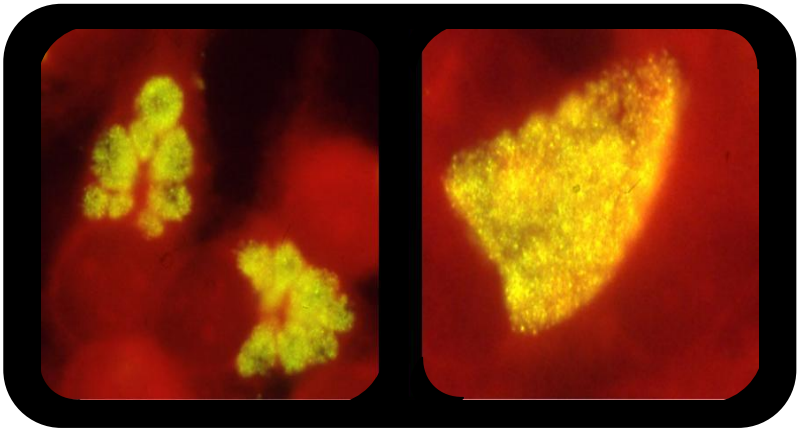
9th AACM

Ninth Annual Amsterdam

Chlamydia Meeting



Hotel Mercure Amsterdam aan de Amstel

7 February 2014
9.00 – 17.00

Preface

Welcome: this year we organize our Annual Amsterdam Chlamydia Meeting (AACM) for the ninth time, and we included, like the last three years, all *Chlamydiae* species.

The symposium will be opened by Dr. Ingrid van de Broek updating us on the "*Chlamydia* Control in Europe 2012: a cross-national survey". In addition we have many senior and junior speakers including 6 PhD students with in total 17 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).

Studies in twins and adopted children have shown that host genetic factors form an important element in the susceptibility to and the severity of infectious diseases such as *Chlamydia trachomatis*, *C. pneumoniae*, and *C. psittaci* infections in humans. Bacterial, environmental, and host genetic factors determine the clinical course of *Chlamydiae* infections and an integrated multi-disciplinary approach is used to study these factors.

Acknowledgements: We would like to thank our sponsor, without his support this meeting would not be possible in the current format. We would also like to thank those involved in the organization of this meeting.

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 Prevention, 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.

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Floor plan (1st Floor, rooms 1+2)

Programme

9.00 – 9.30 **Registration to the symposium (1st floor, Foyer outside Rooms 1-2)**

9.30 Dr. Ingrid van den Broek (NL)
Chlamydia Control in Europe 2012: a cross-national survey

9.55 Prof. Servaas Morré (NL)
Reference Laboratory for Chlamydia trachomatis 2009-2013

10.15 Dr. Remco Peters (NL / SA)
Sexually transmitted infections in rural South Africa

10.35 Drs. Jannie van der Helm (NL)
The role of Surinamese migrants in the transmission of Chlamydia trachomatis between Paramaribo, Suriname and Amsterdam, the Netherlands

10.55 – 11.15 **Coffee Break (In front of the meeting room)**

11.15 Dr. Sylvia Bruisten (NL)
Strain types of Chlamydia trachomatis in relation to ethnicity and symptoms in a young screening population in Amsterdam

11.40 Dr. Reinier Bom (NL)
Molecular Epidemiology of C. trachomatis

12.00 Drs. Anne Dirks (NL)
Chlamydia trachomatis load in population-based screening and STI-clinics: implications for screening policy

12.20 – 13.00 **Lunch (In font of the meeting room)**

13.00 Dr. Yvonne Pannekoek (NL)
Chlamydia Genome State-of-the-Art: Analysis of genome variation at the population level in BIGSdb

13.25 Dr. Vitaly Smelov (RU)
Multilocus sequence typing of genital Chlamydia trachomatis in Russia

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Programme

13.45 Dr. Janneke Heijne (NL)
Control of sexually transmitted Chlamydia trachomatis transmission

14.05 Dr. Nicole Dukers (NL)
Who to screen for anorectal Chlamydia?

14.25 Ing. Dewi de Waaij (NL)
Detection of Chlamydia trachomatis: Presto versus Roche

14.45 – 15.05 **Coffee break (In front of the meeting room)**

15.05 Drs. Stephan Verweij (NL)
C. trachomatis and Chlamydia-likes in subfertility

15.25 Drs. Natascha Lie (NL)
Case report: A C. caviae infection in a human

15.45 Elise Oud (NL)
Case reports: problems in LGV diagnostics and treatment

16.05 Drs. Bart Versteeg (NL)
No indication for tissue tropism for Chlamydia trachomatis strains defined by using multilocus sequence typing

16.25 Drs. Martijn van Rooijen (NL)
Oropharyngeal Chlamydia infections and persistence

16.45 – 16.55 **Closing remarks**

16.55 – 18.00 **Drinks (Foyer, lobby level)**

Ingrid van den Broek, PhD

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Curriculum Vitae

Ingrid van den Broek (1969) has worked as an epidemiologist at the Center for Infectious Disease Control of the RIVM since 2006. She worked on various research topics within the field of control and surveillance of STI's, mainly related to the epidemiology and risk groups for *Chlamydia* as well as on monitoring the development of STI care in the general practice in the Netherlands. She was involved in the evaluation of the *Chlamydia* Screening Implementation (2007-2012).

Before 2006, her research focussed on malaria control and emergency health. She coordinated several studies on the effectiveness of antimalarial therapy and performed rapid health assessments in field projects of 'Medecins sans Frontières' in various tropical countries around the world. In 1999 she completed her PhD at the University of Groningen, in a more experimental biological setting (Dept. Animal Physiology), on the role of the olfactory system of the malaria mosquito *Anopheles gambiae*. She studied Biology in Utrecht (graduation in 1993).

Abstract

Introduction

Chlamydia trachomatis (*chlamydia*) is a priority for infectious disease prevention and control in several European Union (EU) countries. In 2007 the European Centre of Disease Control (ECDC) published a first survey on activities to control *chlamydia* in the EU. In 2009 the ECDC issued a guidance document based on those findings. Here we present the results of the second ECDC survey, showing the current *chlamydia* prevention and control activities, changes between 2007 and 2012 and suggest recommendations to improve *chlamydia* prevention and control in EU countries.

