and treatment failure among men who have sex with men (MSM), heterosexual men and women, diagnosed with repeat chlamydia infection within 1- 4 months after treatment with azithromycin.

Methods Participants completed an online survey capturing treatment and sexual behaviour data since initial diagnosis. Specimens from initial and repeat infections were included in the study. Chlamydia serovars were determined using quantitative PCR assays. When the same serovar was detected in both specimens for participants, MLST was used to further discriminate between genotypes. An algorithm based on genotype and sexual behaviour data was used to differentiate treatment failure from reinfection.

Results There were 600 participants (200 MSM, 200 heterosexual males, 200 females) diagnosed with chlamydia. Of 301/600 who retested between 1–4 months: 258/301 (85.7%) were cured (treated and negative on retest); 4/301 (1.3%) had a definite reinfection (positive retest and different genotype); 19/301 (6.3%) had probable reinfection (positive retest, same genotype and reported unprotected sex with the same or a different partner); 17/301 (5.6%) had possible treatment failure (positive retest, same genotype and reported not having sex or always using condoms); 1/301 (0.3%) had a persistent infection (positive retest, same genotype and no documented treatment); and 2/301 (0.7%) could not be categorised due to insufficient information. Possible treatment failures were more common in MSM (11.3%, 12/106) vs other groups (2.6%, 5/195; $p < 0.01$). Among the possible treatment failures in MSM, 10/12 (83.3%) were initial rectal samples.

Conclusion Treatment failure was common in MSM with rectal chlamydia, suggesting the need for treatment efficacy trials.

Disclosure of interest statement No conflict of interest is declared.

O15.4 AZITHROMYCIN TREATMENT FAILURE IN WOMEN INFECTED WITH GENITAL CHLAMYDIA INFECTION

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Introduction Repeat infections of chlamydia are very common and may represent a new infection, re-infection from an untreated partner or treatment failure. The aim of this cohort study is to estimate the proportion of women infected with chlamydia who experience failure after treatment with 1 gram azithromycin.

Methods Women diagnosed with chlamydia were followed for 8 weeks post treatment with 1 gram azithromycin and provided weekly genital specimens for further assay. The primary outcome was the proportion of women classified as having treatment failure at least 4 weeks after recruitment. Comprehensive sexual behaviour data collection and the detection of Y chromosome DNA in vaginal swabs and genome sequencing were used to differentiate between chlamydia re-infection and treatment failure. Chlamydia culture and MIC was also undertaken.

Results There were 305 women recruited with a response rate of 66%. A total of 36 women were diagnosed with repeat chlamydia infection during follow up (11.8%; 95% CI: 8.4%, 16.0%). The median time till repeat infection was 7 weeks, with 25% of repeat infections diagnosed within 5 weeks. The risk of repeat infection increased with increasing organism load of initial infection (OR = 1.6; 95% CI: 1.2, 2.8 for each additional log increase in load). Of the 36 women with repeat infection, 16 (44.4%; 95% CI: 27.9%, 61.9%) were classified as treatment failure with an overall risk of treatment failure of 5.2% (95% CI: 3.0%, 8.4%). There was no detectable shift in MIC between initial and repeat infections with MIC within reported antimicrobial susceptibility ranges.

Conclusion Using a combination of advanced laboratory techniques and comprehensive sexual behaviour data, we estimate that about 1 in 20 women with chlamydia infection treated with 1 gram of azithromycin will fail treatment. Further laboratory investigation will determine whether there are any genomic characteristics of the infections associated with treatment failure in our cohort.

Disclosure of interest statement This study was funded by the NHMRC.

O15.5 THE NATURAL HISTORY OF *CHLAMYDIA TRACHOMATIS* INFECTION IN WOMEN: A MULTI-PARAMETER EVIDENCE SYNTHESIS

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Introduction The National Chlamydia Screening Programme (NCSP) was initiated in England in 2003. However, the evidence base supporting it has been questioned repeatedly, with little consensus on modelling assumptions, parameter values, or evidence sources to be used in cost-effectiveness analyses.

Methods We reviewed all the available evidence on the *Chlamydia trachomatis* (CT) in the UK and its sequelae. Evidence was identified using "high yield" strategies. Bayesian Multi-Parameter Evidence Synthesis models were constructed for separate subparts of the clinical and population epidemiology of CT. Where possible different types of data were statistically combined to derive coherent estimates. Where evidence was inconsistent, evidence sources were re-interpreted and new estimates derived on a *post hoc* basis.

Results An internally coherent set of estimates was generated, consistent with a multi-faceted evidence base. Among the key findings were: the risk of pelvic inflammatory disease (PID), both symptomatic and asymptomatic, following an untreated CT infection is 17% (6,29), and the risk of salpingitis is 7% (2,14). In women aged 16–24 screened at annual intervals, at best 61% (55,67) of CT-related PID and 22% (7,43) of all PID could be prevented. For women aged 16–44 in the UK, the proportions of PID, ectopic pregnancy and tubal factor infertility (TFI) that are attributable to CT are estimated to be 20% (6,38), 5% (1,12), and 29% (9,56) respectively.

