020.5

PATTERNS OF SEXUAL AND SOCIAL MIXING AMONG HETEROSEXUAL COUPLES LIVING TOGETHER IN ENGLAND: ANALYSES OF A PROBABILITY SAMPLE SURVEY

doi:10.1136/sextrans-2013-051184.0201

P Prah, C H Mercer, A M Johnson. UCL Centre for Sexual Health and HIV Research, London UK

Background Patterns of social and sexual mixing are a major determinant of STI transmission. In particular, discordant mixing is an important driver of STI dissemination when high risk populations mix with low risk populations. However patterns of mixing are poorly understood.

Method We analysed data from a probability sample survey of households in the Health Survey for England 2010. 1,891 heterosexual couples living together were included, all individuals were aged 16–69 years. Self-completion questionnaires were used to collect data on previous STI diagnosis/es, same-sex experience, condom use, age at first sex, and number of sexual partners.

Results Males were on average 2 years older than their female partners, though this age difference ranged from a mean of 0 years in those aged 16–24 to a mean of 3 years in those aged over 55. 85.1% of couples had matching characteristics of reporting previous STI diagnosis/es. After adjusting for age, socio-economic class and marital status, an association was found between males reporting previous STI diagnosis/es and their female partners also reporting the same, AOR: 3.02 (95% CI: 1.78–5.13). Males who reported 10+partners were more likely to be in a couple with a female who also reported this AOR: 2.71 (95% CI: 1.79–4.11). A positive correlation was found between men and women with respect to their age at first sex. There was also a correlation in socio-economic class but with greatest mixing between intermediate and higher/lower categories. A correlation was also found with respect to education level and drinking alcohol.

Conclusion We found evidence of significant levels of assortative mixing amongst heterosexual couples living together in England with respect to reporting previous STI diagnosis/es, numbers of partners, frequent drinking, socio-economic class and education. These analyses of probability sample survey data support the observed skewed distribution of STI transmission in the population.

020.6

SEXUAL PARTNERSHIP PATTERNS AMONG YOUNG PEOPLE IN RURAL TANZANIA

doi:10.1136/sextrans-2013-051184.0202

¹**A M Doyle**, ²J Changalucha, ¹H A Weiss, ^{1,3}D Watson-Jones, ¹R J Hayes, ¹B Zaba, ¹A Ross. ¹*London School of Hygiene & Tropical Medicine, London, UK;* ²*National Institute for Medical Research, Mwanza, Tanzania;* ³*Mwanza Intervention Trials Unit, Mwanza, Tanzania*

Background Sexual partnership patterns influence risk of STI transmission. We describe the pattern of partnerships reported by youth in a survey in rural Tanzania and calculate the UNAIDS recommended measure of concurrency.

Methods In 2007/8, sexual partnership histories were collected, through a face-to-face questionnaire, from 13,814 15–30 y-olds (90% aged 19–25 y) in 20 communities, in Mwanza, Tanzania. Partnership patterns of sexually active participants were described based on reported dates of first and last intercourse with their last 3 partners in the past year. One-off partnerships had the same date of first and last intercourse. Point prevalence of concurrency was calculated at 6 months prior to the survey.

Results Females and males had mean age of 21 and 22 years respectively. In the year prior to the survey, 87% of females and 79% of males reported at least one sexual partner, and 15% of females and 44% of males reported > 3 partners. Among those reporting 1–3

partners, 47% of one-off partnerships started within 4 months of the survey suggesting reporting bias and/or censoring of data. Only 3% of females reported > 2 new partners in the previous year compared to 26% of males, and 3% of females reported > 1 partner in the last 4 weeks compared to 18% of males. The point prevalence of concurrency was 2.3% for females and 10.7% for males. Partnership patterns varied by sex and marital status (Table). The 'Previously married' group were the most likely to report multiple partners.

Conclusions High levels of multiple and concurrent partnerships were reported by males and the 'previously married'. Further analysis of the characteristics of the specific partners and partnerships will be completed to understand the risk associated with each pattern of partnerships. Analyses will also be adjusted for the bias introduced by restricting questions to the last 3 partners.

Abstract 020.6 Table 1 Reported patterns of sexual partnership (last 3 partners in past year) by sex and marital status

	Never married		Currently married		Previously married	
Reported pattern of partnerships (%)	Males N = 3951	Females N = 1740	Males N = 2458	Females N = 3689	Males N = 215	Females N = 608
Abstinent	20.9	16.2	0.04	0.5	6.1	10.7
Single partner	35.7	71.2	50.6	93.4	19.1	55.3
Multiple partners	43.4	12.7	49.1	6.1	74.9	34.0
- no overlap in timing of partnerships	22.6	6.6	4.7	1.4	34.0	20.1
- overlap in timing of at least 2 partnerships	20.7	5.9	44.4	4.7	40.9	13.5
- timing unknown	0.1	0.3	0.2	0.03	0.0	0.5

0.21 - Antimicrobial resistance mechanisms in STI pathogens

021.1

MYCOPLASMA GENITALIUM INFECTIOUS LOAD AND TREATMENT FAILURE DUE TO SELECTED MACROLIDE RESISTANCE

doi:10.1136/sextrans-2013-051184.0203

^{1,2}**J Twin**, ^{3,4,5}C Bradshaw, ^{2,4}S Garland, ³M Bissessor, ³M Chen, ⁴J Walker, ^{3,4}C Fairley, ⁴J Hocking, ^{1,2,4}S Tabrizi. ¹Murdoch Childrens Research Institute, Melbourne, Australia; ²Royal Women's Hospital, Melbourne, Australia; ³Melbourne Sexual Health Centre, Melbourne, Australia; ⁴University of Melbourne, Melbourne, Australia; ⁵Monash University, Melbourne, Australia

Background Treatment failure due the development of macrolide resistance seen at Melbourne Sexual Health Centre (MSHC) has risen from 15 to 46% over the last six years (p < 0.01). Macrolide resistance is conferred through point mutations in the M. genitalium 23S rRNA gene. Treatment failure with 1g azithromycin is either due to an infection with a pre-existing resistant strain or development of resistance during treatment, but the mechanism is not yet fully understood.

Methods A subset of M. genitalium positive cases seen at MSHC between 2007–9 (n = 67) and 2012 (n = 70) underwent detection of resistance mutations via high resolution melt analysis, with real-time PCR quantifying M. genitalium infectious load.

Result Of those M. genitalium cases that successfully responded to 1g azithromycin, the pre-treatment median loads for 2007–9 (n = 40) and 2012 (n = 48) were 8.5 x 102 and 1.7 x 103 copies per reaction respectively. For M. genitalium strains that possessed resistance in the pre-treatment sample, the loads were remarkably similar to those successfully treated, with 2.2 x 103 copies per reaction detected for 2007–9 (n = 9) and 5.7 x 103 copies for 2012 (n = 22). However, for M. genitalium cases that appeared to develop resistance following