to go for clinical collection. Aim of this study was to evaluate the performance of a new Home-based Self Vaginal FLOQUswab™ (HBSVF - COPAN Italia, Brescia) in combination with a commercially available real-time PCR assay, Anyplex II STI-7 (Seegene, Seoul, Korea) which detects seven major pathogens in a single reaction (Chlamydia trachomatis - CT, Neisseria gonorrhoeae - NG, Trichomonas vaginalis - TV, Mycoplasma hominis - MH, Mycoplasma genitalium - MG, Ureaplasma urealyticum - UU, and Ureaplasma parvum - UP).

Methods A total of 78 asymptomatic donors, employees of a private industry (aged 18 to 45 years) were voluntarily enrolled to STIs screening. The subjects answered to a standardise anonymized questionnaire regarding the easy of use of self vaginal collection. The new HBSV swab was collected in a domestic context by following the detailed “how to use it” instructions. After collection, the HBSV swabs were shipped at room temperature to the laboratory in Pievesestina and processed within five weeks. The threshold cycle value (Ct) of a human genomic target (internal control, I C) and Ct of pathogens (CT, NG, TV, MH, MG, UU, UP) were taken as parameters to assess respectively, the efficiency of self-sampling and presence of any inhibitor effects, the stability of nucleic acids on dry swabs.

Results No failure results have been observed, the IC of all samples were amplified (average Ct 30). The real time PCR assay was able to identified 2/78 CT, 4/78 UU, 40/78 UP, 6/78 MH, 1/78 TV positive patients. No MG and NG positive patients have been detected. Women reported self-collection with HBSV easy and comfortable (100%).

Conclusion The new HBSV device showed excellent recovery and stability of nucleic acid of STI pathogens up to 5 weeks at room temperature. The HBSV is suitable for screening of STIs with real-time PCR assay.

P1.59 GENOMIC CHARACTERISATION OF URETHRITIS-ASSOCIATED NEISSERIA MENINGITIDIS

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Introduction Mainly case reports have shown that N. meningitidis, typically a resident of the oropharynx and the causative agent of meningococcal meningitis and meningococcemia, is capable of invading and colonising the urogenital tract. This can result in urethritis, akin to the syndrome caused by N. gonorrhoeae, the etiologic agent of gonorrhoea. Recently, meningococcal strains associated with outbreaks of urethritis were reported to share genetic characteristics with gonococcus, raising the question of the extent to which these strains contain features that promote adaptation to the genitourinary niche, making them “gonococcus-like” and distinguishing them from other N. meningitidis.

Methods A total of 31 urethritis-associated N. meningitidis, representing multiple serogroups and independently collected over a decade and 3 continents, underwent genome sequencing and analysis. The genomes were compared with serogroup-matched N. meningitidis strains isolated from carriage and invasive disease and N. gonorrhoeae strains isolated from men with urethritis.

Results Intact nitrite reductase (AniA), disrupted factor-H binding protein (fHbp), and the lack of capsule are features previously speculated to promote urogenital colonisation. However, we found that a considerable number (n=11) of meningococcal urethritis isolates harbour mutations in AniA predicted to result in truncated peptides and a minority (n=4) of these isolates contained alleles associated with frameshifted fHbp. We noted substantial diversity in the capsule biosynthetic locus, including intact, disrupted, and absent capsules, indicating urogenital colonisation is possible across a range of capsular phenotypes.

Conclusion The meningococcal urethritis strains in this study do not share the allelic patterns of AniA, fHbp, or the capsule locus previously reported for urethritis-associated N. meningitidis. The allelic patterns likely reflect diversity in the underlying meningococcal population, rather than novel adaptation to the urogenital tract.