ulcer swabs, skin biopsies, and rabbit-passaged clinical isolates was enriched for Tp using pooled, parallel whole-genome amplification and/or RNA baits before Illumina short-read sequencing. We adopted hybrid comparative genome assembly analysis that involved de novo and reference-based assembly strategies to generate whole-genome consensus sequences. Repetitive and paralogous loci are being finished using Oxford Nanopore Technologies long-read sequencing and outer membrane protein (OMP) variability assessed using three-dimensional structural modelling.

Results We whole-genome sequenced 20 newly collected strains and analyzed publicly available sequencing data from 605 Tp samples. We observed a higher proportion of Nichols-like strains (6 of 20 [30%]) than expected in newly sequenced samples. Macrolide resistance-associated 23S rRNA alleles were not observed in samples from Columbia or Malawi. Initial analysis of bamA, lptD, and fadL-like loci suggests a spectrum of OMP variability that supersedes clade assignment. Analyses of newly collected samples and publicly available genomes is ongoing.

Conclusion Sampling from geographically diverse sites suggests that Tp strains are more genetically diverse than previously appreciated. Nichols and SS-14 clades were well represented, and macrolide susceptibility was maintained in some localities. Representative sampling complemented by analysis of robust clinical data and paired biological samples is critical to the development of a globally effective syphilis vaccine.

020.5 LOVE IN LOCKDOWN: RELATIONSHIP STRESS, DATING VIOLENCE AND STI RISK IN ADOLESCENT AND YOUNG ADULT RELATIONSHIPS DURING THE COVID-19 PANDEMIC

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Background Adolescents and young adults (AYA) who experience dating violence (DV) are at increased STI risk. Social restrictions during the COVID-19 pandemic have stressed AYA relationships and may cut them off from sources of support. AYA have been shown to respond to relationship stressors with behaviors that increase STI risk. This work examines whether relationship stressors (jealousy and worry about the relationship) exacerbate violence and STI risk among urban AYA during the COVID-19 pandemic.

Methods Participants from four sexual and reproductive health studies in Baltimore, Maryland (USA) were invited to complete a cross-sectional telephone survey on relationship experiences/sexual behavior during the pandemic. March 16, 2020 'stay-at-home' order was used to define the pandemic period. Partner support, jealousy, worry about the relationship making it through the pandemic, current DV, change in DV during pandemic, and condom use at last sex were evaluated using regression analyses. Data collection is still underway in 2021.

Results Of 194 participants surveyed, mean (sd) age 22.7 (2.8) years, 61% were in a romantic/sexual relationship. Of these, 14% reported current TDV, 6% experienced an increase in DV, 66% did not use a condom at last sex. AYA who worried

their relationship would not make it through the pandemic were more likely to experience DV (OR: 5.64, 95%CI: 1.69, 18.9). AYA who felt jealous of other people their partner was talking to/hanging out with during the pandemic were more likely to experience DV (OR: 4.51, 95%CI: 1.39, 14.6). Greater partner support was associated with experiencing less DV (OR: 0.71, 95%CI: 0.56, 0.90). Relationship stressors were not associated with condom use.

Conclusions Relationship insecurity exacerbated by the COVID-19 pandemic may increase risk for DV among AYA. As DV and STI are interconnected, romantic relationship context must be a key focus of STI prevention strategies during and after the pandemic.

020.6 CHLAMYDIA TRACHOMATIS VIABLE LOAD AT SIX DIFFERENT ANATOMICAL SAMPLE SITES IN WOMEN (CHLAMOUR)

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Background Nucleic acid amplification tests (NAATs) have revolutionized our ability to diagnose Chlamydia trachomatis (CT). Sometimes, in addition, assessment of CT viability would help to gain more insight in the clinical impact of a positive NAAT. Methods to assess the CT viability have become available in research settings (e.g. viability-PCR; V-PCR). Here we assess viability in six different anatomic sites in women.

Methods Immediately prior to treatment (STI clinic South Limburg), 28 vaginal NAAT-CT-positive (COBAS4800 CT/NG) adult women, were included in the 'CHLAMOUR' study. We used V-PCR to assess CT viable load (log₁₀ CT/ml) in same clinician taken standardized samples from the cervix, vagina, perineum, anus, optional rectum, and pharynx. Mean loads were compared using t-tests.

Results Twenty-eight women were included of whom 68% (19/28) consented to proctoscopic examination (rectal). NAAT-CT-positive rate was 75% for cervix, 79% vagina, 64% perineum, 64% anus, 74% rectum, and 21% for pharynx. Viable load was detected in 90% (19/21) CT positive cervix, 77% (17/22) vagina, 11% (2/18) perineum, 61% (11/18) anal, 93% (13/14) rectal, and 0% (0/6) pharynx samples. The mean viable load was marginally higher in cervical compared to vaginal samples (4.37 [SD:1.35] vs. 3.45 [SD:1.05], p=0.055). Mean viable load was higher in rectal compared to anal samples (3.51 [SD:0.51] vs. 2.70 [SD:0.42], p=0.01). Viable load was 2.72 [SD:1.69] CT positive perineum samples.

Conclusions The amount of viable CT varied by anatomic site, and were highest 'upward in the body', which is thus likely to represent actual site of infection. Still, the vaginal and anal sites (that are usually self-sampled) had high concordance with the cervical and rectal sites. CT at the perineum may indicate