = 356) | Black men (n = 122) | White women (n = 434) | Black women (n = 199) |
|--------------------------------------|----------------------------------|---------------------------------|-------------------------------|---------------------------------|
| Age (y) | 36.5 \pm 4.4 | 36.5 \pm 4.4 | 36.3 \pm 4.4 | 35.4 \pm 4.9 |
| BMI (kg/m ²) | 28.9 \pm 5.5 | 29.4 \pm 7.3 | 28.0 \pm 6.7 | 31.6 \pm 8.7 ^a |
| Waist (cm) | 98.7 \pm 14.0 ^x | 96.9 \pm 17.9 | 86.4 \pm 15.9 | 93.7 \pm 18.6 ^a |
| MAP (mm Hg) | 92.7 \pm 8.7 ^x | 100.5 \pm 13.3 ^{a,x} | 86.8 \pm 8.8 | 92.7 \pm 11.8 ^a |
| LDL-C (mg/dL) | 130.0 \pm 33.9 | 122.3 \pm 40.6 | 124.3 \pm 32.5 ^a | 116.3 \pm 31.2 |
| HDL-C (mg/dL) | 41.4 \pm 11.8 | 49.9 \pm 16.3 ^a | 50.8 \pm 12.7 ^x | 51.9 \pm 13.0 |
| TG (mg/dL) | 159.4 \pm 118.4 ^{a,x} | 125.7 \pm 108.2 ^x | 119.5 \pm 68.7 ^a | 87.5 \pm 38.3 |
| TC/HDL-C ratio | 5.0 \pm 1.5 ^{a,x} | 4.1 \pm 1.5 ^x | 4.0 \pm 1.2 ^a | 3.7 \pm 1.0 |
| Insulin (μ U/mL) | 12.5 \pm 9.2 | 12.1 \pm 9.5 | 11.1 \pm 7.4 | 14.4 \pm 11.3 ^{a,x} |
| Glucose (mg/dL) | 84.9 \pm 10.3 ^x | 83.6 \pm 11.3 | 81.1 \pm 8.7 | 82.7 \pm 11.2 |
| HOMA-IR | 2.7 \pm 2.3 ^x | 2.6 \pm 2.4 | 2.3 \pm 1.8 | 3.3 \pm 4.7 ^{a,x} |
| CRP (mg/L) | 1.7 \pm 1.9 | 2.1 \pm 2.2 | 2.5 \pm 2.3 ^x | 2.5 \pm 2.3 |
| Adiponectin (μ g/mL) | 7.5 \pm 3.5 ^a | 6.9 \pm 5.5 | 10.3 \pm 4.6 ^{a,x} | 8.2 \pm 4.2 ^x |
| EGFR (mL/[min 1.73 m ²]) | 90.8 \pm 15.3 | 96.7 \pm 20.7 | 92.2 \pm 21.3 | 108.2 \pm 22.9 ^{a,x} |

Race-sex difference (adjusted for age): the superscript *a* (for race) and *x* (for sex) denote higher ($P < .05$) value compared with other race or sex.

waist circumference (women only), MAP, HDL-C (men only), insulin (women only), HOMA-IR (women only), and EGFR (women only) and lower low-density lipoprotein cholesterol (LDL-C) (women only), TG, TC/HDL-C ratio, and adiponectin. Men vs women displayed higher waist circumference (whites only), MAP, TG, TC/HDL-C ratio, and glucose (whites only) and lower HDL-C (whites only), insulin (blacks only), CRP (whites only), adiponectin, and EGFR (blacks only). Furthermore, white men and black women had higher HOMA-IR than their counterparts.

Mean and selected percentiles of HbA_{1c} in the study cohort by race and sex are given in Table 2. Blacks vs whites and women vs men had significantly higher values.

Table 3 shows trends of CV risk factor variables (adjusted for age, race, sex, and smoking status) by quartiles of HbA_{1c}. Significant adverse trends were noted for BMI, waist, LDL-C, HDL-C, TC/HDL-C ratio, insulin, glucose, and HOMA-IR across HbA_{1c} quartiles. Trends were not significant for TG, MAP, CRP, adiponectin, and EGFR.

