to document the population structure of the LGV cases over the years.

**Methods** The complete outer membrane protein A gene (*ompA*) of remnant positive LGV samples (previously confirmed by an in-house qPCR; target: *pmpH* gene) was amplified and sequenced using automated DNA sequencing. The obtained aligned sequences were compared with all L-variants described in literature and with all CT ompA sequences using the BLAST search.

**Results** All samples were from men who have sex with men; mostly HIV positive (82.2%) and from anorectal origin (94.1%). Sequencing of *ompA* (n=118) revealed that, in total, L2 and L2b genotypes were equally found (42.4%) followed by variants of L2 genotypes: L2bV2 (6.8%) and L2bV1 (3.4%). Curiously, one strain defined as L2a had one additional mutation (A515C – Lys172Thr) which is also found in L2bV2 (hereafter named L2aV2). Three L1 strains were identified over the years (one in 2016 and two in 2017) but no link between the three could be found. Two strains could not be characterized due to mixed infection with non-L genotypes. Most of infections were symptomatic (80.7%) with proctitis (71.1%) as predominant symptom. Re-infections were common in our population (9.3%) and sequencing showed that individuals could become infected by different strains in a short period of time. No significant association was found between HIV status, presence of symptoms and the L-variants.

**Conclusion** The LGV strains in Belgium are more genetically diverse than initially thought as a total of two L-variants and five L2-genotypes have been identified. No firm conclusions can be made concerning an association between clinical symptoms and specific L-variants as asymptomatic infections were found with all L2 variants.

**Disclosure** No significant relationships.

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**A NOVEL RAPID REAL-TIME PCR TEST FOR THE DETECTION OF CHLAMYDIA TRACHOMATIS IN PATIENT SAMPLES**

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**Background** Point of care (POC) testing for infectious diseases can provide actionable diagnostic information as soon as individuals present to healthcare systems. POC testing for sexually transmitted infections could have a significant impact on sexual health by enabling screening programs, reducing loss to follow-up and enabling immediate and targeted treatment. We have developed a novel rapid real-time PCR assay which can detect *Chlamydia trachomatis* in clinical samples.

**Methods** DNA was extracted from 122 residual genital swab and urine samples previously tested in the Roche cobas CT/NG assay using the Qiagen DNA mini kit and the DNA extracts were tested for *C. trachomatis* using the rapid real-time PCR assay.

**Results** Of the 122 samples, forty were negative in both the new rapid real-time PCR assay and the Roche cobas assay; 78 samples were positive in both assays and four samples were positive in the cobas assay but negative in the new novel assay. The specificity of the novel assay was 100% and its sensitivity was 95.1% respectively. The four samples which were negative in the new assay had high Ct values in the cobas test indicating low levels of chlamydia organisms were present in the samples.

**Conclusion** The rapid real-time PCR system is rapid, sensitive and specific for the detection of *C. trachomatis* in clinical samples from patients with chlamydia infection. The rapid real-time PCR assay for *C. trachomatis* forms the basis for a low cost, disposable sample to answer diagnostic assay cassette, which will run on the QuantuMDx Q-POC™ platform.

**Disclosure** No significant relationships.