Methods

Experts in sexually transmitted infection surveillance and control from EU countries completed a questionnaire between December 2012 and February 2013, which addressed 13 pre-defined 'key indicators' covering six main topics of *chlamydia* control: 1) guidelines on *chlamydia* case management and testing; 2)

laboratory diagnosis; 3) strategies, plans and organisation of care for sexually transmitted infection control; 4) strategies, plans and activities for primary prevention; 5) surveillance; and 6) *chlamydia* screening programmes. Scores were used to assign countries to one of five categories of *chlamydia* control. Category 3, assigned to countries with *chlamydia* case management guidelines that included recommendations for partner management, was defined as a minimum EU target level.

Results

Twenty-eight of 30 EU/EEA countries responded to the survey (93%).

- *Chlamydia* case management guidelines exist in 22/28 countries and cover *chlamydia* diagnosis and treatment for use by one or more medical professional groups. Partner notification is addressed in 19 countries'case management guidelines.
- Reliable diagnostic tests for *chlamydia* (NAAT) are available in all countries that participated in the survey; in 23/28 countries this method is used for more than 90% of diagnoses;
- 11/28 countries have a strategy or plan for sexually transmitted infection control; six of these documents explicitly include *chlamydia* control. 24/28 countries have specialised healthcare services and/or other providers offering STI care within the general health system
- Primary prevention to improve knowledge about and awareness of *chlamydia* was implemented in 22/27 countries that responded to this question.
- Opportunistic *chlamydia* testing is recommended in 18/28 countries' clinical guidelines. One country (UK) has an organised screening programme.

Amongst 25 countries that took part in both surveys, more countries in 2012 (72%, 18/25) had *chlamydia* control activities in at least category 3 than in 2007 (44%, 11/25). Countries with opportunistic chlamydia testing or an organised screening programme report more diagnosed chlamydia cases than those with less intensive *chlamydia* control activities.

Conclusion

Overall, the infrastructure for *chlamydia* prevention and control activities has increased in 2012 compared to 2007. More countries in 2012 than in 2007 reported organised chlamydia control activities, NAATs for *chlamydia* diagnosis and surveillance of diagnosed cases.

1. National Institute of Public Health (RIVM), Bilthoven, The Netherlands
2. STI/AIDS Foundation and AMC, Amsterdam, The Netherlands
3. Julius Centre, UMC Utrecht, The Netherlands
4. University of Bern, Switzerland
5. European Centre for Disease Prevention and Control, Stockholm, Sweden

Prof. Servaas A. Morré, PhD

Laboratorium Immunogenetica, dept. Medical Microbiology & Infection Prevention, VU University Medical Centre, Amsterdam
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Curriculum Vitae

Professor Servaas A. Morré, PhD – who graduated at the VU University, the Netherlands, in Biochemistry and Molecular Biology in 1994 – has been working on *Chlamydia trachomatis* (epidemiology, diagnostics, immunopathogenesis and immunogenetics) for almost 18 years. He is Head of the Laboratory of Immunogenetics (VUmc, Dept of Medical Microbiology), which he joined from November 1st 2001. His research is focused on the immunogenetics of infectious diseases with special attention to *Chlamydia trachomatis.* 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". A series of grants ran and run on the immunogenetics of CT infections including 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)". He was the organizer of the 7th Meeting of the European Society for *Chlamydia* Research 1-6 July 2012 in Amsterdam. From the first of January 2008 he is head of the Laboratory of Immunogenetics. Since 1st of Sept 2009 he coordinates with the RIVM the *Chlamydia trachomatis* Reference Laboratory and from the 1st of January 2014 he does this together with Prof.dr. Christian Hoebe. From the 1st of June 2011 he is Director of the Institute of Public Health Genomics, Dept of Genetics and Cell Biology, Maastricht University where we works Thursdays and Fridays, and he is since Februari 1st 2012 Professor Host Pathogen Genomics in Public Health.

Abstract

Most commercial NAATs for the detection of *C. trachomatis* rely either on conserved regions of 16S ribosomal RNA or on the 7.5 kb cryptic plasmid of the organism as the target for amplification. Mutations in the primer and probe sequences and plasmid free variants could have devastating effects on control of *C. trachomatis* infections. Indeed, a *C. trachomatis* variant with a deletion in the plasmid was identified in Sweden, after an apparent 25% decrease in *C. trachomatis* infections was noted with major effects on the control of the STI. This

variant had a 377 bp deletion in the region of the plasmid targeted by two commercially NAATs, the M2000 (Abbott Laboratories, Abbott Park, IL, USA) and Amplicor CT/NG PCR (Roche Diagnostic Systems, Branchburg, NJ, USA) tests, and it therefore yielded false negative results with both of these tests. However, this strain remained detectable by another plasmid based NAAT, the ProbeTec ET (BD Biosciences, Sparks, MD, USA), because the deletion did not affect the target region of that test. Naturally occurring plasmid free clinical isolates are rare, indicating the potential plasmids' importance in chlamydial pathogenesis. Based on the Swedish findings where significant numbers of *C. trachomatis* infections were missed (up to 80% in some regions), the Centre for Infectious Disease Control, National Institute of Public Health and the Environment (RIVM) in Bilthoven, the Netherlands defined a monitoring system in the Netherlands carried out by the Laboratory of Immunogenetics at the VU University Medical Center Amsterdam (Prof.dr. Servaas Morré), to monitor potential emerging variants. Here we present the monitoring and the findings of *C. trachomatis* reference tasks from 1st Sept 2009- 1st Jan 2014.

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

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Curriculum Vitae

Remco Peters is a clinical epidemiologist with prime interest in infectious diseases. He works as clinical programme specialist for the Anova Health Institute in South Africa and is affiliated with the Department of Medical Microbiology at the Maastricht University Medical Centre. He obtained is Master of Science degree at the Erasmus University Rotterdam and moved to the VU University Medical Center, Amsterdam, to obtain his MD (2006) and his PhD (2007) in clinical microbiology and infectious diseases. After graduation, he worked as medical doctor at the municipal STI clinic in The Hague before moving to South Africa where he worked as senior medical officer in rural Mopani District. In 2010 he was promoted to programme manager of Anova's district health support project in Mopani named Khutso Kurhula. He successfully grew the project from 30 to 90 employees with expansion of support activities, sustaining and diversifying funding, and implementing a high-profile research agenda with special interest in sexually transmitted infections, diagnosis and management of tuberculosis, paediatric antiretroviral therapy, and eye infections in the context of HIV. During this period he completed his Master in Epidemiology and the London School of Hygiene and Tropical Medicine. In his current job at Anova Health Institute he provides strategic and scientific direction as well as clinical supervision to all of the organization's projects across South Africa. He supervises several PhD students and has published in high-ranked journals. His research interest is in the field of translational and molecular epidemiology and public health of infectious diseases, with special focus on STI. He works in close collaboration with several national and international academic institutions and governmental organizations.

