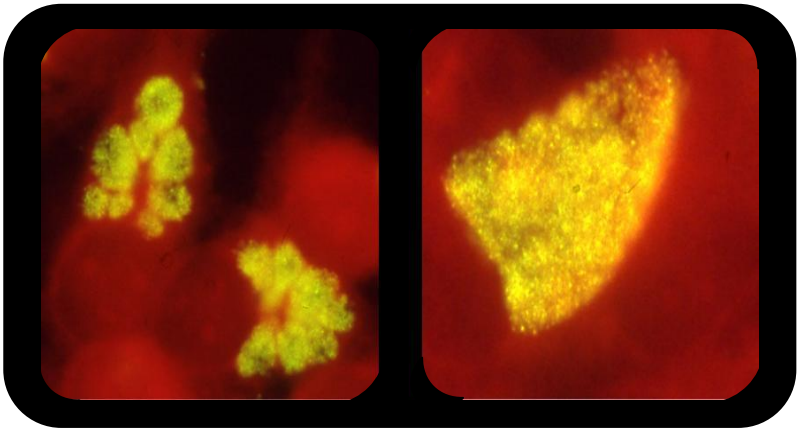
10th AACM

Tenth Annual Amsterdam

Chlamydia Meeting



Hotel Mercure Amsterdam City

6 February 2015
9.00 – 17.00

Preface

Welcome: This is a special occasion, we organise this year our Lustrum meeting, the tenth Annual Amsterdam *Chlamydia* Meeting (10th AACM)! To celebrate this we have this year for the first time a Prize for the best oral presentation by a PhD student, and the quality of the orals will be assessed by the 5 Moderators of our sessions.

Each session will have its own keynote speaker and most are from abroad, including Dr. Georg Stary (Austria), Dr. Remco Peters (South Africa), Dr. Anthony Croxatto (Switerland), and Elisabeth Delaroque-Astagneau (France). The meeting will be opened by Dr. Georg Stary (Austria) on Chlamydial immunology. As from the first AACM forward, we have many junior speakers including PhD students with in total 18 speakers. We are confident that the speakers will spark the minds of both young as well as established Chlamydiologists and trigger valuable discussions this day!

The Laboratory of Immunogenetics: it was established by Emeritus Prof. A. Salvador Peña in 1992, and has become part of the Department of Pathology in 2005 (Prof. Chris J.L.M. Meijer) and since 2012 it became part of the Department of Medical Microbiology and Infection Control. The Laboratory links fundamental scientific research and clinical applications (translational research). Research is divided into two interactive and productive lines: chronic inflammatory diseases (J.B.A. Crusius, PhD) and infectious diseases (Prof. S.A. Morré, PhD; from Jan 1st, 2008, Head of the Laboratory of Immunogenetics and Dr. Sander Ouburg) with *Chlamydia trachomatis* as main pathogen. In addition, we coordinator the Dutch *Chlamydia trachomatis* Reference Laboratory for the Dutch National Institute of Public Health and the Environment (RIVM) since 2009 and since 1 jan 2014 together with Prof.dr. Christian Hoebe (UM).

Acknowledgements: We would like to thank our sponsors, without their support this meeting would not be possible in the current format: Main sponsor Roche, our partners, Becton Dickinson, Mediphos, Cepheid, TubaScan, Hologic (including GenProbe) and our Ambassadors DiaSorin and Goffin Molecular Technologies. We would also like to thank those involved in the organization of this meeting from our Laboartory of Immunogenetics and the Klinkhamer Group.

Dr. Servaas A. Morré
Head of the Laboratory of
Immunogenetics

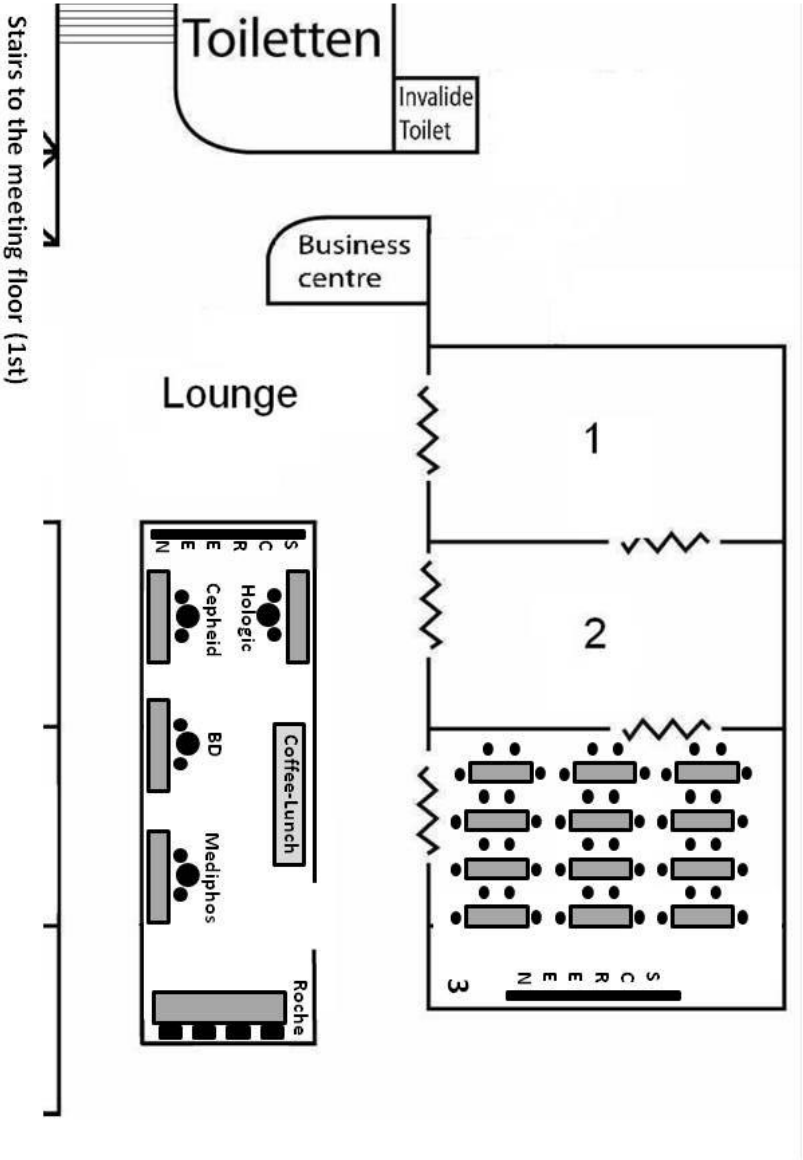
Dr. Sander Ouburg
Senior Postdoc
Infectious Diseases

Laboratory of Immunogenetics, Dept. Medical Microbiology and Infection Control, VUmc, Amsterdam, The Netherlands

Cover photographs: Immunofluorescence staining of *Chlamydia trachomatis* within epithelial cells. HeLa cells were infected with a clinical isolate and stained with a monoclonal antibody specific for the major outer membrane protein (OmpA) of *C. trachomatis*. The left panel shows a nonfusogenic phenotype, while the right panel shows a fusogenic phenotype. Images courtesy of Yvonne Pannekoek, Department of Medical Microbiology, Academic Medical Center, Amsterdam, The Netherlands.

Amsterdam, 6 February 2015

Floor plan (1st Floor, room 3)


Stairs to the meeting floor (1st)
Toiletten
Invalide Toilet
Business centre
Lounge
1
2
3
meeting rooom
SCREEN
Hologic
Cepheid
BD
Mediphos
Roche
Coffee-Lunch

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Programme

9.00 – 9.30 **Registration to the symposium (1st floor, Foyer outside Room 3)**

9.30 Prof. Servaas Morré (NL)
Opening of the symposium

Session: Clinical *Chlamydia trachomatis* diagnostics
Moderator: Prof. Henry de Vries

9.35 Dr. Georg Stary (AT / US)
A mucosal vaccine against Chlamydia trachomatis generates two synergistic waves of protective memory T cells

10.15 Dr. Jannie van der Helm (NL)
What is the optimal time to retest STI clinic patients with a urogenital Chlamydia infection?

