



ESCAIDE

ABSTRACT BOOK

European Scientific Conference on Applied Infectious Disease Epidemiology

**Saint Julian's, Malta,
21-23 November 2018**



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Parallel Session Abstracts

Neisseria gonorrhoea, *Mycoplasma genitalium* and *Trichomonas vaginalis* using self-collected rectal and pharyngeal swabs, and urine samples. PCR-based APTIMA® STI-assays were used. We collected information on sociodemographics, HIV-status, clinical symptoms, sexual behaviour and PrEP-use. We calculated prevalence ratios (PR) to identify risk factors and stratified for HIV-status and PrEP-use.

Results:

As of 22/04/2018, 1,199 MSM were included: 50.4% (603/1,199) were HIV-positive, median age was 39 years [range 18-71]. Overall STI positivity was 31.4% (*Mycoplasma genitalium*=17.8%, *Neisseria gonorrhoea*=9.9%, *Chlamydia trachomatis*=9.1%, *Trichomonas vaginalis*=0.1%) and was not significantly higher in HIV-positive participants (PR=1.0; CI95%=0.8-1.1). 66.3% (230/347) of STI-positive participants did not report STI-related symptoms. 30.1% (162/539) of HIV-negative participants currently took PrEP. In PrEP-users, the number of male sexual partners (median 12 vs. 5; $p<0.05$), sex without condom (91.7% vs 65.9%; $p<0.05$), use of party drugs such as liquid ecstasy (42.8% vs. 26.6%; $p<0.05$) within last 6 months and STI positivity (PR=1.8; CI95%=1.4-2.3) were significantly higher.

Conclusions : A high proportion of mainly asymptomatic MSM are positive for STI in Germany. Health insurance covered regular STI screenings of PrEP-users amongst MSM, independent of symptoms, would facilitate early treatment and thereby reduce further spread.

Subject: Burden of disease

Keywords: Sexually Transmitted Diseases, Men Who Have Sex With Men, HIV Pre-Exposure Prophylaxis, Risk Factors

ABSTRACT ID: 324

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Parallel Session 17 DAY 3, Friday, 23. November 2018 11:00-12:40

Influenza and other respiratory viruses(1): epidemiology and surveillance

Moderator

Julien Beauté

Abstracts

17.1. Whole genome analysis of influenza A(H3) viruses detected between 2016-2018 in the scope of EuroEVA/I-MOVE vaccine effectiveness study

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Background:

NGS techniques, allow a much deeper genetic analysis of influenza viruses, compared to traditional Sanger sequencing of hemagglutinin gene. The present study aims to perform phylogenetic and mutational analysis at whole-genome level in order to search for genetic features related to vaccine failure.

Methods:

Nasopharyngeal swabs were collected during 2016/17 and 2017/18 winter seasons, from ILI patients participating in EuroEVA/I-MOVE study. Whole genome sequences were obtained for 179 influenza A(H3) viruses by NGS in a MiSeq platform and subsequent bioinformatics analysis using the web-based platform INSaFLU (<https://insaflu.insa.pt/>). Additional fine-tune sequence analysis was performed using MEGA-7.

Results:

All sequenced viruses clustered in 2 HA-based genetic groups: 58 (32.4%) in 3C.2a group and 121 (67.6%) in 3C.2a1. Vaccine failure cases were detected in a higher proportion in 3C.2a1 group (20/121, 16.5%) than in 3C.2a (8/58, 13.8%). WGS analysis further revealed intra-subtype reassortments based on the closest genetic relatedness of each viral segment to the representative virus of seasonal A(H3) genetic (sub-) groups, with viruses being distributed in 6 different patterns of genome constellation. The group with all genomic segments most closely related to A/Singapore/INFIMH-16-0019/2016 harboured a higher number of vaccine failure cases (14/69, 20.3%). Despite 16 viruses (from 28 detected in vaccinated cases) presented amino acid substitutions not found in unvaccinated cases, these substitutions revealed a sporadic pattern.

Conclusions:

Vaccine failure cases were not exclusive of any genetic group or reassortment pattern, although they were found in slightly higher proportion among 3C.2a1 viruses and in viruses with all genetic segments mostly similar to A/Singapore/INFIMH-16-0019/2016. The further use of WGS in flu surveillance is essential to better understand genetic determinants of infection and evolutionary dynamics of influenza virus.

Subject: Novel methods in microbiology (e.g. new diagnostic tools)

Keywords: influenza virus, whole genome analysis, vaccine effectiveness, vaccine failure

ABSTRACT ID: 458

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17.2. Predicting peak influenza activity in primary and secondary care in Scotland – is the Moving Epidemic Method the way forward?

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