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.

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

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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 *porA* mutant strain. These strains were phenotypically characterised by antibiogram, serovar, and prolyliminopeptidase (PIP) screening; and genetically in regards of resistance plasmid types, polymorphisms in divergent genetic resistance-mediating loci (n = 14), *porB* sequencing, *N. gonorrhoeae* multiantigen 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.
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P05.10 ANTIMICROBIAL RESISTANCE OF NEISSERIA GONORRHOEA IN GERMANY, RESULTS FROM THE GONOCOCCAL RESISTANCE NETWORK (GORENET)

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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.