The independent multivariate relationship between HbA_{1c} and CV risk factor variables is presented in Table 4. Significant independent predictors of HbA_{1c} in both model 1 (without waist circumference) and model 2 (with waist circumference) were black race, female sex, and TC/HDL-C ratio. In addition, HOMA-IR entered as predictor variable in model 1. However, waist replaced

HOMA-IR as an independent predictor in model 2. Overall, the identified predictor variables in model 1 and model 2 accounted for 5.7% and 6.3% of the variance in HbA_{1c}, respectively.

Fig. 1 illustrates the relationship between prevalence of excess HbA_{1c} (top decile) and status (yes/no) of metabolic syndrome, and parental histories of CV disease and type 2 diabetes mellitus in the study cohort. Prevalence of excess HbA_{1c} was 1.6-fold higher among those with metabolic syndrome ($P < .05$), 2.1-fold ($P < .001$) higher among those with positive parental history of CV disease, and 1.5-fold ($P < .05$) higher among those with parental type 2 diabetes mellitus.

4. Discussion

This community-based study provides normative distribution of HbA_{1c} by race and sex in nondiabetic black and white younger adults, and demonstrates that excess HbA_{1c} relates to metabolic syndrome trait and positive parental histories of CV disease and type 2 diabetes mellitus. It is noteworthy that these observations are based on an apparently “healthy” cohort, free of selection bias.

The observed race (blacks > whites) difference in HbA_{1c} levels in the study cohort is in agreement with an earlier report [6]. The excess in HbA_{1c} in blacks vs whites, although modest and within reference range, may reflect their adverse profile of parameters related to glucose homeostasis such as insulin sensitivity, secretion, and clearance in childhood and adulthood, and higher prevalence of type 2 diabetes mellitus [14–17]. The black-white difference in HbA_{1c} noted in this study was independent of measures of body fatness and insulin resistance, known correlates of HbA_{1c} [6,7,18]. Whether genetic or other factors related to HbA_{1c} metabolism could account for this racial divergence is not known. With respect to sex difference, previous studies have found no difference [6,7,19]; however, women vs men displayed higher HbA_{1c} in the current study, independent of measures

Table 2
Mean and percentile distribution of HbA_{1c} in young adults by race and sex

| | Mean \pm SD * (%) | Selected percentiles | | | | | | |
|--------------|------------------------|----------------------|------|------|------|------|------|------|
| | | 5th | 10th | 25th | 50th | 75th | 90th | 95th |
| White men | 5.7 \pm 0.4 | 5.1 | 5.3 | 5.5 | 5.7 | 6.0 | 6.2 | 6.3 |
| Black men | 5.8 \pm 0.4 | 5.0 | 5.2 | 5.6 | 5.8 | 6.0 | 6.2 | 6.3 |
| White women | 5.8 \pm 0.3 | 5.2 | 5.4 | 5.6 | 5.8 | 6.0 | 6.2 | 6.3 |
| Black women | 5.9 \pm 0.4 | 5.4 | 5.5 | 5.7 | 5.9 | 6.1 | 6.5 | 6.7 |
| Total sample | 5.8 \pm 0.4 | 5.2 | 5.3 | 5.6 | 5.8 | 6.0 | 6.2 | 6.4 |

* $P < .0001$ for comparison of blacks vs whites and men vs women, adjusted for age and race (or sex).

