

Conclusion Women with a history of testing for an STI are at significantly higher risk of not having a pregnancy and reporting a higher use of ART, suggesting that STI testing and a positive CT or NG test result is associated with adverse reproductive health outcomes.

Disclosure No significant relationships.

P479 **IMMUNOPROFILING OF *CHLAMYDIA TRACHOMATIS* COMBINING WHOLE-PROTEOME MICROARRAYS AND HIGH-THROUGHPUT MULTIPLEX SEROLOGY**

Katrin Hufnagel*, Nadine Gassert, Julia Butt, Michael Pawlita, Tim Waterboer. *German Cancer Research Center (DKFZ), Infections and Cancer Epidemiology, Heidelberg, Germany*

10.1136/sextrans-2019-sti.561

Background Chronic infections with *Chlamydia trachomatis* (Ct) can give rise to sequelae that include pelvic inflammatory disease (PID), chronic pelvic pain (CPP), ectopic pregnancy (EP) and tubal factor infertility (TFI), and may contribute to cervical and ovarian cancer development in women. The humoral immune system of an infected individual recognizes and responds to different Ct antigens by eliciting a variety of antibodies. Based on differential protein expression, antibody patterns may represent infection-specific phases of the chlamydial life cycle or disease-specific stages. The selection of potential antigens for the development of serological assays is usually based on prior knowledge about antigenic properties and thus restricted to few selected proteins.

Methods To overcome this bias, we have developed a novel method to generate Ct whole-proteome microarrays directly from bacterial genomic DNA using a combination of multiple spotting technique and cell-free, on-chip protein expression based on expression constructs generated by two successive PCRs. Based on e.g. case-control comparisons, informative antigens are identified and validated in sero-epidemiological studies using low-density, high-throughput Luminex-based multiplex suspension array technology.

Results Establishment of the method for Ct serovar D with 895 open reading frames (ORFs) yielded several novel infection markers, and revealed an association between specific Ct antibodies and the development of cervical carcinoma (adjusted odds ratio (OR) 3.9, 95% confidence interval (CI) 1.8–8.3 for CT_117, and OR 3.1, 95% CI 1.3–7.1 for CT_223).

Conclusion Following this initial screening we aim to identify Ct antigens associated with PID, EP, TFI and ovarian cancer as well as antibody responses associated with protection from Ct re-infection. The newly developed technique for generation of fast and efficient proteome immunoassays can easily be adapted to other complex microorganisms, not only in the field of sexually transmitted infections but in all areas of infection research.

Disclosure No significant relationships.

P480 **ENHANCED PREVALENCE OF *CHLAMYDIA TRACHOMATIS* DNA IN CLINICAL SAMPLES OF PATIENTS WITH STIS CO-INFECTION**

¹Valentina Feodorova*, ¹Sergey Zaitsev, ¹Yury Saltykov, ²Irina Grashkina, ³Charlotte Gaydos, ⁴Thomas Quinn, ⁵Vladimir Motin. ¹Federal Research Center for Virology and Microbiology, Branch in Saratov, Saratov, Russian Federation; ²Saratov State Medical University, Skin Diseases, Saratov, Russian Federation; ³Johns Hopkins University, Division of Infectious Diseases, Baltimore, USA; ⁴National Institute of Allergy and Infectious Diseases, Division of Intramural Research, Baltimore, USA; ⁵University of Texas Medical Branch, Galveston, USA

10.1136/sextrans-2019-sti.562

Background *Chlamydia trachomatis* (CT) is one of the most commonly diagnosed asymptomatic bacterial cause among sexually transmitted infection (STI) worldwide. We assessed the prevalence of CT in random STI patients to evaluate the presence of CT as either a single infection or in co-infection with other STI.

Methods A total of 422 urogenital samples were collected from patients who attended the Diagnostic Centre in Saratov Region to be tested for specific DNA of CT and other STIs (*Neisseria gonorrhoeae*/*Trichomonas vaginalis*/*Mycoplasma hominis*/*Mycoplasma genitalium*/*Human papillomavirus* (HPV 16/18)/*Cytomegalovirus*/*Herpes simplex virus* (HSV 1/2)/*Candida albicans*/*Gardnerella vaginalis*/*Ureaplasma species*). Each clinical sample was carefully screened with the use of commercial kits, either as conventional PCR targeting CT plasmid, or real-time multiplex set (Vector-Best, Russia) validated further by additional confirmatory PCR for the CT-positive samples.