Abstract

South Africa is affected by high a burden of sexually transmitted infections (STI) including HIV. The STI control program is based on the syndromic approach, *i.e.* individuals presenting with a specific clinical syndrome are treated empirically with a combination of antibiotics. However, the aetiology of these syndromes, *e.g.* vaginal or urethral discharge syndrome, is diverse and predictive value of this approach for bacterial STI is low. Individuals with asymptomatic infection are not treated which may cause long-term complications and provides a reservoir to sustain the epidemic.

There are only limited data of the epidemiology of urogenital chlamydia and gonorrhoea in South African women and MSM; no data are available of rectal and pharyngeal infection. We present data of chlamydial and gonorrhoeal infection in two distinct South African populations: 604 women in rural Mopani District and 200 men having sex with men (MSM) in Cape Town. We recruited sexually active women of reproductive age (18-49 years) at 25 primary healthcare (PHC) facilities across the district, regardless of reason for visiting the clinic. MSM were recruited during regular clinic visit at the Ivan Tom's Centre for Men's Health, Woodstock, Cape Town. We present prevalence data of chlamydia and gonorrhoea per anatomic site in both study populations showing high prevalence of asymptomatic infection. For the cohort of women, determinants of infection and the frequency of *Mycoplasma genitalium* and *Trichomonas vaginalis* coinfection are presented. The implications of our study results for the STI control program are discussed.

Jannie J. van der Helm, MSc

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Curriculum Vitae

Jannie van der Helm studied Biomedical Science at the Radboud University Nijmegen. She is currently employed as epidemiologist at the Public Health Service (GGD) Amsterdam, the Netherlands. She will finish her thesis in 2014, which includes international epidemiological studies of HIV, Hepatitis C, *Chlamydia* and other STI. The research regarding *Chlamydia* was conducted in Suriname to determine the prevalence of *Chlamydia*, and to identify the role of Surinamese migrants in the transmission of *C. trachomatis* between Suriname and the Netherlands. Furthermore, she evaluated a point-of-care test for detection of *C. trachomatis* in Suriname.

Abstract

Background/Aim

Surinamese migrants travel extensively between the Netherlands and Suriname. We assessed whether the Surinamese migrants in the Netherlands form a bridge population facilitating transmission of *C. trachomatis* between Suriname and the Netherlands.

Materials/Methods

Between March 2008 and July 2010, participants were recruited at clinics in Paramaribo, Suriname and in Amsterdam, the Netherlands. Risk behavior was recorded and *C. trachomatis* positive samples were typed through multilocus sequence typing (MLST).

Results

Sexual mixing between Surinamese migrants and Dutch and Surinamese natives occurred frequently. A minimum spanning tree of samples from 426 participants showed four MLST clusters. Yet, the MLST strain distribution of Surinamese migrants differed significantly from both the native Surinamese and Dutch populations, and was not an intermediate state between these two populations.

Discussion/Conclusion

Sexual mixing occurred between Surinamese migrants in Amsterdam and the native populations of Suriname and the Netherlands. These migrants did not

seem to form an effective bridge population for *C. trachomatis* transmission between the native populations. Although our data do not seem to justify the need for joint campaigns to reduce the transmission of *C. trachomatis* strains between both countries, preventive campaigns in both Suriname and the Netherlands are required to decrease the *C. trachomatis* burden.

Sylvia Bruisten, PhD

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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 perform 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 coöperative 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. She was the chair organiser of a European Virology congress in 2009 at the VU Medical center.

Abstract

Studies using conventional *ompA* typing have focused on variations in ethnicity and clinical manifestations by *C. trachomatis* serovar types. However, results were conflicting when studying urogenital *C. trachomatis* strain types. This may be due to the use of *ompA* based genotyping which is less discriminatory than the recently developed multilocus sequence typing (CT-MLST) method from Sweden and our group.
In the Netherlands, a *Chlamydia* Screening Implementation (CSI) pilot study was performed offering samples and data of a sexually active population of mostly heterosexual individuals aged 16 to 29 years old. We aimed to investigate differences in *C. trachomatis* sequence type distribution in association to ethnicity and to self reported symptoms in this CSI study.

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All samples from participants living in Amsterdam that were positive for *Chlamydia* by the screening assay (TMA) (n=580) were included for typing by CT-MLST. DNA isolates from TMA samples with a positive in house LGV/nonLGV PCR were sequenced for the regions *ompA*, CT046 (*hctB*), CT058 (*inc*), CT144, CT172 and CT682 (*pbpB*). A minimum spanning tree was generated of all 359 samples with a full CT-MLST profile. We found 29 *ompA* variants, comprising 9 different genovars: the major types being D (n=40;11.1%), E (n=155; 43.2%) and F (n=77; 21.4%). The minimum spanning tree consisted of 5 large clusters and residual strains (small clusters and singletons).
Participant characteristics were compared for the 5 large clusters and the residual group. No significant differences were observed between clusters regarding age, gender, level of education, residence, living conditions, number of partners in the preceding 6 months and history of STI. And no significant differences were observed regarding the proportion of participants with self-reported symptoms (P=0.479), suggesting that al strains are equally capable of causing symptomatic infections.
However, we did observe a significant difference in the proportion of predefined ethnic groups between clusters (P=0.013). Cluster IV had a larger proportion of participants from Surinamese, Antillean, or other non-Dutch origin compared to the other clusters. Participants in cluster IV reported more unsafe sex compared to participants in other clusters and the residual group.

In conclusion, we found in this population of young heterosexuals that participants of non-Dutch ethnicity were over-represented in one *C. trachomatis* cluster (cluster IV). We did not find an association however, between the CT-MLST strain of *C. trachomatis* and symptomatic infections. This suggests that all strains defined by CT-MLST are equally capable of causing symptomatic infections.

