O.20 - HIV transmission in MSM

O20.1 THE CHALLENGES OF DIVERSITY: HIV-1 SUBTYPE DISTRIBUTION AND TRANSMISSION NETWORKS WITHIN THE AUSTRALIAN MOLECULAR EPIDEMIOLOGY NETWORK-HIV 2005–2012

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Introduction Rates of new HIV diagnoses are increasing in Australia, with evidence of an increasing proportion of non-B subtypes reflecting a growing impact of sexual networks, migration and travel. This present study aims to further define HIV-1 subtype diversity and investigate HIV-1 transmission networks within Australia.

Methods The Australian Molecular Epidemiology Network (AMEN) HIV collaborating sites in Western Australia, South Australia, Victoria, Queensland and Western Sydney, provided baseline HIV-1 partial *pol* sequence, age and gender information for a total of 4929 patients during 2005–2012. HIV-1 phylogenetic analyses utilised MEGA V6, with a stringent classification of transmission clusters (bootstrap ≥98%, genetic distance ≤1.5%).

Results HIV-1 B subtype represented 74.9% of 4929 sequences (WA 59.3%, SA 68.6%, W Syd 75.2%, Vic 75.7%, Qld 82.3%), with a greater proportion of clusters compared to non-B subtypes (27.6% vs 22.4% of sequences, p = 0.003), larger cluster size (36.0% with >2 sequences vs 24.8% of non-B clusters, p = 0.03) and more male-only groups (90%). The largest cluster comprised 29 B subtype sequences from Vic + WA (age range 23–70 years). HIV-1 subtype C networks (38 groups) included more female/male groups (73.6%) and a smaller proportion of groups >2 (16%), while CRF01_AE networks (44 groups) included 59.1% male-only groups, with groups >2 accounting for 22.7%.

Conclusion This nationwide study of HIV-1 sequences involving 4929 patients' highlights the increasing diversity of HIV-1 subtypes within the Australian epidemic, as well as differences in transmission networks within Australia that are associated with these HIV-1 subtypes. These findings provide epidemiological insights not readily available using standard surveillance methods and can inform the development of effective strategies for prevention of new HIV-1 diagnoses across Australian state boundaries.

Disclosure of interest statement None declared.

O20.2 HIV-1 SEQUENCE DIVERSITY AND TRANSMISSION NETWORKS IN WESTERN AUSTRALIA FROM 2000–2014, AND THEIR IMPACT ON BASELINE CLINICAL CHARACTERISTICS

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Introduction We have previously described Western Australia as a "hotspot" for HIV-1 subtype diversity in Australia. This investigation characterises this further by studying phylogenetic transmission networks in relation to HIV clinical parameters, from 2000–2014.

Methods Baseline clinical data and HIV-1 pol sequences were assessed over 4 notification eras for 1021 patients. Phylogenetic tree construction (MEGA V6) was utilised to identify transmission networks, using clustering criteria of bootstrap ≥98 and genetic distance ≤1.5%.

Results The proportion of non-B-subtype HIV-1 has remained stable from 2008–2014 (35% of males (subtype CRF01_AE > C); 80% of females (subtype C > CRF01_AE). Non-B-subtype HIV-1 was associated with reduced baseline CD4 count (p = 0.005) after adjusting for effects of baseline viral load and age (p < 0.001).

More and larger transmission clusters were identified among the B-subtype group (p < 0.05), with one cluster of 53 individuals evolving from 2008, characterised by higher baseline CD4 count (p = 0.001) and viral load (p = 0.01) than ungrouped patients. This cluster has expanded in 2014 (12 new cases) despite high proportions of early diagnoses (25% with acute HIV-1 serology) and treatment uptake (76% with HIV VL <40cpm by 2014).

Conclusion This 14-year study highlights several challenges in HIV-1 prevention, including delayed diagnosis among cases of non-B-subtype HIV-1, namely migrants and overseas travellers. We have also identified a substantial increase in baseline viral load over time, with higher viral load levels within a large transmission cluster that continues to expand despite frequent early diagnosis and high treatment uptake. These results can inform strategies to end HIV transmission within Australia.

Disclosure of interest statement None to disclose.

O20.3 HIV TRANSMISSION IN MALE SERODISCORDANT COUPLES IN AUSTRALIA, THAILAND AND BRAZIL

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Background Numerous prospective studies have demonstrated that HIV transmission is greatly reduced in heterosexual HIV serodiscordant couples when the HIV-positive partner (HPP) is receiving combination anti-retroviral therapy (cART) with undetectable viral load (UVL). Comparable data in homosexual male serodiscordant couples (HM-SDC) are extremely limited. We report a pre-specified interim analysis of the relationship between UVL and HIV transmission in the Opposites Attract observational cohort study of HM-SDC in Australia, Bangkok and Rio de Janeiro.

