

screening arm had 7.1 times higher odds (95% CI 5.7–8.8) of being identified as at-risk for suicide, 7.8 times higher odds (95% CI 4.6–13.1) of confirmed follow-up needs, and 4.0 times higher odds (95% CI 2.0–7.9) of initiating mental health treatment. Using a PHQ-8 screen potentially missed 30.2% of at-risk students (positive response to PHQ-9 item #9, but negative on the PHQ-8).

**Conclusions:** Even with a MDD screening tool, which is not optimized for suicide risk assessment, universal screening increased identification of and treatment initiation for suicide risk among identified adolescents. This both confirms the value of this approach and suggests a suicide-specific risk assessment may have even greater impact on treatment engagement of at-risk youth.

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## PLATFORM RESEARCH PRESENTATION II: CHARLES E. IRWIN JR. NEW INVESTIGATORS

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### MOLECULAR BACTERIAL VAGINOSIS AND PROSPECTIVE RISK OF CERVICOVAGINAL CHLAMYDIA TRACHOMATIS INFECTION IN ADOLESCENTS

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**Purpose:** Adolescents make up only a quarter of the population but account for over half of all incident sexually transmitted infections. Bacterial vaginosis has been associated with cervicovaginal Chlamydia trachomatis (CT), although the mechanisms of their association remain poorly characterized. This study investigated the prospective association between the cervicovaginal microbiome (CVM) and the risk of acquiring CT infection in adolescents.

**Methods:** We conducted a nested case-control study of CT within an HPV longitudinal cohort study of sexually active adolescents from a large adolescent health center in New York City. Controls were matched to incident (newly diagnosed) CT cases using risk set sampling based on age, date of study enrollment, and prior history of CT infection. For this study, cervicovaginal swab samples collected from three time points were analyzed: approximately six months before CT infection (V1), at the time of CT diagnosis (V2), and six months after infection treatment (V3). Clinical CT was diagnosed using a GEN-PROBE APTIMA assay. The CVM was evaluated using 16SV4 rRNA bacterial gene amplicon next-generation sequencing. Sequence reads were clustered into amplicon sequence variants using DADA2 and taxonomy was assigned using a custom cervicovaginal microbiome specific database employing a Naive Bayesian classifier. We assessed the presence of bacterial vaginosis (BV) using a previously validated molecular score from the 16SV4 reads (molBV) that provides a Nugent-like score on a scale from 0 - 10. At V1, 232/502 (46.2%) cervicovaginal samples were molBV-BV negative (score 0-3), 79/502 (15.7%) were molBV-BV intermediate (4-6), and 191/502 (38.0%) were molBV-BV positive (7-10). The relative risk (RR) of incident CT based on the molBV-BV score was assessed by comparing participants who were BV positive to those intermediate and negative using

multivariable conditional regression adjusting for patient BMI, number of sexual partners within the last 3 months, and condom use.

**Results:** 16SV4 rRNA gene amplicon sequencing yielded an average of 33,339±13,280 bacterial reads with no significant differences based on case status (p=0.08). Subclinical detection of BV by the molBV score at V1 significantly predicted risk of CT diagnosis at V2, 6 months later (RR=1.78, 95%CI=1.05-3.03). Adjusted cross-sectional analysis of V2 samples revealed an even stronger association between molBV-BV positive status and clinical detection of CT (RR=2.90, 95%CI=1.74-4.85), whereas following CT treatment (V3) there were no differences between cases and controls in their BV scores (p=0.5).

**Conclusions:** While it is known that having a clinical diagnosis of BV is associated with cervicovaginal CT, to our knowledge this is the first study to prospectively demonstrate an association between sub-clinical detection of BV by next-generation molecular sequencing of the CVM and the risk of acquiring a cervicovaginal CT infection.

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### EXPLORING THE IMPACT OF RACISM ON BLACK YOUTH: A MULTIDIMENSIONAL EXAMINATION OF DISCRIMINATORY EXPERIENCES ACROSS PLACE AND TIME

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**Purpose:** Black youth are disproportionately impacted by community violence. Experiences of racism and discrimination may confer additional stress and create greater challenges for youth attempting to recover following violence exposure. We know little about how experiences of violence and discrimination intersect over place and time as well how these intersections relate to changes in stress, post-traumatic stress, and safety. This study linked innovative social network and ecological momentary assessment (EMA) methods to elucidate how perception of racism may influence stress and perceptions of safety among Black youth following a violent event.

**Methods:** This project engaged 25 Black youth (ages 14-19 years old, 58% female) who had witnessed community violence within the past three months. Using an intensive longitudinal design, we sought to understand how the interrelatedness of people, places, and time may impact youth's recovery following exposure to community violence. Youth were recruited in partnership with community-based youth-serving programs and agencies in Pittsburgh, PA. A baseline survey assessed experiences of discrimination (Experiences of Discrimination Scale), stress (Cohen's global measure of stress), posttraumatic stress symptoms (PTS; Child PTSD Symptom Scale; CPSS-5) and also included an egocentric social network survey to identify key sources of support. Youth were given a cell phone with a mobile app, MetricWire, and were asked to complete EMA app-based surveys three times daily for two weeks about the spaces that they were in, the people they were with, and their current emotional state. EMA surveys prompted youth to report their in-the-moment perceptions of racism, stress, PTS symptoms, safety, and social support. A total of 513 EMAs were completed (49% response rate). Multilevel models