10.30 Drs. Martin Singer (NL)
Chlamydia and cytokine expression profiles

10.45 – 11.05 **Coffee Break (In front of the meeting room)**

Session: Dilemmas in human *Chlamydia trachomatis* control
Moderator: Prof. Christian Hoebe

11.05 Dr. Tanja Geelen (NL)
Oro-pharygeal Chlamydia infections in STI control efforts

11.30 Drs. Geneviève van Liere (NL)
Anorectal chlamydia, a hidden reservoir?

11.45 Drs. Anne Dirks (NL)
Natural course of Chlamydia trachomatis bacterial load

12.00 Dr. Louise van Oeffelen (NL)
Risk of late complications after CT infection

12.15 – 13.00 **Lunch (In font of the meeting room)**

Programme

Session: *Chlamydial trachomatis* infections outside of Europe
Moderator: Dr. Remco Peters

13.00 Dr. Remco Peters (NL / SA)
Chlamydia trachomatis and the global health agenda

13.40 Drs. Menne Bartelsman (NL)
POC Diagnostics for CT using Gramm staining

13.55 Dr. Sylvia Bruisten (NL)
Analysis of high resolution-MLST data of Chlamydia trachomatis strains from 16 countries in different continents

14.10 – 14.25 **Coffee break (In front of the meeting room)**

Session: Non-CT Chlamydial infections
Moderator: Prof. Daisy Vanrompay

14.25 Dr. Antony Croxatto (CH)
Chlamydia-like bacteria

14.50 Drs. Sarah van Lent (BE)
Transcriptional and translational analysis C psittaci pmp's

15.05 Dr. Stephan Verweij (NL)
Waddlia chondrophila and female infertility

15.20 Dr. Yvonne Pannekoek (NL)
Chlamydia Genomics

Session: *Chlamydia trachomatis* Epidemiology, Detection, and Research
Moderator: Prof. Servaas Morré

15.35 Dr. Elisabeth Delarocque-Astagneau (FR)
Prevention strategies for Chlamydia trachomatis control in France: Research still needed to refine current recommendations

16.00 Drs. Bart Versteeg (NL)
High resolution multilocus sequence typing reveals unique urogenital Chlamydia trachomatis strains in women in Mopani District, South Africa

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Programme

16.00 Drs. Bart Versteeg (NL)
High resolution multilocus sequence typing reveals unique urogenital Chlamydia trachomatis strains in women in Mopani District, South Africa

16.15 Drs. Nynke de Vrieze (NL)
Epidemiology of urethral LGV infections

16.30 Dr. Arjen Speksnijder (NL)
The vaginal microbiome as a predictor for acquiring Chlamydia trachomatis (Ct)

16.45 Moderators meet to select the best oral presentation by a PhD student

Closing remarks: Prof. dr. Servaas Morré

17:00 - 18:00 Drinks with "bitterballen" (Foyer, lobby level)

18:00 Diner (Restaurant Mercure Amsterdam City)

Georg Stary, PhD

Division of Immunology, Department of Microbiology and Immunobiology, Harvard Medical School, Boston, USA
Division of Immunology, Allergy and Infectious Diseases, Department of Dermatology, Medical University of Vienna, Vienna, Austria
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Curriculum Vitae

Georg Stary is a dermatologist with prime interest in immunology and infectious diseases. He graduated from medical school in 2004 and was trained as dermatologist at the Department of Dermatology in Vienna. During his residency he performed studies on the immune system of the human skin with a focus on the cutaneous dendritic cell network. In 2010 he started a four-year postdoc in Prof. von Andrian's lab at Harvard Medical School, Boston, and evaluated new strategies for mucosal vaccination. He used *Chlamydia trachomatis* as model pathogen for mucosal infections. In 2014 he returned to Vienna and is currently working at the Department of Dermatology as senior physician and group leader of his newly established lab.

Abstract

Vaccines that are administered via non-mucosal routes are often poorly protective against mucosal pathogens, presumably because such vaccines do not generate memory cells that migrate to mucosal surfaces. Although mucosa-tropic memory cells are inducible by mucosal immunization, few mucosal vaccines are currently used clinically because live vaccine vectors pose safety risks and many antigens are weak immunogens when applied to intact mucosa. Moreover, the mechanisms of immune protection against many mucosal infections are not well understood. One case in point is *Chlamydia trachomatis* (Ct).
Genital Ct infection induces protective immunity that is thought to depend on interferon-γ (IFN-γ) producing CD4 T cells. By contrast, we observed that mucosal exposure to UV-inactivated Ct (UV-Ct) generates tolerogenic Ct-specific regulatory T cells, resulting in exacerbated bacterial burden upon subsequent Ct infection. Here, we show that mucosal immunization with UV-Ct complexed with charge-switching synthetic adjuvant particles (cSAP) did not exert the tolerogenic effect of UV-Ct alone but elicited long-lived protection against genital Ct infection. This differential effect of UV-Ct-cSAP versus UV-Ct was because the former was preferentially presented by immunogenic CD11b+CD103– dendritic cells (DCs), while the latter was primarily acquired by tolerogenic CD11b–CD103+ DCs. Notably, genital protection was achieved after either intrauterine or intranasal, but not subcutaneous immunization with UV-Ct-cSAP and was inducible. Only

mucosal vaccination, like mucosal infection with live Ct, induced a wave of Ct-specific CD4+ effector cells that accessed the genital mucosa during the first week and established long-term resident memory T cells (TRM). For optimal clearance of Ct upon rechallenge, a second memory cell wave needed to be recruited to infected tissue from the circulating pool.
Thus, using a novel platform for mucosal immunization, we demonstrate that protection against Ct depends on synergistic actions of two discrete memory T cell subsets with distinct migratory properties.

Jannie van der Helm, PhD

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Curriculum Vitae

Jannie van der Helm is an epidemiologist with prime interest in infectious diseases. After obtaining her Master degree in Biomedical Science at the Radboud University Nijmegen in 2006 she worked as datamanager at the Public Health Service Amsterdam and two years later combined this with her PhD research. In September 2014 she graduated at the University of Amsterdam, thesis entitled “International epidemiological studies on HIV, Hepatitis C and STI”, supervised by Prof. H.J.C. de Vries and Prof. M. Prins. During her PhD project she closely collaborated with various research groups and institutes in Europe, Canada, Australia and Suriname. She published in high impact journals and received several prizes for her work. She is currently employed as a postdoctoral fellow at the Public Health Service (GGD) Amsterdam.

Abstract

Background

Chlamydia trachomatis (Ct) is a common and often recurring sexually transmitted infection.

Retesting can be an effective strategy to prevent onward transmission and late sequellae. However, the recommendation of when to retest varies widely by current guidelines. Therefore, we assessed the optimal time to retest following treatment of urogenital Ct.

Methods

Included in the study were heterosexual clients of the Amsterdam STI outpatient clinic who were positive for urogenital Ct by a nucleic acid amplification test (NAAT). After diagnosis, treatment and counselling, they were offered retesting for Ct. Participants were randomly assigned for retesting after 2, 4 or 6 months. Participants could choose between two retest options: collect a sample (urine for men, vaginal swab for women) at home or return to the clinic, in both cases using the same type of self-collection kit. Participation and Ct positivity rates at follow-up of individuals randomized to the 3 retest intervals were calculated. An intention-to-treat analysis was performed using follow-up data until 8 months after the recruitment visit.

Results

Between May 2012 and March 2013, 2257 individuals were included (45% were male, median age 23 years [IQR 21-26]). The participation rate of retesting was significantly higher in the 2-months-group (65.8%) compared to the 4- (50.5%) and 6-months-group (40.9%, p<0.001) while the positivity rate was comparable between the three groups (9%, p=0.859). Retesting more than 1 week before the scheduled retest moment occurred significantly more often in the 6-month group (20%) compared to the 2-months-group (5%, p<0.001), however the positivity rate was significantly higher in the 2-months group (36% vs 21%, p=0.026). The intention-to-treat analysis showed that the return rate within 8 months after the initial visit (regardless of timing) was significantly higher in the 2-months-group (76.7%) compared to the 6-months-group (63.8%, p<0.001); however the positivity rates were comparable (p=0.998).

Conclusion

We recommend to offer retesting to STI clinic patients not later than 4 months following an initial diagnosis of urogenital Ct. The participation rate was higher when earlier retesting was offered and positivity rates were comparable. Moreover, 20% of individuals scheduled in the 6 month group re-tested >1 week before their scheduled retest moment, indicating that a 6 month interval is too long.

Martin Singer, MSc

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Curriculum Vitae

Martin Singer, born 26th of July 1989, has a bachelor of applied sciences degree and a master degree in biomedical sciences (VU University of Amsterdam). During internships at the laboratory of immunogenetics at the department of Medical Microbiology and Infecton Control, he worked on *Chlamydia trachomatis* among other bacterial STDs. He studied genetics that influence the susceptibility and severity of a *Chlamydia trachomatis* infections as well as the influence of cytokines on the severity of the infections. He's now a PhD student at the laboratory of immunogenetics.

