P489 *CHLAMYDIA TRACHOMATIS* -SPECIFIC GENE TRANSCRIPTS AS A MORE ACCURATE MARKER FOR INFECTION STATUS

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Background Current routine diagnostic methods for the detection of *Chlamydia trachomatis* (CT) do not provide information on CT viability. Previously, detection of messenger-RNA (mRNA) has been utilized as a marker for bacterial viability, as mRNA molecules are generally short-lived (half-life of minutes). However, only one study evaluated CT mRNA half-life times [$t_{1/2}$] of two clinical isolates (serovar L2b and E) which ranged from 1 to $\geq$5000 minutes. Here we assess and confirm mRNA half-life times of serovar D to further facilitate evaluation of CT viability.
Methods CT serovar D was propagated in HeLa cells until 30 h post infection and treated with rifampicin to arrest gene transcription. Total RNA was isolated at 0 min (before treatment), and 10 min, 30 min and 60 min after treatment. RNA was converted to cDNA using random hexamers. RT-qPCR was used to amplify fragments of the unprocessed 16S (intermediate molecules in 16S rRNA synthesis), 16S (early), *rpoD* (early), *omcB* (mid), and *hctA* (late) gene transcripts. Half-life time was based on the fit of an exponential decay between values obtained at before and after transcriptional arrest.
Results In this study showed that the obtained $t_{1/2}$ values for CT serovar D mRNA (median $t_{1/2}$18 min) were similar as previously reported for the CT serovars L2b and E (median $t_{1/2}$ 15 and 17 min, respectively). The observed half-lifes of *rpoD* (9 min), *hctA* (12 min), *omcB* (18 min), and unprocessed 16S (18 min) transcripts were relatively short, while 16S gene transcripts were more stable over time ($t_{1/2}$54 min).
Conclusion The detection of *rpoD*, *hctA*, *omcB*, and unprocessed 16S gene transcripts showed the most promising results as a potential marker for an active CT infection. Currently we are evaluating the time to clearance of mRNA molecules in patients after being treated.
Disclosure No significant relationships.

P490 LGV IN PATIENTS ATTENDING AN STI OUTPATIENT CLINIC IN BERLIN: AN URBAN EMERGENCE WITH HIGH PROPORTION OF HIV-COINFECTIONS

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Background Lymphogranuloma venereum (LGV) is the infection of the lymphatic system caused by Chlamydia trachomatis (CT) serovars L1-L3. The first emergence of LGV in networks of men, who have sex with men (MSM) began in Europe (2003), followed by a series of outbreaks worldwide. In the absence of national passive surveillance systems for LGV, we evaluated prevalence and characteristics of LGV in a high-risk population (MSM) attending a STI Outpatient Clinic in Berlin.
Methods We performed a retrospective analysis of all tested CT samples (pharyngeal, urethral, rectal) from 2012–2017. All positive rectal samples underwent additional testing for L1-L3 genotype. For this purpose a PCR was performed of a L-specific region (polymorphic H-gene).
Results A total of 12,390 samples (5,316 patients) were collected and resulted in 486 L+ swabs (191 patients). The number of tested swabs increased from 1,370 (2012) to 3,634 (2017). The proportion of CT+ swabs fluctuated between 10% and 15%. Among the CT+ patients, the proportion of L+ patients decreased continuously from 37% (2012) to 21% (2017). The majority of patients tested were male, between 26–35 years of age. We observed the highest rate of L-infections in older patients (maximum in the age-group 46–55 years, CT+/L+ 46%). The majority of patients infected with L+ came from central metropolitan districts. The HIV-coinfection rate among CT+ patients decreased continuously from 39% (2012) to 12% (2017). The proportion of HIV+ patients among L+ patients remained high and decreased from 80% (2012) to 50% (2017).
Conclusion Our data display the largest epidemiological development of LGV in Germany and demonstrate a high prevalence of genotype L1-L3, which require a prolonged antibiotic treatment compared to other CT serotypes. As the routine screening of anorectal swabs in high-risk population is still not recommended, our results strongly suggest a need for genotyping positive CT rectal specimens.
Disclosure No significant relationships.

P491 DETERMINING RECOMMENDED CHLAMYDIA AND GONORRHEA TREATMENT USING LINKED MEDICAL CLAIMS, PRESCRIPTION AND LABORATORY DATA

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Background The Centers for Disease Control and Prevention (CDC) recommends specific regimens for treatment of chlamydia and gonorrhea. Dual therapy is recommended for gonococcal infection to mitigate antimicrobial resistant gonorrhea (250 mg ceftriaxone plus 1g azithromycin). Previous studies examining adherence to these recommendations have had limited information on medical claims, prescription claims, and laboratory data in private practices in the United States.
Methods We used the OptumLabs® Data Warehouse (OLDW) a comprehensive, longitudinal, real-world data asset with de-identified lives with linked private insurance claims and clinical information to identify persons aged 15–60 years who had valid nucleic acid amplified testing results demonstrating gonorrhea or chlamydia in 2016–2017. We defined valid lab results as positive or negative, but did not include lab records with indeterminate or missing results in our analysis. We then assessed the time of their first positive test and the type of

treatment within 30 days to determine if there was evidence in the claims record that the CDC recommended treatment was provided.

