Methods: As part of a CRN pilot project, focus groups were conducted with Kaiser Permanente Colorado members in 2009 to determine individual perspectives and public opinion about the importance and value of family history, DTC genetic testing, and DTC advertising and other media representations of DTC genetic tests. Focus groups were conducted by concordant population groups: General population KPCO members, members who self-identify as African American, members who self-identify as Hispanic/Latino, women with a recent referral for BRCA1/2 testing, KPCO primary care providers, and KPCO specialty care providers. **Results:** Results on focus group demographics, media use, trust in information, and most trusted information sources are presented. Additional results include coding focus group transcripts for value and polarity (positive/negative) of opinion on family history and genetic testing. Additional coding for how different population groups frame opinion on the issue (progressive, deterministic, caution) include results on whether frames are similar or different across population groups. Finally, information on the impact of media presentations on member opinion and decision-making were assessed. **Conclusions:** Individual opinions about the value of family history and genetic testing for disease risk vary greatly. Salience of themes related to genetic testing and DTC genetic tests specifically may vary across concordant population groups.

Keywords: Direct-to-consumer genetic testing, Health and family history, CRN pilot project

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PS1-10:

Response to Metformin and Genetic Variants of Organic Cation and Multidrug and Toxin Extrusion Transporters

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Background and Aims: Metformin is the most widely-used anti-diabetic drug in the United States. However, medication management fails to achieve therapeutic goals in ~20% of patients. This study attempted to identify genetic polymorphisms associated with metformin treatment failure. We studied the associations between polymorphisms in two liver and kidney organic cation transporter genes (OCT1 & OCT2) and two kidney multidrug and toxin extrusion transporter genes, (MATE1 & MATE2K) and response to metformin monotherapy. **Methods:** At Kaiser Permanente Southeast and Marshfield Clinic Research Foundation we identified 304 type 2 diabetes (T2DM) patients on metformin monotherapy who: were enrolled for ≥6 months prior to initiation; remained on metformin ≥90 days following initiation; and had a HbA1c measured prior to first metformin prescription and then after initiation. From this group we selected 171 patients who had not received metformin or other anti-diabetics previously, and had baseline HbA1c levels >7.0% prior to metformin initiation. We genotyped 10 SNPs, and assessed response by measuring absolute and relative change in HbA1c after metformin initiation. **Results:** Three SNPs were identified that were significantly associated with reduced response to metformin, after adjustment for baseline HbA1c, dose, and ethnicity. In a dominant model, heterozygosity or homozygosity for minor A allele in the MATE1 intronic SNP, rs2289669, resulted in a smaller absolute change in HbA1c (mean of 0.45% less reduction in absolute change in HbA1c; 95% CI 0.17 to 0.74%) compared to individuals homozygous for major G allele. In a recessive model, homozygosity for minor A allele in MATE2K 5'-UTR SNP, rs12943590, resulted in smaller absolute change in HbA1c (mean of 0.43% less reduction in absolute change in HbA1c, 95% CI 0.053 to 0.86%). The reduced function SNPs in OCT1 & OCT2 were not associated with metformin response, except for rs34059508 (G465R). This SNP showed a positive (but not statistically significant) association with smaller absolute change in HbA1c (mean of 0.49%; 95% CI -0.06354 to 1.045%). **Conclusions:** These three variants of metformin transporter genes may be important for

personalizing treatment for patients with T2DM. A replication study in a larger population is currently being planned.

Keywords: Genetic polymorphisms, Metformin transporter genes, Metformin treatment

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PS1-11:

Specimen Collection Within the Cancer Research Network: A Critical Appraisal

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Background and Aims: The Genomics Working Group (of the Cancer Research Network (CRN) Pharmacovigilance Project) explored single-site experiences with genomic studies to understand challenges and opportunities for collecting and using biological specimens. Its specific aims were to: (i) describe the availability of existing biospecimens; (ii) document successful past specimen collection strategies; (iii) identify potential barriers to selected recruitment strategies; and (iv) develop standardized study documents for future genomic research. **Methods:** We distributed a survey on existing biospecimen availability to principal investigators at all CRN Pharmacovigilance sites. Information collected included the number of specimens, storage methods, and type of specimens available. Investigators were also asked to identify past and current studies at their institutions in order to collect information on successful specimen collection strategies. A literature review was conducted both to identify potential barriers to participation and to understand the feasibility of various recruitment procedures. Benefits and limitations of 'opt-out' and 'opt-in' specimen collection methods were examined. Lastly, we developed study documents, including recruitment letters and informed consent forms, for future saliva and blood specimen collection efforts. **Results:** Two of the CRN HMOs currently have large-scale banked blood or saliva specimens (>20,000) within existing repositories. One site has two large-scale studies (>20,000 participants each) with banked specimens able to provide DNA for future research. Whole blood or blood components are the most commonly collected specimen types, and multiple CRN sites have access to banked tumor blocks. There were 33 past or current studies that included biospecimen collection. There was a trade-off between intensive data collection requirements and recruitment yield, cost, and participation burden. **Conclusions:** There is great potential for collection, storage, and use of biospecimen samples for research within the CRN. For future collection efforts, 'opt-out' models allow fast sample accrual, but impact data de-identification requirements. 'Opt-in' models allow for broad data collection, but are resource and time intensive. Pathology time and support may be a barrier to future use of stored samples.

Keywords: Genomics Working Group, Specimen collection strategies, Genomic research

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PS1-12:

Use of Tumor Registry to Obtain Family History Information

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Background: The Human Genome project has revolutionized the field of medicine to move toward personalized medicine. The family history is a screening tool to identify families at risk for common conditions allowing for personalized care. For breast cancer syndromes, genetic testing, counseling and prophylactic treatment are available. While there are data about the efficacy and clinical utility of the family history, there are areas that still need investigation. Does obtaining the family history lead to patient