

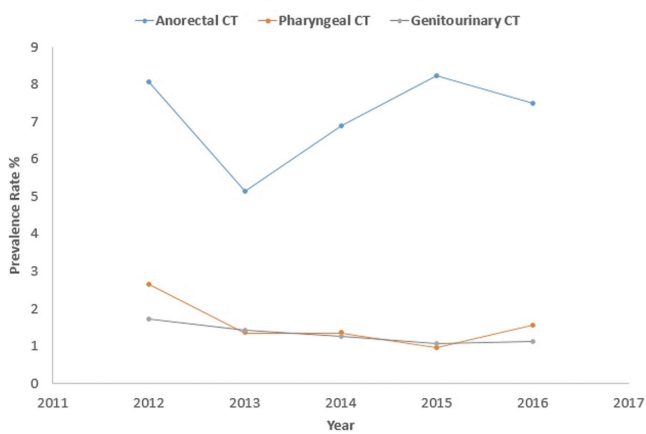
infections in the US Military HIV Natural History Study (NHS), a cohort of HIV-infected Department of Defense beneficiaries.

Methods. Since 2012, willing NHS subjects have undergone nucleic acid-based tests (NAAT) to identify anorectal (AR)/ pharyngeal (PH) GC/CT infections. Incident cases had a positive test following an initial negative test. Risk factors for incident GC/CT infections were assessed with a multivariate Cox proportional hazards model.

Results. A total of 405 GC and 457 CT infections were observed among 1998 subjects (median age 28.7 years, 94% male, 44.1% African-American [AA]); 21% of GC and 18% of CT cases were re-infections. The incidence of AR GC, PH GC, and AR CT increased over time ($P = 0.02$, $P = 0.03$ and $P = 0.02$, respectively). Incident GC infections were associated with younger age [HR 0.61 per 5 year increase (0.57–0.66)], AA ethnicity [HR 1.46 (1.06–2.00)], higher viral load [HR 1.63 per log increase (1.47–1.80)] and a prior history of syphilis [HR 2.20 (1.62–2.99)]. Incident CT infections were associated with younger age [HR 0.7 per 5 year increase (0.66–0.74)], male gender [HR 5.82 (1.86–18.20)], higher viral load [HR 1.61 for each log increase (1.47–1.76)], lower CD4 count [HR 0.86 per 200 cell increase (0.79–0.95)], prior GC [HR 1.55 (1.15–2.08)] and prior syphilis [HR 2.16 (1.67–2.79)].

Conclusion. Incident AR GC and CT infections are increasing in the NHS and approximately 20% of infections were repeat infections. The increased incidence is attributable at-least in part to the increased uptake of EG testing. Our study highlights the importance of prevention in positive programs to reduce the risk of HIV transmission.