Results 4,972 patients were identified as having gonorrhea only. Of this group, 77% were male, and 70% were 15–35 years of age. Additionally among this group, 35% had evidence of receiving the CDC recommended combination therapy for gonorrhea, 26% had evidence of receiving 250 mg ceftriaxone without evidence of receiving 1g azithromycin, and 16% had evidence of receiving 1g azithromycin without ceftriaxone. A separate group of 24,044 patients were identified as having chlamydia only. Among this group, 40% were male, and 88% were 15–35 years of age. Additionally among this group, 65% had evidence of receiving a CDC-recommended chlamydia treatment, and 11% also had evidence of receiving 250 mg ceftriaxone.

Conclusion There is variation in claims data regarding the treatment regimens administered for gonorrhea and chlamydia treatment. Further studies are needed to evaluate treatment claims data against medical record reviews.

Disclosure No significant relationships.

P492 PREDICTING CHLAMYDIA REINFECTION IN AFRICAN AMERICAN WOMEN USING IMMUNOGENETIC DETERMINANTS IN A BAYESIAN MODEL

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Background African Americans have the highest rates of *Chlamydia trachomatis* (CT) infection in the U.S., nearly six-fold higher than Caucasians. Even after controlling for sociodemographic factors, African American women have higher CT infection rates, suggesting immunogenetic factors could influence infection risk. The primary objective of this study is to develop a Bayesian model to predict CT reinfection in African American women.

Methods We are using data from a study cohort of CT-infected women who were enrolled when they returned to a STD clinic in Birmingham, AL, USA, for treatment of a positive screening urogenital CT nucleic acid amplification test. They had repeat urogenital CT NAAT performed at enrollment and 3- and 6-month follow-up visits. We modeled the probability of CT reinfection within 6 months after treatment using conditional logistic regression in a Bayesian framework and weakly informative priors. Primary predictors of interest were immunogenetic risk factors specified by the presence of at least one HLA-DQB1*06 allele and absence of a CT-specific $CD4^+$ IFN-γ response. Additional predictors evaluated include the modifying effects of unprotected sex and concomitant bacterial vaginosis (BV).

Results To date, we have evaluated 75 participants for whom complete data were available. Modeling both HLA-DQB1*06 and a CT-specific $CD4^+$ IFN-γ response performed best for expected predictive accuracy of CT reinfection within 6 months after treatment. Under this model, the probability of reinfection for those with a CT-specific $CD4^+$ IFN-γ response and no HLA-DQB1*06 alleles was 23.1% (95% CI: 7.6%–47.5%), whereas probability of reinfection for those without a CT-specific $CD4^+$ IFN-γ response and at least one HLA-DQB1*06 allele was 75.0% (95% CI: 52.5%–89.1%).

Conclusion Our model evaluating immunogenetic factors predicting CT reinfection demonstrated that presence of an HLA-DQB1*06 allele and absence of a CT-specific $CD4^+$ IFN-γ response may be a significant predictor in African American women.

Disclosure No significant relationships.

P493 DETERMINATION OF *CHLAMYDIA TRACHOMATIS* ORGANISM LOAD IN MEN WITH NON-GONOCOCCAL URETHRITIS (NGU)

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Background The ability to quantify the organism load of *Chlamydia trachomatis* (CT) using a commercial assay could expand insights from epidemiological studies. This approach can be applied to routine diagnostic testing, and multiple specimen types. Approximate CT organism load was determined in urine from men with NGU, with and without co-infections, by comparing the results from each positive sample to a set of CT standards using the Abbott Real*time* *m*2000 (*m*2000) platform.

Methods Urine specimens, collected from men participating in the Idiopathic Urethritis Men's Project (IUMP), were tested on the *m*2000 for CT. Additional testing included *Neisseria gonorrhoeae*, *Mycoplasma genitalium*, *Trichomonas vaginalis*, and *Ureaplasma urealyticum*. Standards were prepared by diluting CT elementary bodies (EB) into the collection device at six concentrations. CT organism load was determined by comparing the instrument generated delta cycle (DC) value from each CT positive urine to the standard curve. Calculated means were compared by t-test ($p<0.05$).

Results Two hundred and six men were tested for CT and 83 (40.3%) were positive. The DC values for 81/83 (97.3%) CT positive samples fell within the range of the standard curve. The mean DC value was 12.15 (range 0.19–16.96) which equated to a mean CT organism load of 1.4×10^6 EB/ml urine (range 2.22×10^2-9.97×10^6). There was no difference between the mean organism load in specimens from men who did and did not have co-infections with other STIs, 2.04×10^6 versus 1.38×10^6 EB/ml, ($p\geq0.05$).

Conclusion CT load determination can be performed on urine specimens using the *m*2000. This could facilitate straightforward load determination in settings where routine testing is performed. In men with NGU, the CT organism load is high and no difference in CT load was observed in men with CT mono-infections and men co-infected with CT and other STIs.

Disclosure No significant relationships.