cervix, and 18.3% were both local and systemic IgA antibody negative.

Conclusion After the third vaccination, there is a strong agreement between cervical and systemic IgG antibody responses and a weak agreement between cervical and systemic IgA antibody responses. The induction of IgA antibodies seems to be secondary to that of IgG antibodies in response to HPV intramuscular vaccination.

P1.04 DEVELOPMENT OF AN ELISA-ASSAY FOR DETECTION OF IGA AND IGG AGAINST HUMAN PAPILLOMA VIRUS

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Introduction The interest in human papilloma virus (HPV) seropositivity has increased considerably since HPV vaccines have become available worldwide. The aim of this study was to assess the performance of enzyme-linked immunosorbent assay (ELISA) in analysing serum samples provided from women with and without genital DNA-HPV infection confirmed by polymerase chain reaction (PCR), for detection of specific antibodies of the isotypes IgG and IgA recognising HPV-16 and −18, as well as virus-like particles (VLPs).

Methods 50 sexually active female patients between 18 and 35 years of age from the outpatient clinic at the university hospital were enrolled. In order to test them, positive controls were obtained from patients with HPV-induced lesions and who were DNA-HPV positive confirmed by PCR. A specific assay was used to identify antibodies to HPV VLPs by ELISA. The samples were divided into HPV positive and negative, and an ELISA detecting IgA and IgG anti-HPV-VLP was carried out.

Results The effectiveness of ELISA and the kappa (k) index was obtained from the values entered in the receiver operating characteristic (ROC) curves for IgG and IgA. IgG-VLP-HPV-16 showed a good correlation between ELISA and PCR (k=0.75), and IgG-VLP-HPV-18 showed a very good correlation between ELISA and PCR (k=0.84). While the IgA antibody correlation was also positive, although weaker, IgA-VLP-HPV-16 was moderate (k=0.45) and IgA-VLP-HPV-18 good (k=0.66). The efficacy of the assay concerning IgG was: sensitivity, specificity, and accuracy were 82.3%, 92%, and 88% to IgG-VLP-HPV-16, and 100%, 92%, and 94% to IgG-VLP-HPV-18. The assay concerning IgA was: sensitivity, specificity, and accuracy were 64.7%, 80%, and 73.8% to IgA-VLP-HPV-16, and 100%, 80%, and 84.8% to IgA-VLP-HPV-18.

Conclusion IgG and IgA antibodies against HPV-16 and −18 can be detected in unvaccinated individuals by using the VLP that serve as the basis for bivalent HPV vaccine. The values for ELISA assays and the values found for IgG correlate good/very good with HPV-16/18 detected by PCR.

P1.05 CURRENT USE AND PERCEIVED OBSTACLES TO USE OF POINT-OF-CARE TESTS IN SUB-SAHARAN AFRICA

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Introduction Sexually transmitted infections (STIs) continue to be a significant global public health issue. Rapid, inexpensive and easy-to-use point of care tests (POCTs) for syphilis, HIV, and trichomonas have become available and WHO pre-qualified. We surveyed public health workers from Africa to determine current STI POCT practices.

Methods From March to October 2016, we invited 7584 healthcare workers (HCW) to participate in an email survey using Qualtrics software. Email addresses were obtained from the Ministry of Health and a database of training attendees at the Infectious Diseases Institute over the last 6 years.

Results 555 participants (50% male) took the online survey. 91% were from Uganda. Most (n=449, 81%) were clinicians including 336 (61%) nurses and 113 (20%) clinical officers of Level III/IV health centres (40%). Among 449 clinician respondents, 312 (69%) reported seeing HIV/general patients and 309 (70%) diagnose at least one patient with an STI daily. Of 555 participants, common POCTs used were pregnancy test (74%), urine dipstick (71%), syphilis rapid test (66%) and Gram's stain (53%). Clinicians reported that 86% of POCTs were performed by HCWs and 54% read the test while the patient was present. Most clinicians sent blood specimens for HIV (79%) and syphilis (64%) confirmation but only 18% routinely sent cultures for gonorrhoea. The majority of clinicians (74%) practiced syndromic diagnosis for STDs/HIV. Among all, lack of availability of POCTs (43%), increased patient wait time (25%), and lack of training to perform the test (21%) were leading barriers to scale up POCTs. Comparing those who use syphilis POCTs to those who do not, a interruption of work flow was the greatest barrier identified (20% versus 12%, p=0.042). 60% of clinician participants felt that having increased access to POCTs for STIs would be useful.

Conclusion Increase of POCT availability and training could improve uptake of POCTs for STIs in Uganda and decrease the need for syndromic management which may lead to overtreatment and emergence of antibiotic resistance.

P1.06 IN SILICO MULTILOCUS SEQUENCE TYPING OF *CHLAMYDIA TRACHOMATIS* PLASMIDS SHOWS CLUSTERING OF ISOLATES ACCORDING TO THE DISEASE RELATED BIOVARS

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Introduction Nucleotide sequencing of the *ompA* gene, encoding the outer membrane protein MOMP, divides *C. trachomatis* into 15 main genovars comprising three biovars associated

with different disease phenotypes along with distinct tissue tropisms. The extra chromosomal plasmid of *Chlamydia trachomatis* is suggested to encode genes essential for chlamydial infection *and transmission. Using an in silico plasmid MLST scheme, the clustering of C. trachomatis* isolates was investigated in association with previously defined *ompA* biovars.

