recommendations? Do patients act on recommendations? Are there barriers to action and are there improved outcomes? One established barrier is the time to obtain a pedigree and knowledge basis for interpretation. Options for obtaining and interpreting a family history are necessary due to these barriers. We examined the use of tumor registry data as a cost effective option for providing family history, and age information. **Methods:** The tumor registry data were examined to identify women that were diagnosed with breast cancer between 2004-2008. These data were then substratified for age and family history. A family history was considered positive if it met the US Preventative Health Task Force criteria for breast cancer. The EMRX allowed identification of patients who had genetic counseling and or testing recommended and how many patients followed up on those recommendations. **Results:** Between 2004-2008 there were 1,594 patients with a newly diagnosed breast cancer. Of these, 113 had no information (7%). There were 1,112 (75%) that had at least one 1st or 2nd family member with a significant malignancy. There were 61 patients that met criteria for a positive family history. Fourteen patients were at or below age 50, and 47 over age 50. Of the 61 patients, 37 (60.7%) were offered genetic counseling and/or testing. **Conclusions:** The tumor registry data did identify individuals with a positive family history of breast cancer and was cost effective. In conjunction with the EMRX, it is possible to see if the appropriate recommendations were made and whether individuals followed the recommendations. These individuals present opportunities for future research in barriers to care, and biomarker research in individuals with a familial risk.

Keywords: Tumor Registry, Personalized medicine, Family history screening

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PS1-13:

Using the PMRP Cohort to Develop a Model for Incorporating Genetic and Environmental Factors into Prostate Cancer Screening Decisions

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Background: Prostate cancer screening with PSA has decreased the average age of prostate cancer detection and increased the number of men who undergo prostate biopsies. Currently two thirds of the prostate biopsies performed due to a high PSA test are negative for prostate cancer leading to unnecessary expense and distress for the individual. One way to decrease the unnecessary procedures associated with PSA screening would be to identify individuals who are either at increased or reduced risk of prostate cancer using newly discovered genetic and environmental risk factors. **Aims:** Using the males in the Personalized Medicine Research Project (PMRP) population that have had a PSA test, determine if genetic and environmental factors can be incorporated into the PSA screening model to better discriminate individuals who will have a diagnosis of prostate cancer from those with negative biopsies. **Methods:** Individuals in PMRP who were diagnosed with prostate cancer (N=466) were compared with the entire Marshfield Clinic population to determine cancer screening characteristics such as rate of PSA screening and average age at cancer diagnosis. All men in PMRP who have had a PSA test (N=4659) were genotyped for at least 12 polymorphisms that have been associated with prostate cancer in GWAS studies and dietary history was collected if available. **Results:** Individuals diagnosed with prostate cancer in the PMRP population tend to have more PSA tests prior to diagnosis than the general population (an average of 7) with 69% (N=320) having at least one PSA test prior to a prostate biopsy. A total of 935 of the 4659 men in the study have had a prostate biopsy with a positive biopsy rate of 34%. Using a panel of 12 previously identified polymorphisms; seven were significantly associated with prostate cancer in our population. Individuals with 1 or fewer risk alleles (15.6% of the population 146 of 935) were less likely to have a diagnosis of prostate cancer on biopsy (OR 1.6). **Conclusions:** The PMRP population that has experienced at least one PSA screen is a viable population for testing new screening algorithms that incorporate genetic and environmental factors for better identification of prostate cancer risk.

Keywords: Prostate cancer screening, PSA screening, Genetic and environmental risk factors

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PS1-14:

Utilization and Effectiveness of KRAS Testing for Colorectal Cancer

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Background: New genomic and personalized medicine (GPM) applications have the potential to enhance our ability to screen for disease predisposition and treatment responsiveness. Surveying colorectal cancer (CRC) tissue for mutations in the KRAS gene is one such test that can help decide how to treat patients with metastatic colorectal cancer (mCRC). KRAS testing provides an opportunity for oncologists to tailor the use of anti-EGFR therapy to increase treatment effectiveness and potentially minimize adverse events. The FDA has recently changed the labeling of anti-EGFR therapies to indicate that it is not effective for the treatment of patients with KRAS mutations. KRAS testing has already become standard clinical practice in many settings. In this study, we will assess the patterns of diffusion and utilization of KRAS testing and evaluate the characteristics of patients, providers, and health systems as they relate to the uptake of KRAS testing. We will also conduct a comparative analysis of KRAS testing for mCRC patients treated in community practices to evaluate its effectiveness in terms of both progression-free survival and overall survival. **Methods:** This study will include a total of 800 mCRC cases diagnosed between January 1, 2005 and July 31, 2010 from 7 HMORN sites. Using electronic records at each site, we will capture information on relevant patient characteristics including disease characteristics, comorbidities, history of all cancer-directed therapies, acute complications, receipt of palliative care and contextual socioeconomic variables. We will use chart review to supplement, or in some cases verify, the electronic data. **Conclusion:** The study will serve as a model for evaluating the potential impact of GPM applications to improve health outcomes, reduce costs, and influence patient and physician decision-making in the area of personalized therapies.

Keywords: KRAS testing, Patient treatment, Genomic and personalized medicine applications

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Cancer

C-B2-01:

A Panel of Markers with Potential Clinical Diagnostic Application

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Background and Aims: Distinguishing low/intermediate grade neuroendocrine carcinoma (carcinoid and atypical carcinoid) from a high grade neuroendocrine carcinoma [small cell carcinoma and large cell neuroendocrine carcinoma (LCNEC)] of the lung can be difficult, especially in small biopsy specimens. Patients diagnosed with a low/intermediate grade carcinoma would be treated surgically white patients diagnosed with small cell carcinoma with chemotherapy. Biomarkers may increase the diagnostic accuracy. **Methods:** We studied 42 consecutive cases of neuroendocrine tumors of the lung (20 small cell carcinomas, 7 large cell neuroendocrine carcinomas, 12 carcinoids and 3 atypical carcinoids) with the objective of comparing the expression of the panel of biomarkers (CD117, KOC, Ki-67, pVHL and p16) between the low and high grade neuroendocrine tumors of the lung. Tissue microarrays were constructed and expression of each biomarker was evaluated using immunohistochemistry. Staining was standardized and scored as “0” = Negative, “1+” = Focal, “2+” = 30 -49% cells staining and “3+” = 50-100% cells staining positively. For the purpose of the present study, a specimen scored as “0” or “1+” was classified as negative, while a specimen scored as “2+” or “3+” was considered positive. In estimating the likelihood of expression of the biomarkers, specimens were