Abstract

Bacterial urogenital infections like chlamydia are widespread inflammatory diseases with severe symptoms if the infection goes untreated. These symptoms can range from inflammation to infertility and ectopic pregnancy. Host cytokines play a vital role in both the initial and long term immune response, indirectly affecting the symptoms experienced by the host. However, levels of cytokine expression vary between individuals. Meta-analysis of previous literature on the subject confirms severity of *Chlamydia* infections is strongly affected by a number of cytokines related to both the innate and adaptive immune response. Further review of scientific articles showed the level of cytokine expression during the Th1 based response against *C. trachomatis* was shown to vary substantially between infected hosts. Inflammation related cytokines TNFα and IFNγ affect the clinical outcome of the disease most noticeably. Similarly, other bacterial urogenital infections were also shown to be affected by varying cytokine expression levels. Cytokine expression levels, especially for IL-6, IL-17, and TNFα, during *N. gonorrhoeae* infections affect the outcome of that disease as well. During *T. pallidum* infections the effect of cytokine expression levels varies between different stages of the disease due to differences in immune response during these different stages. However, it was clearly shown that IFNγ variation in hosts greatly affected the ability and time needed to clear the infection. All studied pathogens were shown to be affected in some way by cytokine expression variations in TNFα or IFNγ. This potentially opens the way to potential joint therapies in the future, and may mean that conclusions drawn for these cytokine

during infection with one pathogen may be found later on for the other studied pathogens as well.

Tanja Geelen, PhD

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Curriculum Vitae

Tanja Geelen received her MSc-degree in 2008 at the University of Maastricht where she studied Clinical Molecular Science. She completed her PhD in 2013, at the University of Maastricht, Dept. of Medical Microbiology MUMC+, with the thesis entiteld: '*Haemophilus influenzae* in respiratory disease, from the bug to the body'. After her graduation, she joined the STI research group from the Dept. of Medical Microbiology. Her research interests are both the general epidemiology of several STI as well as more experimental research on Chlamydia trachomatis. At the same time she started the training for medical molecular microbiologist (MMM) under supervision of Prof. P. Savelkoul and Dr. ir. P. Wolffs.

Abstract

Introduction:

There is increasing data concerning the prevalence of extra-genital *C. trachomatis* (CT) infections. CT can infect the pharynx asymptomatically as the only site of infection, and, as such, might have the potential for pharyngeal-to-genital transmission.

Aims:

Studying pharyngeal CT infections to gain more insight in the prevalence and bacterial load, critical for sexually transmitted infection (STI) control efforts.

Material & Methods:

We retrospectively analysed all oral CT requests, assessed using the Cobas 4800-CT/NG-assay (Roche) performed from 2012 until 2014.

Results:

Oral swabs (n=5946) were obtained for men (70%) and women (30%), with a CT detection rate of 0.8% (n=48). Oral CT infection involved a single site in 56% of the cases (n=27). Multiple anatomical (anorectal or genital) site CT infection were observed for the remaining cases, with 21% being positive at all sites tested. The majority of oral tests were requested by the STI clinics (97% of requests) based on reported risk behaviour. The median cycle threshold (Ct) for oral swabs was

36.5 (range: 24.57-40.57), whereby 90% of the samples had Ct values >30. These are relatively high Ct values compared to genital infection (median:24.35, range:14.93-39.85). No differences were observed between Ct values in single infections or multiple anatomical site CT infections.

Discussion/Conclusion:
These results showed that screening of oral samples for CT infection contributes to STI detection, as most of the cases involved single site infections. Furthermore the relatively high Ct values (low bacterial load) observed warrants further exploration as this could affect the risk of pharyngeal-to-genital transmission.

Geneviève van Liere, PhD

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Curriculum Vitae

Geneviève van Liere (1987) graduated in Health Sciences - Infectious Diseases in 2010 at the VU University in Amsterdam. She completed her Master thesis in Valencia, Venezuela. Results of the study were published in Acta Tropica. In October 2010 she started working as a researcher/datamanager at the Public Health Service (GGD) South Limburg. Since October 2011 she is also working as a PhD student at the Public Health Service (GGD) South Limburg in collaboration with Research school CAPHRI and the department of Medical Microbiology, Maastricht University Medical Center. Her PhD project is about epidemiology of *Chlamydia trachomatis* with focus on testing policy.

Abstract

Background

Anorectal chlamydia (Ct) is frequently diagnosed in men who have sex with men (MSM) and women. It is unknown whether anorectal Ct in MSM and women detected by NAAT are comparable in clinical impact and transmission potential. Bacterial load quantification of anorectal Ct and knowing which determinants are associated with (high) bacterial load could provide more insight.

Methods

A convenience sample of anorectal Ct positive MSM who reported anal sex (n=90) and women with concurrent urogenital/anorectal Ct who reported anal sex (n=51) and who did not report anal sex (n=61) were selected from the South Limburg Public Health Service's STD unit. Bacterial load (Ct/ml) was quantified for all samples and log transformed for analyses. Samples with undetectable HLA (n=9) were excluded from analyses.

Results

MSM who reported anal sex had a similar mean log anorectal Ct load (3.5) as women who reported anal sex (3.80) (P=0.21). Anorectal Ct load was significantly higher in women who reported anal sex (3.80) compared to women who did not report anal sex (2.76, P=0.001). The proportion with load samples undetectable was 8.9% (n=8) in MSM who reported anal sex, 9.8% (n=5) in women who

reported anal sex and 27.9% (n=17) in women who did not report anal sex (P=0.03). Detectable load values ranged between 1.81-6.32 for MSM, between 1.74-7.33 for women who reported anal sex this was, and between 1.84-6.31 for women who did not report anal sex. Symptoms and other determinants were all not associated with anorectal Ct load.

Conclusions

Anorectal chlamydial load was comparable between MSM and women who reported anal sex, suggesting comparable transmission potential. Women who did not report anal sex had lower anorectal load, but within comparable range as observed in MSM and in women who reported anal sex. Possibly, autoinoculation plays a role in anorectal Ct load in women.

Anne Dirks, MD

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Curriculum Vitae

Jeanne Agnes Maria Catharina Dirks was born in 's-Hertogenbosch on July 29, 1986. After completing the Gymnasium in 2004, she commenced her Bachelor of Science at University College Roosevelt in Middelburg. Her university education was continued in Maastricht, with the Physician-Clinical Investigator programme, resulting in an MD and MSc-degree in 2011. Hereafter a PhD-trajectory was started under supervision of CJPA Hoebe, PFG Wolffs and NH Dukers-Muijrers in Maastricht. The topic of the PhD is the bacterial load in *Chlamydia trachomatis* infections, and its relation to both bacterial and host factors. Since September 2014, Anne is a registrar in medical microbiology at the Maastricht University Medical Centre.

Abstract

Chlamydia trachomatis (CT) has an incubation time of approximately 1-3 weeks [1], and it is recommended that testing take place at least 2 weeks after unsafe sexual contact [2], to avoid the chance of false negatives. However, nucleic acid amplification techniques, the most commonly used diagnostic method nowadays, have a much higher sensitivity and specificity than older techniques like enzyme immunoassay or culture. Therefore, we investigated the bacterial CT load at two time-points during an infection, to determine the optimal testing time based on the natural course of the bacterial load.

Patients from the STI-clinic in South Limburg were asked to provide two samples per anatomical location per time point; the moment of screening (T1) and the moment of treatment (T2). 287 CT-positive patients (30% men) were included, which resulted in 312 paired samples; 81 urine samples, 191 vaginal swabs and 40 anal swabs (12 male; 28 female). Time between samples ranged from 3 to 63 days. Patients who used antibiotics in the interval between T1 and T2 were excluded. CT-load was determined using quantitative PCR. A difference of ≤1 log between paired samples was deemed normal intrapersonal PCR variation.

The majority of samples showed an equal CT load in the interval between T1 and T2; 68% of vaginal swabs, 72% of urines and 50% of anal swabs. Surprisingly, 22% of vaginal swabs, 17% of urines and 40% of anal swabs showed a decrease in CT load in the interval between screening and treatment. While only ±10% of

samples showed an increase in load in this interval. Excluding samples with more than 14 days difference (13.5%) did not alter the results. The number of days between samples did not influence the difference in CT load, e.g. the load difference did not increase with more time between samples.
If the natural course of CT follows the same curve observed in animal studies, our results seem to indicate that 90% of patients get tested during the plateau- or declining phase of the infection, but only rarely during the upward phase. Thus, our results seem to indicate that the majority of patients visit the STI-clinic when the infection has already been established or is in its downward phase. Although this needs to be evaluated on a larger scale, our results seem to indicate that it is not necessary to wait 2 weeks after unsafe sexual practices before CT testing, but that this period can be shortened without any missed diagnoses.

[1] NHG-standaard: Het soa consult. 2014.
[2] Soa-aids: www.soaaids.nl/nl/soas/de-soa-test

Louise van Oeffelen, PhD

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Curriculum Vitae

Louise van Oeffelen (1984) obtained her bachelor degree in Nutrition and Dietetics at the Hogeschool van Arnhem en Nijmegen in 2008. In the same year she started her academic education by studying Nutrition and Health at the Wageningen University, with a specialisation in Epidemiology and Public Health. Her master thesis was performed at the National Institute for Public Health and the Environment (RIVM), where she investigated the relation between serum micronutrient concentrations and the development of asthma in children. After she graduated in 2010, she worked four months at the RIVM as a junior researcher on a project about the prevalence and consequences of chronic diseases in children. In February 2011 she started her PhD research at the UMC Utrecht concerning ethnic inequalities in cardiovascular disease incidence, prognosis and health care use. She combined her PhD project with the post-master program Clinical Epidemiology at the Utrecht University. After obtaining her doctor's degree in June 2014, she began working as an epidemiologist at the STI group of the RIVM. She is mainly involved in the development and execution of the Netherlands Chlamydia Cohort Study, which aims at determining the risk of late complications after a *Chlamydia trachomatis* infection in women, and at identifying (genetic) factors that may contribute to the development of these complications.

