clinic visitors. In view of the extensive resistance against doxycyclin and ciprofloxacin, these antibiotics are not appropriate treatment options for gonorrhoea; instead, extended spectrum cephalosporins are advised.

Disclosure of interest statement The study is funded by Indonesian government through Beasiswa Unggulan (The Excellence Scholarship Program), Ministry of Education and Culture Republic of Indonesia and Public Health Service (GGD) of Amsterdam, The Netherlands. The authors declare that there is no conflict of interest.

P05.06 PROLONGED INFECTION OF PHARYNGEAL GONORRHOEA AFTER TREATMENT WITH CEFTRIAXONE
1,2,3IPy Hananta*, 2,3M. Schim van der Loeff, 3AP van Dam, 1H Soebono, 2,3HIC. de Vries.
1Department of Dermatology and Venerology Faculty of Medicine Universitas Gadjah Mada, Yogjakarta, Indonesia; 2Academic Medical Center, Universiteit Van Amsterdam, The Netherlands; 3Public Health Service (GGD) of Amsterdam, The Netherlands
10.1136/sextrans-2015-052270.292

Introduction Previous studies reported that in a considerable proportion of pharyngeal gonorrhoea cases treated with extended-spectrum cephalosporins, the infection remains detectable after several weeks. We examined the occurrence of prolonged pharyngeal gonorrhoea infections after treatment with ceftriaxone at a sexually transmitted infection (STI) outpatient clinic in Amsterdam.

Methods A retrospective cohort study was conducted based on routine electronic medical records at the STI clinic of the Public Health Service (GGD) of Amsterdam. Eligible for inclusion were: adults diagnosed with pharyngeal gonorrhoea between January 2012 and July 2013, who were treated with ceftriaxone (500 mg IM), and who returned for a test of cure (TOC) between 7 and 21 days after treatment.

Definitive diagnosis of gonorrhoea was based on Gen-Probe Apta-Combo 2 Assay™ using Tigris DTS™ system. Some patients also received additional antibiotics with ceftriaxone.

Information on patients’ characteristics and clinical history were available, but data on sexual re-exposure after treatment were not.

Results In the study period, 880 pharyngeal gonorrhoea cases were diagnosed; 290 cases (32.9%) returned for a TOC visit and were eligible (253 males and 35 females, median age 34 and 25 years, respectively). In 17 cases (5.9%) N. gonorrhoeae infection was detected again. Prolonged infection was not associated with gender (p = 0.49) or age (p = 0.87), but appeared to be associated with sex work (OR = 3.24 [95% CI 0.83–12.45], p = 0.07). Prolonged infection was significantly more common among those who were treated with ceftriaxone only vs a combined-regimen (OR = 4.07, [95% CI 0.90–18.39]; p = 0.048).

Conclusion Prolonged pharyngeal gonorrhoea infection after appropriate treatment was not uncommon, and was more often observed in those who were treated with ceftriaxone only. This could be the result of re-infection after treatment or of treatment failure possibly due to poor tissue penetration. Treatment failure due to antimicrobial resistance seems unlikely.

Disclosure of interest The study is fully funded by Public Health Service (GGD) of Amsterdam, The Netherlands. The authors declare that there is no conflict of interest.
Introduction Neisseria gonorrhoeae resistance to extended-spectrum cephalosporins as well as treatment failures with ESCs has been increasingly reported in many countries globally. These increasing trends together with the limitation of drugs of choice lead gonorrhoea to become a global health concern. Herein, we aimed to reveal more understanding on the physiological response of gonococci to ESCs using proteomic approach.

Methods N. gonorrhoeae reference strain was grown with or without a subinhibitory dose of ESCs. Protein expression was determined by 2-dimensional gel electrophoresis in conjunction with MALDI-TOF/TOF MS analysis.

Results In total, 14 and 13 proteins were significantly altered expression following exposure to ceftriaxone and cefixime, respectively. Most of expressed proteins shared a similar expression pattern in response to ceftriaxone and cefixime reflecting similarities in antibiotic mechanisms. ESC antibiotics triggered proteins in a variety of functions, such as membrane protein, transport system, energy metabolism, and stress response, which would help gonococci to survive under drug stress. Interestingly, the subinhibitory dose of ESCs also triggered the expression of gonococcal virulence factors (e.g. azurin and peptidyl-prolyl isomerase), which might be an adaptation mechanism of gonococci in ESC stress and also affect the outcome of gonococcal infection.

Conclusion The present work might provide new insights into physiological adaptive networks of gonococci to antimicrobial agents and more understanding toward the mechanism of action, which subsequently may benefit for the further drug discovery of new antimicrobials to combat with resistant gonococci.

