Society for Epidemiologic Research

47th Annual Meeting
Final Program (as of 6/9/2014)
June 24 – 27, 2014

TUESDAY, JUNE 24, 2014

7:00 - 8:30 pm **Welcome Reception and Poster Session 1** Grand Ballroom 3

AGING

001 Birth Weight as a Predictor of Grip Strength in the Seventh Decade of Life
Mark Pearce

002 Bladder Antimuscarinics and Cognitive Decline in Elderly Patients Enrolled in the National Alzheimer's Coordinating Center Cohort
Daniela Moga

003-S From Forgetful to Disabled: Does Physical Inactivity Accelerate Onset of IADL Limitations among Memory Impaired Adults?
Pamela Rist

004 Leukocyte Telomere Length and Mortality in the National Health and Nutrition Examination Survey, 1999-2002
Belinda Needham

005-S Polypharmacy among Adults Aged 65 and Older in the United States: 1988-2010
Christina Charlesworth

006-S The Study on Global Ageing and Adult Health (SAGE): Depression and Body Composition among Aging Populations
William Olson

007-S Use of Electronic Medical Records and Health Risk Assessments to Understand Sedentary Time in Older Adults
Dori Rosenberg

008 Is Spousal Caregiving Associated with Physical Activity Prevalence?: Evidence from the Health and Retirement Study
Benjamin Capistrant

009 Objectively Measured Physical Activity among Older Adults in an Urban Setting in India: Results of a Study on Global Ageing and Adult Health (SAGE) Sub-Study
Josh Snodgrass

010-S Physical Activity, Functional Abilities, and Health: Results of a WHO SAGE Sub-Study among Older Adults in an Urban Setting in India
Tyler Barrett

011-S A Prospective Assessment of Cardiac Biomarkers for Hemodynamic Stress and Necrosis and the Risk of Falls among Older People
Dhayana Dallmeier

012-S Validation of Self-Reported Hypercholesterolemia Accounting for Lipid-Controlling Drug Use
Michael Passarelli

013 Walking Speed Modifies the Association between Diastolic Blood Pressure and Outcomes: The Health, Aging, and Body Composition Study
Michelle Odden

014-S Association between Exposure to Secondhand Smoke and Telomere Length: Cross-Sectional Study of 1,433 Non-Smokers
Liya Lu

015-S Cadmium and Lead Exposure and Risk of Age-Related Cataract in US Adults: The National Health and Nutrition Exam Survey
Weiye Wang

ALTERNATIVE MEDICINE

016 Withdrawn

CANCER

017 A Comprehensive Model of Colorectal Cancer by Risk Factor Status and Sub-Site Using Data from the Nurses' Health Study
Esther Wei

018-S Alcohol, Smoking and Non-Hodgkin Lymphoma in Twins
Amie Hwang

The "-S" designation indicates that the work was completed while the presenter was a student

337 Environmental Phenols and Reproductive Hormones in Premenopausal Women
Anna Pollack

338-S Hair Mercury and Clinical Outcomes among Women Undergoing In Vitro Fertilization
Myriam Afeiche

339-S Phthalate Exposure and Age at Menarche in US Girls
Taara Bhat

340-S Residential Proximity to Agricultural Pesticides and Risk of Cardiac Birth Defects
Kristen M Rappazzo

341 Trimester Specific PM2.5 Exposure and Fetal Growth in Ohio, 2007-2010
Aimin Chen

342-S Risk of Chronic Obstructive Pulmonary Disease (COPD) Due to Biomass Fuels among Women in Kurram Agency, Federally Administered Tribal Area (FATA): A Case-Control Study
Mehreen Mujtaba

343-S Olfactory Perception and Fragranced Product Use in a Sample of Twins
Matthew O Gribble

344-S Objective Measurement of Erythemal Ultraviolet B Radiation (UVB) from 1979-2009 and Implications for Exposure Assessment
Marvin Langston

GENETICS

345 A Systematic Appraisal of Field Synopses in Genetic Epidemiology
Orestis Panagiotou

346-S Clinical and Genetic Associations with Cognitive Impairment Assessed Using TICS-M in Multiple Sclerosis
Michaela George

347-S Race Versus Ancestry: Does Socially or Genetically Defined Race Predict Dementia Risk in Older Americans?
Jessica R Marden

348-S Using an Alzheimer's Disease Polygenic Risk Score to Predict Memory Decline
Jessica R Marden

349-S A Trans-Ethnic, Genome-Wide Association Study of Ventricular and Supraventricular Ectopy
Melanie D Napier

350 Admixture Mapping of Type 2 Diabetes in African American Women
Edward A Ruiz-Narvaez

351 Epigenome-Wide Study Identifies Novel Methylation Loci Associated with Plasma Adiponectin
Stella Aslibekyan

352 Genetically Predicted 17?-Estradiol and Systemic Inflammation in Women: A Separate-Sample Mendelian Randomization Analysis in the Guangzhou Biobank Cohort Study
C Mary Schooling

353 An Epidemiologic Insight from the Twin and Family Studies: Health Effects of Kimchi Eating Trial and Salt Intake and Habits as an Example
Joohon Sung