Abstract

Rationale:

Chlamydia trachomatis (Ct) is a common sexually transmitted infection (STI) among young people. Although the course of infection is often asymptomatic, Ct may lead to severe complications in women, such as pelvic inflammatory disease (PID), prolonged time to pregnancy, ectopic pregnancy, and tubal infertility. Since various transmission control strategies have not been successful in reducing Ct prevalence, it may be more effective to focus on prevention of complications after a Ct infection. Until now, the risk of complications after Ct has not been assessed directly in a prospective cohort study, but only in modelling studies. The estimates of complication risk after Ct vary widely between these modelling studies.

Furthermore, factors that contribute to the development of complications after Ct remain to be elucidated.

Objective:

The aim of the Netherlands Chlamydia Cohort Study (NECCST) is to assess the risk of developing complications and the time to pregnancy in women with and without a known previous Ct infection. Furthermore, this study aims at determining host genetic biomarkers and behavioural, demographic, and pathogen factors that are associated with the development of these complications.

Study design:

NECCST will be a cohort study and a continuation of the Chlamydia Screening Implementation (CSI), which was executed between 2008 and 2011 in Rotterdam, Amsterdam, and South Limburg, among people between 16 and 29 years of age. In the CSI, persons were invited to be tested for Ct. Of all participants who gave informed consent, biological samples have been stored in a Biobank. In NECCST we will recruit all CSI women who consented to be approached for follow-up (2,371 CSI Ct positive women and 12,314 CSI Ct negative women), and prospectively follow them until 2022. Samples stored in the CSI Biobank will be used to measure the presence of candidate host genetic biomarkers (Single Nucleotide Polymorphisms (SNPs)). In case the sample is absent or of insufficient quality, a new buccal sample will be obtained in 2015. During NECCST, four data collection moments are foreseen: in 2015, 2017, 2019, and 2021. Participants will be asked to fill in an online questionnaire at every data collection moment. At the first and last data collection moment, participants will also be asked to provide a blood spot sample at home (bloodspot on paper) in order to measure Immunoglobulin G (IgG) antibodies for Ct, as a marker of a previous Ct infection.

Conclusion:

We expect that NECCST will provide us accurate data on the risk of late complications after a Ct infection in women. Furthermore, NECCST will give us insight into factors that may contribute to the development of these complications. This may benefit targeted secondary preventive measures in high-risk women and can aid triage of women requiring laparoscopy in fertility clinics.

Remco P.H. Peters, MD, PhD, DLSHTM

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Curriculum Vitae

Dr Remco Peters works as clinical programme specialist for the Anova Health Institute in South Africa. He is affiliated with the departments of medical microbiology of the Maastricht University Medical Centre and the University of Pretoria. He obtained his medical degree (2006) and PhD (2007) in clinical microbiology and infectious diseases at the VU University in Amsterdam and an MSc in Epidemiology from the London School of Hygiene and Tropical Medicine. He has worked as medical intern, doctor and researcher in various countries in Africa and Central America.

In his current job Dr Peters provides leadership to Anova's research agenda as well as senior clinical expertise in the field of infectious diseases, with a specific focus on the HIV, tuberculosis and sexually transmitted infection programmes. His research interest is in the field of clinical, molecular and translational epidemiology and public health aspects of infectious diseases. He has a particular passion for STI research.

Abstract

Chlamydia trachomatis infectious occur worldwide, but there are interesting geographical differences. The global epidemic of *C. trachomatis* infection is diverse, but the public health and clinical research agendas are dominated by developed, resource-rich countries. This presentation aims a) to provide insight in the burden of *C. trachomatis* infections in developing countries, b) to discuss specific challenges associated with *C. trachomatis* management and control in these settings, c) to elaborate on ways to increase awareness and to promote *C. trachomatis* control on the international public health agenda.

Amsterdam, 6 February 2015

Menne Bartelsman, MD

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Curriculum Vitae

Menne Bartelsman (1978) graduated as a phycisian at the University of Amsterdam. After graduation he was (among other things) member of the editorial board of the *Nederlands Tijdschrift voor Geneeskunde* (Dutch Journal of Medicine) and a phycisian at Jellinek Verslavingszorg (addiction clinic). The past two years he has been working as a physician and PhD researcher at the STI clinic of the Public Health Service Amsterdam. His PhD research is focussed on the cost-effectiveness of point-of-care (POC) diagnostics of Chlamydia and gonorhoeae.

Abstract

Objectives

To compare two diagnostic point-of-care (POC) algorithms for urogenital chlamydia in male high-risk patients with respect to: diagnostic accuracy, loss to follow-up, correctly managed consultations, and costs.

Methods

Retrospective comparison of the diagnostic accuracy and cost-effectiveness of Gram stained urethral smear analysis for the POC management of urogenital *Chlamydia trachomatis* infections. Between 2008-2009 Gram stained urethral smear analysis was offered to all men irrespective of symptoms; between 2010-2011 only to those with symptoms. The Aptima CT assay was the reference diagnostic test.

Results The number of examined Gram stained smears in the two periods was respectively 7185 (2008-2009 period) and 18852 (2010-2011 period). The sensitivity of the Gram stain analysis was respectively 83.8% (95%CI 81.2-86.1) and 91.0% (95%CI 89.5-92.3) (p<0.001). The specificity was respectively 74.1% (95%CI 73.0-75.2) and 53.1% (95%CI 51.8-54.4) (p<0.001). The positive predictive value (PPV) was low in both periods, respectively 31.7 (95%CI 29.8 to 33.6) and 35.6% (95%CI 34.1 to 37.1) (p=0.002), whereas the negative predictive value (NPV) was high, respectively 97.0% (95%CI 96.4 tot 97.4) and 95.4% (95%CI 94.6 to 96.1) (p=0.002).

The loss to follow-up rate between 2008-2009 and 2010-2011 was respectively 1.8% (95%CI 1.0 to 2.9) versus 2.3 % (95%CI 1.7 to 3.0) (p=0.36). There was a small difference in overtreatment, 68.0% (95%CI 66.0 to 69.8) versus 64.1% (95%CI 62.6 to 65.5) (p=0.001). The cost per correctly managed consultation was 14.3% lower in the 2010-2011 period, (€ 94.31 versus € 80.82).

Conclusions

With a high sensitivity in male high-risk patients, the Gram stained urethral smear is a useful POC test to detect urogenital *Chlamydia trachomatis*. When offered only to men with urogenital symptoms the specificity decreases but the cost per correctly managed consultation is reduced with 14.3% without a significant difference in loss to follow-up.

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Curriculum vitae

Sylvia Bruisten is a medical molecular microbiologist. She is currently employed as the head of the department of molecular diagnostics at the Public Health laboratory of the Municipal Health Service (GGD) Amsterdam, the Netherlands. She is also supervisor of several PhD students who performed molecular epidemiological studies on hepatitis viruses (HAV, HBV and HCV) and also on several sexually transmitted bacteria such as *Neisseria gonorrhoeae*, *Treponema pallidum*, and *Chlamydia trachomatis*.
Sylvia studied Biology/Biochemistry in Nijmegen after which she started her PhD project on 'the regulation of Complement genes in the mouse' at the Netherlands Cancer Institute in Amsterdam at the Department of Immuno-Genetics supervised by Prof dr. P. Borst. After completing her thesis in 1989, she worked as a molecular biologist at the CLB (now called 'Sanquin'). She participated in studies with the Academic medical center and the GGD Amsterdam, on the Amsterdam Cohort studies, that all involved the early detection of HIV-1 sequences in blood and blood products. She is currently a member of several boards of committees (CTB-MMO, CK) of the Dutch Microbiology organisation, NVMM.
Under her guidance 6 PhD students completed their thesis on Molecular epidemiological studies. The last thesis in 2014 was on the molecular epidemiology of *Chlamydia trachomatis*, using high resolution-MLST. Another 3 PhD students are currently working with her on their thesis, of whom one is studying tissue tropism and bacterial characteristcs of *Chlamydia trachomatis*.