Conclusion The study establishes a set of interpretations of the major studies and study designs, under which a coherent set of estimates can be generated for UK decision-makers. CT is a significant cause of PID and TFI. CT screening is of benefit to the individual, but detection and treatment of incident infection may

be more beneficial. Further research is required to confirm predictions, and to improve the precision of key estimates. The cost-effectiveness of screening should be re-evaluated using these estimates.

Disclosure of interest statement This study was funded by the Medical Research Council grant G0801947. No pharmaceutical grants were received in the development of this study. PH has received funding from Cepheid directly and indirectly for lecturing on point of care testing and undertaking research on the cost effectiveness of their CT/NG assay. Has also received payment from Atlas Genetics for an article in the Parliamentary Review on the benefits of point of care technology in improving the cost effectiveness of sexual health services. Has also received an honorarium from Hologic for an education talk on STI diagnostics.

O15.6 IMPACT OF THE LNG-IUS ON CERVICAL PERSISTENCE OF *CHLAMYDIA TRACHOMATIS* AND VAGINAL MICROBIOTA IN A BABOON MODEL

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Introduction Alterations in vaginal microbiota associated with intrauterine contraception may impact host susceptibility to sexually transmitted infection. We evaluated the effect of the levonorgestrel intrauterine system (LNG-IUS) on cervical persistence of *Chlamydia trachomatis* (CT) in a baboon model and whether CT persistence was correlated with vaginal microbial community structure.

Methods 20 wild caught female olive baboons (*Papio abubis*) were randomly assigned to receive either LNG-IUS and CT inoculation (n = 8), LNG-IUS and sham inoculum (n = 2), CT inoculation alone (n = 8), or sham inoculation (n = 2). Animals were acclimated to the LNG-IUS for 24 weeks after which animals were cervically inoculated once weekly for 5 weeks. Vaginal swabs were collected weekly for microbiome analysis by 16S rRNA-encoding gene sequence analysis. Presence of CT in the cervical epithelium was confirmed with weekly nucleic acid amplification testing (NAAT) and culture.

Results Use of the LNG-IUS was significantly associated with positive CT culture (p = 0.04) but not NAAT (p = 0.07). Median time to cervical clearance of CT as detected by NAAT was 12.5 days (range 5–16) for LNG-IUS animals in comparison to 7 days (range 3–10) for non-implanted animals (p = 0.14). Similarly, median time to cervical clearance of CT by culture was 12 days (range 5–15) for LNG-IUS animals and 5 days (range 1–10) for non-implanted animals (p = 0.05). We did not detect significant within group differences between vaginal microbial community structure at baseline and following LNG-IUS insertion, CT inoculation, or LNG-IUS and CT in combination.

Conclusions Use of the LNG-IUS was associated with a trend towards cervical persistence of CT in a baboon model. However, this persistence is not explained by alterations in vaginal microbial communities.

Disclosure of interest statement The authors have no disclosures to report.

O16 - HPV vaccination: hits and misses

O16.1 THE RAPID AND NEAR ELIMINATION OF HUMAN PAPILLOMAVIRUS (HPV) TYPE 6, 11, 16 AND 18 AMONG YOUNG HIGH-RISK WOMEN WITHIN THREE YEARS OF THE NATIONAL HPV VACCINATION PROGRAMME IN AUSTRALIA: FINDINGS FROM A 10-YEAR CROSS-SECTIONAL STUDY

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Introduction The national quadrivalent human papillomavirus (HPV) vaccination programme was launched in Australia in April 2007. The aim of this study was to explore the proportion of vaccine targeted HPV genotypes contained in the quadrivalent (4vHPV) and the nine-valent (9vHPV) vaccines detected among young women diagnosed with *Chlamydia trachomatis*.

Methods Women ≤25 years attending Melbourne Sexual Health Centre from 1-July-2004 to 30-June-2014 and diagnosed with chlamydia were included in the analysis. Detection of HPV genotypes was performed on stored cervical or high vaginal samples. The proportions of women who had 4vHPV types (6/11/16/18) and the other five types within the 9vHPV grouping (31/33/45/52/58 alone) excluding 4vHPV types were calculated for each Australian financial year and stratified by age and vaccine eligibility. The proportions of HPV types among unvaccinated women in the post-vaccination period were also calculated to assess herd protection.

Results A total of 1,202 women were included in this study. The proportion of samples with 4vHPV types dramatically decreased among Australian-born ≤25 year old females over the 10 year period (6/11 decreased from 16% to 2% [p_{trend} <0.001]; 16/18 decreased from 30% to 4% [p_{trend} <0.001]). In women ≤21 years old, HPV 6/11 remained at zero and HPV16/18 were detected in <5% of samples for all years after 2008/2009. A significant decline in 4vHPV types in unvaccinated Australian-born women was also observed, from 41.3% to 18.5% in the pre- and post-vaccination eligible periods respectively ($p = 0.031$), but no decline was seen in the other five types within the 9vHPV grouping (22.5% vs. 25.9%; $p = 0.805$).

Conclusion Coverage achieved using the 3-dose vaccine was sufficient to largely eradicate 4vHPV types in Australian born women ≤21 years old, within three years of the introduction of the national HPV vaccination program. A strong herd protection was observed among women, with a significant decline in the proportion of 4vHPV in unvaccinated women.

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