354-S Body Size and Obesity Gene Variation Contribute to Multiple Sclerosis Susceptibility
Milena Gianfrancesco

355-S Modification of Genetic Susceptibility to Increased Body Mass by Measures of Acculturation among United States Hispanic/Latinos: The Population Architecture Using Genomics and Epidemiology Consortium
Lindsay Fernández-Rhodes

356-S Obesity-Related Genetic Variants are Associated with Age at Menarche in the Multiethnic National Longitudinal Study of Adolescent Health
Angela Liu

357 Genome Wide Association Study of Urgency Urinary Incontinence
Nedra Whitehead

HIV/STI

358-S Impact of Prosecution for Non-Disclosure of HIV Status on Attitudes and Behaviour among HIV-Positive Men who Have Sex with Men (MSM) in Toronto, Canada
Maya A Kesler

359 The Consequences of Methodology Changes to National Surveys on Monitoring HIV Testing Trends in the United States
Michelle Van Handel

360 Use of P-Technique to Examine the Dynamic Relationship among STD-Associated Feelings and Perceptions in a Cohort of Adolescent Females
Pamela Matson

361-S Survival by Race/Ethnicity and Sex among Treated, HIV-Infected Adults
Catherine Lesko

362-S The Effect of Providing Combination Antiretroviral Therapy to HIV-Infected Mothers on Loss to Follow-Up among their HIV-Exposed Infants in Kinshasa, Democratic Republic of Congo
Lydia Feinstein

The "-S" designation indicates that the work was completed while the presenter was a student

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AN EPIDEMIOLOGIC INSIGHT FROM THE TWIN AND FAMILY STUDIES: HEALTH EFFECTS OF KIMCHI EATING TRIAL AND SALT INTAKE AND HABITS AS AN EXAMPLE. Joohon Sung*, Jung-Eun Lee, Yun-Mi Song (Seoul National University, Seoul Korea)

Twin studies have contributed to science mainly by discriminating the roles of genes versus environments by comparing the resemblances between monozygotic twins (MZ) and dizygotic twins (DZ). Recently, twin or twin-family studies have evolved; a cotwin-control study is a modern design, in which comparisons are made between two cotwins, instead of unrelated cases and controls. Applications of the design include biomarker, epigenetics and microbiome studies. Clinical trial is another application, where two MZ cotwins are allocated to different intervention groups. We conducted 2 week trial of Kimchi-rich Korean diets (=treatment group), where randomly assigned cotwins are provided DASH diet as controls. In this study, 26 healthy MZ pairs with one or two risk factors of metabolic syndrome components were included. We found that general inflammatory markers (hsCRP) and triglyceride levels were significantly lowered among treatment group, compared with their cotwins (DASH diet) or their own baselines. The author also presented an example of salt intake habits. When the shared environmental effects were analyzed using whole families as shared unit, only genetic influences were evident (explaining 0.30-0.42 of total variances). However, when the analyses were repeated using current cohabitation as unit, sharing environments became significant, explaining 0.07~0.042 of total salt intake levels. This tendency was more evident with the sodium density, a measure reflecting salt taste; 0.22 were explained by current cohabitation. And this tendency was stronger between spouses (r2=0.38) than those between siblings and DZ (r2=0.14). We interpreted this findings that 1) the salt intake habits are not fixed but changeable although it is influenced by moderate genetic effects. 2) the changes in salt intake habits will not take very long, probably a few years by sharing same meals. Although some researchers consider adding twins or families will introduce analytical complexities with few fruits, many epidemiologic studies in fact will benefit from adding twins or families.

354-S

BODY SIZE AND OBESITY GENE VARIATION CONTRIBUTE TO MULTIPLE SCLEROSIS SUSCEPTIBILITY. Milena Gianfrancesco*, Farren Briggs, Ling Shen, Hong Quach, Alan Bernstein, Catherine Shaefer, Lisa Barcellos (UC Berkeley School of Public Health, Berkeley, CA United States)

Multiple sclerosis (MS) is a demyelinating autoimmune disease and one of the most common neurological diseases in young adults. Studies confirm a strong genetic component for MS; however, evidence for environmental risk factors, such as childhood and adolescent obesity, has also been reported. We investigated the relationship between MS and 40 established obesity genes while controlling for effects of several established genetic and environmental risk factors. A gene-environment investigation assessed whether variation within significant obesity genes modifies MS risk conferred by body size and body mass index (BMI) during various age periods. White, non-Hispanic members of Kaiser Permanente Medical Care Plan, Northern California (KPNC) aged 18-69 (1,099 cases, 640 controls); and participants from the Kaiser Permanente Research Program on Genes, Environment, and Health (RPGEH) (11,572 controls). Association analysis between obesity SNPs and MS was conducted using KPNC and RPGEH datasets, adjusted for ancestry, gender and HLA-DRB1*15:01, the strongest genetic risk factor for MS (1,099 cases, 12,212 controls). Within KPNC only, logistic regression models estimated odds ratios (ORs) of having MS with 95% confidence intervals (95% CI) adjusted for year of birth, as well as established genetic and environmental risk factors associated with MS (1,099 cases, 640 controls). Across the 40 obesity genes, five SNPs were associated with MS status in KPNC and RPGEH datasets after correcting for multiple testing. When mean body size in 20's was also considered in the model for the KPNC dataset alone, rs822391 and rs5594391 were independently associated with MS risk (p=0.03 and p=0.05, respectively), after adjusting for established genetic and environmental risk factors. This study is the first to examine the relationship between genetic factors related to obesity and MS susceptibility. Combined, the two SNPs are associated with 1.26 increased odds of MS after controlling for environmental and genetic factors related to the disease. Future studies should examine whether MS risk as related to obesity genes is mediated through increased body mass or other biological pathway.