Results CT was detected in 17/194 (4,02%) patients who were screened only for the presence of CT DNA (194/422, 45,97%). However, when all 422 patients were systematically screened for CT, along with all other STIs, CT infections were significantly higher (about 4-fold larger) in the patients with other STIs (70/422, 16,58%). Moreover, 56/70 (80%) CT DNA samples were successfully genotyped as CT genovars: E (50%), G (21,42%), D (17,85%), J (5,35%) and K (3,57%).

Conclusion Chlamydial asymptomatic infection cases can be frequently masked by clinical symptoms of other STIs. Diagnostic testing for multiple STIs should provide a broader diagnostic coverage for asymptomatic CT patients in order to improve significantly CT early detection, prevention of transmission, and treatment strategies.

Disclosure No significant relationships.

P481 **PATIENTS WITH REPEAT *CHLAMYDIA TRACHOMATIS* AND *NEISSERIA GONORRHOEAE* ARE DIFFERENT COMPARED TO THOSE WITH SINGLE INFECTIONS**

¹Juliën Wijers, ¹Nicole Dukers-Muijters, ²Christian Hoebe, ³Petra Wolffs, ²Geneviève Van Lier. ¹Public Health Service South Limburg, Sexual Health Infectious Diseases and Environmental Health, Heerlen, Netherlands; ²Public Health Service South Limburg, Maastricht University Medical Center (MUMC), Sexual Health, Infectious Diseases and Environmental Health, Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Heerlen, Netherlands; ³Maastricht University Medical Center (MUMC), Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Maastricht, Netherlands

10.1136/sextrans-2019-sti.563

Background Recently it was proposed that patients repeatedly infected with *Chlamydia trachomatis*(CT) or *Neisseria gonorrhoeae*(NG), so called core groups, likely have high impact on

circulating STIs within the population. To substantiate such proposition, more information is needed on (1) whether the characteristics of those single infected patients differ from the repeat infected patients and (2) the proportion of patients who were not retested.

Methods Laboratory data from all CT/NG tests by the STI clinic, general practitioners or hospital physicians between 2011–2016 of patients aged 15–64 years were obtained (24,051 tests: 2,317 CT positive, 405 NG positive). The outcome ‘repeatedly infected’ was defined as patients with ≥ 2 CT or ≥ 2 NG infections. Chi-square tests were used to compare characteristics of repeatedly infected versus single infected patients, for CT and NG separately.

Results Patients with repeat CT-infections 12%(215/1,845) were more often women, HIV positive, NG positive, diagnosed at the STI clinic or hospital compared to the GP, had ≥ 1 sex partner, reported urogenital symptoms, proctitis and oropharyngeal symptoms ($p < 0.05$). Of the patients with a single CT infection, 50%(814/1,630) was not retested. Patients with repeat NG-infections 13%(38/296) were more often men, older (≥ 25 years), living in non- and modest urban areas, HIV positive, diagnosed at the STI clinic or hospital and reporting oropharyngeal symptoms ($P < 0.05$). Of the patients with a single NG infection, 27%(69/258) was not retested.

Conclusion Patients with repeat CT/NG infections differed from patients with a single infection. Also, characteristics of repeatedly infected patients differed between CT and NG. Indeed, patients with repeat CT or NG infections have impact on STI transmission. However, 27–50% of CT/NG positive patients were not retested. Probably those patients also have impact on circulating STIs, as reinfections are common. Focus should be on infected patients who do not retest or even not test at all as they enable ongoing transmission.

Disclosure No significant relationships.

P482

WOMEN VISITING GENERAL PRACTITIONERS HAVE HIGHER *CHLAMYDIA TRACHOMATIS* BACTERIAL LOADS THAN WOMEN VISITING THE STI CLINIC

¹Juliën Wijers, ²Geneviève Van Liere, ³Petra Wolffs, ²Christian Hoebe, ⁴Nicole Dukers-Muijers*. ¹Public Health Service South Limburg, Sexual Health Infectious Diseases and Environmental Health, Heerlen, Netherlands; ²Public Health Service South Limburg, Maastricht University Medical Center (MUMC), Sexual Health, Infectious Diseases and Environmental Health, Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Heerlen, Netherlands; ³Maastricht University Medical Center (MUMC), Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Maastricht, Netherlands; ⁴Public Health Service South Limburg, Sexual Health, Infectious Diseases and Environmental Health, Heerlen, Netherlands

10.1136/sextrans-2019-sti.564

Background The bacterial load of *Chlamydia trachomatis* (CT) infected individuals may indicate the likelihood of further transmission and development of sequelae. For the first time, we compared the urogenital CT-load of men and women diagnosed by general practitioners (GPs), hospital physicians and the STI clinic.