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Curriculum Vitae

Reinier Bom (1982) graduated in Medical Biology at the University of Amsterdam in 2008. During his study he took courses in population genetics, epidemiology, evolutionary biology, and microbiology. After his graduation he started a PhD project on the molecular epidemiology of *Chlamydia trachomatis* at the Public Health Laboratory of the Public Health Service of Amsterdam. During this project he developed and evaluated various multiple typing techniques for *C. trachomatis* and, in cooperation with the University of Uppsala, he developed a public database for *C. trachomatis* typing. For his PhD project he collaborated with various research groups in the Netherland, as well as institutes in Sweden, England, the United States, Suriname, China, and Tunisia. He successfully defended his PhD thesis on January 14, 2014. Currently he is working at the Condomerie, where he is estimating the effect of condom distribution at sex locations throughout the Netherlands on the transmission of various sexual transmitted infections, including HIV, hepatitis C and *C. trachomatis*.

Abstract

Chlamydia trachomatis infections are the most prevalent bacterial sexually transmitted infections (STI) worldwide. A better understanding of the transmission of *C. trachomatis* may contribute to improved screening and prevention programs. Through the use of typing methods, better understanding can be achieved by discriminating between clinically, biologically or epidemiologically different *C. trachomatis* strains.

Using *ompA* genovar typing, heterosexuals were mainly infected with genovars E, F, and D, while MSM had predominantly genovars D, G, and J infections. When multilocus sequence typing (MLST) was applied, differences in *C. trachomatis* strain distribution proved to be much more apparent. Eight clusters were identified of which 4 consisted of samples from MSM, with genovars D, G, J, and L2b. The other 4 clusters consisted mainly of samples from heterosexuals with genovars D, E, F, I, and J. Genetic diversity was much lower in the MSM clusters than in heterosexual clusters. The distribution of urogenital strains found among MSM in the Netherlands was very similar to the distribution found among MSM in Sweden and the United States, while much more differences were seen between the distribution of strains found among heterosexuals in the Netherlands and

Sweden. Within the Netherlands, the distribution of *C. trachomatis* strains found among the heterosexual Surinamese migrant population differed from the native Dutch heterosexual distribution, as it did from the native Surinamese heterosexual distribution. Within Suriname, all major ethnic groups were represented in all *C. trachomatis* clusters, but the proportion from various ethnic groups differed significantly between the clusters. When the distribution of *C. trachomatis* genotypes found among heterosexuals from Nanjing, China were compared with those found in Amsterdam, the Netherlands, we found that most strains were specific to Nanjing. This demonstrates geographical variation in *C. trachomatis* previously left undetected.

We found that the MSM and heterosexual populations harbour distinct *C. trachomatis* strains. In addition, within the MSM-associated *C. trachomatis* strains less variation was observed compared to the heterosexual-associated strains. Among heterosexuals, the distribution of strains varied between countries and between subgroups within one country. This variation was absent among MSM. These differences could arise from biological differences between the risk group-associated strains or can be accounted to differences in the transmission networks between the two risk populations. Future research should elucidate these differences and how these findings can be exploited to improve screening and prevention programs.

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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 at the *Chlamydia trachomatis* reference laboratory in Maastricht. The topic of the PhD is the bacterial load in *Chlamydia trachomatis* infections, and its relation to both bacterial and host factors.

Abstract

Chlamydia trachomatis (CT) bacterial load is estimated to be higher in high-risk populations than in the general population, possibly affecting the efficacy of CT-screening incentives. We investigated the CT load in 2 CT-positive cohorts: (1) attendants of a sexually transmitted infection (STI)-clinic and (2) participants of the Dutch population-based screening (PBS), thereby taking into account symptoms as well as other determinants relevant for bacterial load. CT-load was determined using quantitative PCR in 1085 CT-positives from the PBS-cohort (n=629; 467 women) and STI-clinic in South Limburg (n=456; 292 women). Loads were converted into tertiles. Using multinominal logistic regression analyses with load as outcome, the independent association of cohort, symptoms, risk-behaviour and cell count were assessed. In men, STI-clinic-cohort, cell count and urethral discharge were positively associated with CT load. In women, PBS-cohort and cell count were positively associated with CT load. Within cohorts, no difference could be demonstrated between CT load in the highest CT category. Our results indicate a similar height of bacterial CT load in the general population and in a high-risk population, highlighting the relevance of population-based CT-screening.

Amsterdam, 7 February 2014

Yvonne Pannekoek, PhD

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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

Multi Locus Sequence Typing (MLST) indexes the sequences of multiple (usually seven) housekeeping gene fragments of approximately 500 bp in length. Each unique allele is assigned an arbitrary integer identifier with unique combinations of the alleles, allelic profiles, are identified by a sequence type (ST) number. Allele and ST definitions are stored in the pubMLST databases overseen by a curator for each species or group of species[1].

We have successfully applied MLST to investigate the population structure and evolution of *Chlamydia*. Phylogenetic analyses of seven housekeeping gene fragments of *C. trachomatis* strains revealed three non-overlapping clonal complexes among *C. trachomatis* strains, while the *C. pneumoniae* strains from patients formed a single group. The LGV strains grouped in a single cluster, while the urogenital strains were distributed over two separated groups, one consisted solely of strains with frequently occurring serovars (E, D, F)[2]. This grouping was

congruent with the phylogenetic analysis and grouping of *C. trachomatis* strains based on whole genome sequences[3]. In addition, phylogenetic analyses of the concatenated allele sequences of *C. psittaci* revealed an association between *C. psittaci* genotype and host species[4]. More recently, the application of MLST to *C. pecorum* strains and demonstrated an association between *C. pecorum* genotype and host species (Pannekoek *et al*. unpublished).

Wider population genomic research on *Chlamydia* requires the linkage of whole genome sequence (WGS) data with detailed clinical information, provenance, genotypic and phenotypic properties, thereby allowing integrated studies, irrespective of the origin and diversity of the isolates. Recently, the MLST paradigm was extended to WGS data, so that different combinations of loci can be analysed depending on the question being addressed[5]. This system, the Bacterial Isolate Genome Sequence Database (BIGSdb), is a scalable, open source, web-accessible database system that is capable of the storage, retrieval, and analysis of linked phenotypic and genotypic information in a computionally efficient manner. BIGSdb incorporates the capacity to define and identify any number of loci and genetic variants at those loci within stored nucleotide sequences. These loci can be further organised into 'schemes' for isolate characterization or for evolutionary or functional analyses. Isolates and loci can be indexed by multiple names and any number of alternative schemes can be accommodated, enabling cross-referencing of different studies and approaches. The data can be easily linked to external databases and fine-grained authentication of access permits multiple users to participate in community annotation by setting up or contributing to different schemes within the database[5].