Abstract

Typing of *C. trachomatis* strains has longtime relied on polymorphism in the ompA gene (genovar) and the encoding major outer membrane protein (MOMP), defining its serovar. In most countries almost half of all urogenital chlamydia infections are of serovar E type, mostly the /E/Bour genovar.
The high resolution *Chlamydia trachomatis* multilocus sequence type (hr-CT-MLST) database (http://mlstdb.bmc.uu.se) is based on five target regions (non-housekeeping genes) and the ompA gene. Each target region has varying numbers of alleles; these are known presently as 89 for hctB, 51 for CT058, 30

for CT144, 38 for CT172, and 35 for pbpB. Our aims were to perform an overall analysis of all *C. trachomatis* MLST sequence types (STs) in the database and to examine STs with a global spread to see if these succesful strains could be 'founder strains'.
A total of 414 STs were recognized from 2089 specimens. The addition of 49 ompA gene variants created 459 profiles. ST variation and their geographical distribution was characterized using minimum spanning tree analyses. Men who have sex with men (MSM) provided 609 samples of which 63% were present in 4 STs, that centered 4 large clusters. Four other predominating STs were found to occur among 1383 heterosexual cases reflecting 31% of this group. The heterosexual STs centered genetically more diverse clusters. The cluster representation thus seems to reflect sexual behaviour from the hosts and not, as we discovered also, tissue tropism.
The diversity in ocular trachoma cases was lower compared to that found in sexually transmitted chlamydia infections.
Predominating STs were identified in 12 available *C. trachomatis* whole genomes which were compared to 22 *C. trachomatis* full genomes without predominating STs. No specific gene in the 12 genomes with predominating STs could be linked to successful spread of certain STs. Concatenated sequence analysis showed that MLST targets provided a similar tree to that based on whole genome analysis (Harris et al, 2012). The presented hr-CT-MLST method identifies *C. trachomatis* strains with global spread and provides a tool for epidemiological investigations such as resolving sexual networks.

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Curriculum Vitae

Antony Croxatto is currently working as an assistant Lab Manager at the diagnostic microbiology laboratory of the Lausanne University hospital centre. He obtained his Master of Science degree at the University of Lausanne in 1998. He moved to Umeå University at the department of microbiology and molecular biology, Sweden, to obtain his PhD in 2006 working on the role of bacterial cell-cell signalling (quorum sensing) in the virulence mechanisms of *Vibrio* species. He spent one more year in Sweden as a postdoc working on the establishment of quorum sensing signalling as a potential therapeutic target for the prevention of the disease before obtaining a postdoctoral position focusing on *Chlamydia*-like bacteria in the group of Prof. Gilbert Greub at the University of Lausanne, Switzerland. His research projects included three major topics: (i) Characterisation of the virulence mechanisms (type III secretion, intracellular trafficking) of *Chlamydia*-like organisms recognised as emerging pathogens of pneumonia (*Parachlamydia acanthamoebae*) and miscarriage (*Waddlia chondrophila*), (ii) development of molecular tools to conduct diagnostic, epidemiological and prospective studies, including real-time PCRs, immunofluorescence and ELISA, (iii) genome sequencing projects on *Chlamydia*-like bacteria comprising sequencing, gap closure and annotation. Antony started a degree in medical microbiology in 2012 and is now involved in diagnostic microbiology, R&D in bacteriology laboratory automation and in research projects on *Chlamydia*-like bacteria at the Lausanne University hospital, Switzerland.

Abstract

The order *Chlamydiales* includes the *Chlamydiaceae*, *Parachlamydiaceae*, *Waddliaceae*, *Simkaniaceae*, *Criblamydiaceae*, *Rhabdochlamydiaceae*, and *Piscichlamydiaceae* families. Members of the *Chlamydiales* order are obligate intracellular bacteria that replicate within eukaryotic cells of different origins including humans, animals, and amoebae. Many of these bacteria are pathogens or emerging pathogens of both humans and animals but their true diversity is largely underestimated and their ecology remains to be investigated. Considering their potential threat on human health, it is important to expand our knowledge on the diversity of *Chlamydiae* but also to better understand the pathogenic potential

of *Chlamydia*-like bacteria. *Parachlamydia* and *Waddlia* represents newly identify pathogens causing respiratory tract infections and abortion in both humans and mammals. Several studies on these two *Chlamydia*-like bacteria focused on essential conserved virulence mechanisms among *Chlamydiae* such as T3SS, intracellular trafficking and bacterial cell division. The results showed that *Chlamydia*-like microorganisms have evolved specific virulence mechanisms adapted towards their natural hosts but also that these bacteria represent a good model to study the biology of bacteria belonging to the *Chlamydiales* order. Thus, using a new pan-*Chlamydiales* PCR, we analyzed the prevalence of *Chlamydiales* DNA in ticks, which are important vectors of several viral and bacterial infectious diseases. To conduct this study, 1340 *Ixodes ricinus* ticks prepared in 192 pools were collected in Switzerland and 55 ticks belonging to different tick species were harvested in Algeria. In Switzerland, the prevalence of *Chlamydiales* DNA in the 192 pools was equal to 28.1% (54/192) which represents an estimated prevalence in the 1340 individual ticks comprised between 4.0 to 28.4% (average 16.2%). The pan-*Chlamydiales* qPCR was positive for 45.5% (25/55) of tick samples collected in Algeria. The sequencing of the positive qPCR amplicons revealed a high diversity of *Chlamydiales* species. Most of them belonged to the *Rhabdochlamydiaceae* and *Parachlamydiaceae* families. Thus, ticks represent an important host reservoir for *Chlamydiales* and should be considered as potential central vectors for *Chlamydiales* propagation to both humans and animals.

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Curriculum Vitae

Sarah Van Lent, born on June 21st 1988, graduated from Ghent University in 2011 with a minor in Biomedical Biotechnology and a major in Microbial Biotechnology. In her master thesis she identified potential virulence genes of *Paenibacillus larvae*, the causative agent of American foulbrood in honey bees. In 2011 she started her PhD in the laboratory of Immunology and Biotechnology of the Animal Cell at Ghent University. Her work mainly focuses on the polymorphic membrane proteins of *Chlamydia psittaci*.

Abstract

Currently, little is known about the mechanisms by which *Chlamydia* species manipulate host cells and induce disease in their different hosts. In spite of diverse infection strategies and symptoms, all *Chlamydiae* share a conserved, unique, biphasic developmental cycle. Chlamydial proteins are differentially expressed in EBs and RBs. Proteins present on the surface of EBs are of particular interest for vaccine development, as they are putative targets for neutralization of the infection. Polymorphic membrane proteins (Pmps) form the largest membrane protein family and are unique to the *Chlamydiae*. In the last decade, the Pmps have been studied intensively because of the abundance of the pmp genes (~ 4.1%) within the highly reduced chlamydial genome and the presence of the Pmp family in all currently sequenced chlamydial genomes. Molecular analyses of the Pmp family of *Chlamydia trachomatis*, *C. pneumoniae,* and *C. abortus* indicated the usability of these proteins for the development of a chlamydial vaccine. As no vaccine is currently available for *C. psittaci* and no molecular studies were done on its Pmps before, we determined the transcriptional and translational expression profile of PmpA, PmpB, PmpD, and PmpH, using RT-qPCR and an immunofluorescense assay (IFA). In addition, immuno-electron microscopy (EM) was used to assess their subcellular localization. As previous studies suggested a unique role in chlamydial pathogenesis for Pmps expressed during stress, analyses were done under both normal and stress conditions. PmpA was found to be the most notable Pmp in *C. psittaci*. Firstly, it is the most conserved Pmp in *C. psittaci*, secondly, it is the only Pmp protein that is expressed in most inclusions as early as 12 hpi, and finally, it

is more abundantly labeled at the chlamydial surface than the major outer membrane protein (MOMP). These data suggest a critical role for this Pmp in the pathogenesis of *C. psittaci* and thus suggest it might be a promising vaccine candidate.

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Curriculum vitae

Stephan Verweij graduated in Biomedical sciences in 2012 at the VU University Amsterdam. He successfully defended his PhD thesis entitled "*Chlamydia trachomatis* in the Dutch population: epidemiology, serological responses, and host genetics" and received his PhD-title on March 12, 2014. In 2009, Stephan completed an internship in the Laboratory of Immunogenetics of the VU University medical center under supervision of Prof. dr. Servaas A. Morré. The subject was immunogenetic and serological correlates of human *Chlamydia trachomatis* infections. After this project he decided to continue working in the lab of Prof. Morré. Stephan participated in the EpiGenChlamydia student training challenge in Oxford, United Kingdom (2009), and won this challenge with three peer students. From March to July 2012, he undertook an apprenticeship at the Anova Health Institute, Tzaneen, South Africa. The objective of this epidemiological project was to determine the prevalence of *C. trachomatis* and *Neisseria gonorrhoeae* in women living in remote areas within South Africa. He was selected for, and participated in the ECDC training programme "Bacterial sexually transmitted infections - diagnostics, antimicrobial resistance and molecular typing" at Public Health England, London from November 17-21, 2014. Stephan is currently enrolled in the accelerated medical programme of the VU University medical center ("zij-instroom"). He recently extended his finished apprenticeship in the Department of Microbiology of CHUV hospital, Lausanne, Switzerland, where he conducted research on clinical and biological aspects of Waddlia chondrophila, a *Chlamydia*-like bacterium.

