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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