References:

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Curriculum Vitae

Vitaly Smelov is an urologist with a strong interest in the "grey area" between urological diseases and sexually transmitted infections. He was graduated from the Military Medical Academy, St. Petersburg, Russia in 1993 and defended his thesis on the treatment of *Chlamydia infections* in men with chronic inflammation in the prostate in 2008. Recent research topics involve: the viral pathogenesis of anogenital malignancies (cervical and anal cancers), prostate inflammation and cancer, HPV and *Chlamydia* infections.
He initiated and was involved in several research projects together with research groups from the VU University and GGD Amsterdam, which was possible through the UNESCO-ASM Travel Award in 2006 and European Urology Scholarship Program Clinical Fellowship in 2007, respectively.
In 2011-2013 he was awarded with Swedish Cancerfonden grants and worked as a Postdoc on several HPV-related projects in Karolinska Institutet (Stockholm), combining this with his work in St. Petersburg as a clinician in an infertility clinic in and as a Docent in North-Western State Medical university named after I.I. Mechnikov.
Since October 2013 he is a Postdoc Fellow at the International Agency for Research on Cancer – World Health Organization (Lyon, France).

Abstract

HPV and *C. trachomatis* (CT) infections are among the most often diagnosed viral and bacterial STIs in the world, respectively. The infections potentiate each other's impact and acquisition and might be involved in urogenital carcinogenesis in both genders. An advanced multilocus sequence typing (MLST) scheme detects CT strains that circulate among the population and is a useful molecular epidemiologic tool for discriminating strain types beyond the level of *ompA* genotype. The epidemiological data about the prevalence of CT among the Russian population is limited and the data on CT ethno-demographic characteristics is lacking. Limited data is available on Russian CT strain types and geographical differences. There is a need for the molecular epidemiological study on CT strains among HPV+/- Russian populations, to better understand the role

of ethnicity, cross-border transmissions and their role in the tissue tropism and a possible role of CT strains in development of genital malignancies.

Janneke Heijne, PhD

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Curriculum Vitae

Janneke Heijne is a researcher in the STI group at the National Institute for Public Health and the Environment (RIVM) in Bilthoven. She studied Biomedical Sciences at the VU University in Amsterdam. During these studies she discovered her interests in both biology and mathematics. She did a bachelor internship at the department of theoretical biology of the VU University, in collaboration with the RIVM. This was Janneke's first introduction to mathematical modelling of infectious disease dynamics. Her master's internship, at the Institute for Research in Extramural Medicine (EMGO) of the VU Medical Centre in Amsterdam, introduced her to the field of epidemiology. After finishing her studies in 2003, Janneke started working as a researcher at the RIVM in the infectious disease surveillance group and later in the mathematical modelling group. In 2008 Janneke moved to Bern, Switzerland to do a PhD at the Institute of Social and Preventive Medicine (ISPM) of the University of Bern, under supervision of Prof. Nicola Low. The overall aim of her PhD was to use mathematical modelling and epidemiological data to investigate the impact of interventions to control *chlamydia* transmission. After obtaining her doctorate degree in 2012 she moved back to the Netherlands where she is currently working at the RIVM.

Abstract

Background: Re-infections within partnerships are an important contributor to sustaining *chlamydia* transmission. The objective of this study was to determine the optimal time interval for a repeated *chlamydia* test by combining epidemiological data analyses and mathematical modelling.

Methods: Claims data for US women aged 15-25 years who were enrolled in commercial health insurance plans between 2002 and 2006 is used. The numbers of initial positive and negative tests that were followed by a repeated test and the positivity of repeated tests is determined. A dynamic transmission pair model is used that reflects the partnership formation and separation processes in 15 to 25 year olds to determine the impact of screening interventions and the time course of repeated infections in women under different levels of notifying the current partner. Last, the additional impact of repeated testing uptake on reducing *chlamydia* prevalence is explored.

Results: 40% (4949/12 413) of positive tests were followed by a repeated test compared with 22% (89 119/402 659) of negative tests at any time. Positivity of repeated tests followed by an initial positive test was high: 15% (736) after a positive test versus 3% (2886) after a negative test. The transmission model showed a peak in repeated infections between 2 and 5 months after treatment. For a *chlamydia* testing uptake of 10% per year, the additional impact of repeated testing on reducing *chlamydia* population prevalence was modest.
Conclusions: The mathematical model predictions support the recommended interval for repeat *chlamydia* testing. This study provides information that can be used to design randomised controlled trials to determine more effective interventions to prevent chlamydial reinfection.

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Curriculum Vitae

Dr. Nicole HTM Dukers-Muijrers (1972) is infectious diseases epidemiologist and coordinator research at the department of infectious diseases, public health service South Limburg, and also works at Caphri, Dept. Medical Microbiology (affiliated National *Chlamydia* reference laboratory), University Medical Centre, Maastricht. With a master's degree in Biological Health Sciences & Epidemiology, University of Maastricht, she obtained her doctorate (2002) at the University of Amsterdam. In total she has 18 years of relevant international work experience as a researcher and project leader in The Netherlands (GGD South Limburg and GGD Amsterdam, Universities of Maastricht and of Amsterdam, RIVM) and also worked in San Francisco US (UCSF), China and Ethiopia. She published over 70 papers in international peer-reviewed journals including high impact journals as Journal of Infectious Diseases, New England Journal of Medicine, AIDS, American Journal of Epidemiology.

Her research interest is in the field of public health, with a major focus on prevention of sexually transmitted infections, including *Chlamydia*. In her projects, she combines biological, psycho-behavioural and network assessments to gain a deeper understanding of the processes underlying acquisition, spread and control of infections. Examples of ongoing projects by current PhD students under her supervision include the multi-anatomic site evaluation of *Chlamydia* infections to inform testing policies and using an innovative online targeting of sexual and social networks with *Chlamydia* home-delivered tests. She was applicant of several funded grant proposals and an ad-hoc reviewer for high impact peer-reviewed journals and for research project funds. She is a member of the editorial board of the journal BMC Public Health.