Abstract

Damage to the Fallopian tubes, or tubal pathology, is a common cause of subfertility in women. Tubal damage is thought to occur when pathogenic microorganisms, such as *Chlamydia trachomatis*, ascend from the lower genital tract and infect the tubes, inducing inflammation. This may cause scarring of the Fallopian tubes, resulting in sub- or infertility, known as tubal factor infertility (TFI). Other less known microorganisms capable of colonising the genital tract of women may as well be responsible for the onset of TFI. Recently it has been shown that *Waddlia chondrophila*, like *C. trachomatis* a member of the

Chlamydiales order, is capable of causing adverse pregnancy outcomes in ruminants and human. Since *W. chondrophila* is closely related to *C. trachomatis*, we hypothesise that antibodies against *W. chondrophila* may also be associated with tubal pathology in women. The aim of this study is to assess the prevalence of antibodies against *W. chondrophila* in women attending the gynaecology department of the University Medical Center Groningen, the Netherlands. Additionally, we associate the *W. chondrophila* antibody titre with severity of tubal pathology and compare this to *C. trachomatis* antibodies with the aim to obtain a better predictive value for women with tubal pathology than the normal *C. trachomatis*-MOMP serology currently used. Five hundred fifty-seven serum samples meeting the inclusion criteria (*C. trachomatis*-MOMP antibody test result available, laparoscopic and/or hysterosalpinography data available), were selected. Of the 557 serum samples, 472 (84.7%) were *C. trachomatis*-MOMP negative, 85 (15.3%) were positive. A total number of 174 (31.2%) women has had laparoscopic diagnosis or hysterosalpinography performed, and were graded in class 1 to 4. Prevalence of *W. chondrophila* antibodies was 45.3%. The most remarkable finding was that the statistical difference between antibody positivity to both *W. chondrophila* and *C. trachomatis*-MOMP between controls and laparoscopy status 4 was much stronger than the difference for MOMP antibodies alone, showing very high specificity to identify occlusion of both tubes.

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Curriculum Vitae

Yvonne Pannekoek received her M.Sc. in 1987 at the University of Amsterdam where she studied Biology with emphasis on Molecular Microbiology. She graduated in 1993, at the University of Amsterdam, Dept. of Medical Microbiology of the Academic Medical Center, thesis entitled “Identification of Neisserial stress proteins: Molecular and immunological properties of Neisserial Hsp60”. A part of her PhD work was carried out at the Max-Planck-Institut für Biologie, Abt. Infectionsbiologie, Tübingen, Germany, former laboratory of Prof. dr. Thomas F. Meyer were she worked as a visiting research fellow. After her graduation she joined the laboratory of Prof. dr. Patrik M. Bavoil, at that time situated in the University of Rochester, Dept. of Microbiology and Immunology, NY, US, where she worked as a postdoctoral fellow on the pathogenesis of *Chlamydia* infections. During that period she discovered the type III secretion system of *Chlamydia*. For this work she, together with other members of the Bavoil lab, received the best poster award during the Third European *Chlamydia* meeting that was held in 1996 in Vienna, Austria. In 1995 she returned to the Dept. of Medical Microbiology at the AMC in Amsterdam were she currently is appointed as Assistant Professor. Her main interests are the pathogenesis and molecular epidemiology of infections caused by *N. meningitidis*, *S. pneumoniae*, and *Chlamydiae*.

Abstract

Chlamydiaceae are obligate intracellular pathogens that have evolved to colonize a diverse range of hosts. There are currently 11 described species of *Chlamydia*, most of which have a significant impact on the health of humans and/or animals. Expanding chlamydial genome, including plasmid sequence information, has revolutionized our understanding of their unique biology. Aspects of their unique lifecycle, host–pathogen interactions, and genetic differences between *Chlamydia* strains can now be better understood and some associations with different host and tissue tropisms can be made. Here, I will highlight some aspects of chlamydial genomics including the emerging role of plasmid encoded virulence factors. In addition, I will highlight some methodology to analyze the evolution, phylogeny, and molecular epidemiology of these pathogens.

Amsterdam, 6 February 2015

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Abstract

In this talk, we will review current recommendations to control *Chlamydia trachomatis* (Ct) genital infections in France, recent data indicating possible increase in prevalence in young adults, gaps in knowledge in Ct infections and pelvic inflammatory disease (PID) natural history, rationale and overview of a community based trial evaluating early screening for *Chlamydia trachomatis* in young women for primary prevention of pelvic inflammatory disease and the need for cost effectiveness evaluation of different control strategies.

In France, the national chlamydia control strategy includes sexual health education, awareness campaigns, promotion of condoms and at-risk population screening. Systematic (routine) screening in young sexually active women has not been implemented. This screening is offered to 18-24 year old women only if they visit STI clinics, reproductive health services or abortion centres (Anaes, 2003).

The number of Ct diagnoses has increased in the past ten years in France as well as in other European countries. The proportion of positive tests reported by the national laboratory network increased from 3% in 2004 to 6.5% in 2010 among women (Renachla, InVS, december 2011; La Ruche 2013). Although these trends may be partly explained by an increase in screening activities, particularly targeting at-risk people, they may reflect an increase in incidence. Thus, in 2012, the proportion of positive tests reached 8.3% of the 18-24 year old women participating in a web-based study promoting home screening (de Barbeyrac 2013; Kersaudy-Rahib 2013).

Key characteristics of Ct infection natural history, i.e. rate and timing of progression of lower genital tract infection to PID, are not sufficiently documented. Yet, accurate estimates of these characteristics are needed to better anticipate the benefit of early and systematic screening of infection. Also, duration of Ct infection in the absence of treatment is not well established and could possibly last one year or longer (Geisler 2010). Finally, reinfection is common after therapy (10%-20% patients within 12 months) (LaMontagne 2007, Hosenfeld 2009), even possibly increasing (Rekart 2013), thus raising questions about host immune response and relevance of and time to re-testing.

The context of increasing prevalence in young women and recent improvements in the diagnosis of Ct infection and in the procedure (i.e. availability of reliable self-taken devices) allows reconsidering current recommendations. However, there is a need to evaluate the efficacy of early screening in preventing PID and to better understand the natural history of Ct infection and progression to PID in young women to elaborate a well-adapted screening program for mid-term in France. As systematic screening in young sexually active women has not been implemented in France, it leaves an opportunity to conduct a community-based randomized trial to evaluate the efficacy of early screening and treatment in preventing PID. The control group of the randomized trial, following current screening recommendations, will allow to better document the natural history of Ct infection, in particular the rate of and time to progression to PID.
This trial will be part of a comprehensive approach to refine strategies to control Ct infections in France. This approach already includes recent studies that aimed at establishing well accepted methods of screening i.e. self-taken samples, home- versus clinic-based screening (Kersaudy-Rahib 2013). Data from the trial will be used to develop a dynamic transmission model of Ct infection and PID. This model will allow testing prevention strategies to reduce both the incidence of PID and the prevalence of Ct infection. The model will serve as a basis for cost-effectiveness analysis. If proved efficient the screening strategy may be implemented in the future.

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Curriculum vitae

Bart Versteeg was born on April 15th 1987 in Zaltbommel (Netherlands). After finishing his bachelor in Applied Science at the Hogeschool Utrecht in 2010, he studied Biomedical Science at the VU University in Amsterdam. In 2013, he started as a PhD student at the Public Health Laboratory of the Public Health Service (GGD) Amsterdam, the Netherlands. His PhD project is about the molecular epidemiology of *Chlamydia trachomatis*.

Abstract

Background

Recently, we reported a high prevalence (16%) of urogenital *C. trachomatis* infections among women in a rural setting in South Africa. Molecular epidemiological studies on *C. trachomatis* infections could provide insights in the characteristics of this epidemic, yet such data are not available. The objective of this study was therefore to assess the distribution of *Chlamydia trachomatis* strains among South African women and to compare the distribution with a sample of strains from Amsterdam, the Netherlands.

Methods

High resolution multilocus sequence typing (MLST) was used to study urogenital *C. trachomatis* infections in women visiting primary healthcare facilities across rural Mopani District in Limpopo Province, South Africa. Sequence types (STs) were compared to 100 strains from women visiting the STI clinic in Amsterdam, the Netherlands.

Results

Full MLST data was obtained for *C. trachomatis* infection in 43 women from Mopani District. Using the complete MLST profile of all 43 women from Mopani District, 26 STs could be identified, of which 18 (69%) were novel and unique to Mopani District. The remaining STs clustered together with strains from Amsterdam.

Conclusion

MLST revealed a diverse molecular epidemiology with novel and unique STs and a specific cluster for the Mopani district. These results demonstrate worldwide geographic variation of *C. trachomatis*.