Methods HM-SDC reporting regular anal intercourse with each other were recruited through clinical sites. Detailed information on sexual risk behaviours was collected at each visit from the HIV-negative partner (HNP). HNPs were tested at baseline and follow-up for HIV antibodies and STIs (sexually transmitted infections), and HPPs for HIV viral load and STIs. Incidence rates were calculated per couple-year of follow-up (CYFU) using person-year methods, and stratified by whether different forms of condomless anal intercourse (CLAI) were reported. UVL was defined as <200 copies/mL. One-sided confidence intervals (CI) were calculated using the exact Poisson method. Linked HIV transmission in couples was defined by phylogenetic analysis.

Results By December 2014, 234 HM-SDC were enrolled: 135 from Australia, 52 from Bangkok and 47 from Rio de Janeiro. There were a total of 150.0 CYFU in 152 couples with at least one follow-up visit of whom 65 (42.8%) were in a non-monogamous relationship. At baseline, 84.2% of HPPs were on cART and in total 82.9% had UVL. STI prevalence was 11.2% in HPPs and 6.6% in HNPs. There were 90.8 CYFU in periods where CLAI was reported with a total of 5,905 acts of CLAI in 88 couples. There were no linked HIV transmissions. The upper limit of the 95% CI of the transmission rate was 4.06/100 CYFU for periods in which CLAI was reported, and 6.46/100 CYFU for periods in which receptive CLAI was reported.

Conclusions There were no linked HIV transmissions in 150 CYFU in these HM-SDC, despite close to 6,000 acts of CLAI. The upper confidence limit of the transmission rate during follow-up in periods during which CLAI was occurring was 4.06/100 CYFU. These data add to emerging evidence that the rate of HIV transmission in HM-SDC is very low when the HIV-positive partner is on ART. Further follow-up of a larger sample size is required to accurately delineate any residual risk.

O20.4 TRANSMISSION RISK BELIEFS INFLUENCE SEXUAL RISK BEHAVIOUR OF HIV-POSITIVE MSM

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Introduction Beliefs about the efficacy of antiretroviral treatment for decreasing risk of HIV transmission may influence a person's sexual risk behaviour. We examined whether individuals' HIV transmission risk beliefs predicted subsequent engagement in unprotected anal intercourse (UAI) among men who have sex with men (MSM).

Methods HIV-positive and HIV-negative MSM were recruited for the longitudinal study in San Francisco using time-location sampling. Participants who completed both the baseline and 6-month follow-up behavioural surveys were included in the analysis (N = 773). Beliefs regarding HIV transmission risk at baseline and reported UAI with any sexual partner during the 6-month interval between the baseline and follow-up surveys were evaluated.

Results UAI at baseline was associated with an increased likelihood of UAI at follow-up among both HIV-positive MSM (OR = 6.45, $p < 0.01$) and HIV-negative MSM (OR = 13.59, $p < 0.01$). UAI was more frequently reported at follow-up among HIV-positive MSM who agreed with the statements, "Because of combination drug treatment for HIV, I am less concerned about infecting someone," (OR = 2.49, $p = 0.04$) and "I am less worried about having UAI now that treatments can be taken after unprotected sex," (OR = 6.52, $p = 0.02$). HIV-positive MSM who agreed with statement, "My sexual practices are safer because someone who is positive can become re-infected with HIV," were less likely to report UAI at follow-up (OR = 0.13, $p < 0.01$). Transmission risk beliefs were not associated with UAI at follow-up among HIV-negative MSM.

Conclusion HIV-positive MSM who believed there was less risk of transmitting HIV due to the availability of antiretroviral treatment and post-exposure prophylaxis were more likely to engage in UAI. Concerns about the possibility of re-infection may have influenced some HIV-positive men to refrain from engaging in UAI. These findings suggest the need for prevention messages to highlight treatment adherence and viral suppression as important factors that affect the efficacy of antiretrovirals for reducing HIV transmission risk.

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O20.5 TRENDS IN UNDIAGNOSED HIV AND HIV TESTING BEHAVIOUR IN COMMUNITY SAMPLES OF MEN WHO HAVE SEX WITH MEN IN LONDON, UK: RESULTS FROM REPEAT CROSS-SECTIONAL SURVEYS BETWEEN 2000–2013

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Background HIV testing can reduce undiagnosed and late HIV diagnosis. We examine trends between 2000–2013 of overall and undiagnosed HIV prevalence, HIV testing among men who have sex with men (MSM), and factors associated with undiagnosed HIV.

Methods Repeat cross-sectional anonymous behavioural surveys with oral specimens for HIV antibody (Ab) testing were conducted in community venues in London. Participants were treated as undiagnosed HIV+ if they tested HIV Ab+, and had never tested for HIV, last tested or perceived themselves as HIV negative, or did not know their HIV status. Undiagnosed fraction is the proportion of undiagnosed HIV Ab+ results of the total number of HIV Ab+ results. Trends between 2000–2013 and factors associated with undiagnosed HIV (2011 and 2013 data) were examined using logistic regression. Adjusted odds ratios (AOR) and 95% confidence intervals (CI) were calculated.