Abstract

Introduction: In addition to infection of the urogenital tract, chlamydia and gonorrhoea can also cause anorectal infections. These might play a major role in the persistence of urogenital STI infection and the transmission of STIs to others. While urogenital testing is a routine procedure in STI care services in the UK, US, and the Netherlands, guidelines in these countries state that anorectal testing is

not routine but restricted to people who are in high-risk groups, report anal sexual behaviour, or have anal symptoms (selective testing on indication). It is likely that selective testing on indication misses infections in the STI clinic population. Adequate treatment for anorectal *chlamydia* is currently under debate and therefore, anorectal control strategies (treatment and testing) may thus be in critical need of revision. Current studies (ongoing work of PhD student Genevieve van Liere) are the first to assess the proportion of anorectal *chlamydia* by routine universal testing in the diverse target groups of STI clinics (high risk groups (MSM, prostitutes and swingers) and the general female population) and to examine the associations with medical and behavioural history. We aim to estimate the number of infections missed by current selective testing on indication and to formulate recommendations for control strategies.
Methods: Between January 2010 and July 2013, high risk groups and the general female population attending our sexually transmitted infections clinic were routinely tested for anorectal, oropharyngeal and urogenital *Chlamydia trachomatis* and *Neisseria gonorrhoeae*. Data were collected on demographics and sexual behaviour.
Results: Prevalence of anorectal *Chlamydia* ranged from 5% to 9% in MSM and women and was lower in heterosexual males with 1%. Current selective testing (*i.e.* based on report of symptoms and/or anal sex) misses 55.0% anorectal *chlamydia* infections in homosexual MSM, 43% in bisexual MSM, 50% in bisexual male swingers, 75% in heterosexual male swingers, 48% in female swingers and 71% in the general female population. For gonorrhoea this was 29%-80%. Most of the anorectal *chlamydia* cases were combined with genital *Chlamydia* infections in 54%-94% of women, while MSM showed mostly isolated anorectal Chlamydia infections (62%).
Discussion: Current selective testing on indication of symptoms and sexual history is not an appropriate control strategy for anorectal *chlamydia* and gonorrhoea in high risk groups and the general female population visiting an STI clinic. There is an urgent need to optimise the testing guidelines at different anatomic sites. Routine universal anorectal testing is feasible and should be considered as a possible control strategy for MSM and female swingers. For the general female population, when more restricted control measures were to be preferred, we advise (1) doing anorectal testing for all women who test positive for urogenital *chlamydia*, or (2) not doing anorectal testing but providing direct treatment for urogenital *chlamydia* that is effective for anorectal *chlamydia* as well (*e.g.* doxycycline).

Dewi J. de Waaij, BAs

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Curriculum vitae

Dewi de Waaij, born 1 December 1989, has a bachelor of applied sciences degree and is currently a bachelor student of medicine at the VU University of Amsterdam. During her internship in 2011 at the laboratory of immunogenetics at the department of Pathology, she worked on *Chlamydia trachomatis*. She studied genetics that influence the susceptibility and severity of a *Chlamydia trachomatis* infection. She's now a PhD student at the laboratory of immunogenetics.

Abstract

Objectives: Comparison of the new GMT Presto-Plus Assay with the cobas 4800 CT/NG test (Roche Molecular Diagnostics, Pleasanton, CA, US) for the detection of Chlamydia trachomatis (CT) and Neisseria gonorrhoea (NG) using dry collected vaginal and rectal swabs of South African women. Performances (sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) were assessed for both assays and discrepancy analyses were performed with a third assay.

Methods: Sample collection: a cross-sectional study was conducted at primary healthcare facilities across the Mopani District, South Africa. From 612 women vaginal and rectal swabs were obtained (Copan,Diagnostics, Brescia, Italy). Swabs were frozen for storage without buffer (dry swabs). Patient information was provided and written consent obtained. CT and NG detection: DNA was isolated by the High Pure PCR Template Preparation Kit (Roche), and processed using the new CE-IVD certified PRESTO-PLUS test (Goffin Molecular Diagnostics, Houten, The Netherlands) and the cobas 4800 CT/NG test (Roche Molecular Diagnostics). Discrepant samples were analyzed by the TibMolBiol CT or NG assay. The gold standard was defined as two concurring results for the PRESTO-PLUS and cobas 4800 tests, or, with discrepant results, two concurring results of either test together with the TibMolBiol assay.

Results: 100 (16.3%) samples gave positive results for CT and/or NG. Only three samples were discrepant: 1 vaginal sample for NG and 2 rectal samples for CT. Sensitivities, specificities, and positive and negative predictive values between the cobas 4800 CT/NG Test and the new GMT assay were comparable resulting in the following CT and NG prevalences: Vaginal CT: 12.4%, Vaginal NG: 3.4%,

Rectal CT: 6.4%, and Rectal NG: 1.6%. Overall, 14.9% of women were infected vaginally with NG and/or CT, and 7.2% of women were infected rectally with NG and/or CT. Finally, 16.3% of the women were infected NG or CT at any site.
Conclusion: The new GMT assay showed comparable performance compared to the frequently used cobas 4800 CT/NG Test for both vaginal and rectal dry swabs for detection of infection with CT or NG. The use of dry swabs is off label but appears to be suitable.

Stephan P. Verweij, MSc

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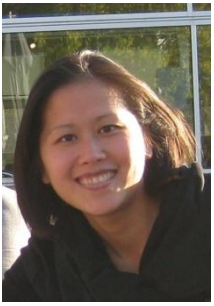
Curriculum vitae

Stephan Verweij graduated in Biomedical sciences in 2012 at the VU University Amsterdam. He is currently finishing his PhD project, which he will defend on March 12th of this year. 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. Stephan is currently enrolled in the accelerated medical programme of the VU University medical center ("zij-instroom"). He recently finished his scientific 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

Natascha Lie studied Health Sciences and Medicine at Maastricht University. After finishing her master in Biological Health Sciences and graduating as a medical doctor in 2006, she worked at the emergency department of St Elisabeth Hospital in Tilburg. During this time she gained a lot of clinical experience and developed her skills for patient care. In 2009 she started her training as a resident in Pulmonology at Atrium Medical Center in Heerlen.

