

compared to GLP-1s, BMS was associated with lower risks of MI (RR 0.65, 95% CI 0.51-0.83,  $p < 0.001$ ), CVA (RR 0.62, 95% CI 0.48-0.79,  $p < 0.001$ ), sleep apnea (RR 0.41, 95% CI 0.37-0.45,  $p < 0.001$ ), and dementia (RR 0.56, 95% CI 0.23-1.00,  $p = 0.047$ ). A trend toward reduced mortality (RR 0.80, 95% CI 0.62-1.01,  $p = 0.060$ ) was also observed. Unmatched analyses favored BMS for all outcomes.

**CONCLUSION** In this large real-world cohort, BMS was associated with lower cardiovascular risk, reduced sleep apnea, and decreased dementia compared with GLP-1 receptor agonists in obese patients. In patients with severe obesity, surgical intervention may be associated with greater long-term protection against obesity-related complications than GLP-1 therapy.

**POSTER CONTRIBUTIONS**

**26-A-14259-ACC  
ASSOCIATIONS BETWEEN ACCULTURATION LEVEL AND BEHAVIORAL METRICS OF LIFE'S ESSENTIAL 8 IN ASIAN AMERICAN IMMIGRANTS**



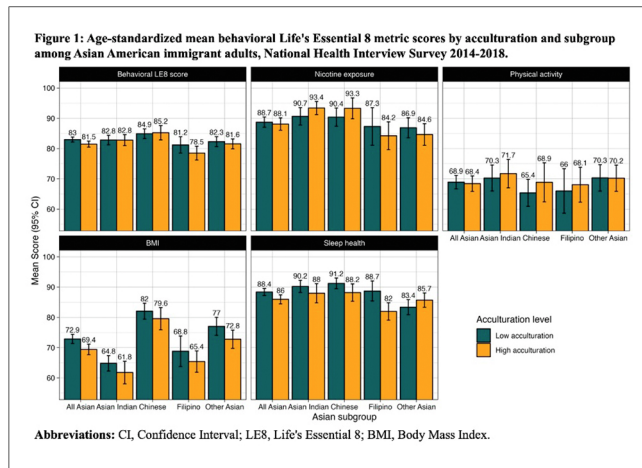
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**BACKGROUND** The associations between cardiovascular behavioral risk factors and acculturation remain poorly characterized among immigrant Asian American subgroups.

**METHODS** We analyzed data from the 2014-2018 National Health Interview Survey to examine associations between acculturation and behavioral Life's Essential 8 (LE8) scores. Acculturation was assessed using a composite measure (years in the US, US citizenship, and English proficiency) and categorized as low versus high. The behavioral LE8 (range 0-100) was derived from an average of four components: nicotine exposure, physical activity, body mass index (BMI), and sleep health. Age-adjusted LE8 scores were compared across acculturation levels within Asian American subgroups using survey-weighted Wald tests.

**RESULTS** Among 3,166 participants (52.4% female, mean age 52.3 years), high versus low acculturation was associated with lower behavioral LE8 scores (81.5 vs 83.0), driven by BMI (69.4 vs 72.9) and sleep health (86.0 vs 88.4). Subgroup analyses showed lower scores for sleep health among Filipino adults (82.0 vs 88.7) and BMI among "other" Asian adults (72.8 vs 77.0) with higher acculturation (all  $p < 0.05$ ).

**CONCLUSION** High acculturation is associated with lower behavioral LE8 scores, with significant variation across Asian subgroups, highlighting the need for research to guide tailored prevention strategies.



**POSTER CONTRIBUTIONS**

**26-A-14523-ACC  
GENOMIC EXPLORATION OF ATHEROGENIC LIPOPROTEINS IN A CARIBBEAN POPULATION: FINDINGS FROM THE GENESIS-ATHERO STUDY**



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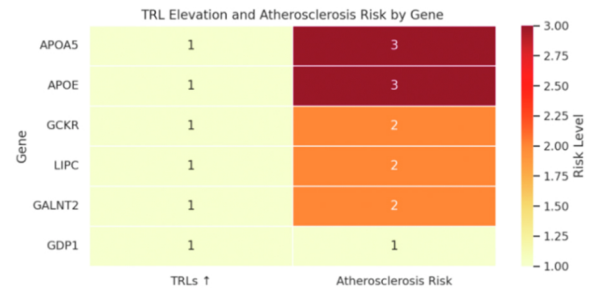
**BACKGROUND** Inherited dyslipidemias, including familial hypercholesterolemia (FH), contribute to premature atherosclerotic cardiovascular disease (ASCVD). The genetic landscape of these disorders remains unexplored in the Caribbean.

**METHODS** A cross-sectional study was conducted on 17 adults who underwent genetic testing from a registry of 465 patients with suspected inherited dyslipidemia (2022-2025). Targeted sequencing analyzed lipid-related genes (LDLR, APOB, PCSK9, APOA5, APOE, GCKR, LRP6, GPD1, LIPC, GALNT2). Data on zygosity, inheritance, ClinVar classification, comorbidities, and lipid phenotypes were recorded.

**RESULTS** Heterozygous variants with autosomal dominant inheritance predominated (100%). Pathogenic LDLR variants (c.590G>A, c.331C>T) confirmed classical FH in 11.8% of cases. The most frequent variants were APOA5 and APOE (35.3% each), associated with hypertension (HTN, 64.7%), diabetes/prediabetes (DM/Pre-DM, 35.3%), and coronary artery disease (CAD, 29.4%). A TRL-risk heatmap identified them as major contributors to residual atherogenic risk.

**CONCLUSION** In this cohort, LDLR mutations confirmed FH in some samples, while APOA5 and APOE alleles were strongly linked to hypertriglyceridemia. Atherogenic risk is driven not only by classical FH mutations but also by triglyceride-rich lipoprotein pathways. Early identification and management of LDL-C, non-HDL-C, and TRL-related variants is essential to reduce premature ASCVD in high-risk individuals.

**Figure 1. Heatmap of Atherogenic Risk and TRL Elevation by Gene**



**Figure 1 Heatmap :** A heatmap visually displays the contribution of individual gene variants to atherogenic risk and TRL (triglyceride-rich lipoprotein) elevation. Genes with the highest impact, such as APOA5 and APOE, appear in intense red, indicating strong association with remnant accumulation and cardiometabolic burden. Moderate-risk genes (GCKR, LIPC, GALNT2) are shaded orange to yellow, while GPD1 appears neutral, reflecting emerging polygenic potential. This visual reinforces the relevance of expanding gene panels beyond LDL-C-centric approaches. Targeted sequencing was performed on lipid-related genes: APOA5 (apolipoprotein A-V), APOE (apolipoprotein E), GCKR (glucokinase regulatory protein), LIPC (hepatic lipase), GALNT2 (polypeptide N-acetyl-galactosaminyltransferase 2), GPD1 (glycerol-3-phosphate dehydrogenase 1).