Methods: *In silico* analysis using publicly available whole genome sequence data (WGS) of *C. trachomatis* isolates deposited in the *Chlamydiales* pubMLST database (http://pubmlst.org/chlamydiales/) was performed. Only data from WGS were investigated ensuring that complete sequence data in all eight known plasmid genes and *ompA*, were included. An *in silico* plasmid MLST scheme was developed to assign allele numbers and plasmid sequence types to all included isolates. Clustering of *C. trachomatis* plasmids was assessed using minimum spanning tree analysis. Moreover, we performed a polymorphism analysis of each plasmid gene.

Results Using the *in silico* plasmid MLST scheme, plasmid alleles and sequence types were successfully assigned to 157 *C. trachomatis* isolates. Overall, 47 unique plasmid sequence types were detected. Minimum spanning tree analysis identified 5 large clusters, which showed clustering of *C. trachomatis* plasmids according to the *ompA* defined biovars. Further analysis of individual plasmid genes showed that besides specific STs, each biovar also had distinct plasmid alleles. Moreover, analysis of the polymorphic variation of plasmid genes confirmed that the *C. trachomatis* plasmid was highly conserved with all isolates sharing >99% sequence identity.

Conclusion: *In silico* multilocus sequence typing of *C. trachomatis* plasmids showed clustering of isolates according to biovars, suggesting that the *C. trachomatis* plasmid along with specific plasmid genes may play a role in the distinct disease phenotypes found in *C. trachomatis* infections.

P1.07 CONTRIBUTION OF PCR IN THE BIOLOGICAL DIAGNOSIS OF *TRICHOMONAS VAGINALIS* INFECTION AT INSTITUT PASTEUR OF COTE D'IVOIRE

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Introduction The urogenital trichomonasis remains the most common non-viral sexually transmitted infection. Classically, its biological diagnosis relies on the use of microscopy which is often negative because of the fragility of the parasite. PCR is thus an alternative method. So, this study aims to show the importance of PCR in the diagnosis of *Trichomonas vaginalis*.

Methods This cross-sectional study was conducted among 194 women received at the Institut Pasteur of Côte d'Ivoire from July to October 2013 for an STD through a vaginal sample with three swabs. Direct examination was made on each sample, Gram stain and Giemsa, culture as well as a multiplex PCR (*T. vaginalis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* and *Mycoplasma genitalium*). The sociodemographic and clinical data were collected using a questionnaire.

Results In total, 194 women were received with an average age of 31.35 years (SD=8.60 years). At microscopy, 2 cases (1.03%) of *T. vaginalis* were revealed. After DNA extraction, a PCR amplification has allowed to identify 7 cases (3, 61%) of *T. vaginalis* with a sensitivity of 100% and specificity of 97.4%. Other germs were identified by PCR, *Chlamydia trachomatis* (4.12%), *Neisseria gonorrhoeae* (2.58%) and *Mycoplasma genitalium* (1.03%).

Conclusion Routine testing of *Trichomonas vaginalis* by PCR has shown the importance of this method in the diagnosis of *Trichomonas vaginalis* infection because of its high sensibility and specificity. Its might be an alternative after the initiation of classical microscopy.

P1.08 DEVELOPMENT, VALIDATION AND TESTING COSTS OF AN IN-HOUSE REAL-TIME POLYMERASE CHAIN REACTION ASSAY FOR THE DETECTION OF *CHLAMYDIA TRACHOMATIS*

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Introduction In Brazil, the Digene Hybrid Capture II DNA test (HCII CT-ID - Qiagen) is the only molecular test used to identity *Chlamydia trachomatis* (CT). This test has shown sensitivity and specificity ranging from 93.8%–97.7% and 95.9%–100.0%, respectively, compared to that of culture. However, up to 27.7% of negative results are false. Real time polymerase chain reaction (qPCR) offers both high sensitivity and specificity. The objective of this study is to describe the development, assess the performance, and costs, of a new in-house qPCR assay for the diagnosis of genital chlamydial infection.

Methods Asymptomatic women aged 14–25 years who attended primary health services in Manaus, Brazil, were screened for CT using the HCII CT-ID-test. A subset of cervical specimens were tested using an in-house qPCR and a commercial qPCR (Artus qPCR) as a reference test. A primer/probe based on the sequence of cryptic plasmid was designed. An economic evaluation was conducted from the provider's perspective. Overall, 292 specimens were tested by both the commercial kit qPCR and the in-house qPCR.

Results The primers and probe designed for the CP target showed specificity, because no cross–reaction was observed for other STI species tested or with the human DNA. We were able to standardise this reaction in 10 µL and 5 µL volumes for the CP and β-actin set primers, respectively. The sensitivity, specificity, positive and negative predictive values of in the in-house qPCR were 99.5% (95% confidence interval [CI]: 97.1–100), 95.1% (95% CI: 89–98.4), 97.4% (95% CI: 94–99.1), and 99.0% (95% CI: 94.5–100), respectively. The cost per case of CT was $0.55 for HCII CT-ID, $1.45 for Artus qPCR and $1.33 for in-house qPCR.

Conclusion In conclusion, we have developed an in-house qPCR to detect cervical CT targeting CP primers. The in-house qPCR method was its lower cost. Findings from this study can help to revise the national recommendation of using HCII CT-ID. The in-house qPCR should be considered as a good candidate for the diagnostic method for screening programs in Brazil.