from 46 public STD clinics in the 4 provinces. Specimens that tested positive for *C. trachomatis* by polymerase chain reaction were genotyped for the infecting *C. trachomatis* strain by amplifying and sequencing the genovar-specific ompA gene, which encodes the chlamydial major outer membrane protein. Nine *C. trachomatis* genovars were identified from 129 specimens; they consisted of the F (25.6%, n = 33), E (17.1%, n = 22), J (16.3%, n = 21), D (15.5%, n = 20), G (11.6%, n = 15), K (5.4%, n = 7), H (3.9%, n = 5), I (1.6%, n = 2), and B (0.8%, n = 1) genovars. Nine genovars were found in specimens from Guangxi province, 6 were found in specimens from each of Guangdong and Hainan provinces, but only 5 were found in specimens from Jiangsu province. Significant differences were observed in *C. trachomatis* genovar distributions between different provinces: G/Ga was absent among male STD clinic patients (MSPs) while being prevalent in the 3 southern provinces.

**P3.261** GLOBAL MULTISEQUENCE TYPE (MLST) ANALYSIS OF CHLAMYDIA TRACHOMATIS STRAINS FROM 16 COUNTRIES


J Isaksson, 1R Bom, 1I Saleh, 2B Hermann, 1S Bruisten. 1Department of Clinical Microbiology, Uppsala, Sweden; 2Public Health Laboratory, Public Health Service of Amsterdam, Amsterdam, The Netherlands

**Background** The *Chlamydia trachomatis* MLST database was established in 2007 and is based on five target regions (non-housekeeping genes) and the conventional *ompA* gene. It enables worldwide epidemiological analyses.

**Methods** Samples were included from 11 studies focusing on specific risk groups and with different study objectives. Geographical distribution of MLST profiles was carried out and eBURST analysis was performed.

**Results** A total of 414 MLST profiles were recognised from 2087 entries. Polymorphism of target regions was reflected in varying numbers of alleles; *hctB* 2087 entries. Polymorphism of target regions was reflected in identified genetic founders. The genetic diversity was much lower in the MSM clusters compared to clusters in heterosexuals. The 8 predominating profiles as founders, and another 3 as subgroup founders. The genetic diversity was much lower in the MSM clusters compared to clusters in heterosexuals.

**Conclusions** Worldwide a few *C. trachomatis* MLST profiles predominate. Different MLST profiles predominate among MSM and heterosexuals.

**P3.262** COMPARISON OF URINE SAMPLES AND PENILE SWABS IN THE DETECTION OF HUMAN PAPILLOMA VIRUS IN MEN USING THE SPF 1 LINE PROBE ASSAY


P3.263 DO MEN HARBOUR THE SAME STRAIN OF GONOCoccus AT MULTIPLE ANATOMICAL SITES?


K Eastick. Scottish Bacterial STI Reference Laboratory, Royal Infirmary of Edinburgh, Edinburgh, UK

**Background** All *N. gonorrhoeae* clinical isolates in Scotland are routinely typed by *Neisseria gonorrhoeae* multi-antigen sequence typing (NG-MAST). The frequency with which individuals harboured the same *N. gonorrhoeae* strain at > 1 anatomical site concurrently was examined.

**Methods** Episodes of gonorrhoea between 2004 and January 2013 comprising typed isolates from two or more anatomical sites of the same male individual submitted within a one-month period were analysed for similarity.

**Results** 410 episodes of gonorrhoea were identified with > 1 site cultured. The table shows differences in sequence type (ST) within episodes. Forty episodes with three cultures are included in all three pair-wise combinations. Overall 91.2% of episodes had identical STs at all sites.

Where STs differed at only one allele, the sequences were compared using CLUSTALW. Thirteen of 14 alleles compared were at the *povB* locus. Nine pairs were 99.8% similar, representing a difference of 1 nucleotide. The remaining pairs showed 88.4%, 98.2%, 97.8%, 96.9% and 75.1% (<i>ibpB</i>) similarity.