Abstract

A case of severe community-acquired pneumonia requiring intensive care admission and mechanical ventilation is described. Psittacosis was diagnosed based on a positive PCR for *'C. psittaci*' performed on sputum, broncho-alveolar lavage fluids and even acute phase serum sample. However, no contact with birds was reported after investigation by public health authorities and further genotyping did not reveal a known *C.psittaci* genotype. As thorough questioning revealed that the patient purchased two pet guinea pigs recently, *Chlamydophila caviae* was searched for as the diagnostic *'C. psittaci*' PCR detects this species as well. *C. caviae* was finally found by use of *C. caviae* specific PCR and sequence analysis. The patient slowly recuperated and was discharged in weakened but relatively good condition. After long term rehabilitation he made a full recovery.

Amsterdam, 7 February 2014

Elise V. Oud, BSc

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Curriculum Vitae

Elise Oud was born on November 27th, 1988. She graduaded in BSc Biomedical Sciences in 2010 at the VU University in Amsterdam. During her bachelor internship at the Department of Pathology, laboratory Immunogenetics of the VU University in Amsterdam, she focused the genetic perspective of *Chlamydia trachomatis* and female infertility. In 2013 she graduated in BSc in Medicine at the Academic Medical Centre, University of Amsterdam. Recently she wrote a case series about pitfalls in the diagnosis and management of inguinal lymfogranuloma venereum, in cooperation with the Department of Dermatology, Academic Medical Centre, University of Amsterdam and the STI outpatient clinic, Public Health Service, Amsterdam.

Abstract

Objectives Current lymphogranuloma venereum (LGV) guidelines mainly focus on anorectal infections. Inguinal LGV infections have been rare in the current epidemic among men who have sex with men (MSM), but might require a different approach not yet recommended in current guidelines for the treatment and diagnosis of LGV.

Methods Description of 4 inguinal LGV cases presented at the STI outpatient clinic in Amsterdam.

Results 4 MSM developed inguinal LGV infection several weeks after a previous STI consultation. Initially 2 men had received 1000 mg azithromycin after being notified by a partner with LGV. During follow up of the 4 inguinal LGV cases, 3 failed to clear the infection after the advised 21 days doxycycline regimen and required a prolonged course of antibiotic therapy.

Discussion The presented inguinal LGV cases highlight 3 relevant pitfalls in the current clinical guidelines for the management of LGV. 1) Urethral *chlamydia* infections in MSM can be caused by LGV biovars that in contrast to non-LGV biovar infections require prolonged courses of antibiotic therapy. 2) The recommended presumptive treatment of contacts notified for LGV with one gift of azithromycin seems insufficient to prevent established infections. 3) Inguinal LGV with bubo formation may require prolonged courses of doxycycline, exceeding the currently advised 21 days regimen.

Amsterdam, 7 February 2014

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Curriculum vitae

Bart Versteeg finished his bachelor in life sciences in 2010 at the Hogeschool Utrecht. Subsequently, he started studying biomedical sciences at the VU university in Amsterdam where he obtained his master diploma in 2012. Currently, he is working as a PhD student at the Public Health Service (GGD) Amsterdam. His PhD project is about tissue tropism and molecular epidemiology of *Chlamydia trachomatis*.

Abstract

Introduction

A recently developed high resolution *Chlamydia trachomatis* multilocus sequence typing (CT-MLST) system has improved the characterization of different *C. trachomatis* strains infecting populations at risk. Studies using this CT-MLST method revealed separate transmission networks for men having sex with men (MSM) and heterosexuals [1]. The different distributions of *C. trachomatis* strains may be a reflection of differences in sexual behavior of MSM and heterosexuals. However, in studies mentioned, samples from MSM were primarily obtained from the anorectal tract whereas samples from heterosexuals were obtained from the urogenital tract. Therefore another explanation might be tissue tropism, causing specific *C. trachomatis* sequence types to be preferentially associated with either the urogenital or the anorectal tract.

Methods

A retrospective analysis was performed using routinely collected data and samples (from 2012) of women diagnosed with *chlamydia* at the STI outpatient clinic of the PHS, Amsterdam .This analysis was restricted to women who were diagnosed with either concurrent *C. trachomatis* infections at multiple anatomic locations, or with a solitary rectal infection. Epidemiological data were retrieved from electronic patient records. Samples were typed using CT-MLST from which minimum spanning trees were generated. For the comparison of rectal infections between MSM and women, we selected samples from MSM with a rectal *C. trachomatis* infection from a previous study, for which full MLST data and epidemiological data were available [1].

Results

Full MLST data were obtained for 207 MSM and 185 heterosexual women with rectal infections from which a minimum spanning tree was generated. This tree again showed a clear separation between samples from MSM and women which were dispersed over 6 large clusters. Of these, 3 clusters consisted predominantly of samples from women whereas the other 3 large clusters consisted of samples from MSM. So, in spite of the fact that only anal samples were used we observed the same phenomenon of separate transmission networks in MSM and heterosexuals.

Furthermore, we obtained full MLST data from 434 samples of 206 women with *C. trachomatis* concurrent infections at multiple anatomical locations comprising 316 (72.8%) urogenital, 101 (23.3%) rectal, and 17 (3.9%) pharyngeal samples. Using the complete MLST profile of all 434 samples another minimum spanning tree was generated in which 4 large clusters could be identified. This tree showed a heterogeneous distribution of STs found per anatomic location. If a cluster stands for a distinct *C. trachomatis* strain it was clear that each anatomical location could be infected with each of the strains defined by CT-MLST.

Conclusion

In rectal samples we still observed largely distinct *C. trachomatis* strains infecting MSM and women making tissue tropism unlikely. We observed no significant differences in the proportion of urogenital, rectal or pharyngeal infections for each *C. trachomatis* strain, arguing against tissue tropism. Most likely the separate transmission patterns in MSM and heterosexuals are due to network associated factors.

[1] Bom et al. J Clin Microbiol 49:2844-2853, 2011.