Table 3

Trends of CV risk factor variables by HbA_{1c} level in young adults

| Variable (mean ± SD) | Quartile of HbA _{1c} (range, %) | | | | P for trend* |
|-------------------------------------|--|----------------------|----------------------|----------------------|--------------|
| | 1 (4.5–5.5), n = 273 | 2 (5.6–5.7), n = 288 | 3 (5.8–5.9), n = 273 | 4 (6.0–6.9), n = 277 | |
| BMI (kg/m ²) | 27.9 ± 6.3 | 28.9 ± 6.9 | 28.9 ± 6.4 | 30.6 ± 7.8 | .0002 |
| Waist (cm) | 90.4 ± 16.2 | 92.4 ± 17.0 | 93.4 ± 16.7 | 94.9 ± 17.7 | .0001 |
| MAP (mm Hg) | 91.1 ± 10.9 | 90.8 ± 10.6 | 91.1 ± 10.3 | 92.1 ± 11.4 | .380 |
| LDL-C (mg/dL) | 123.2 ± 35.3 | 122.9 ± 32.6 | 126.7 ± 34.6 | 125.5 ± 33.5 | .020 |
| HDL-C (mg/dL) | 49.1 ± 14.5 | 48.4 ± 14.2 | 46.5 ± 12.9 | 47.5 ± 12.8 | .0003 |
| TG (mg/dL) | 129.9 ± 96.8 | 129.1 ± 87.5 | 131.0 ± 101.4 | 118.8 ± 82.6 | .524 |
| TC/HDL-C ratio | 4.2 ± 1.5 | 4.2 ± 1.4 | 4.4 ± 1.4 | 4.3 ± 1.3 | .0002 |
| Insulin (μU/mL) | 11.7 ± 9.9 | 12.0 ± 8.7 | 12.0 ± 8.3 | 14.1 ± 16.9 | .013 |
| Glucose (mg/dL) | 82.6 ± 10.3 | 82.7 ± 8.9 | 81.4 ± 9.5 | 84.9 ± 11.4 | .011 |
| HOMA-IR | 2.5 ± 2.6 | 2.5 ± 2.0 | 2.5 ± 1.9 | 3.1 ± 4.0 | .006 |
| CRP (mg/L) | 2.1 ± 2.1 | 2.2 ± 2.2 | 2.3 ± 2.3 | 2.2 ± 2.3 | .924 |
| Adiponectin (μg/mL) | 8.9 ± 5.2 | 9.0 ± 4.6 | 8.4 ± 4.2 | 8.4 ± 3.8 | .283 |
| EGFR (mL/[min 1.73m ²]) | 91.9 ± 18.3 | 94.6 ± 21.8 | 96.9 ± 20.1 | 97.2 ± 22.4 | .088 |

* Adjusted for age, race, sex, and smoking (yes/no).

of body fatness and insulin resistance. The reason(s) for the discrepancy between studies is not clear.

Besides race and sex, TC/HDL-C ratio and waist circumference, measures related to metabolic syndrome [12,20], were independent correlates of HbA_{1c} in this study cohort. Although insulin resistance/hyperinsulinemia is pathologically linked to dysglycemia, the observed increases in HbA_{1c} appear to be mediated primarily through excess body fatness because HOMA-IR was no longer significant when waist circumference was introduced in the multivariate regression model. Because obesity is commonly linked to insulin resistance and the compensatory hyperinsulinemia [21], it may as well play a role as an initiating factor in the development of dysglycemia. This is consistent with our earlier observations showing a temporal association between the degree of baseline adiposity and the incidence of hyperinsulinemia in children, adolescents, and younger adults alike, independent of baseline insulin level [22], and childhood obesity rather than insulin resistance as a powerful predictor for developing metabolic syndrome in young adulthood [23].

Table 4

Predictors of HbA_{1c} in young adults

| Predictors | Standardized coefficient | |
|--------------------------|--------------------------|---------|
| | Model 1 | Model 2 |
| Race (black > white) | 0.16 § | 0.16 § |
| Sex (female > male) | 0.14 ‡ | 0.16 § |
| TC/HDL-C ratio | 0.11 † | 0.10 † |
| HOMA-IR | 0.11 † | |
| Waist | | 0.11 * |
| Model R ² (%) | 5.8 | 6.3 |

Model 1: age, race, sex, smoking (yes/no), MAP, TC/HDL-C ratio, HOMA-IR, CRP, adiponectin, and EGFR.

Model 2: model 1 + waist.

* $P < .05$.† $P < .01$.‡ $P < .001$.§ $P < .0001$.

In studies including the present one, the predictor variables associated with higher HbA_{1c} accounted for only 3% to 7% of its variance among persons without diabetes [6,7]. Although not examined in the present study, hematologic factors, known correlates of HbA_{1c} metabolism [24], were found to contribute little to its variance in healthy population [7]. Whether genetic factors may be involved in the physiological differences in HbA_{1c} metabolism among persons without diabetes is not known.