Prevalence of Chlamydial Infections by Anatomical Site



Prevalence of Gonococcal Infections By Anatomical Site

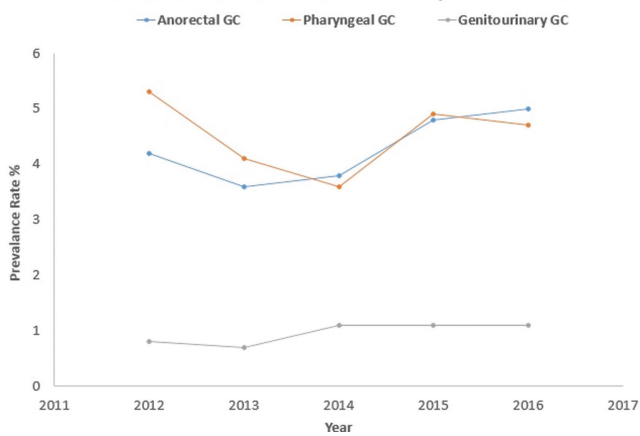


Table. Incidence rate per 100 person-years (95% confidence interval) by site

| Year | GC | | | CT | | |
|------|-----------------|-----------------|---------------|-----------------|---------------|---------------|
| | AR ^a | PH ^a | GU | AR ^a | PH | GU |
| 2012 | 1.3 (0.7–2.3) | 1.9 (1.1–2.9) | 2 (1.2–3) | 2.7 (1.8–4) | 1 (0.5–1.9) | 4.4 (3.2–5.9) |
| 2013 | 1.8 (1.1–2.6) | 2 (1.3–2.8) | 1 (0.6–1.7) | 2.5 (1.8–3.5) | 0.5 (0.2–1) | 2.2 (1.5–3.1) |
| 2014 | 1.2 (0.7–1.9) | 1.3 (0.7–2) | 1.2 (0.7–1.9) | 2.4 (1.7–3.4) | 0.4 (0.2–1) | 1.5 (0.9–2.2) |
| 2015 | 2.1 (1.4–3.1) | 2.3 (1.6–3.2) | 1.1 (0.6–1.8) | 3.1 (2.3–4.3) | 0.8 (0.4–1.5) | 1.8 (1.1–2.6) |
| 2016 | 2 (1.3–3) | 2.4 (1.6–3.4) | 1.1 (0.6–1.8) | 3.8 (2.7–5) | 0.8 (0.4–1.5) | 1.5 (0.9–2.4) |

^aSignificant change over time.

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2505. Integration of Next-Generation Sequencing, Viral Sequencing, and Host-Response Profiling for the Diagnosis of Acute Infections

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Background. To guide treatment of infectious diseases, clinicians need sensitive, specific, and rapid diagnostics. We aim to incorporate complementary methods of microbial sequencing and host-response profiling to improve the diagnosis of patients at risk for acute infections.

Methods. We enrolled 200 adult patients with systemic inflammatory response syndrome (SIRS) at the Stanford Emergency Department. Physicians with specialty training in infectious diseases conducted retrospective two-physician chart review to establish likely admission diagnoses. Blood samples were tested with a previously described 18-gene host-response integrated antibiotics decision model (IADM) that distinguishes noninfectious SIRS, bacterial infections and viral infections. Plasma samples were tested with shotgun metagenomic next-generation sequencing (NGS) and viral sequencing with VirCapSeq. A novel statistical algorithm was developed to identify contaminant organism sequences in NGS data.

Results. The physician chart review classified 99 patients (49%) as infected, 69 (35%) possibly infected and 32 (16%) non-infected. Compared with chart review, the IADM distinguished bacterial from viral infections with an area under curve of 0.85 (95% confidence interval 0.77–0.93). NGS results to date confirmed positive blood cultures in seven of nine patients, with two of four blood culture-positive *E. coli* patients turning up negative on NGS due to *E. coli* contamination. NGS also confirmed positive cultures from other sites in two of six patients with negative blood cultures. Preliminary VirCapSeq data from 23 patients confirmed positive viral tests in five of six patients with Hepatitis C, BK Virus, Cytomegalovirus and Epstein-Barr Virus infections. VirCapSeq did not identify a causative agent in the plasma of 11 patients with confirmed respiratory viral infection and intestinal Norovirus infection, and six patients with idiopathic illness. Interestingly, VirCapSeq found viral reactivation in 8 of 12 immunocompromised patients.

Conclusion. The diagnosis of suspected infections may be enhanced by integrating host-response and microbial data alongside clinical judgment. Our results and large cohort lay the foundation to demonstrate the utility of this approach and in which patients these tools may be most useful.

Disclosures. T. E. Sweeney, Inflammatix, Inc: Employee and Shareholder, Salary; T. Briese, Roche: Columbia University has licensed VirCapSeq to Roche, Licensing agreement or royalty; W. I. Lipkin, Roche: Columbia University has licensed VirCapSeq to Roche., Licensing agreement or royalty; P. Khatri, Inflammatix, Inc.: Co-founder, Scientific Advisor and Shareholder, Licensing agreement or royalty and ownership stock; D. A. Relman, Karius: Consultant, Stock options; Arc Bio LLC: Consultant, Stock options