of rectal CT infection underwent additional testing to identify LGV serovars utilizing novel real-time PCR assays specific for the L serovars of CT *Chlamydia trachomatis*.

Results. From 28 April 2014–19 July 2016, 420 men underwent screening for rectal STIs, including 66 (15.7%) who had prevalent rectal infection with CT. An additional 68 participants developed incident infections during 208 person-years of follow-up. Of 134 eligible rectal swab specimens, 128 underwent further testing for LGV serovars. Seven (5.5%) of the tested samples were identified as LGV serovars of CT. None of the seven participants with LGV reported any symptoms such as fever or rectal pain. Two of the participants with LGV were simultaneously co-infected with rectal gonorrhea. HIV co-infection was common among participants with both LGV and non-LGV serovars of CT (71% and 77%, respectively, $P = 0.74$).

Conclusion. LGV was uncommon but present among Nigerian MSM in this study. LGV needs to be considered even in asymptomatic cases, particularly if anorectal CT infection fails to respond to the usual course of therapy. Consistent screening for L serovars of CT, or empiric treatment for LGV in cases with a high suspicion for this diagnosis, could potentially improve patient outcomes and decrease transmission.

Disclosures. **All authors:** No reported disclosures.

2501. Real-Time PCR Targeting Mosaic *penA* XXXIV for Prediction of Extended-Spectrum Cephalosporins Susceptibility in Clinical *Neisseria Gonorrheae* Isolates

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Session: 279. STIs - Diagnostics and Therapy
Saturday, October 7, 2017: 2:00 PM

Background. Antimicrobial-resistant *Neisseria gonorrheae* (NG) is a global public health problem, resulting in limited empirical treatment options. Due to increasing minimum inhibitory concentrations (MICs) of ESCs against NG in the US, it is critical that susceptibility to ESCs be monitored. Since few laboratories routinely perform culture and susceptibility testing for NG, there is a need for a rapid test to predict susceptibility to ESCs. More than 98% of isolates with decreased susceptibility to cefixime (CFM) in the US carry mosaic *penA* XXXIV. In this study, we developed a multiplex real-time PCR for mosaic *penA* XXXIV and previously validated *gyrA* to predict ESCs MICs and ciprofloxacin (CIP) susceptibility.

Methods. 150 NG isolates with known cefpodoxime (CPD), CFM, ceftriaxone (CRO) and CIP MICs were obtained from Neisseria Reference Laboratory at University of Washington and CDC Antimicrobial Resistance Bank. DNA extracted from culture was used in multiplex HybProbe real-time PCR on Lightcycler 480. *gyrA* was genotyped by melt curve and served as internal control, while presence of mosaic *penA* XXXIV was detected by selective amplification.

Results. All 32 (100%) CIP-susceptible and 118 (100%) CIP-resistant isolates, as determined by Clinical and Laboratory Standards Institute breakpoints, demonstrated wild-type and Ser91 mutant *gyrA* genotype, respectively. Melt curve genotyping demonstrated mosaic *penA* XXXIV melt patterns in 66/68 (97%) isolates with at least one ESC MIC above alert value set forth by the CDC (CPD and CFM MICs ≥0.25 µg/ml; CRO MIC ≥0.125), while all 82 (100%) isolates with ESC MICs under alert values did not amplify. The first of the 2 false-negative isolates had MICs above alert values for all ESCs tested and harbored IX mosaic type, while the second one had CRO MIC above alert value and harbored XII mosaic type. Both of these mosaic types did not share homology with mosaic *penA* XXXIV in the region targeted by the assay.

Conclusion. The mosaic *penA* XXXIV assay demonstrated 97% sensitivity and 100% specificity in predicting alert ESCs MIC values among clinical isolates tested, and was successfully multiplexed with *gyrA* assay. Clinical utility of this assay may be limited due to false negativity in isolates with non-XXXIV mosaic types, but it could serve as a useful surveillance tool for XXXIV mosaic.

Disclosure. **R. Humphries**, Roche: Consultant, Consulting fee

2502. Electronic Reminder Notifications Improve Uptake of Targeted Ciprofloxacin Therapy for *Neisseria gonorrheae* Infections at the University of California, Los Angeles Health System

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Session: 279. STIs - Diagnostics and Therapy
Saturday, October 7, 2017: 2:00 PM

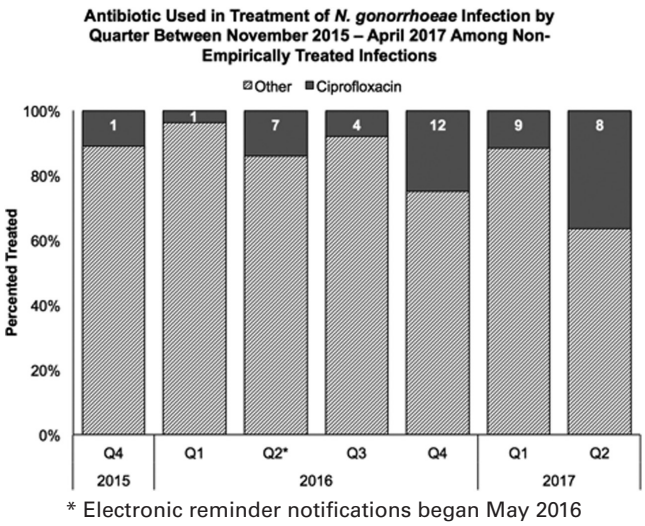
Background. A wild-type gyrase A (*gyr*A) genotype of *N. gonorrheae* reliably predicts susceptibility to ciprofloxacin, which can reduce selection pressure for ceftriaxone-resistant infections, an urgent public health threat. In November 2015, UCLA Health began *gyr*A genotyping all *N. gonorrheae* positive specimens. In May 2016, we began sending reminder notifications of treatment recommendations to providers of patients with wild-type infections.

