endometrial cancer (EC) are well documented, but differences in distress have not been previously explored. Here we characterize the association between race/ethnicity, distress scores, and stressors reported by patients with EC. METHODS/STUDY POPULATION: Patients presenting to a single academic outpatient gynecologic oncology practice for initial evaluation of known EC from January 2013-May 2020 were included. The electronic health record was used to abstract demographics, National Comprehensive Cancer Network Distress Thermometer and Problem List (NCCN DT) scores and stressor categories (physical, emotional, spiritual, practical, and family) from the initial encounter. Referral to support services occurs at NCCN DT score ≥4. We excluded women who received prior cancer-directed therapy and those without an initial NCCN DT score. Summary statistics were tabulated for demographics. Mann-Whitney U tests were used for inter-group difference on continuous variables and 2-sample tests for equality of proportions were used for binary variables. RESULTS/ANTICIPATED RESULTS: 412 non-Hispanic White (NHW, mean age 63) and 149 non-Hispanic Black (NHB, mean age 65) women were included in our analysis. More NHB women presented with high-grade EC (53.7%) vs NHW women (21.9%) and fewer NHB women were privately insured (32% vs 52%). Median distress scores were higher in NHW women compared to their NHB counterparts (4 vs. 2, $p<0.001$) and NHB women were more likely to report a distress score of 0 compared to their NHW counterparts (32% vs 19%, $p=0.001$). 50.5% NHW women had a score ≥4 and thus qualified for referral to services compared to 20.7% of NHB women ($p=0.02$). Of those referred, NHB and NHW women declined referral to support services at similar rates (35.1% vs 34.5%; NS). There was a significant difference in the median number of stressors reported by NHW and NHB women, (4 vs 3 stressors; $p=0.02$). DISCUSSION/SIGNIFICANCE OF FINDINGS: The NCCN DT, a widely used tool in cancer clinics, may fail to adequately measure distress in NHB women presenting with a diagnosis of EC, despite >30% more high-risk histology cancers in this cohort. This difference leads to disparities in referral to additional support services, which may affect quality of care and quality of life.

Mechanistic Basic to Clinical

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10061

Assessing immunogenicity of an Ebola vaccine in humans using a systems biology approach*

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ABSTRACT IMPACT: Understanding gene expression changes after viral vaccination and booster may help predict vaccine efficacy. OBJECTIVES/GOALS: Utilize a systems biology approach to identify gene expression changes after administration of Zaire Ebola virus glycoprotein expressed in a Chimp Adeno3 vector (ChAd3-EBOZ) and either boosted ~7 weeks later with modified vaccinia Ankara MVA expressing Zaire and Marburg GPs plus Tai forest NP (MVA-BN ®Filo) or given saline (placebo). METHODS/STUDY POPULATION: As part of the phase 1b, open-label vaccination trial of ChAd3-EBO-Z in Mali, West Africa, peripheral blood mononuclear cells were isolated from eight volunteers for whole genome transcriptomics analysis. Four subjects received the MVA-BN ®-Filo booster and four received saline. Samples were taken prior to receipt of the booster or placebo, as well as 1, 7, and 14 days afterwards. Significant differentially expressed genes were identified using RNA-seq between baseline and post-MVA-BN ®Filo. Functional enrichment analysis against the GO Ontology Database and the Immune Signatures C7 collection of MSigDB (ImmuneSigDB) was performed. These differentially expressed genes were also examined for associations with Ebola antibody titers and cell-mediated immune responses. RESULTS/ANTICIPATED RESULTS: The majority of gene expression changes occurred on day 1 post-MVA-BN ®-Filo administration. 870 genes had significantly different expression when day 1 samples were compared to pre-booster baseline (791 upregulated/79 downregulated). Those upregulated genes are mainly involved type I interferon and regulation of viral life cycle pathways. The downregulated genes are involved in regulation of cellular defense response, lymphocyte mediated immunity. Comparing to the C7 Immune Signatures collection datasets, we identified more than 100 upregulated genes from 6 studies of yellow fever vaccination that were also significantly upregulated in our study. The top enriched ontological pathway of those genes is cellular response to type I Interferon. DISCUSSION/SIGNIFICANCE OF FINDINGS: The use of a systems biology approach to compare gene expression changes among vaccine studies utilizing whole genome transcriptomics data allows the identification of genes involved in the immune response to vaccination and might aid in predicting vaccine efficacy.

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Pathogen-specific metabolic pathways and innate immune responses associated with Chlamydia trachomatis infection and other STIs

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ABSTRACT IMPACT: This project seeks to identify unique host responses that are biomarkers for specific urethral pathogens, and which can be used in the development of point-of-care (POC) STI diagnostics. OBJECTIVES/GOALS: How Chlamydia trachomatis (CT) and other common STIs, e.g. Neisseria gonorrhoeae, evade immunity and elicit pathology in the male urethra is poorly understood. Our objective is to determine how STI-infected urethral epithelial cells, as well as the uninfected 'bystander' cells with which infected cells communicate, respond to CT and other STIs. METHODS/STUDY POPULATION: We evaluated how immortalized urethral cell lines - including transduced human urethral epithelial cells (THUECs) - respond to increasing doses of CT infectious particles using in vitro one-step progeny assays performed in the presence or absence of cycloheximide, a drug that inhibits eukaryotic protein synthesis. We will perform concurrent single-cell RNA sequencing (scRNA-seq) and multiplex cytokine analyses to determine how different CT doses impact the transcriptomes of infected and bystander urethral epithelial cells and modulate cytokine production of the overall monolayer. Results of these experiments will inform the feasibility of performing similar analyses in situ using urethral swabs from men with clinically diagnosed urethritis. RESULTS/ANTICIPATED RESULTS: Our results demonstrate that immune-competent urethral cell monolayers strongly resist CT infection, unless most of the cells are simultaneously infected.

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