At-risk cancer genetic syndrome identification (ARCAGEN-ID): Novel EHR integrated system to overcome disparities in identification and testing for cancer genetic syndromes.

Vinit Singh, George Chen, Amanda Sena, Thomas Rafter, Rosa Xicola, Mohamad Sharbatji, Jing Liu, Quiana Brown, Karina Brierley, Claire Healy, Michelle Hughes, Nitu Kashyap, Xavier Llor; Roswell Park Comprehensive Cancer Center, Buffalo, NY; Yale School of Medicine, New Haven, CT; Yale New Haven Health, New Haven, CT; Advent Health, Orlando, FL; Yale New Haven Hospital, New Haven, CT; Emory University School of Medicine, Atlanta, GA

Background: Identifying individuals at-risk for a hereditary cancer syndrome (HCS) is crucial to prevent cancer deaths. While there are established guidelines for genetic testing, less than 30% eligible individuals are tested, with consistently worse rates among underserved. The complexity of guidelines and providers' unconscious bias contribute to these disparities. This project aimed to enhance the identification and testing of at-risk individuals, focusing on underserved populations. **Methods:** NCCN/ACMG criteria for genetic testing were translated into three distinct rule-based conditional logic statements in the EHR. A total of 218 rules that serially evaluate each aspect of an individual criteria, and together roll up into a logic statement of "at-risk for HCS. The rules evaluate personal and/or family history, determine age at onset, and categorize family relationships. A proof-of-concept automated outreach initiative was developed that allowed patients to opt into genetic testing after an informational video was watched was developed. Relevant data were extracted and compared using chi-square test. **Results:** Out of 1.3 million individuals, ARCAGEN-ID identified 59,377 (4.8%) at-risk of an HCS. Of those, 47,000 (79.2%) had not been previously evaluated: 43,051 (79.3%) at-risk for Breast, Ovarian, Pancreas, Prostate related mutation; 3,308 (70.2%) at-risk for Lynch syndrome, and 1,144 (80.5%) at-risk for other HCSs. Among previously identified individuals, 2,340 (18.9%) had a pathogenic variant (PV). Compared to overall population in health system, ARCAGEN group had a higher proportion of female (82% vs 55%, $p < 0.01$), White (78% vs 65%, $p < 0.01$) and non-Hispanic (89% vs 84%, $p < 0.01$) individuals, and had less often Medicaid (16.7% vs 28%, $p < 0.01$). Within ARCAGEN, comparing previously identified individuals with newly identified ones, the latter were significantly more often male (19.9 vs 11.13%, $p < 0.01$), younger (≤45y) (33.6% vs 27.2%, $p < 0.01$), Non-White (22.9& vs 20.5%, $p < 0.01$), and more often on Medicaid (31.5% vs 13%, $p < 0.01$). For the pilot, 126/504 outreached individuals (25%) viewed the video and completed a questionnaire. 43/504 (8.5%) pursued testing, and 7 (16%) had a PV. A total of 7% had prior testing not recorded in discrete fields; 2% declined testing; and 6% sought genetic counseling prior to testing. A higher proportion of African American (AA) individuals opted for testing through this strategy (11%) compared to the overall percentage of this population that was outreached (6%, $p = 0.05$). **Conclusions:** Through this automated system, we were able to identify more non-White individuals and add more Medicaid-insured individuals for testing. Uptake after outreach was higher among AA. Thus, a system like ARCAGEN can help overcome disparities in HCS identification without a relevant increase in resources. Research Sponsor: None.