Based on the association between HbA_{1c} and metabolic syndrome in nondiabetic first-degree relatives of persons with type 2 diabetes mellitus, excess HbA_{1c} has been proposed as a surrogate for the syndrome [18]. In the current study, prevalence of excess (top decile) HbA_{1c} was significantly associated with metabolic syndrome and with positive parental history of CV disease and type 2 diabetes mellitus. Because metabolic syndrome, CV disease, and type 2 diabetes mellitus all have a strong genetic and familial

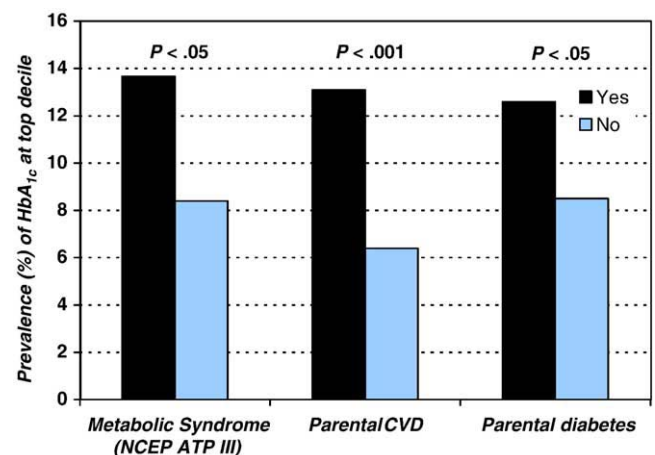


Fig. 1. Prevalence of excess HbA_{1c} (top decile) by status (yes/no) of metabolic syndrome and by parental histories of CV disease and type 2 diabetes mellitus in younger adults. The Bogalusa Heart Study.

component, a positive parental history is recognized as a surrogate indicator of risk in the offspring [25–27]. Furthermore, metabolic syndrome is a strong predictor of CV disease and type 2 diabetes mellitus [28,29]. Taken together, it appears that excess HbA_{1c} within reference range may be a biomarker of risk for developing these conditions.

In this study, HbA_{1c} was not associated with the inflammation-related markers CRP and adiponectin either in bivariate or multivariate analysis. Earlier studies conducted mainly in middle-aged and older adults having type 2 diabetes mellitus and other CV comorbidities showed an association between HbA_{1c} and CRP [30,31]. It should be mentioned, however, that in one study levels increased with HbA_{1c} only among persons with diabetes having HbA_{1c} level greater than 9% [32]; in another study of persons without diabetes, this relationship disappeared after adjustment for body fatness [30]. With respect to adiponectin, no previous data are available for comparison. It is likely that the lack of association of HbA_{1c} with CRP and adiponectin in this study cohort may be due to their younger age and nondiabetic status.

As limitations, this study lacks direct measurements of postchallenge glucose and in vivo insulin action and secretion used in clinical and etiologic studies. Instead, we used well-established simple surrogate measures that are applicable to population studies. Reported parental medical histories were not verified in this study cohort. However, nonsystematic misclassification of self-reported histories would most likely result in an underestimation of the true differences between the groups. Furthermore, because of lack of dietary intake data, this study did not address the known role of diet, in particular calcium, magnesium, and glycemic index of carbohydrates, in the regulation of glucose homeostasis and related risk of obesity, CV disease, and type 2 diabetes mellitus [33–38]. Finally, this study is cross-sectional and observational in nature and cannot address the issue of causality or pathophysiological mechanisms.

In summary, excess HbA_{1c} within reference range is adversely associated with metabolic syndrome and parental histories of CV disease and type 2 diabetes mellitus in nondiabetic, apparently healthy younger adults. These findings underscore the potential value of HbA_{1c} in risk assessments of CV disease and type 2 diabetes mellitus in younger adults. Additional population-based studies are obviously needed to develop consensus regarding cutoff points to define risk status in this age group.

Acknowledgment

The Bogalusa Heart Study is a joint effort of many investigators and staff members, whose contributions are gratefully acknowledged. We are especially grateful to the study participants.

Supported by grants AG16592 from the National Institute on Aging and 0555168B from the American Heart Association.

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