

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 ≥ 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-lives 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 gonorrhoea. Dual therapy is recommended for gonococcal infection to mitigate antimicrobial resistant gonorrhoea (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 gonorrhoea 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