Abstracts

P05.09 PHENOTYPIC, GENETIC AND GENOMIC CHARACTERISATION OF THE 2015 WHO NEISSERIA GONORRHOEAE REFERENCE STRAINS FOR QUALITY ASSURANCE OF LABORATORY INVESTIGATIONS GLOBALLY

M Unemo,* ‡Golparian, †Y Grad, ‡A Liminos, †T Wil, ‡M Lahra, ‡S Harris. †WHO Collaborating Centre for Gonorrhoea and Other Sexually Transmitted Infections, National Reference Laboratory for Pathogenic Neisseria, Department of Laboratory Medicine, Clinical Microbiology, Faculty of Medicine and Health, Örebro University, Örebro, Sweden; ‡Department of Immunology and Infectious Diseases, Harvard T.H Chan School of Public Health, Boston, MA, USA; †WHO Collaborating Centre for STD, Microbiology Department, The Prince of Wales Hospital, Randwick, Sydney, Australia; ‡Department of Reproductive Health and Research, World Health Organization (WHO), Geneva, Switzerland; Pathogen Genomics, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridgeshire, UK

Introduction Gonorrhoea and antimicrobial resistance (AMR) in Neisseria gonorrhoeae are major public health concerns globally. Resistance to all antimicrobials available for treatment of gonorrhoea has now been reported in N. gonorrhoeae. Enhanced quality assured gonococcal AMR surveillance is crucial worldwide and the WHO Global Gonococcal Antimicrobial Surveillance Programme (GASP) was revitalised in 2009. To obtain reliable and comparable AMR data internationally, appropriate and well-characterised N. gonorrhoeae reference strains are essential for quality assurance. The phenotypic and genetic characteristics of the 2008 WHO N. gonorrhoeae reference strains (n = 8) were previously published. Here, we describe the phenotypic, genetic, and genomic characteristics of the 2015 WHO N. gonorrhoeae reference strains.

Methods In the 2015 WHO N. gonorrhoeae reference strain panel (n = 14), six additional strains have been selected to include representation of high-level cephalosporin and azithromycin resistance and porB mutant strain. These strains were phenotypically characterised by antibiogram, serovar, and prolyl-linopeptidase (PIP) screening; and genetically in regards of resistance plasmid types, polymorphisms in divergent genetic resistance-mediating loci (n = 14), porB sequencing, N. gonorrhoeae multilocus sequence typing (NG-MAST), and multilocus sequence typing (MLST). Fully characterised finished reference genomes for all the 2015 WHO N. gonorrhoeae reference strains were produced using PacBio and Illumina sequencing technologies.

Results The 2015 WHO reference strains represent all available main phenotypes of resistance and susceptibility to antimicrobials previously and currently used for treatment of gonorrhoea, as well as several considered for future use. All corresponding resistance genotypes and molecular epidemiological types were also elucidated. Finally, references genomes of each strain were obtained and characterised in detail.

Conclusion The 2015 WHO N. gonorrhoeae reference strains are intended for internal and external quality assurance in all types of laboratory investigations, i.e. particularly in GASP but also for phenotypic (e.g. culture) and molecular diagnostics, species determination, genetic AMR detection, molecular epidemiology, and genome sequencing as well as other novel molecular technologies.

Disclosure of interest statement This work was funded by the Örebro County Council Research Committee and the Foundation for Medical Research at Örebro University Hospital, Sweden, the WHO, and The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridgeshire, United Kingdom.

P05.10 ANTIMICROBIAL RESISTANCE OF NEISSERIA GONORRHOEA IN GERMANY, RESULTS FROM THE GONOCOCCAL RESISTANCE NETWORK (GORENET)

S Dudaeva-Vyule, 5 S Buter, °K Jansen, °A Loenzenbach, °S Nikinsins, °A Sailer, †E Guhl, ‡P K Kohl, †V Bremer. °Department for Infectious Disease Epidemiology, Robert Koch Institute, Berlin, Germany; °German Reference Laboratory for Gonococci, Department of Dermatology and Venerology, Vivantes Hospital Berlin, Germany; ‡Department of Infectious Diseases, Robert Koch Institute, Berlin, Germany; European Public Health Microbiology Training (EUPHEM) Programme, European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

Introduction Neisseria gonorrhoeae (NG)-infections are not reportable in Germany and only limited data on NG-epidemiology and antimicrobial resistance (AMR) are available. With GORENET we monitor the NG-AMR and patterns of resistance testing in Germany in order to guide treatment algorithms and targeted prevention strategies.

Methods We recruited laboratories based on geographic distribution and number of NG-isolates. From April 2014 prospective data on all performed NG-AMR-tests together with patient-related information were collected. Laboratories send a part of the isolates to the national reference laboratory (NRL) for culturing and AMR-testing towards ceftriaxone, cefixime, azithromycin, ciprofloxacin, and penicillin by using E-Test, as well as beta-lactamase. Results are interpreted according to European Committee on Antimicrobial Susceptibility Testing 4.0.

Abstracts

Sex Transm Infect 2015;91(Suppl 2):A1–A258