Methods. We reviewed records for all laboratory confirmed *N. gonorrheae* cases from November 1, 2015–April 30, 2017. Infections in different anatomic sites were considered unique infections, while unique infections in a single patient on the same date were considered a case. Empiric therapy was defined as treatment within 1 day of specimen collection. We also collected test-of-cure data among patients with wild-type infections treated with ciprofloxacin.

Results. Among 423 patients (23% HIV infected) there were 460 cases and 514 anatomic site-specific *N. gonorrheae* infections. Of infections, 218 (43%) had a wild-type *gyr*A genotype, 138 (27%) mutant, 153 (30%) indeterminate, 4 were not attempted, and 1 had missing data. There were 255 (55%) cases and 283 (55%) infections treated non-empirically. The median time-to-treatment among those cases was 4 days (interquartile range 3–6 days). Ciprofloxacin was used in 2 (3%) of 66 nonempirically treated infections prior to the start of reminder notifications, compared with 40 (18%) of 217 nonempirically treated infections after notifications began ($P = 0.002$). Of the 55 providers who received an email on or before the day of treatment for non-empirically treated patients, 32 (58%) used ciprofloxacin. There was no ciprofloxacin use prior to assay implementation. The trend in treatment by quarter among non-empirically treated infections is shown the Figure.

Among 30 patients treated with ciprofloxacin, 6 had a test of cure at one week, and all (100%; 95% CI 61%–100%) of those tests were negative for *N. gonorrheae*; 5 were from urethral specimens, and 1 was from the pharynx.

Conclusion. Electronic provider notifications augmented targeted ciprofloxacin therapy for *N. gonorrheae* infections. Preliminary test-of-cure data are promising.



Disclosures. **All authors:** No reported disclosures.

2503. Gonorrhea (GC) and Chlamydia (CT) Infection in a Large, Well-Characterized Military Cohort: Prevalence, Incidence, Site of Infection, and Patient Characteristics

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Session: 279. STIs - Diagnostics and Therapy
Saturday, October 7, 2017: 2:00 PM

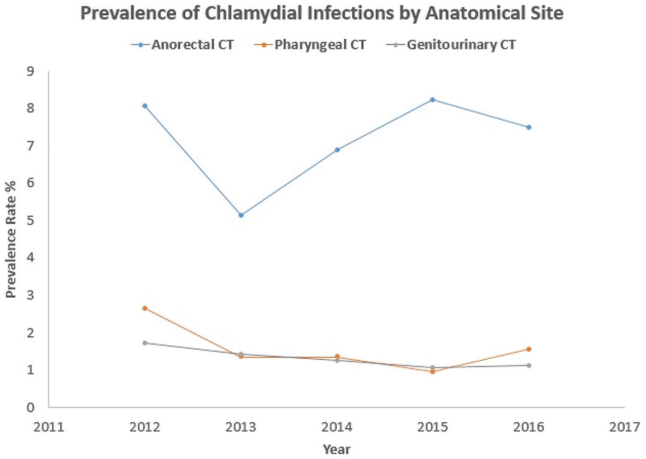
Background. In the US military, routine extra-genital (EG) GC/CT testing in persons living with HIV was implemented in 2012. This study examines the prevalence/incidence and risk factors associated with genital (GU) and EG GC/CT

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.



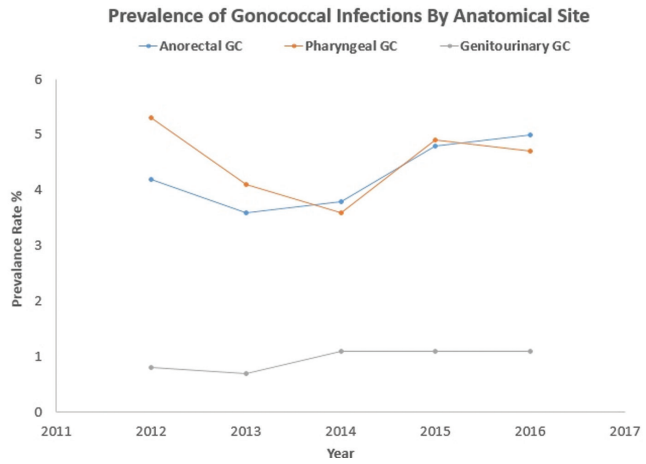


Table. Incidence rate per 100 person-years (95% confidence interval) by site

	GC			CT		
Year	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)

[a]Significant change over time.

Disclosures. **All authors:** No reported disclosures.

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

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Session: 282. Featured Oral Abstract
Saturday, October 7, 2017: 4:45 PM

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