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Curriculum vitae

Martijn van Rooijen graduated in 2005 as a biomedical scientist and teacher in biology at the University of Leiden. Since 2007, he has been working as datamanager at the STI clinic and at the Public Health laboratory of the Municipal Health Service Amsterdam (GGD). Additionally he has been working on a research project on prevalence and persistence of pharyngeal *chlamydia*, and he is evaluating the STI clinic policy of routine Hepatitis C screening in HIV positive men who have sex with men. In collaboration with the Municipal Health Service Rotterdam he has been working on the implementation of the online partner notification tool "suggest-a-test". He will analyze the acceptability and usability of users of this partner notification tool.

Abstract

Background

Pharyngeal *Chlamydia trachomatis* (*chlamydia*) persistence probably contributes to ongoing transmission, yet data on persistence duration is lacking. We examined the prevalence, persistence, chlamydial DNA concentration, and genotypes of pharyngeal *chlamydia* among patients of a sexually transmitted infection (STI) clinic.

Methods

High-risk female patients reporting active fellatio and all male patients having sex with men (MSM) were screened for pharyngeal *chlamydia* using a nucleic acid amplification test (NAAT). A repeat swab was obtained to evaluate persistence in untreated patients with pharyngeal *chlamydia*.

Results

Pharyngeal *chlamydia* was detected in 148/13,111 (1.1%) MSM and in 160/6,915 (2.3%) women but was not associated with pharyngeal symptoms. In 53% MSM and 32% women with pharyngeal *chlamydia*, concurrent anogenital *chlamydia* infections were absent. In 27/43 (63%) MSM and in 35/55 (64%) women the repeat pharyngeal swab was persistently positive (4-58 follow-up days, median follow-up 10 days). Persisting pharyngeal *chlamydia* was associated with an initial

chlamydial DNA concentration above the median (p=0.001). Of 23 selected MSM with pharyngeal *chlamydia*, 2 were lymphogranuloma venereum (LGV) biovar positive (8.7%).

Conclusions
The pharynx is a reservoir for *chlamydia* and LGV, and may play a role in transmission. In high-risk STI clinic patients, the pharynx should be tested for *chlamydia*.

Symposium Organizer
Servaas A. Morré

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Curriculum vitae

Professor Servaas A. Morré, PhD, who graduated at the VU University, the Netherlands, in Biochemistry and Molecular Biology in 1994 has been working on *Chlamydia trachomatis* (epidemiology, diagnostics, immunopathogenesis, and immunogenetics) for almost 18 years. He is Head of the Laboratory of Immunogenetics (VUmc, Dept of medical Microbiology), which he joined from November 1st 2001. His research is focused on the immunogenetics of infectious diseases with still special attention to *Chlamydia trachomatis*, bacterial meningitis (Prof Marceline van Furth, VUmc), and Human Papilloma Virus (Prof. C.J.L.M. Meijer). Together with Prof. Salvador Peña, he organised the "First Mini-symposium *Chlamydia trachomatis* Infections" in December 2004 and we organize our Ninth "Annual Amsterdam *Chlamydia* Meeting" in February 2014. 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". A series of grants ran and run on the immunogenetics of CT infections including 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 (Scientific Consortium Director), with additional funding from amongst others NIH, NGI, and ETB. He was the organizer of the 7th Meeting of the European Society for *Chlamydia* Research 1-6 July 2012 in Amsterdam. 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. From the first of January 2008 he is head of the Laboratory of Immunogenetics. Since 1st of Sept 2009 he coordinates with the RIVM the *Chlamydia trachomatis* Reference Laboratory and from the 1st of January 2014 he does this together with Prof.dr. Christian Hoebe. From the 1st of June he is Director of the Institute of Public Health Genomics, Dept of Genetics and Cell Biology, Maastricht University where we works Thursdays and Fridays, and he is since Februari 1st 2012 Professor Host Pathogen Genomics in Public Health.

Amsterdam, 7 February 2014

Future STI / *Chlamydia* Meetings

12th German *Chlamydia* Workshop
April 2 - 4 2014, Berlin, Germany
http://131.130.66.201/dcw/

13th International Symposium on Human *Chlamydial* Infections
June 22 – 27 2014, Pacific Grove (CA), USA
http://www.chlamydia-symposia.org/

28th IUSTI Europe Meeting
September 18 – 20 2014, Malta
http://www.iustimalta2014.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

10th Annual Amsterdam *Chlamydia* Meeting
2015, Amsterdam, The Netherlands

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

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

Table I: *PhD theses in the Netherlands*

2014 Stephan P. Verweij*	VU University Amsterdam
2014 Reinier Bom*	University of Amsterdam/GGD A'dam
2013 Jonathan Lal	Maastricht University/ VU University Amsterdam
2013 Laura van Dommelen*	Maastricht University
2013 Marlies Heiligenberg	University of Amsterdam/GGD A'dam
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

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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
Dewi de Waaij	VU University Amsterdam
Monique Pereboom	VU University Amsterdam
Esmée Lanjouw	VU University Amsterdam
Jelena Malogajski	VU University Amsterdam/ Maastricht University
Ivan Brankovic	VU University Amsterdam/ Maastricht University
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
Charlotte van der Veer	University of Amsterdam/ Public health services
Jannie van der Helm	University of Amsterdam/ Public health

An overview of PhD work on *Chlamydiae*

Table III: *PhD theses on Chlamydiae*

2013 Lizi Yin	Ghent University, Belgium	CPC
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
Evelien de Clercq	Ghent University, Belgium	CT
Kristien de Puysseleyr	Ghent University, Belgium	C
Leentje de Puysseleyr	Ghent University, Belgium	C
Sarah van Lent	Ghent University, Belgium	CPs

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

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Amsterdam, 7 February 2014

Announcement

10th Annual Amsterdam *Chlamydia* Meeting

2015

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

We hope to welcome you all in Februari 2015

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"Combating reproductive health and associated infectious diseases in Women's Health"

Notes

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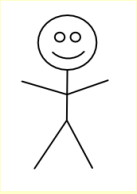
The organisers would like to acknowledge the support in organising this meeting of: Ing. Jolein Pleijster, Ing. Roel Heijmans, Ing. Dewi de Waaij, Drs. Stephan Verweij, Omaima El Tahir, Jerrel Morman



Symposium coordinator
Lay out & design, odd jobs:
Sander Ouburg, PhD
Laboratory of Immunogenetics, Dept. of Medical Microbiology & Infection zzcontrol
VUmc, Amsterdam

This symposium is accredited (5 points) by:

- *The Dutch Society for Medical Microbiology (NVMM)*

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