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Curriculum Vitae

Nynke de Vrieze studied medicine at the Academic Medical Center of the University of Amsterdam.She worked at the STI Outpatient clinic in Amsterdam for almost two years and combined clinical work at the clinic with research. She is currently employed as a dermatology resident at the University Medical Center in Utrecht and is still related to the STI clinic in Amsterdam to finish her thesis which includes epidemiological studies of Lymphogranuloma Venereum and other STI.

Abstract

Urethral lymphogranuloma venereum (LGV) is not screened routinely and is probably key in transmission. We tested urethral samples of MSM positive of *C. trachomatis* further for biovar L and found 8 positive urethral LGV infections. Urethral LGV is missed in current diagnostic algorithm.

Backround/Aim

Various guidelines (BASHH, WHO/IUSTI and CDC) recommend routine diagnostic methods for anorectal LGV in MSM. None recommend routine screening of urethral LGV infections. Our aim was to explore the true prevalence of urethral LGV among MSM tested at the STI clinic in Amsterdam.

Materials/Methods

We tested urethral samples of MSM positive of *C. trachomatis* further for biovar L. We started first of January 2014 and we planned to continue until 1st of January 2016. If the pmpH test was inconclusive (mainly due to insufficient DNA), the result was considered negative for LGV.

Results

From first of January 2014 until fist of January 2015 8.765 MSM were tested for urethral *C. trachomatis* infections. 301 *C. trachomatis* urine positive samples were

tested for biovar L. 238 were negative, 55 inconclusive and eight were positive for Lymphogranuloma venereum.

Discussion/Conclusion

Prevalence of urethral LGV in MSM at the STI clinic in Amsterdam was 0.09%. Urethral LGV is, both in anorectal LGV and their partners, missed in current diagnostic algorithm. Awareness of, screening for, and prompt treatment of LGV is crucial for the individual patient and to prevent ongoing transmission.

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Curriculum Vitae

Arjen Speksnijder studied geobiochemistry at Leiden University and obtained his PhD in microbial ecology at the University of Nijmegen. After a post-doc period in the Natural History Museum of Londen and the University of Aberdeen he became staff researcher molecular microbiology at Plant Research International in Wageningen. In 2007 he became head of the medical microbiology laboratory of the Public Health service of Amsterdam. In this position he was involved in human epidemiological research with a focus on *Chlamydia*, HPV, HCV, and vaginal microflora. In 2013 he moved to Naturalis in Leiden. He is now head of Laboratories for Research and Education. His research interest is assessment of biodiversity by metabarcoding for human impact studies, environmental quality, taxonomy support, and meta community interactions.

Abstract

Objective

This study is the first to present data on the genomic composition of the vaginal microbiome prior to a Ct infection, making it possible to see whether specific compositions of the vaginal microbiome could be a marker for acquiring Ct.

Design

A nested case control study was performed among women at low risk for acquiring Ct. For taxonomic classification, the V3-V4 hyper variable regions of the 16S rRNA gene were sequenced. The genomic composition of the vaginal microbiome was then linked to the socio-demographic data and data on sexual risk behaviour and analysed using logistic regression.

Outcome

Among women in Amsterdam, 5 major community state types (CST) of the vaginal microbiome could be determined. The microbiome of the majority of women was dominated by *Lactobacillus crispatus*, 37%. Another group was dominated by *L. iners*, 33%. The third group was characterized by the absence of *Lactobacillus* spp and the presence of *Gardenerella vaginalis*, 25%. Multivariate analysis revealed CST and type of relationship as independent risk factors.

Women with a *L. iners* dominated CST had an increased risk for acquiring Ct. Women with a steady partner, but not living together also had an increased risk for acquiring Ct.

Conclusion

The distribution of the various CST is as expected in a predominantly white cohort, except for the relatively large group of women with a CST lacking *Lactobacillus* spp. Having a vaginal microbiome that is dominated by *L. iners* increases the risk for acquiring Ct in the long run. Therefore, the composition of the vaginal microbiome can be used as a predictor for acquiring STIs, even over long time periods.

Symposium Organizer
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Curriculum vitae

Prof. Servaas A. Morré, PhD is working on *Chlamydia trachomatis* for almost 20 years and has over 160 publications, from which most are on *Chlamydia trachomatis*. He graduated at the VU University, The Netherlands, in Biochemistry and Molecular Biology in 1994 and is currently working as Head of the Laboratory of Immunogenetics, VU University medical center, Amsterdam and is since 2011 Director of the Institute of Public Health Genomics, Dept of Genetics and Cell Biology, Maastricht University where we works Thursdays and Fridays.

He worked at The Zaadunie, Department of Cell biology on plant genetics: polyploidization of Brassica oleracea (Cauliflower) during cell culture (M. Tan, PhD) and at the Department of Biochemistry and Molecular Biology VU on processing of ribosomal RNAs in Saccharomyces cerevisiae (Prof. H. Raué, PhD, R. van Nues PhD). As an Erasmus Fellow he studied at the Universidade Do Porto, Laboratório de Genética Molecular, Portugal, on POLO: an essential kinase for mitosis in Drosophila melanogaster (Prof. C. Sunkel, PhD). His PhD thesis performed in Department of Pathology (VU University) was on the epidemiology, diagnostics and immunopathogenesis of human urogenital *Chlamydia trachomatis* infections. As a postdoc, the Van Coeverden Adriani Foundation made it possible to extend his Chlamydial research in the Department of Infectious Diseases, The City of Hope Medical Center, California, USA, in collaboration with Dr. Jim Ito and Dr. Joseph Lyons, specialists in murine modelling.

From November 1st 2001, he joined the Laboratory of Immunogenetics, VUmc. His research is for the major part focused on the immunogenetics of infectious diseases with special attention to Chlamydia trachomatis, and Bacterial meningitis (collaboration Paediatrics, VUmc). Together with Prof. Salvador Peña, he organised the “First Mini-symposium *Chlamydia trachomatis* Infections” in December 2004 and this year 2015, we organize our Lustrum meeting, the 10th AACM. In July 2005 at the 16th Biennial meeting of the International Society for Sexually Transmitted Diseases Research (ISSTDR) he was a member of the Scientific Committee and organized amongst others the workshop “Immunogenetics of *Chlamydia trachomatis* Infections”, with Prof. David Mabey (London, UK, Trachoma research). He was organizing Committee member of 6th Meeting of the European Society for Chlamydia Research, University of Aarhus, Aarhus, Denmark, July 1-4, 2008 and at this meeting also session organizer: “Immunogenetics of *Chlamydia trachomatis* infections”. Finally he was the organizer of the 7th Meeting of the European Society for *Chlamydia* Research in 2012 (1-6 July) in Amsterdam.

Since 2007 he is Scientific Consortium Director, of the European Framework Programme 6 (FP6) grant (LIFESCIHEALTH FP6, Co-ordination Actions (CA)) on functional genomics research entitled: “Contribution of molecular epidemiology and host-pathogen genomics to understand *Chlamydia trachomatis* disease (Acronym: EpiGenChlamydia)“ with 20 European, African and US groups. This consortium had his first meeting on 12 December 2007. In 2011 part of the Consortium went forward using new SNE based funding schemes. Since 1st of Sept 2009 he coordinates the the Dutch *Chlamydia trachomatis* Reference Laboratory for the Dutch National Institute of Public Health and the Environment (RIVM) since 2009 and since 1 jan 2014 together with Prof.dr. Christian Hoebe (UM).

Together with Prof. Paul Savelkoul (Medical Microbiology and Infection Control, VUmc), he is co-founder and co-director of a VUmc spin-off company called Microbiome Ltd (Sept 2005), a company specializing in Medical and Microbiological diagnostics, typing, and laboratory consultancy and founded in 2011 the spin-off company TubaScan specializing in diagnostic application based on host genetic markers.

