about whether screening and detection rates vary by race/ethnicity. **Methods:** Data from electronic health records (EHR) in a large ambulatory group practice were used to construct a cohort of persons aged 35 and older without prevalent diabetes ($N = 116,355$). They were followed for diabetes screening (average follow up 17 months in 2007-2011). We computed standardized screening and detection rates in each racial/ethnic group and examined predictors of screening. We compared positive detection rates for those who met the U.S. Preventive Services Task Force (USPSTF) or American Diabetes Association (ADA) screening criteria and those who did not. **Results:** Most patients (82%), including 75% of those meeting neither criteria, were screened during follow-up. Racial/ethnic minority groups had higher screening rates – Latino (82%), Asian subgroups (83% (Japanese) to 90% (Filipino)), non-Hispanic Black (92%) – than non-Hispanic White (80%) ($P < 0.001$). Detection rates were also significantly higher for some minority groups (Latinos (2.1%), Asian Indians (2.4%), and Filipinos (3.8%)) than non-Hispanic White (1.3%) ($P < 0.05$). Among screened, 1.6% had positive test results (number needed to screen (NNS) = 64). The NNS was 46 for those meeting ADA criteria, 36 for USPSTF criteria and 132 for those meeting neither. **Conclusions:** Nearly all patients in our study population received screening, and racial/ethnic minority groups were not less likely to be screened. Current clinical practice screens a high proportion of individuals meeting neither ADA nor USPSTF guidelines. Given low screening costs that may be appropriate because many new cases were detected among those without risk factors. Given the substantial benefit of early detection of diabetes our study suggests that universal, preventive screening for diabetes for asymptomatic individuals may have utility.

Keywords: Diabetes; Screening; Prevention

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Genetics

B4-1:

An Overview of Kaiser Permanente's Research Program on Genes, Environment, and Health

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Background/Aims: The Research Program on Genes, Environment, and Health (RPGEH) is a large, population-based resource for genetic epidemiology developed by scientists at the Kaiser Permanente (KP) Northern California Division of Research. The goal of this program is to link research data for 500,000 broadly consented health plan members, including longitudinal electronic medical records (EMR), genomic data from biospecimens, and environmental exposure data from surveys and geographic information system (GIS) databases in order to support research on many different health conditions. **Methods:** In 2011, the RPGEH established a state-of-the-art biorepository. The KP clinical lab infrastructure is used to collect and transfer blood samples to the biorepository where saliva, serum, plasma, buffy coat and extracted DNA samples are processed and archived. The biorepository includes a facility for separating blood into components for storage, as well as DNA extraction and normalization. Storage capabilities include -80 C and -20 C freezers, an ambient storage unit and LN2 freezers. The biorepository was designed to store blood components for up to 500,000 health plan members. Although initially participant recruitment was by postal mail, electronic methods of recruitment have now been developed. The goal of this effort was to decrease the per person cost of contact and to recruit younger members. By leveraging the KP EMR, blood draw orders are now automatically entered by RPGEH staff for consenting participants. These samples are then stored in the RPGEH biorepository and tracked in a Laboratory Information Management System. **Results:** A survey of adult health plan members has provided data on health-related behaviors and other risk factors for 430,000 RPGEH participants. To date, 190,000 biospecimens from consenting RPGEH participants have been collected. Genome-wide genotyping and telomere length analysis of 100,000 RPGEH participants have been performed. **Conclusions:** At >200,000 participants (with specimens for >100,000 genotyped), the RPGEH is already an extremely unique and valuable resource.

Keywords: Genetic Resource; Biorepository; Recruitment of a General Cohort

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B4-3:

Demographic and Behavioral Influences on Telomere Length and Relationship with All-Cause Mortality: Early Results from the Kaiser Permanente Research Program on Genes, Environment, and Health (RPGEH)

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Background/Aims: Telomere shortening is a biomarker of aging, but it is still unclear whether it directly influences aging-related health changes and mortality, or largely reflects the accumulating influences of environmental influences and declining health. Prior studies have reported associations between short telomeres and many health conditions. Mendelian syndromes and heritability studies demonstrate the biological underpinnings of telomere length (TL), yet other studies show that environmental and behavioral factors also influence telomere lengths. **Methods:** As part of the RPGEH, the Genetic Epidemiology Research Study on Adult Health and Aging (GERA), a multi-ethnic cohort (average age = 63 years) has measured TL from saliva samples on over 100,000 individuals with linked electronic medical records. A survey of demographic and behavioral factors was conducted 2 years prior to saliva collection. With these data, we examined demographic relationships with TL, behavioral influences, and relationship of TL with all-cause mortality following sample collection. **Results:** As expected, TL is inversely correlated with age, and women have longer telomeres than men except as young adults. All analyses controlled for age and gender. As seen in other studies, we find significantly longer TL among African Americans than other groups. TL is positively correlated with education and body mass index (BMI), and negatively correlated with cigarette smoking and alcohol consumption. We found no relationship with major depression or stress-related disorders, even when limited to recent episodes. We found that short TL was prospectively associated with mortality, although only those with the shortest TL were at increased risk; the association suggested a critical threshold of short TL determines effects on mortality. The association persisted even after adjustment of the demographic and behavioral factors such as age, sex, race, education, BMI, smoking, and alcohol consumption. **Conclusions:** While this could indicate a direct effect of TL on health, it will also be important to examine the extent of pre-existing morbidities in these individuals to understand their possible role in the pathway between TL and longevity.

Keywords: Genetics; Mortality; Epidemiology

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B4-4:

Genome-Wide Association Study of Macular Degeneration: Early Results from the Kaiser Permanente Research Program on Genes, Environment, and Health (RPGEH)

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Background/Aims: Age-related macular degeneration (AMD) is the most common cause of vision loss in individuals over the age of 50 in the United States. Genetic factors explain a large portion of the risk of developing AMD, and genetic variants at the CFH, HTRA1/ARMS2, C2/CFB, and C3 gene loci have previously been associated with the disease. **Methods:** We conducted a genome-wide association study (GWAS) of AMD in the Kaiser Permanente Genetic Epidemiology Research on Adult Health and Aging (GERA) cohort. The GERA cohort includes 110,266 subjects with extensive electronic medical record information on eye examinations, diagnoses and treatment of