Methods All urogenital nucleic acid amplification tests (NAAT) CT-positive samples ($n = 3,588$) from the Maastricht Medical Microbiology Laboratory were included in the analyses (2012–2016). The cycle quantification (Cq)-value of the NAAT was used as an inversely proportional measure for CT-load (Cq-values and CT/ml values were highly correlated, Pearson’s $r = 0.8$). Multivariable linear regression analyses

were used to compare urogenital Cq-values between STI care providers (GPs, hospital physicians, STI clinic) and assess potential associated demographic- and coinfection determinants, stratified by sex. Adjusted mean differences of Cq-values are presented using betas (B) and 95% confidence intervals (95%CI).

Results Urogenital Cq-values were similar in men visiting the GPs (B:0.2;95%CI: -0.3 to 0.7) and hospital physicians (B:0.4;95%CI: -0.8 to 1.6) compared to the STI clinic. Women visiting the GP had significantly lower urogenital Cq-values (B:-1.0;95%CI: -1.6 to -0.3) compared to the STI clinic. Women visiting the hospital had higher urogenital Cq-values (B:1.1;95%CI: 0.2 – 2.0) compared to the STI clinic. Among women visiting the STI clinic, urogenital Cq-values were lower in women with concurrent anorectal CT (B: -3.1 ;95%CI: -3.8 to -2.3) compared to anorectal CT-negative women.

Conclusion Male patients visiting different STI care providers had similar CT-loads. The higher CT load of women visiting the GP compared to STI clinic women could be indicative for higher transmission potential and sequelae. Women visiting hospital physicians had lower CT loads likely due to time of diagnosis. Notably, STI clinic women with concurrent anorectal CT had substantially higher urogenital CT-loads. This finding indicates a missed opportunity in GP and hospital physician patient management, as they rarely test anorectally, while anorectal CT is common among women.

Disclosure No significant relationships.

P483

A LOWER GENITAL *CHLAMYDIA TRACHOMATIS* BACTERIAL LOAD IS ASSOCIATED WITH COINFECTIONS WITH *NEISSERIA GONORRHOEAE* AND HIV

¹Juliën Wijers, ¹Nicole Dukers-Muijers*, ²Geneviève Van Liere, ³Petra Wolffs, ²Christian Hoebe. ¹Public Health Service South Limburg, Sexual Health Infectious Diseases and Environmental Health, Heerlen, Netherlands; ²Public Health Service South Limburg, Maastricht University Medical Center (MUMC), Sexual Health, Infectious Diseases and Environmental Health, Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Heerlen, Netherlands; ³Maastricht University Medical Center (MUMC), Medical Microbiology, Care and Public Health Research Institute (CAPHRI), Maastricht, Netherlands

10.1136/sextrans-2019-sti.565

Background The bacterial load of *Chlamydia trachomatis* (CT) infected individuals may indicate the likelihood of further transmission and development of sequelae. This is the first and largest study to date providing results of a complete overview of the bacterial CT-load of genital and extra-genital samples and its associations with *Neisseria gonorrhoeae* (NG) infection and HIV.

Methods All genital ($n = 2,067$ vaginal swabs; $n = 1,793$ urines), anorectal ($n = 828$) and oropharyngeal ($n = 61$) nucleic acid amplification test (NAAT) CT-positive samples from the Maastricht Medical Microbiology Laboratory were included in analyses (2012–2016). The NAAT cycle quantification (Cq)-value was used as an inversely proportional measure for CT-load (Cq-values and CT/ml values were highly correlated for vaginal swabs; Pearson’s $r = 0.9$, and moderately correlated for urine in men; Pearson’s $r = 0.6$; $p < 0.001$). Mean Cq-values were compared between anatomic locations and coinfections with HIV and NG. Mean Cq-values are presented and tested using ANOVA and independent T-tests stratified for sex. Only statistically significant associations ($p < 0.05$) are presented.

Results In men, Cq-values were higher in oropharyngeal swabs and anorectal swabs compared to urine (35.9 and 33.9 vs