Amsterdam, 6 February 2015

Future STI / *Chlamydia* Meetings

13th German *Chlamydia* Workshop
February 11 - 13 2015, Vienna, Austria
http://www.chlamydienworkshop.org/

7th *Chlamydia* Basic Research Society (CBRS)
March 29th – April1st *2015, New Orleans (LA), USA*
http://www.uams.edu/cbrs/2015%20Meeting.htm

14th IUSTI World Meeting & 21st ISSTDR
September 14 – 18 2015, Brisbane, Australia
http://www.worldsti2015.com

11th Annual Amsterdam *Chlamydia* Meeting
2016, Amsterdam, The Netherlands

8th European *Chlamydia trachomatis* meeting
2016, London, United Kingdom

14th International Symposium on Human *Chlamydial* Infections
2018

An overview of PhD work in The Netherlands on *Chlamydia trachomatis*

Table I: *PhD theses in the Netherlands*

2014 Jelena Malogajski	Maastricht University / VU University Amsterdam
2014 Ivan Brankovic	Maastricht University / VU University Amsterdam
2014 Rianne Vriend	University of Amsterdam / Public Health Services (GGD) Amsterdam
2014 Jannie van der Helm*	University of Amsterdam / Public Health Services (GGD) Amsterdam
2014 Stephan P. Verweij*	VU University Amsterdam
2014 Reinier Bom*	University of Amsterdam / Public Health Services (GGD) Amsterdam
2013 Jonathan Lal	Maastricht University / VU University Amsterdam
2013 Laura van Dommelen*	Maastricht University
2013 Marlies Heiligenberg*	University of Amsterdam / Public Health Services (GGD) Amsterdam
2012 Janneke Heijne*	University of Bern / RIVM
2011 Ouafae Karimi	VU University Amsterdam
2011 Koen D. Quint*	VU University Amsterdam
2010 Caroline J. Bax*	University of Leiden / Medical Center Haaglanden
2010 Janneke E. den Hartog*	Maastricht University
2010 Ingrid Rours	Erasmus University Rotterdam
2008 Liesbeth Duijts*	Erasmus University Rotterdam
2007 Denise A.M. Perquin	University of Leiden / Medical Center Haaglanden
2006 Sander Ouburg	VU University Amsterdam
2006 Joke Spaargaren*	University of Amsterdam and VU University Amsterdam
2006 Tanja P. Gijsen*	Maastricht University
2006 Hannelore M. Götz*	Erasmus University Rotterdam
2005 Jan E.A.M. van Bergen*	University of Amsterdam
2004 Joseph M. Lyons*	City of Hope Medical Center, CA, USA, and VU University Amsterdam
2003 Laura S. Murillo	VU University Amsterdam
2002 Monica Molano Luque	VU University Amsterdam
2001 Irene G.M. van Valkengoed*	VU University Amsterdam
1999 Servaas A. Morré*	VU University Amsterdam
1999 Johannes W. Trum	University of Amsterdam
1999 Bernardus W.J. Mol	University of Amsterdam
1998 Yvonne T.H.P. van Duijnhoven	University of Amsterdam
1997 Marita J.W. van de Laar	University of Amsterdam
1995 Jar Lan*	VU University Amsterdam
1994 Josina van Ulsen	Erasmus University Rotterdam
1994 Jacobus M. Ossewaarde*	University of Utrecht
1993 Hans J.H. Theunissen*	Erasmus University Rotterdam
1992 Johannes T.M. van der Schoot*	University of Amsterdam
1992 Arent J.P. Boeke and Janny H. Dekker	VU University Amsterdam
1992 André H. van der Willigen	Erasmus University Rotterdam
1991 Eric C.J. Claas	VU University Amsterdam
1990 Gijsbertus J.H.M. Ruijs*	Rijksuniversiteit Groningen
1989 Henk J. Vonsée	Rijksuniversiteit Limburg
1987 Kie H. Tjiam*	Erasmus University Rotterdam

**Chlamydia trachomatis* is the major focus in the thesis.

Ranking position for number of theses 1987-2014: VU 14, UVA 9, Erasmus 7, UM 5

Table II: *Current PhD fellows working (partially) on* Chlamydia trachomatis.

Geneviève van Liere	Maastricht University / Public Health Service ZL
Anne Dirks	Maastricht University / Public Health Service ZL
Kevin Theunissen	Maastricht University / Public Health Service ZL
Eleanne van Ess	VU University Amsterdam
Martin Singer	VU University Amsterdam
Dewi de Waaij	VU University Amsterdam
Monique Pereboom	VU University Amsterdam
Esmée Lanjouw	VU University Amsterdam
Marleen Jansen	VU University Amsterdam / Maastricht University
Vitaly Smelov	VU University Amsterdam and St. Petersburg State Medical University, Russia
Bart Versteeg	University of Amsterdam / Public Health Services (GGD) Amsterdam
Charlotte van der Veer	University of Amsterdam / Public Health Services (GGD) Amsterdam
Nynke de Vrieze	University of Amsterdam / Public Health Services (GGD) Amsterdam
Menne Bartelsman	University of Amsterdam / Public Health Services (GGD) Amsterdam
Martijn van Rooijen	University of Amsterdam / Public Health Services (GGD) Amsterdam
Amy Matser	University of Amsterdam / Public Health Services (GGD) Amsterdam
Titia Heijman	University of Amsterdam / Public Health Services (GGD) Amsterdam
Roel Achterbergh	University of Amsterdam / Public Health Services (GGD) Amsterdam

An overview of PhD work on *Chlamydiae*

Table III: *PhD theses on* Chlamydiae

2014 Evelien de Clercq	Ghent University, Belgium	C/CT
2013 Lizi Yin	Ghent University, Belgium	CPs/CAb
2011 Veerle Dickx*	Ghent University, Belgium	CPs
2010 Katelijn Schautteet*	Ghent University, Belgium	C / CT
2010 Caroline van Droogenbroeck*	Ghent University, Belgium	CPs
2009 J.J.M. Bouwman	Utrecht University, The Netherlands	CP
2009 Delphine Beeckman*	Ghent University, Belgium	CPs
2008 Kristel Verminnen*	Ghent University, Belgium	CPs
2008 Taher Harkinezhad*	Ghent University, Belgium	CPs
2008 M.D. de Kruif	University of Amsterdam, The Netherlands	CP
2007 Edou R. Heddema*	University of Amsterdam, The Netherlands	CPs
2007 Ellen Boelen*	Maastricht University, The Netherlands	CP
2006 Arnaud Daniël Hauer	Leiden University, The Netherlands	CP
2005 Tom Geens*	Ghent University, Belgium	CPs
2005 Marnix Van Loock*	Catholic University Leuven, Belgium	CPs
2005 Manuela Voorend*	Maastricht University, The Netherlands	CP
2005 Tryphon Vainas	Maastricht University, The Netherlands	CP
2004 H.F. Berg	University of Amsterdam, The Netherlands	CP
2004 Boulos Maraha*	VU Universtiy, Amsterdam, The Netherlands	CP
1997 Roel P.A.J. Verkooyen*	Erasmus University Rotterdam, The Netherlands	CP
1994 Daisy Vanrompay*	Belgium	CPs

Table IV: *Current PhD fellows working (partially) on* Chlamydiae.

Stefanie Lagae	Ghent University, Belgium	CPs
Kristien de Puysseleyr	Ghent University, Belgium	C
Leentje de Puysseleyr	Ghent University, Belgium	C
Sarah van Lent	Ghent University, Belgium	CPs
Cindy de Boeck	Ghent University, Belgium	CPs
Matthias van Gils	Ghent University, Belgium	C

**Chlamydiae* are the major focus in the thesis.
C: Chlamydiae
CAb: C. abortus
CT: C. trachomatis
CP: C. pneumoniae
CPs: C. psittaci

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Amsterdam, 6 February 2015

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Announcement

11th Annual Amsterdam *Chlamydia* Meeting

2016

Organisers: Servaas Morré & Sander Ouburg
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Dept. Medical Microbiology & Infection Control, VUmc, Amsterdam

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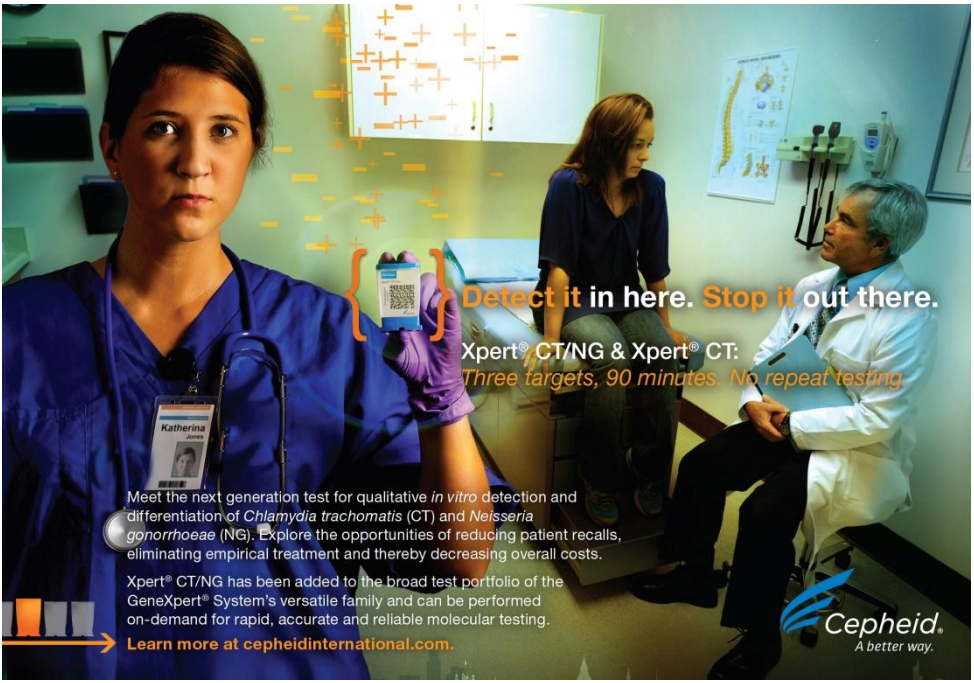

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