355-S

MODIFICATION OF GENETIC SUSCEPTIBILITY TO INCREASED BODY MASS BY MEASURES OF ACCULTURATION AMONG UNITED STATES HISPANIC/LATINOS: THE POPULATION ARCHITECTURE USING GENOMICS AND EPIDEMIOLOGY CONSORTIUM. Lindsay Fernández-Rhodes*, on behalf of the PAGE Obesity Working Group (University of North Carolina at Chapel Hill, Chapel Hill, NC United States)

There are marked obesity disparities in United States (US) Hispanic/Latinos. Although the genetic determinants of obesity have been studied in this diverse ethnic group, little is known about how they may be modified by sociocultural factors like acculturation, of which language use is a common proxy. The aim of this study was to examine if acculturation of Hispanic/Latinos to a US lifestyle, as assessed by self-reported exclusive English language use at home, exacerbates the association of previously established risk variants on adult body mass index (BMI). The community-based Hispanic Community Health Study/Study of Latinos includes 11,609 Hispanic/Latino adults (age: 20-74; BMI: 18.5-70.0 kg/m^2) with genetic data from the Metabochip (Illumina, Inc). We used generalized estimating equations to model lnBMI while adjusting for relatedness, sampling design, age, sex, center and global ancestry. We tested for interactions between 1) 13 loci (minor allele>5%) previously associated with BMI in European decent populations and 2) self-reported language use at home. Seven loci displayed evidence of association with BMI (*SEC16B, TMEM18, GNPDA2, STK33, MTCH2, FTO, MC4R,* p<0.05) and the interaction was significant for one locus (*TMEM18,* p=0.02). A joint test of the main genetic and interaction effects identified an additional locus (*BDNF,* p=0.01). As consistent with our hypothesis, at *BDNF* we observed a 1% higher BMI for one versus no risk alleles among those reporting exclusive Spanish use at home, and a 8% higher BMI for one versus no risk alleles among those reporting exclusive English use at home. Future research will replicate these effects in 11,000 Hispanic/Latino participants in the Population Architecture using Genomics and Epidemiology Consortium. Our preliminary findings highlight the importance of capturing both genetic and sociocultural determinants when studying obesity disparities.

356-S

OBESITY-RELATED GENETIC VARIANTS ARE ASSOCIATED WITH AGE AT MENARCHE IN THE MULTIETHNIC NATIONAL LONGITUDINAL STUDY OF ADOLESCENT HEALTH. Angela Liu*, Misa Graff, Ethan Lange, Kristin Young, Kathleen Harris, Karen Mohlke, Kari North, Penny Gordon-Larsen (University of North Carolina at Chapel Hill, Chapel Hill, NC United States)

There is a known inverse relationship between age at first menstruation (menarche) and obesity. Genetic loci previously associated with obesity have been associated with age at menarche in subjects of European descent, but the contribution of these variants across multiethnic samples is largely unknown. Using females enrolled in Waves II and III of the National Longitudinal Study of Adolescent Health (Add Health, n=5608; age 11-27 years), a multiethnic nationally representative cohort, we assessed the association of 40 established obesity-related single nucleotide polymorphisms (SNPs) with age at menarche (Mean=12.17 years, Standard Deviation=1.43) in 3463 European American (EA), 1254 African American (AA), and 891 Hispanic American (HA) females. Mixed linear, additive genetic models that accounted for sampling design, family relatedness, and geographic region were stratified by race/ethnicity, and then combined for meta-analysis. Five SNPs in EA, 3 in HA and 1 in AA showed a nominally significant relationship (P<0.05) with age at menarche. In EA, rs9939609 within the FTO gene achieved Bonferroni-corrected significance (P<0.0013) with a 1.4-month (Standard Error (SE)=0.033) decrease in age at menarche per obesity increasing allele. The nominally significant SNPs in AA and HA did not achieve Bonferroni-corrected significance. The pooled meta-analysis across race/ethnicity revealed 2 Bonferroni-corrected significant SNPs near FTO and TFPA2B (p<0.002) and 1 nominally significant SNP in POMC negatively associated with age at menarche (1.0-month (SE=0.027), 1.3-months (SE=0.035) and 1.0-month (SE=0.028) decrease per allele, respectively). We have previously shown the variants near FTO and TFAP2B, but not POMC, to be positively associated with BMI during adolescence across race/ethnicity in Add Health. These findings suggest a complex relationship between obesity-related variants and pubertal development.